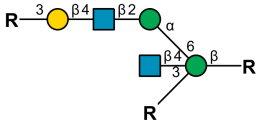
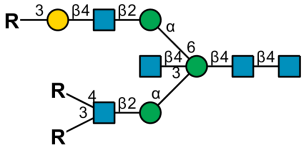
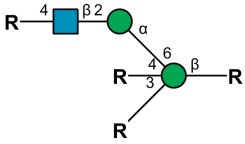
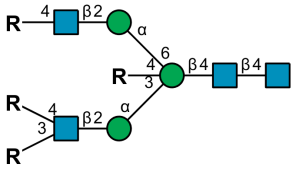
PHA-E

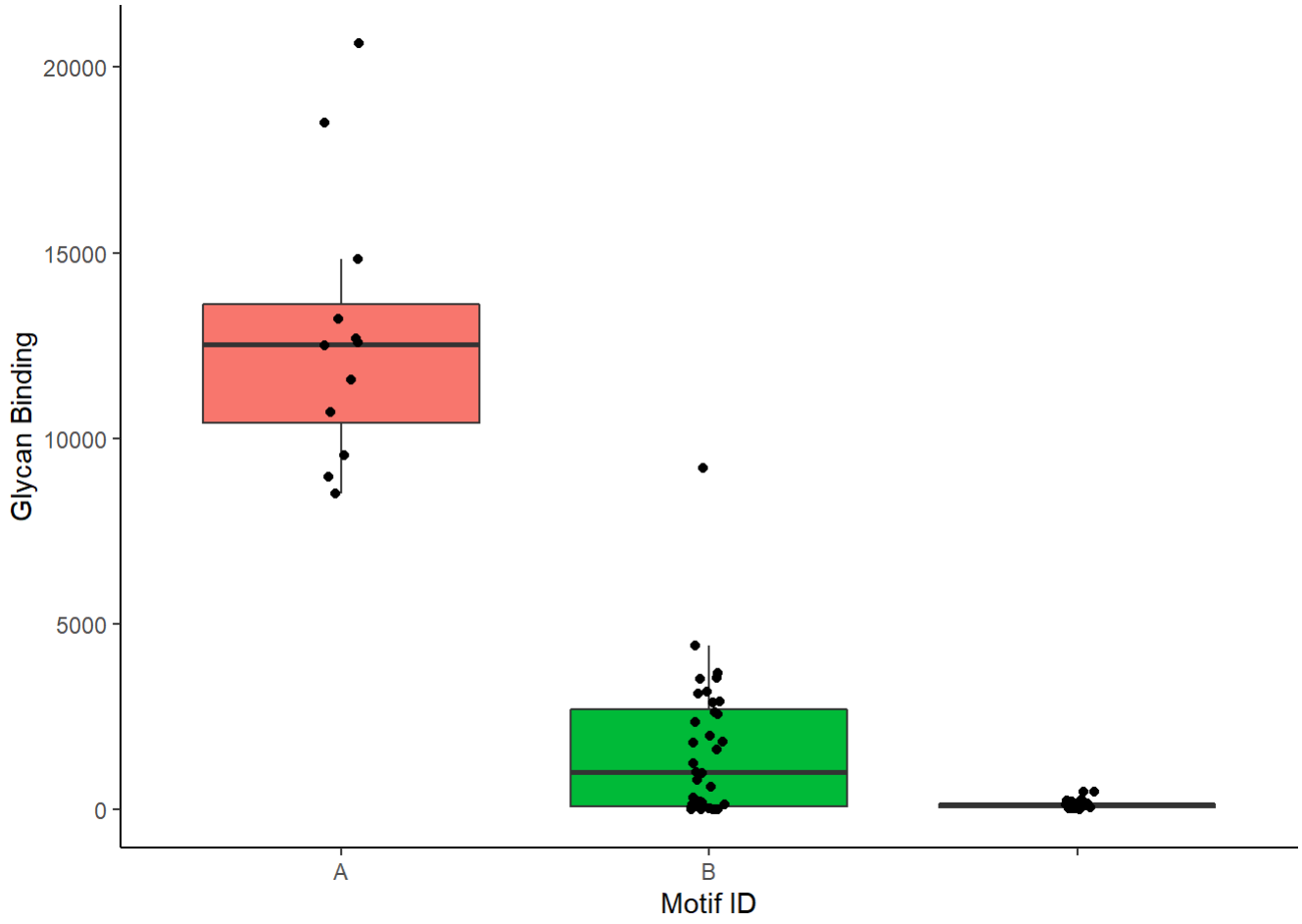
Automated Analysis report for PHA-E evaluated at 1 ug/mL

List of Primary PHA-E Motifs

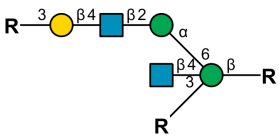
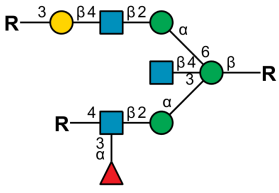
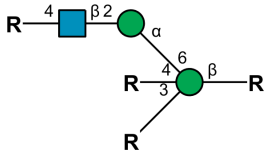
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	12
B			0.14	36
0			0.01	24

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

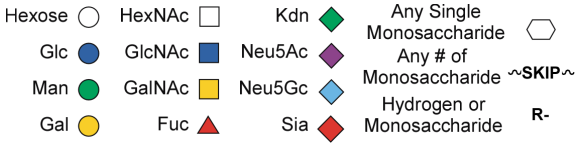
Boxplot of Primary Motifs



List of Fine-Specificity PHA-E Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*			1.00	8	<0.001
A1			0.74	4	<0.001
B0			0.12	36	0.013
0	Non-Binders (100%)		0.00	24	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

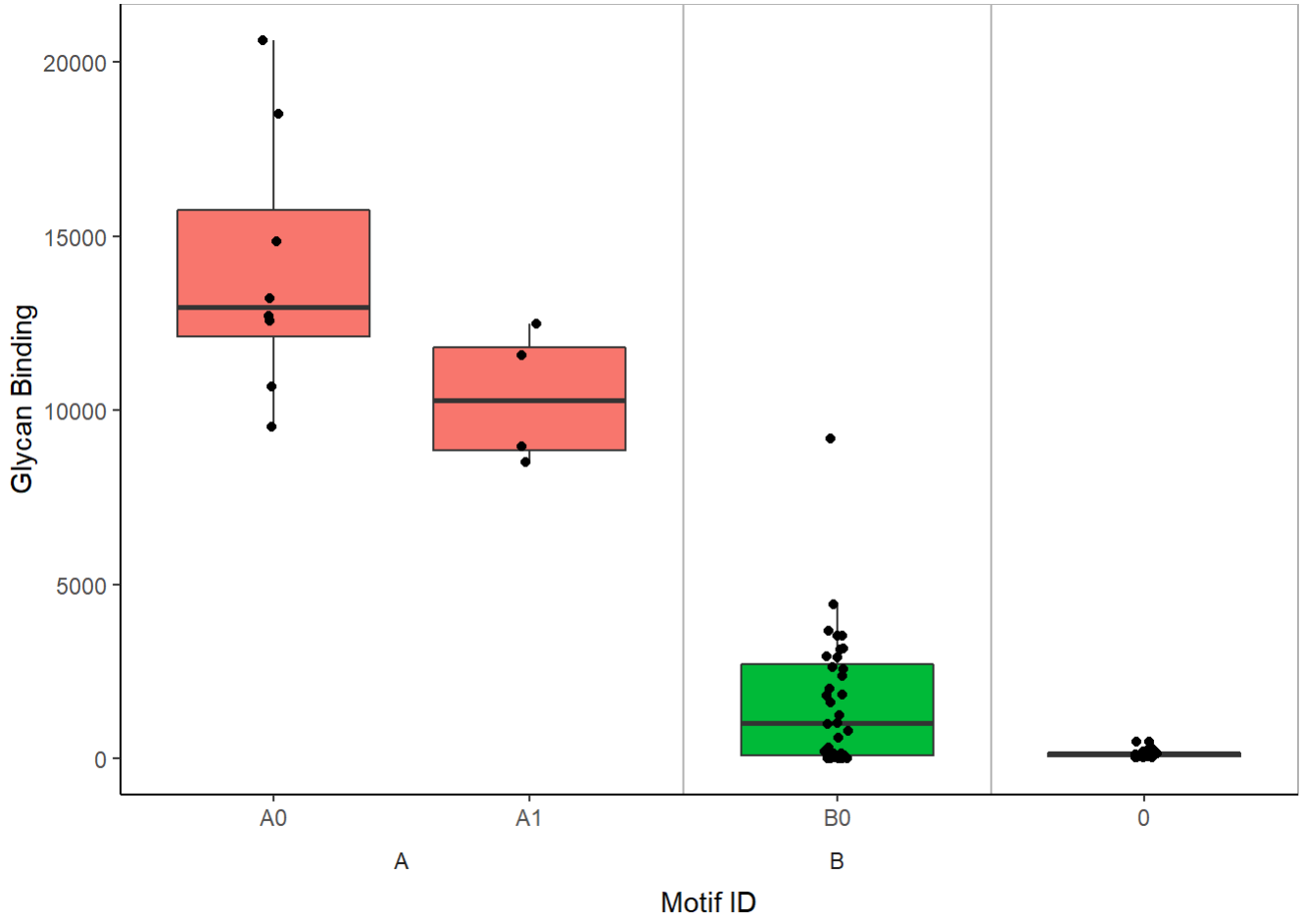


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

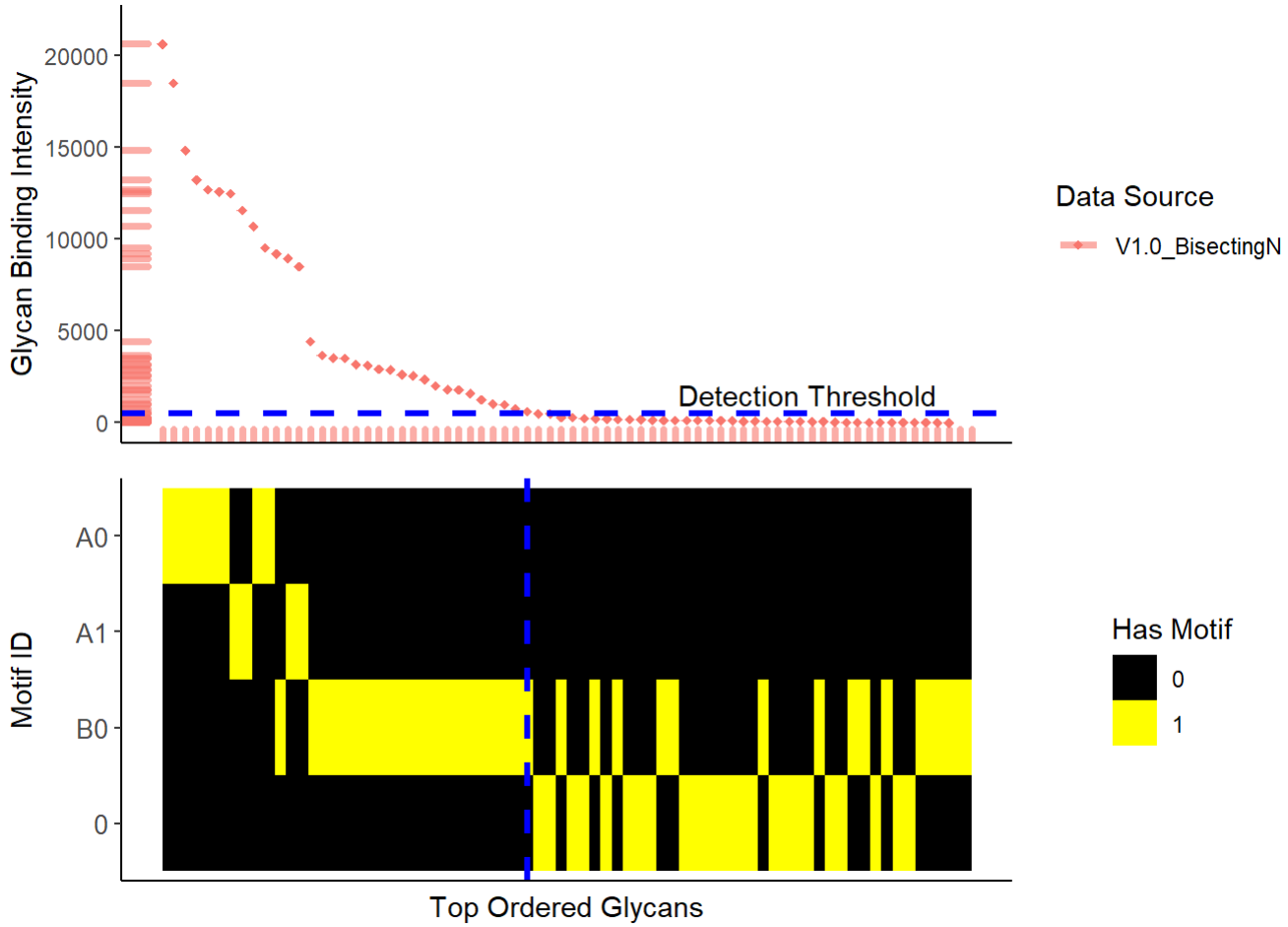
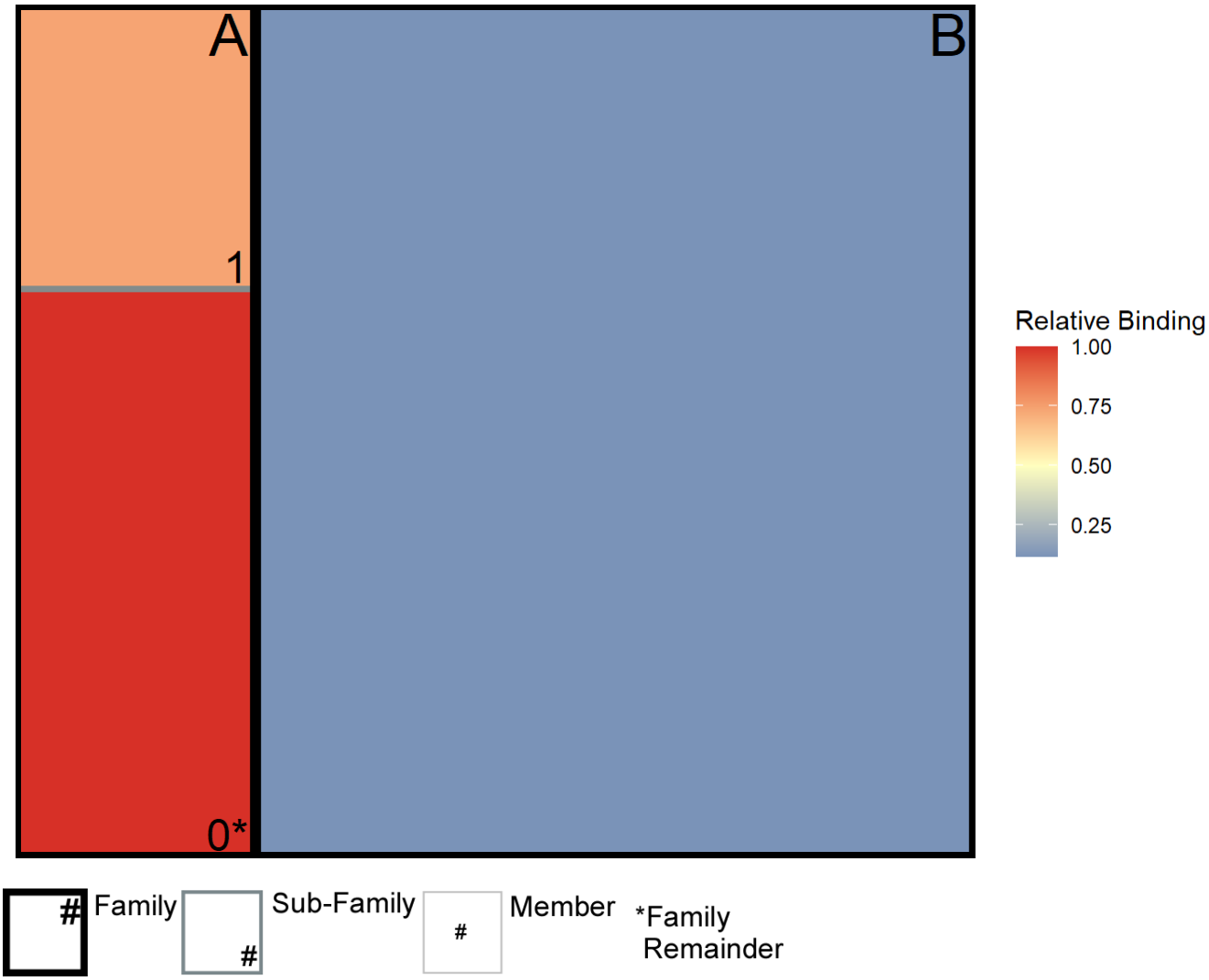


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

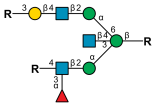
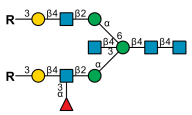
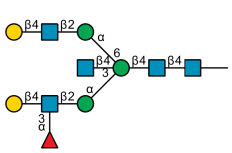
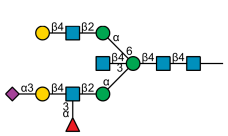
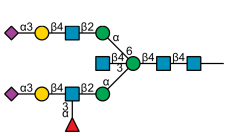


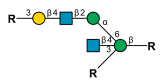
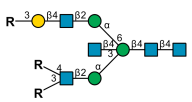
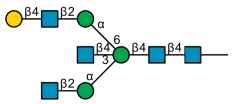
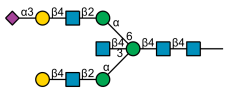
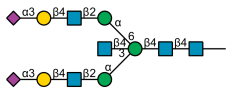
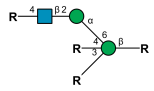
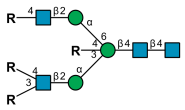
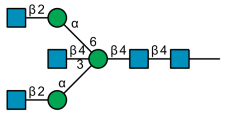
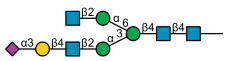
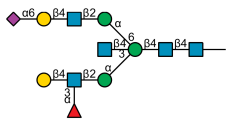
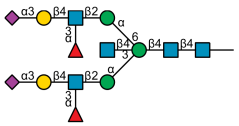
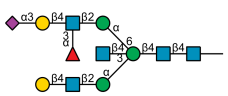
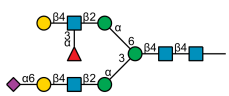
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

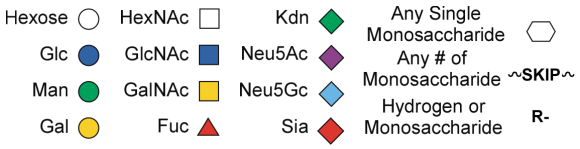
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				14		15		18

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				22		27		3
B0				1		44		19
0				6		30		70

Key:



All Concentration Plots:

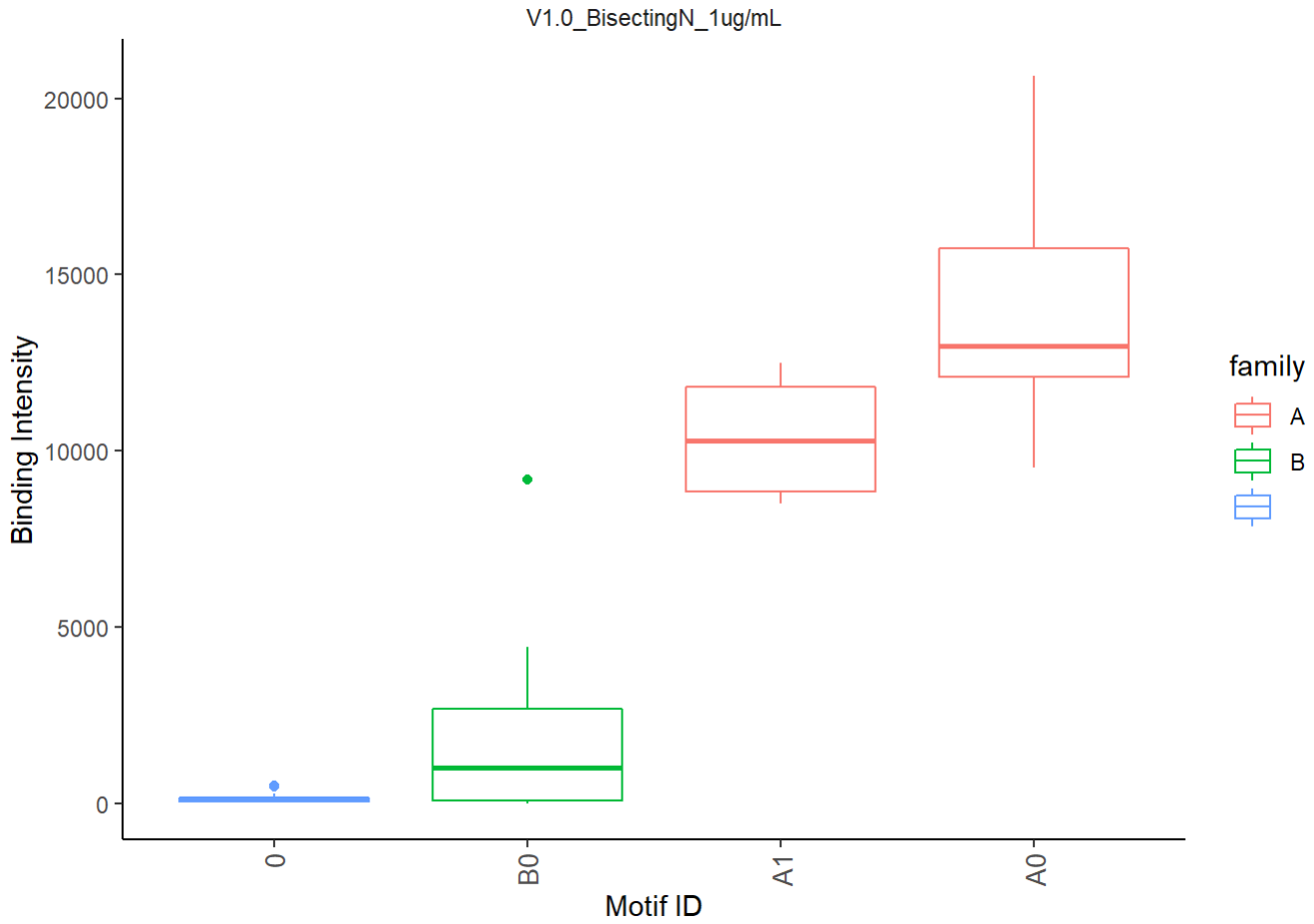
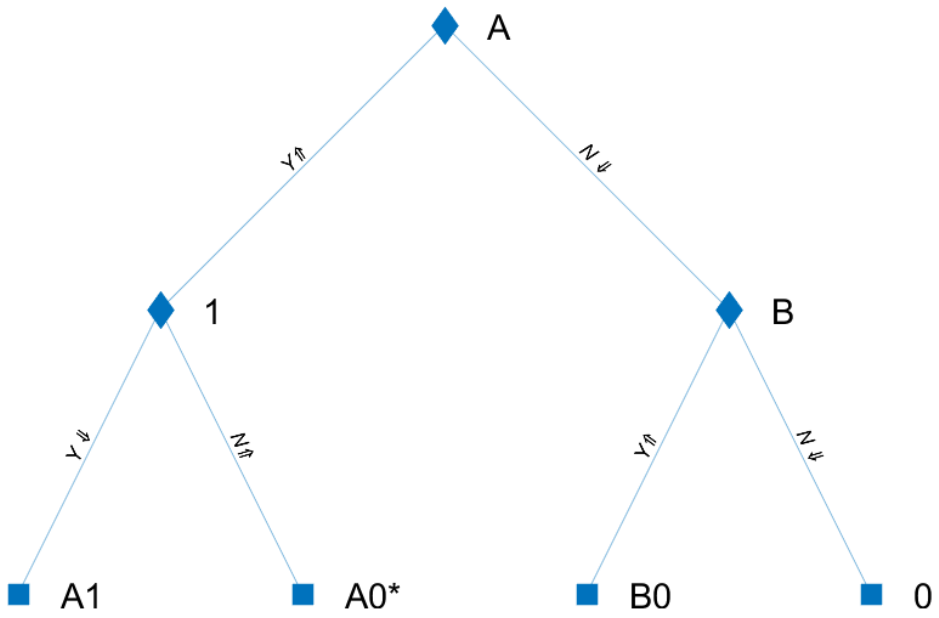


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



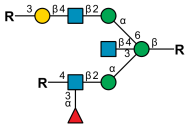
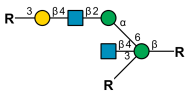
*Motif matches the remaining glycans not matched by earlier motifs in the model.

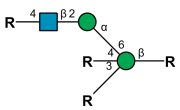
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

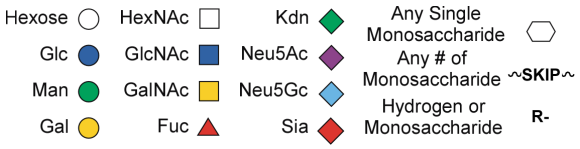
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f3f4f>FucA1-3<6f>GlcNAcB1-2<3f4f6f>ManA1-3)(<3f4f6f>GlcNAcB1-4)<2f>ManB
A0*		<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f4f6f>GlcNAcB1-4)<2f>ManB

Motif ID	Motif Graphic	Motif Text
B0		<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
0		Non-Binders

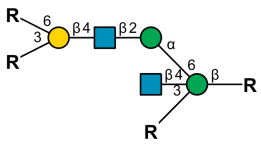
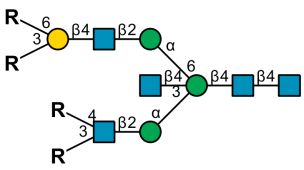
Key:



PHA-L

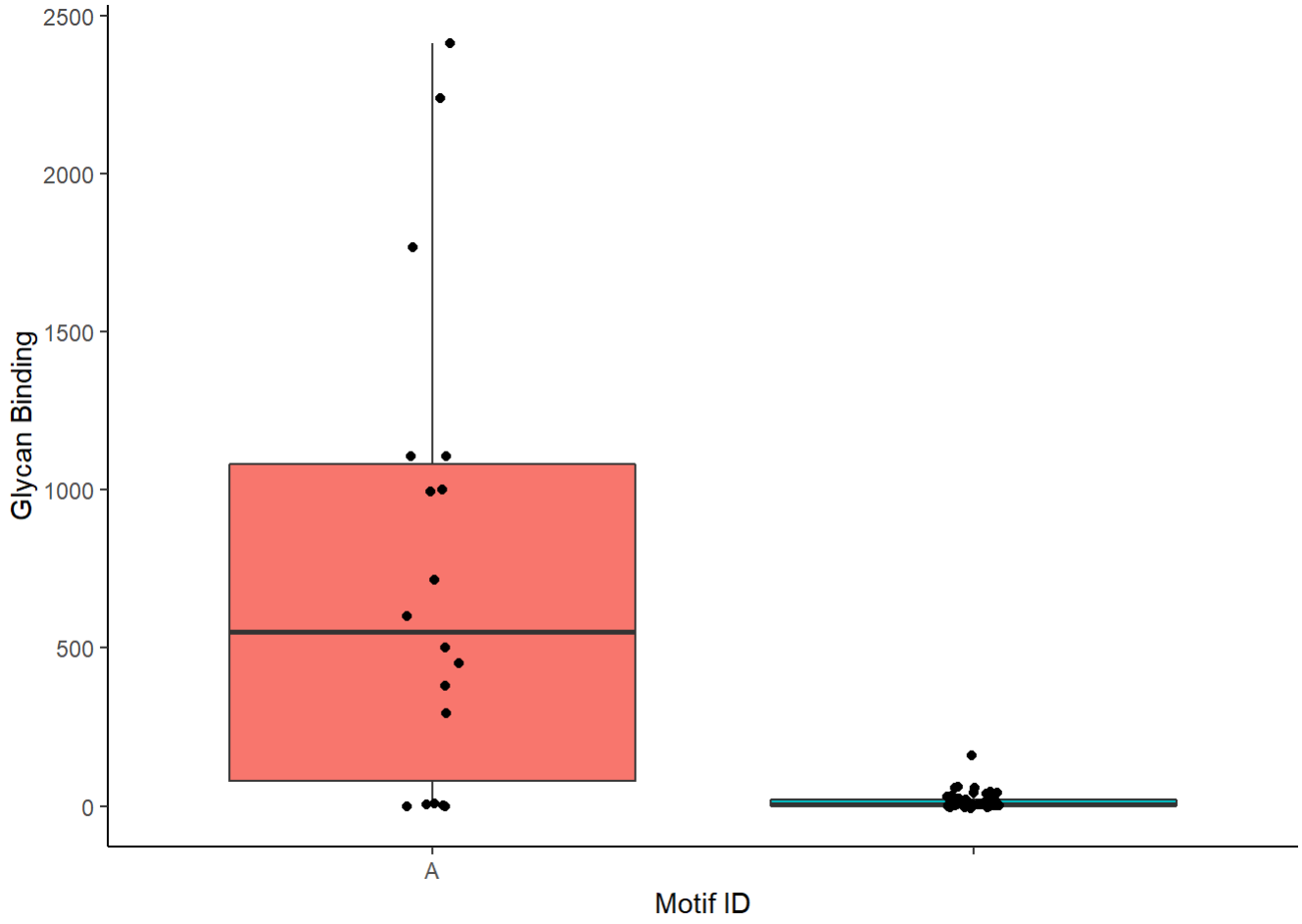
Automated Analysis report for PHA-L evaluated at 10 ug/mL

List of Primary PHA-L Motifs

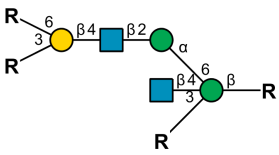
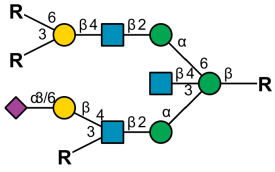
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	18
0			0.02	54

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

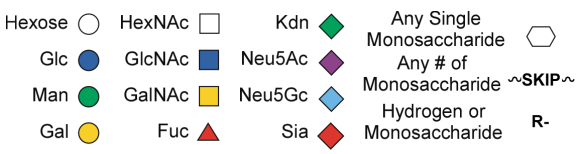
Boxplot of Primary Motifs



List of Fine-Specificity PHA-L Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*			1.00	9	<0.001
A1			0.36	9	0.002
0	Non-Binders (100%)		0.00	54	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

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Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

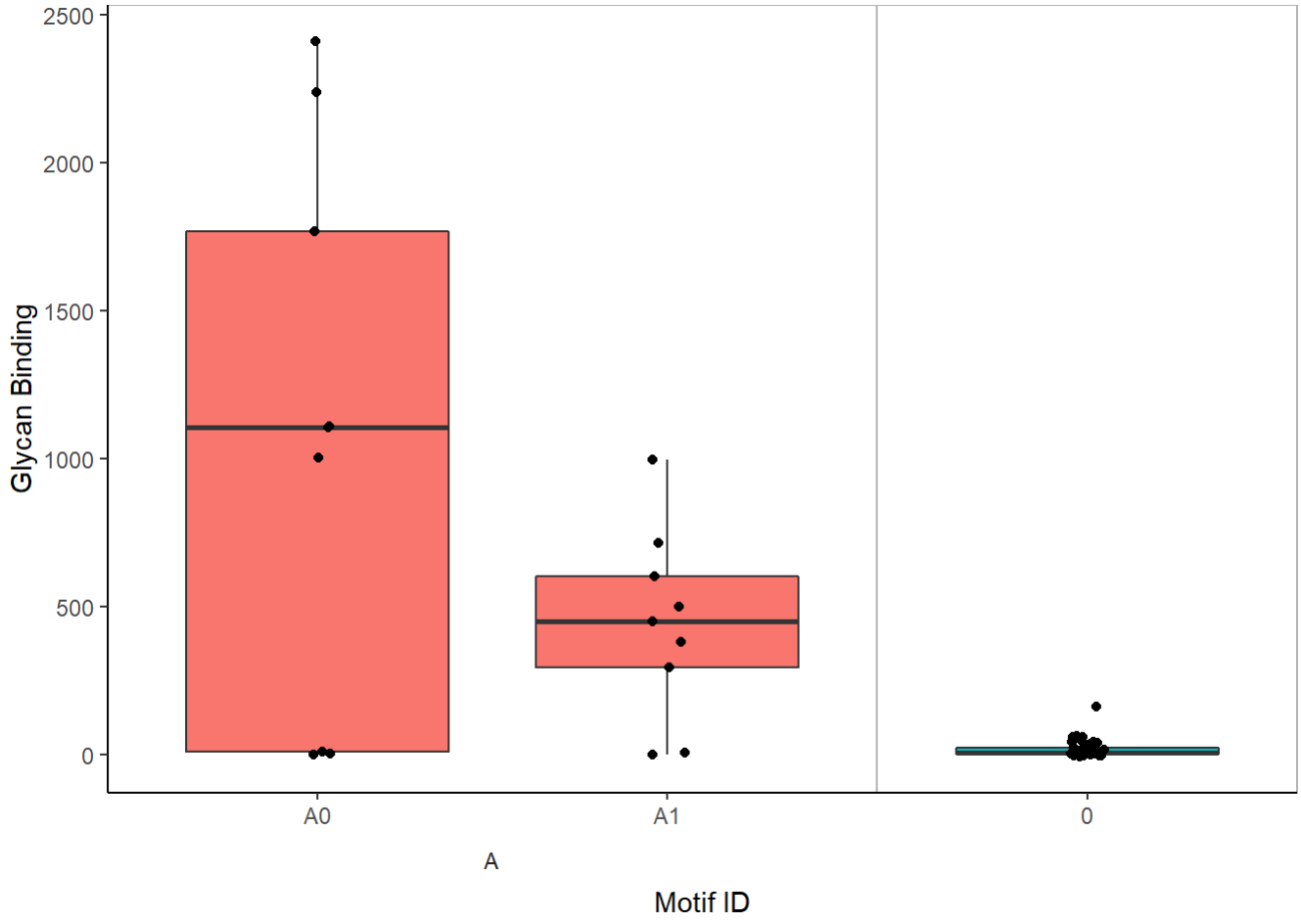


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

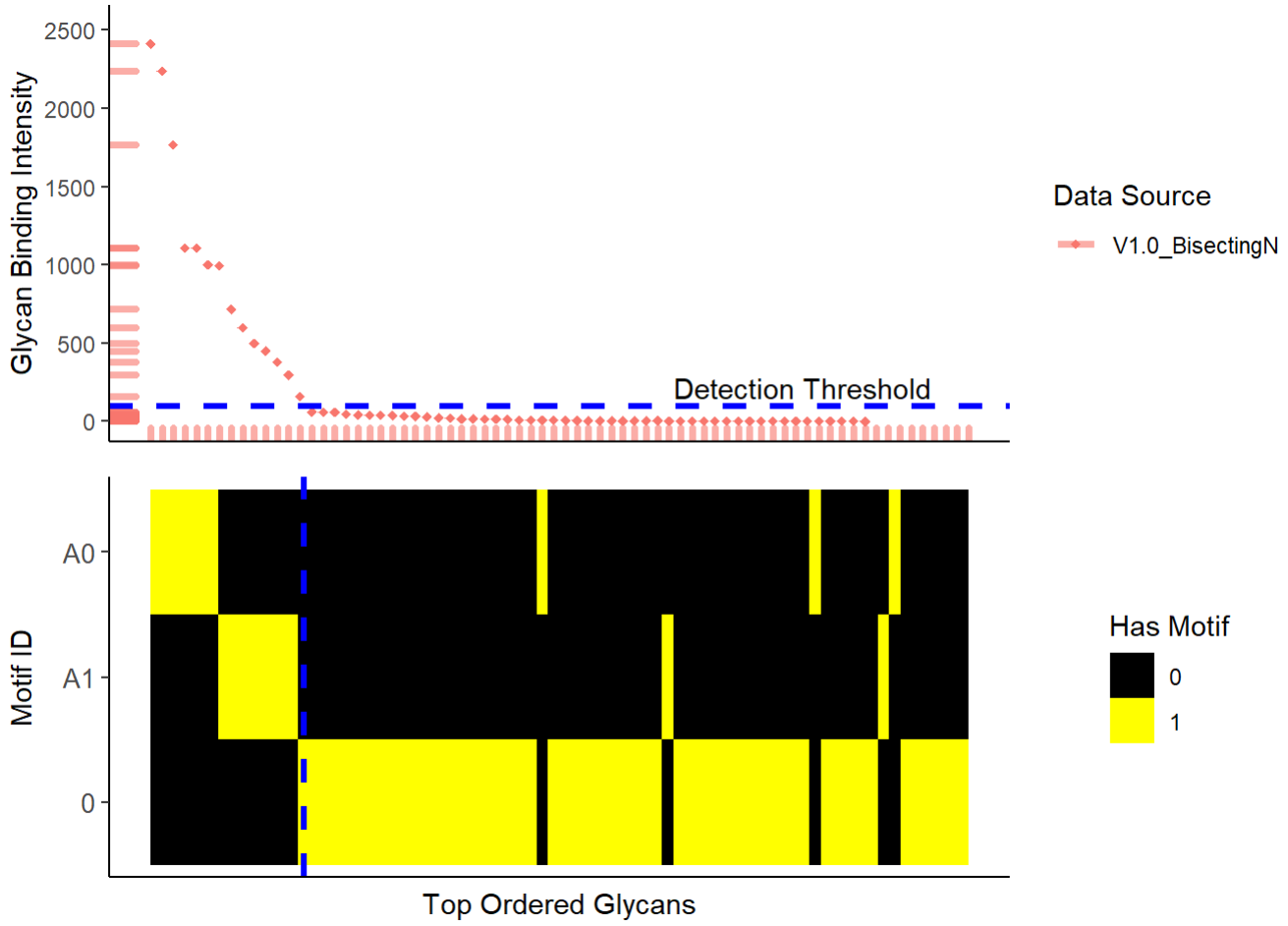
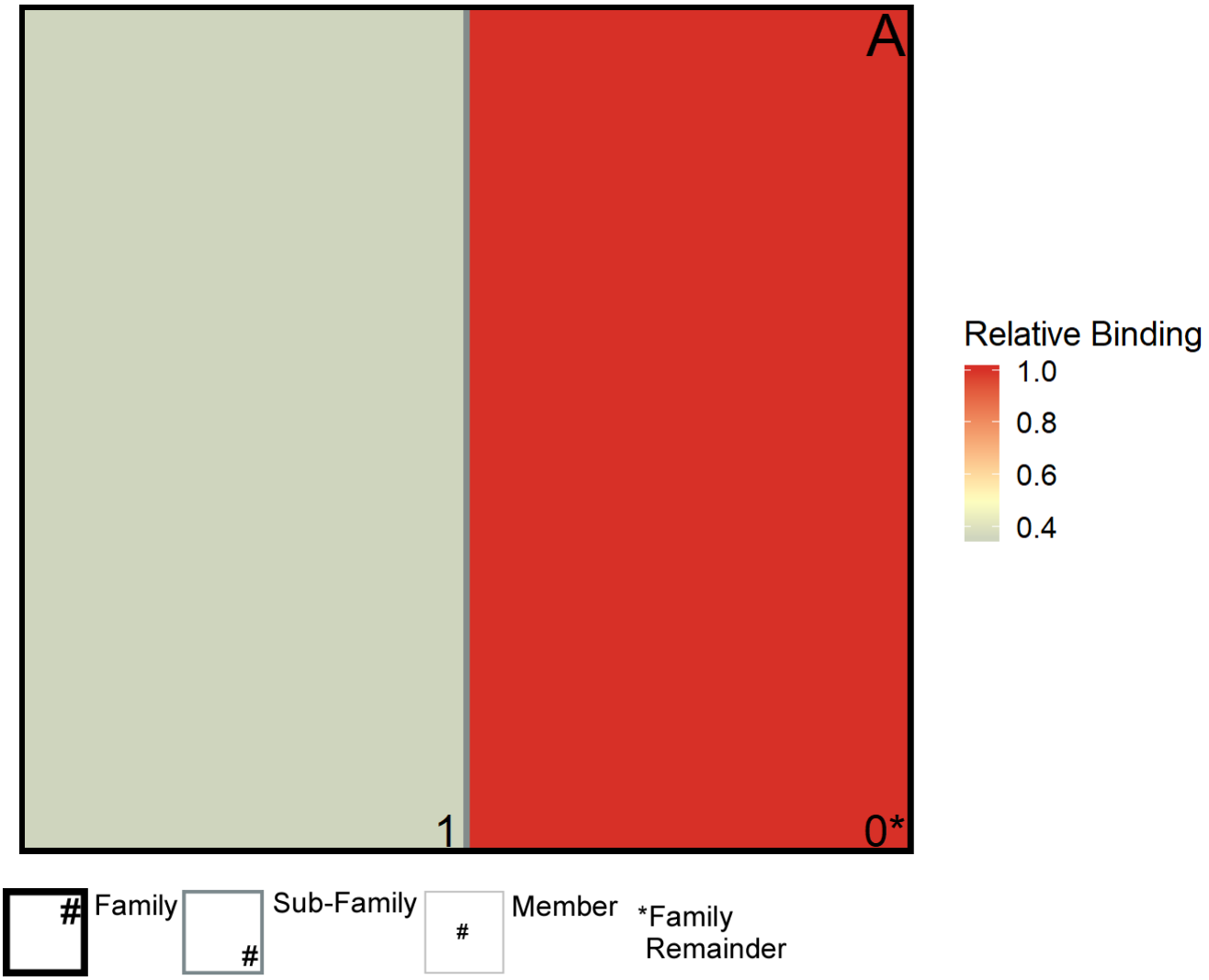


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map



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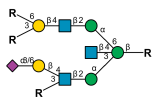
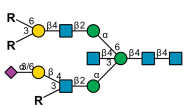
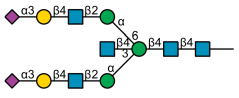
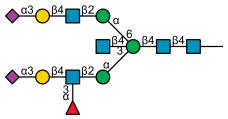
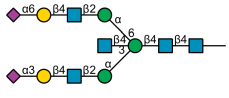
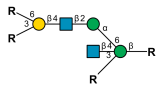
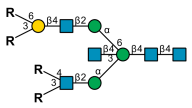
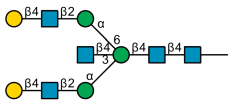
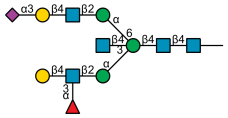
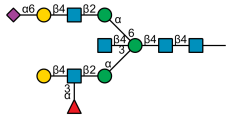
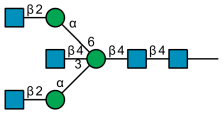
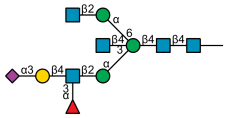
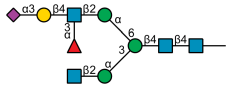
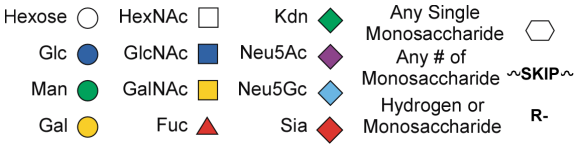
Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				3		18		31

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				2		17		19
0				1		11		62

Key:



All Concentration Plots:

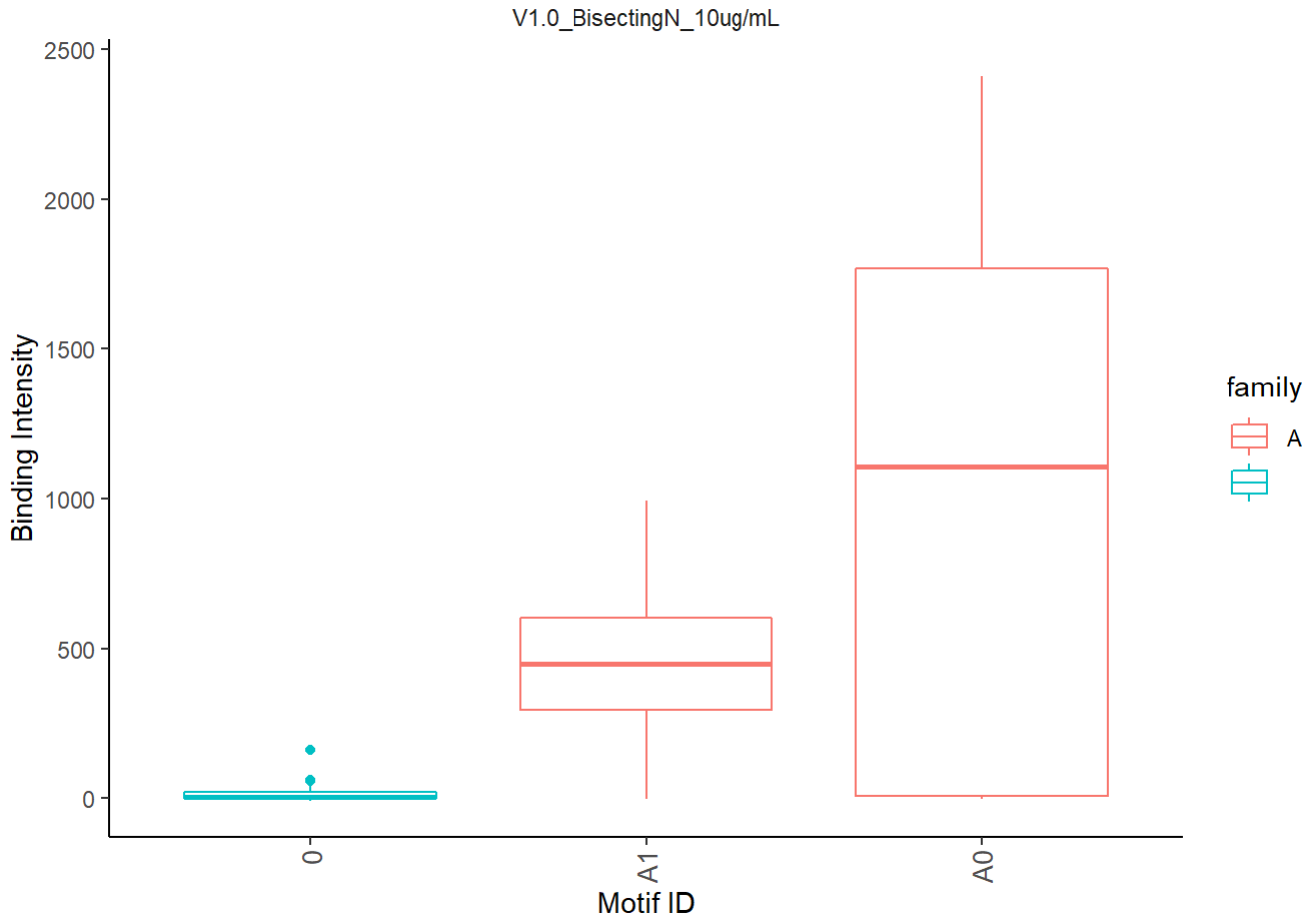
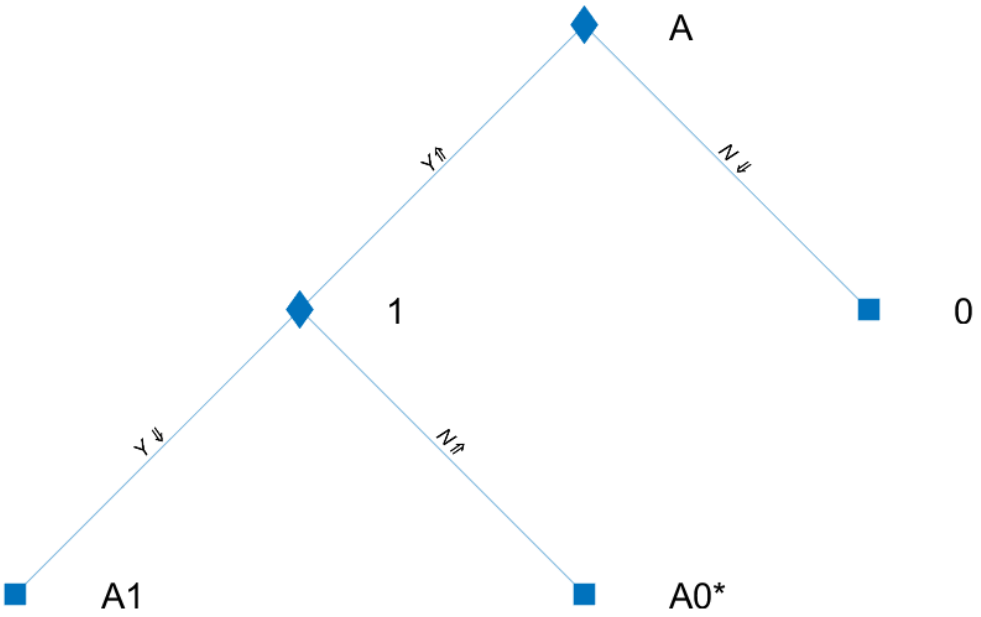


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



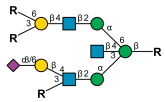
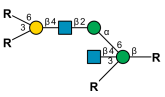
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

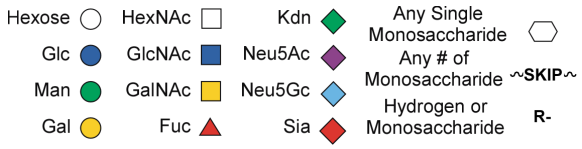
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)(<3f4f6f>GlcNAcB1-4)<2f>ManB
A0*		<2f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f4f6f>GlcNAcB1-4)<2f>ManB
0		Non-Binders

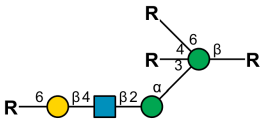
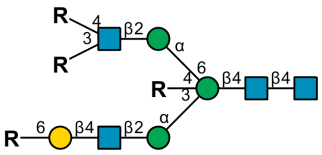
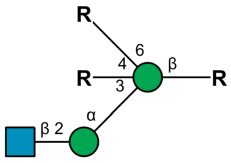
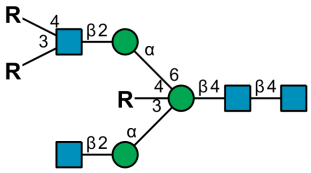
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

Calsepa

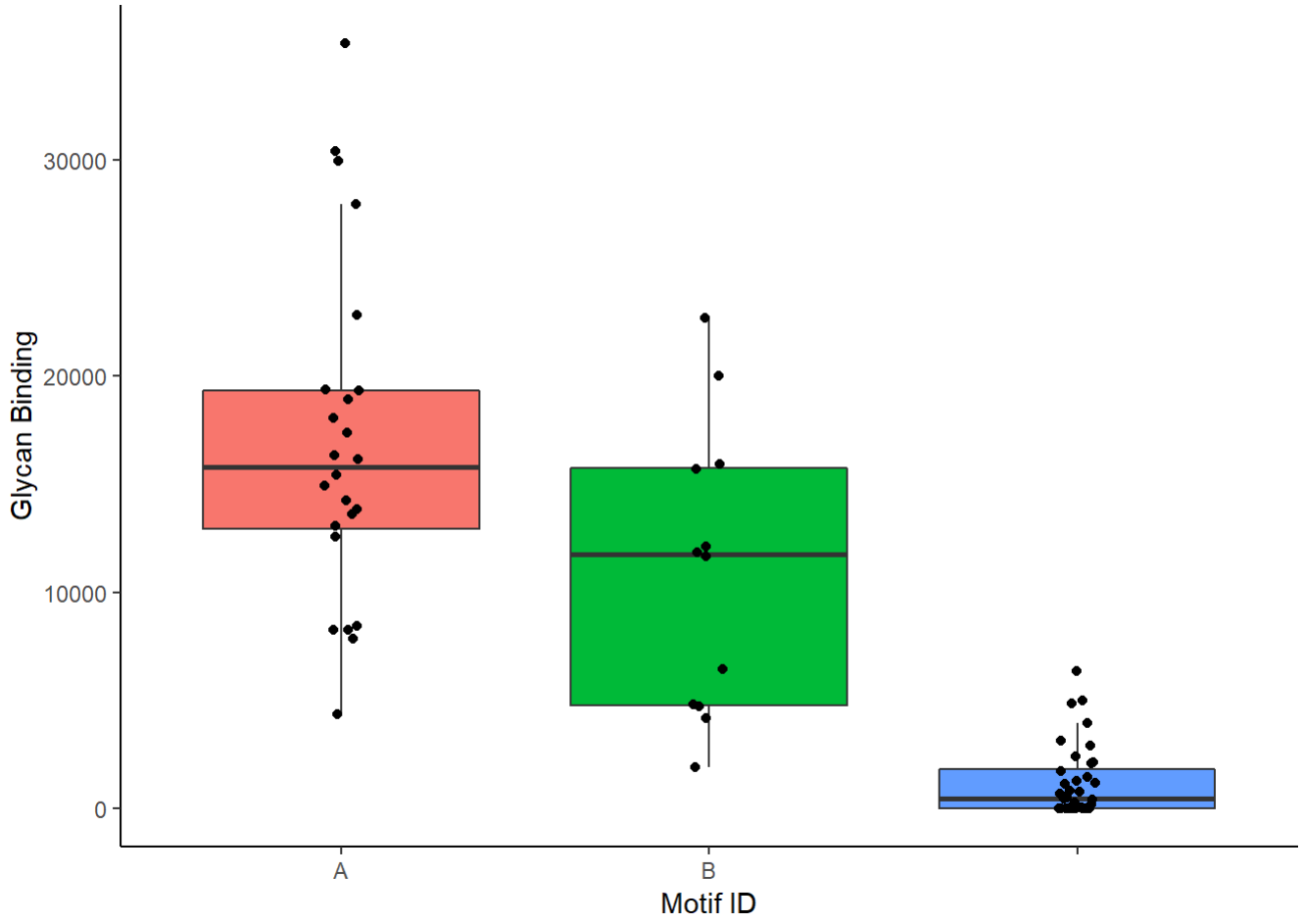
Automated Analysis report for Calsepa evaluated at 2 ug/mL

List of Primary Calsepa Motifs

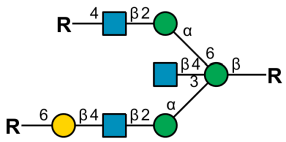
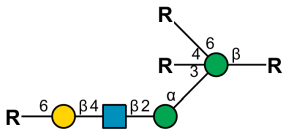
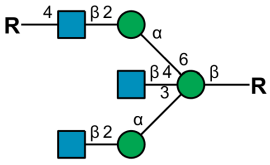
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	24
B			0.65	12
0			0.09	36

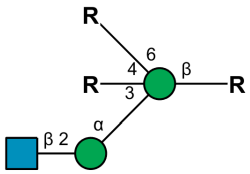
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

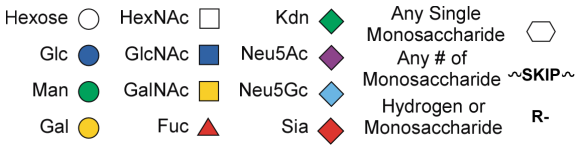


List of Fine-Specificity Calsepa Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A1			1.00	8	<0.001
A0*			0.56	16	<0.001
B1	Terminal N-Glycan N-Acetyl Glucosamine Bisecting N-Glycan (90%)		0.69	4	<0.001

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
B0*			0.30	8	0.001
0	Non-Binders (100%)		0.00	36	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

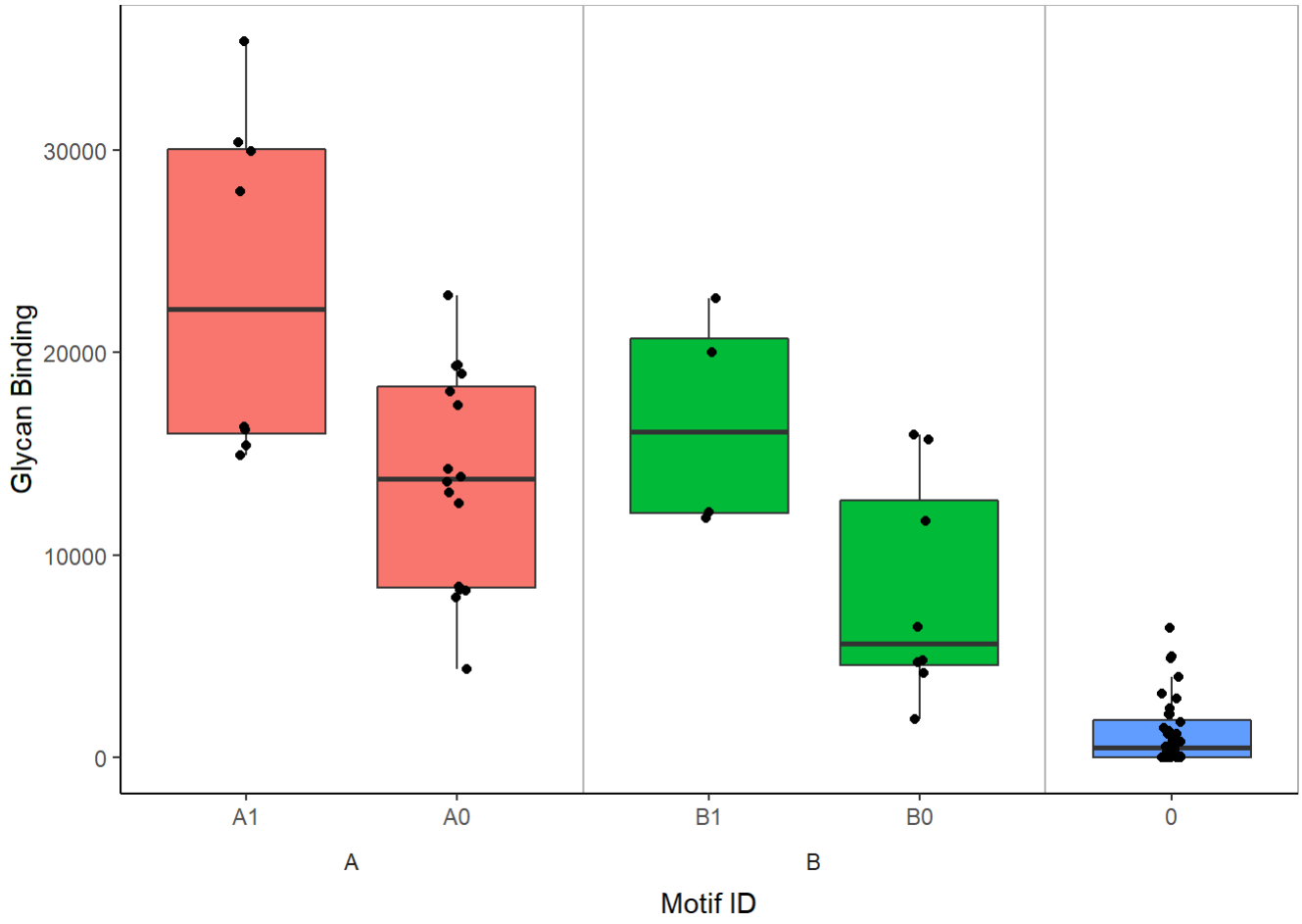


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

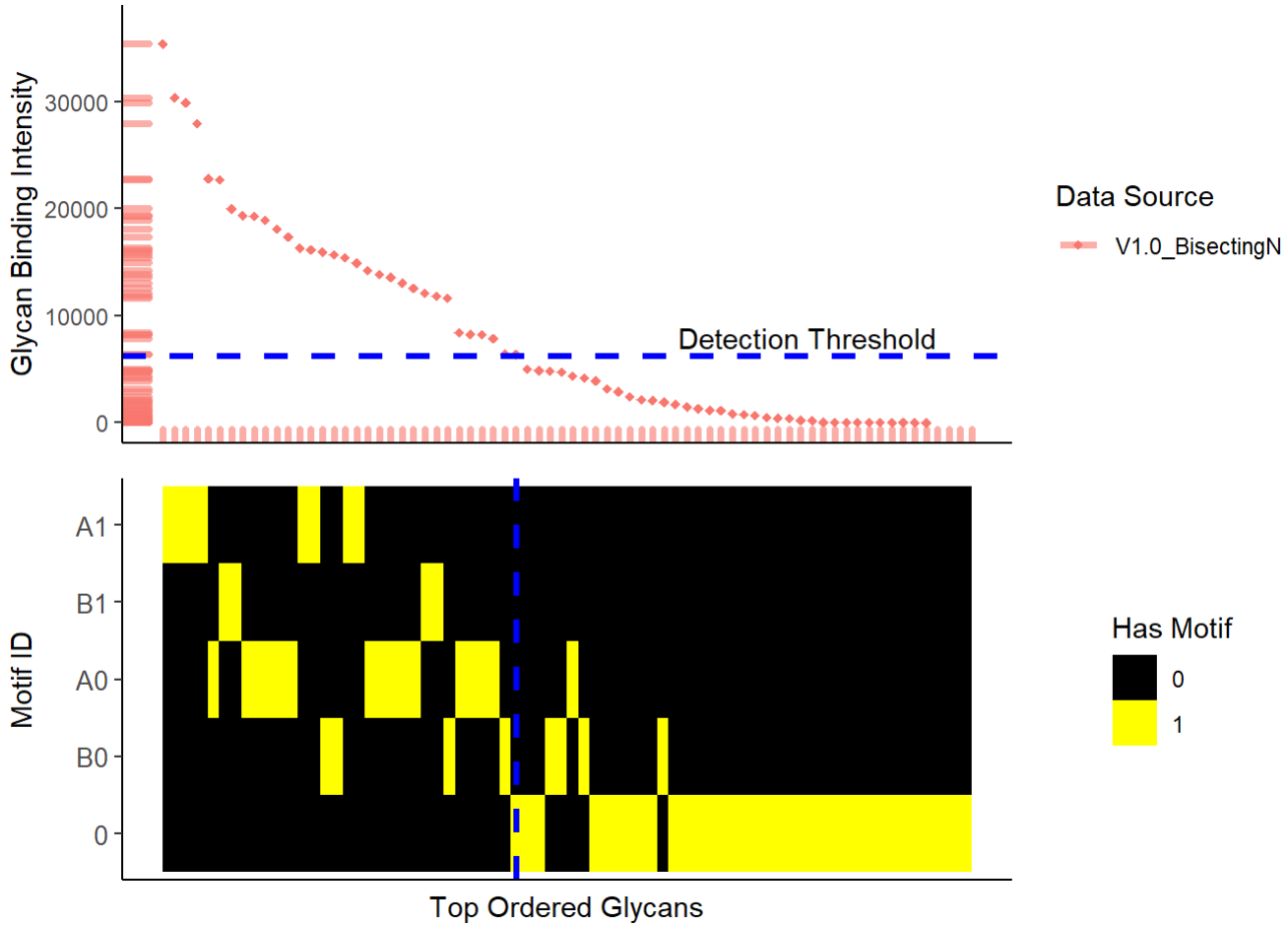
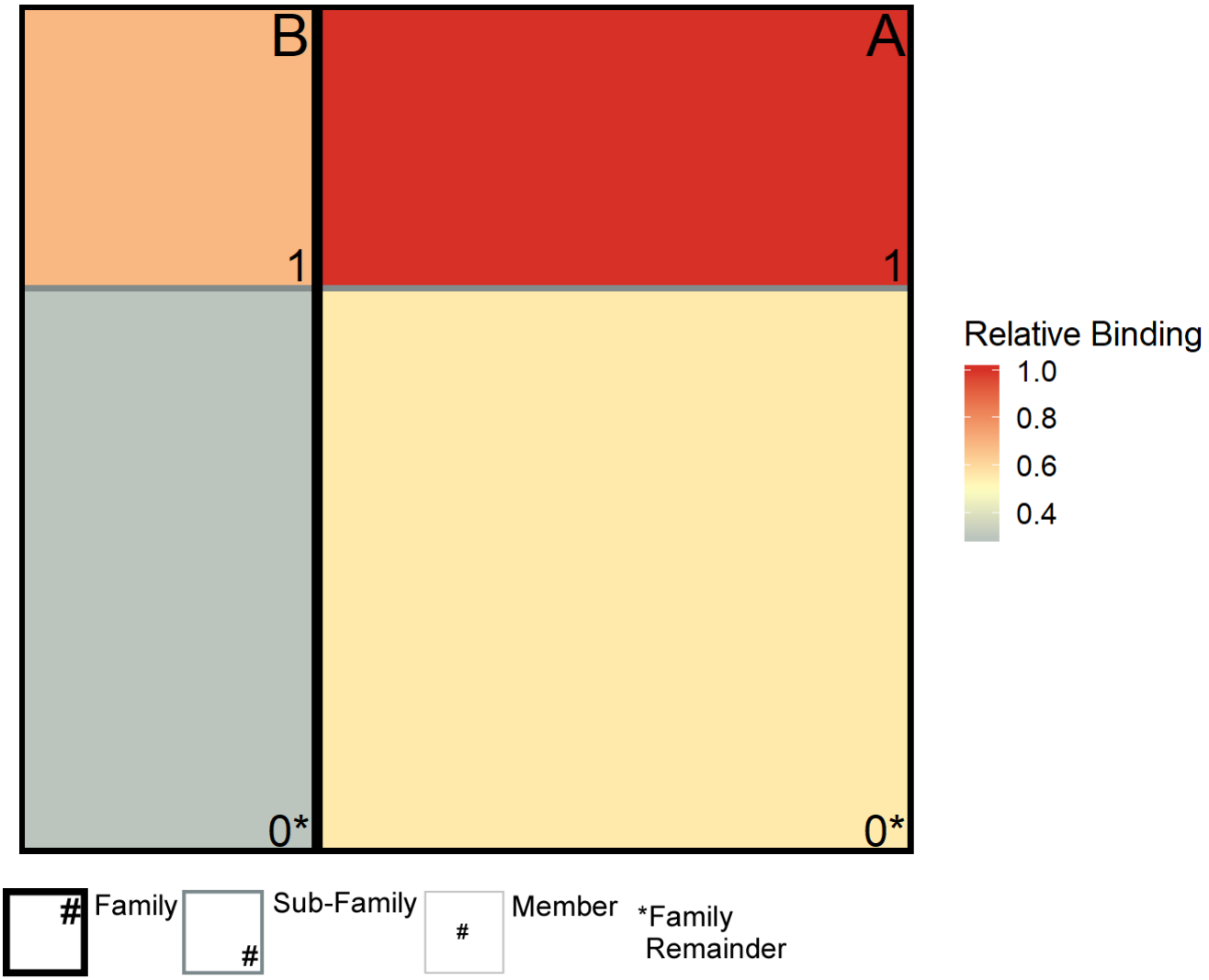


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

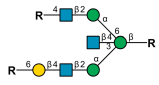
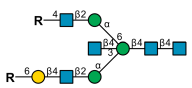
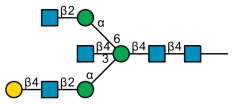
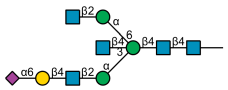
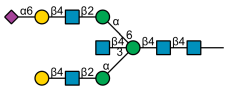
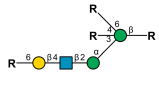
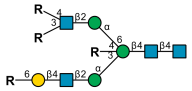
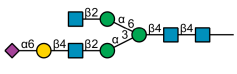
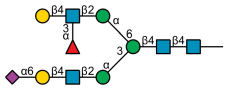
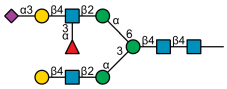


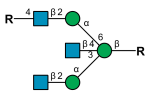
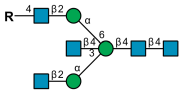
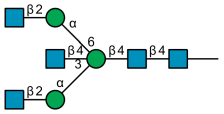
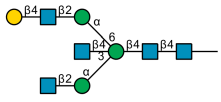
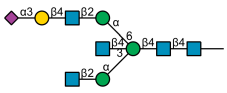
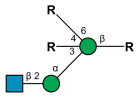
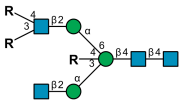
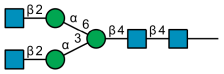
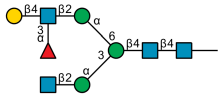
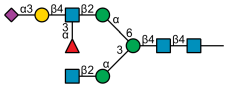
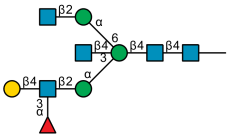
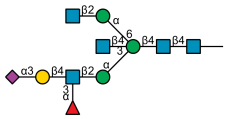
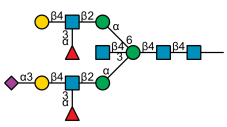
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

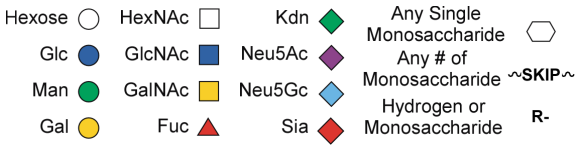
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				7		9		28
A0				45		70		66

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
B1				1		22		23
B0				37		61		62
0				10		11		21

Key:



All Concentration Plots:

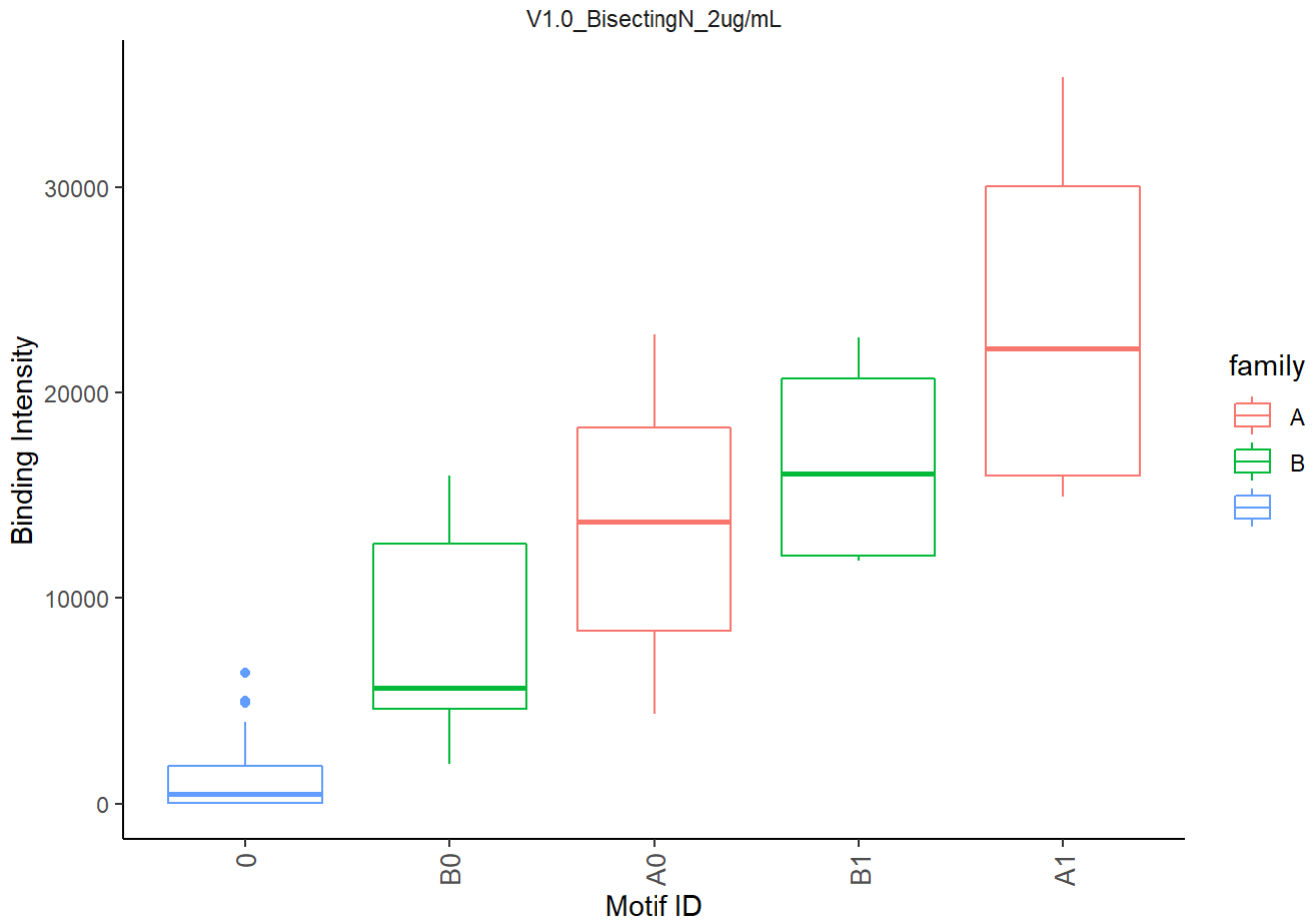
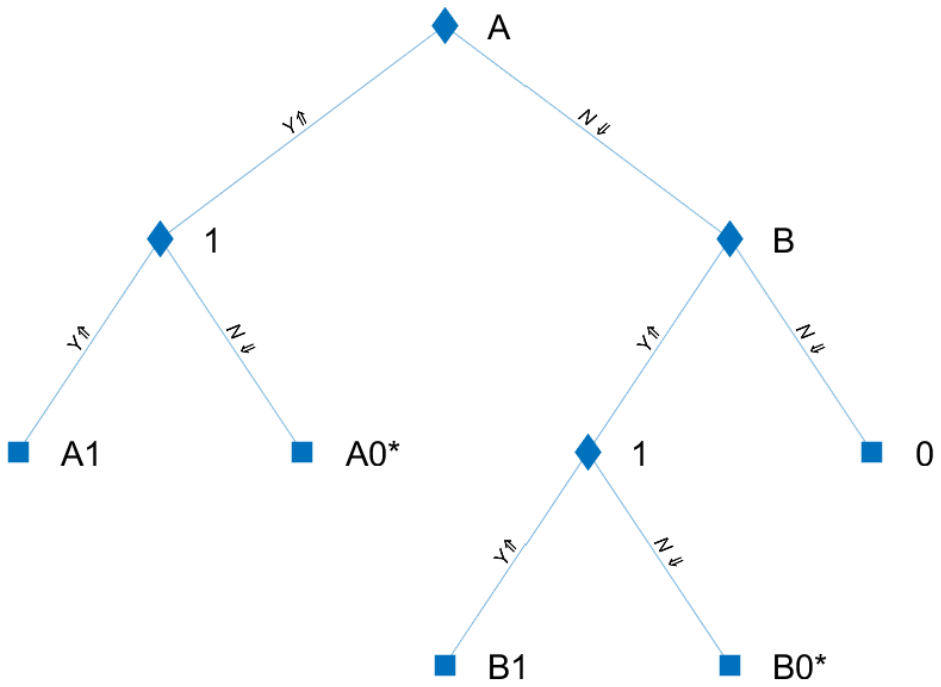


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



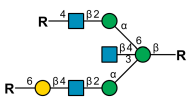
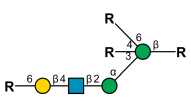
*Motif matches the remaining glycans not matched by earlier motifs in the model.

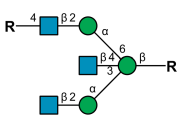
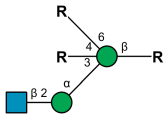
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

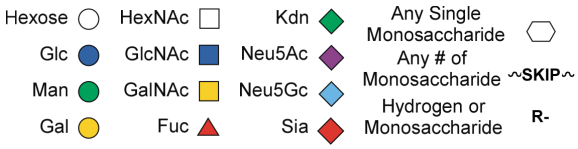
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)(<3f4f6f>GlcNAcB1-4)<2f>ManB
A0*		<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB

Motif ID	Motif Graphic	Motif Text
B1		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)(<3f4f6f>GlcNAcB1-4)<2f>ManB
B0*		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
0		Non-Binders

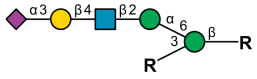
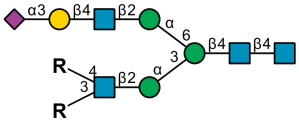
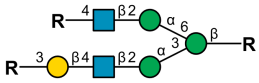
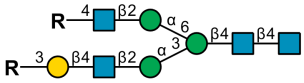
Key:



MAL-I

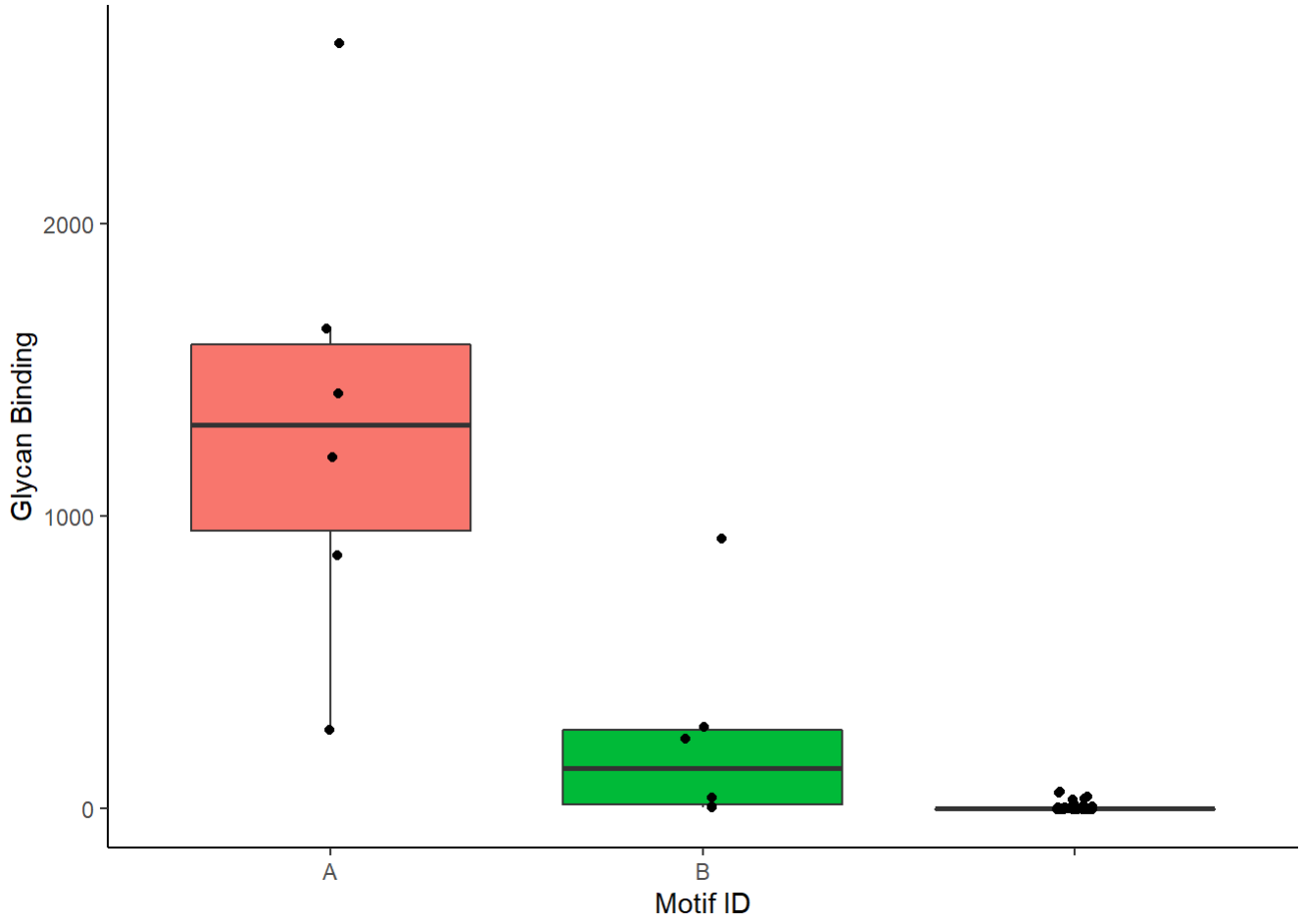
Automated Analysis report for MAL-I evaluated at 10 ug/mL

List of Primary MAL-I Motifs

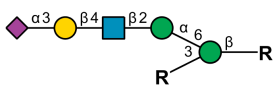
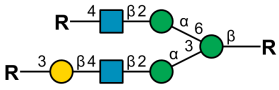
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	6
B			0.23	6
0			0.01	60

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

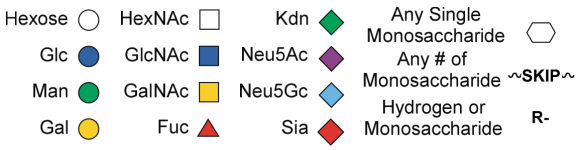
Boxplot of Primary Motifs



List of Fine-Specificity MAL-I Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0			1.00	6	-0.000
B0			0.22	6	0.033
0	Non-Binders (100%)		0.00	60	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

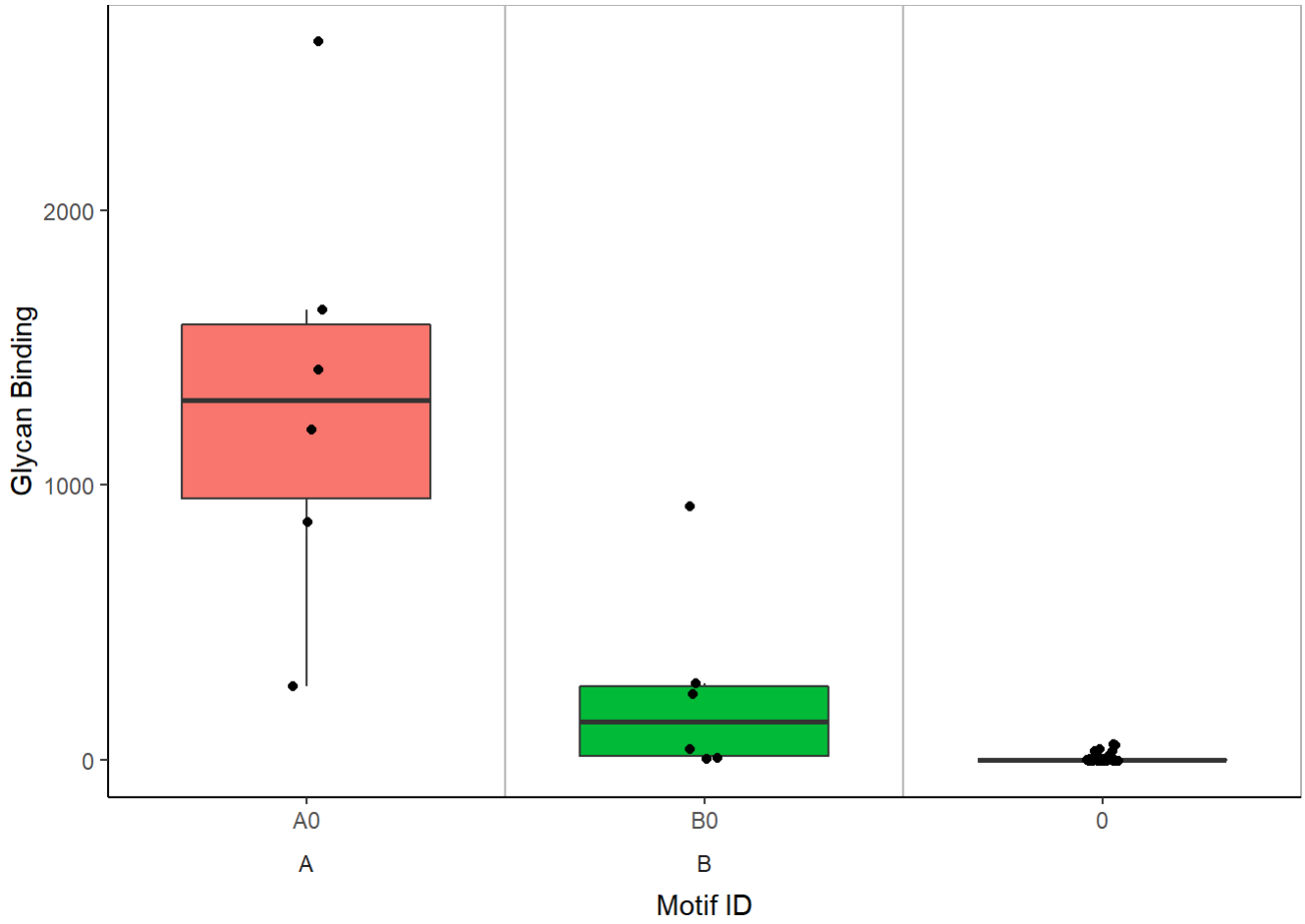


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

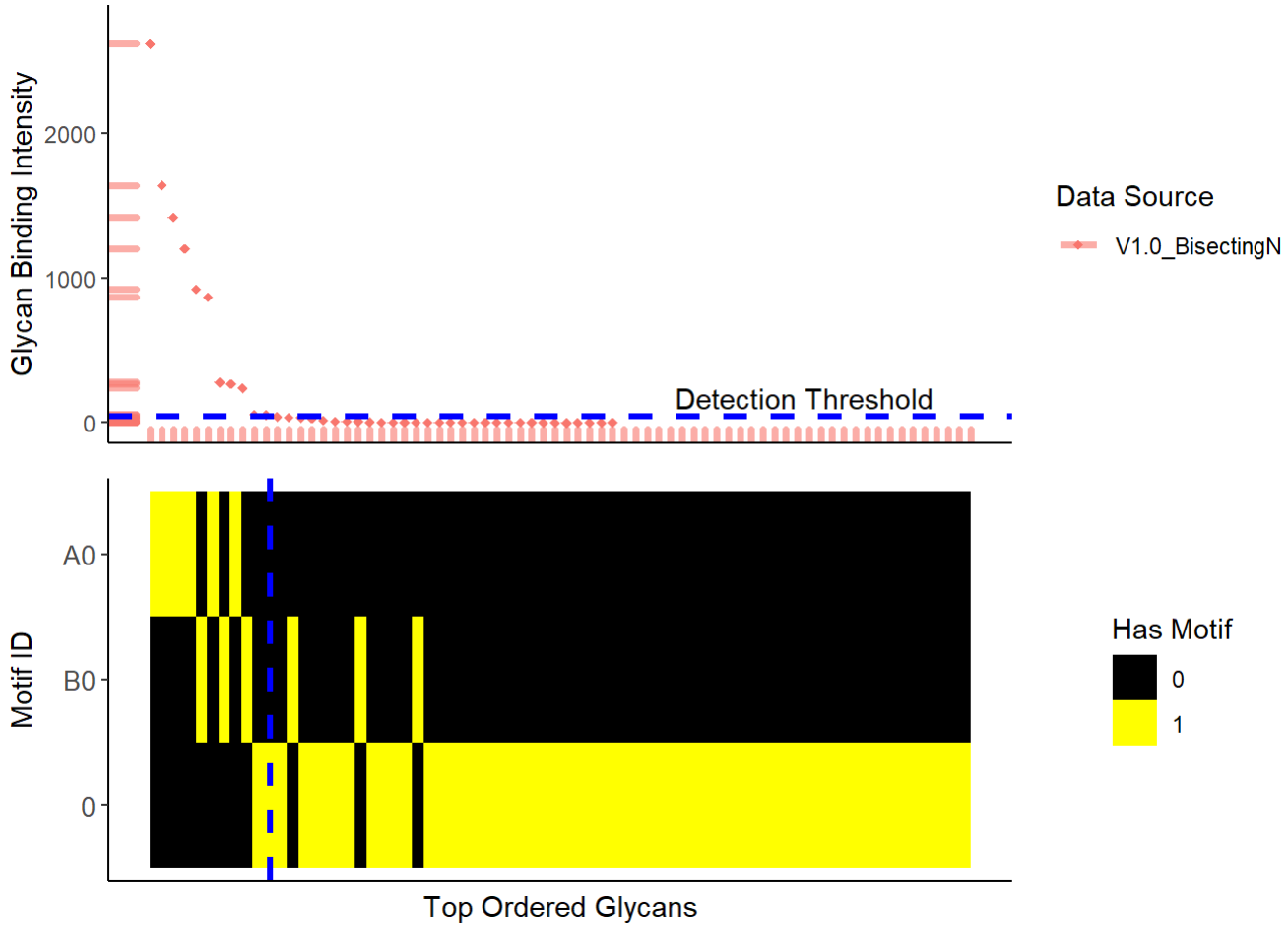
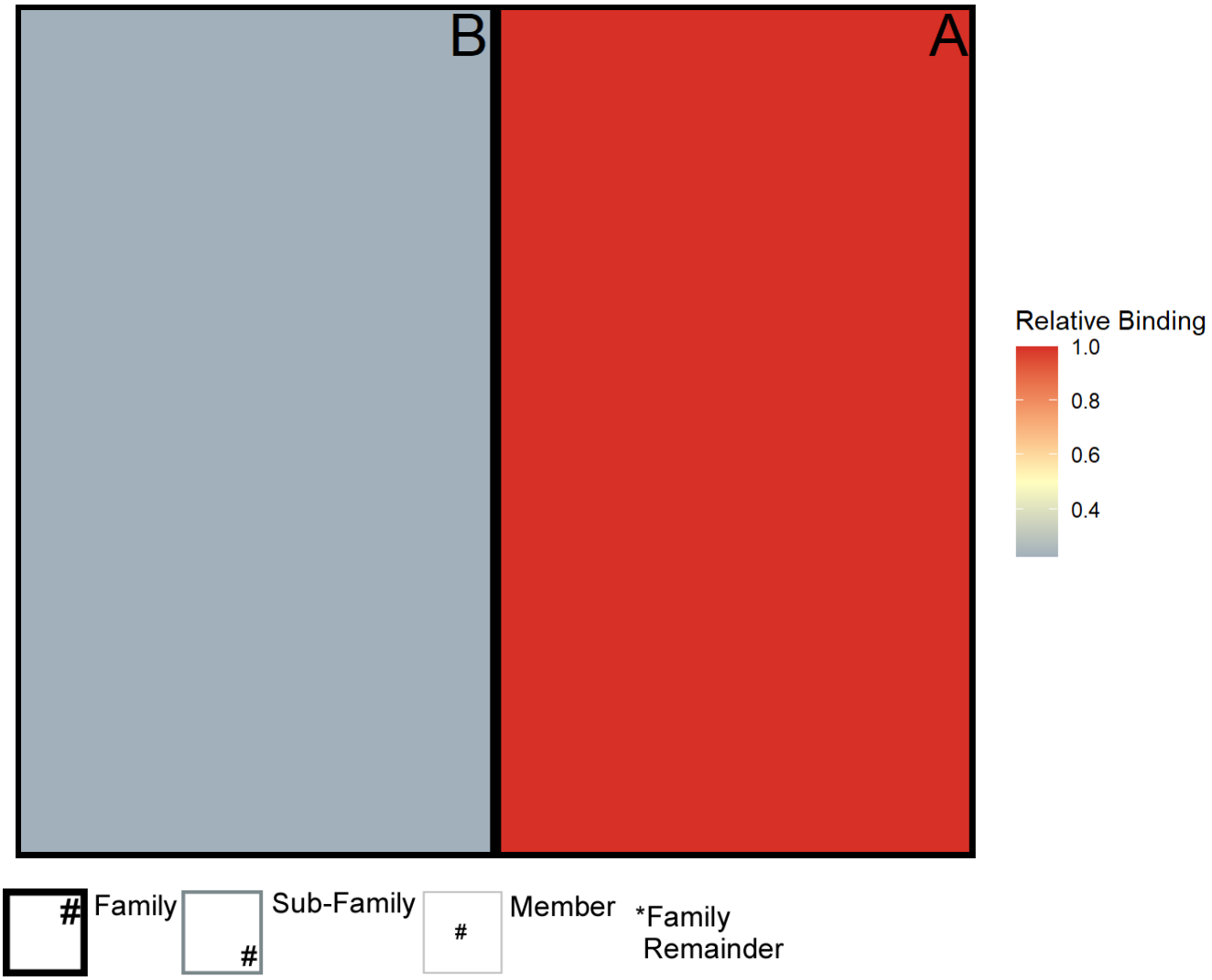


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

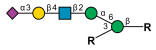
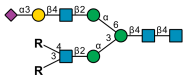
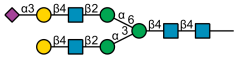
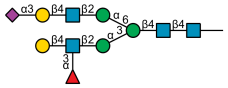
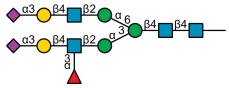
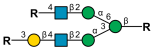
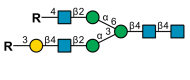
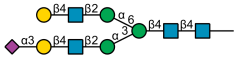
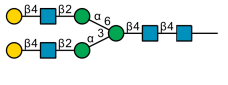
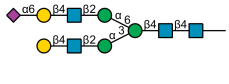


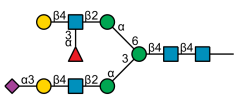
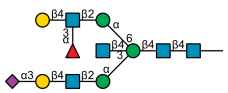
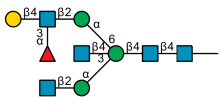
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

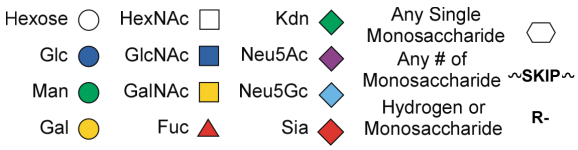
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				63		53		54
B0				48		38		64

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
0			 68	 32	 25

Key:



All Concentration Plots:

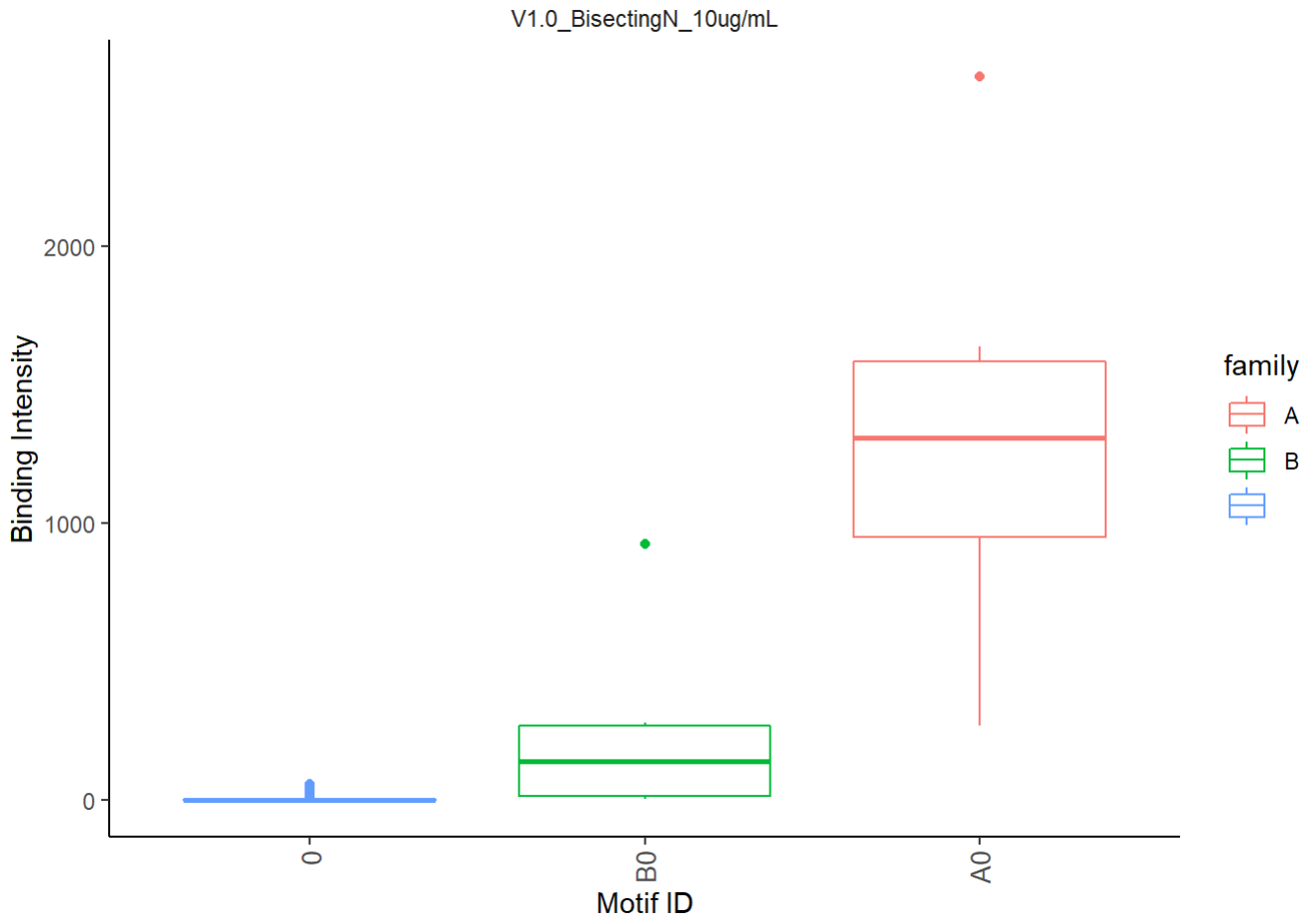
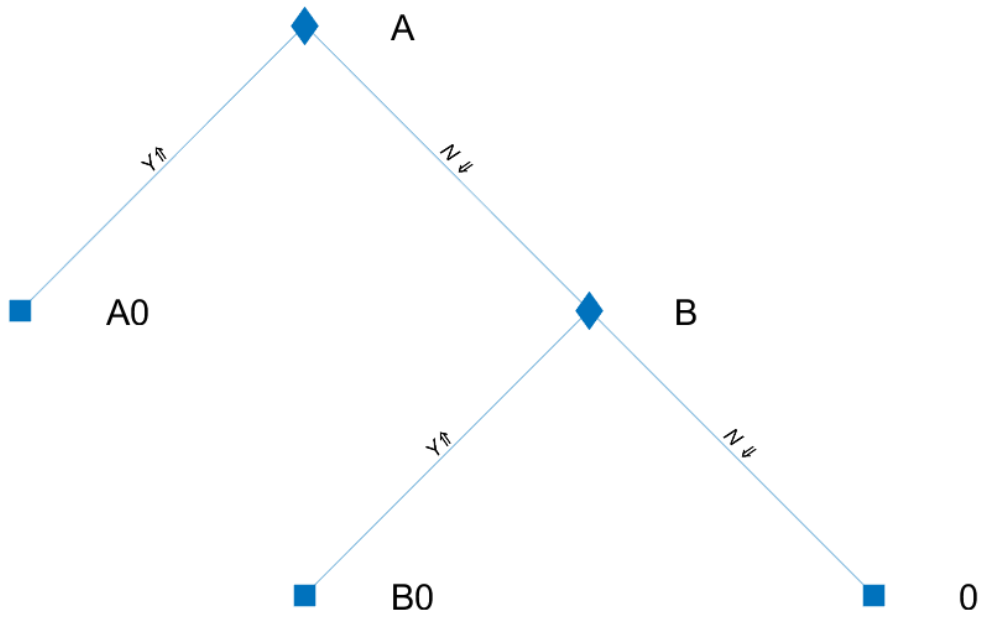


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



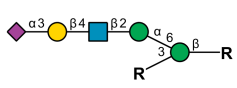
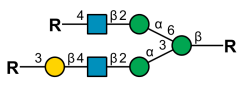
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

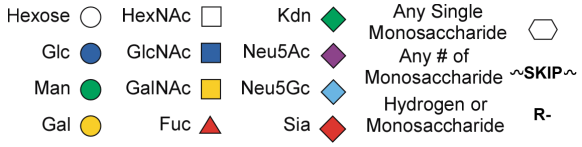
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f4f>ManB
B0		<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f4f>ManB
0		Non-Binders

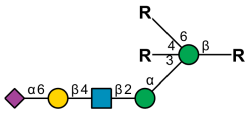
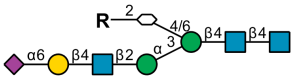
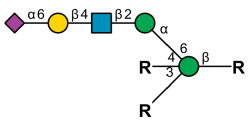
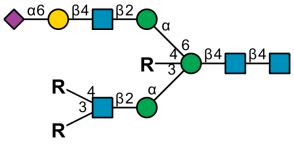
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

SNA

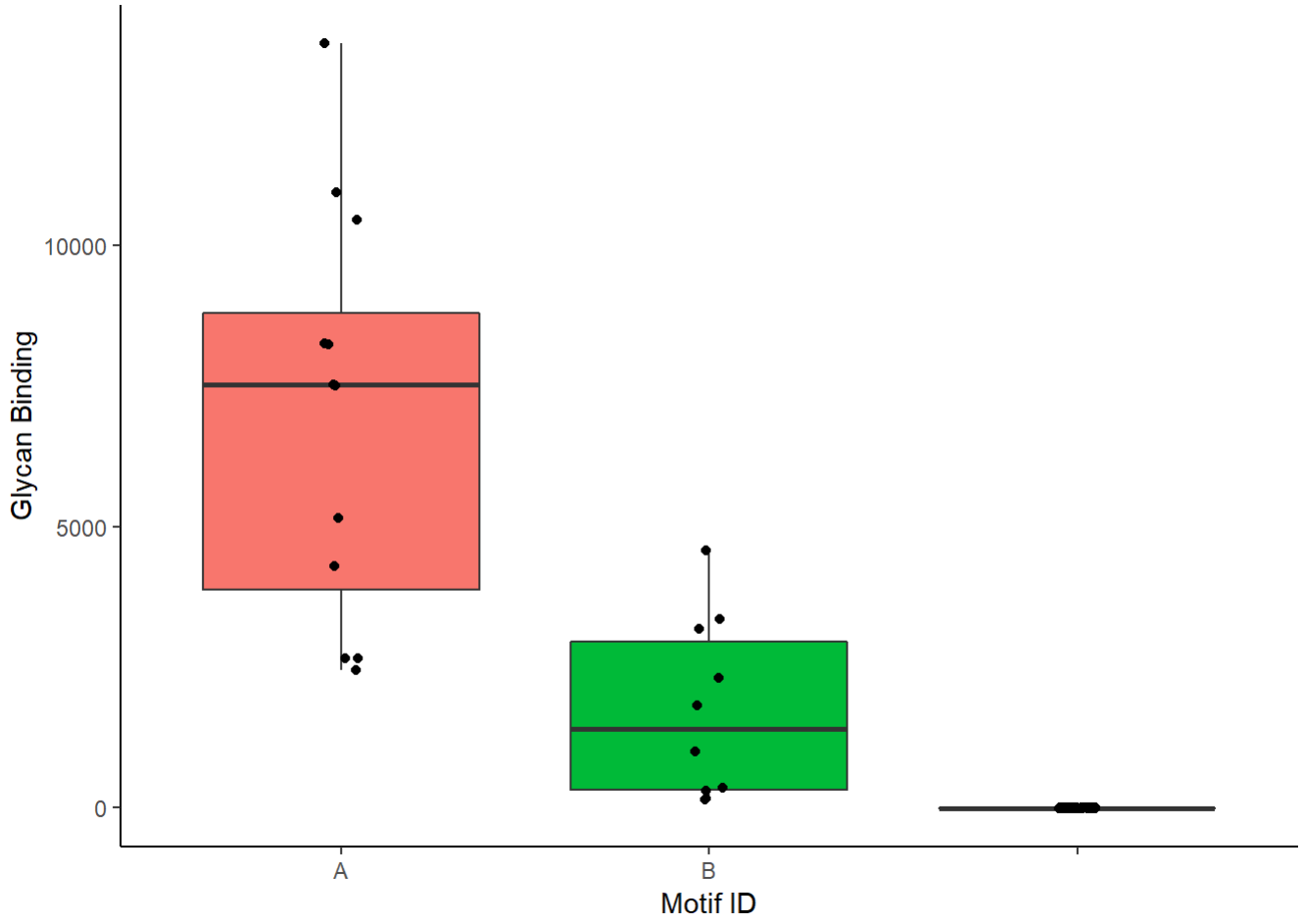
Automated Analysis report for SNA evaluated at 20 ug/mL

List of Primary SNA Motifs

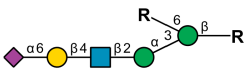
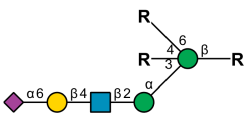
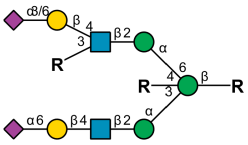
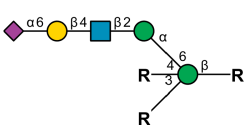
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	12
B			0.26	10
0			0.00	50

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

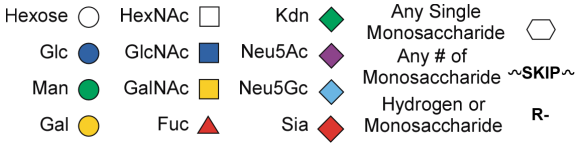
Boxplot of Primary Motifs



List of Fine-Specificity SNA Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A2	a6 Sialyl Type 2 LacNAc Terminal beta-Galactose (90%)		1.00	3	<0.001
A0*	a6 Sialyl Type 2 LacNAc Terminal beta-Galactose (90%)		0.76	3	<0.001
A1	a6 Sialyl Type 2 LacNAc a3 Sialyl Galactose (92%)		0.50	6	<0.001
B0			0.18	10	0.001
0	Non-Binders (100%)		0.00	50	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

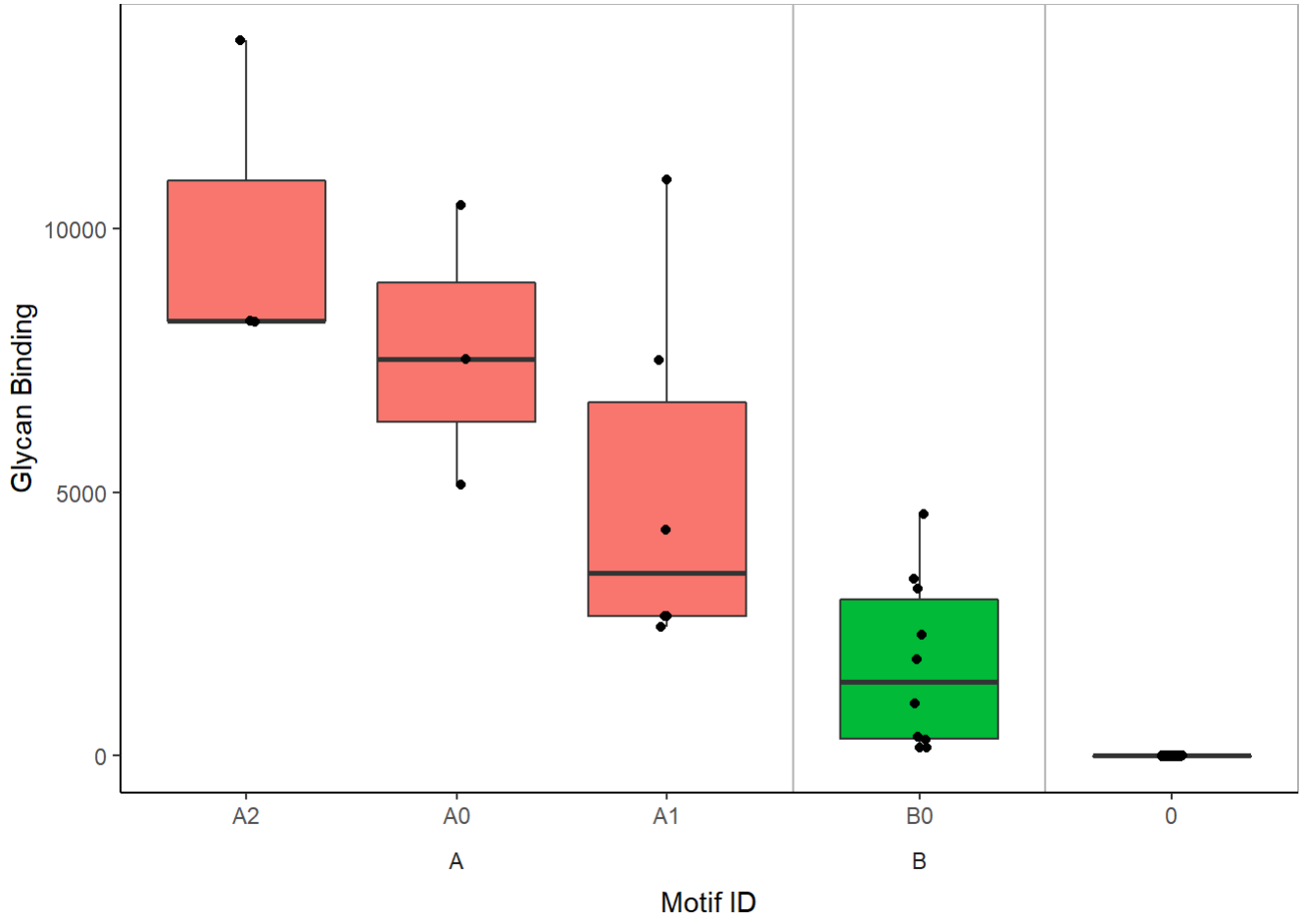


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

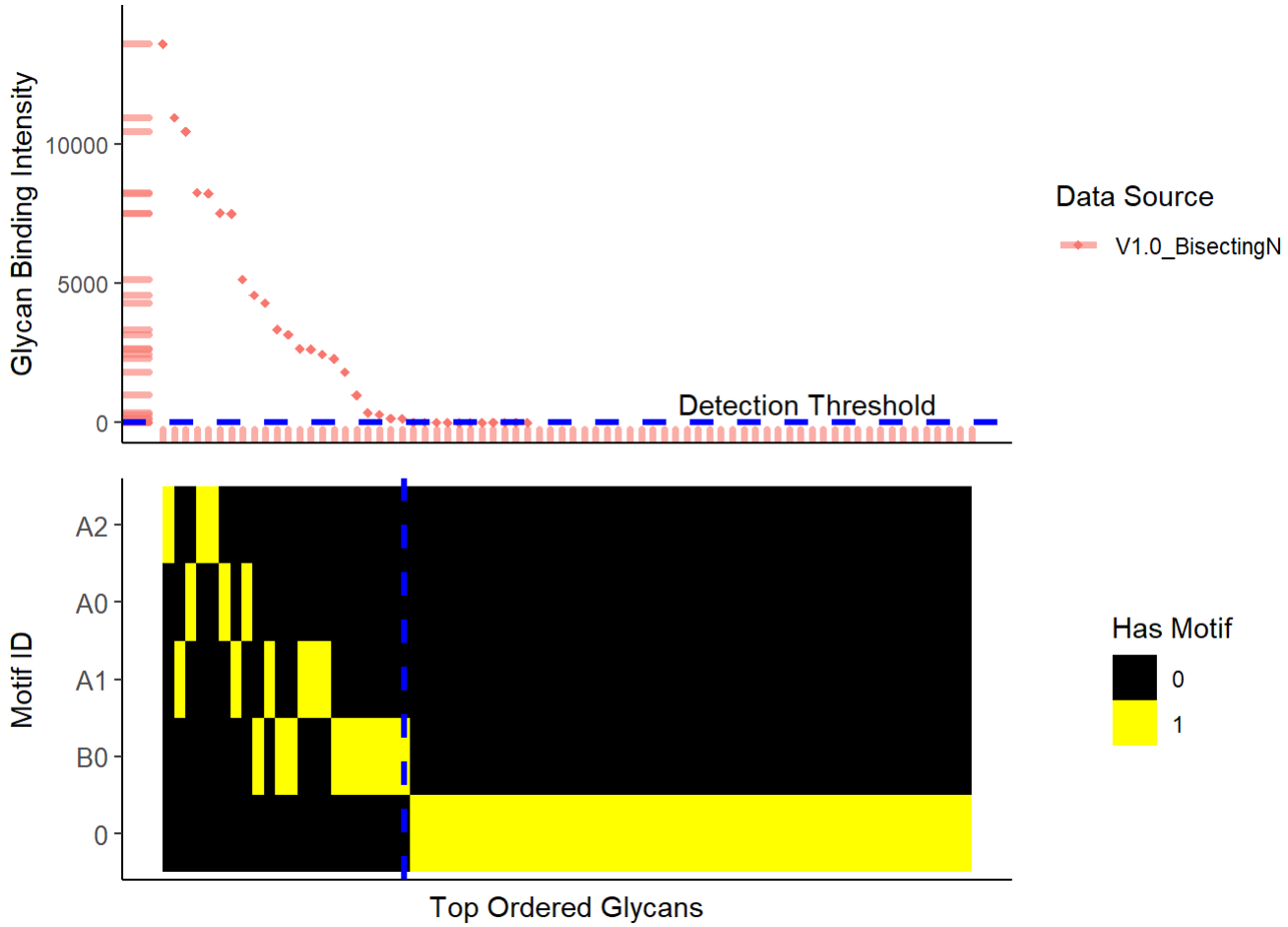
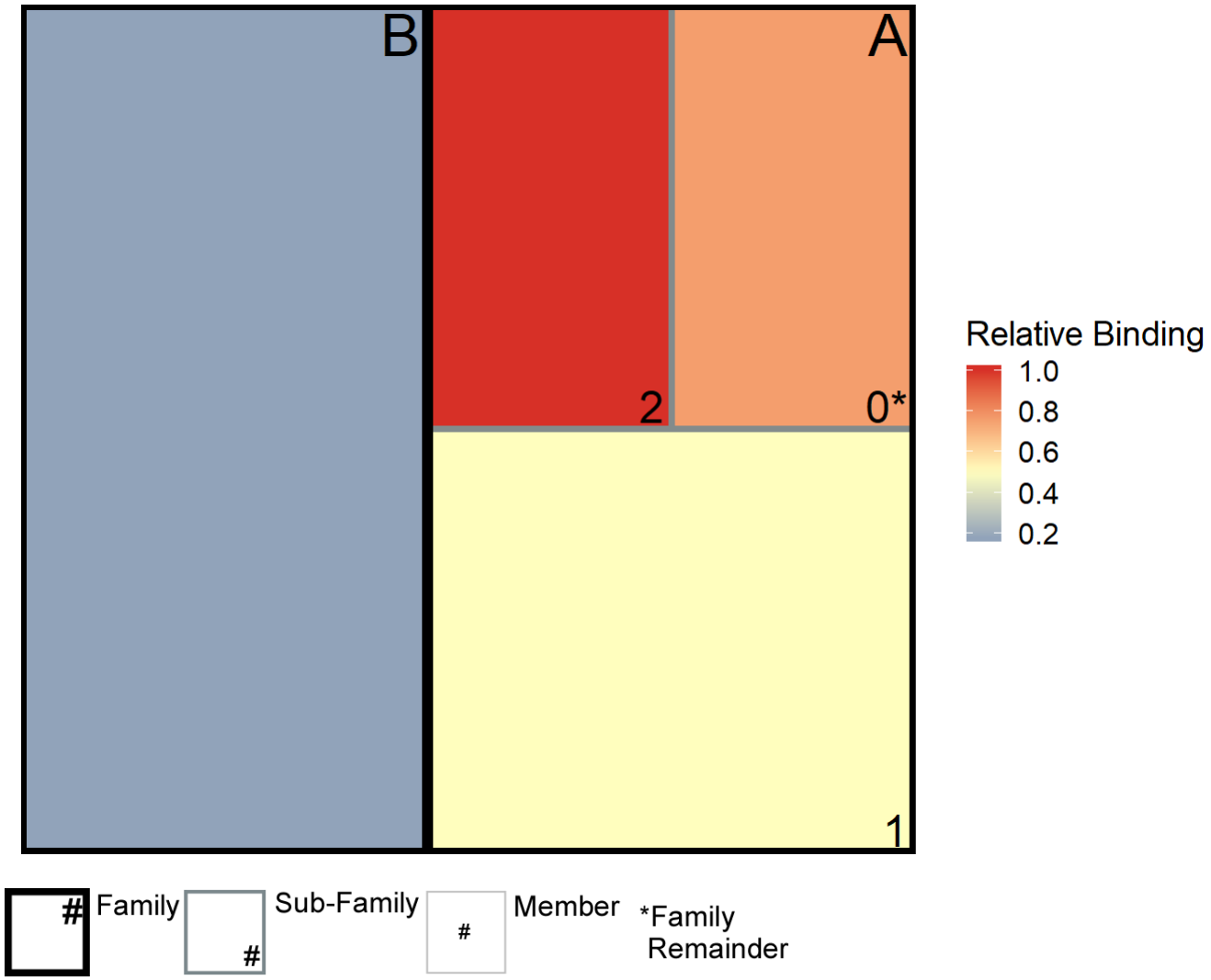


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

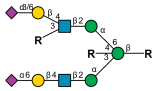
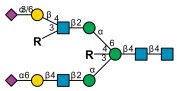
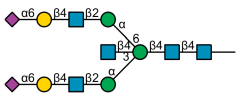
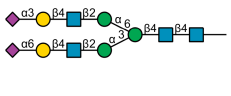
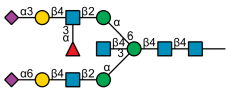
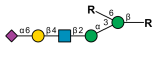
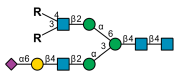
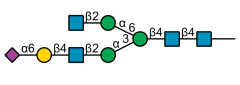
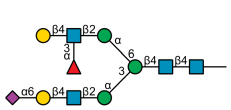
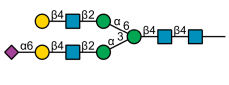


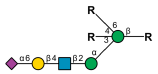
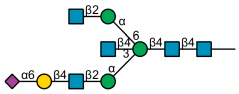
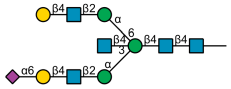
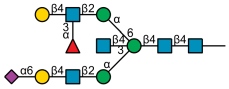
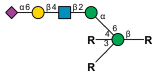
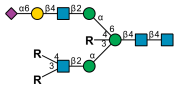
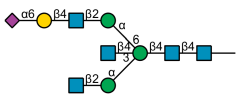
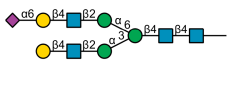
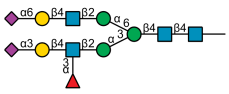
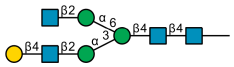
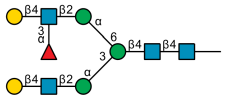
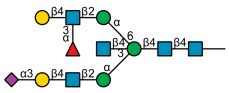
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

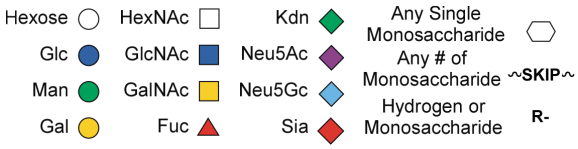
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				4		52		35
A2				45		70		49

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				9		13		34
B0				24		64		56
0				43		65		32

Key:



All Concentration Plots:

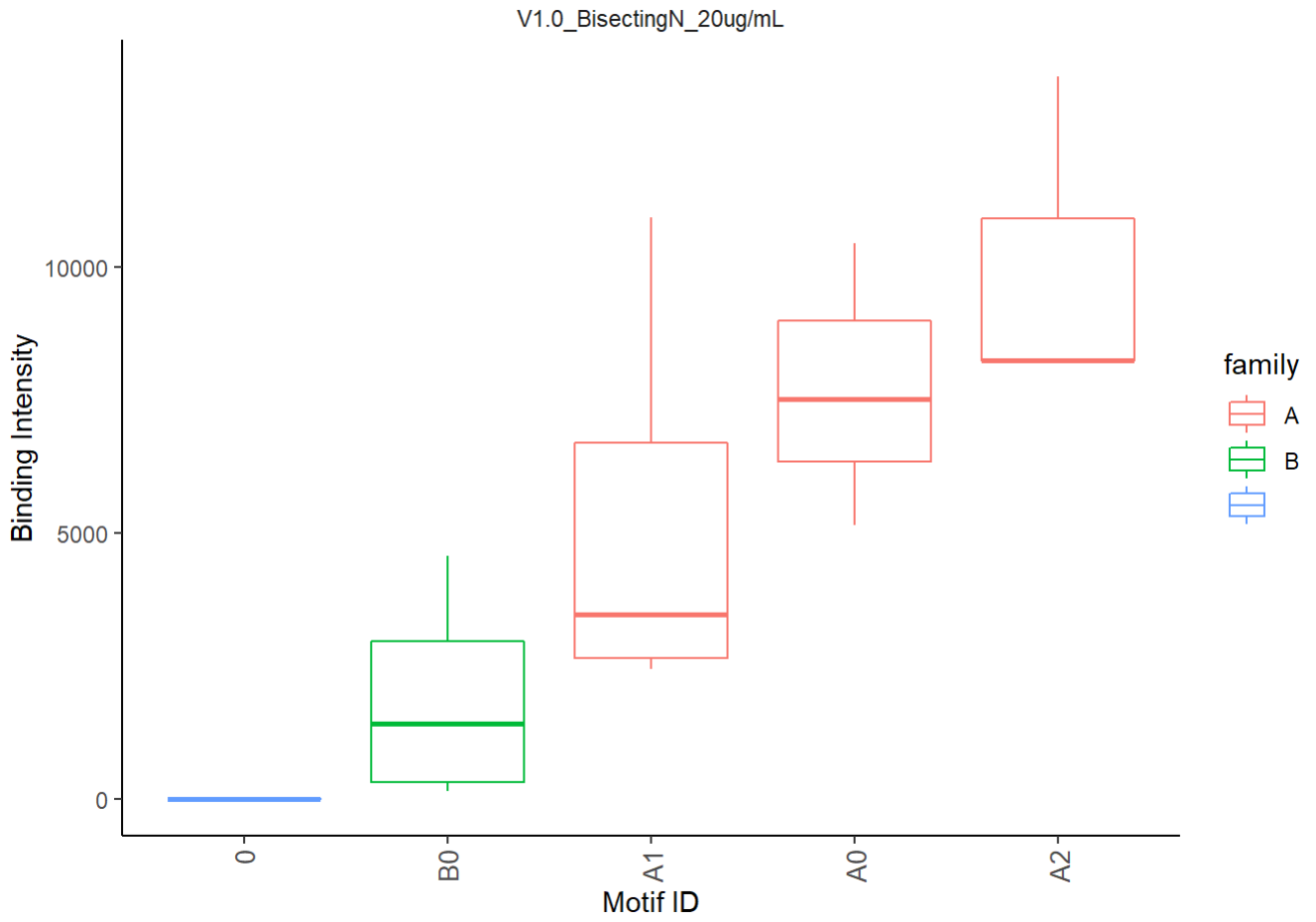
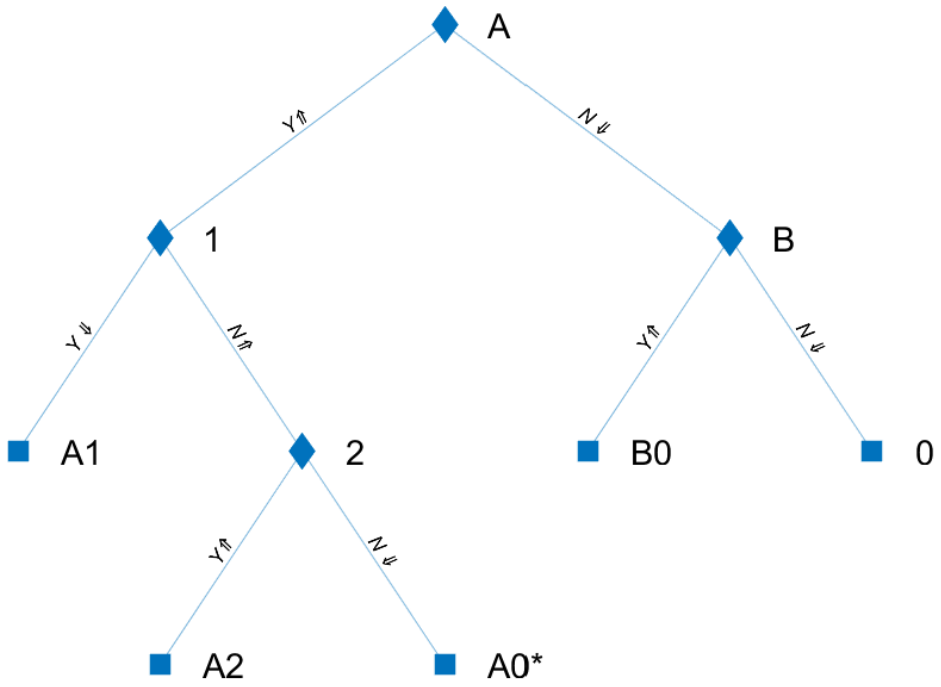


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



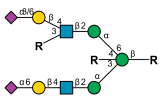
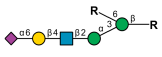
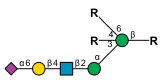
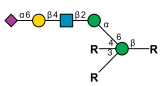
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

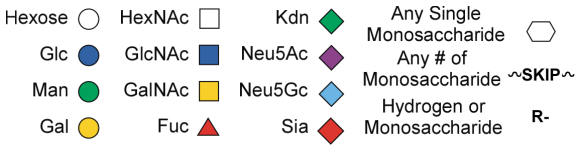
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f>ManB
A2		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f4f>ManB
A0*		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
B0		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB

Motif ID	Motif Graphic	Motif Text
0		Non-Binders

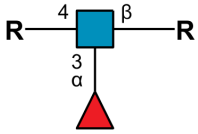
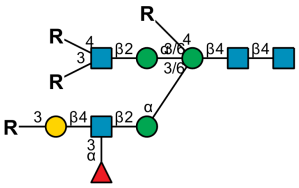
Key:



AAL

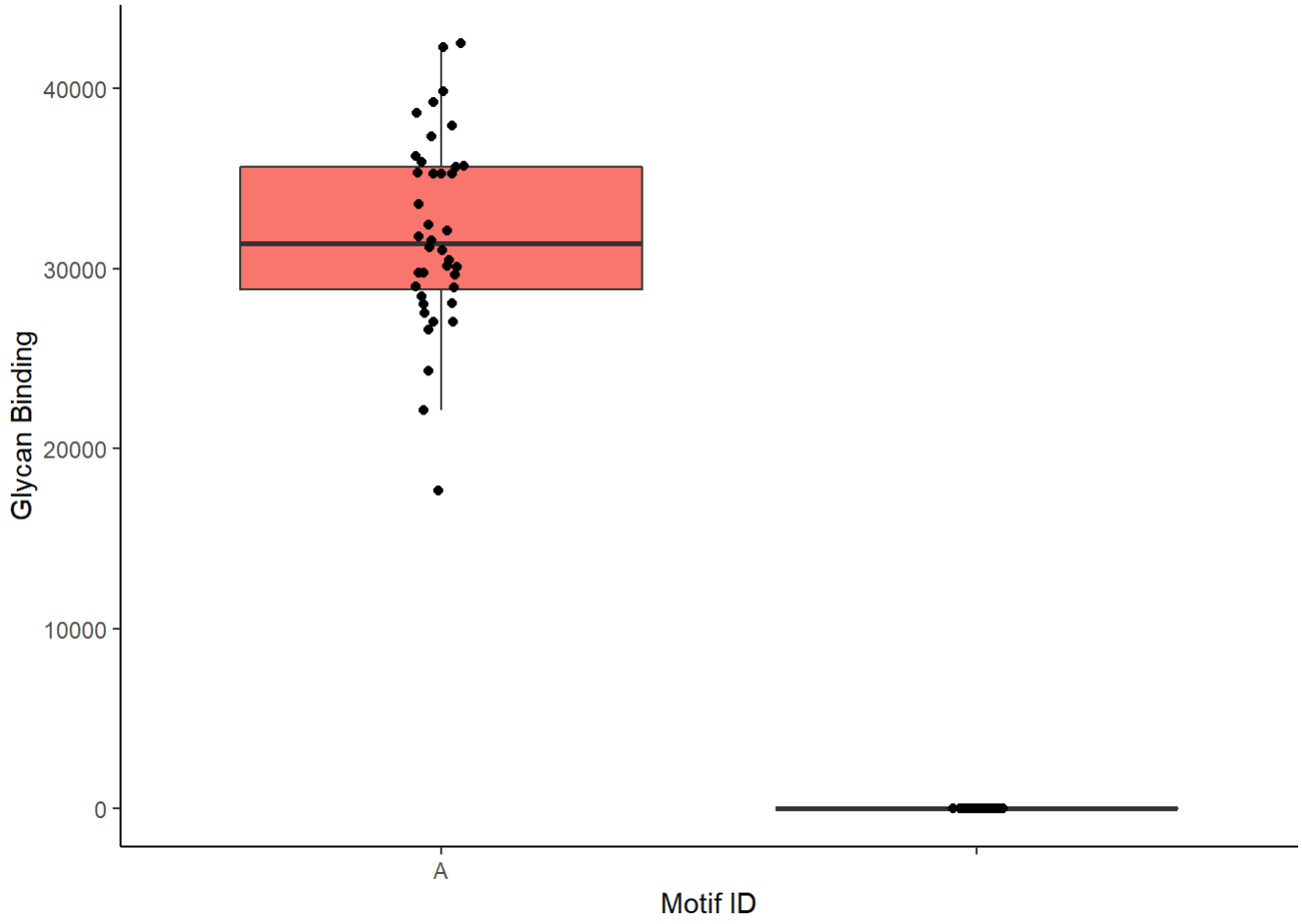
Automated Analysis report for AAL evaluated at 10 ug/mL

List of Primary AAL Motifs

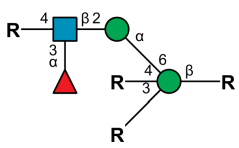
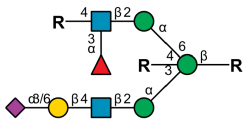
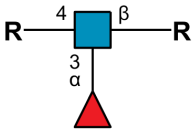
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1	40
0			0	32

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

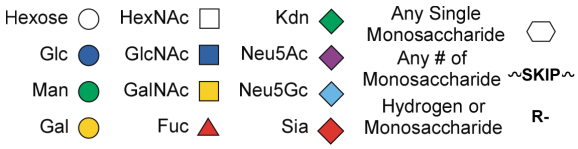
Boxplot of Primary Motifs



List of Fine-Specificity AAL Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A2*			1.00	16	<0.001
A1			0.81	8	<0.001
A0*			0.80	16	<0.001
0	Non-Binders (100%)		0.00	32	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

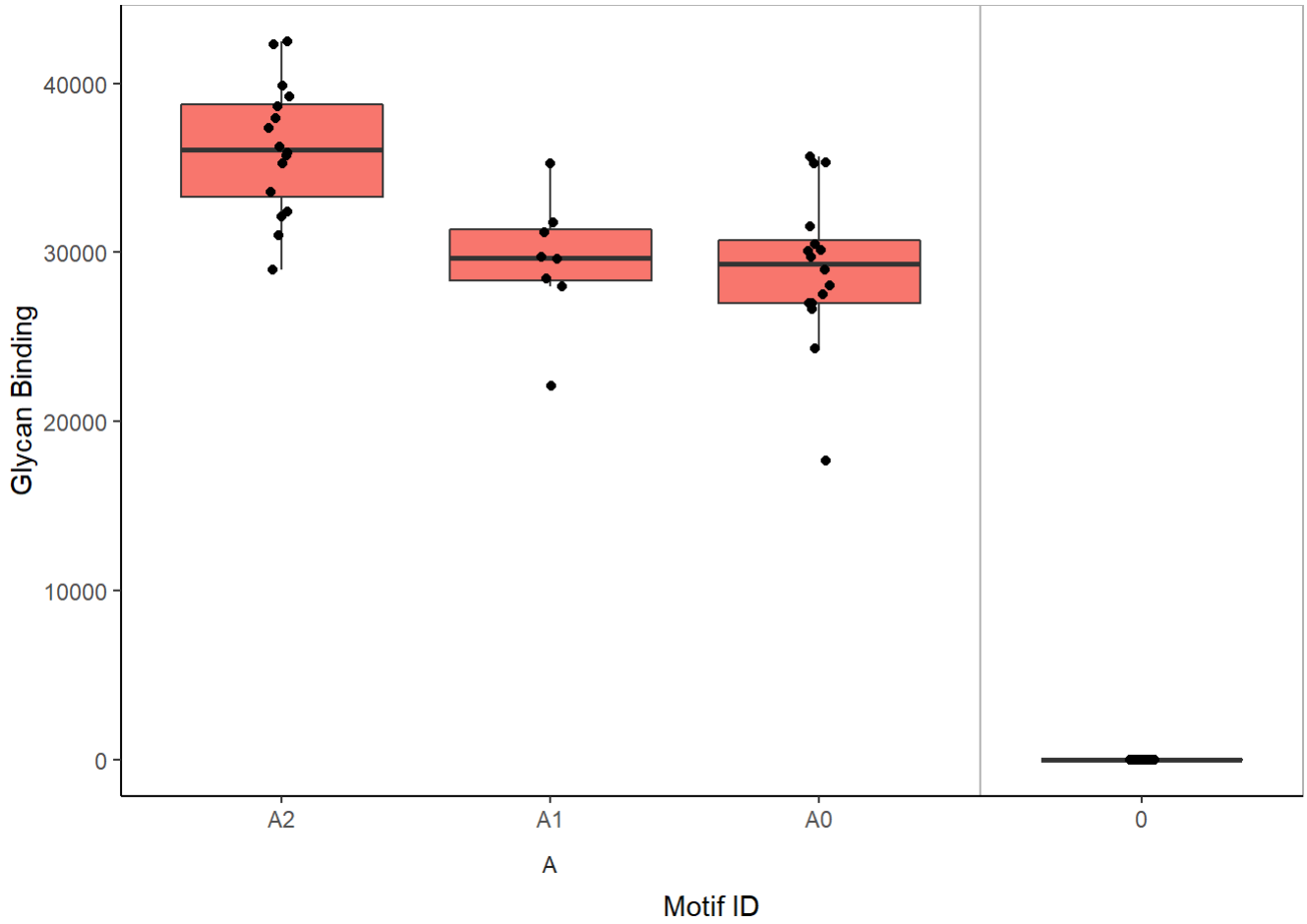


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

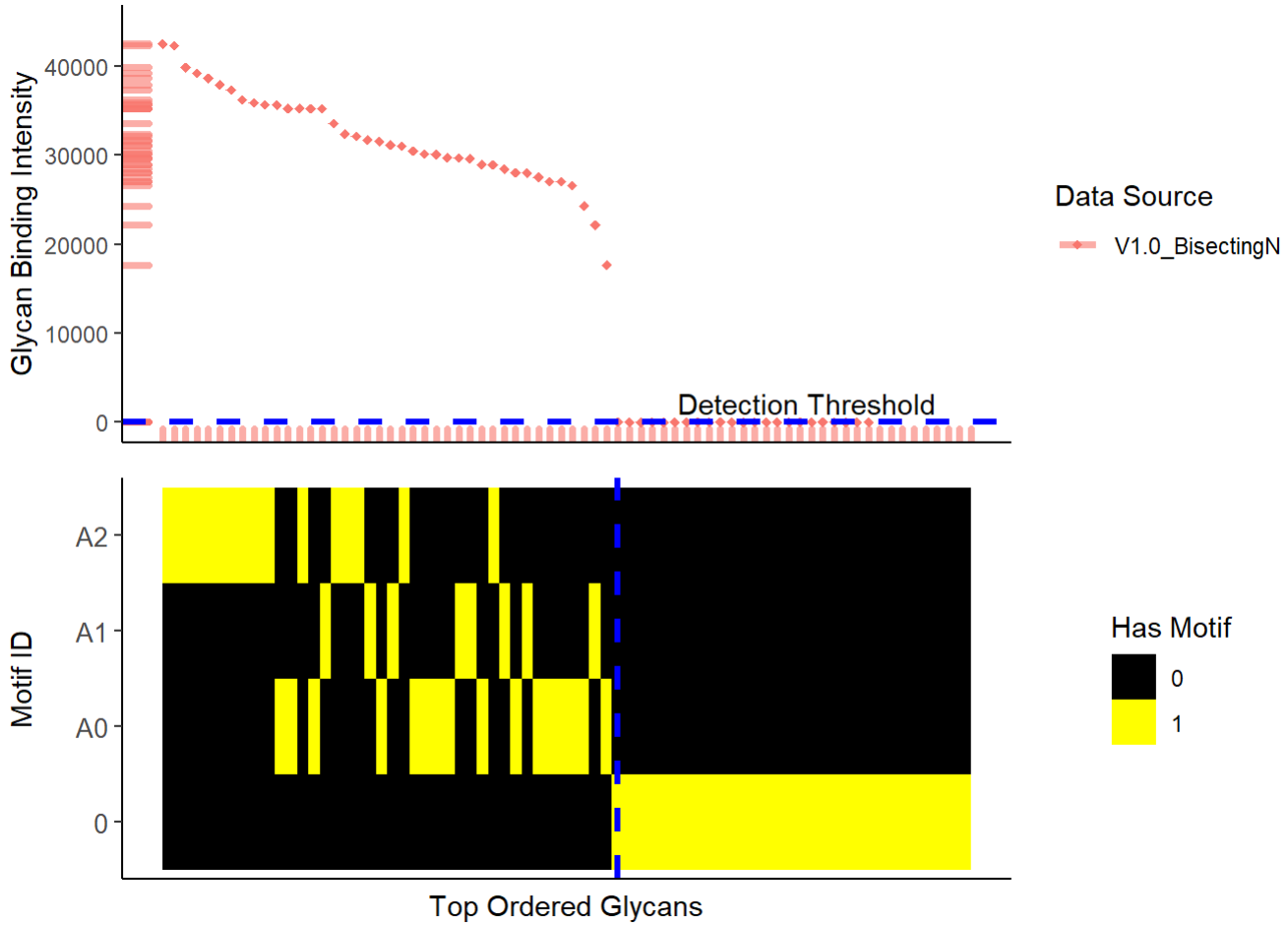
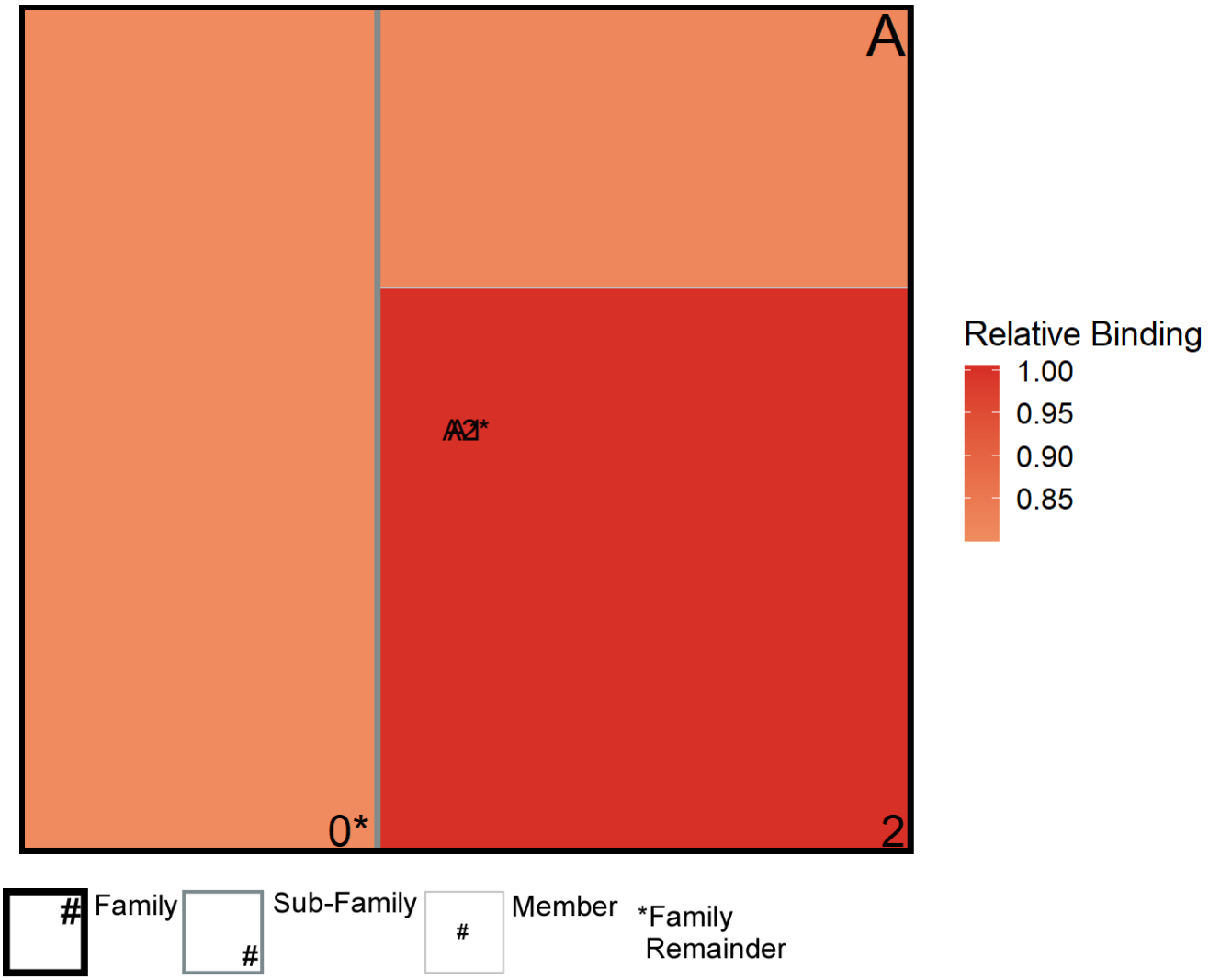


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

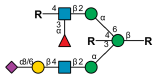
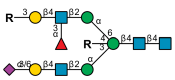
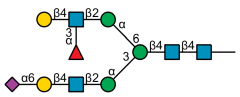
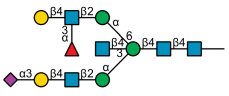
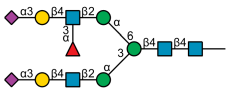


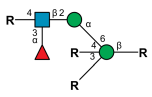
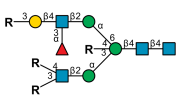
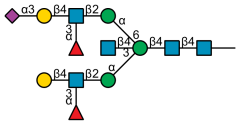
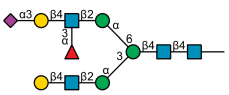
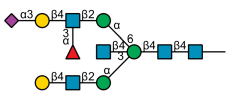
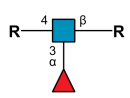
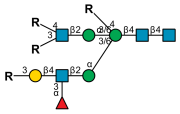
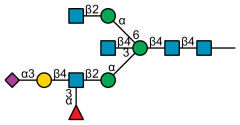
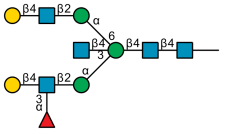
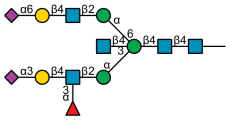
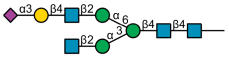
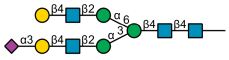
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

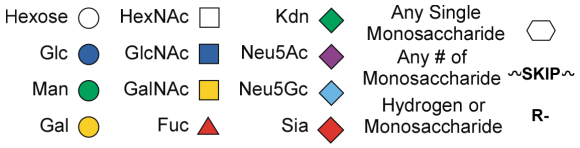
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				70		32		69

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A2				36		66		30
A0				11		14		20
0				49		59		48

Key:



All Concentration Plots:

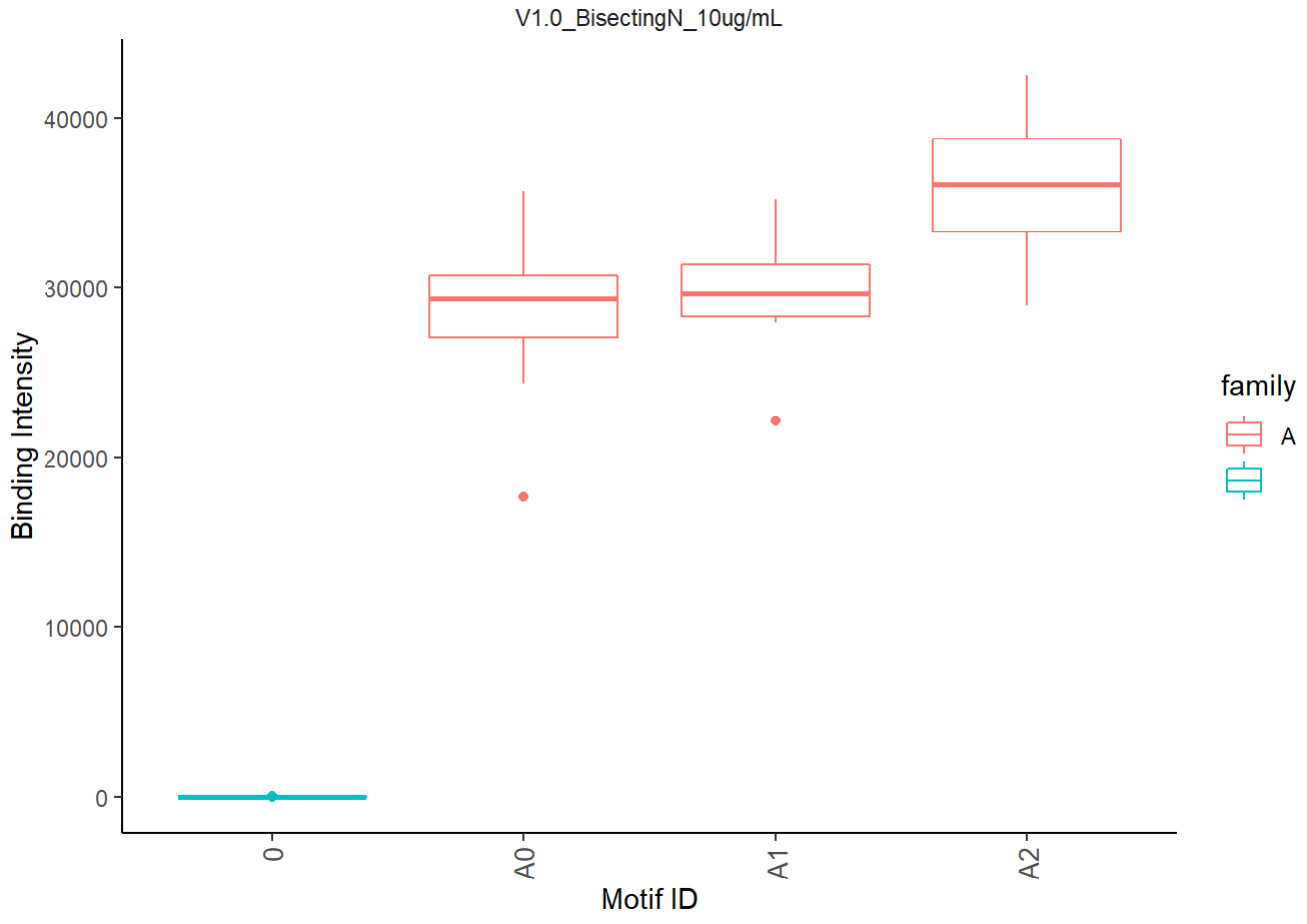
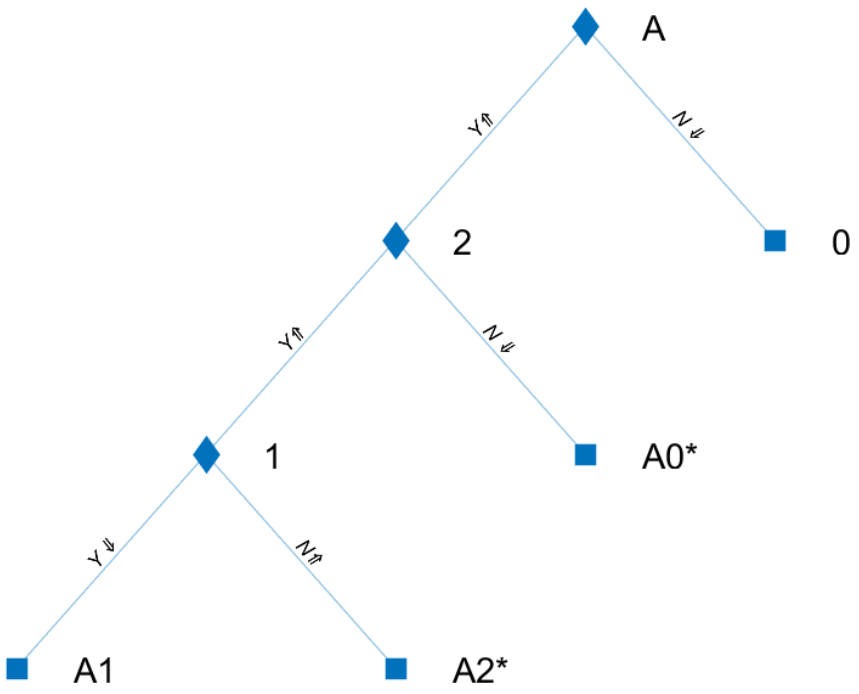


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



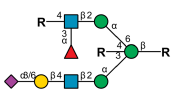
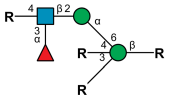
*Motif matches the remaining glycans not matched by earlier motifs in the model.

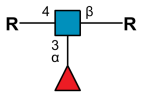
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

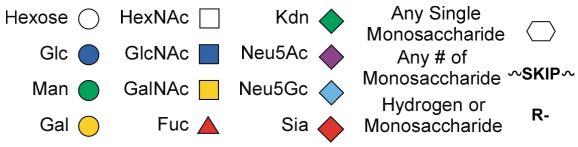
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f3f4f>FucA1-3<6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f>ManB
A2*		<2f3f4f>FucA1-3<6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB

Motif ID	Motif Graphic	Motif Text
A0*		<2f3f4f>FucA1-3<6f>GlcNAcB
0		Non-Binders

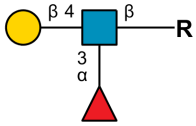
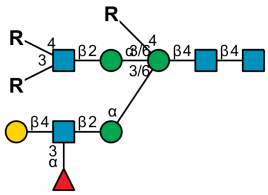
Key:



LTA (LTL)

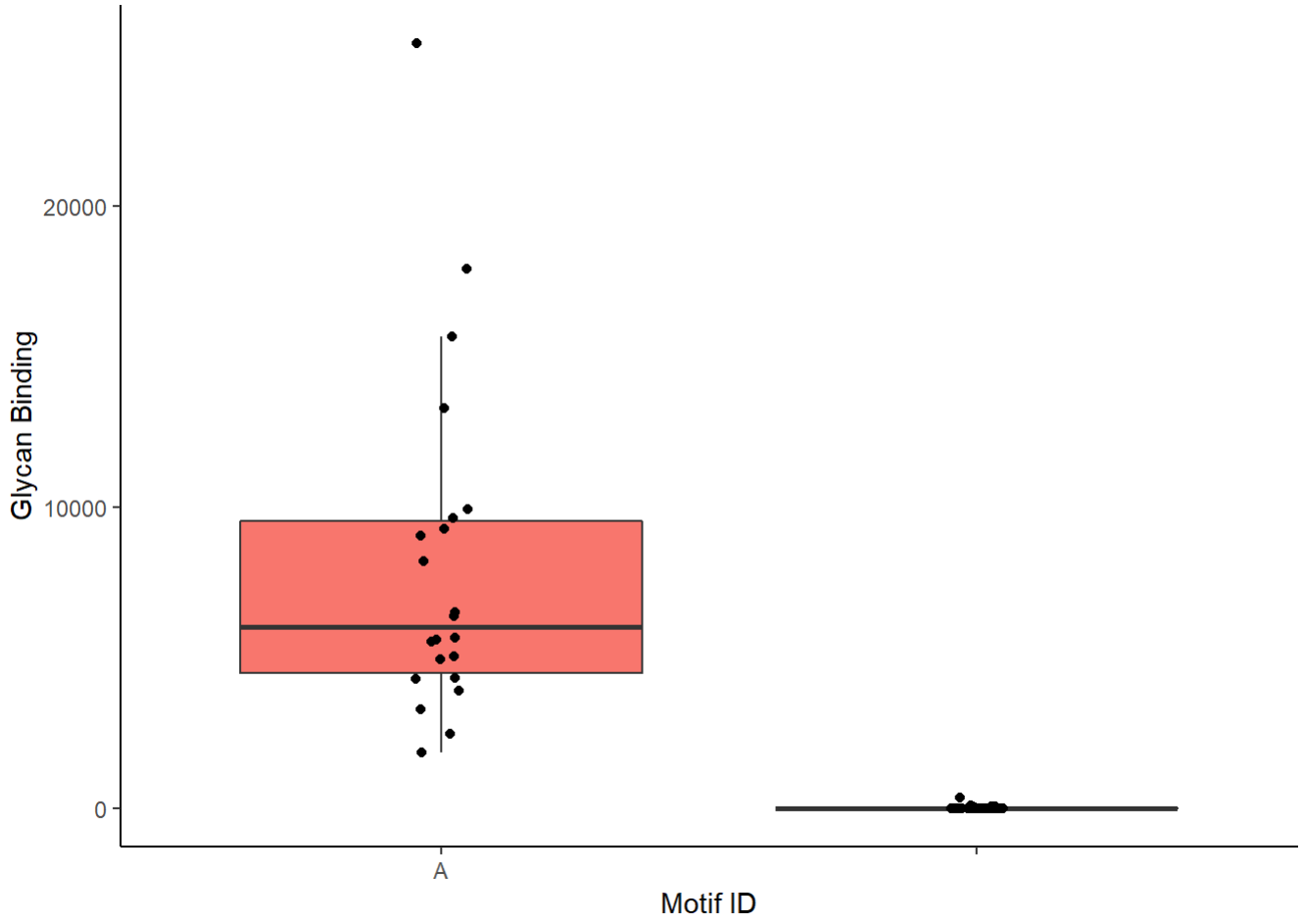
Automated Analysis report for LTA evaluated at 10 ug/mL

List of Primary LTA Motifs

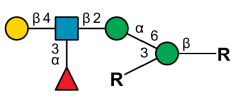
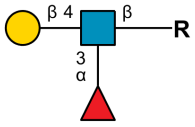
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1	22
0			0	50

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

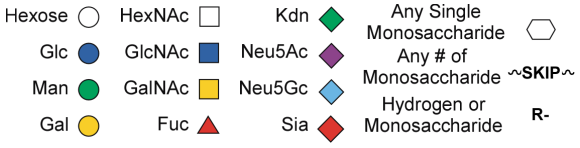
Boxplot of Primary Motifs



List of Fine-Specificity LTA Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A1			1.00	6	<0.001
A0*	Terminal Lewis X (92%)		0.68	16	<0.001
0	Non-Binders (100%)		0.00	50	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

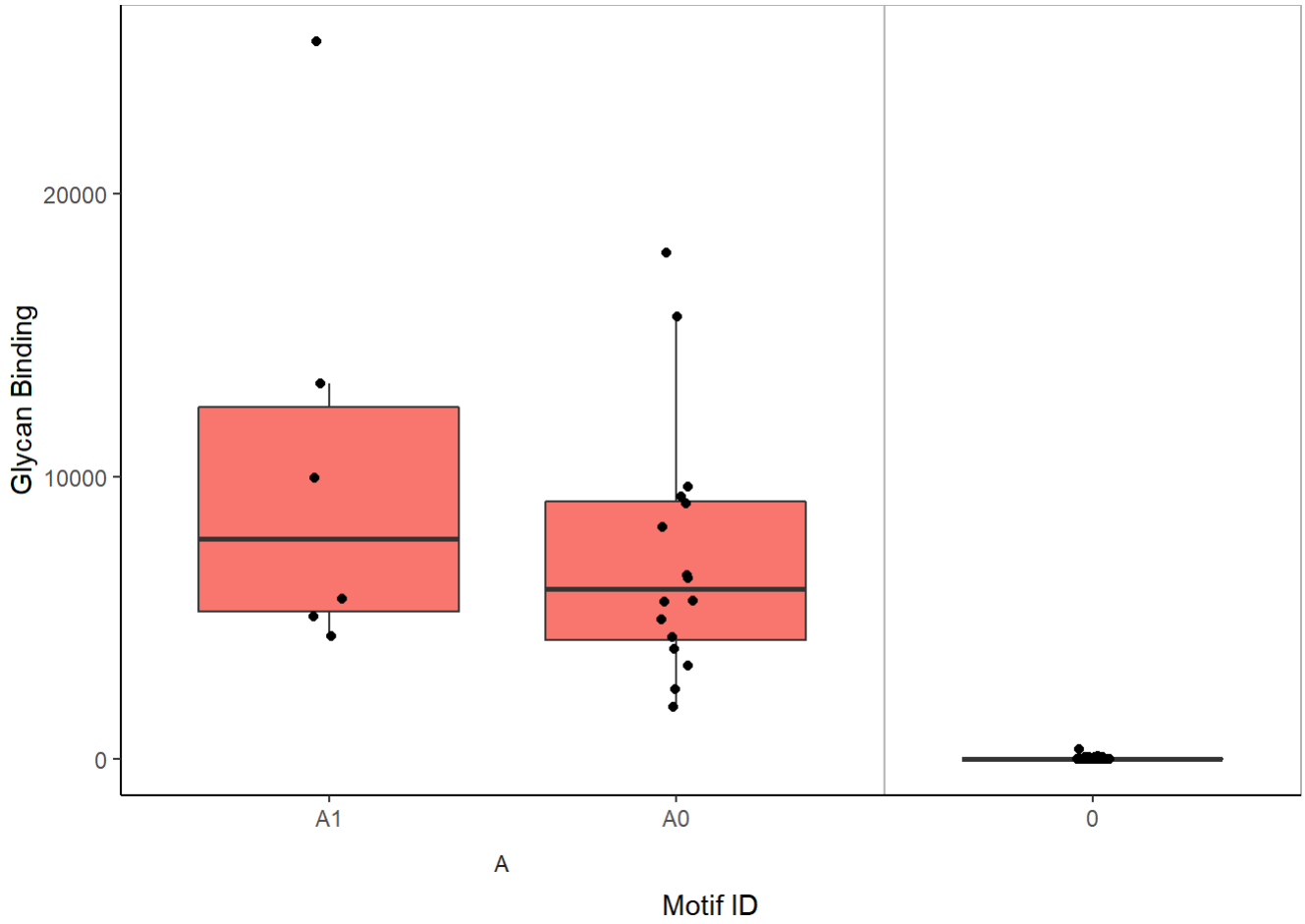


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

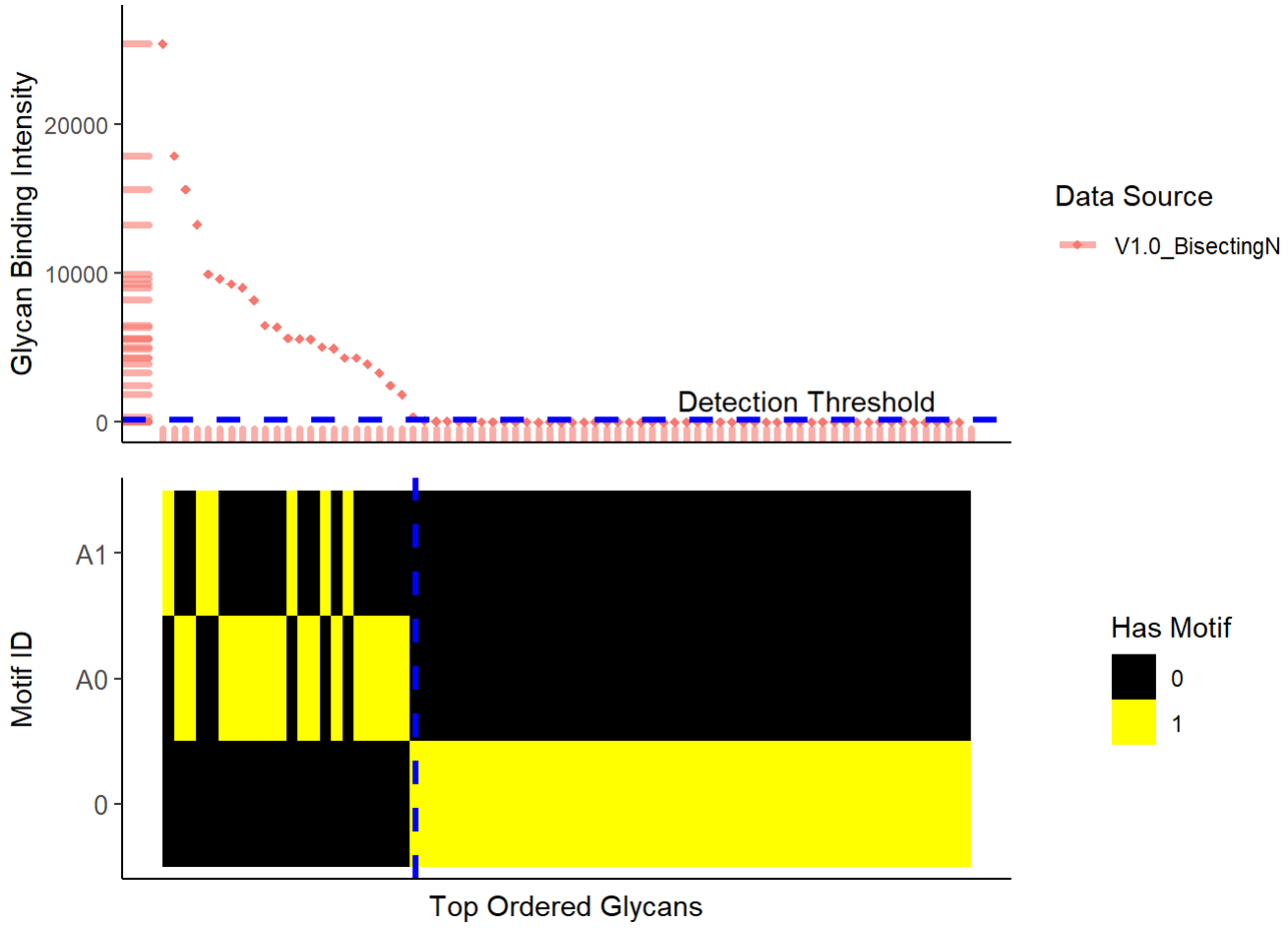
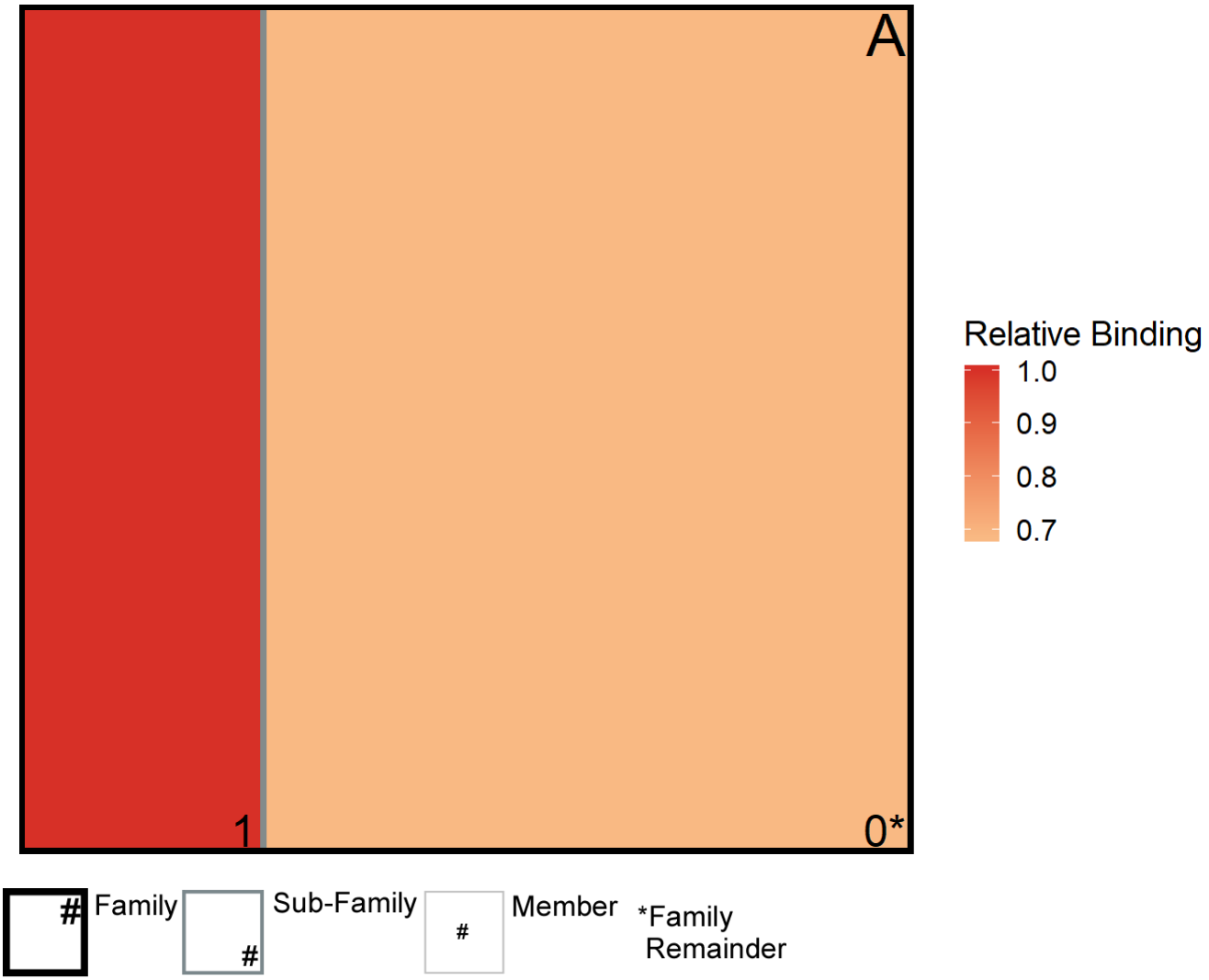


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

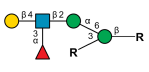
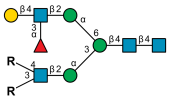
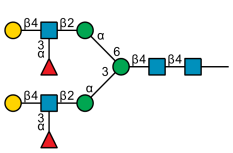
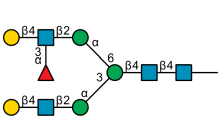
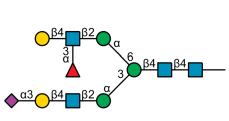


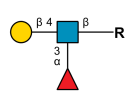
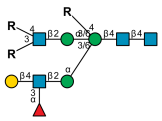
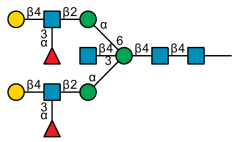
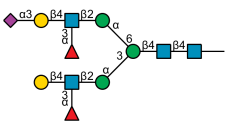
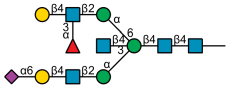
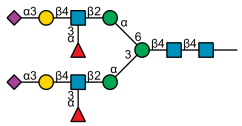
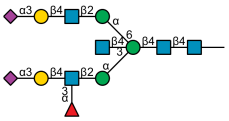
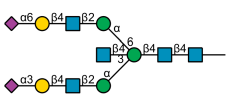
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

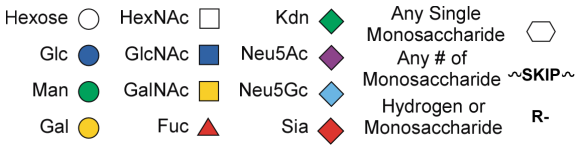
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				41		65		68

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				5		72		34
0				42		18		31

Key:



All Concentration Plots:

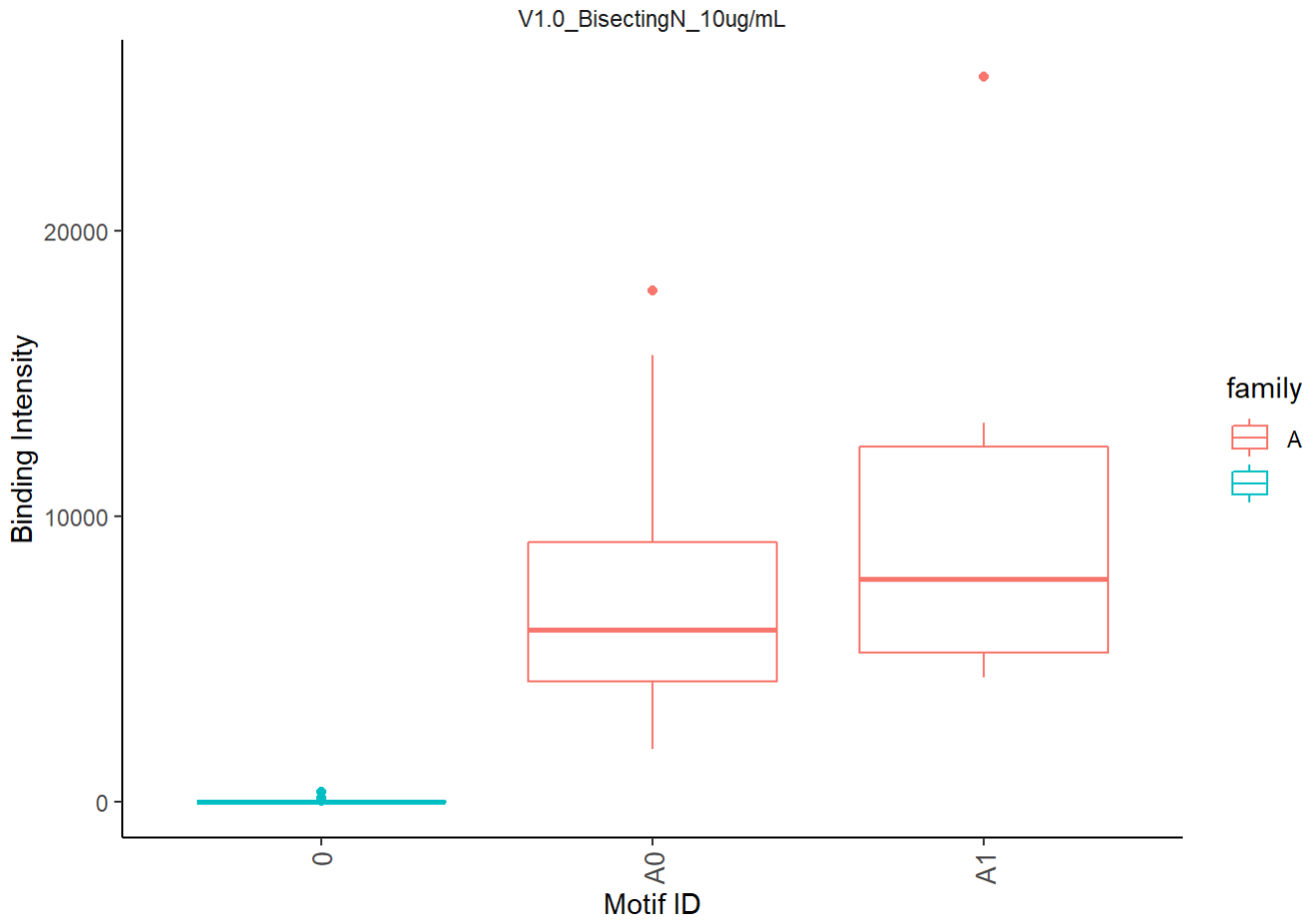
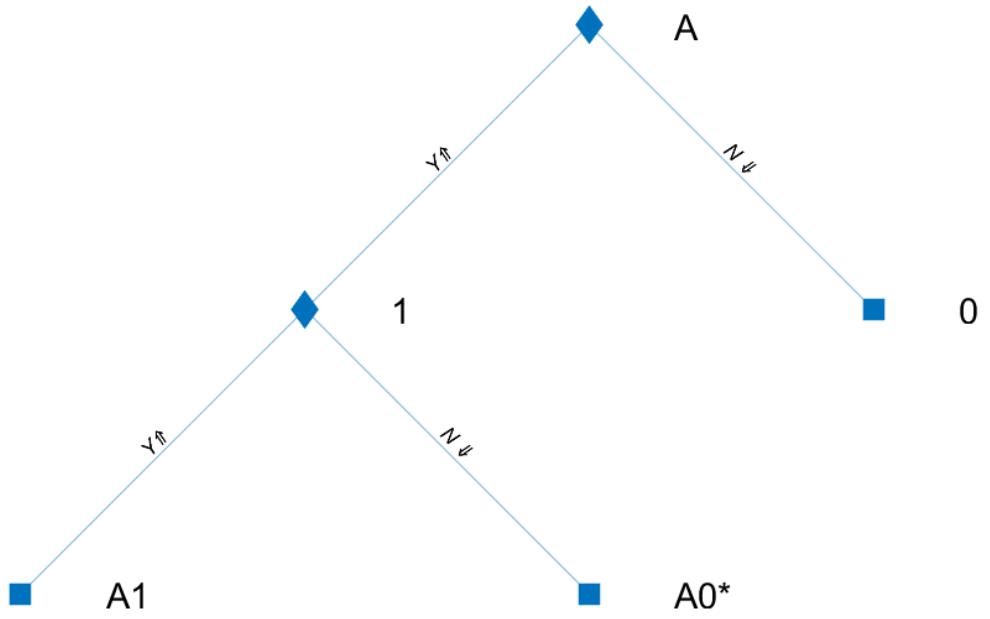


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



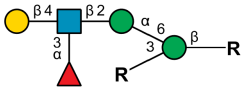
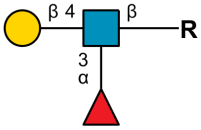
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

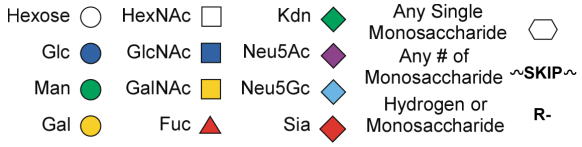
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<2f3f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f4f>ManB
A0*		<2f3f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB
0		Non-Binders

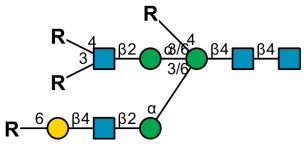
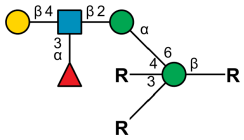
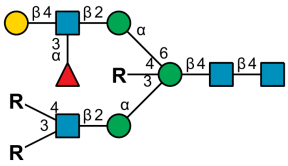
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

RCA-I

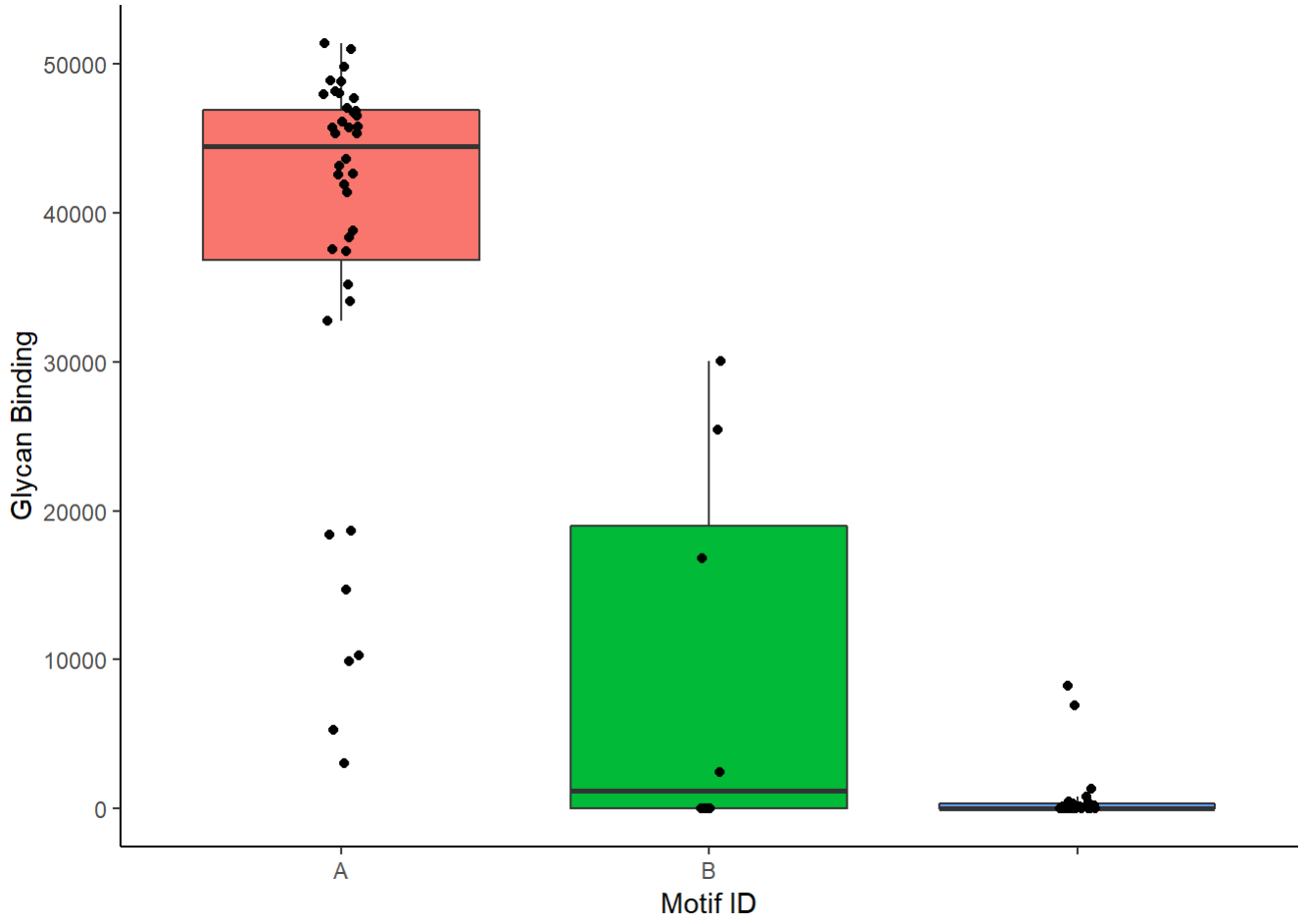
Automated Analysis report for RCA-I evaluated at 2 ug/mL

List of Primary RCA-I Motifs

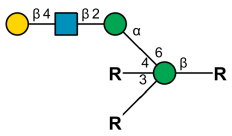
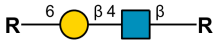
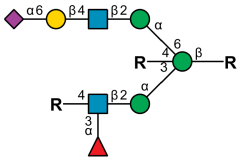
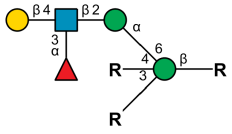
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	40
B			0.29	8
0			0.03	24

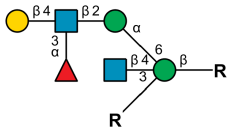
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

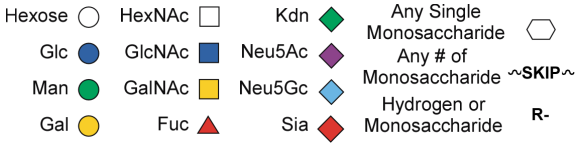


List of Fine-Specificity RCA-I Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A1			1.00	12	<0.001
A0*			0.87	24	<0.001
A2	a6 Sialyl Type 2 LacNAc Terminal Lewis X (94%)		0.28	4	0.035
B0*			0.41	4	0.001

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
B1	Terminal Lewis X Bisecting N-Glycan (90%)		-0.02	4	1.000
0	Non-Binders (100%)		0.00	24	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

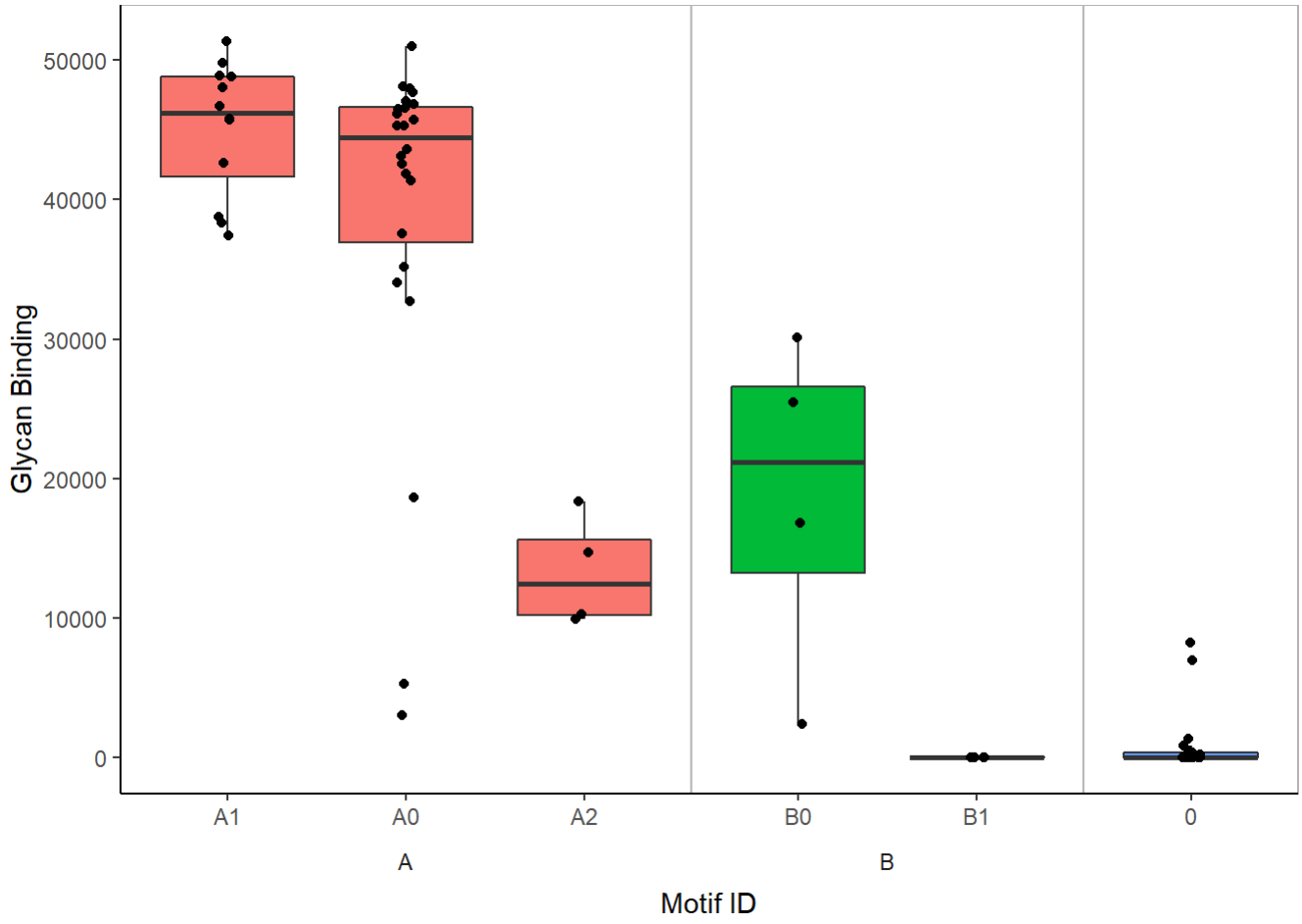


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

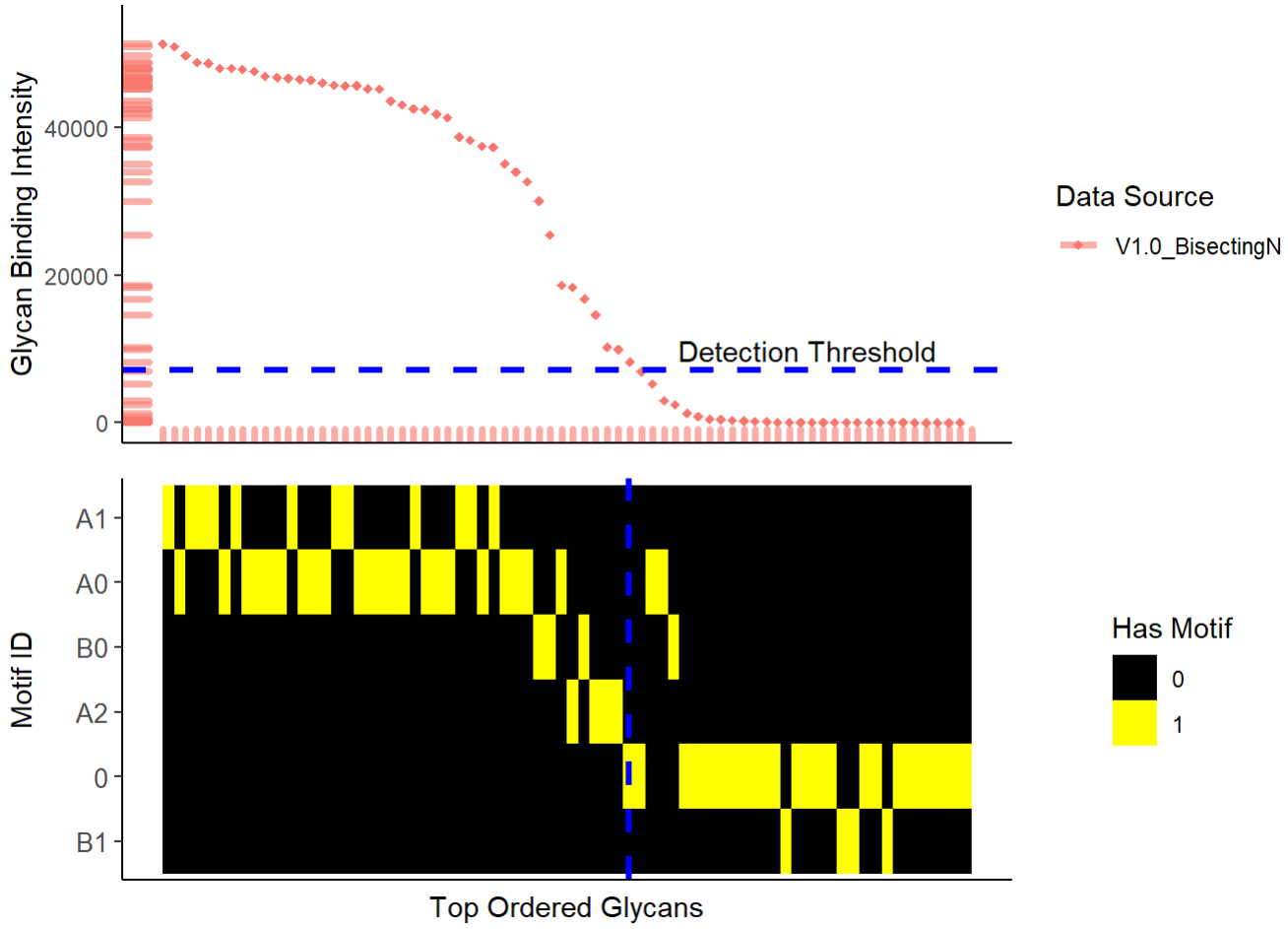
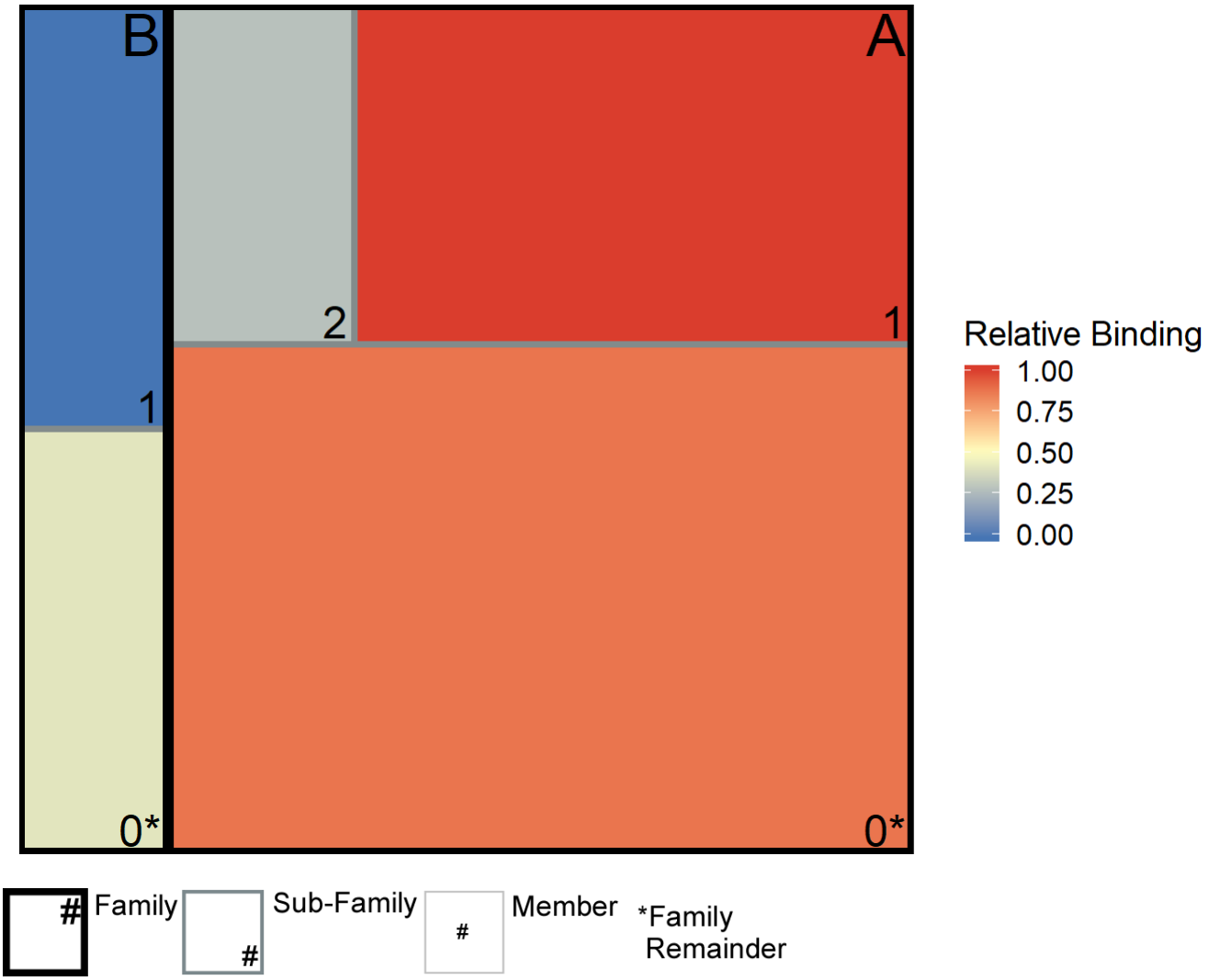


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

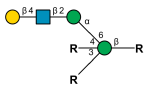
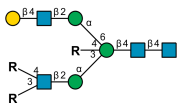
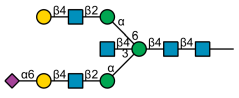
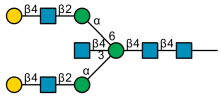
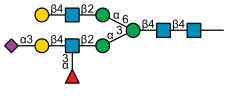


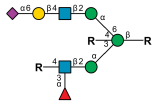
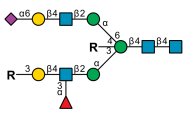
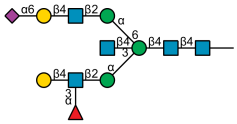
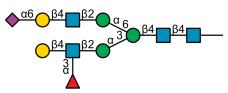
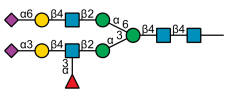
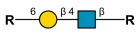
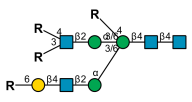
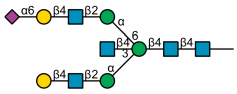
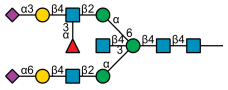
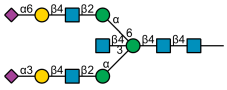
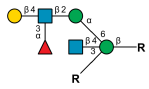
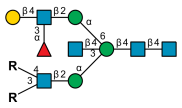
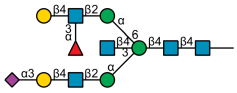
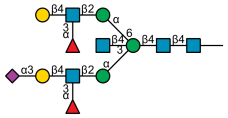
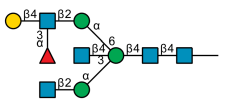
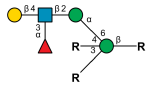
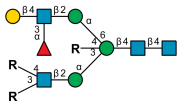
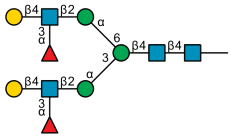
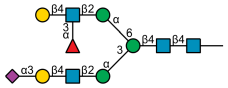
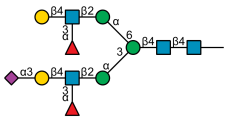
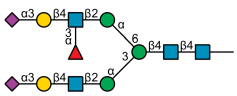
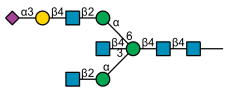
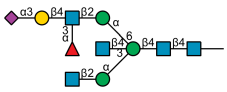
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

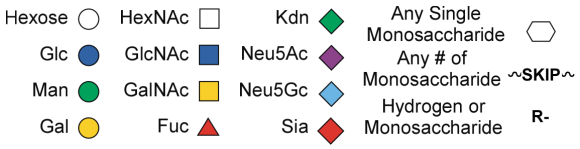
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				13		2		51

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A2				19		55		56
A0				28		35		31
B1				32		21		25
B0				41		68		57
0				69		23		26

Key:



All Concentration Plots:

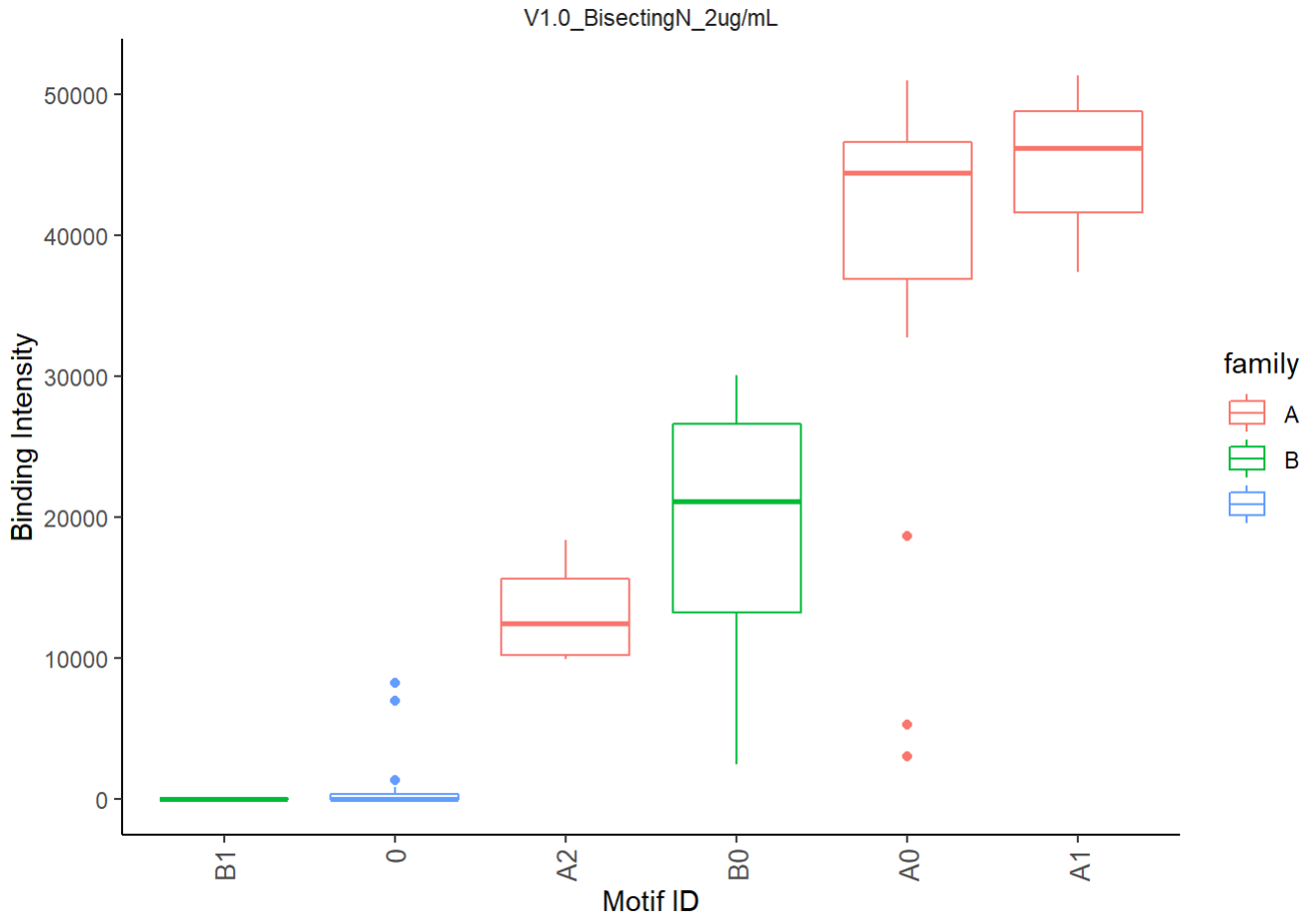
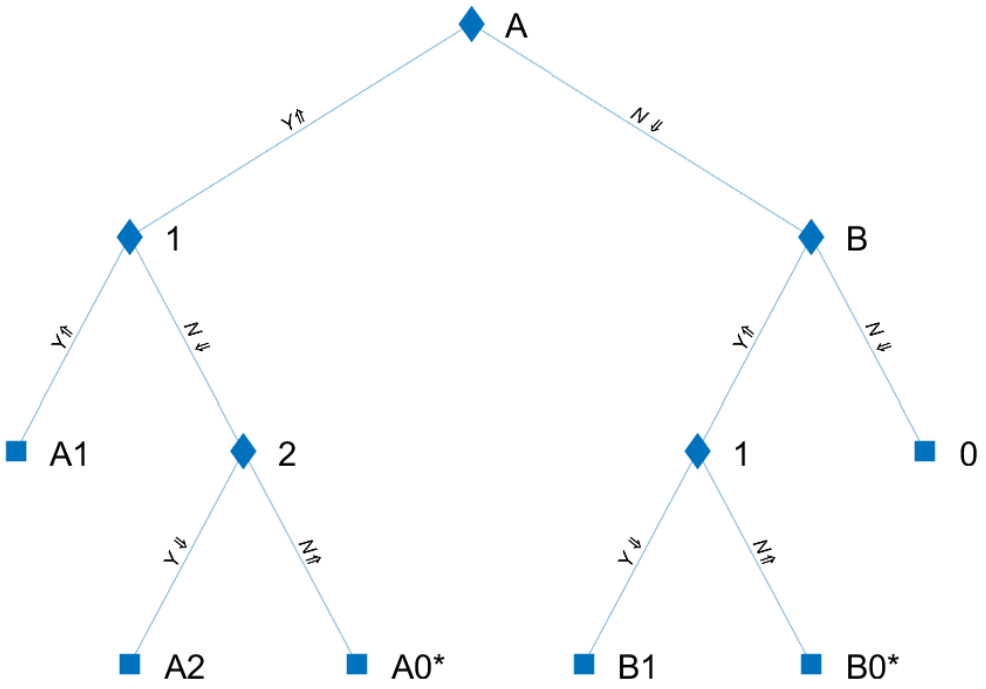


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



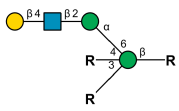
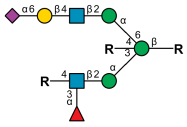
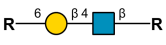
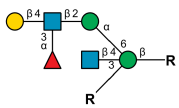
*Motif matches the remaining glycans not matched by earlier motifs in the model.

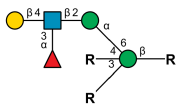
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

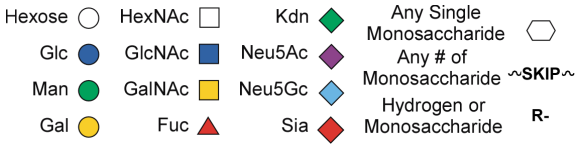
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
A2		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f3f4f>FucA1-3<6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f>ManB
A0*		<2f3f4f>GalB1-4<3f6f>GlcNAcB
B1		<2f3f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f4f6f>GlcNAcB1-4)<2f>ManB

Motif ID	Motif Graphic	Motif Text
B0*		<2f3f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
0		Non-Binders

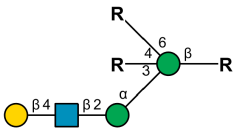
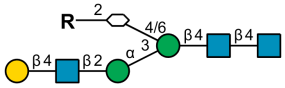
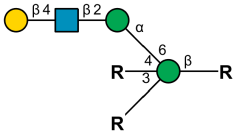
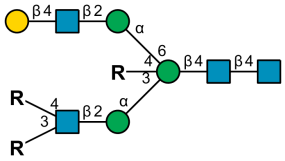
Key:



ECL

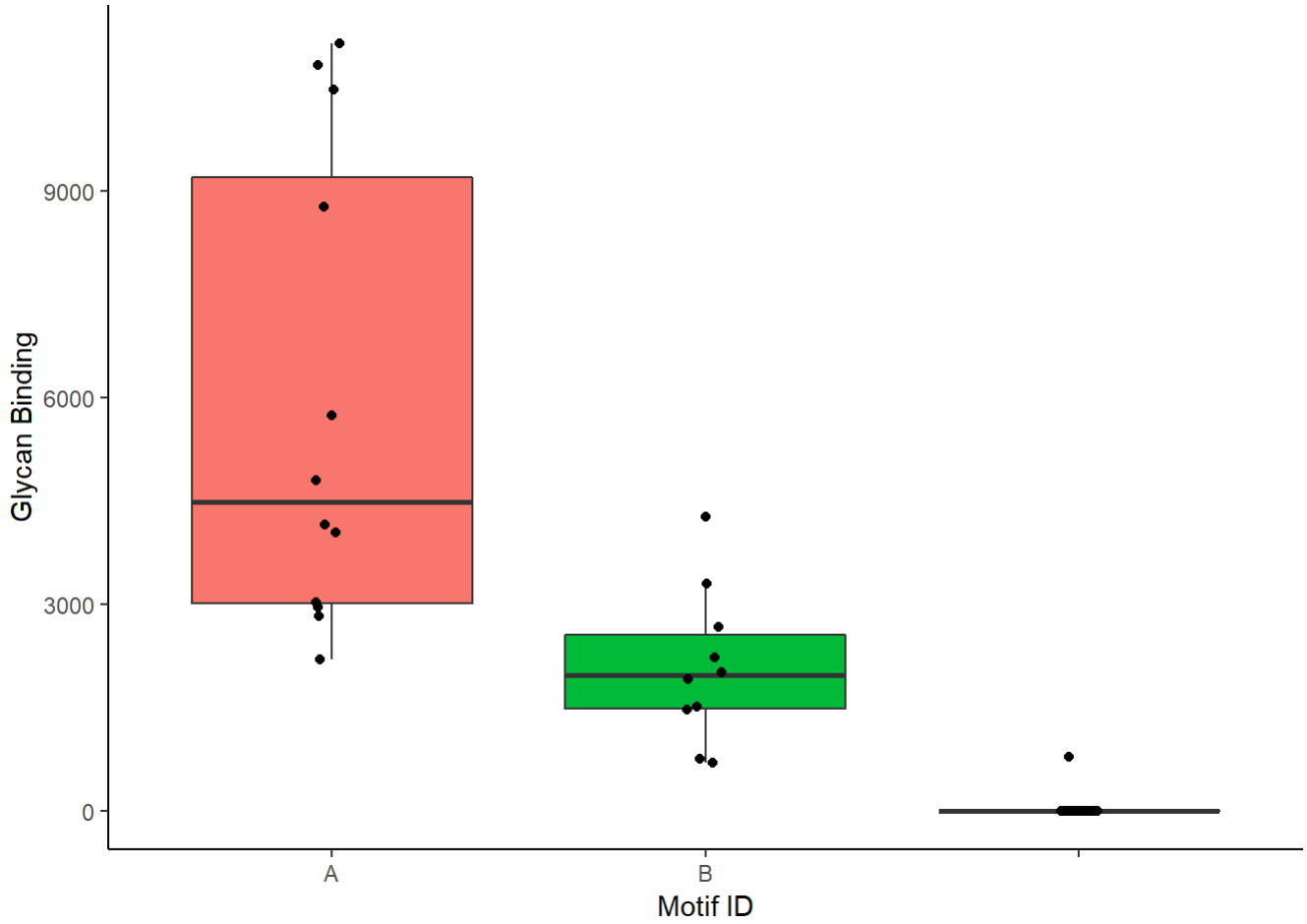
Automated Analysis report for ECL evaluated at 10 ug/mL

List of Primary ECL Motifs

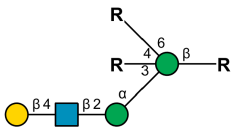
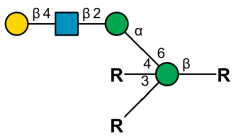
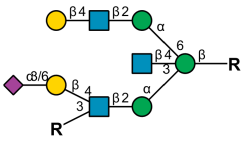
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	12
B			0.34	10
0			0.00	50

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

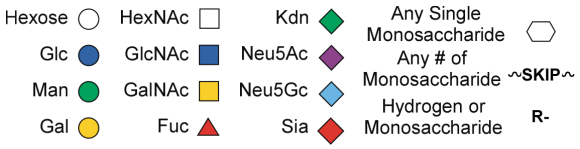
Boxplot of Primary Motifs



List of Fine-Specificity ECL Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0			1.00	12	<0.001
B0*			0.42	7	<0.001
B1	Terminal Type 2 LacNAc a3 Sialyl Galactose (90%)		0.16	3	0.579
0	Non-Binders (100%)		0.00	50	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

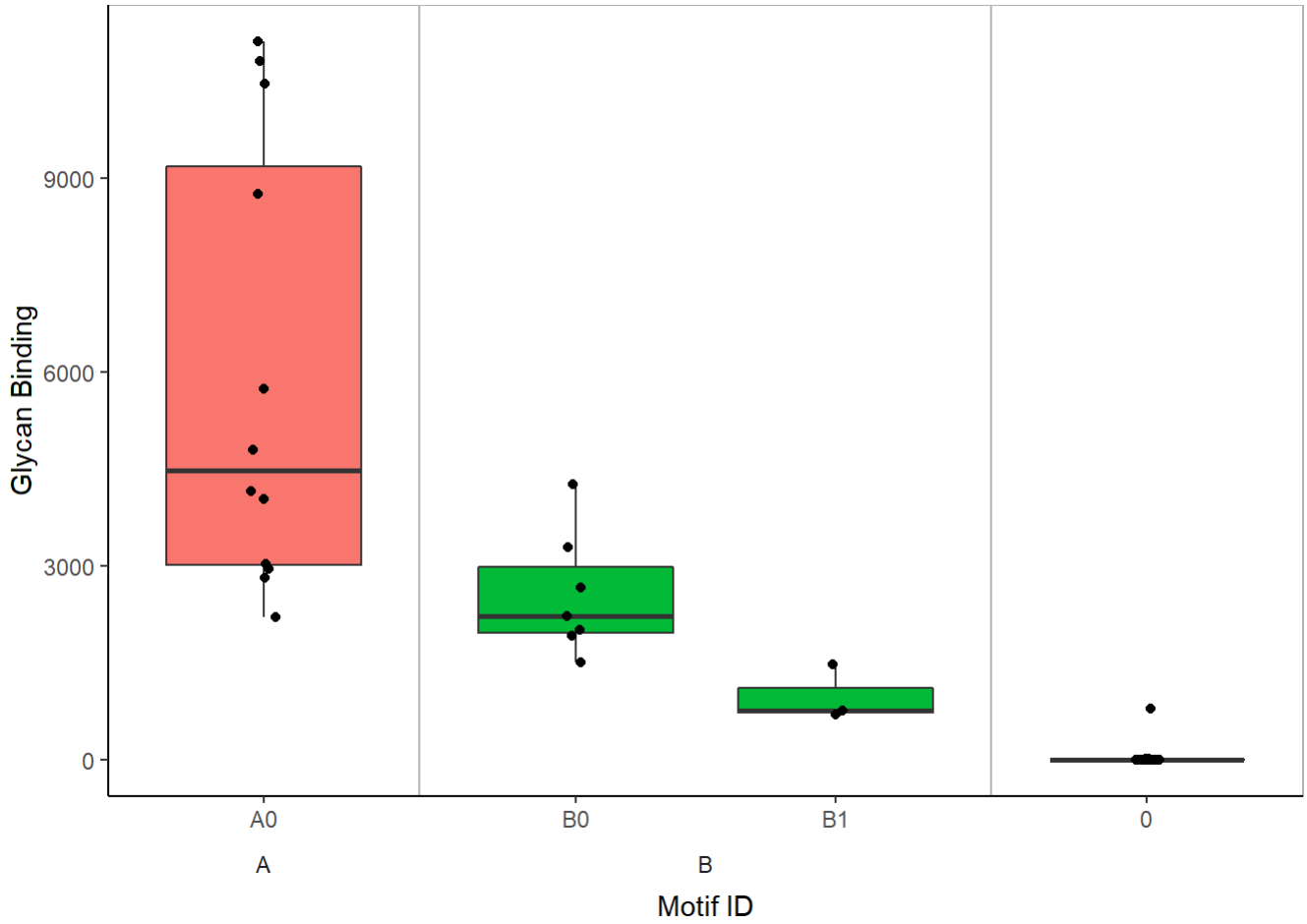


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

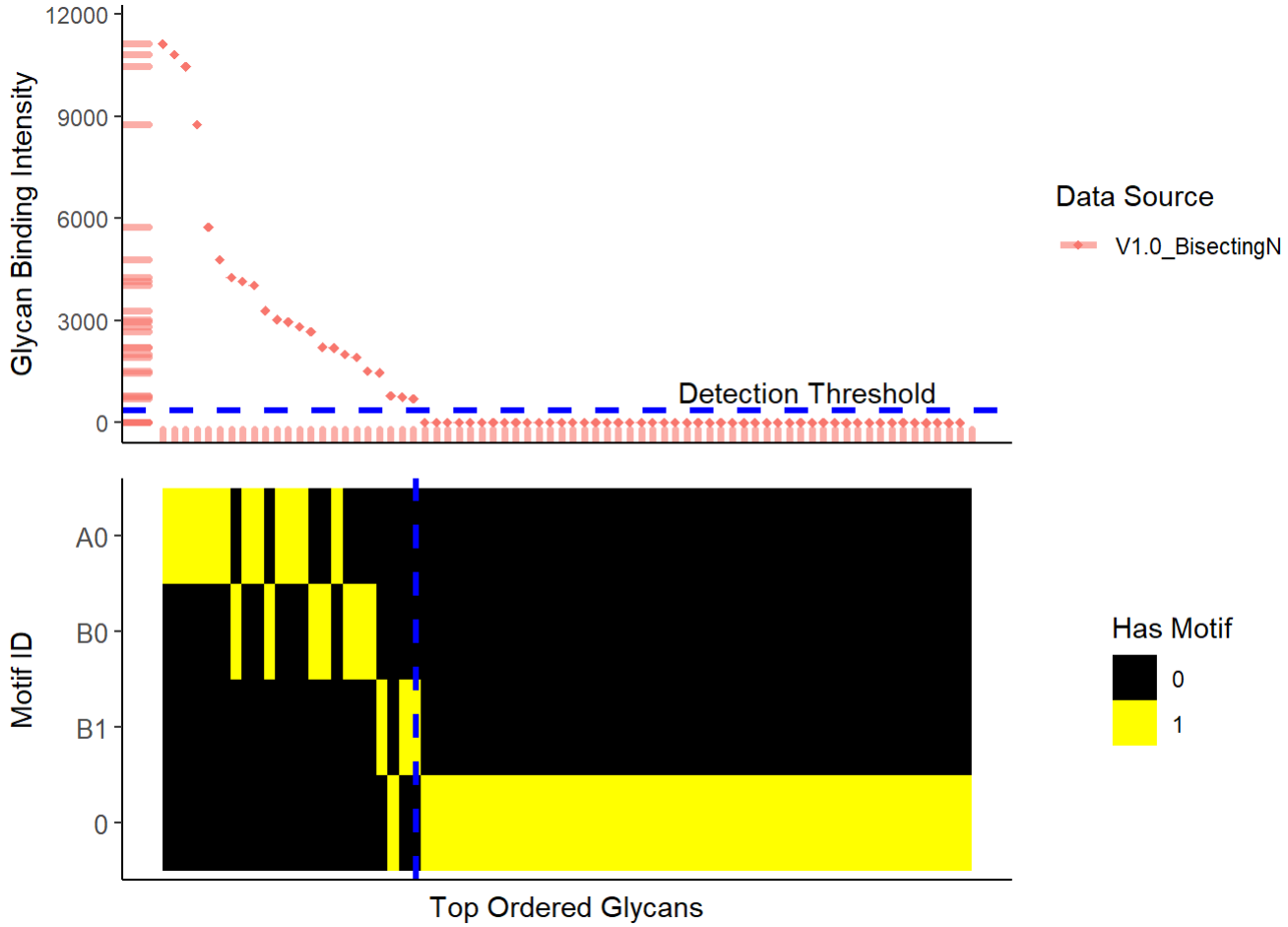
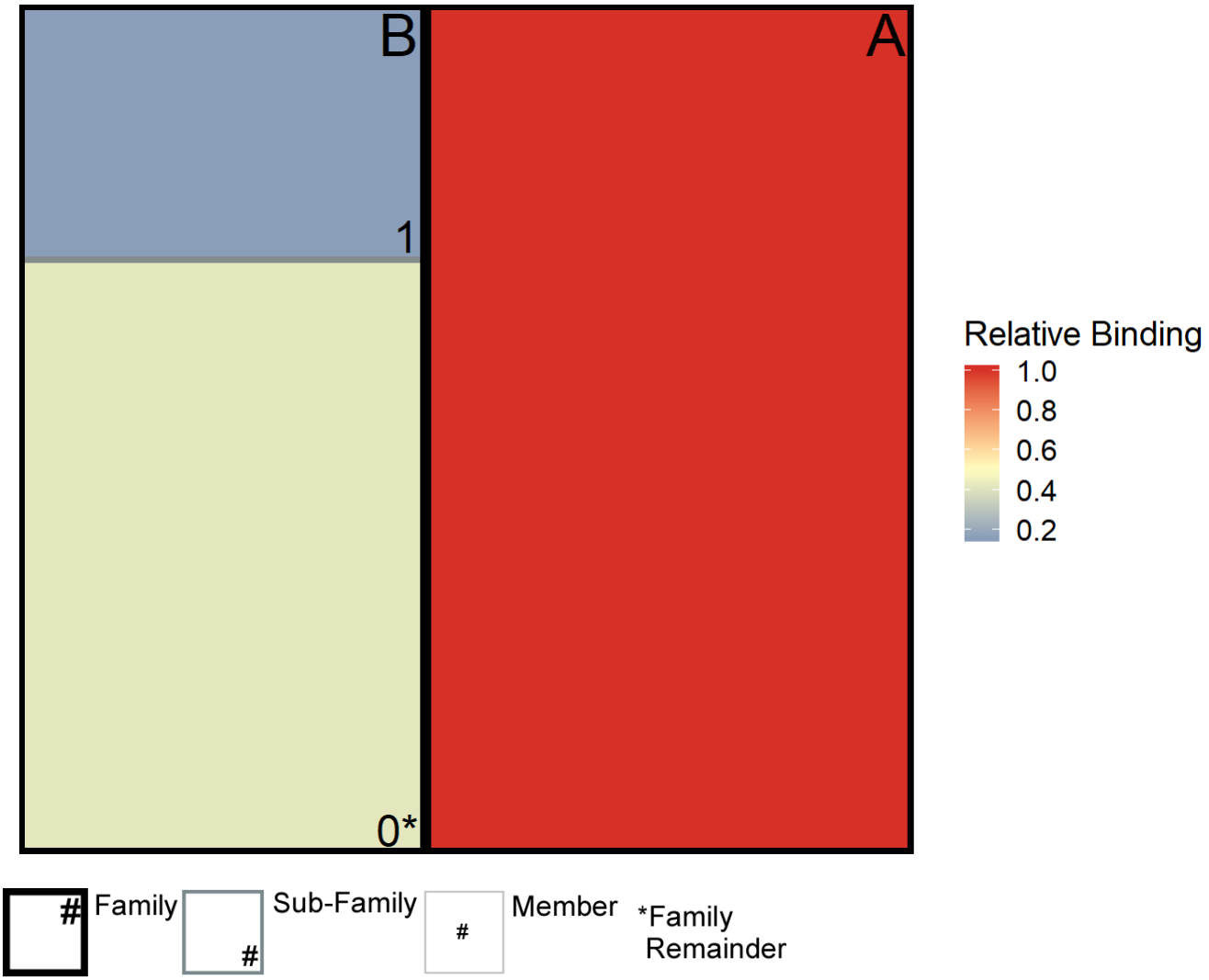


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

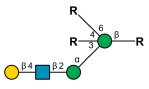
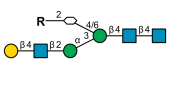
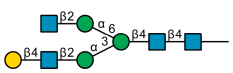
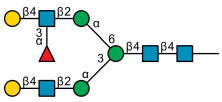
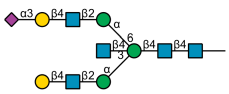


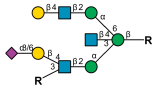
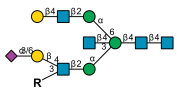
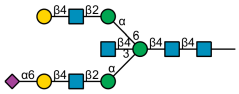
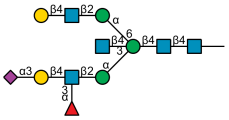
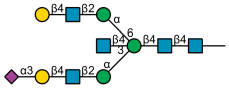
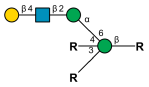
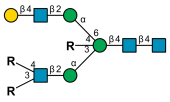
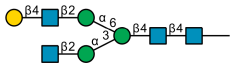
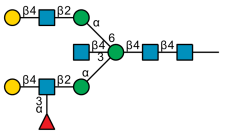
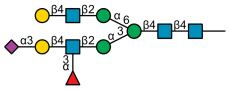
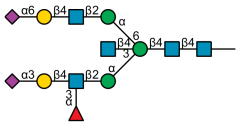
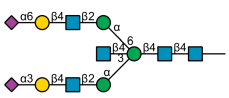
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

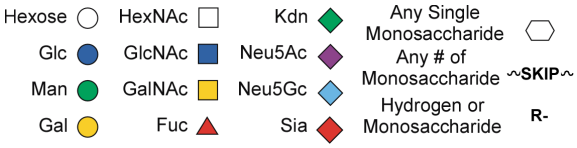
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				43		65		27

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
B1				13		15		12
B0				58		14		51
0				20		40		31

Key:



All Concentration Plots:

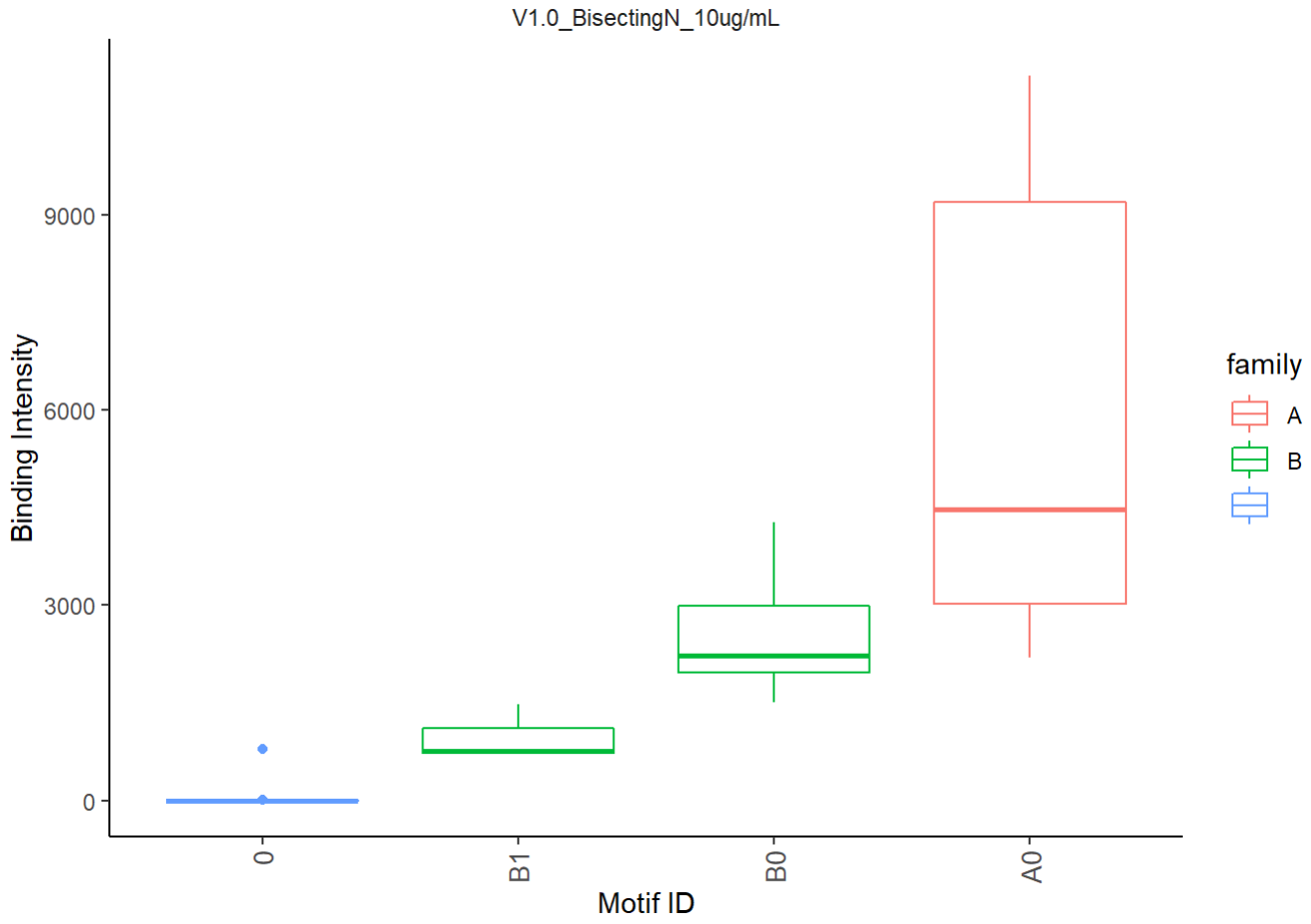
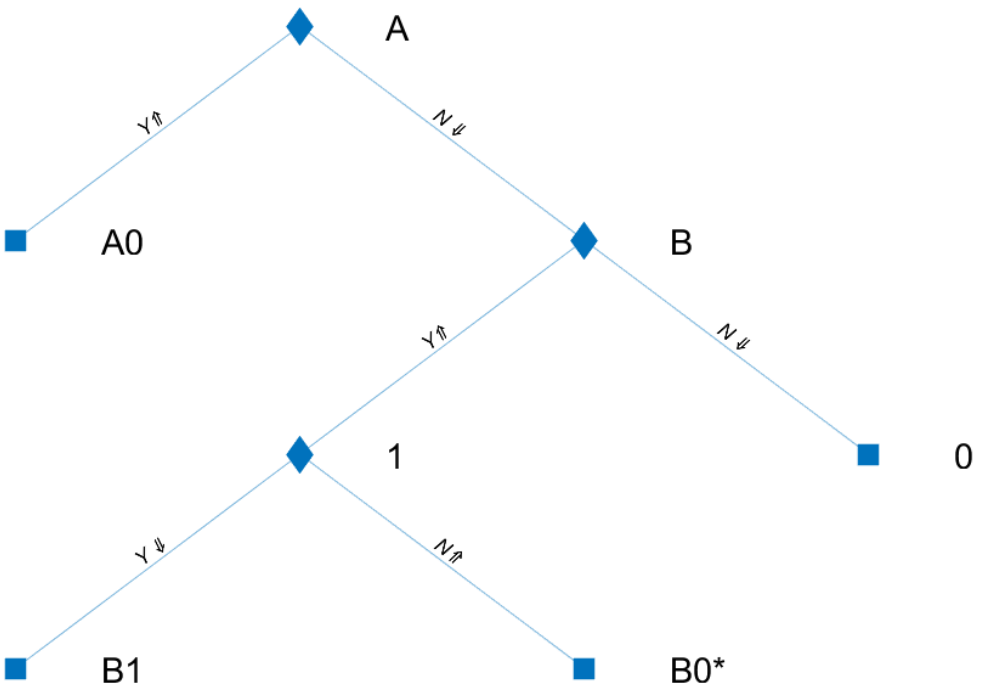


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



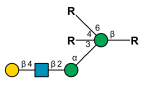
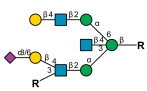
*Motif matches the remaining glycans not matched by earlier motifs in the model.

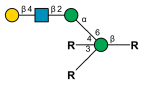
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

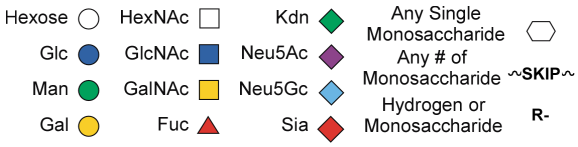
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
B1		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)(<3f4f6f>GlcNAcB1-4)<2f>ManB

Motif ID	Motif Graphic	Motif Text
B0*		<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
0		Non-Binders

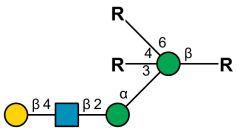
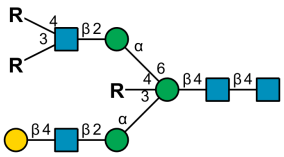
Key:



WFA (WFL)

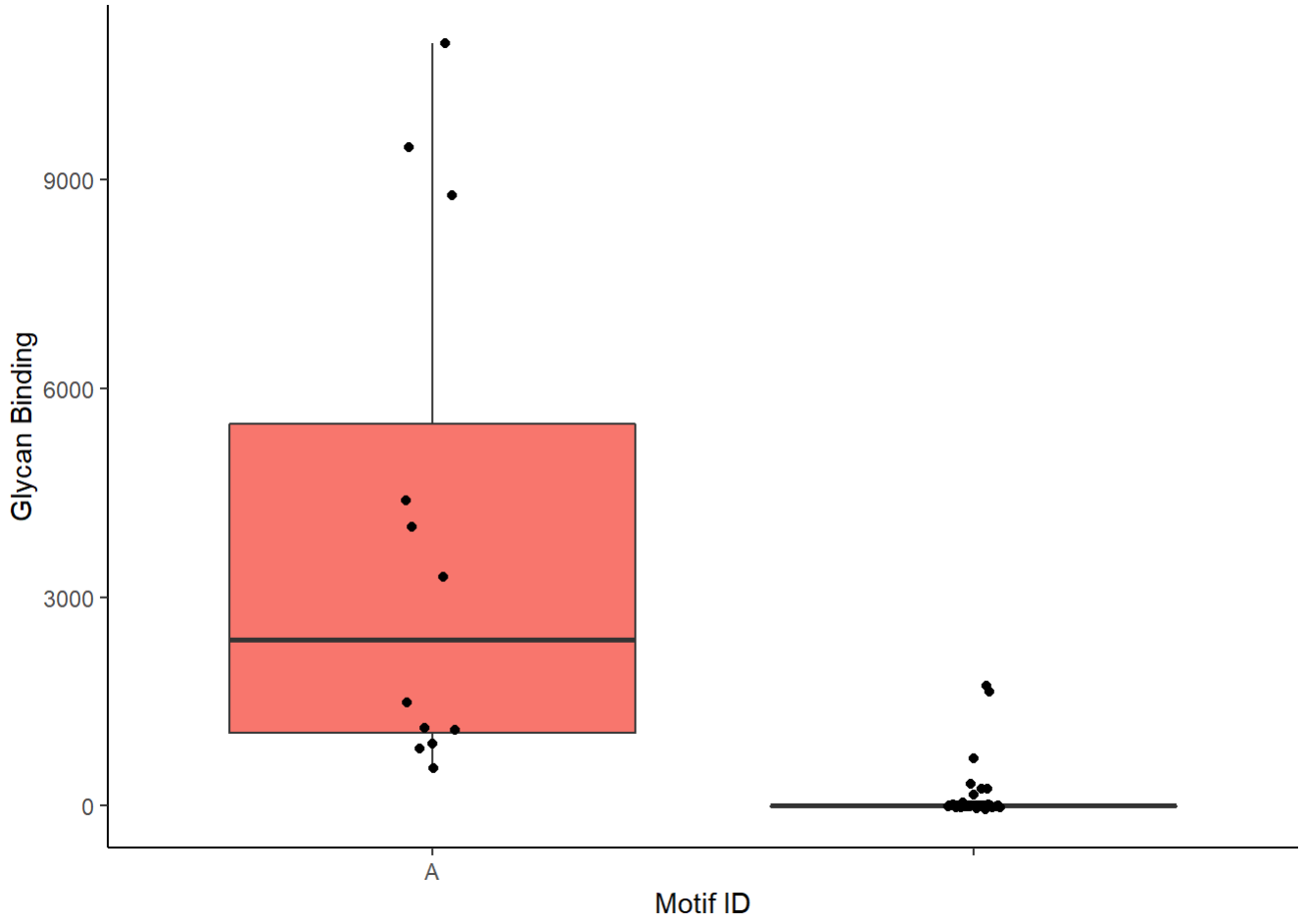
Automated Analysis report for WFA evaluated at 10 ug/mL

List of Primary WFA Motifs

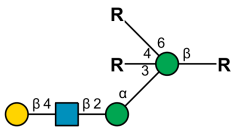
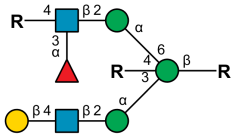
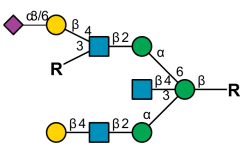
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	12
0			0.04	60

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

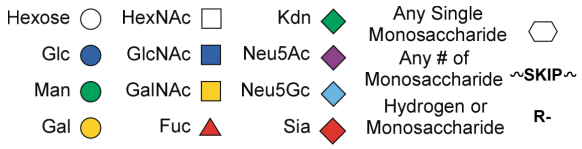
Boxplot of Primary Motifs



List of Fine-Specificity WFA Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*			1.00	6	<0.001
A2	Terminal Type 2 LacNAc Terminal Lewis X (96%)		0.48	3	0.001
A1	Terminal Type 2 LacNAc a3 Sialyl Galactose (90%)		0.11	3	0.736
0	Non-Binders (100%)		0.00	60	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

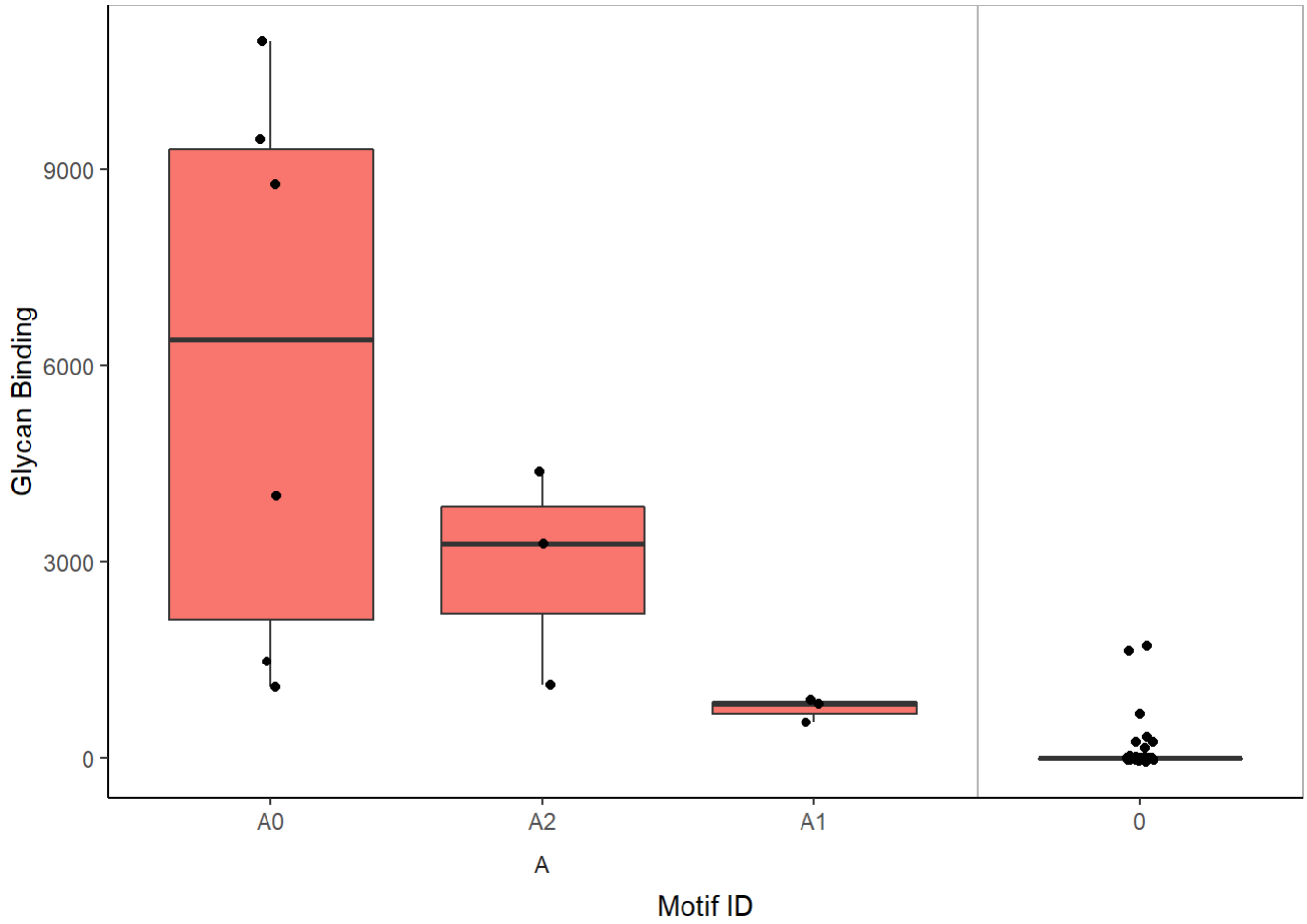


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

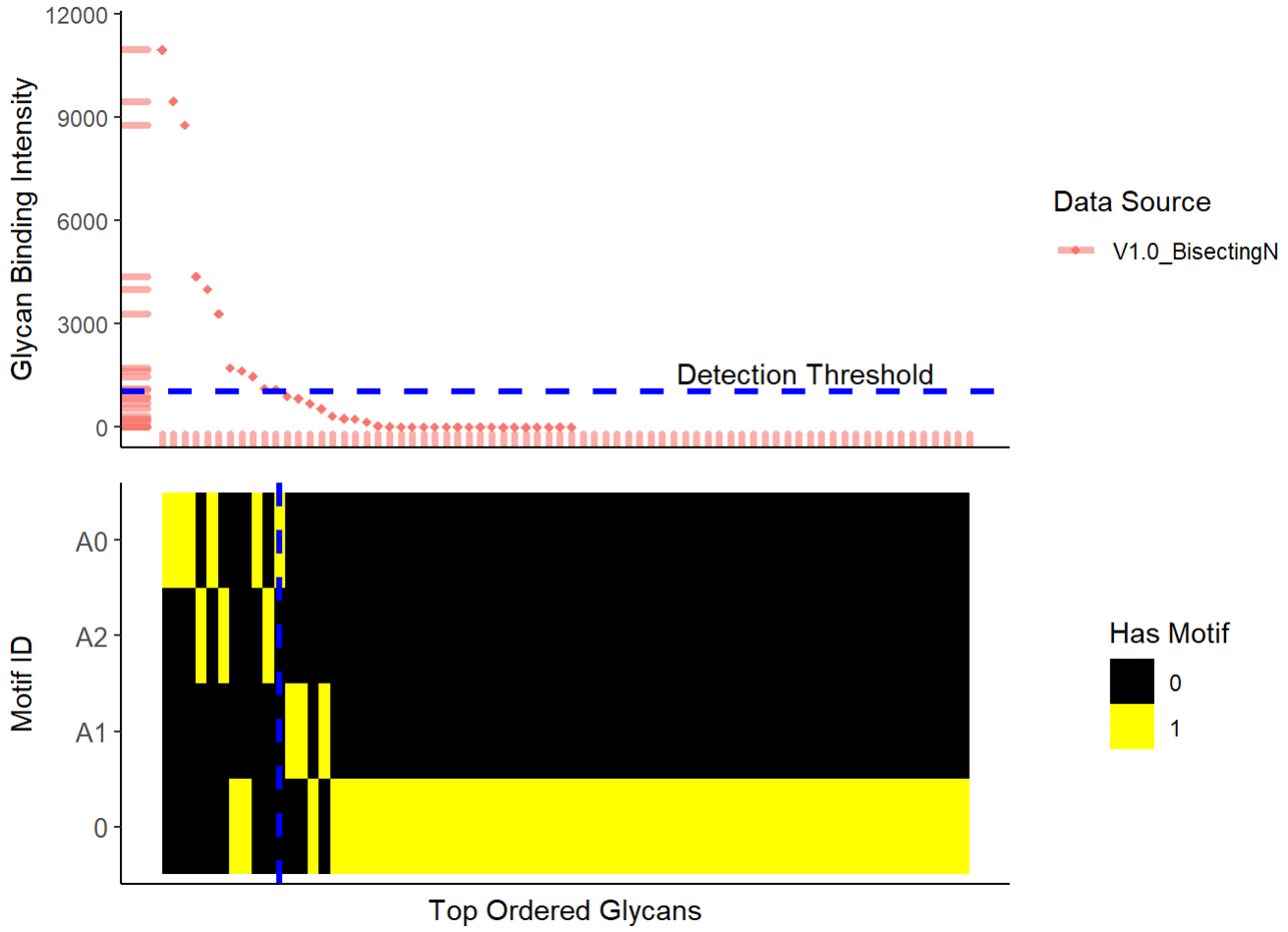
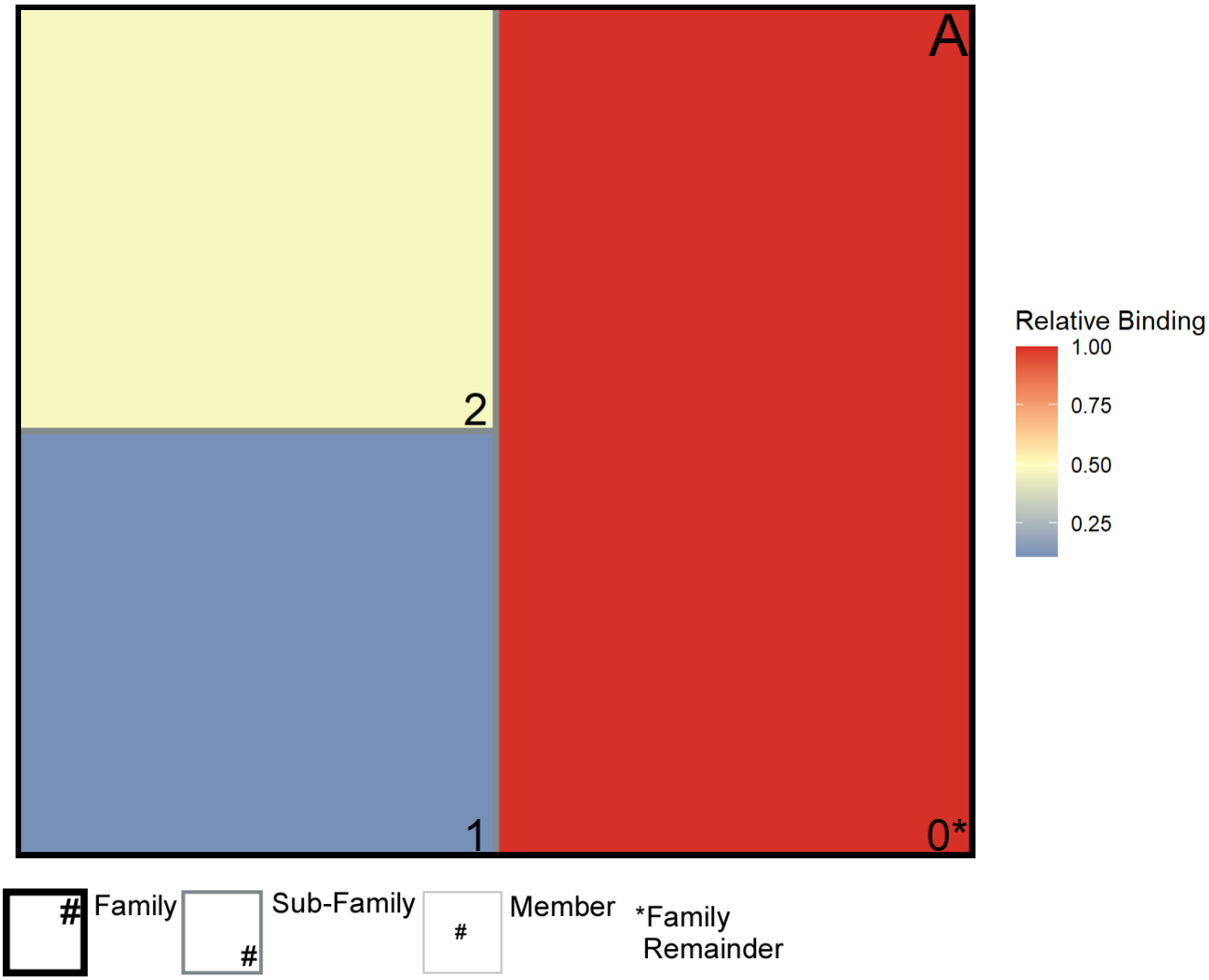


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

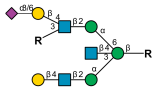
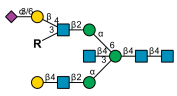
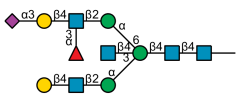
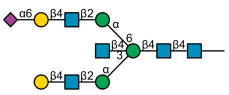
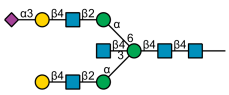
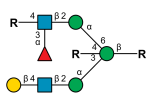
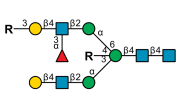
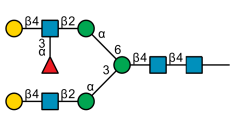
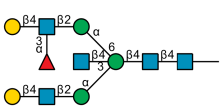
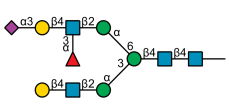


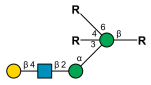
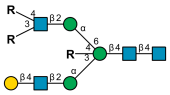
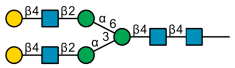
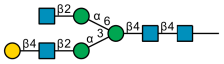
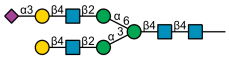
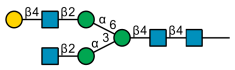
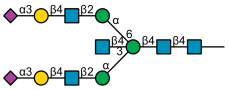
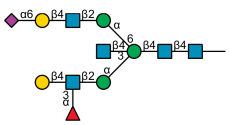
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

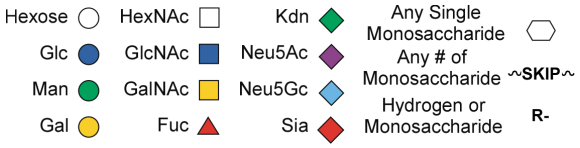
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				30		28		27
A2				65		29		66

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				38		43		63
0				58		3		19

Key:



All Concentration Plots:

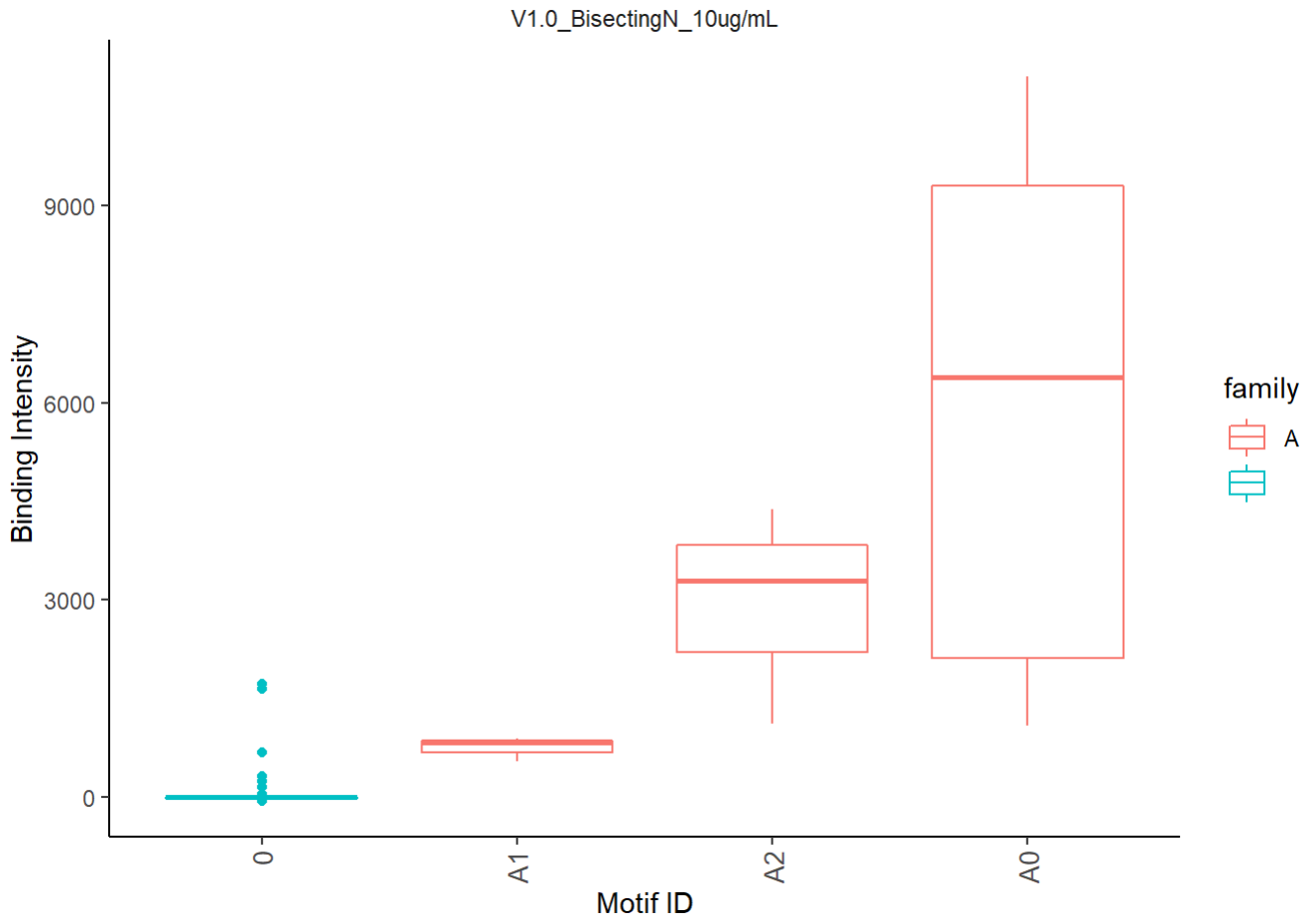
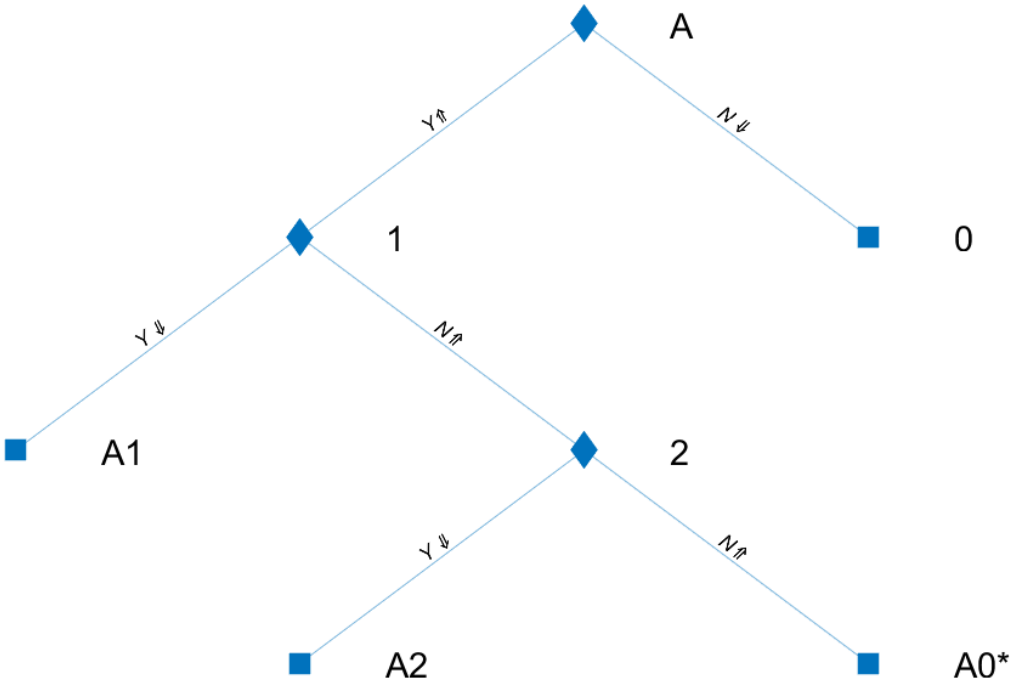


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



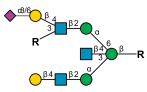
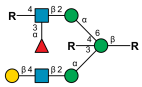
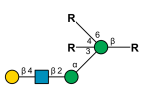
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

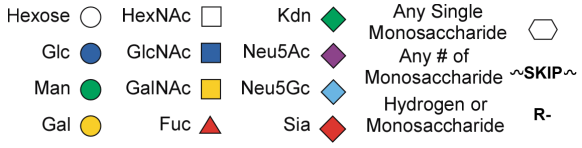
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)(<3f4f6f>GlcNAcB1-4)<2f>ManB
A2		<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f3f4f>FucA1-3<6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f>ManB
A0*		<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
0		Non-Binders

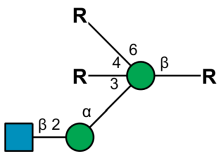
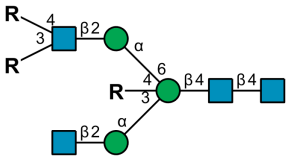
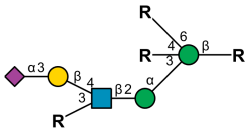
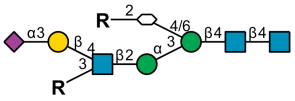
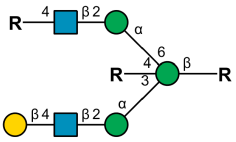
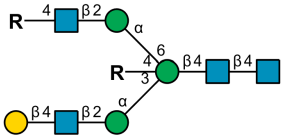
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

WGA

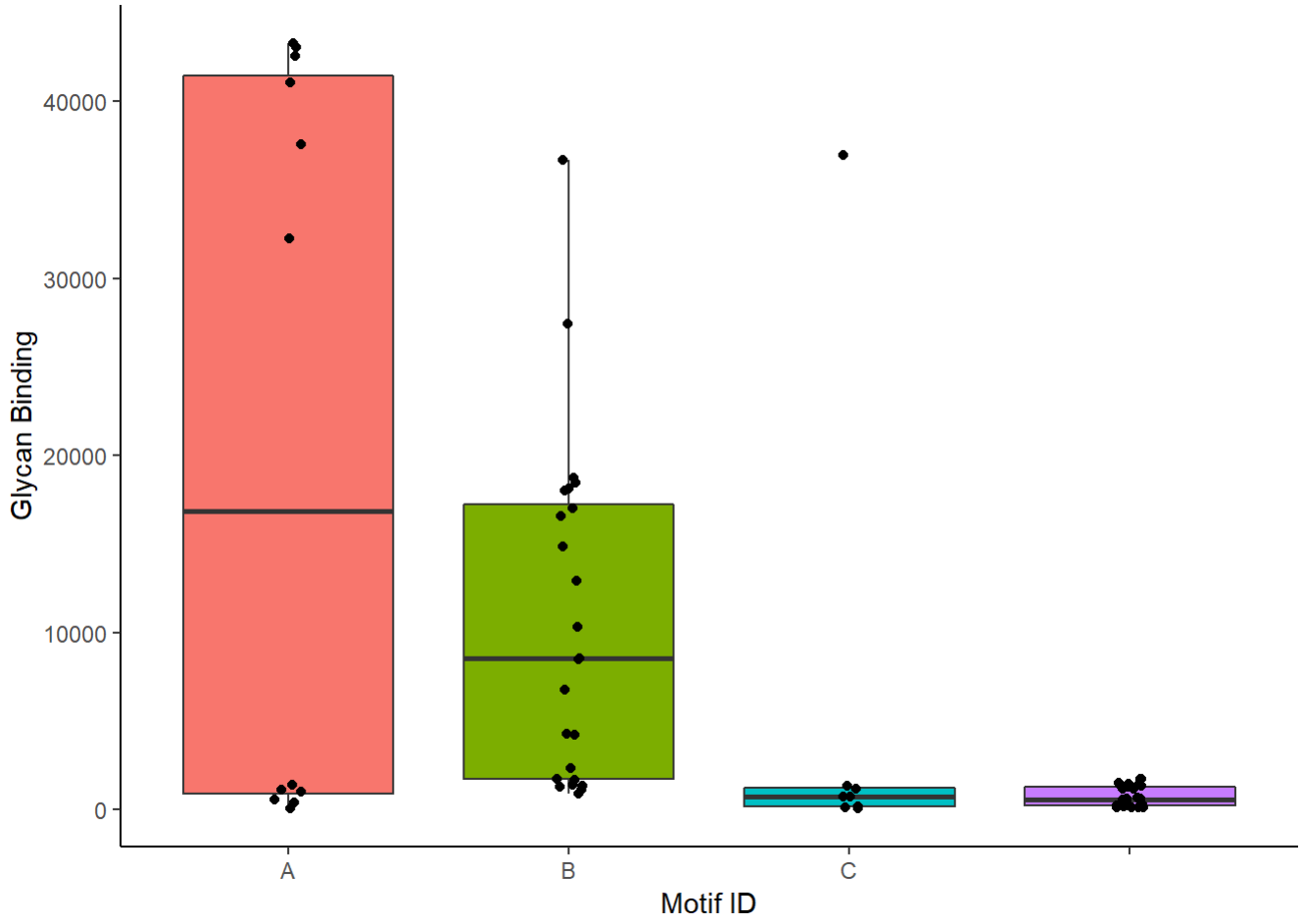
Automated Analysis report for WGA evaluated at 5 ug/mL

List of Primary WGA Motifs

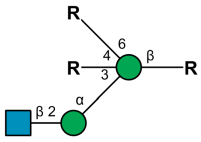
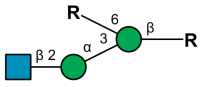
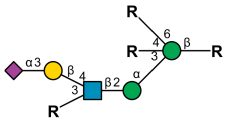
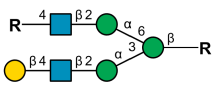
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	12
B			0.48	24
C			0.27	8
0			0.03	28

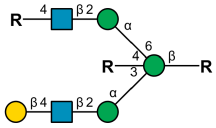
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

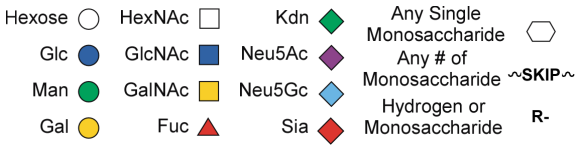


List of Fine-Specificity WGA Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*	Terminal N-Glycan N-Acetyl Glucosamine Bisecting N-Glycan (93%)		1.00	6	<0.001
A1			0.00	6	1.000
B0			0.26	24	<0.001
C1			0.26	4	0.079

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
C0*	Terminal Type 2 LacNAc Bisecting N-Glycan (90%)		0.00	4	1.000
0	Non-Binders (100%)		0.00	28	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

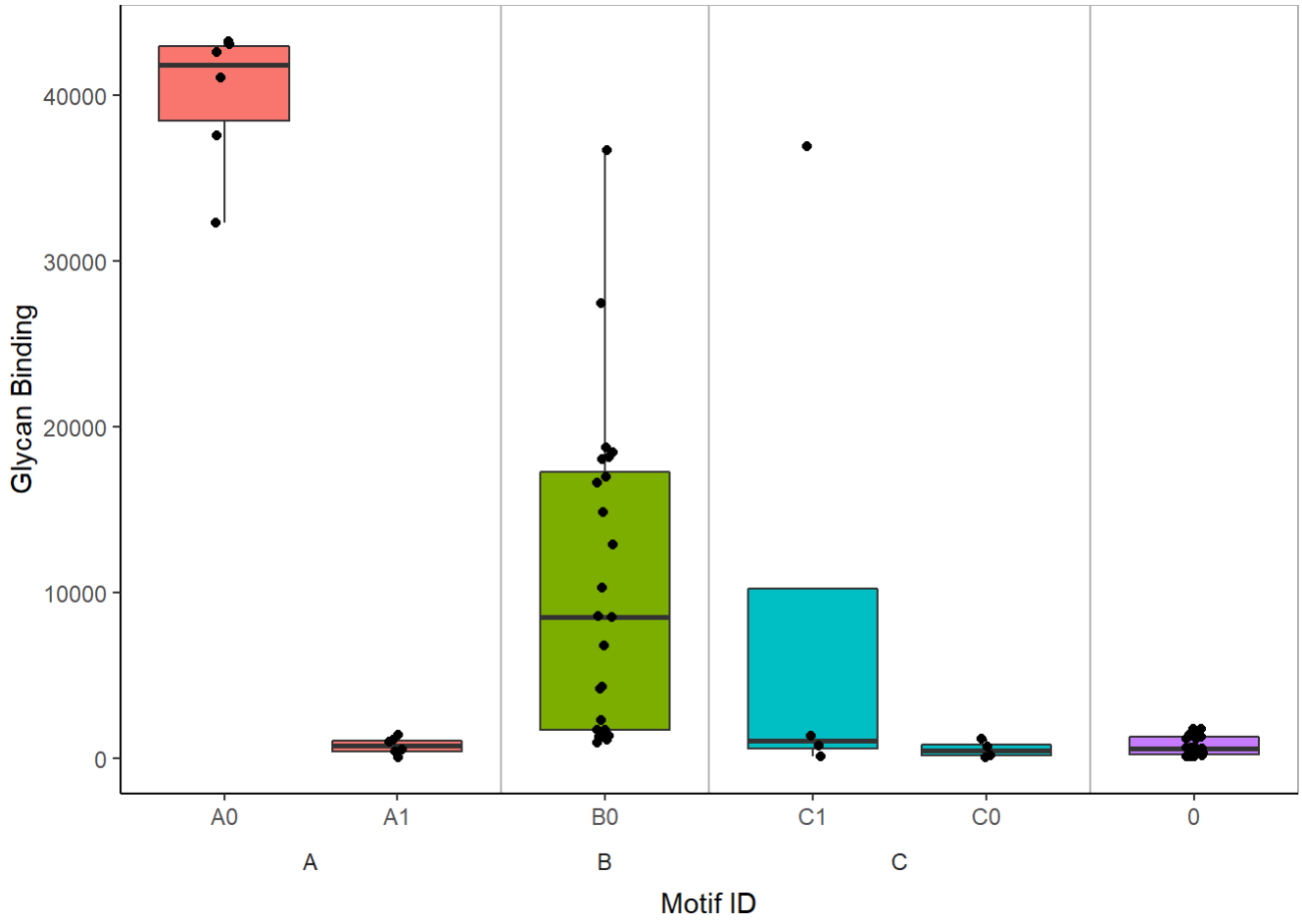


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

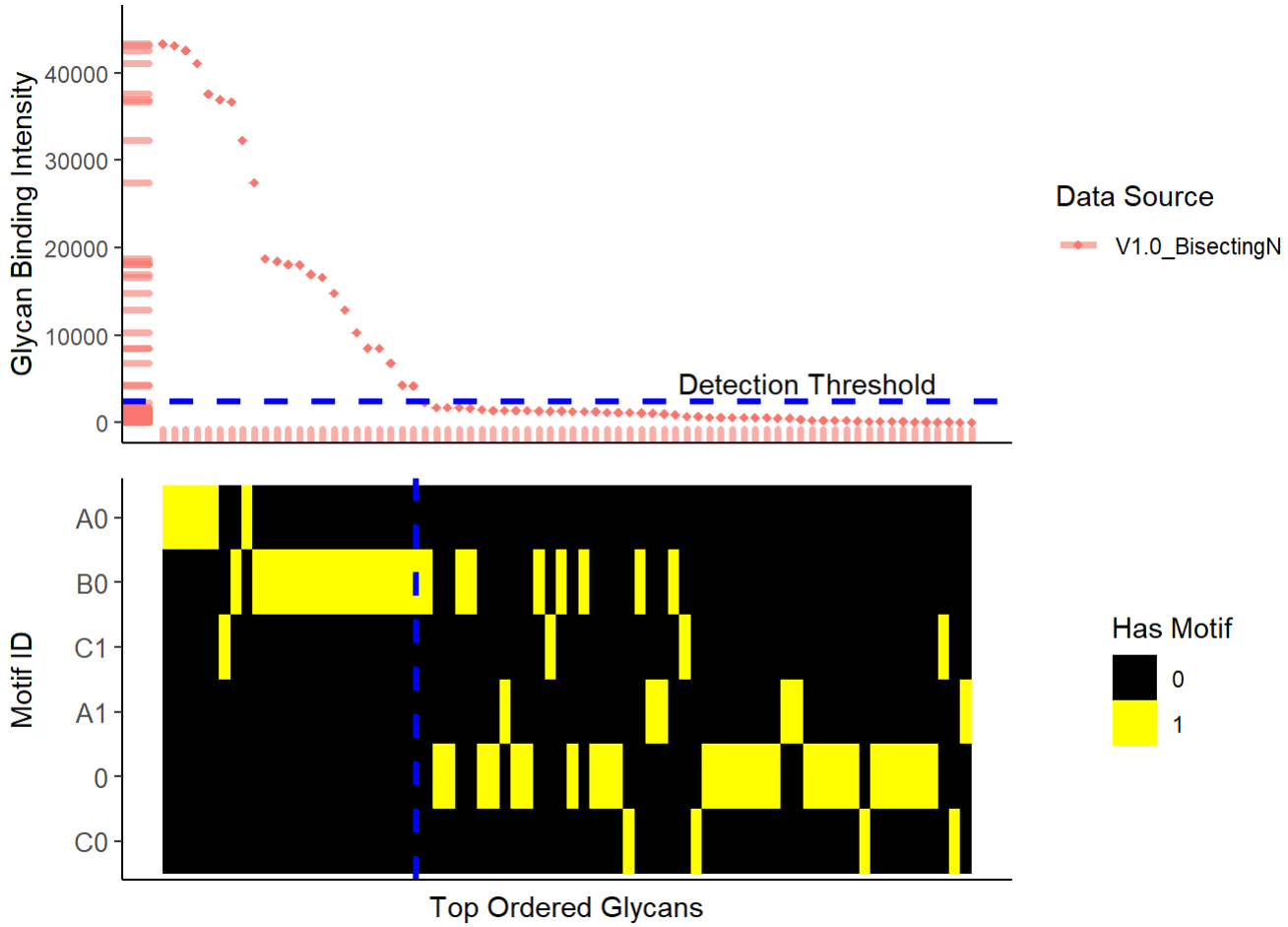
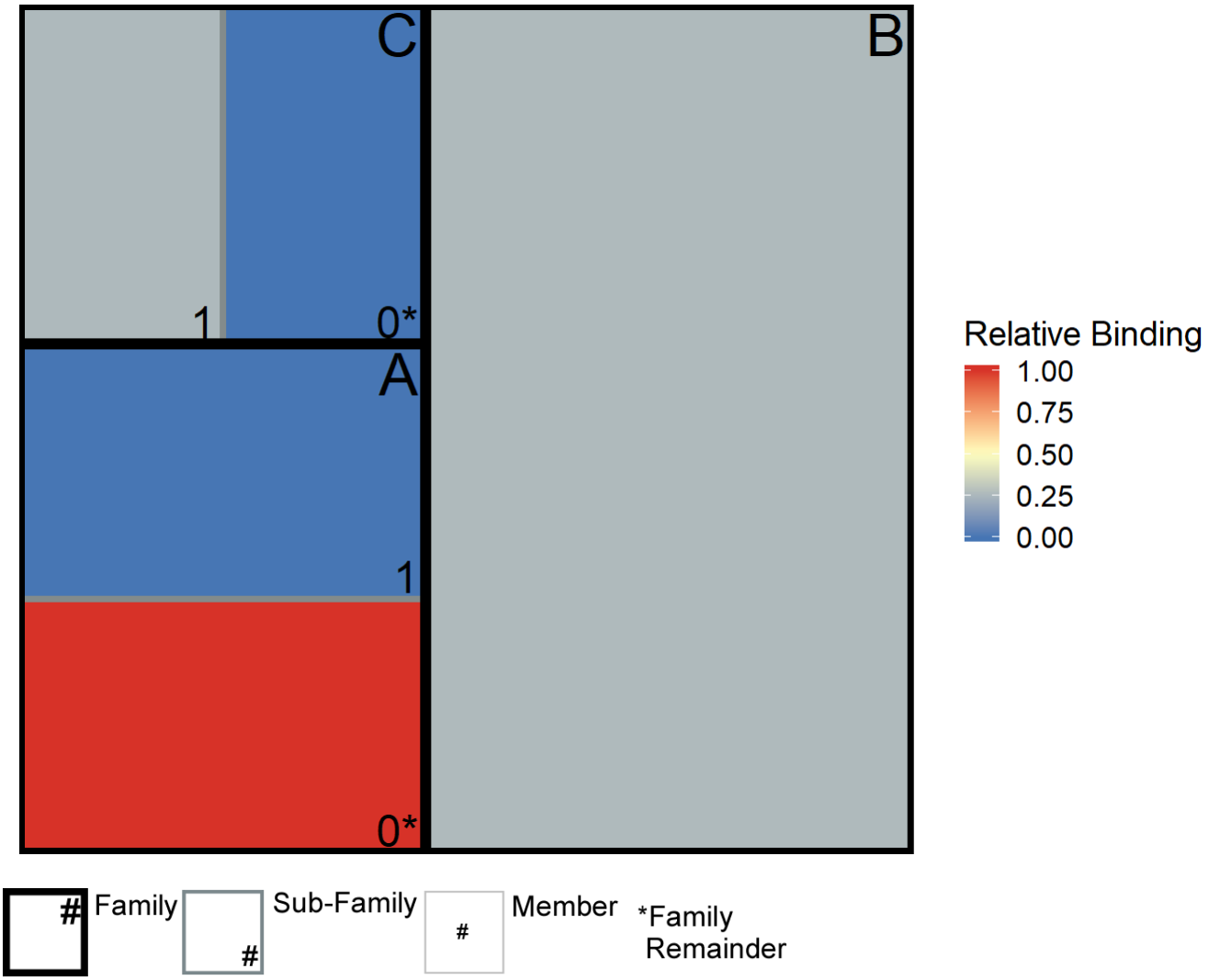


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

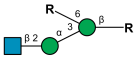
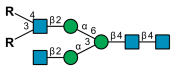
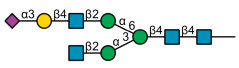
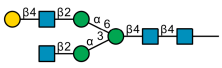
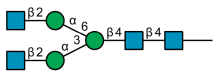
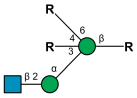
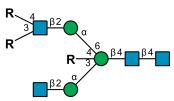
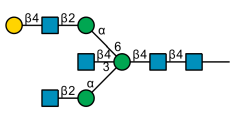
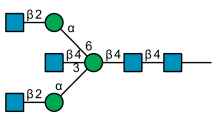
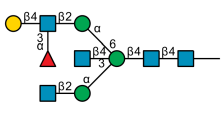


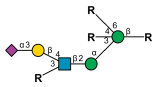
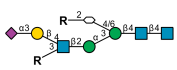
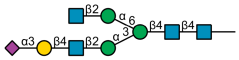
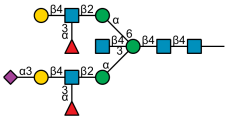
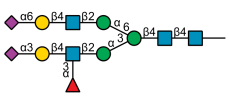
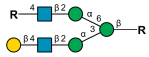
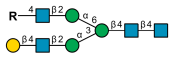
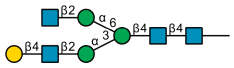
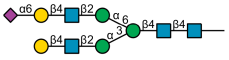
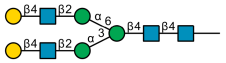
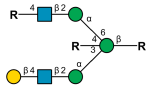
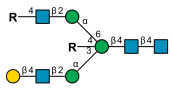
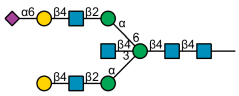
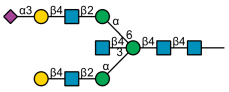
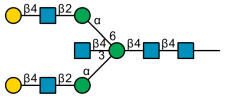
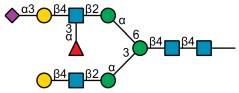
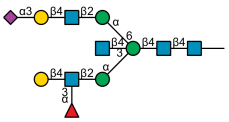
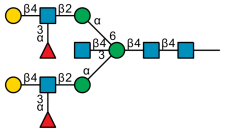
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

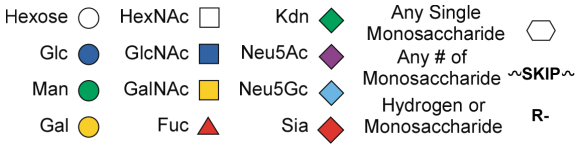
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				59		58		37
A0				22		1		25

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
B0				44		21		56
C1				43		64		38
C0				28		27		2
0				66		17		5

Key:



All Concentration Plots:

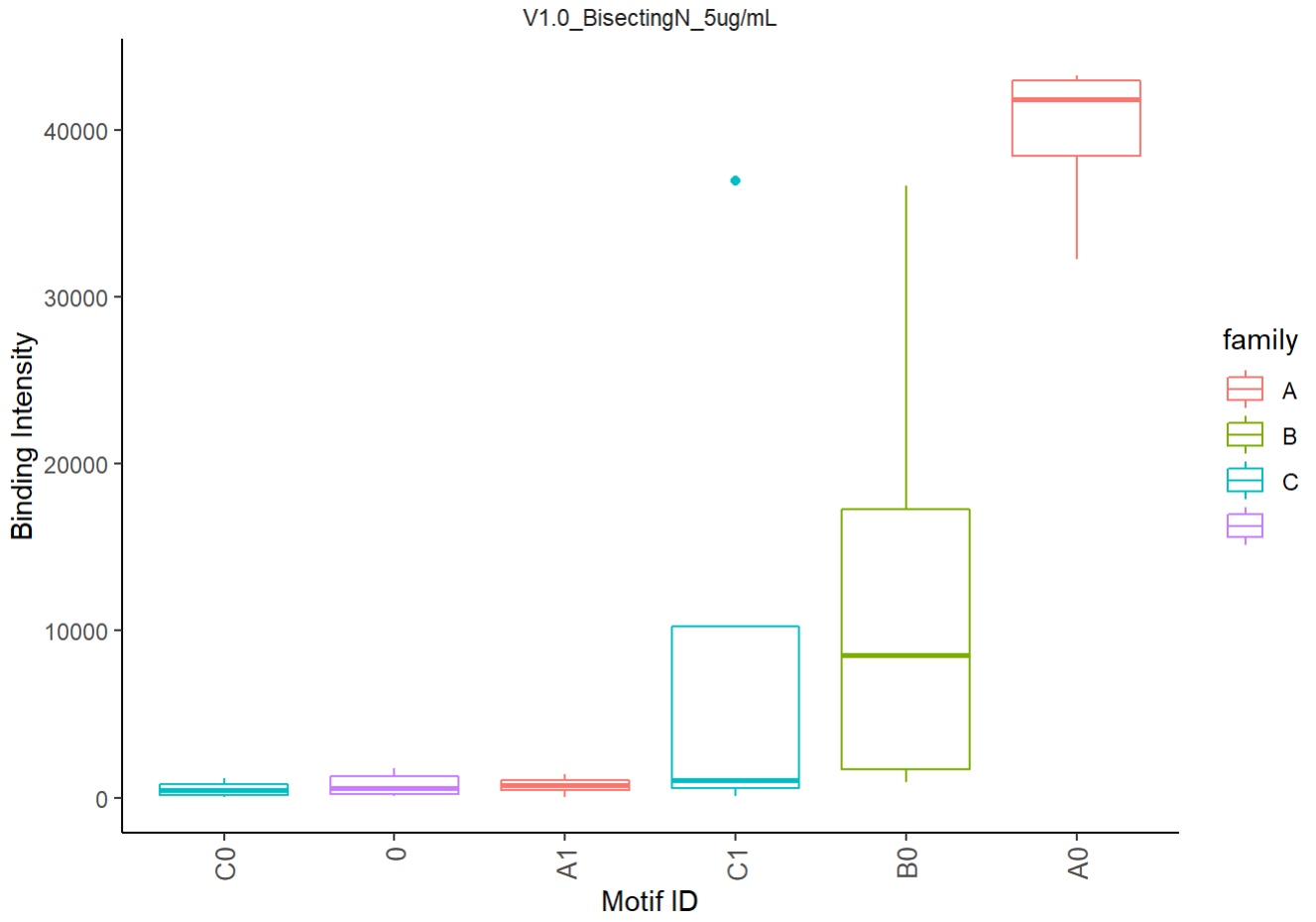
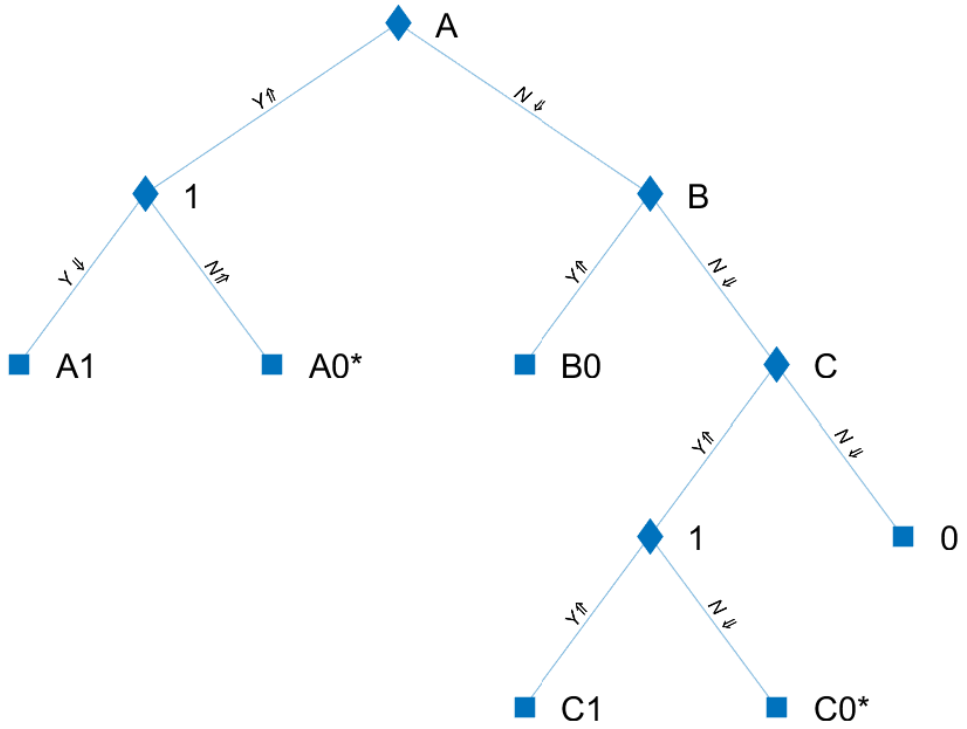


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



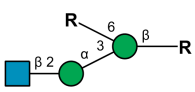
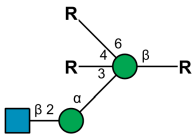
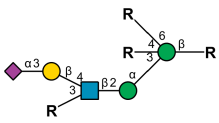
*Motif matches the remaining glycans not matched by earlier motifs in the model.

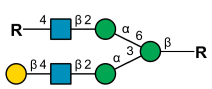
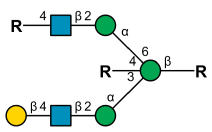
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

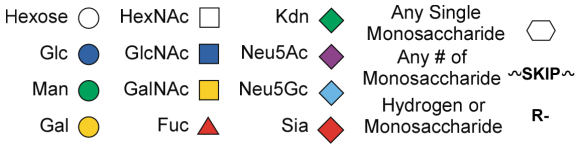
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f4f>ManB
A0*		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
B0		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB

Motif ID	Motif Graphic	Motif Text
C1		<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f4f>ManB
C0*		<2f3f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f>ManB
0		Non-Binders

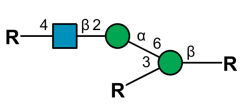
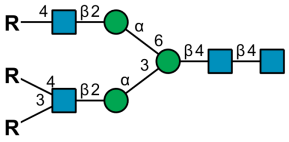
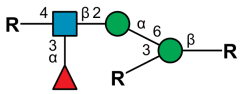
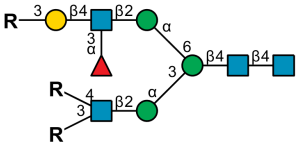
Key:



ConA

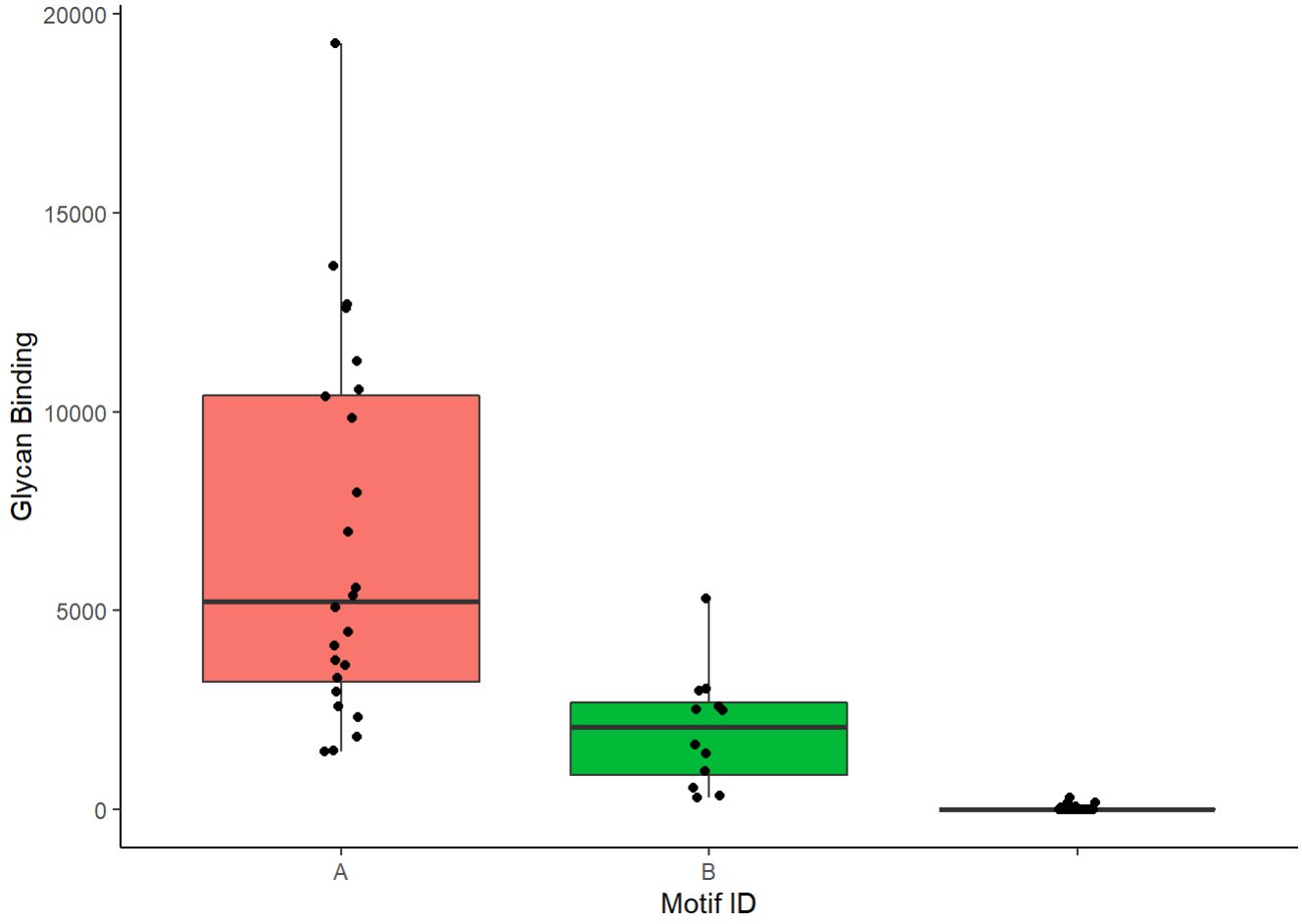
Automated Analysis report for ConA evaluated at 1 ug/mL

List of Primary ConA Motifs

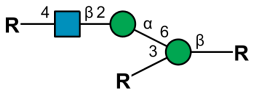
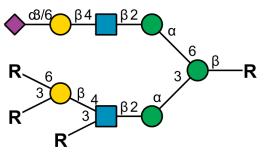
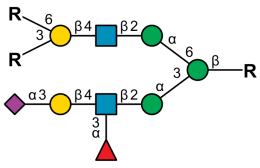
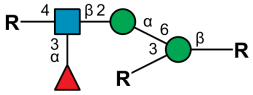
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	24
B			0.30	12
0			0.01	36

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

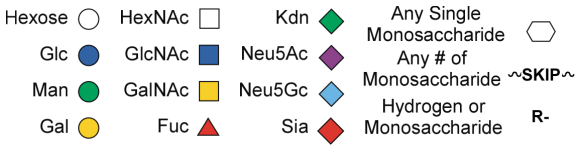


List of Fine-Specificity ConA Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*			1.00	13	<0.001
A2			0.32	8	<0.001
A1			0.22	3	0.209
B0			0.20	12	0.010

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
0	Non-Binders (100%)		0.00	36	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

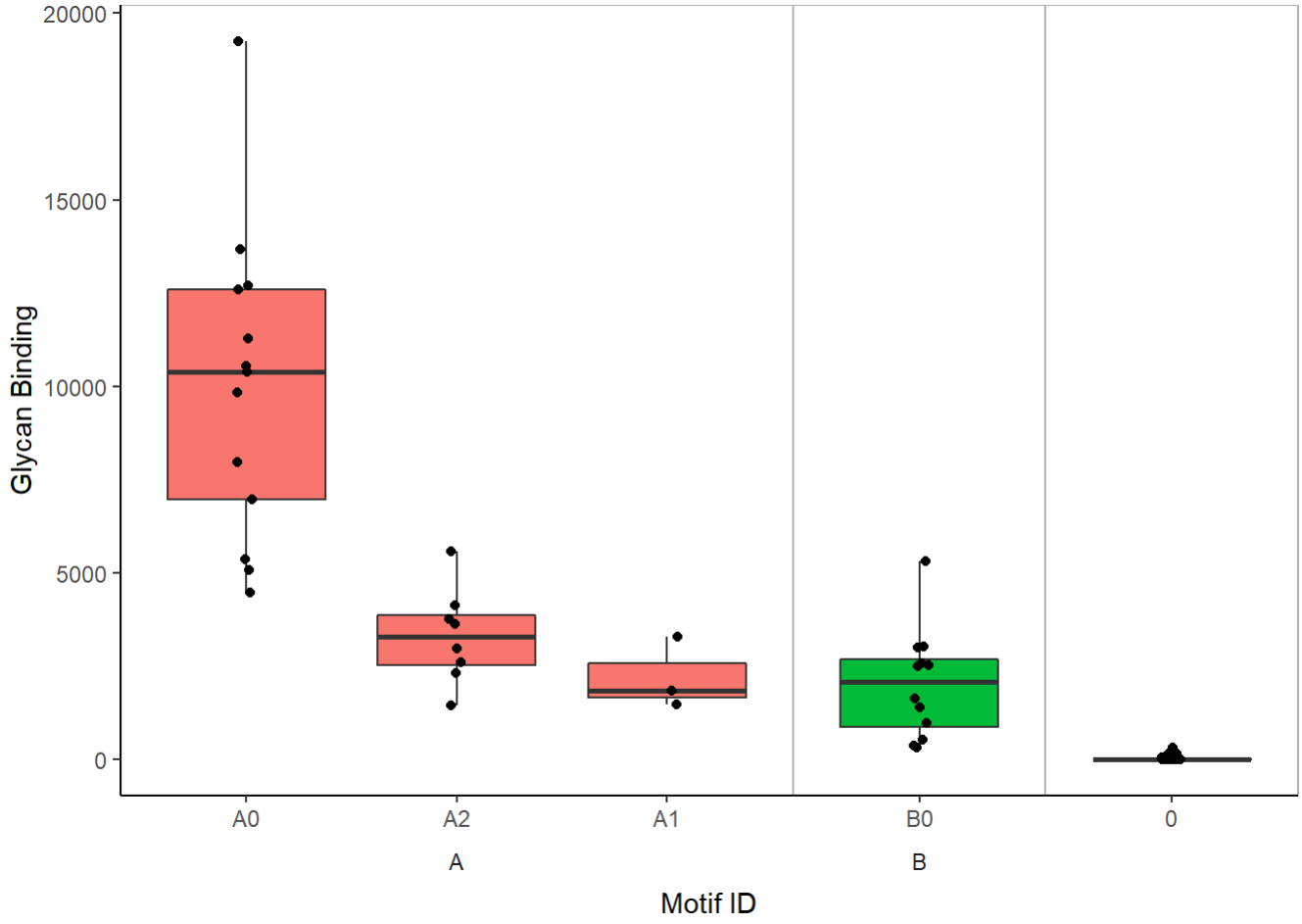


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

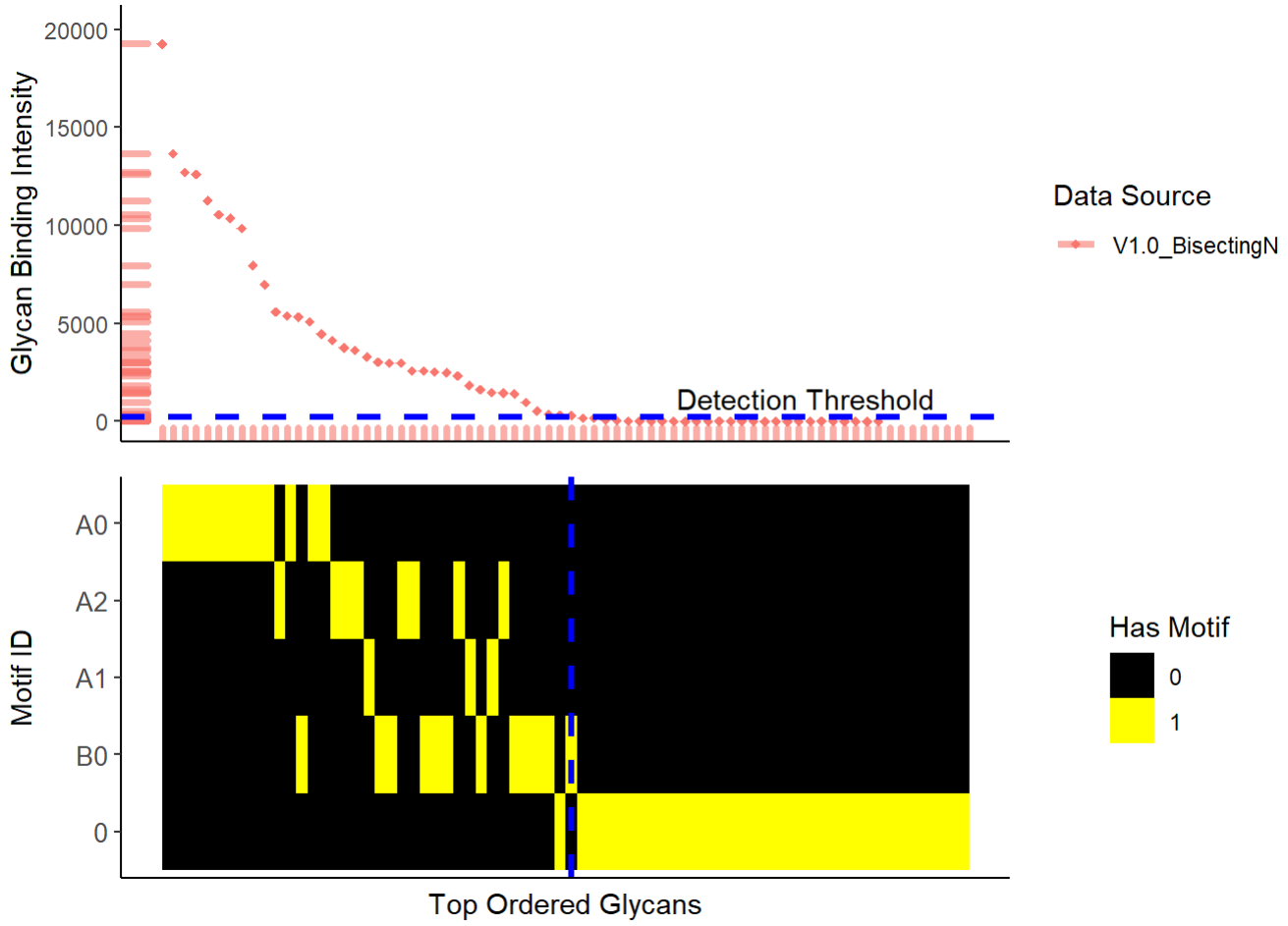
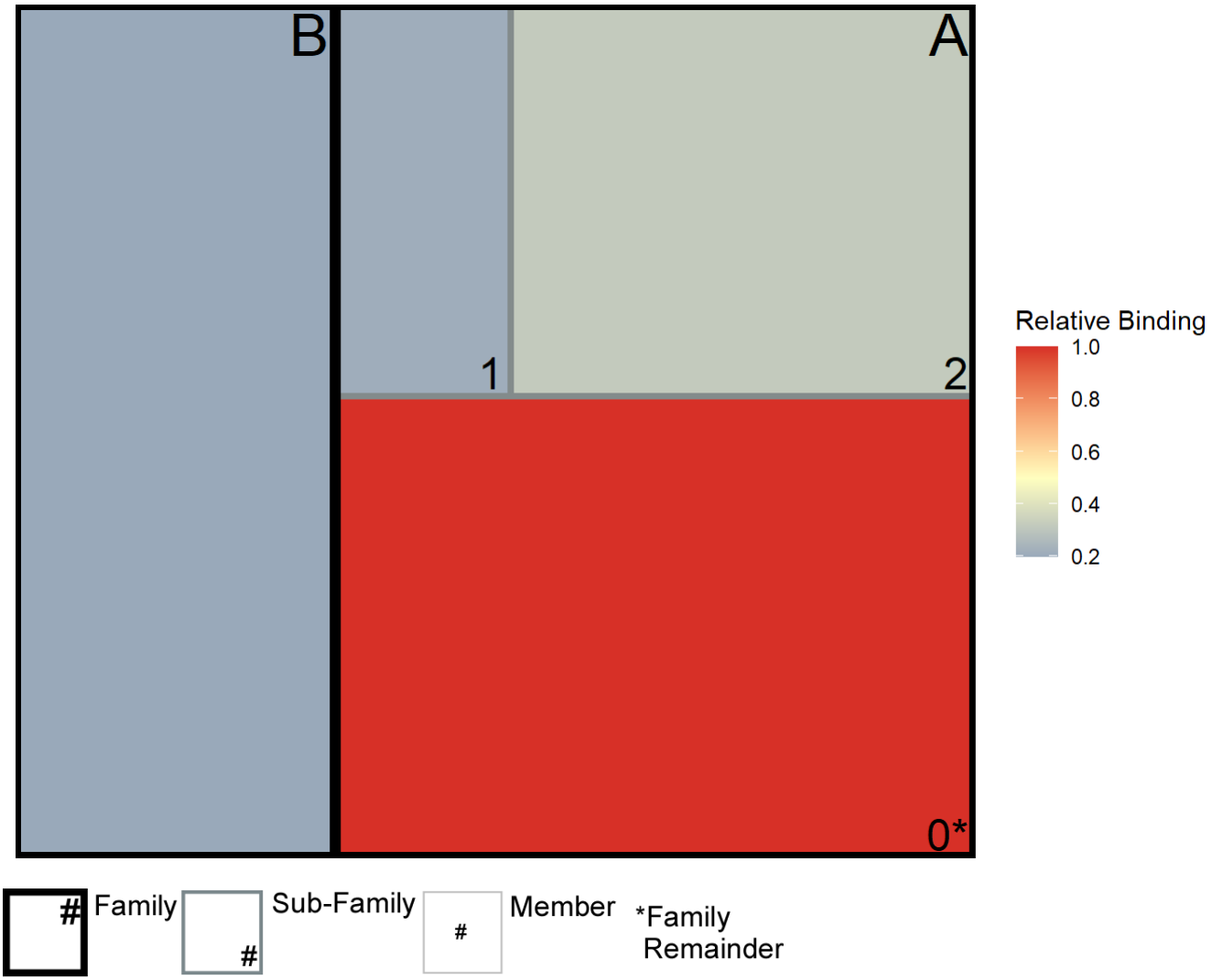


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

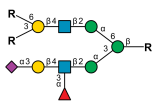
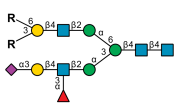
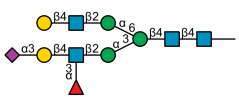
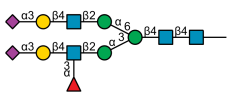
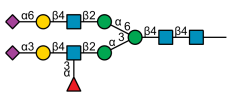
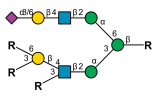
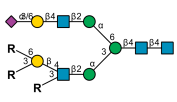
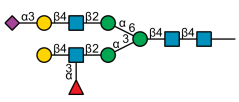
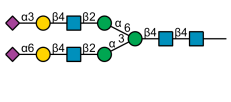
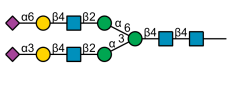


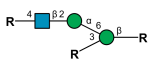
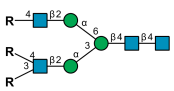
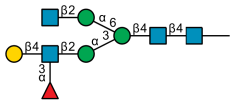
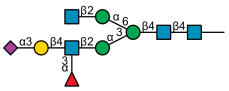
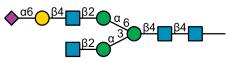
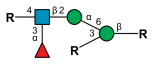
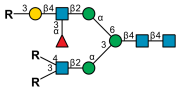
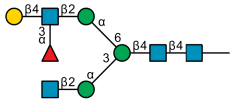
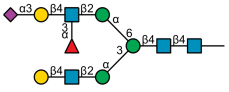
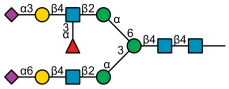
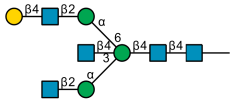
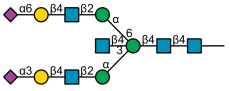
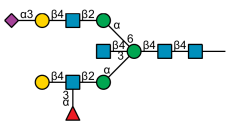
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

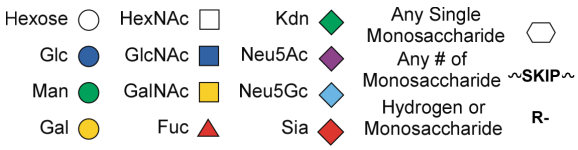
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				51		54		56
A2				53		52		67

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				46		47		60
B0				61		66		71
0				22		31		17

Key:



All Concentration Plots:

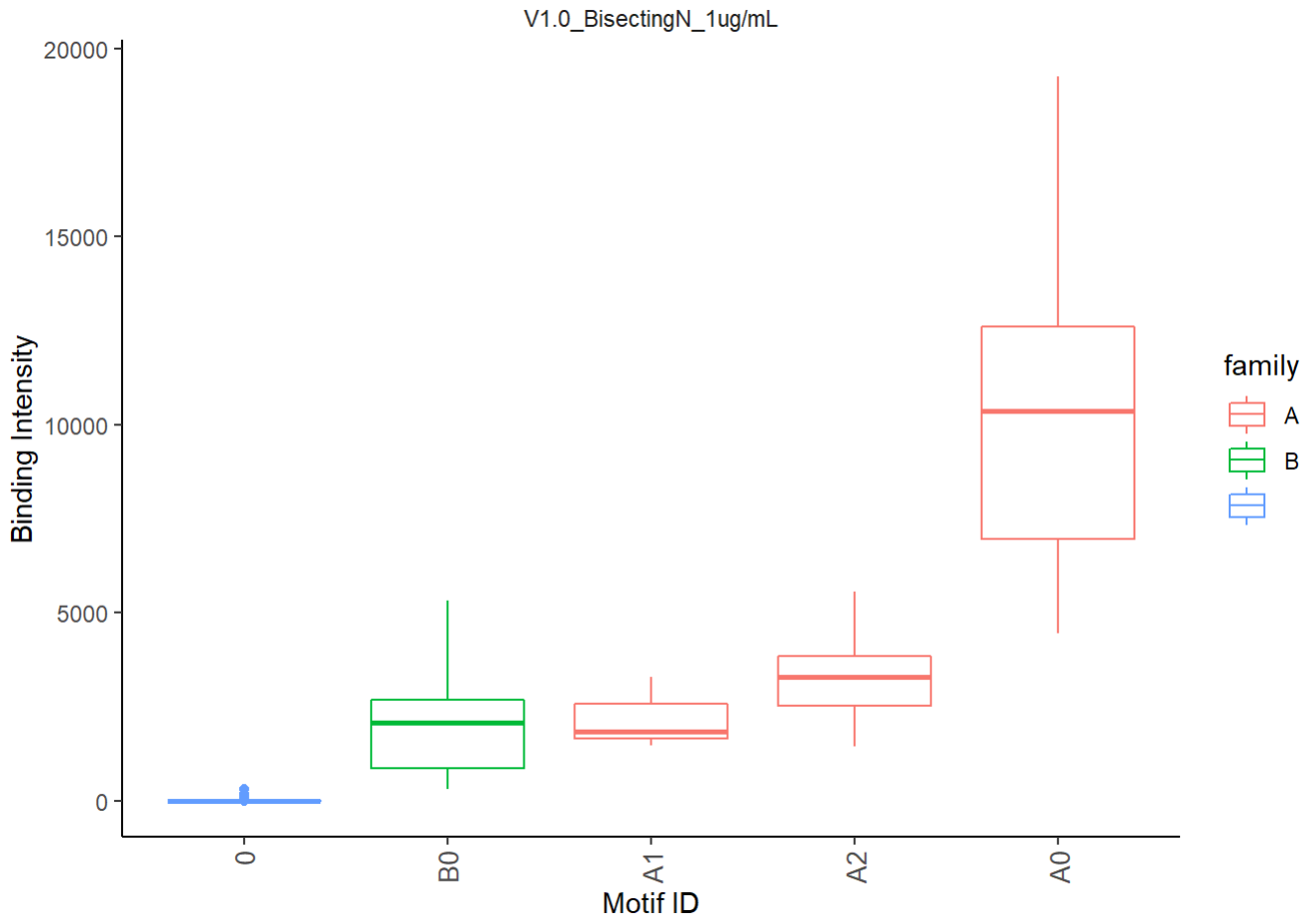
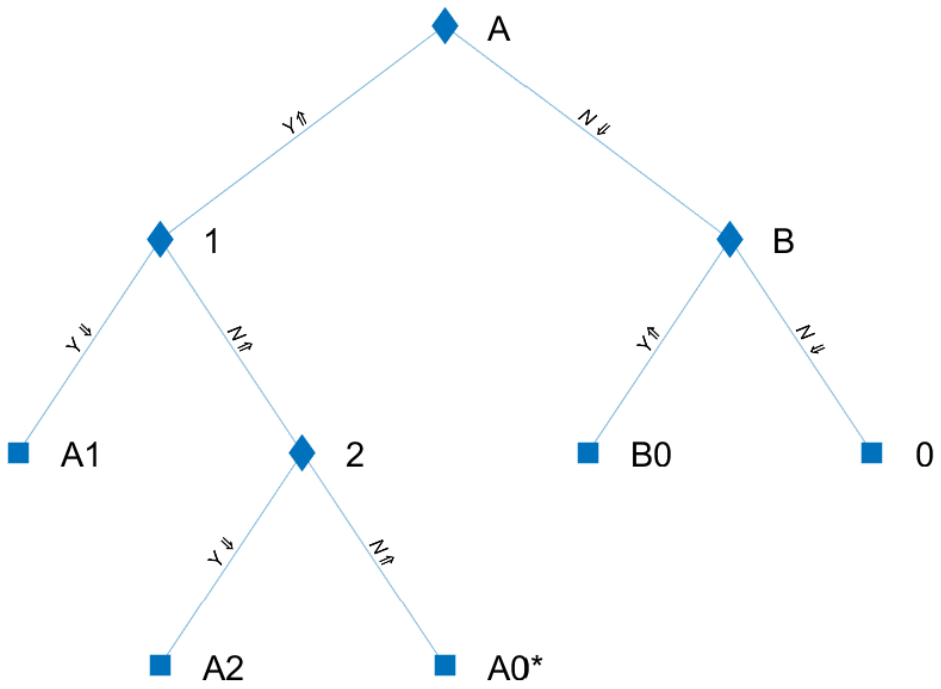


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



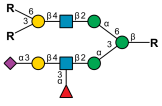
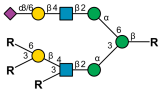
*Motif matches the remaining glycans not matched by earlier motifs in the model.

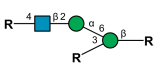
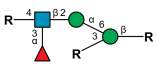
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

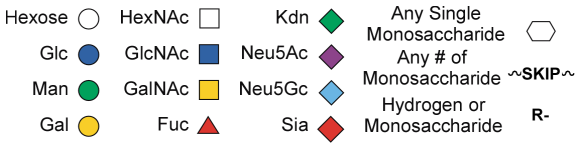
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f4f>ManB
A2		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f4f>ManB

Motif ID	Motif Graphic	Motif Text
A0*		<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f4f>ManB
B0		<2f3f4f>FucA1-3<6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f4f>ManB
0		Non-Binders

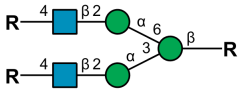
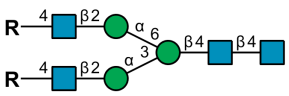
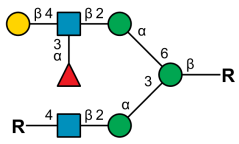
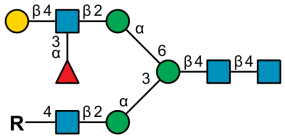
Key:



GNL

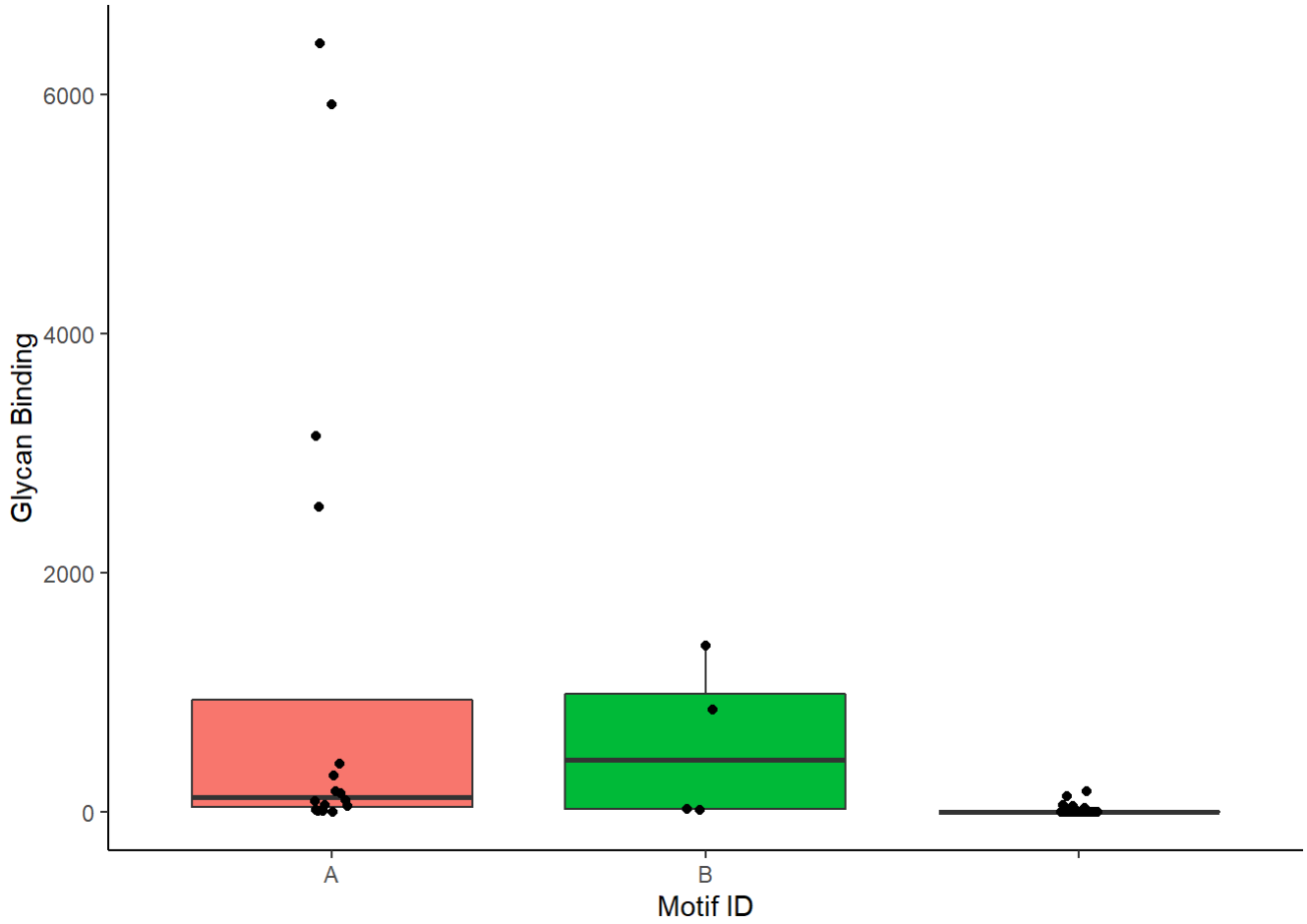
Automated Analysis report for GNL evaluated at 10 ug/mL

List of Primary GNL Motifs

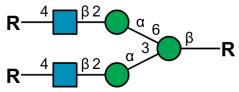
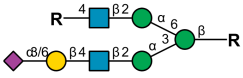
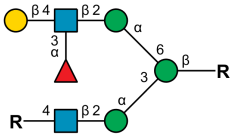
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	16
B			0.54	4
0			0.01	52

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

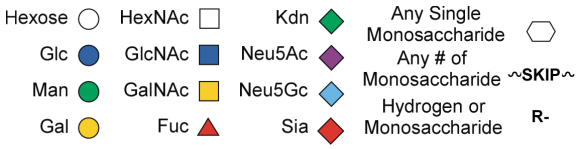
Boxplot of Primary Motifs



List of Fine-Specificity GNL Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*			1.00	8	<0.001
A1			0.02	8	0.999
B0			0.30	4	0.499
0	Non-Binders (100%)		0.00	52	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

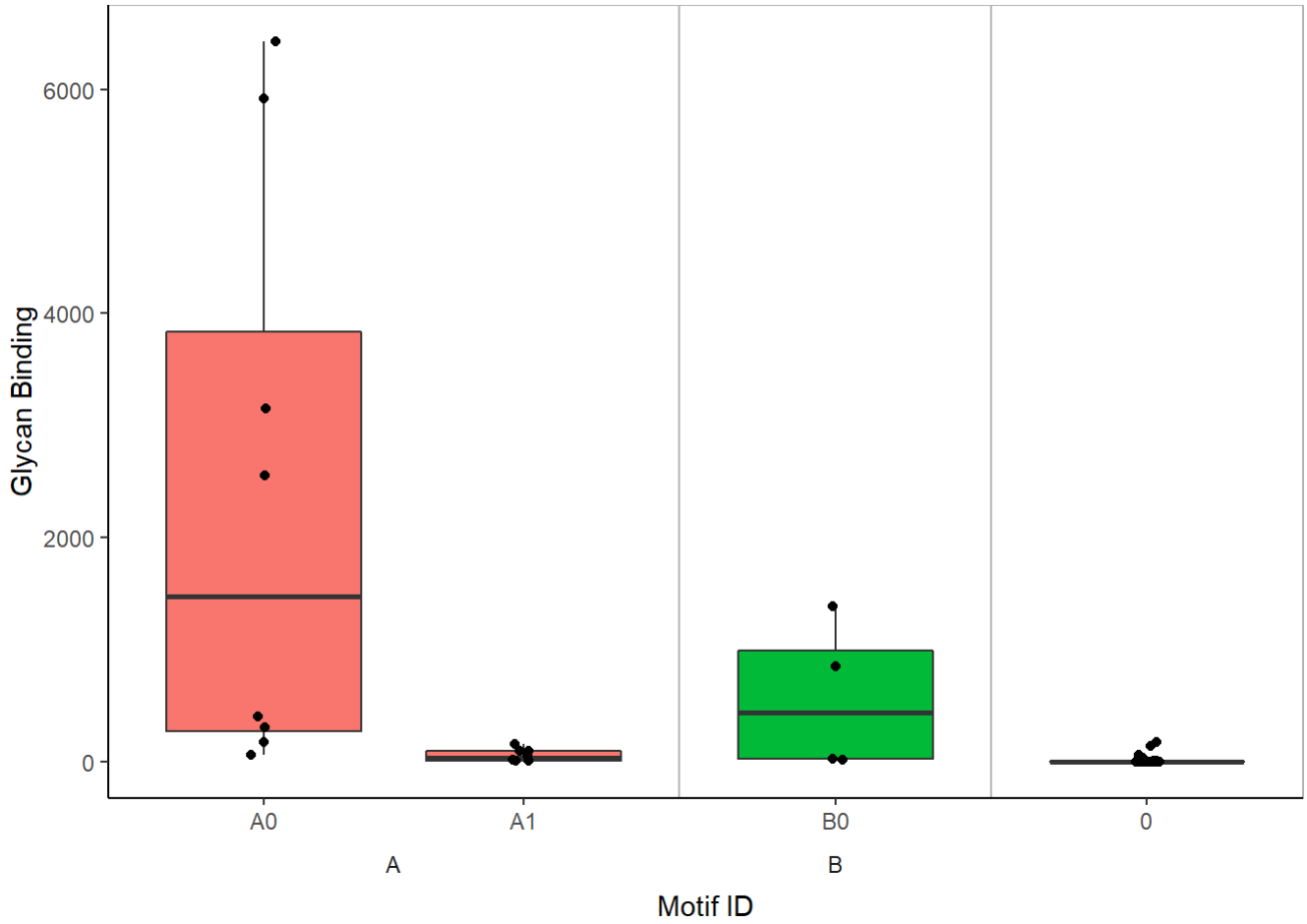


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

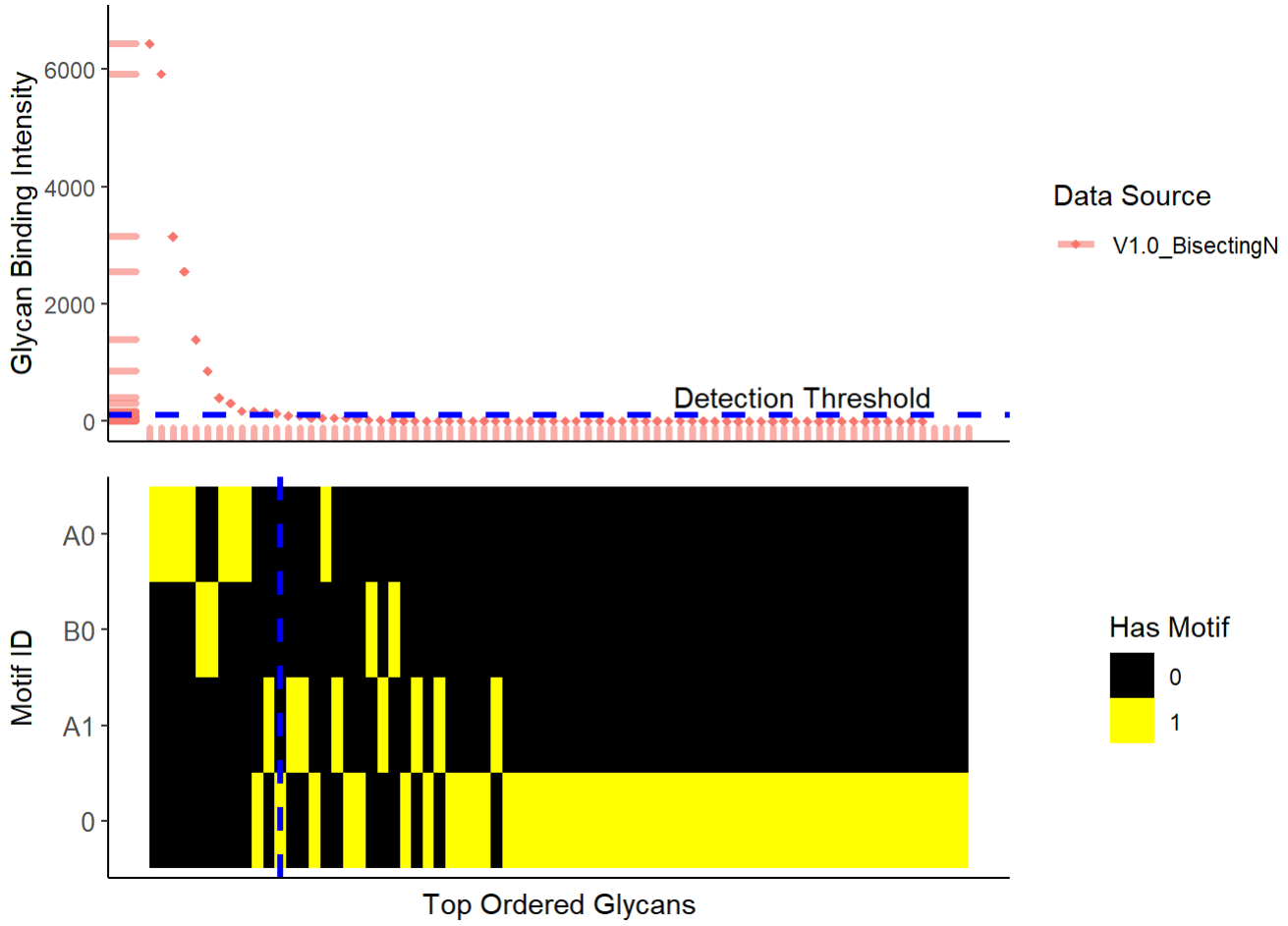
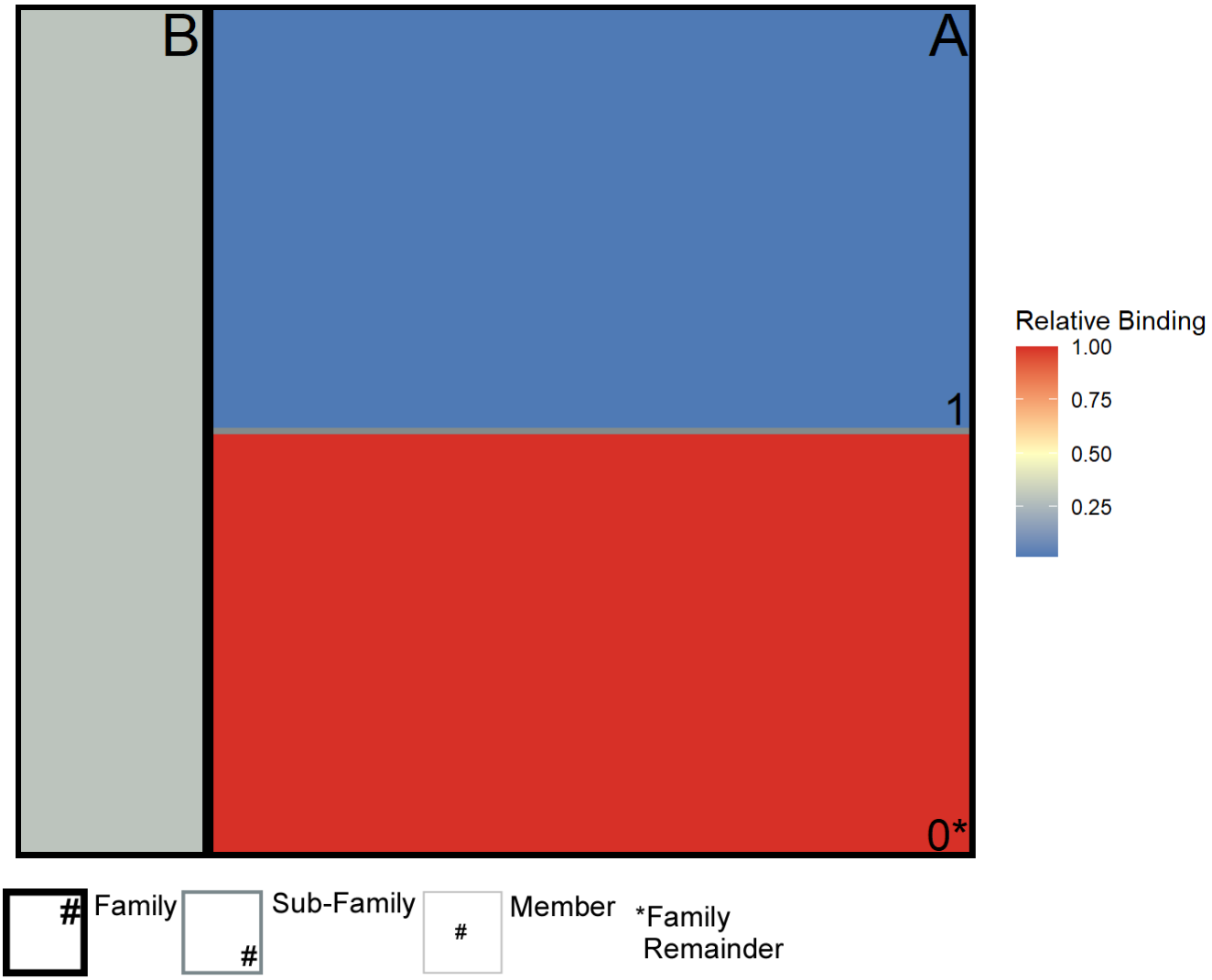


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

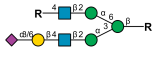
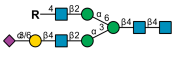
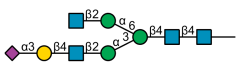
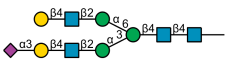
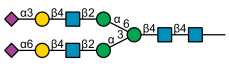
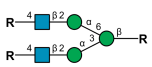
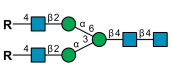
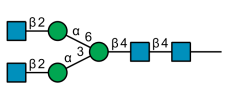
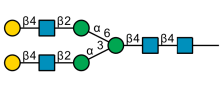
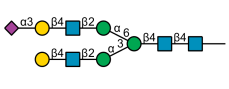


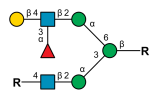
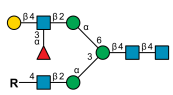
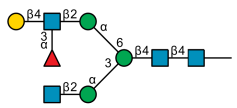
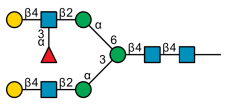
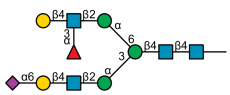
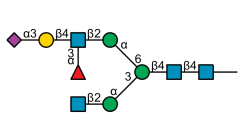
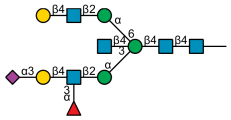
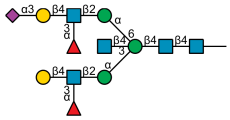
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

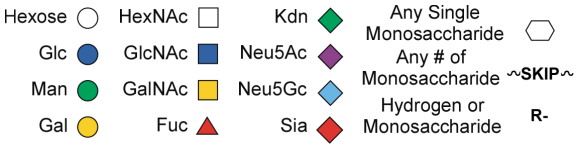
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				44		48		52
A0				37		38		63

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
B0			 61	 65	 70
0			 62	 15	 36

Key:



All Concentration Plots:

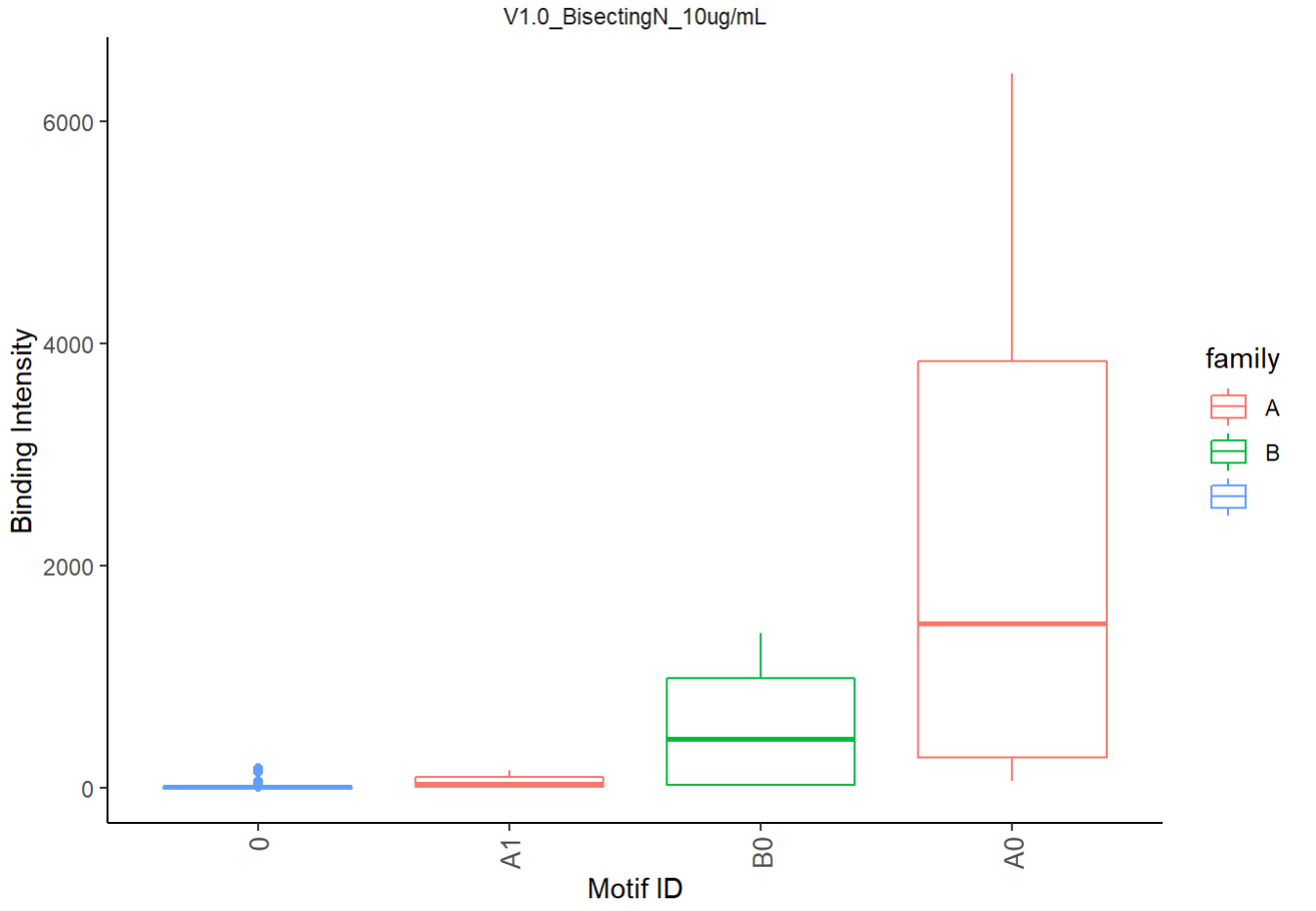
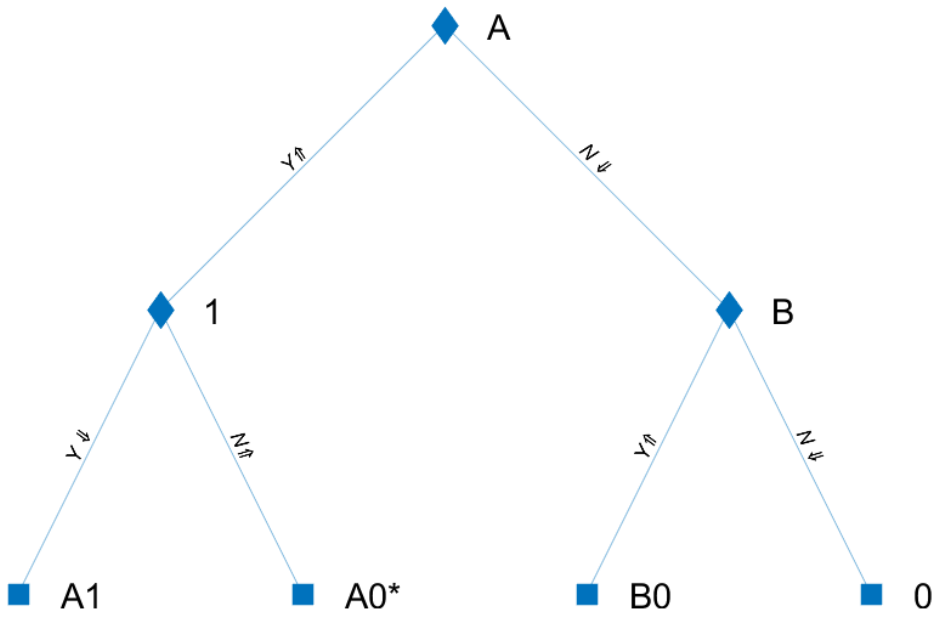


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



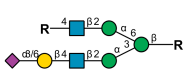
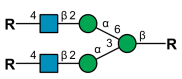
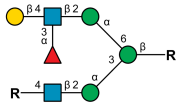
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

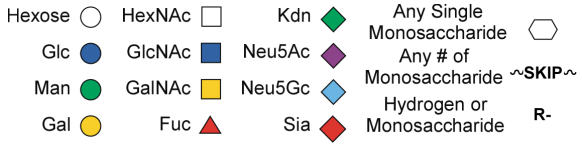
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f4f>ManB
A0*		<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f4f>ManB
B0		<2f3f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f4f>ManB
0		Non-Binders

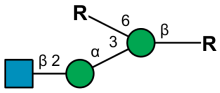
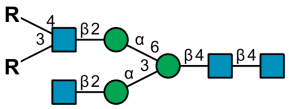
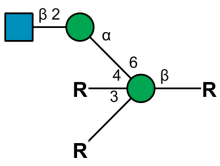
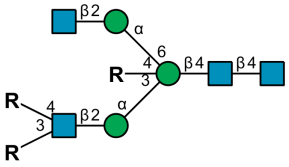
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

GSII

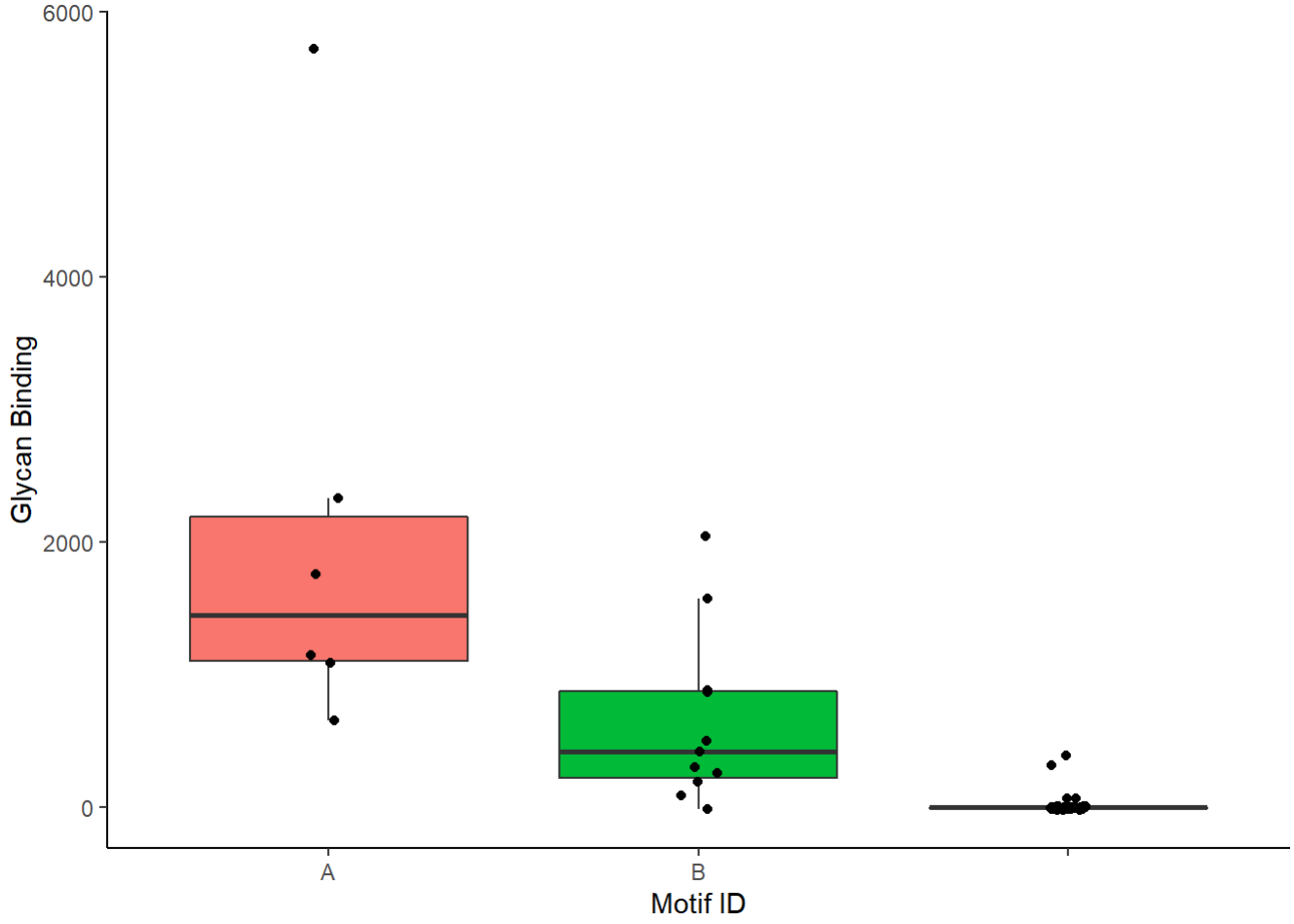
Automated Analysis report for GSII evaluated at 10 ug/mL

List of Primary GSII Motifs

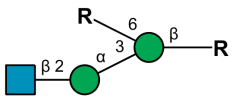
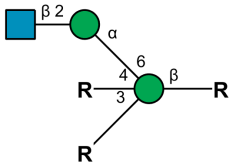
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	6
B			0.33	11
0			0.01	55

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

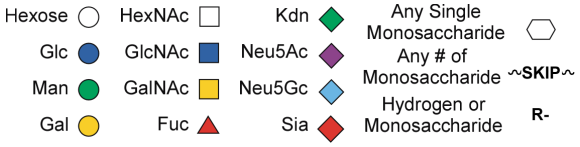
Boxplot of Primary Motifs



List of Fine-Specificity GSII Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0			1.00	6	<0.001
B0			0.32	11	0.002
0	Non-Binders (100%)		0.00	55	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

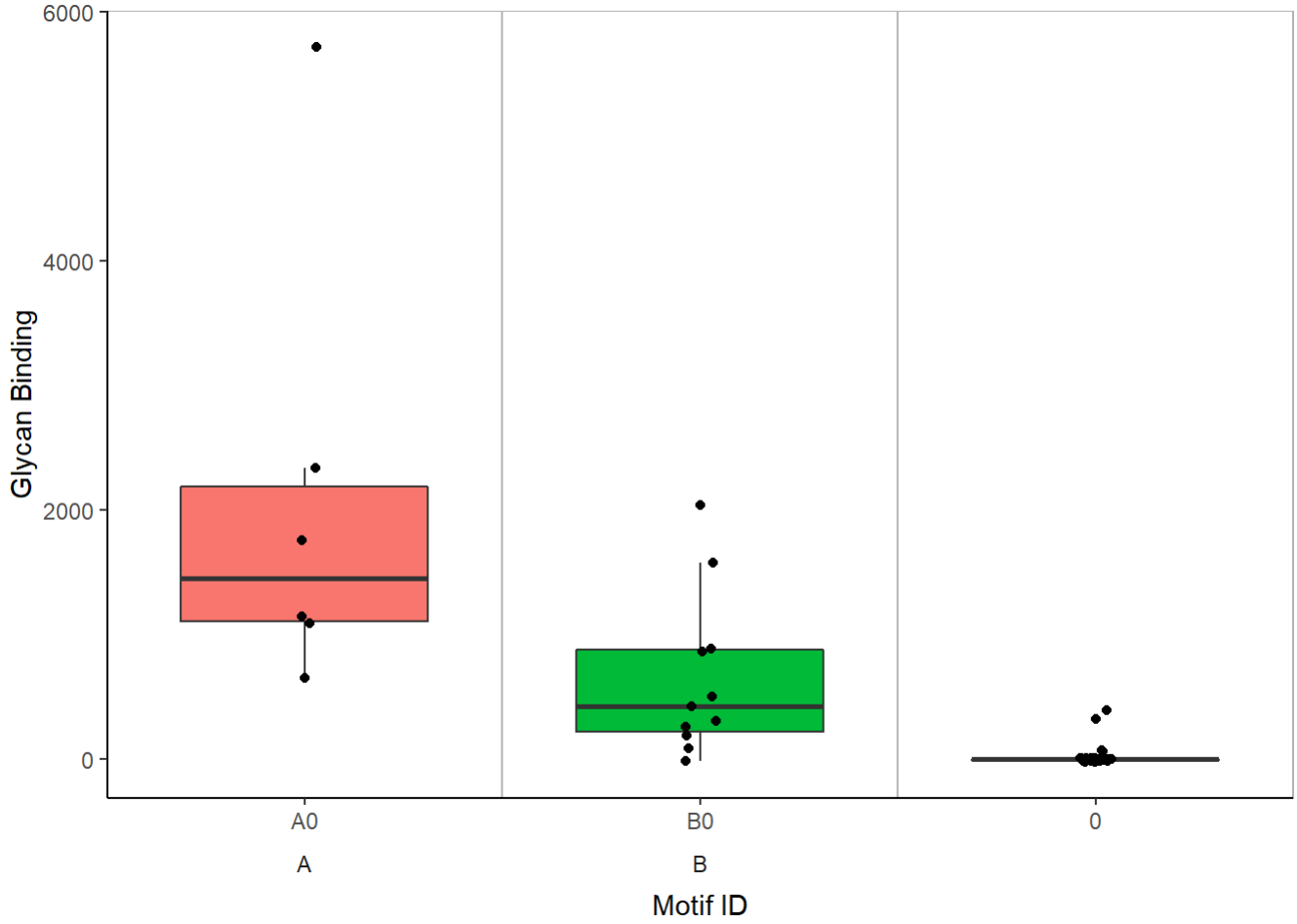


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

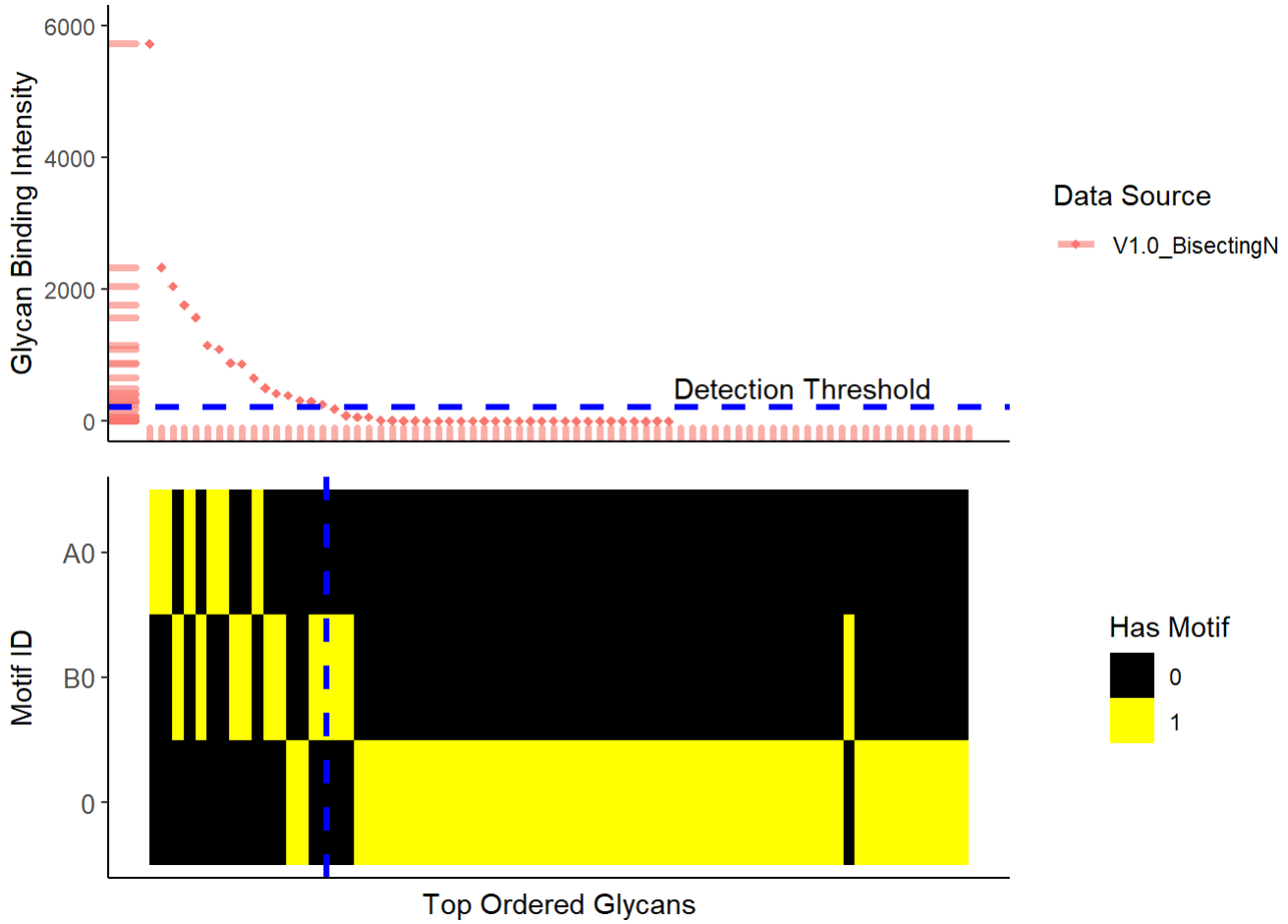
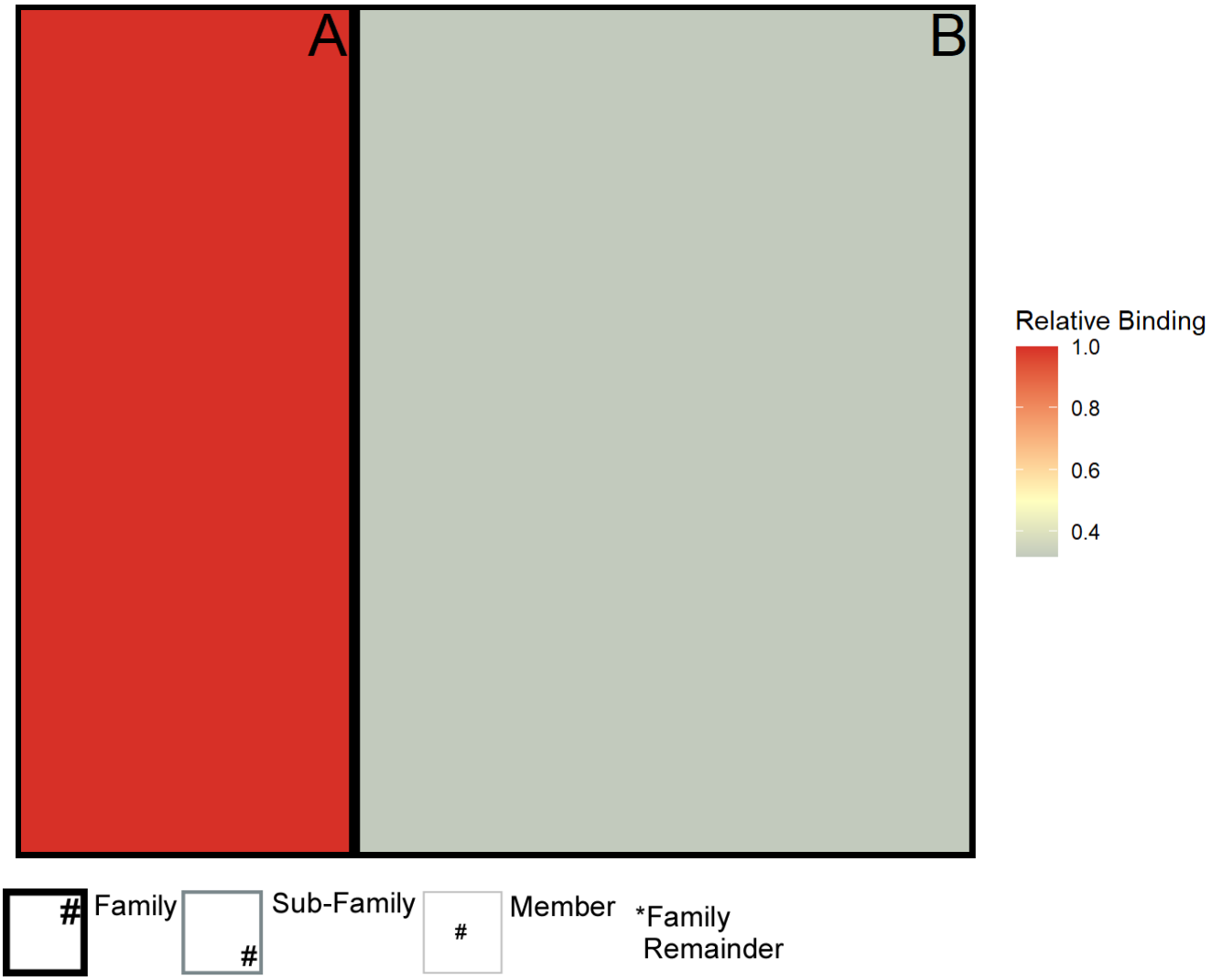


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

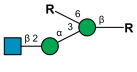
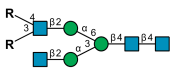
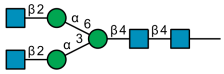
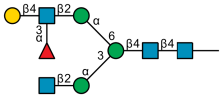
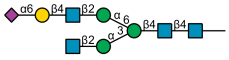
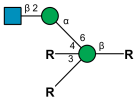
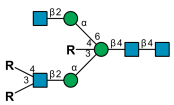
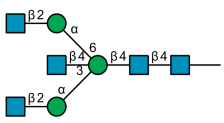
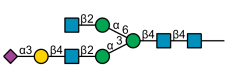
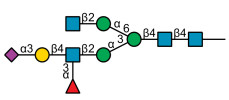


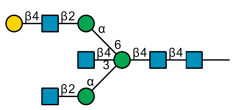
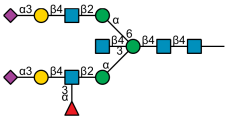
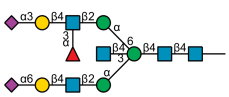
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

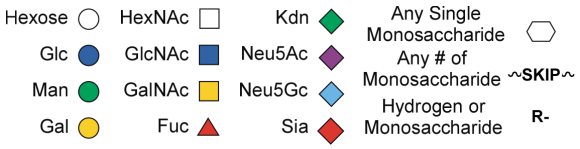
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				37		61		60
B0				1		44		47

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
0			 22	 18	 35

Key:



All Concentration Plots:

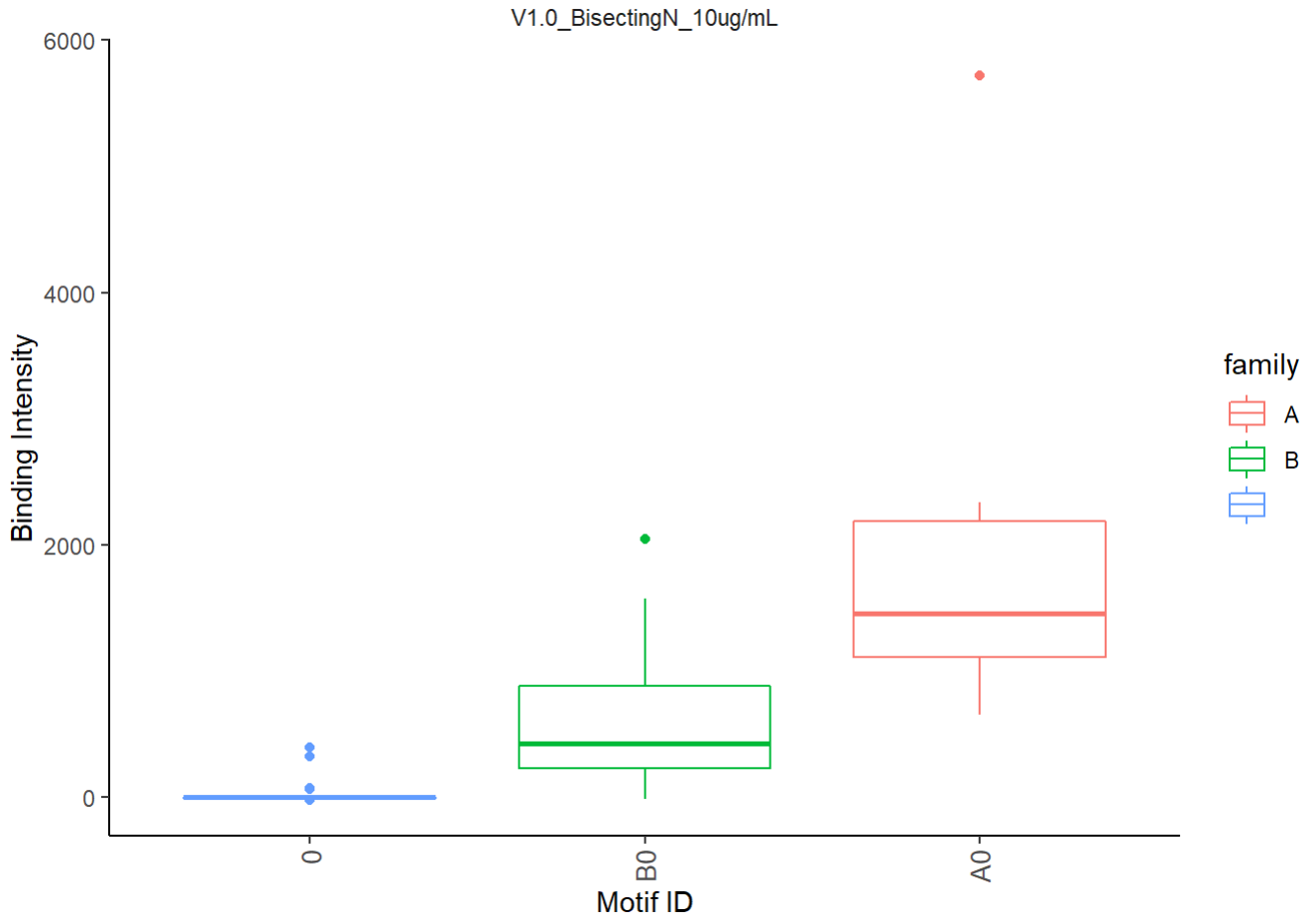
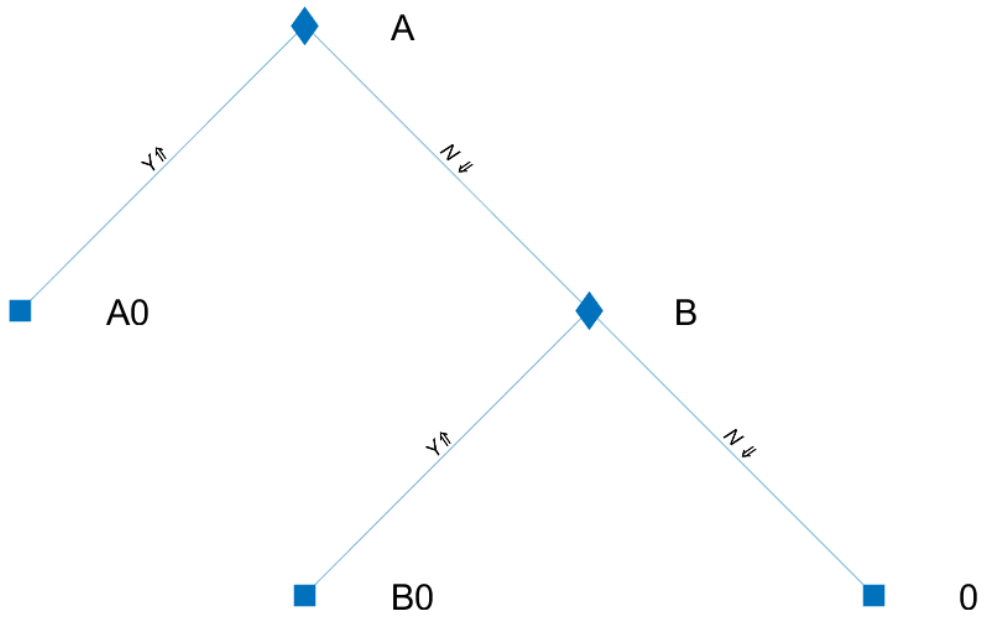


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



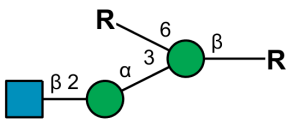
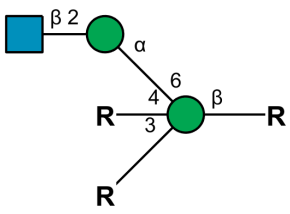
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

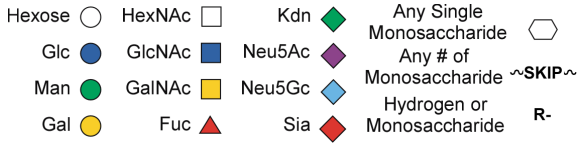
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f4f>ManB
B0		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
0		Non-Binders

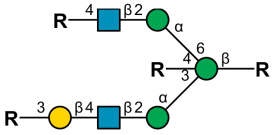
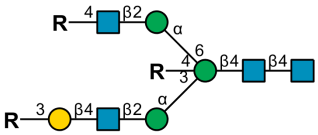
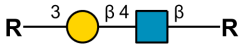
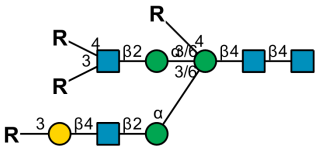
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

Galectin3

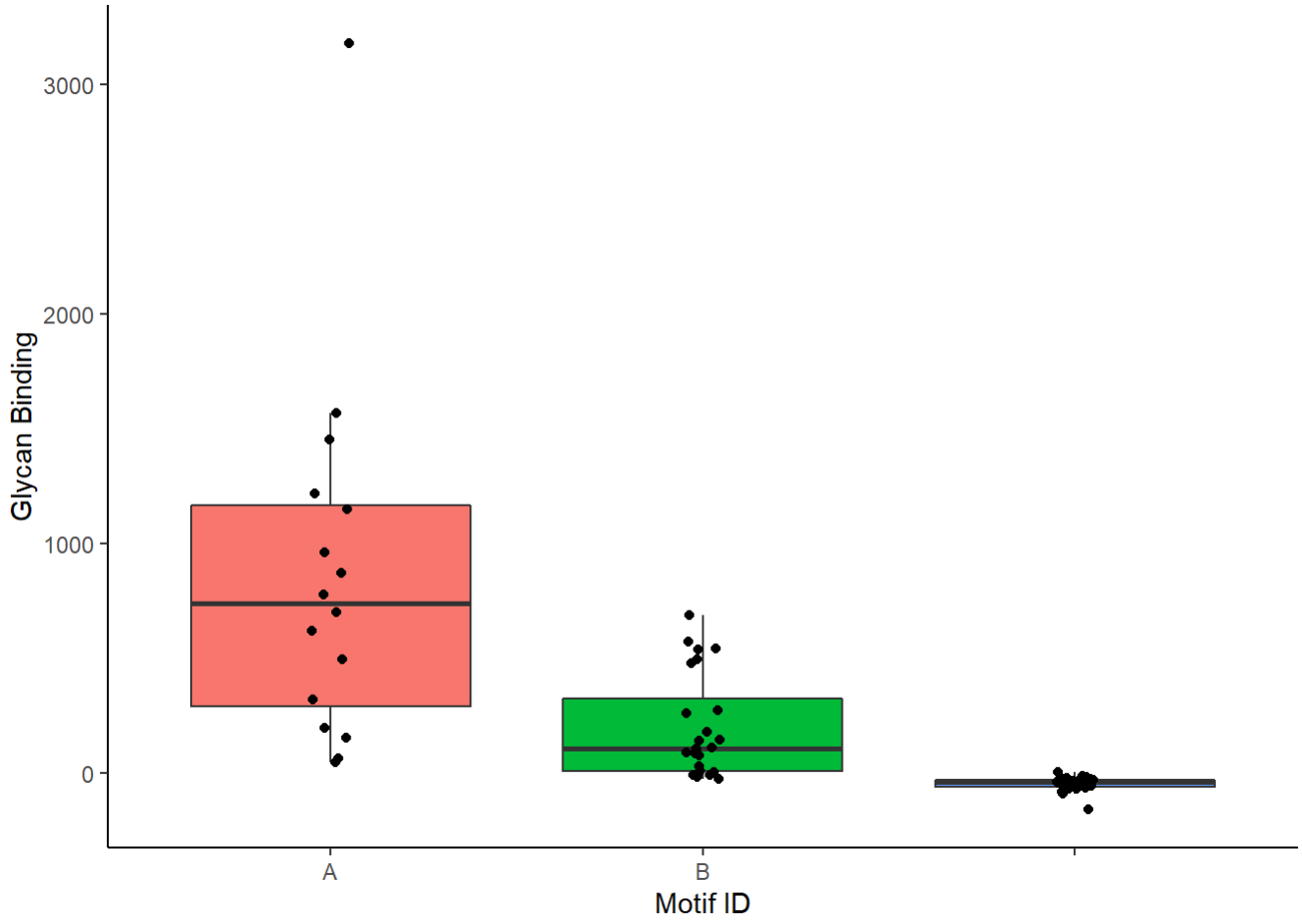
Automated Analysis report for Galectin3 evaluated at 50 ug/mL

List of Primary Galectin3 Motifs

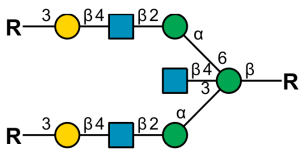
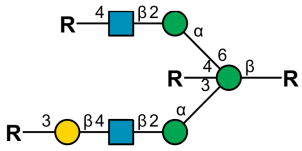
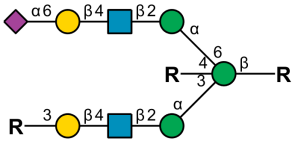
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	16
B			0.25	24
0			-0.05	32

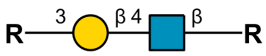
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

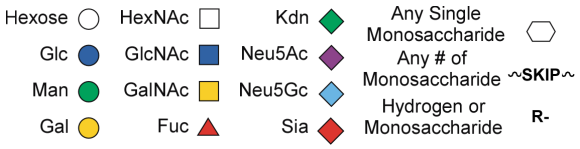


List of Fine-Specificity Galectin3 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A1			1.00	4	<0.001
A0*			0.53	8	<0.001
A2	a6 Sialyl Type 2 LacNAc a3 Sialyl Type 2 LacNAc (94%)		0.18	4	0.328

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
B0			0.17	24	0.018
0	Non-Binders (100%)		0.00	32	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

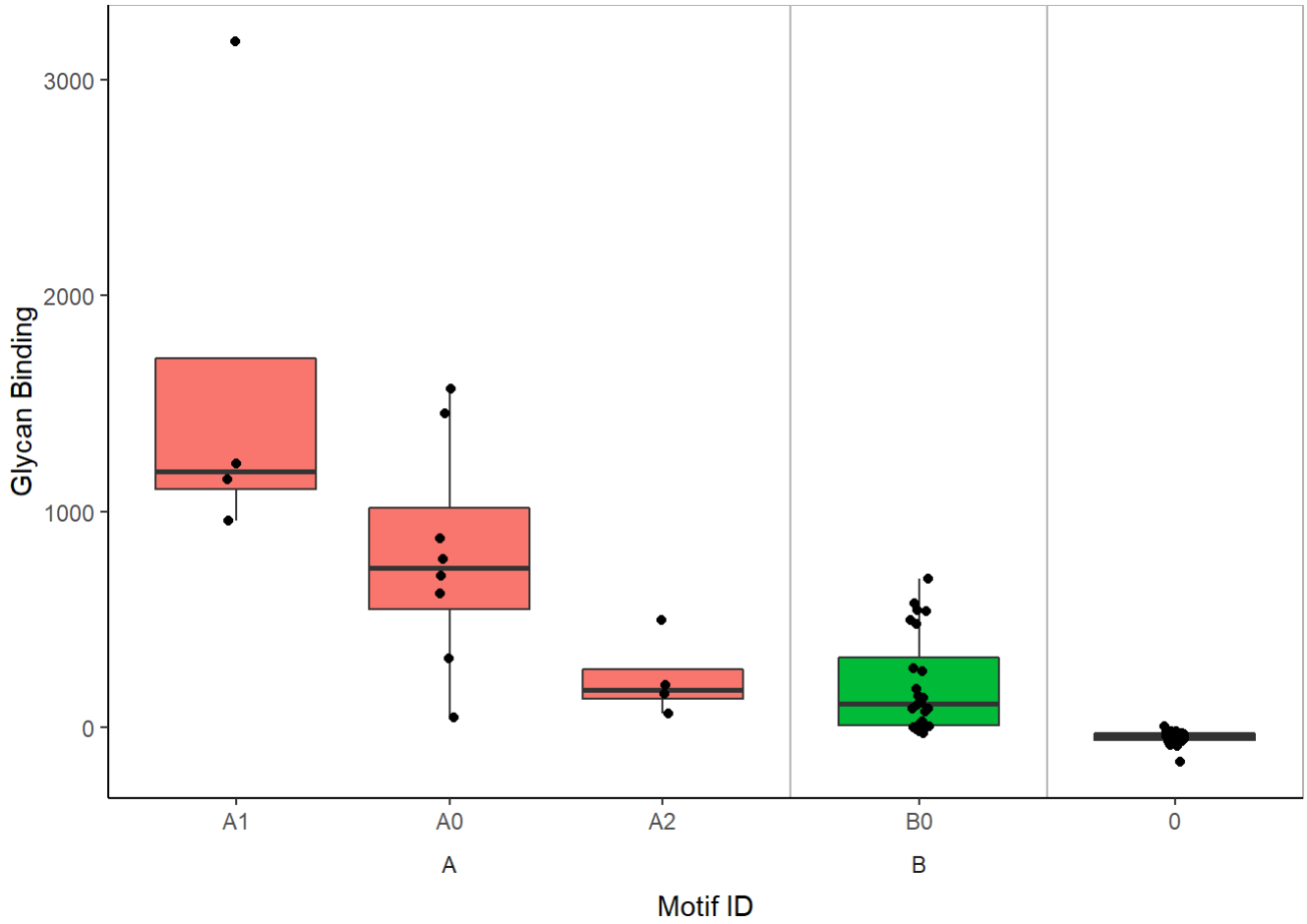


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

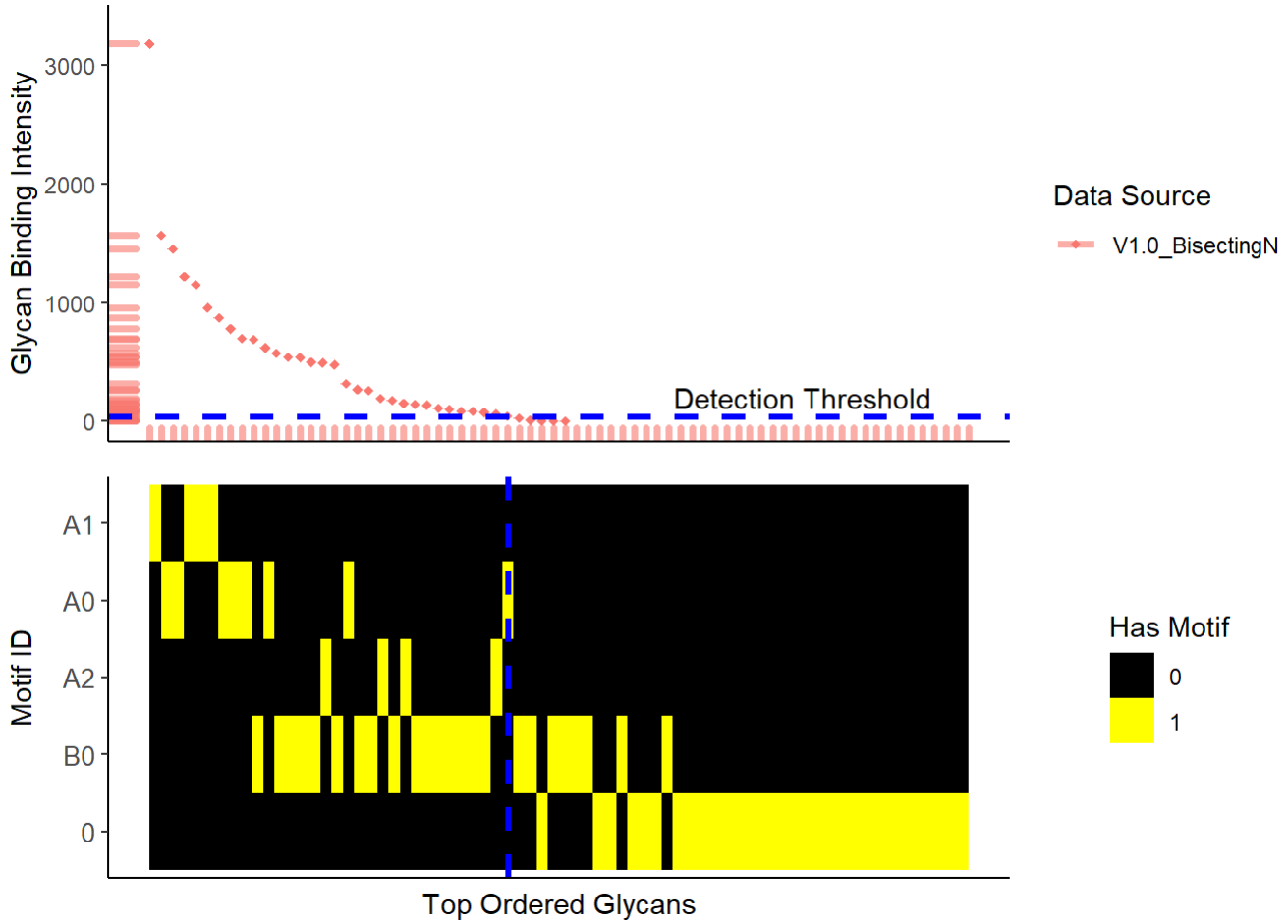
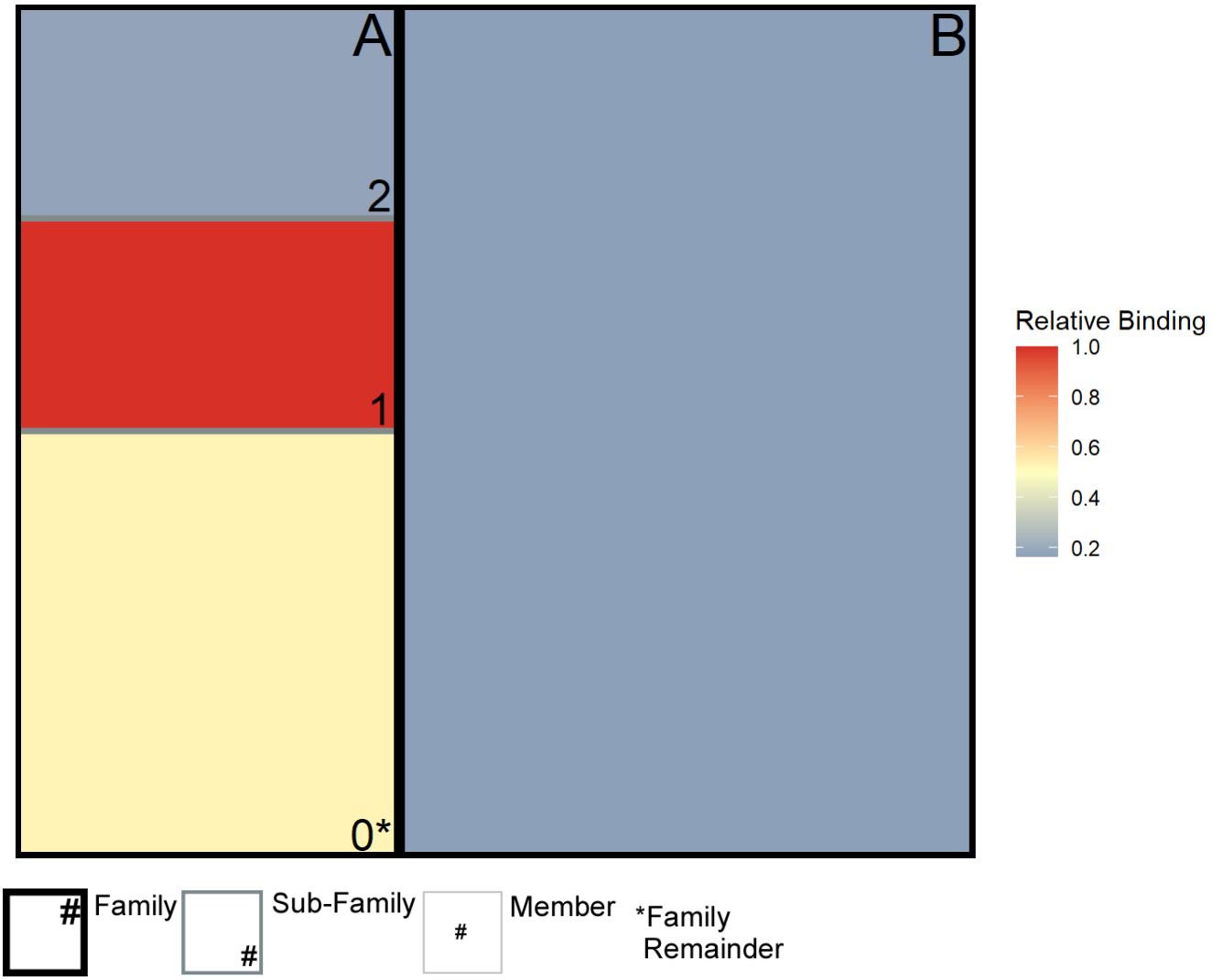


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

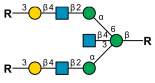
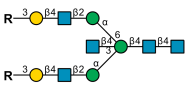
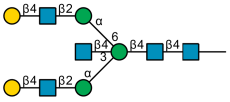
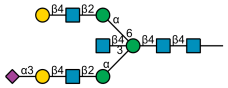
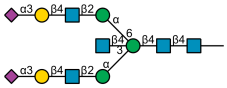
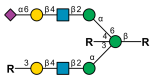
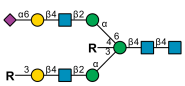
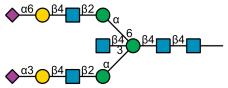
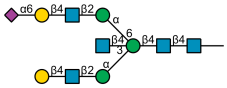


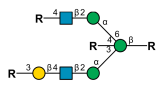
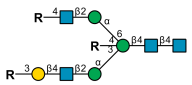
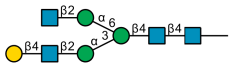
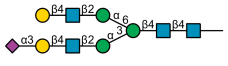
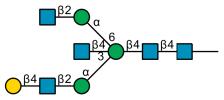
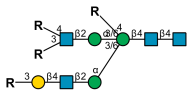
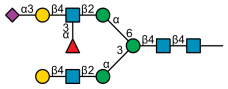
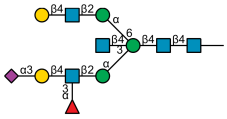
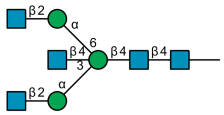
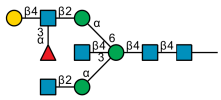
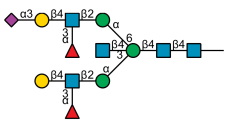
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

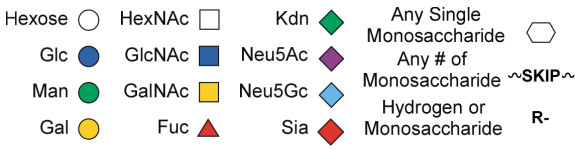
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				2		12		3
A2				67		31		28

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				43		48		7
B0				49		66		15
0				1		25		36

Key:



All Concentration Plots:

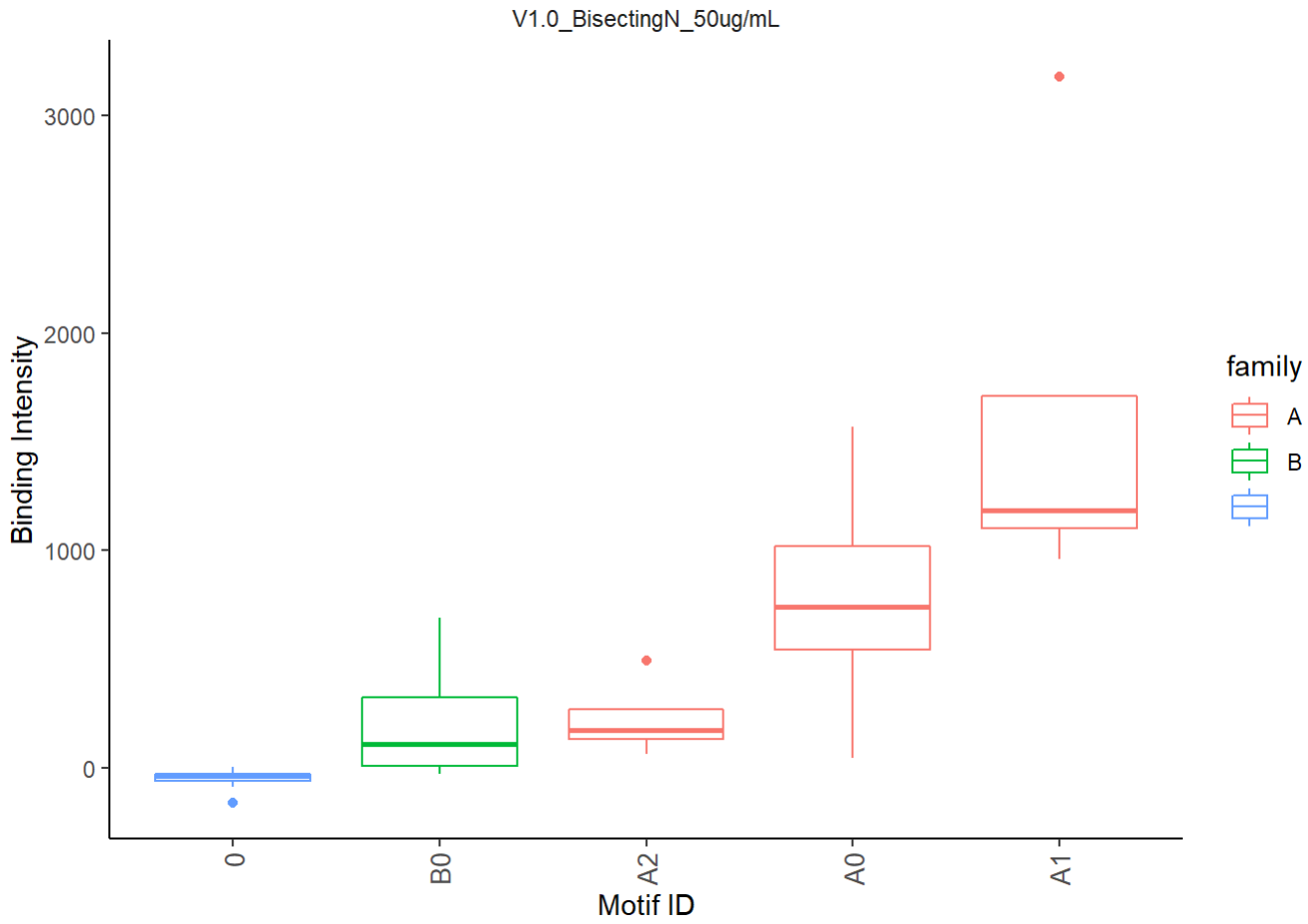
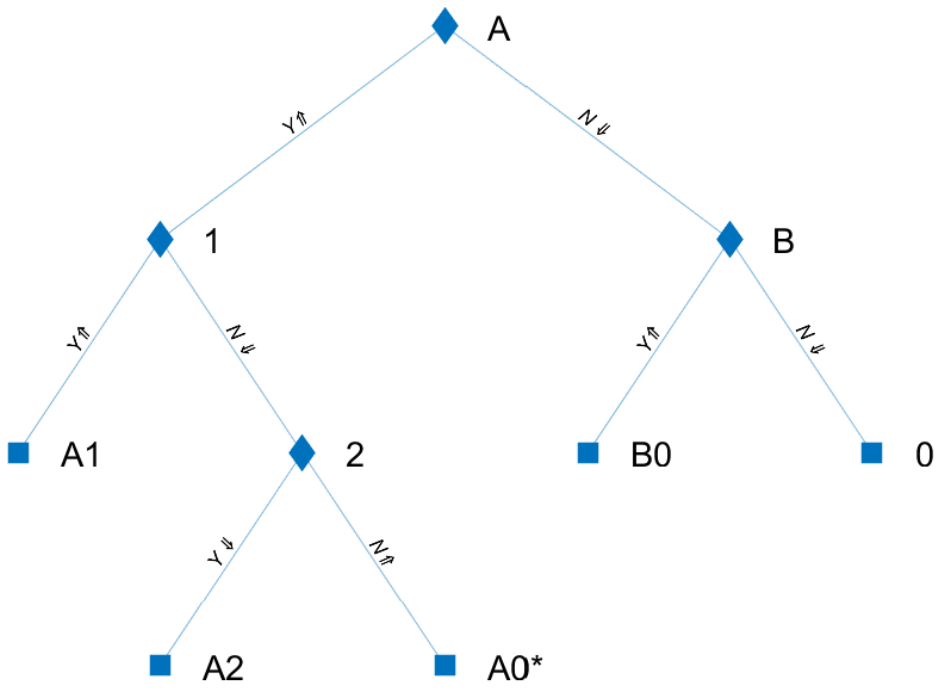


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



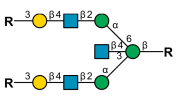
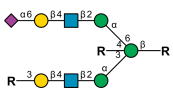
*Motif matches the remaining glycans not matched by earlier motifs in the model.

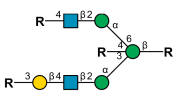
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

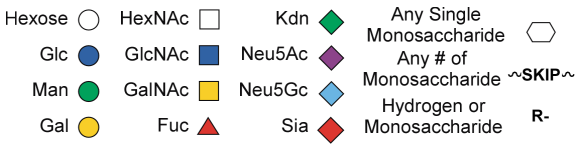
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)(<3f4f6f>GlcNAcB1-4)<2f>ManB
A2		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f>ManB

Motif ID	Motif Graphic	Motif Text
A0*		<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f>ManB
B0		<2f4f6f>GalB1-4<3f6f>GlcNAcB
0		Non-Binders

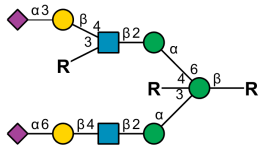
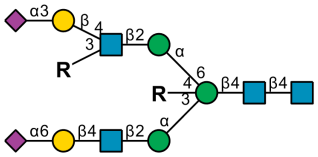
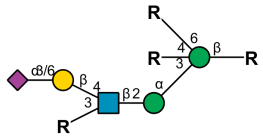
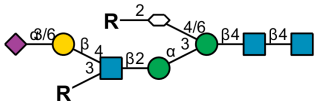
Key:



Siglec3

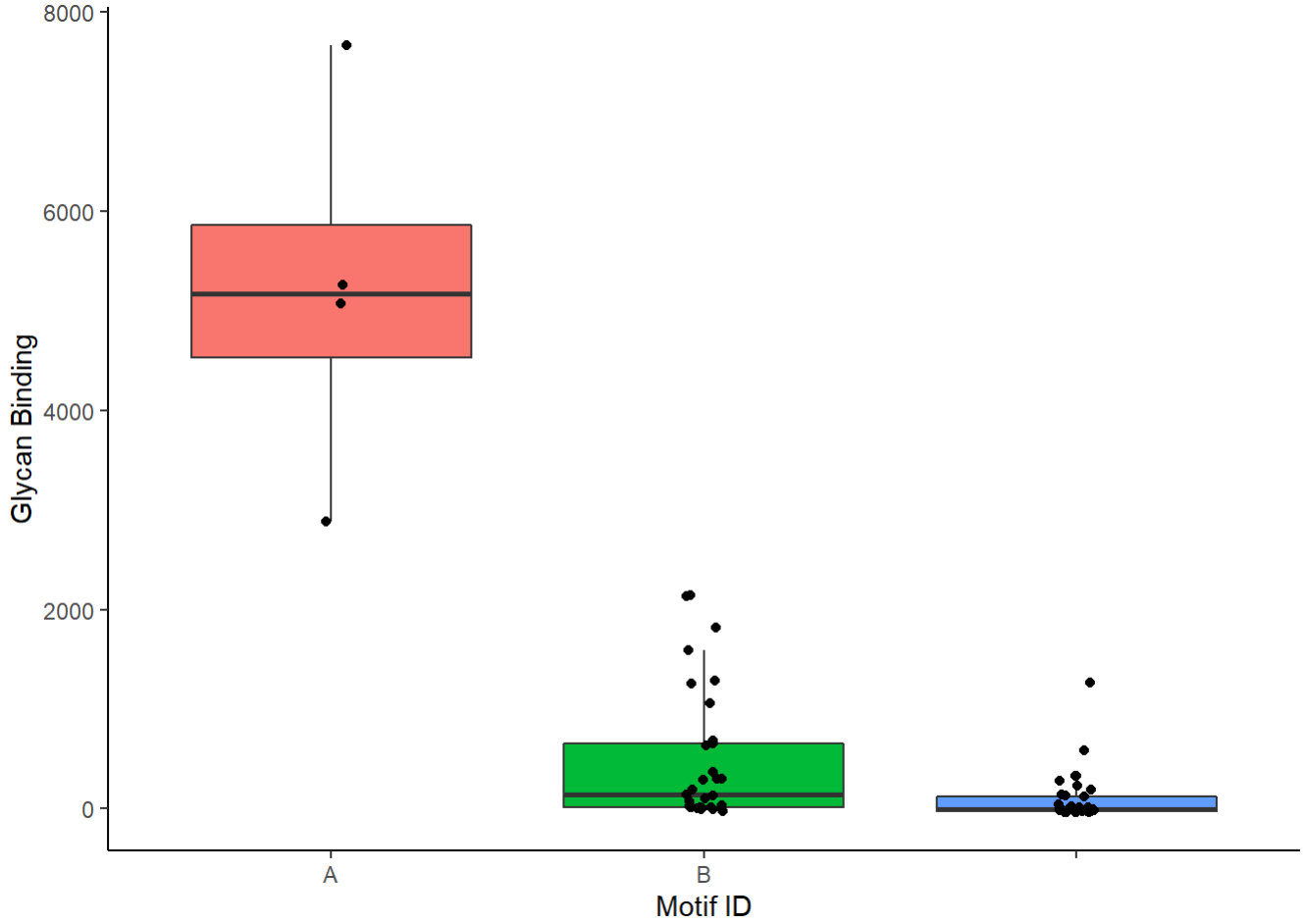
Automated Analysis report for Siglec3 evaluated at 20 ug/mL

List of Primary Siglec3 Motifs

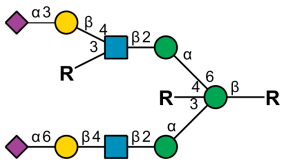
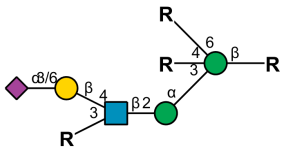
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	4
B			0.10	32
0			0.02	36

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

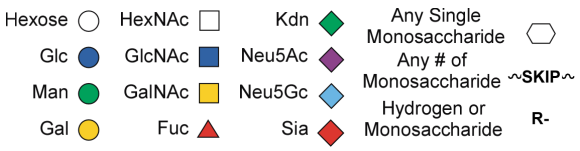
Boxplot of Primary Motifs



List of Fine-Specificity Siglec3 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0	a6 Sialyl Type 2 LacNAc a3 Sialyl Type 2 LacNAc (94%)		1.00	4	<0.001
B0			0.09	32	0.028
0	Non-Binders (100%)		0.00	36	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

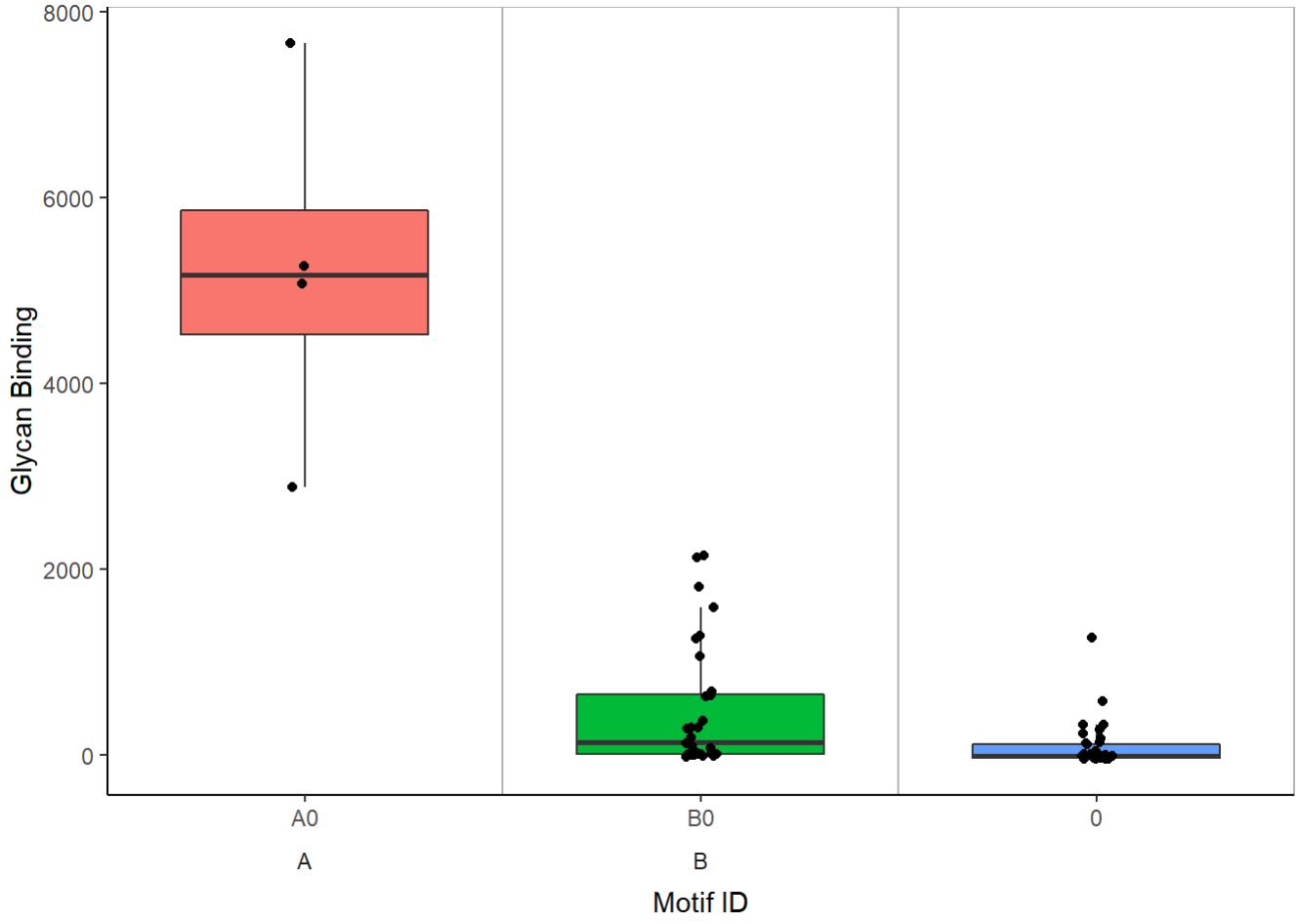


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

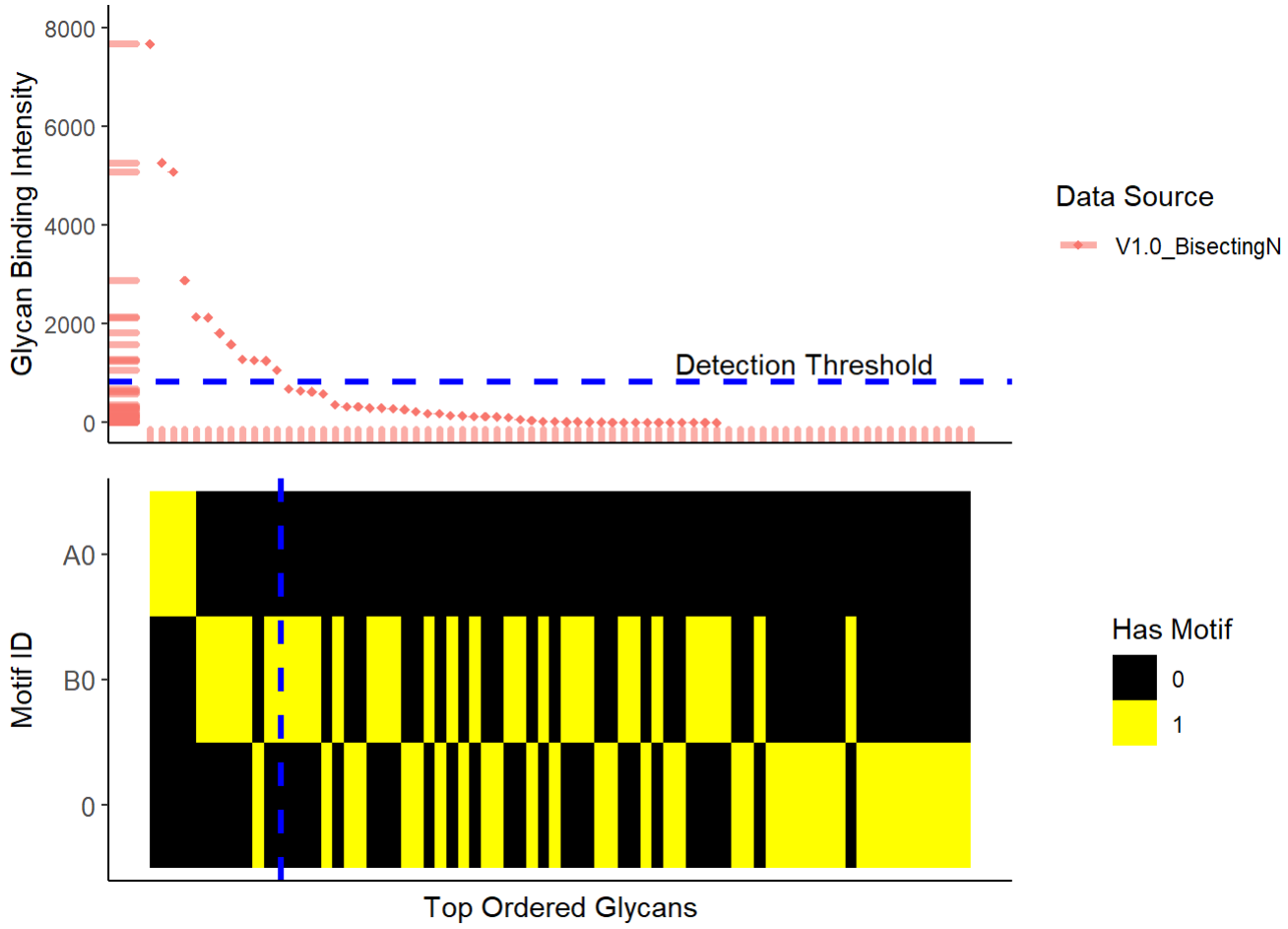
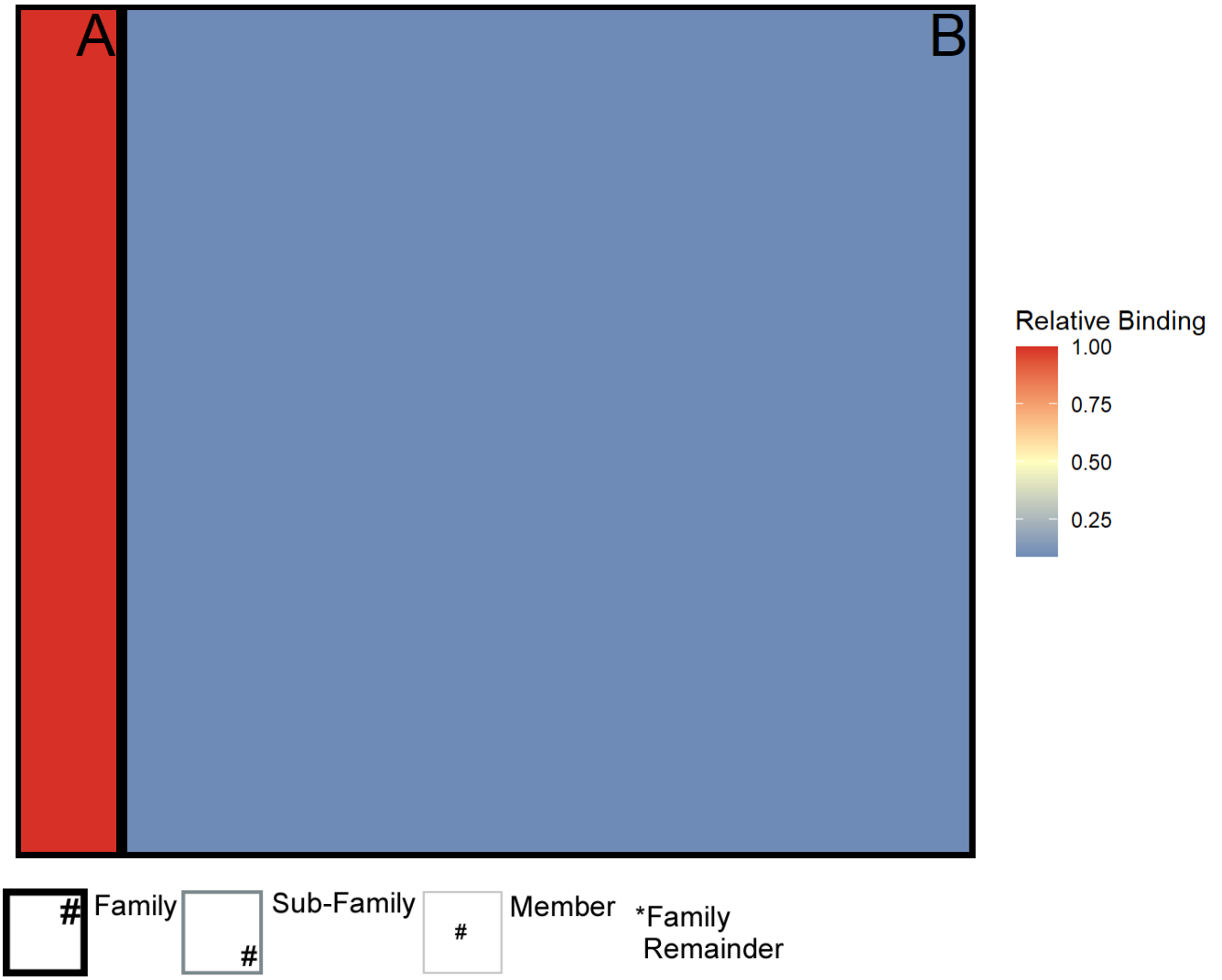


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

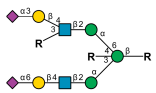
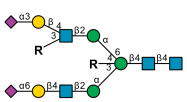
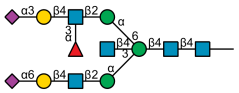
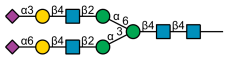
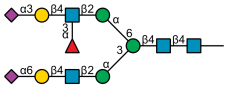
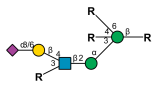
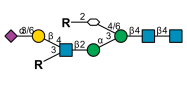
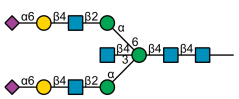
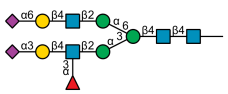
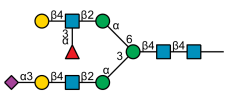


*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

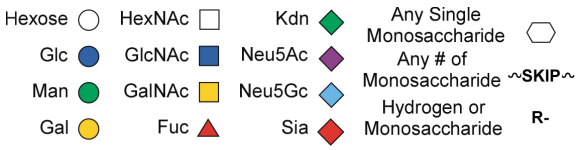
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				35		52		71
B0				4		56		68

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
0			26	62	65

Key:



All Concentration Plots:

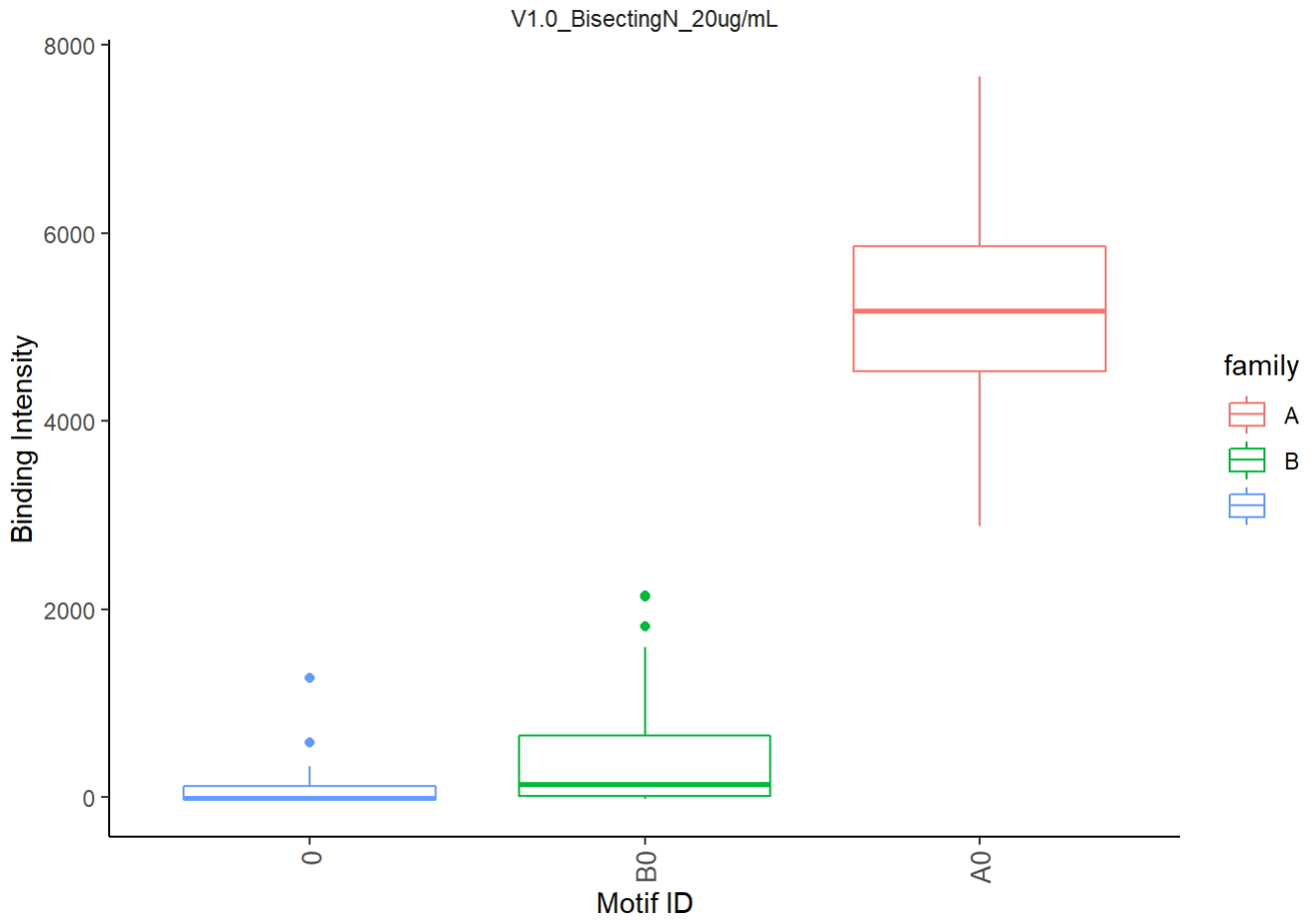
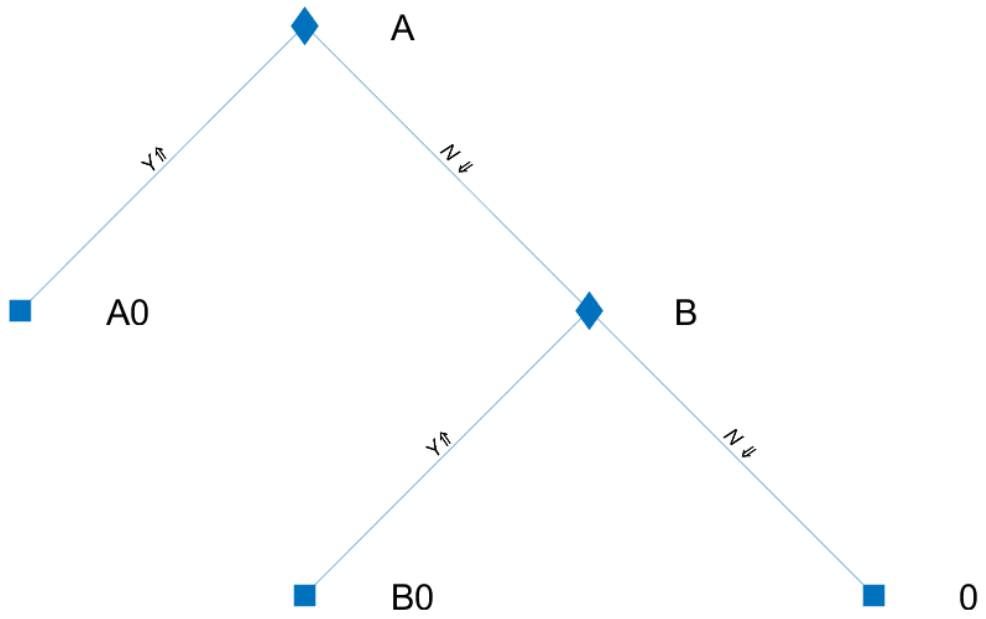


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



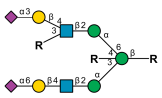
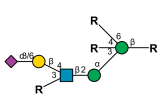
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

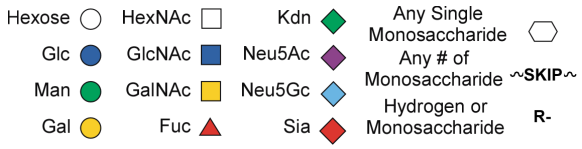
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f>ManB
B0		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
0		Non-Binders

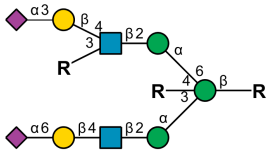
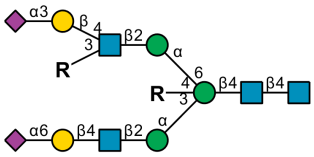
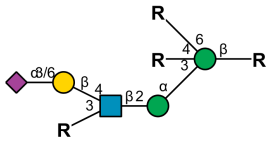
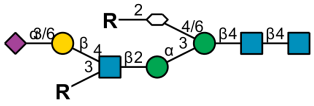
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

Siglec10

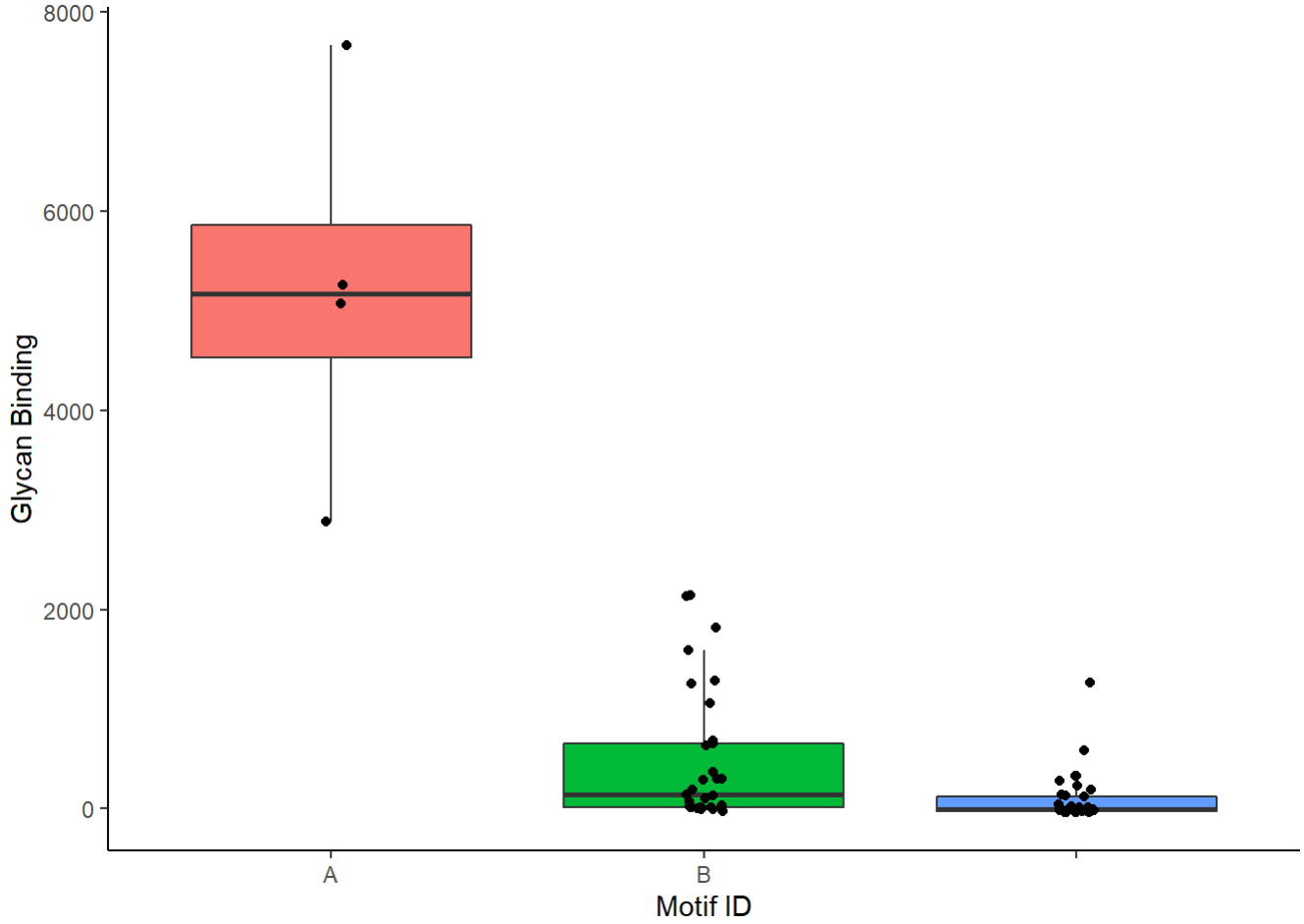
Automated Analysis report for Siglec10 evaluated at 20 ug/mL

List of Primary Siglec10 Motifs

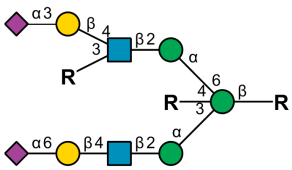
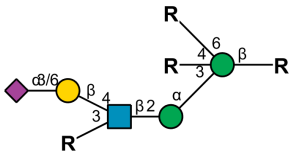
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	4
B			0.10	32
0			0.02	36

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

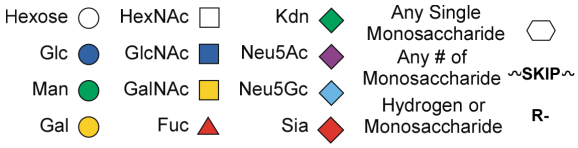
Boxplot of Primary Motifs



List of Fine-Specificity Siglec10 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0	a6 Sialyl Type 2 LacNAc a3 Sialyl Type 2 LacNAc (94%)		1.00	4	<0.001
B0			0.09	32	0.028
0	Non-Binders (100%)		0.00	36	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

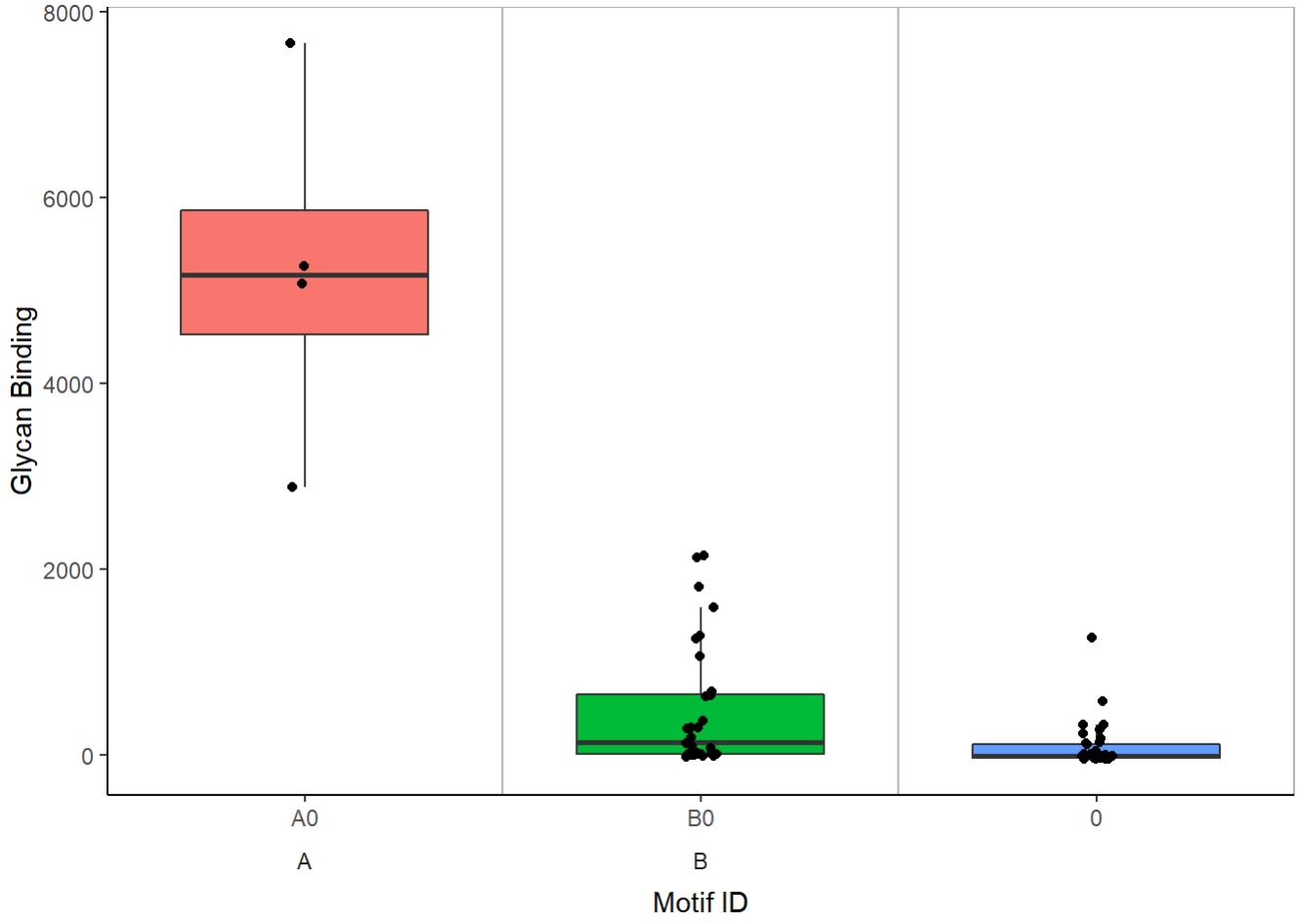


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

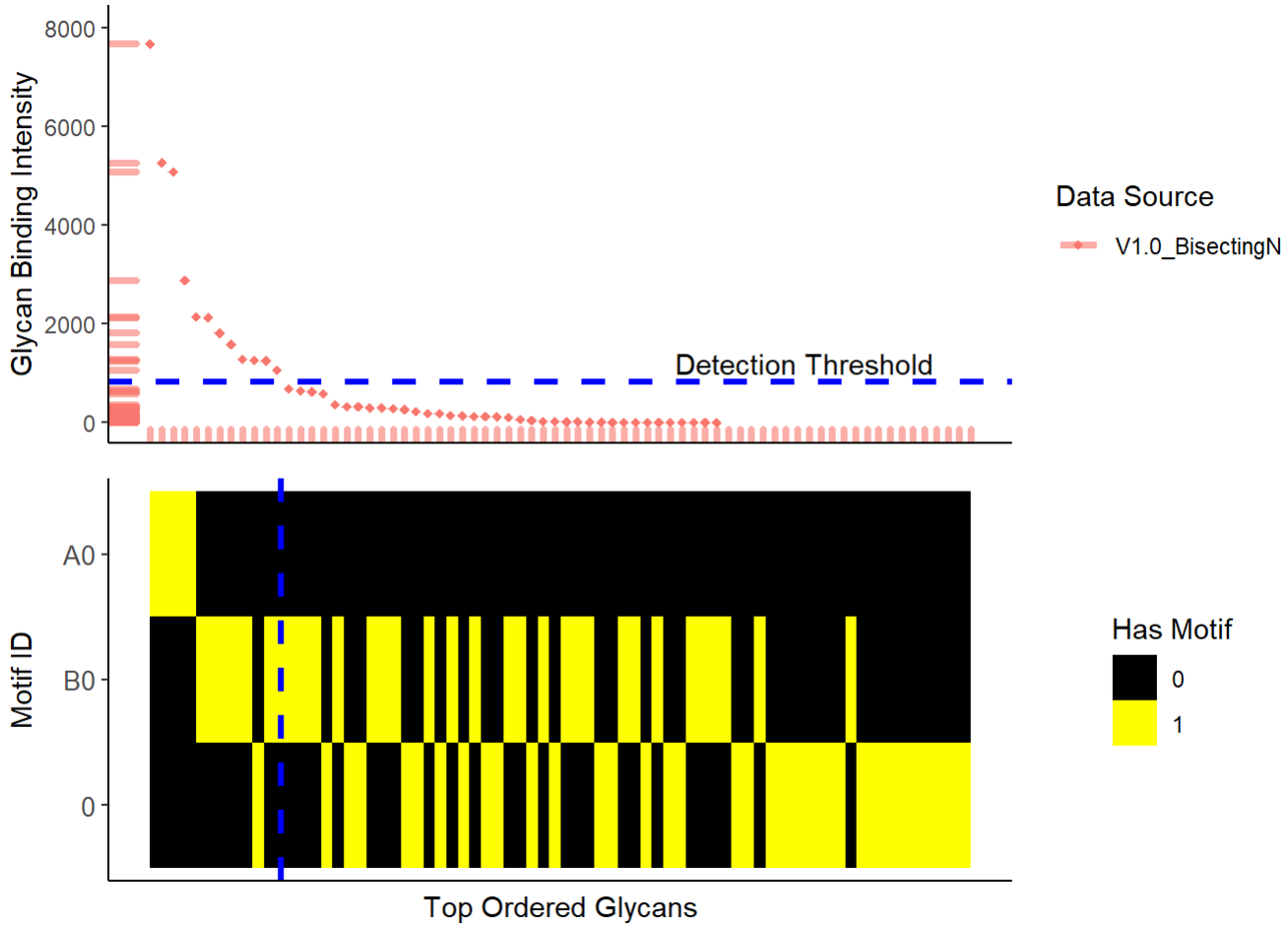
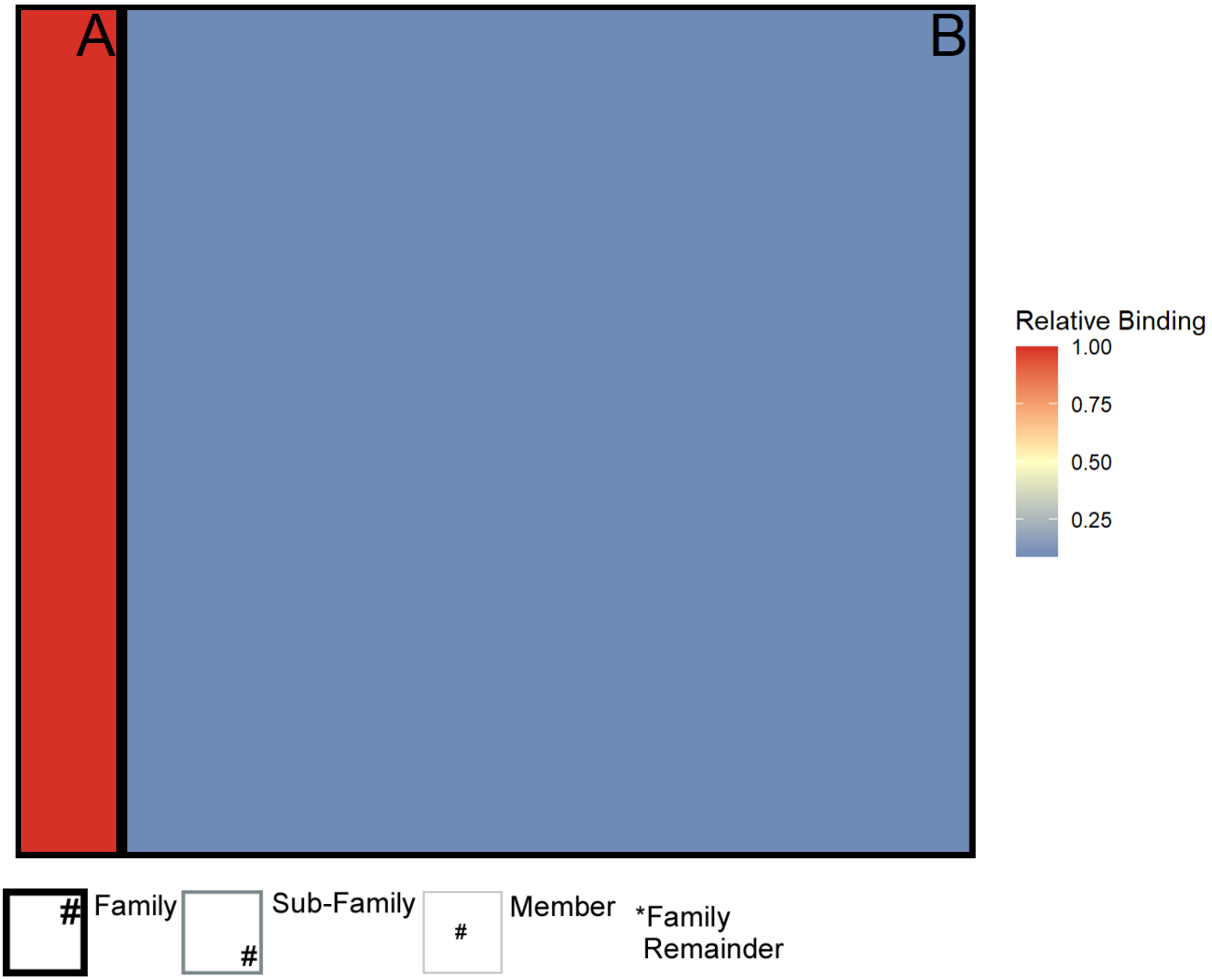


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

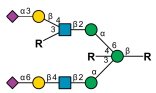
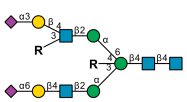
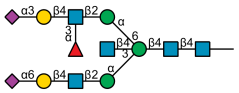
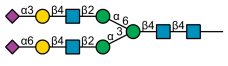
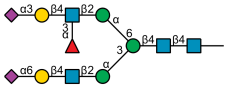
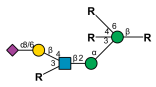
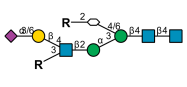
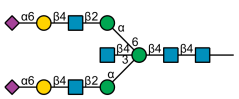
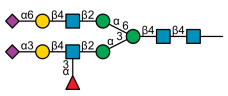
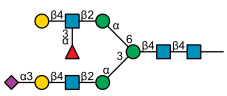


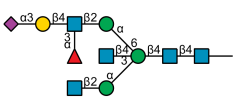
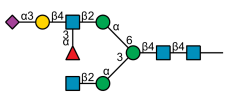
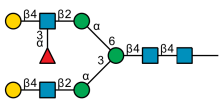
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

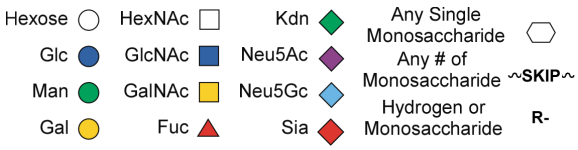
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				35		52		71
B0				4		56		68

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
0			 26	 62	 65

Key:



All Concentration Plots:

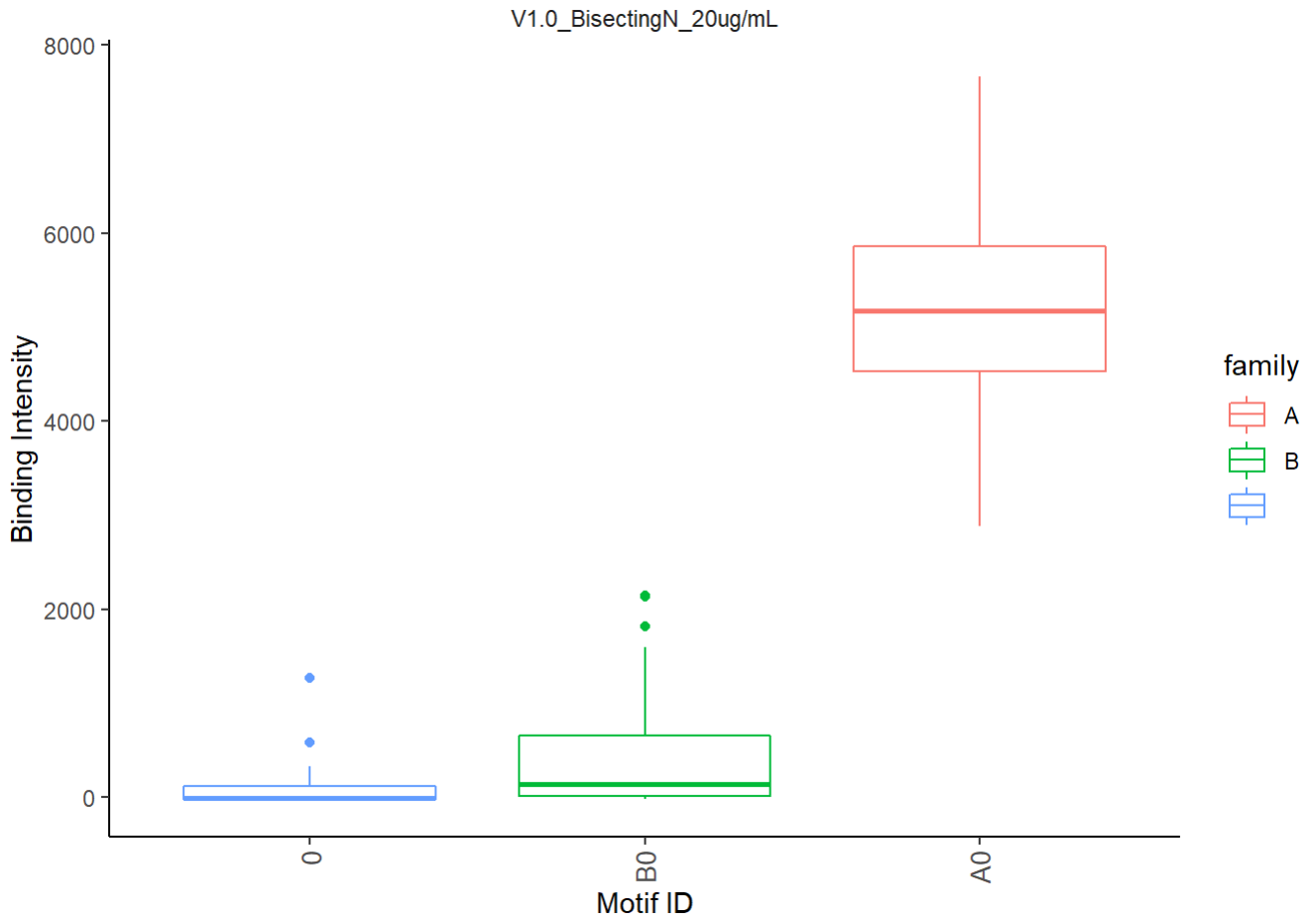
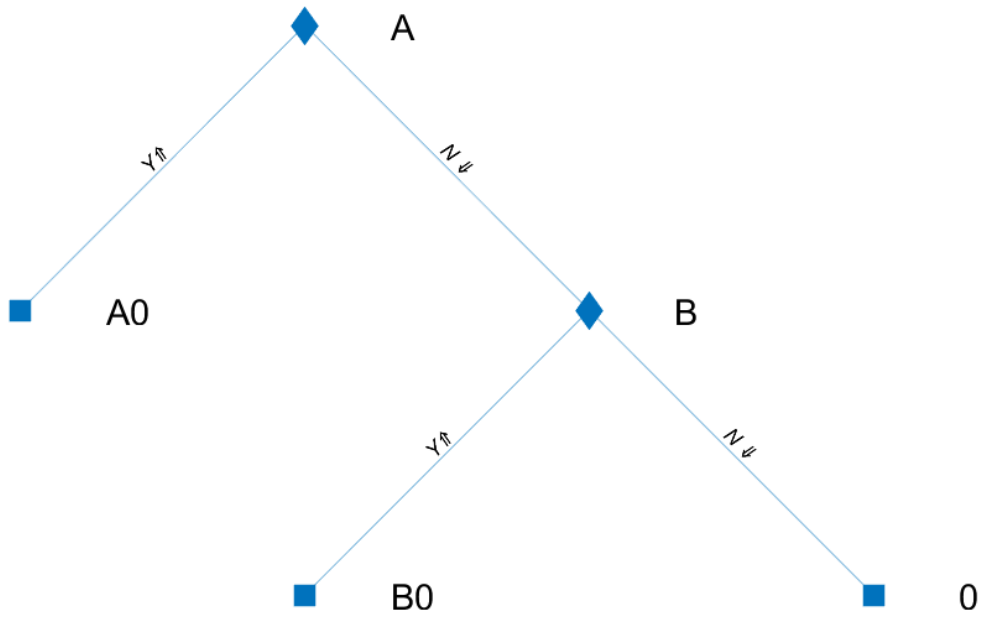


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



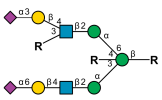
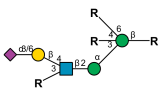
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

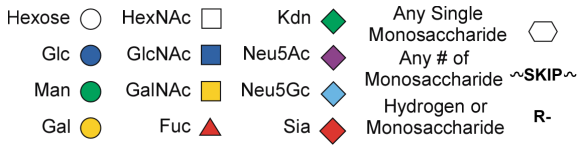
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f>ManB
B0		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
0		Non-Binders

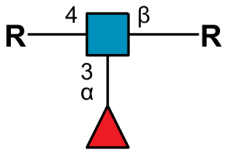
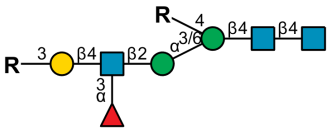
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

E-selectin

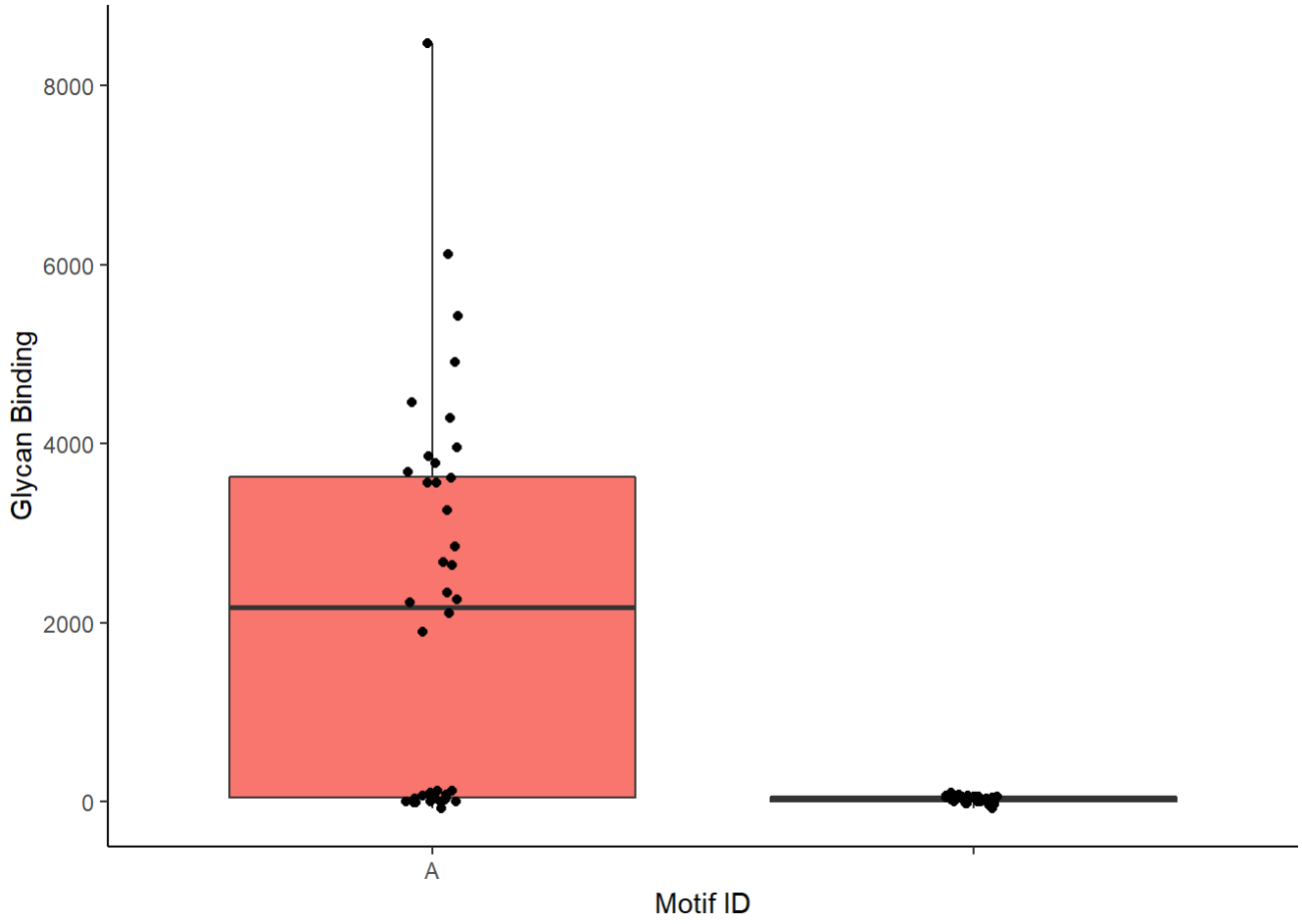
Automated Analysis report for E-selectin evaluated at 10 ug/mL

List of Primary E-selectin Motifs

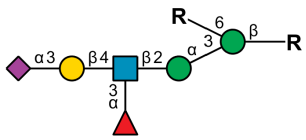
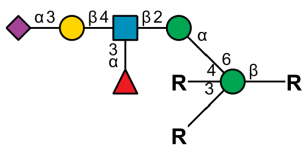
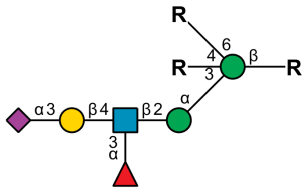
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	40
0			0.01	32

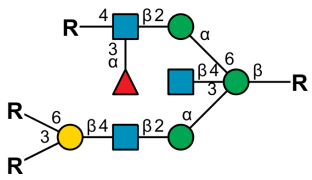
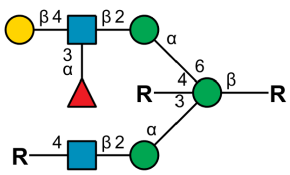
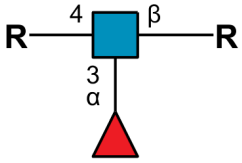
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

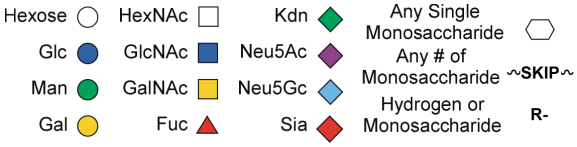


List of Fine-Specificity E-selectin Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A4			1.00	5	<0.001
A2			0.92	9	<0.001
A5*	Sialyl Lewis X Bisecting N-Glycan (92%)		0.70	5	<0.001

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A1			0.41	6	0.023
A3			0.01	5	1.000
A0*			0.00	10	1.000
0	Non-Binders (100%)		0.00	32	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

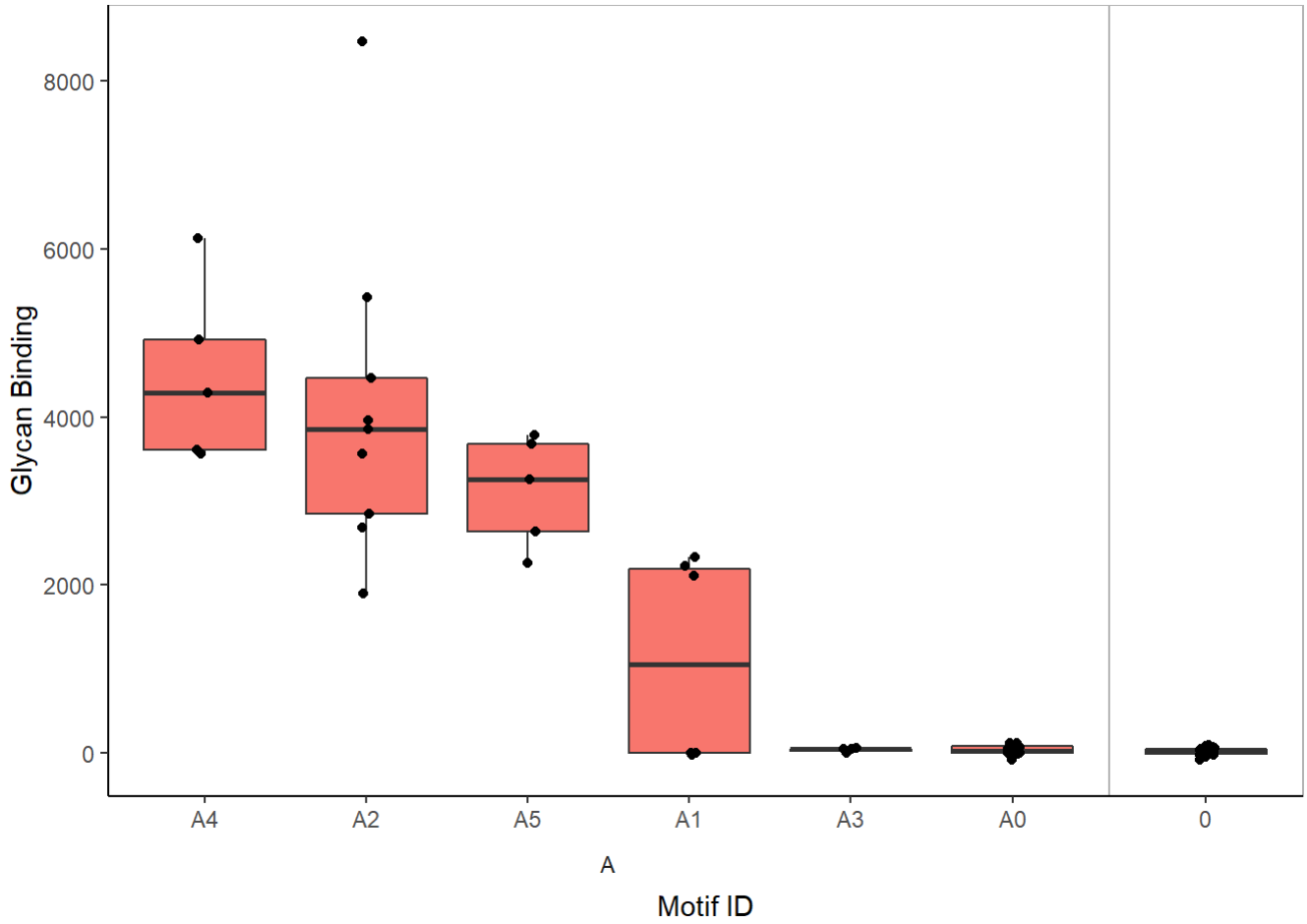


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

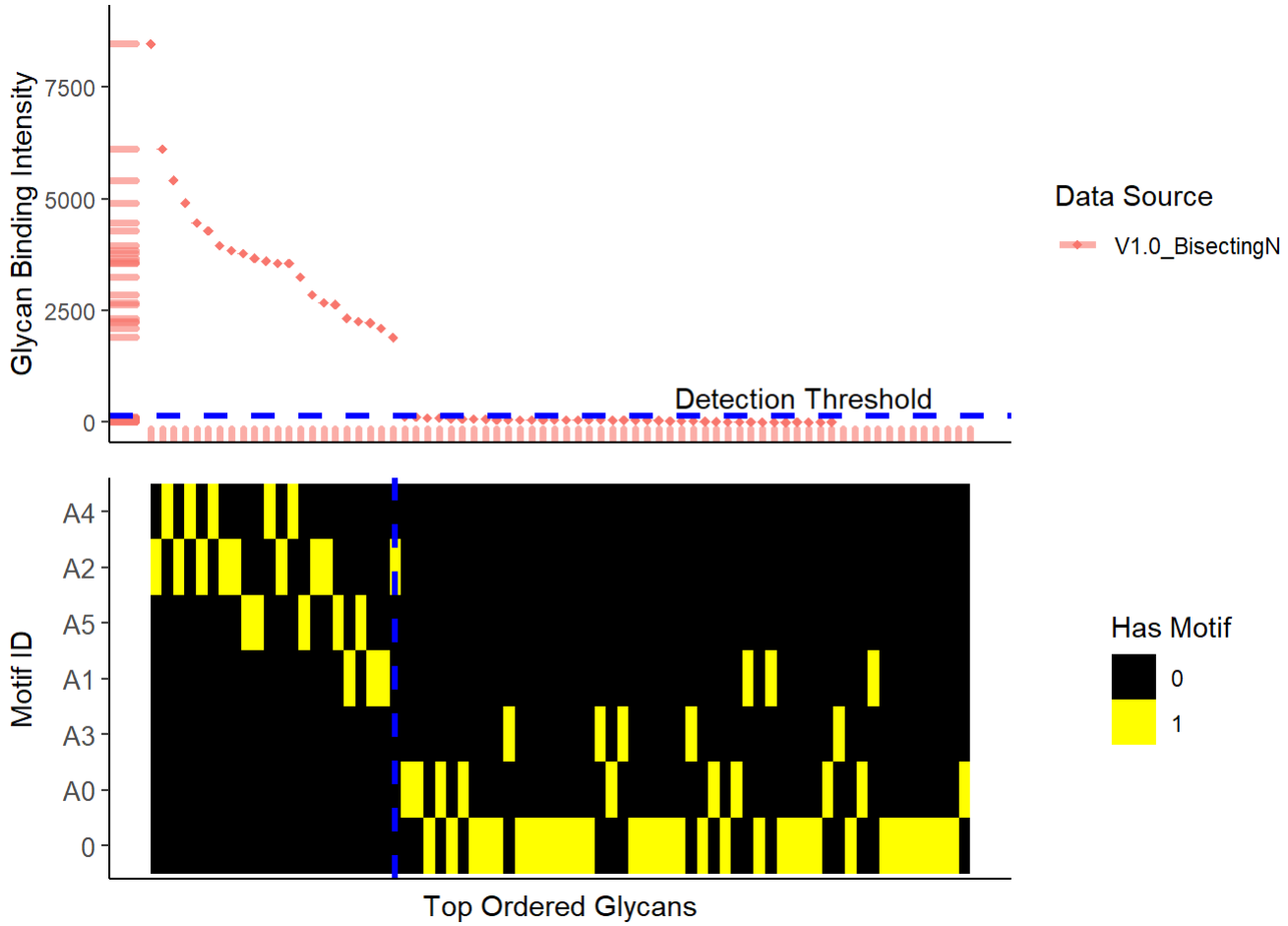
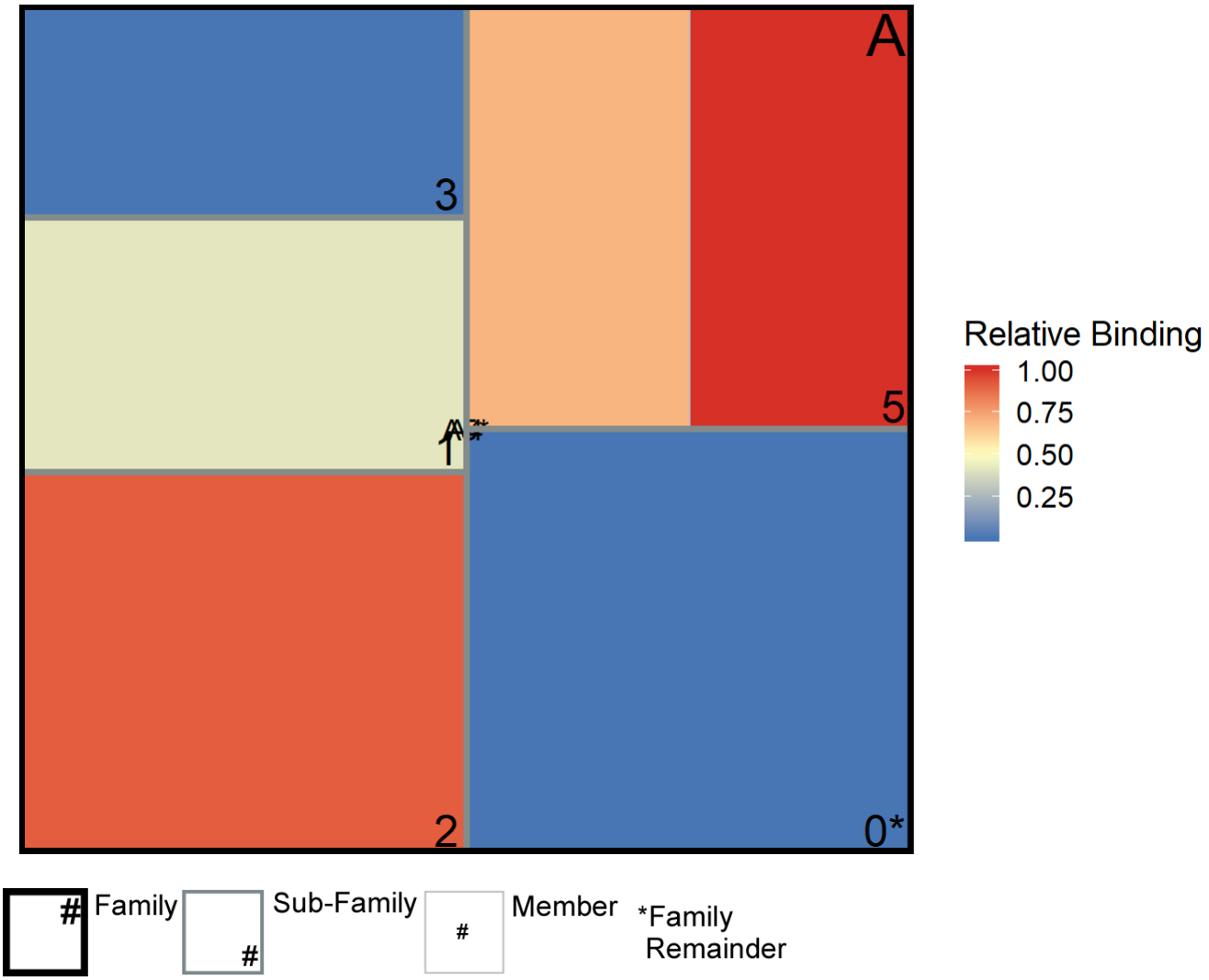


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

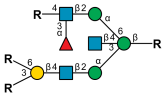
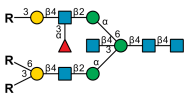
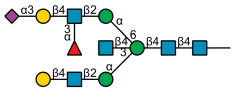
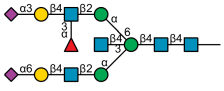
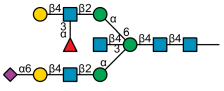


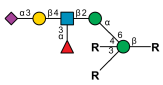
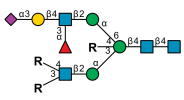
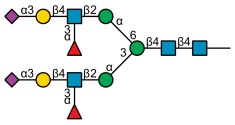
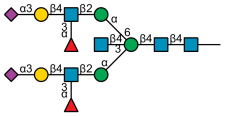
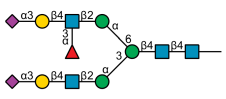
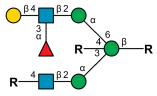
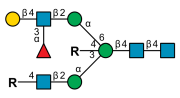
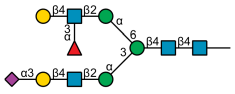
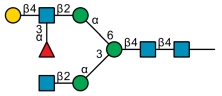
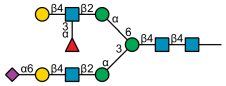
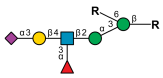
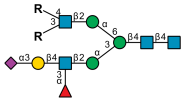
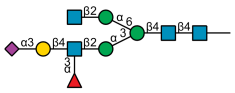
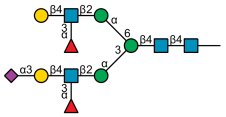
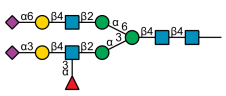
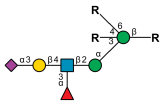
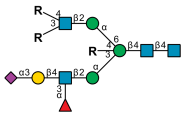
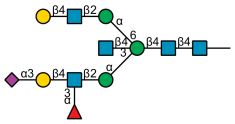
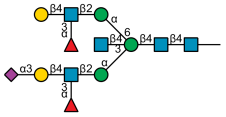
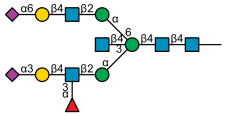
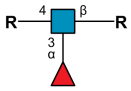
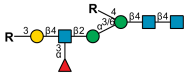
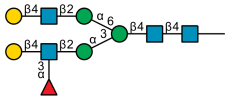
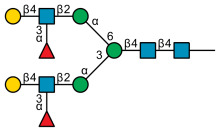
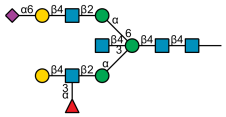
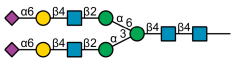
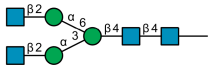
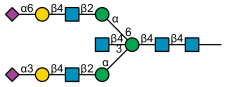
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

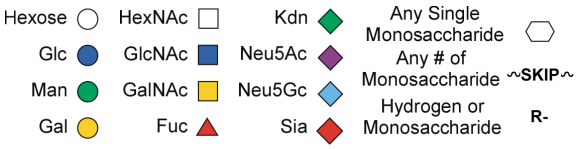
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				30		35		34

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A2				42		6		69
A3				68		61		70
A4				47		57		56
A5				15		21		20
A0				50		41		19
0				40		37		31

Key:



All Concentration Plots:

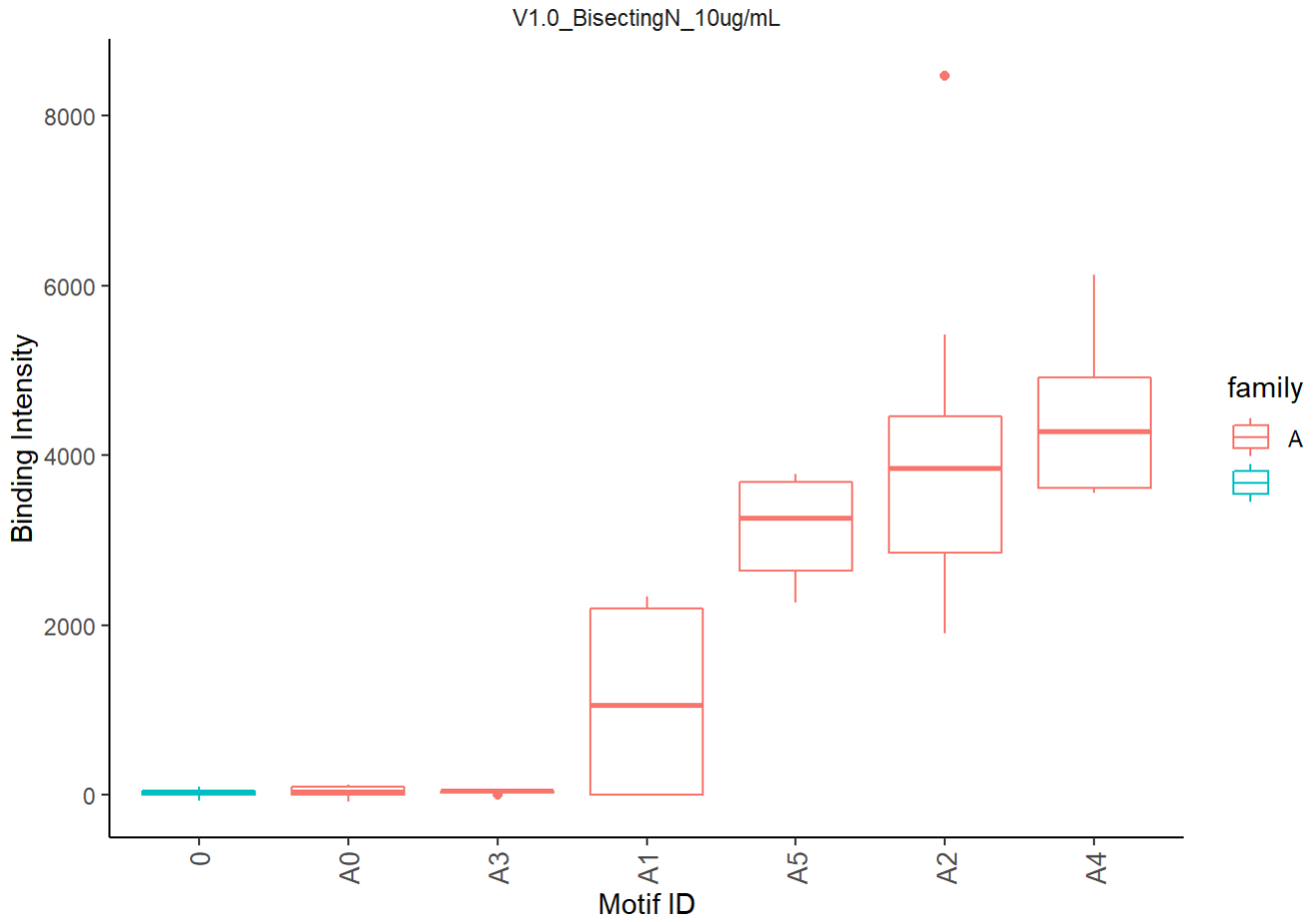
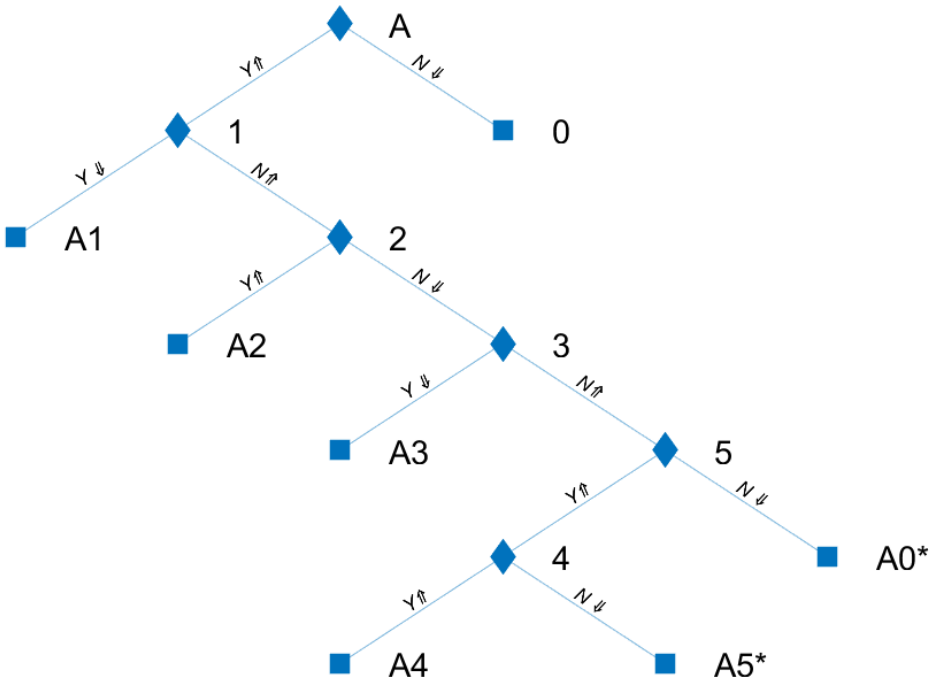


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



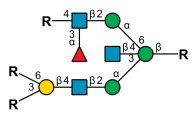
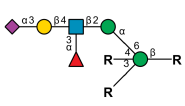
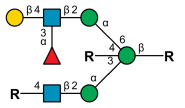
*Motif matches the remaining glycans not matched by earlier motifs in the model.

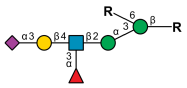
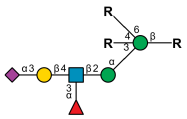
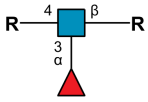
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

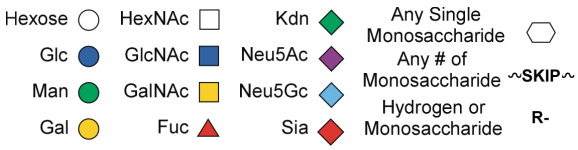
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<2f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f3f4f>FucA1-3<6f>GlcNAcB1-2<3f4f6f>ManA1-6)(<3f4f6f>GlcNAcB1-4)<2f>ManB
A2		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
A3		<2f3f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f>ManB

Motif ID	Motif Graphic	Motif Text
A4		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f4f>ManB
A5*		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
A0*		<2f3f4f>FucA1-3<6f>GlcNAcB
0		Non-Binders

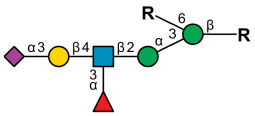
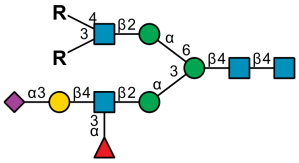
Key:



CD15s

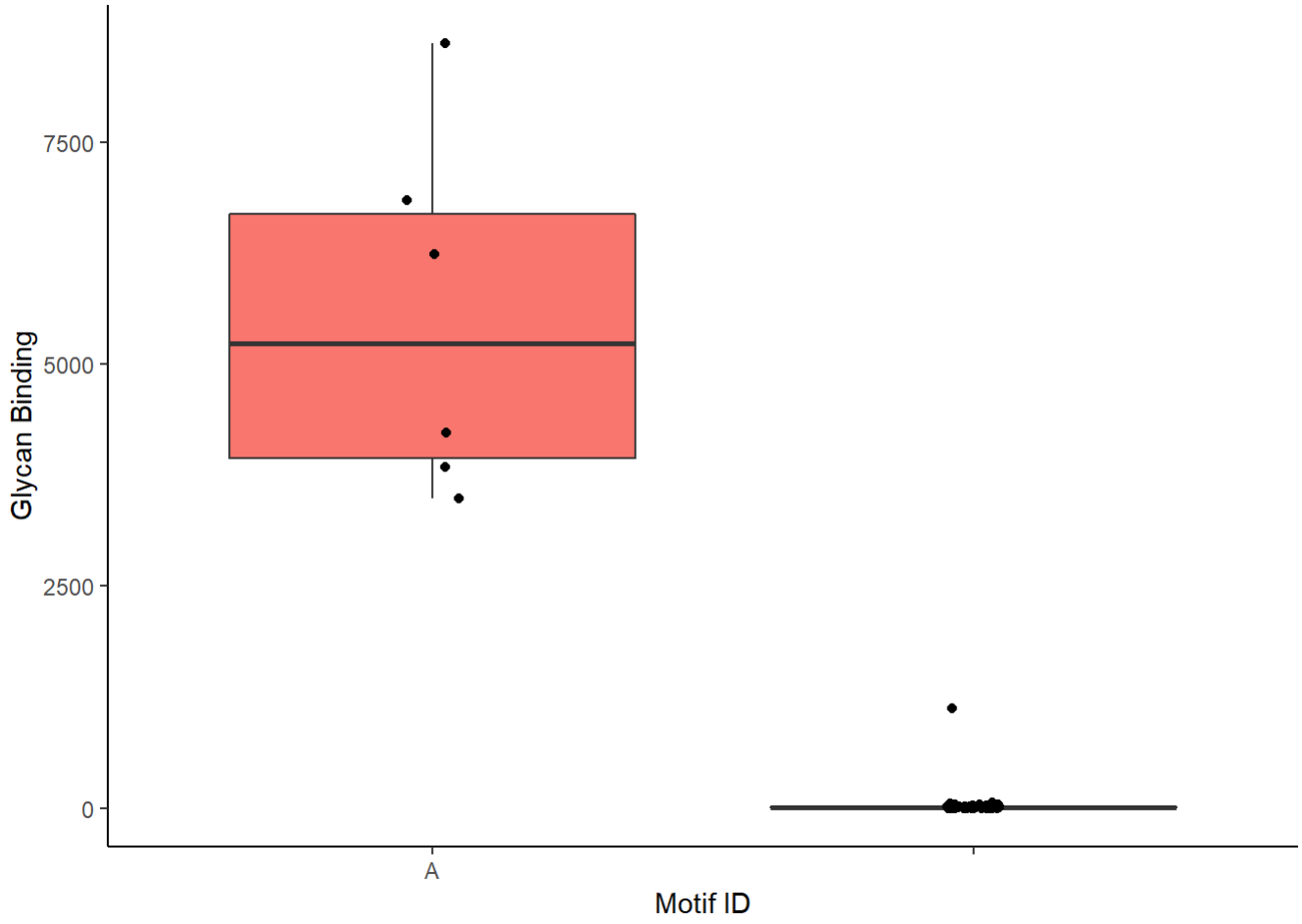
Automated Analysis report for CD15s evaluated at 20 ug/mL

List of Primary CD15s Motifs

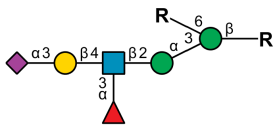
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	6
0			0.01	66

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

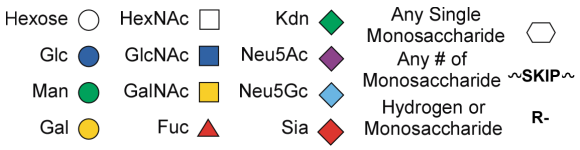
Boxplot of Primary Motifs



List of Fine-Specificity CD15s Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0			1	6	<0.001
0	Non-Binders (100%)		0	66	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

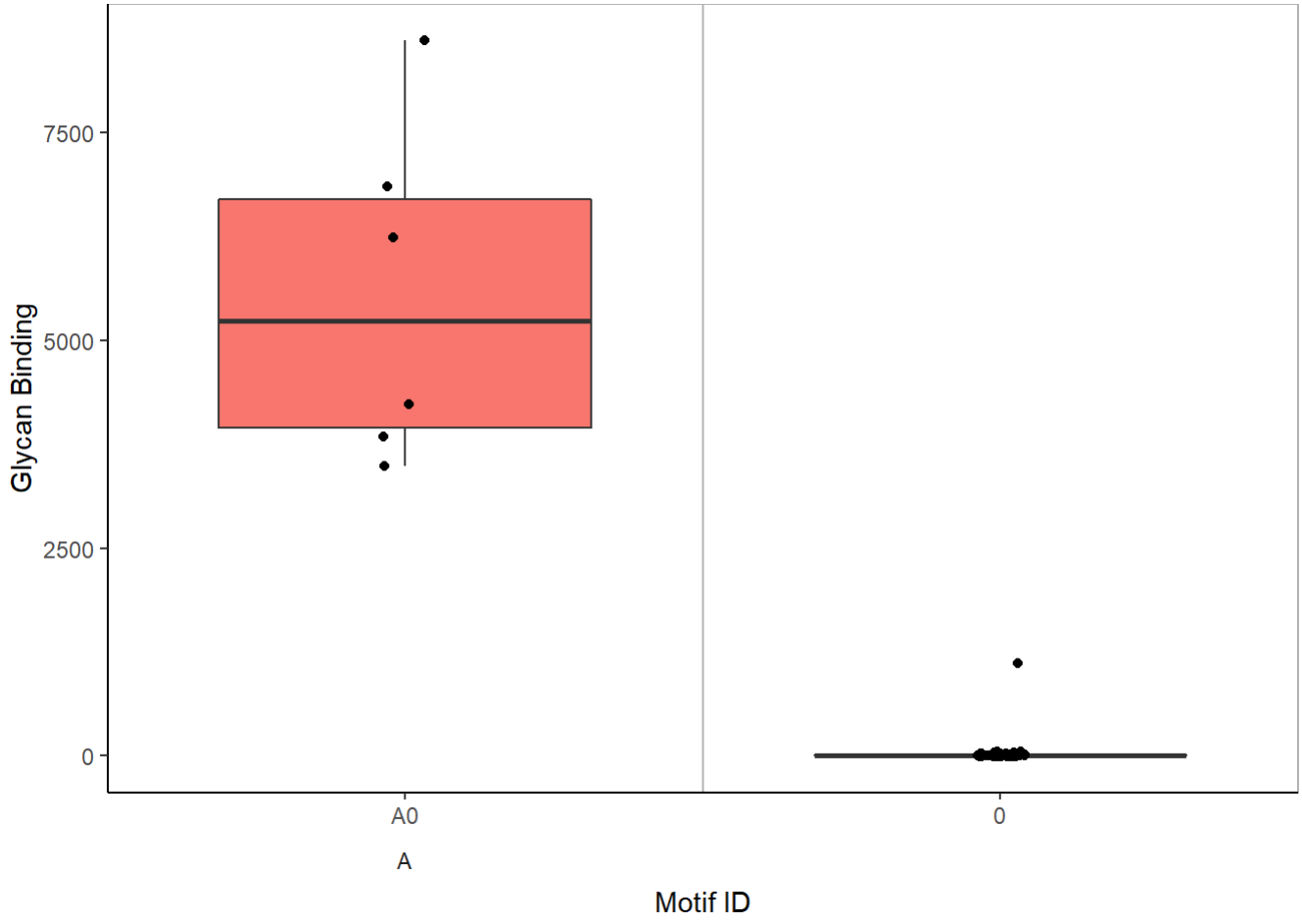


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

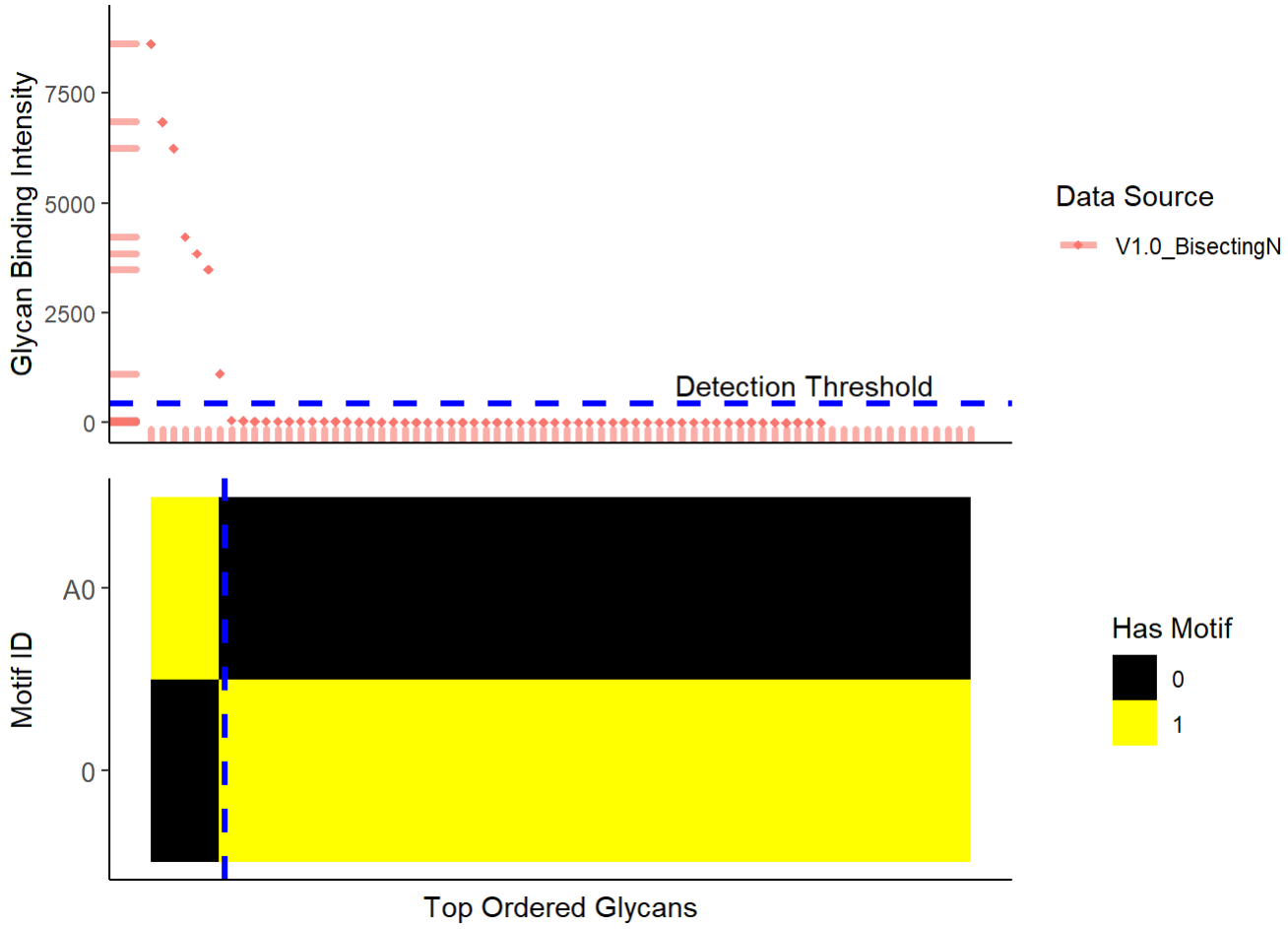
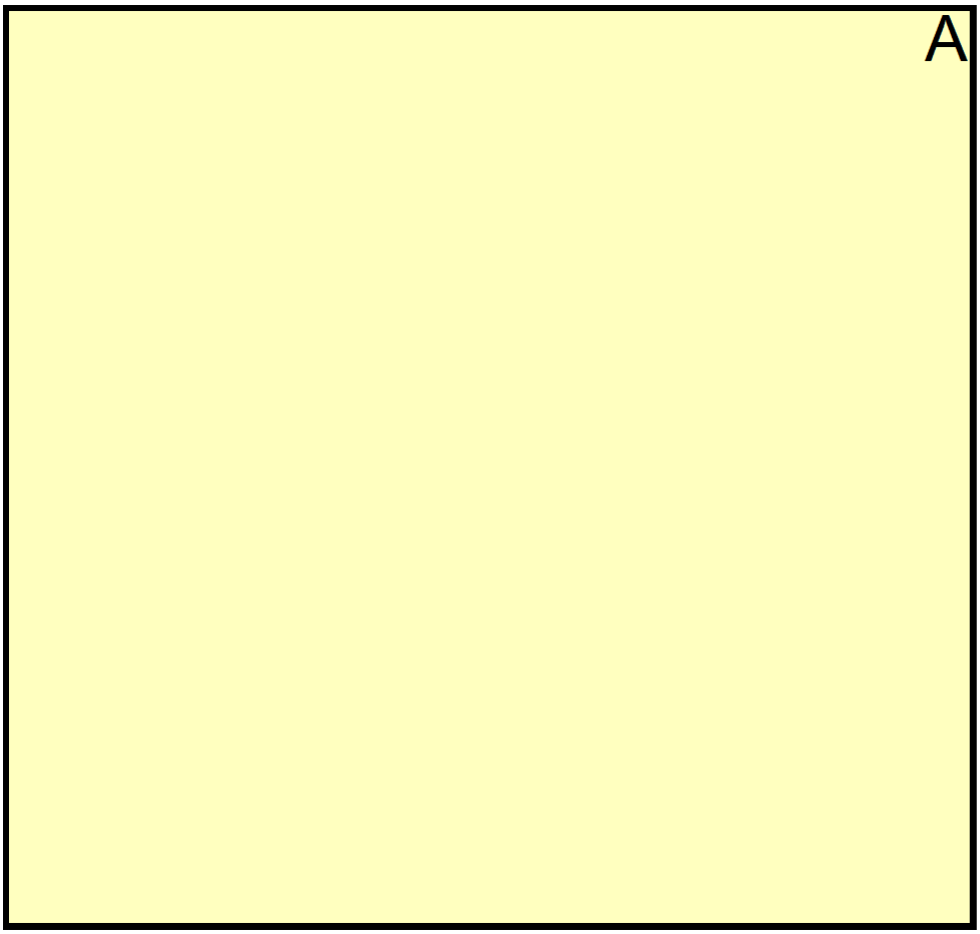
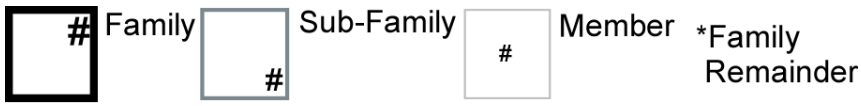
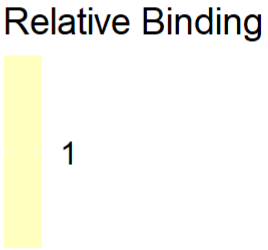


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map





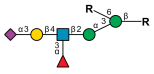
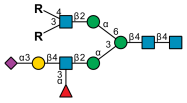
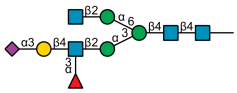
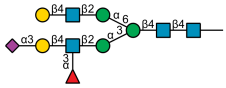
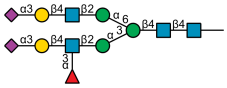


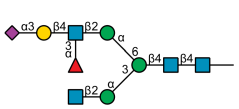
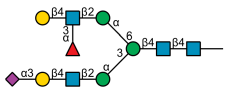
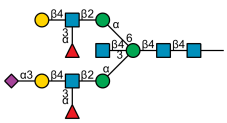
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

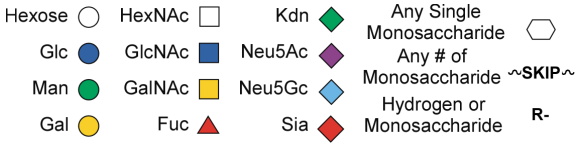
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				47		51		54

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
0			 62	 68	 21

Key:



All Concentration Plots:

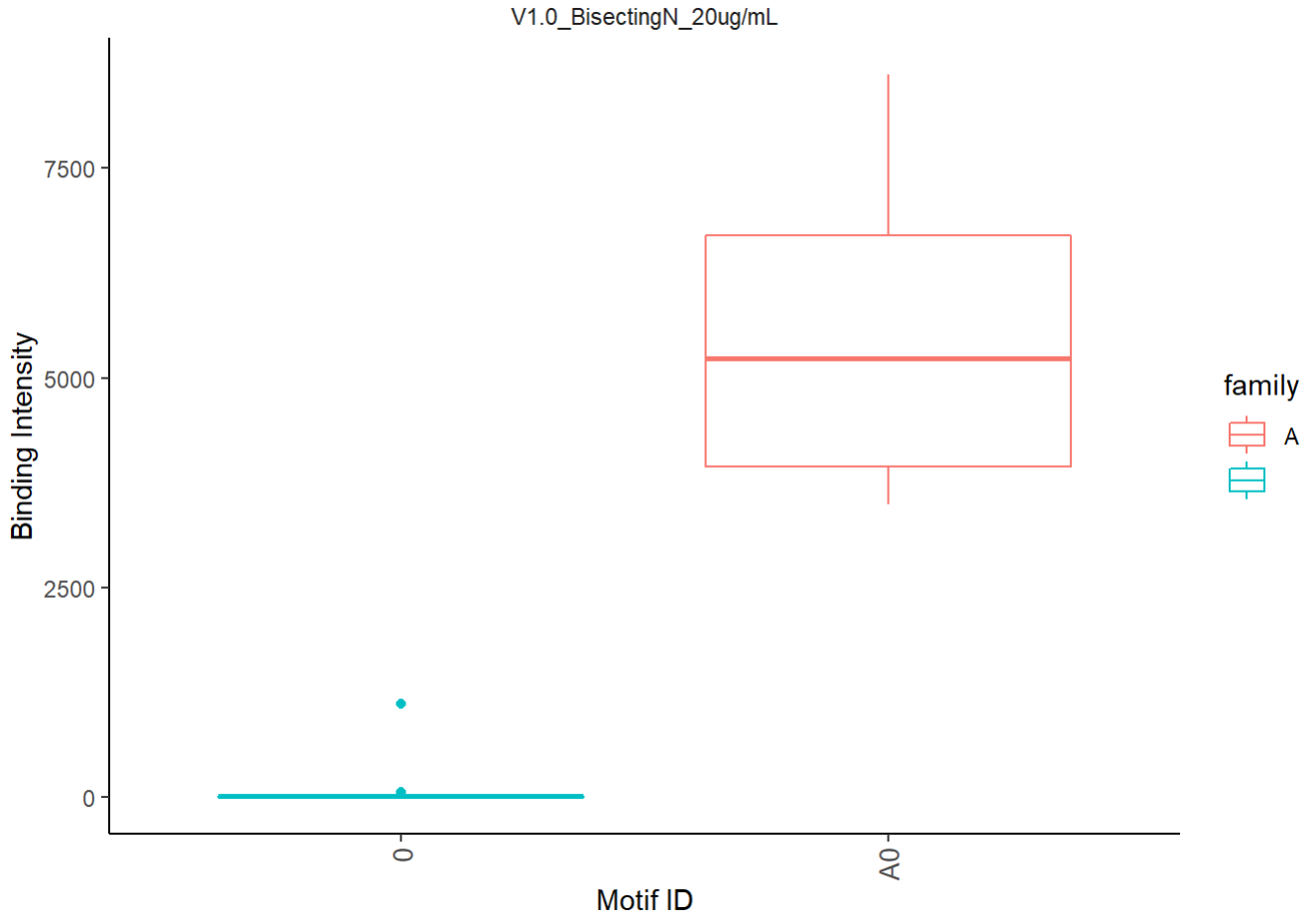
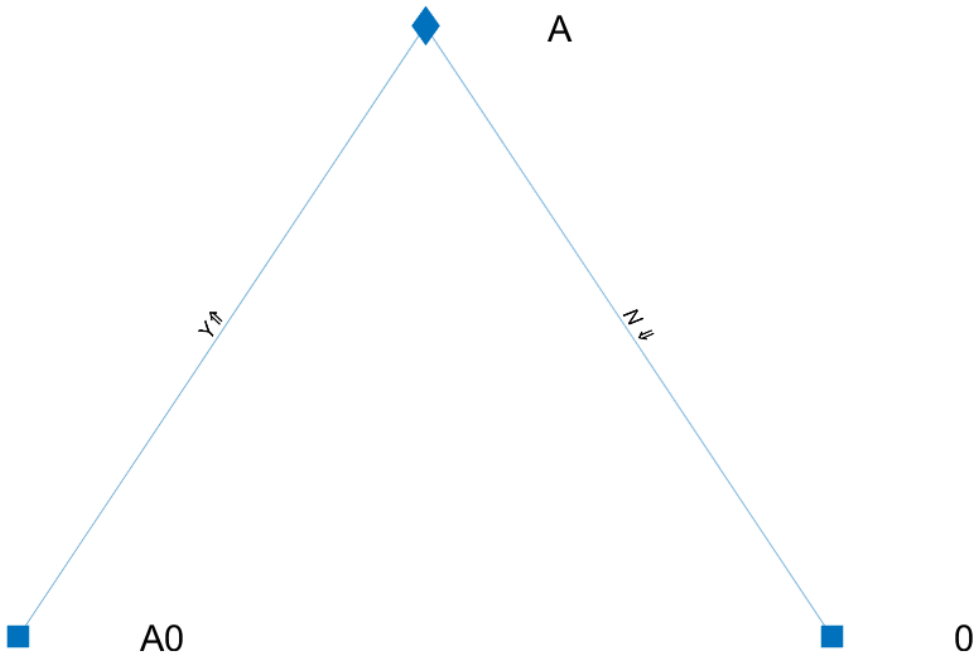


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



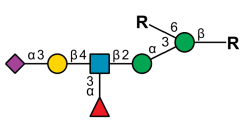
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

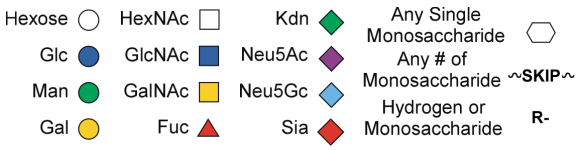
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f4f>ManB
0		Non-Binders

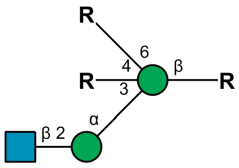
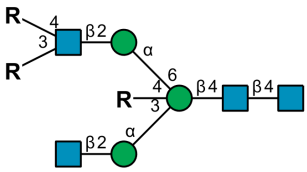
Key:



RatDCIR2

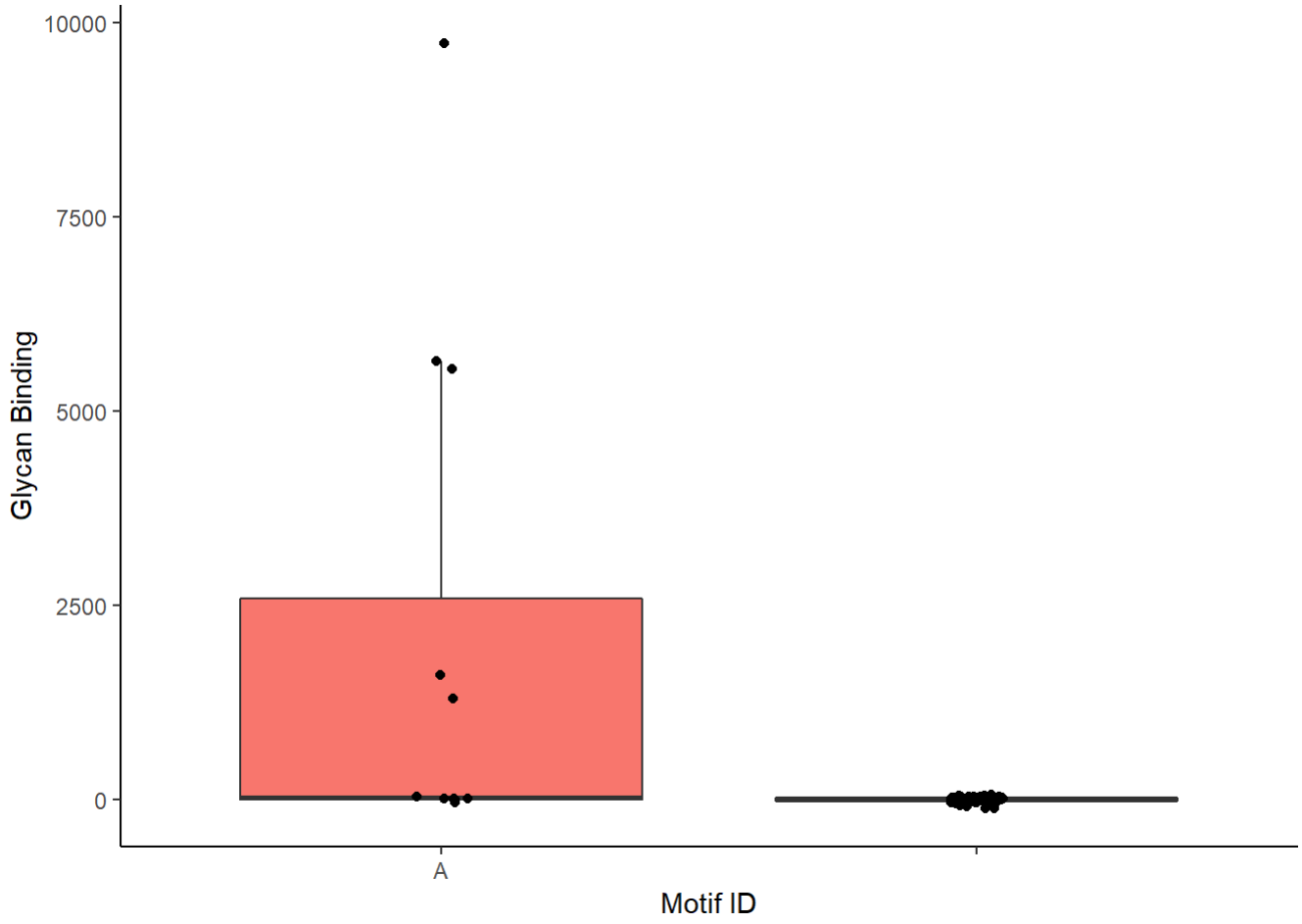
Automated Analysis report for RatDCIR2 evaluated at 20 ug/mL

List of Primary RatDCIR2 Motifs

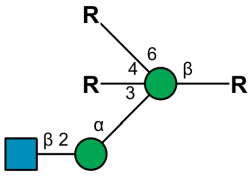
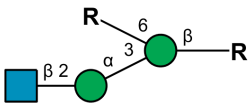
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1	12
0			0	60

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

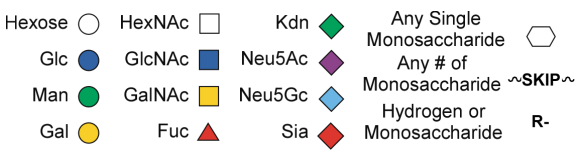
Boxplot of Primary Motifs



List of Fine-Specificity RatDCIR2 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*	Terminal N-Glycan N-Acetyl Glucosamine Bisecting N-Glycan (93%)		1	6	<0.001
A1			0	6	1.000
0	Non-Binders (100%)		0	60	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

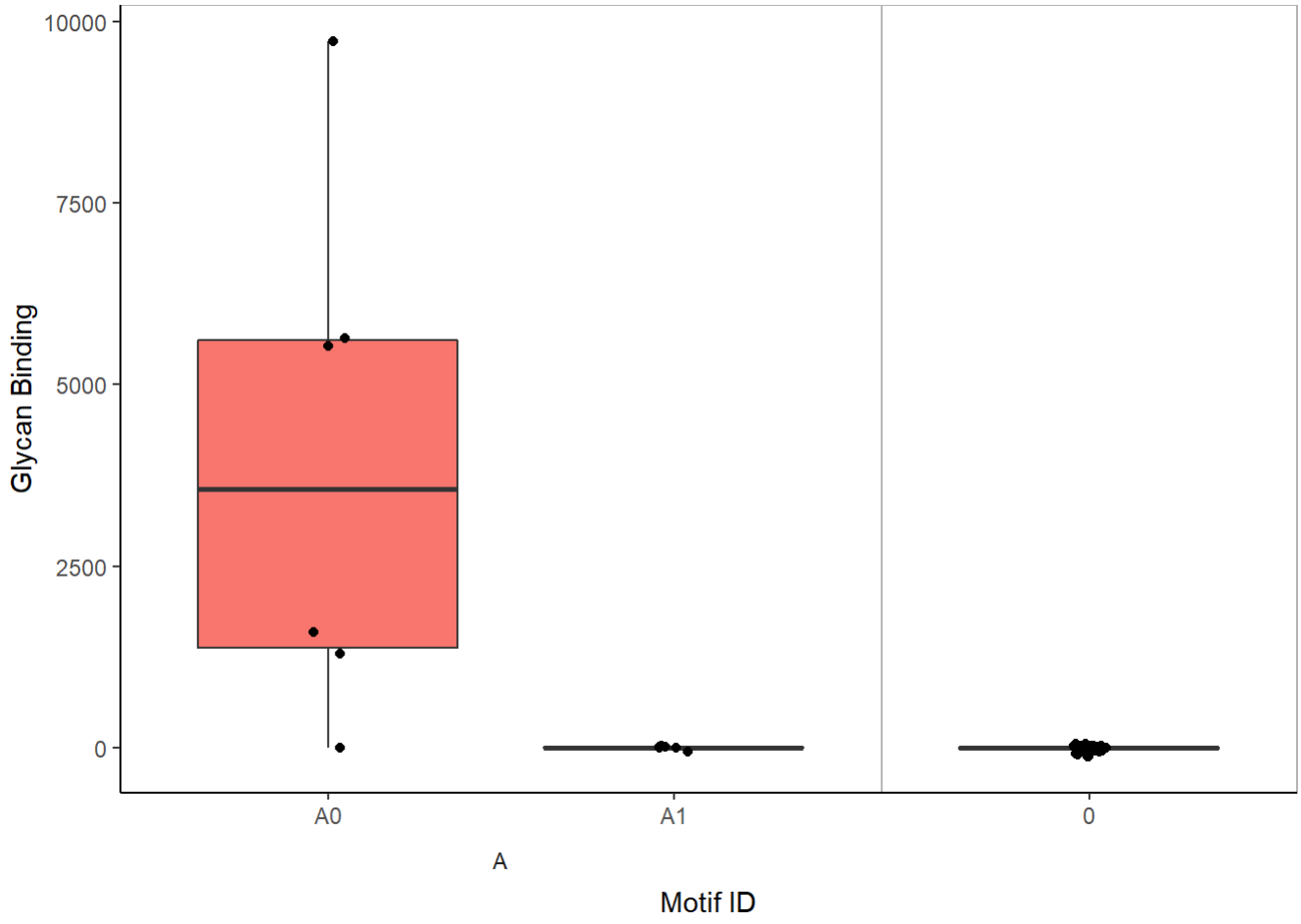


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

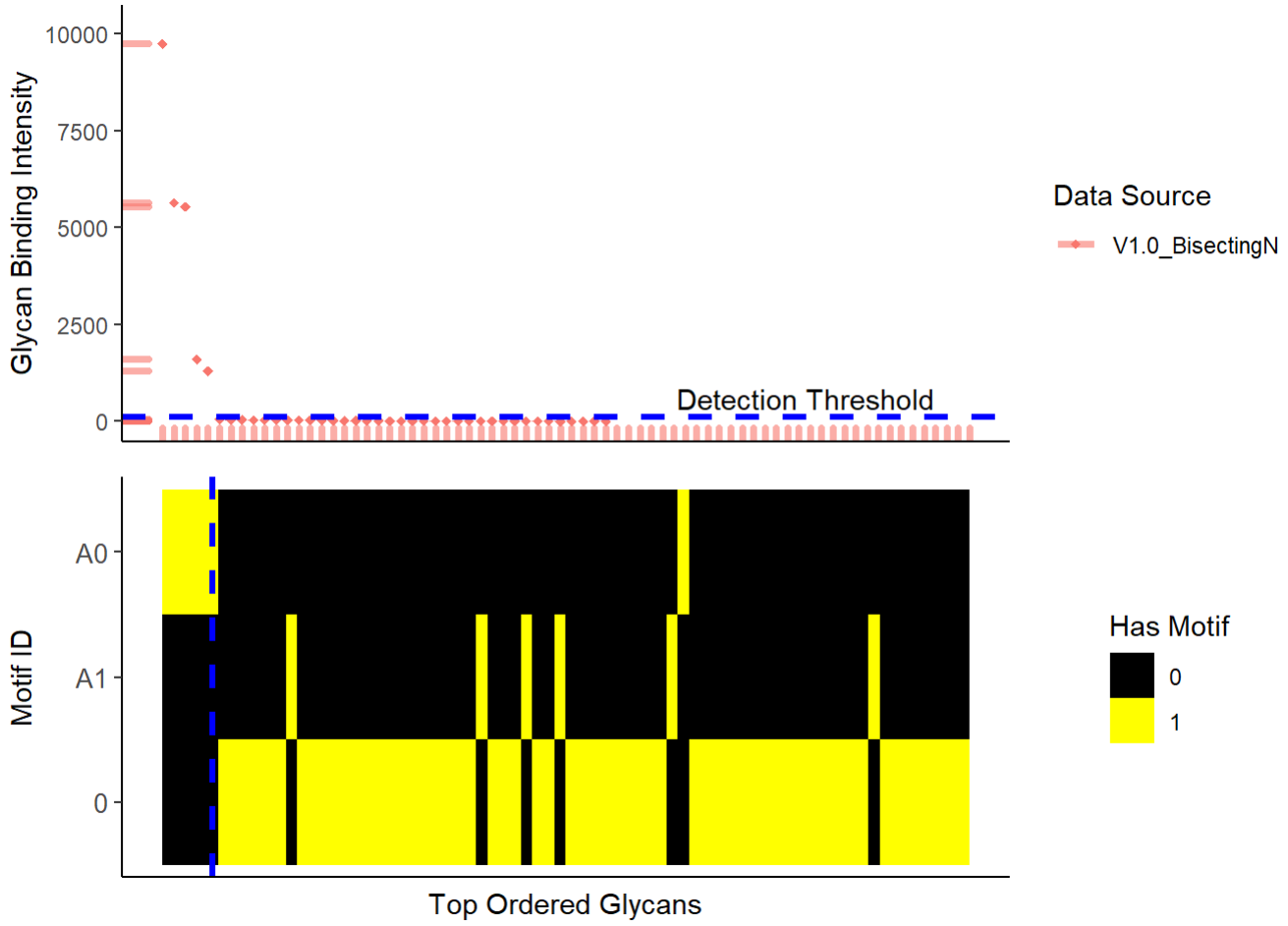
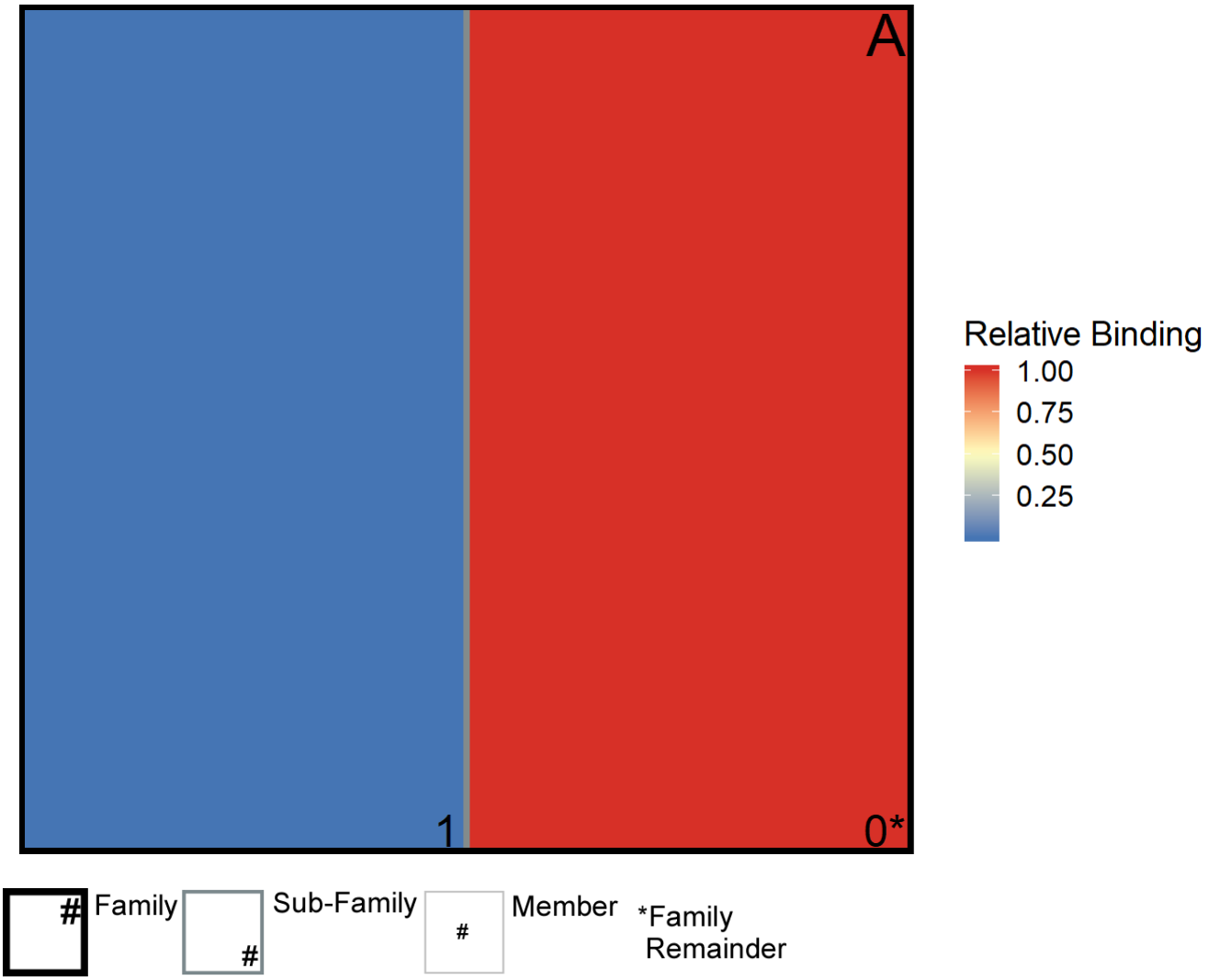


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

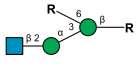
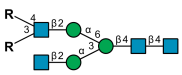
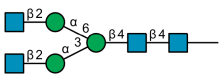
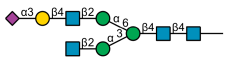
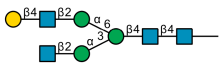
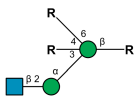
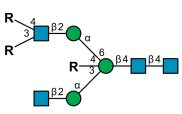
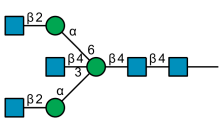
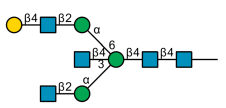
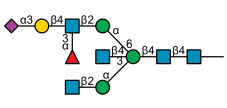


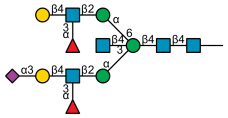
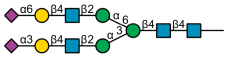
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

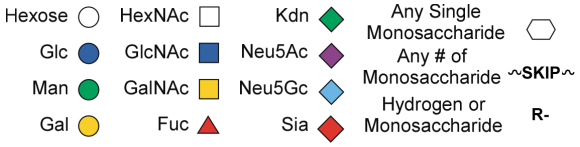
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				37		59		58
A0				1		22		26

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
0			 44	 21	 67

Key:



All Concentration Plots:

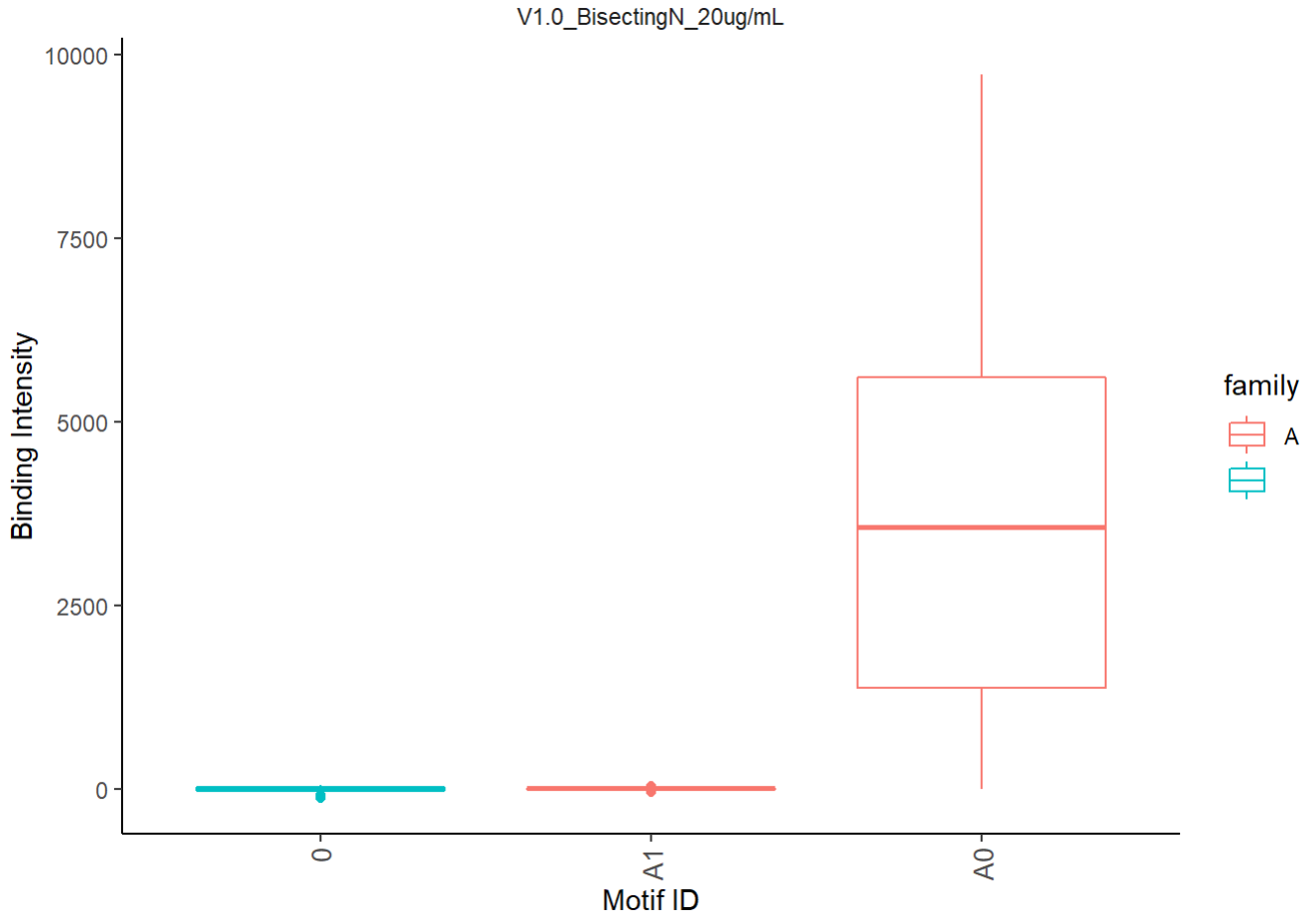
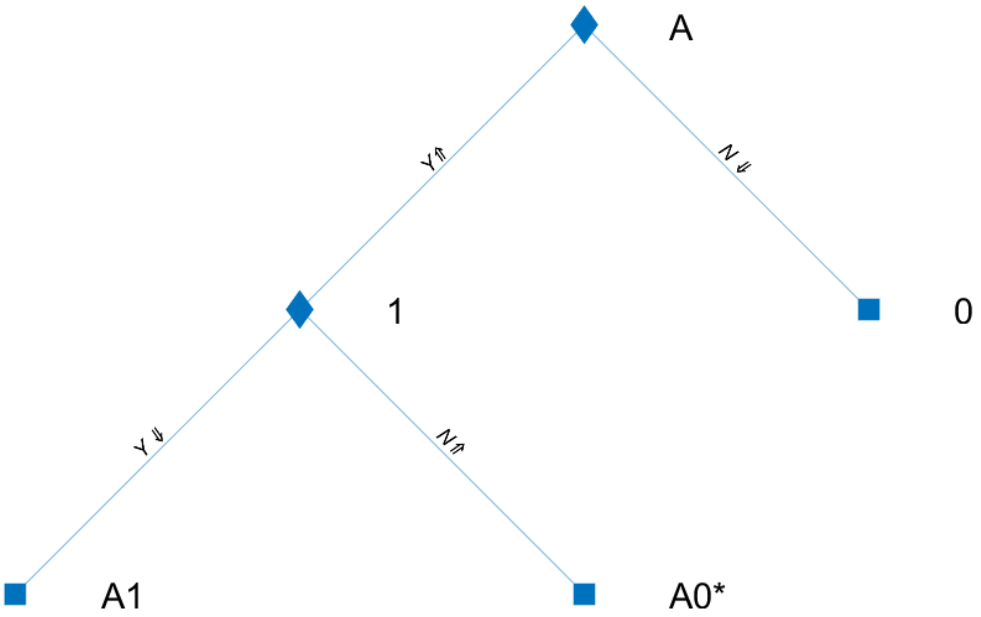


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



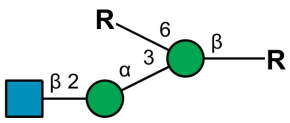
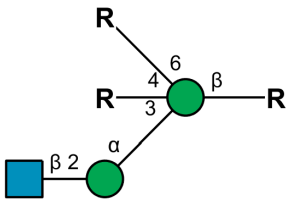
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

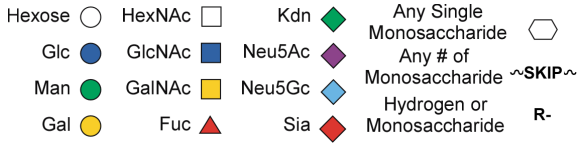
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f4f>ManB
A0*		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
0		Non-Binders

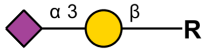
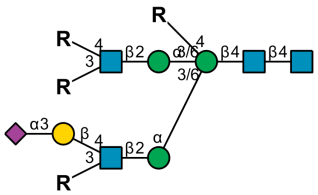
Key:


Hexose
HexNAc
Kdn
Any Single Monosaccharide
Glc
GlcNAc
Neu5Ac
Any # of Monosaccharide
~SKIP~
Man
GalNAc
Neu5Gc
Hydrogen or Monosaccharide
R-
Gal
Fuc
Sia

NR19240 (PR8_H1)

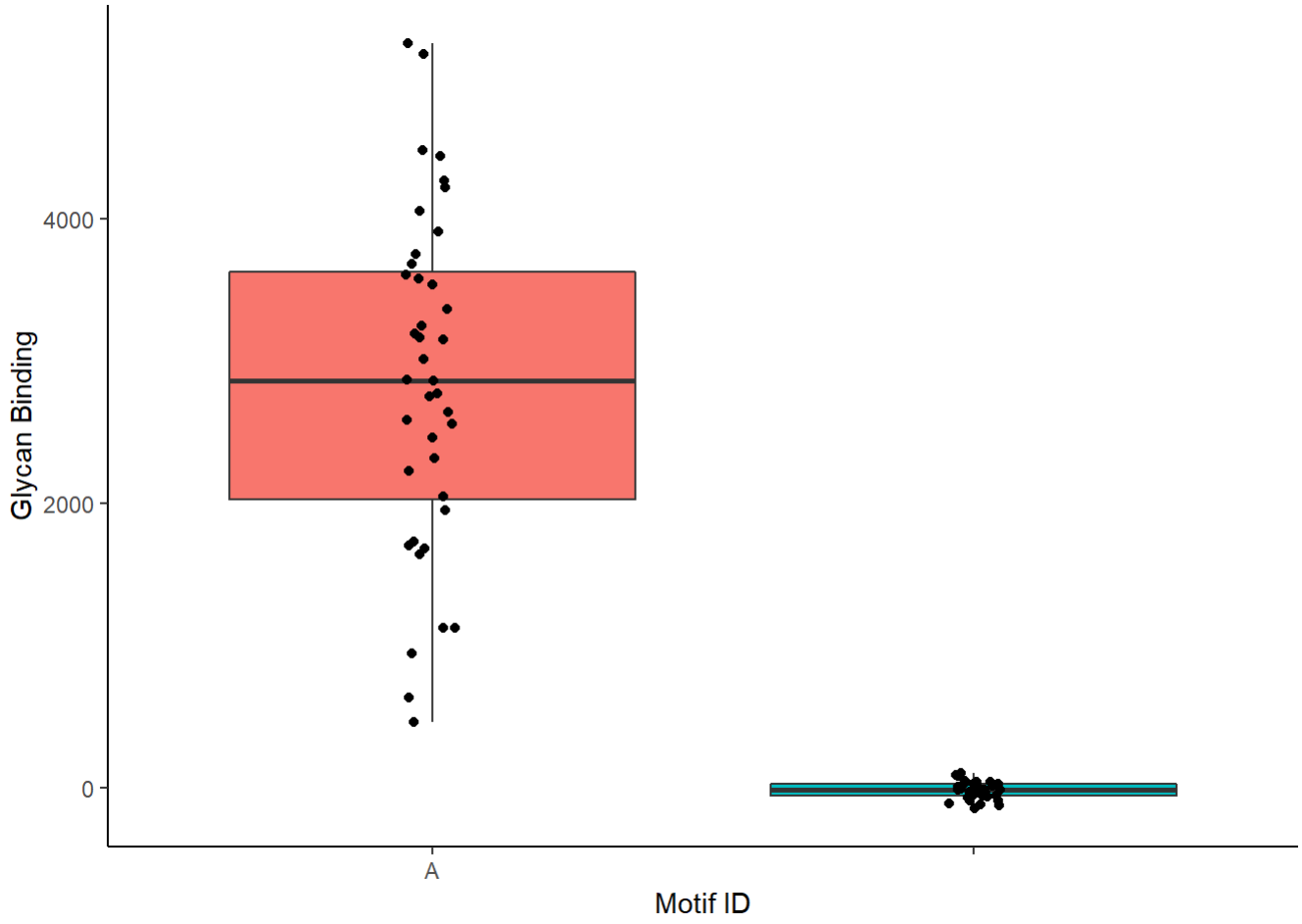
Automated Analysis report for NR19240 evaluated at 20 ug/mL

List of Primary NR19240 Motifs

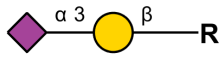
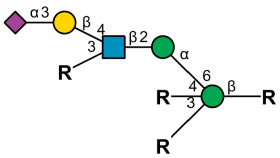
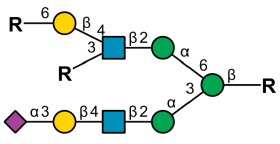
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	40
0			-0.01	32

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

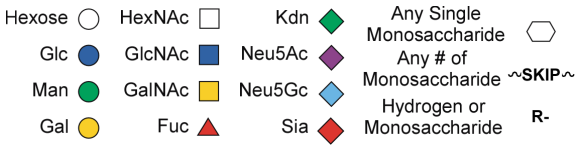
Boxplot of Primary Motifs



List of Fine-Specificity NR19240 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*			1.00	13	<0.001
A1			0.66	24	<0.001
A2	a3 Sialyl Type 2 LacNAc Terminal beta-Galactose (90%)		0.65	3	<0.001
0	Non-Binders (100%)		0.00	32	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

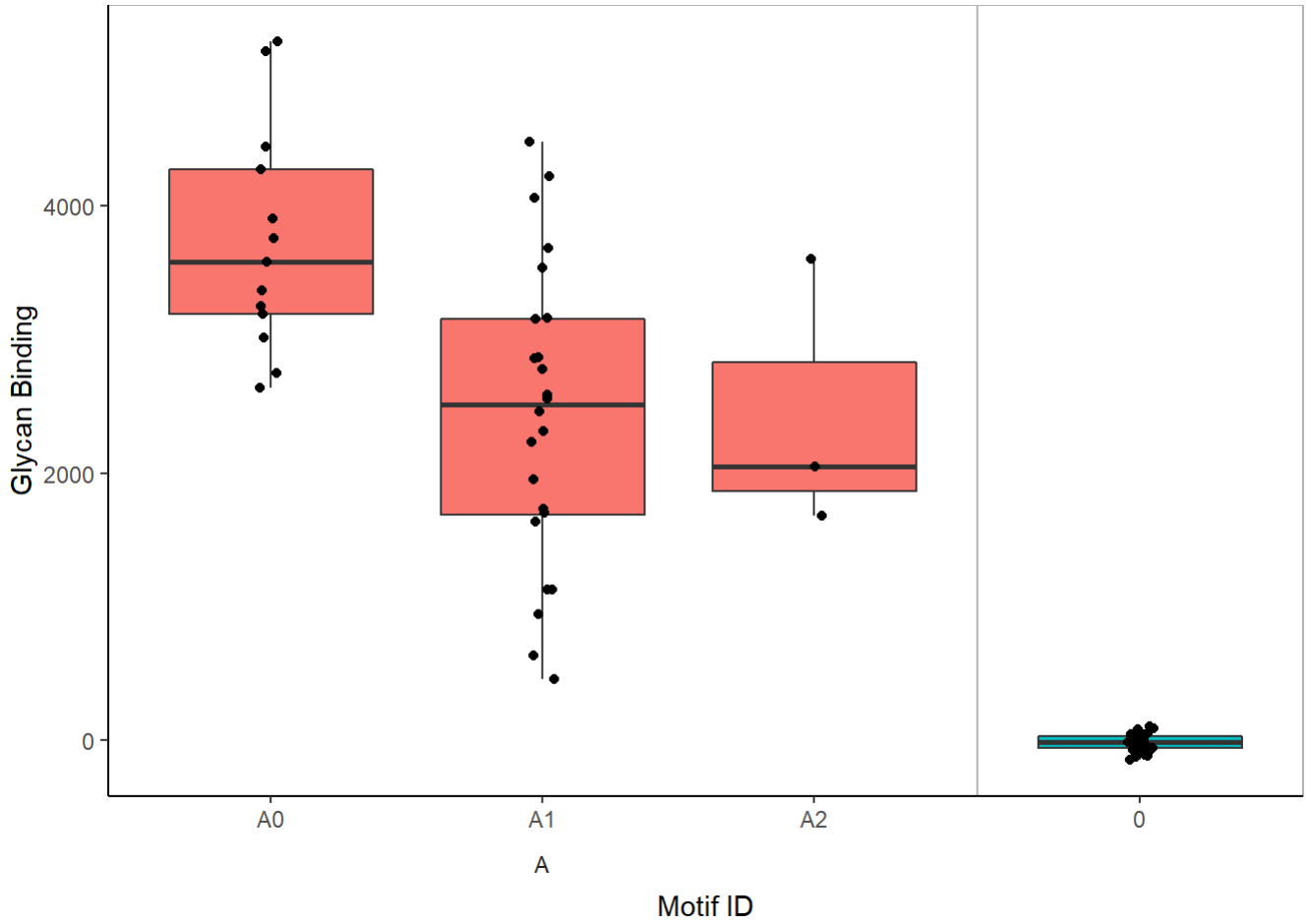


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

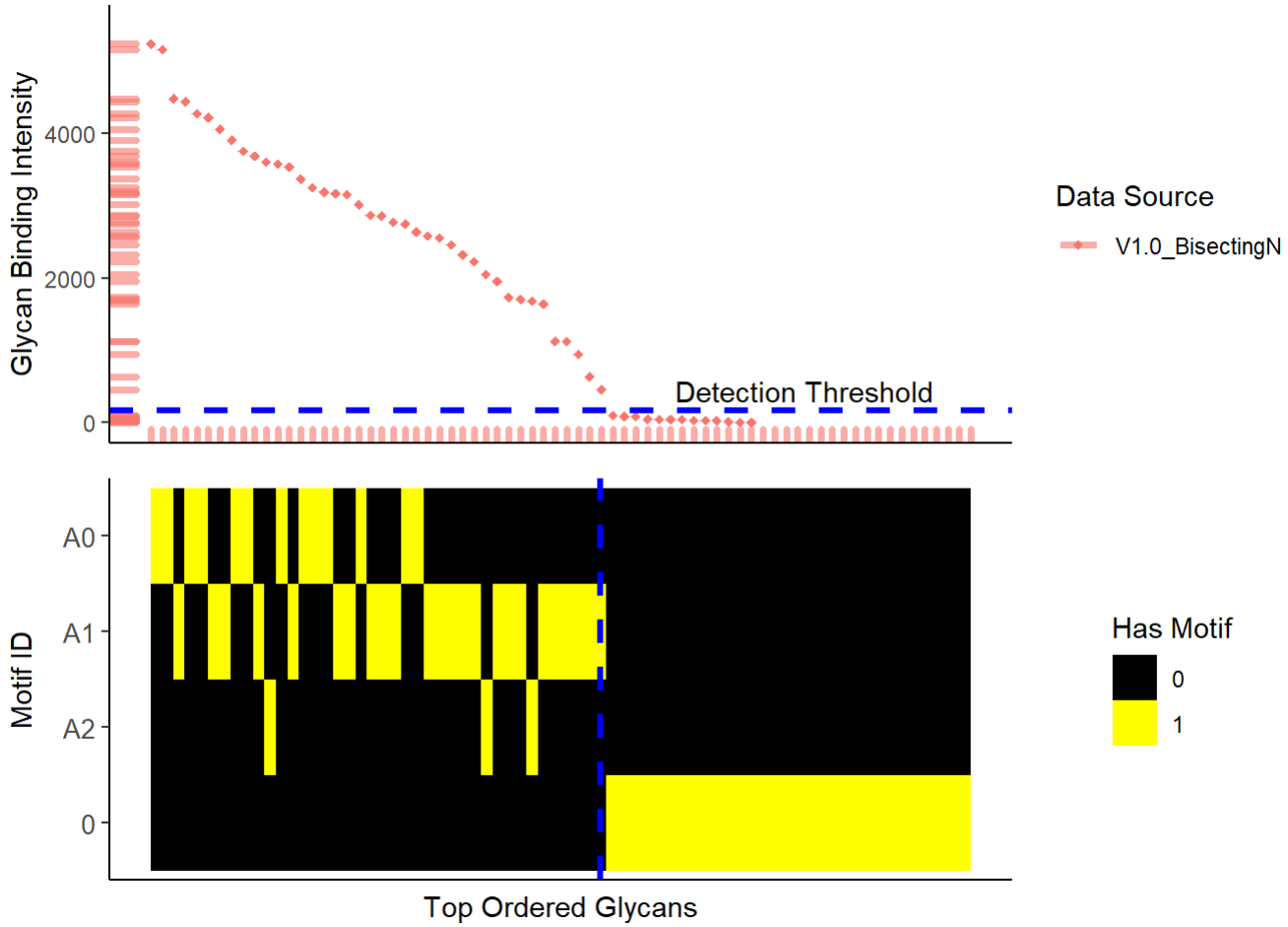
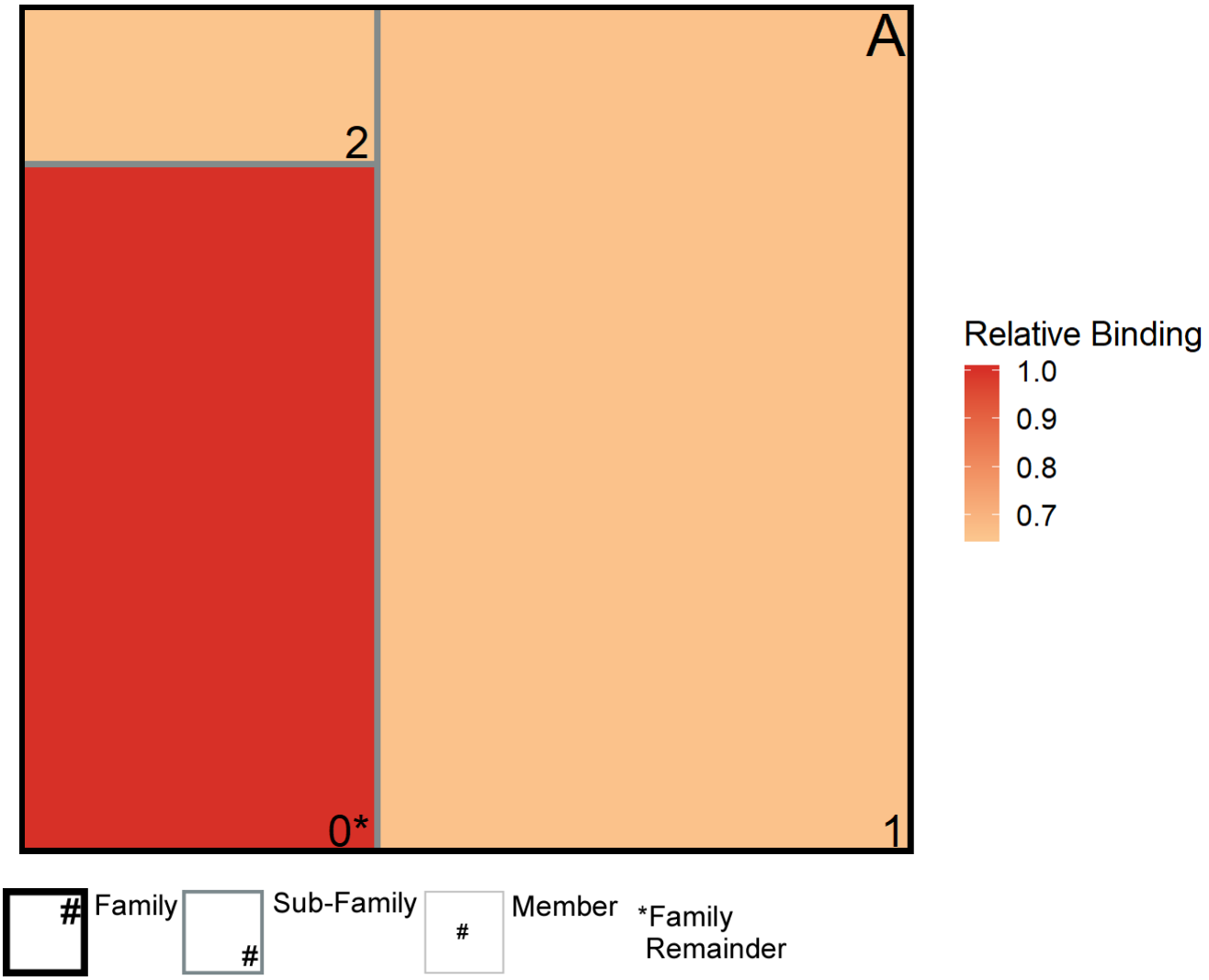


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

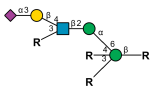
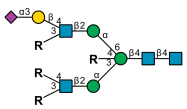
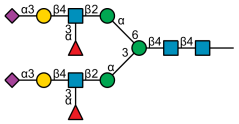
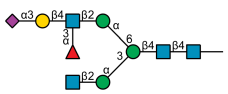
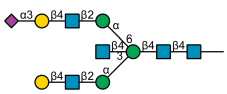


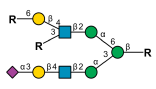
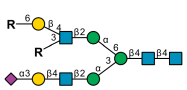
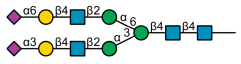
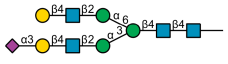
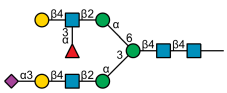
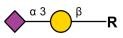
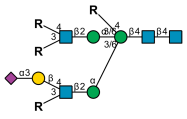
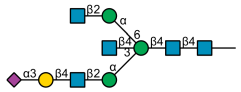
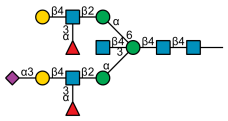
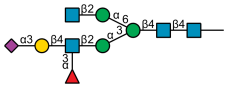
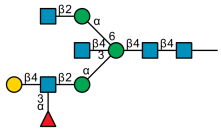
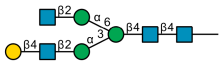
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

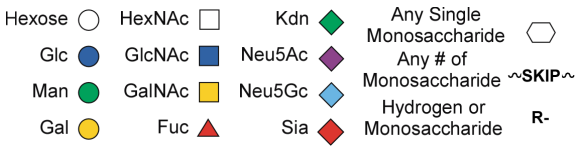
Detailed Model Breakdown

Motif Glycan Examples:

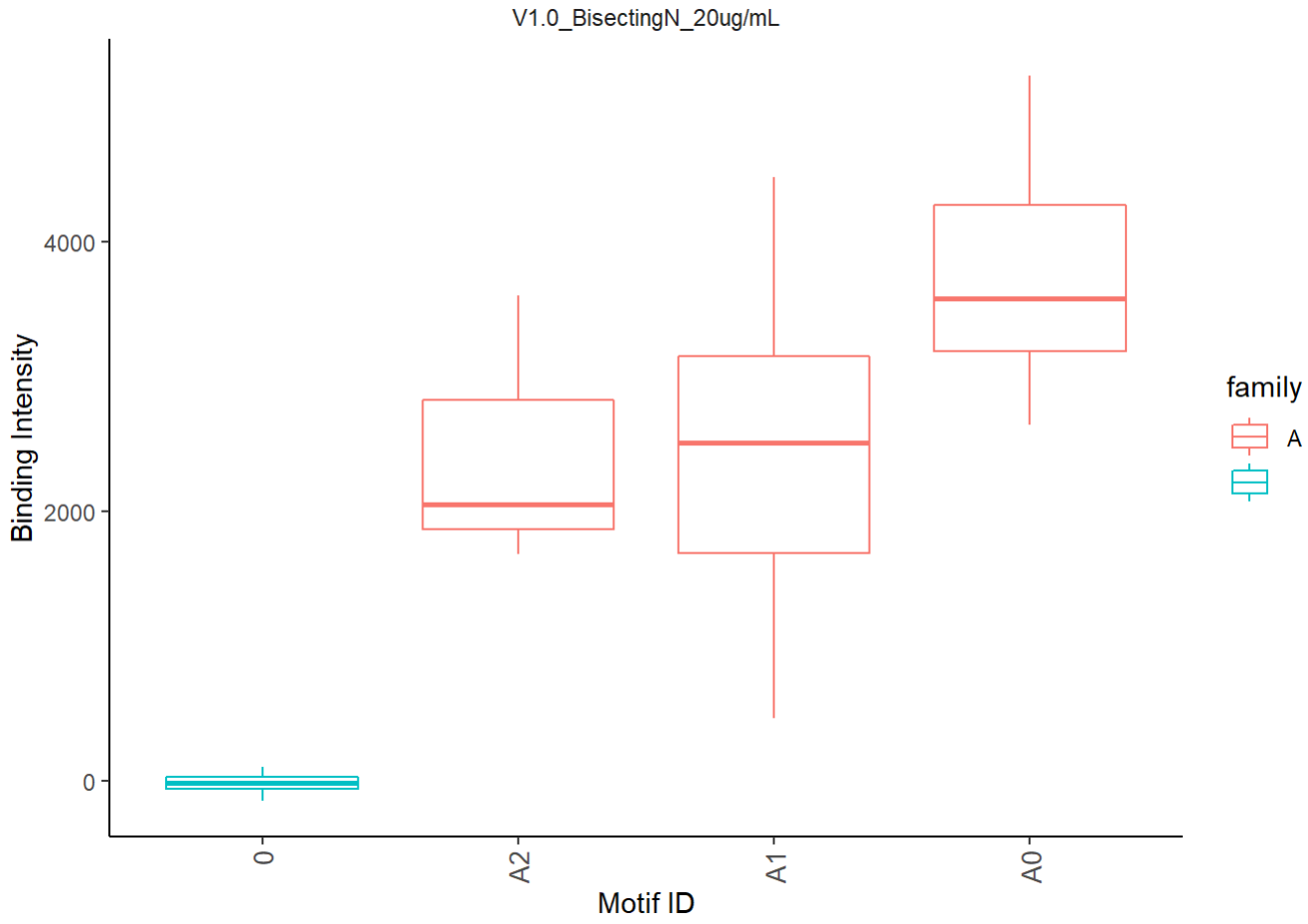
Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				42		62		27

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A2				67		48		68
A0				8		21		47
0				40		10		43

Key:



All Concentration Plots:



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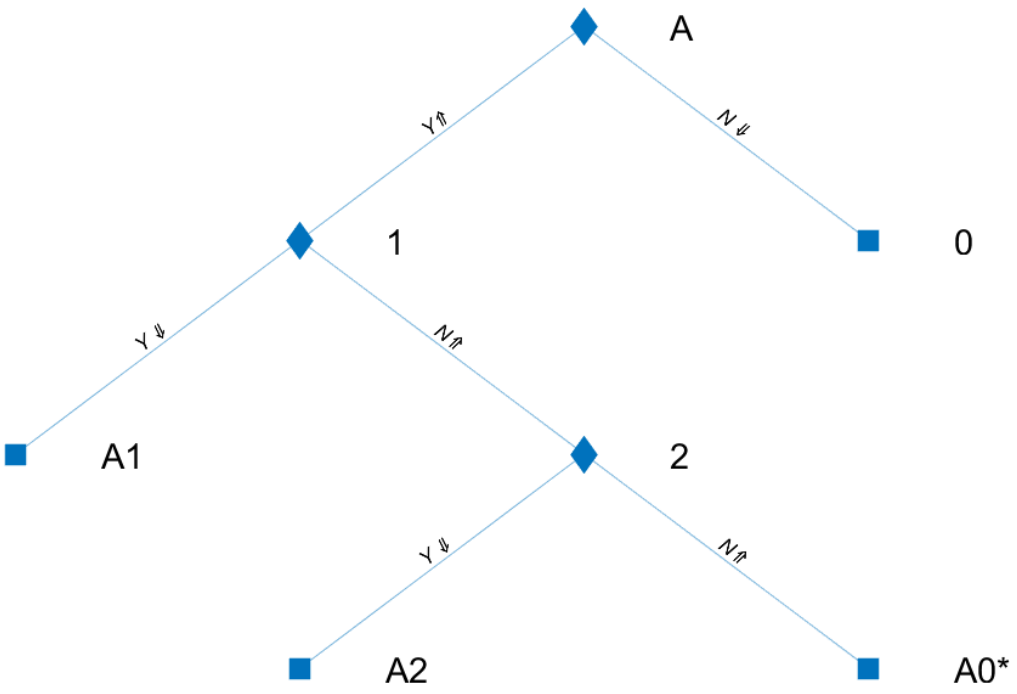
Model Structure:



*Motif matches the remaining glycans not matched by earlier motifs in the model.

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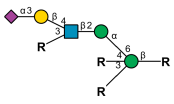
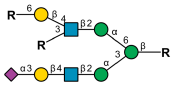
Curve Fitting:

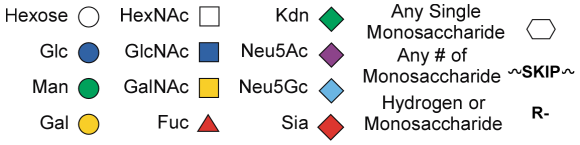
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
A2		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f3f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f4f>ManB
A0*		<6f8f>Neu5AcA2-3<2f4f6f>GalB

Motif ID	Motif Graphic	Motif Text
0		Non-Binders

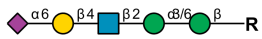
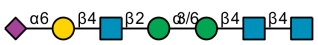
Key:



NR19441 (NY18H1)

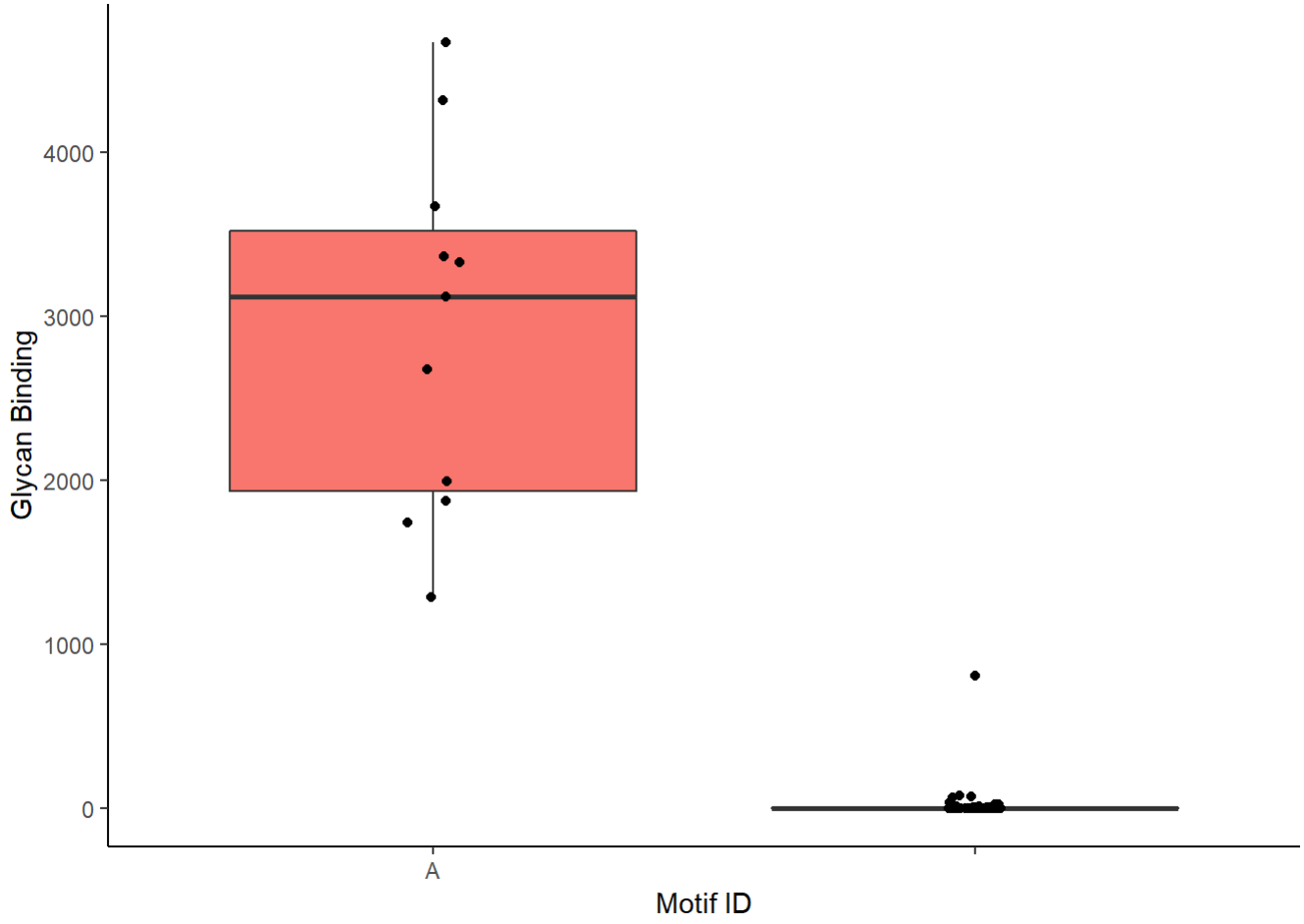
Automated Analysis report for NR19441 evaluated at 20 ug/mL

List of Primary NR19441 Motifs

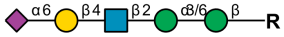
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	11
0			0.01	61

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

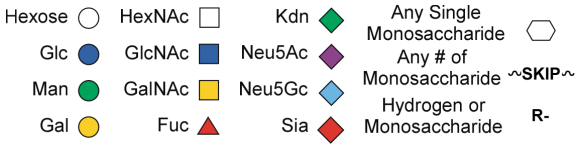
Boxplot of Primary Motifs



List of Fine-Specificity NR19441 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0			1	11	<0.001
0	Non-Binders (100%)		0	61	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

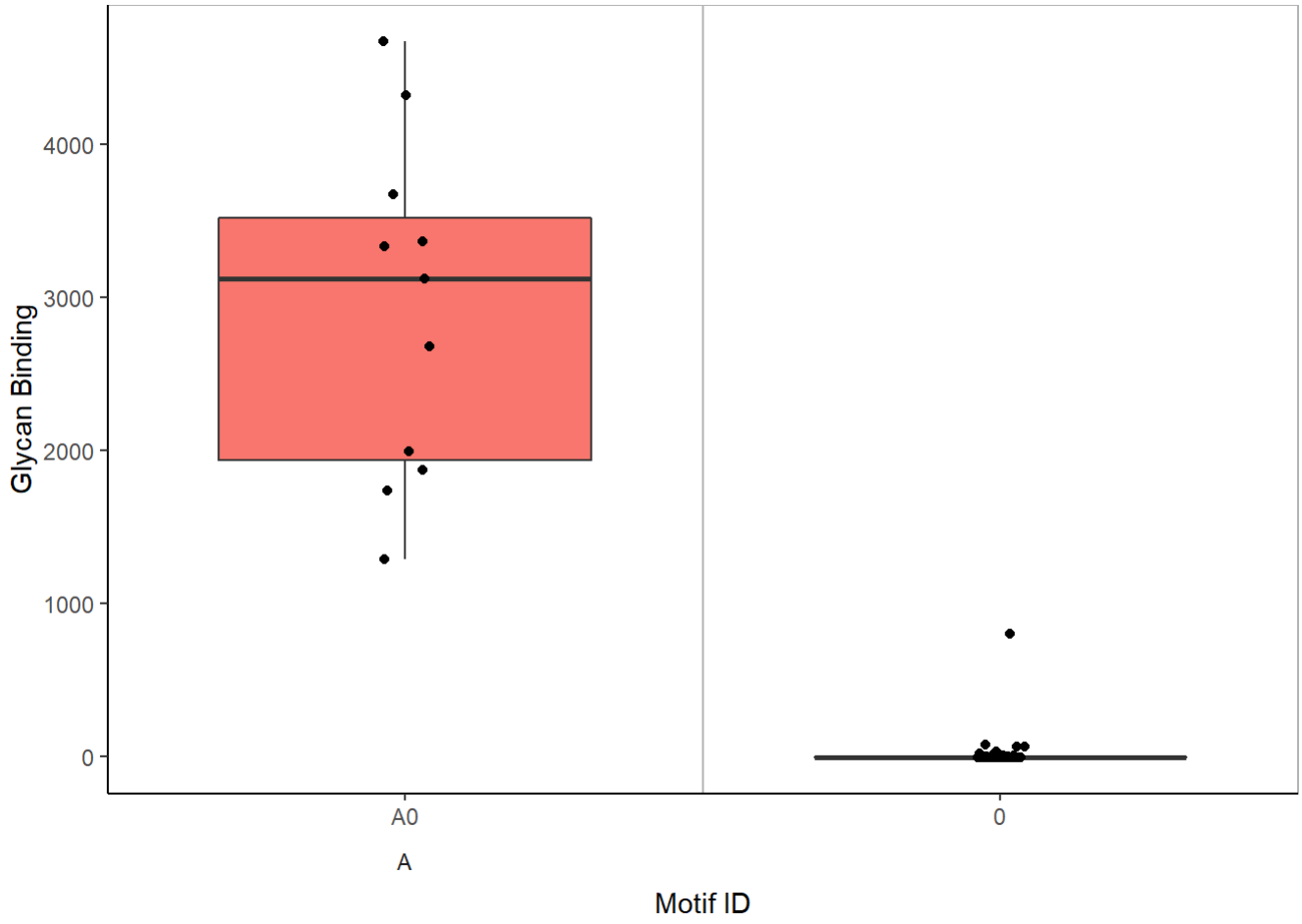


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

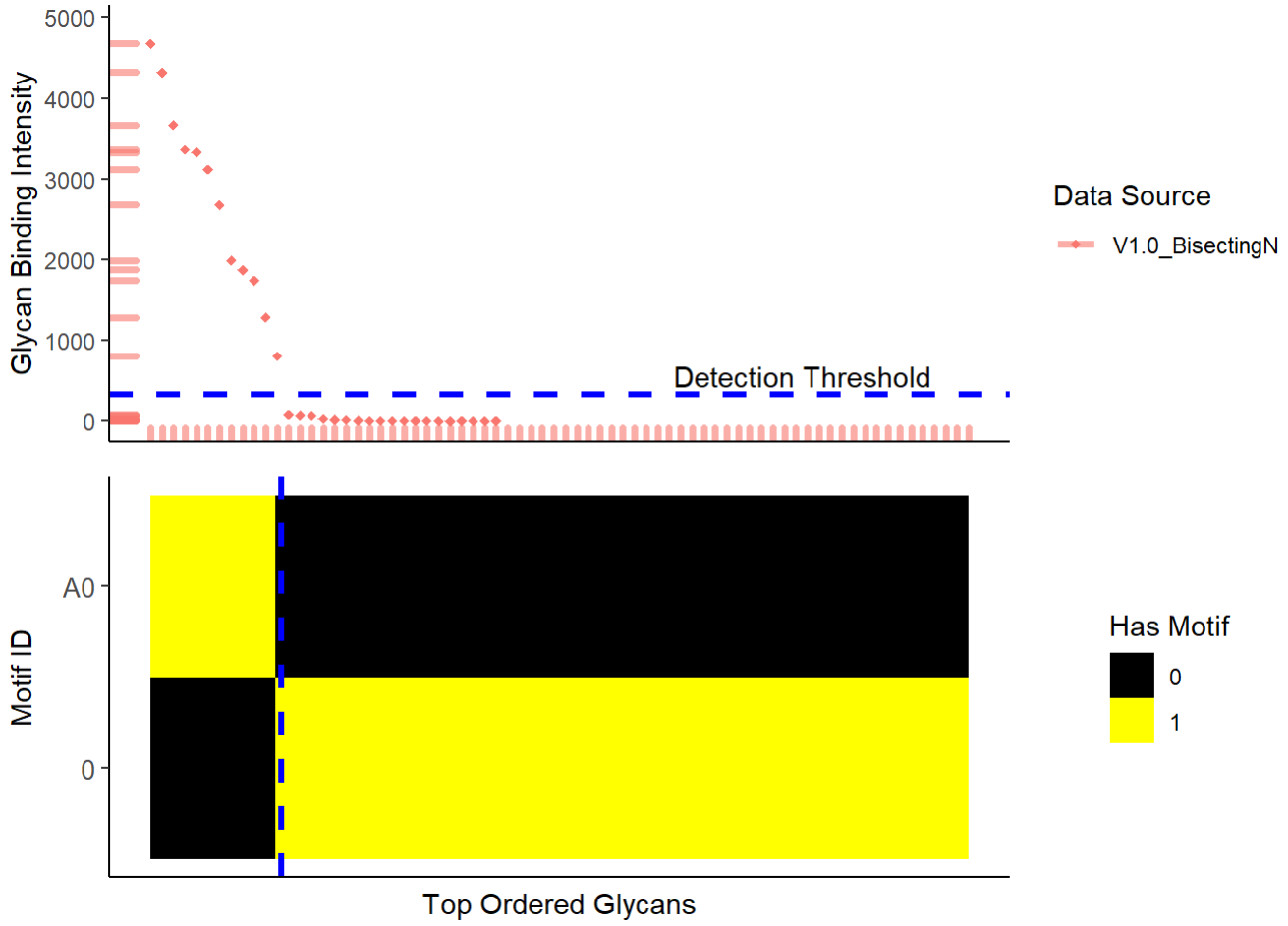
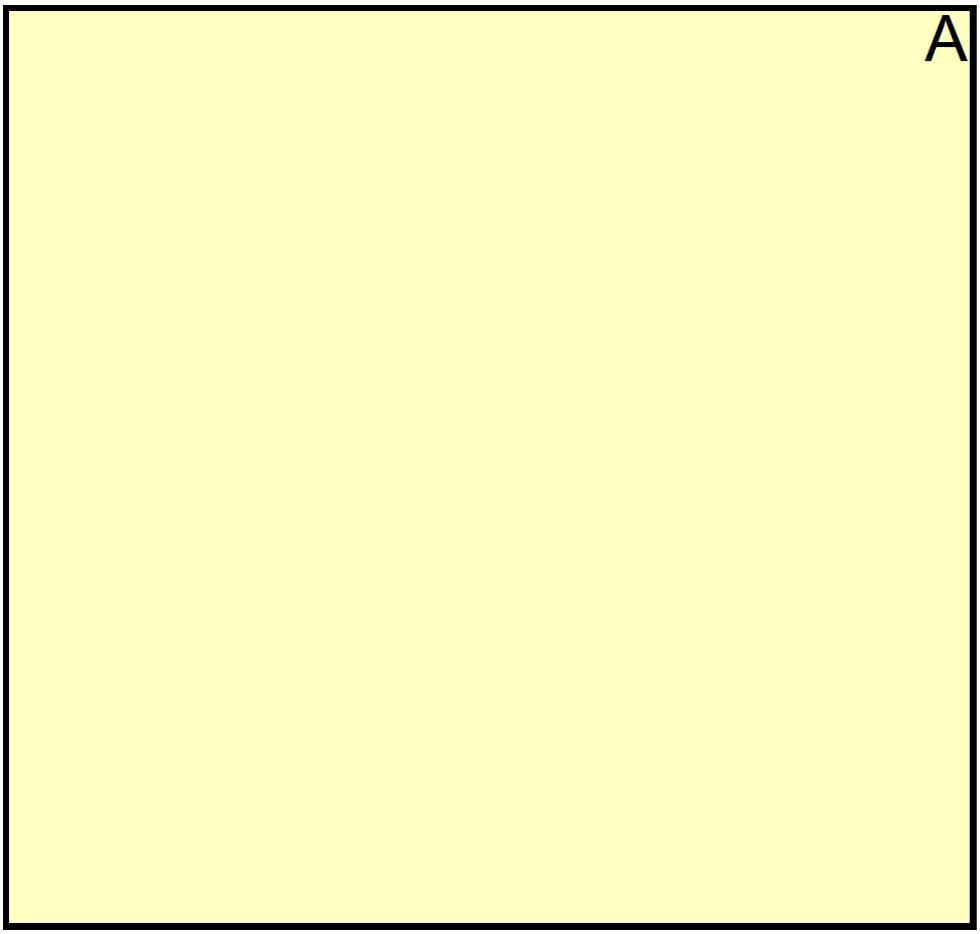
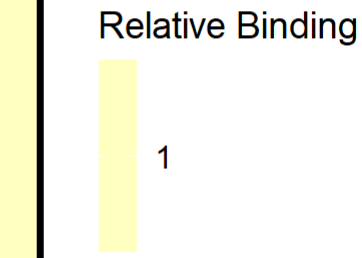
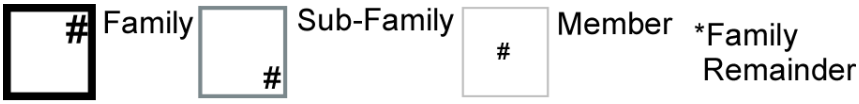


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map





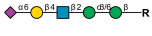
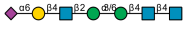
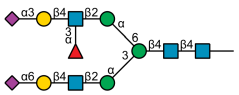
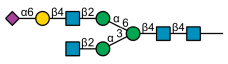
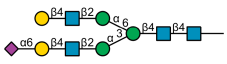
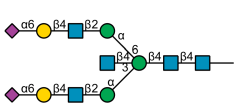
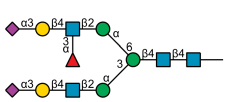
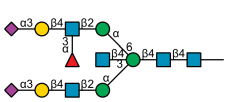


*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

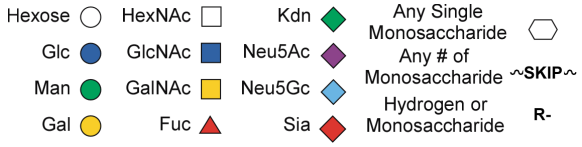
Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				71		60		49
0				4		69		33

Key:



All Concentration Plots:

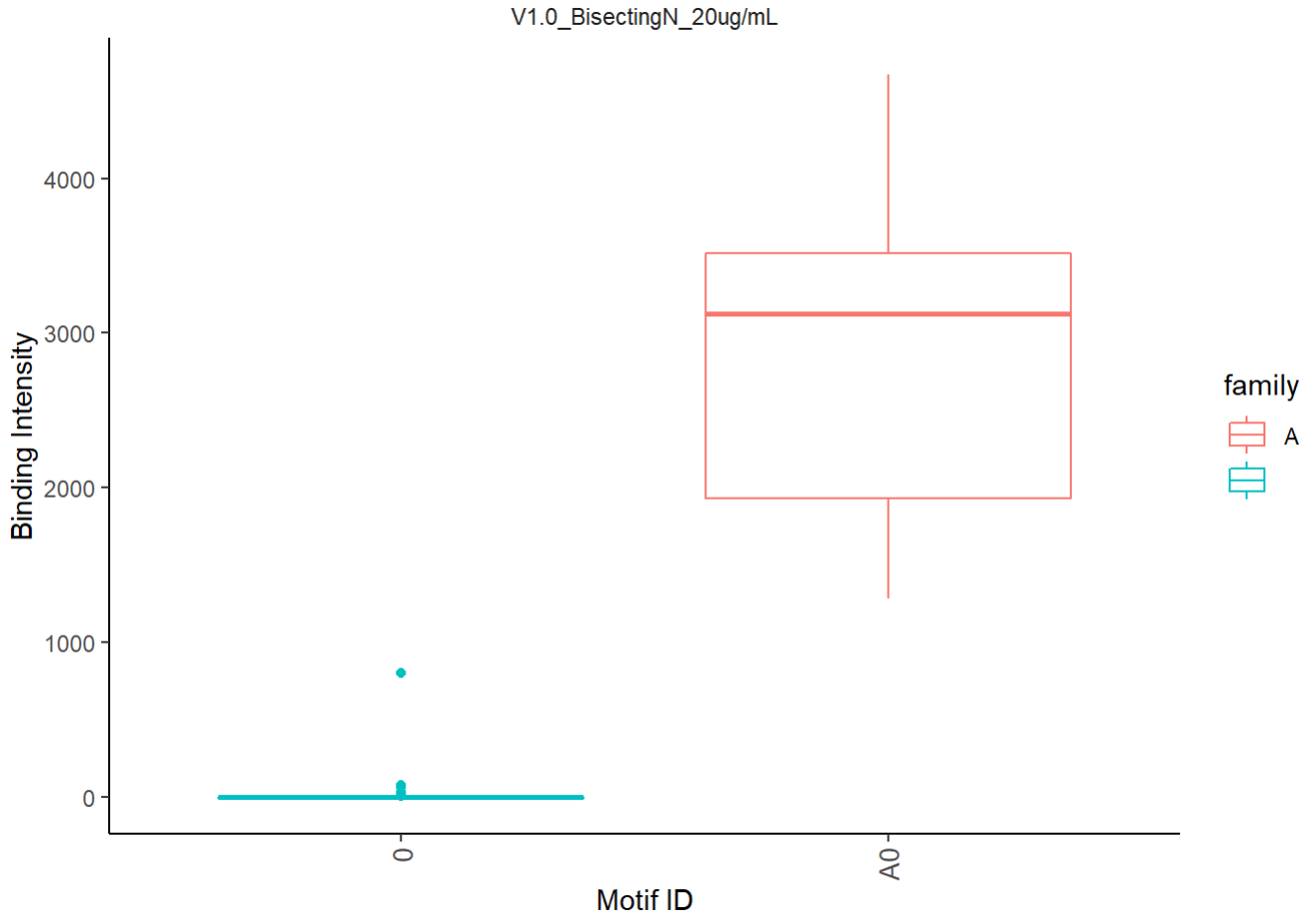
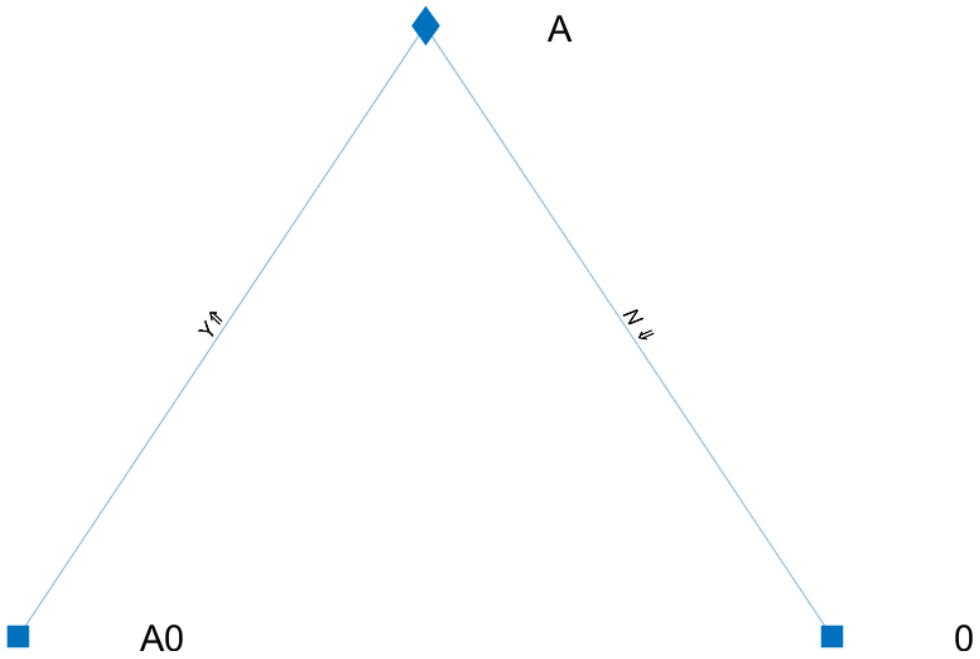


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



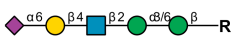
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

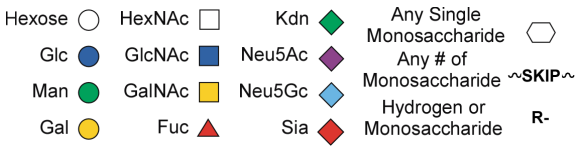
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-<3or6><2f4f>ManB
0		Non-Binders

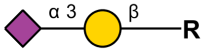
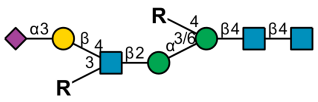
Key:



NR41637 (SP27_H1)

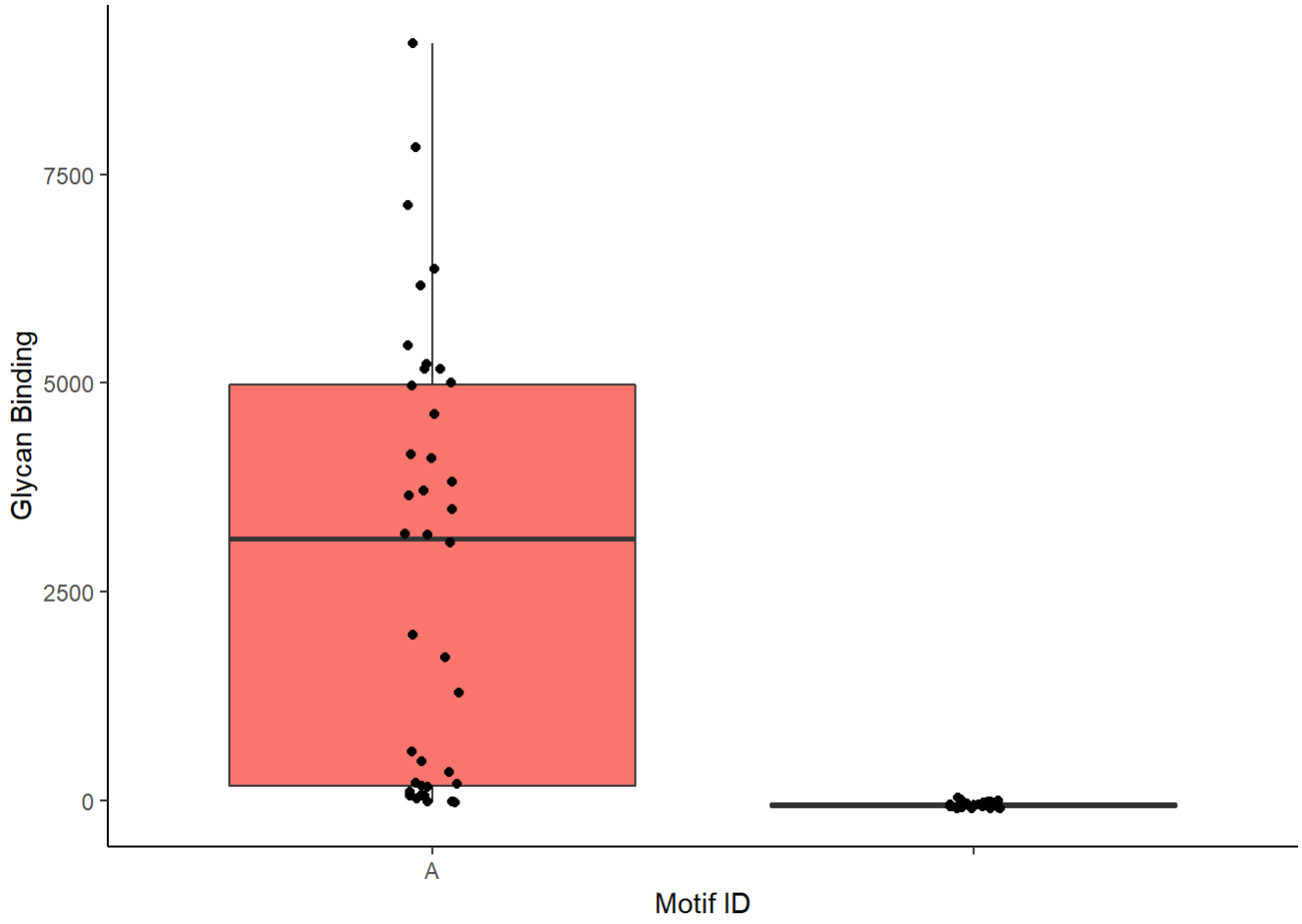
Automated Analysis report for NR41637 evaluated at 20 ug/mL

List of Primary NR41637 Motifs

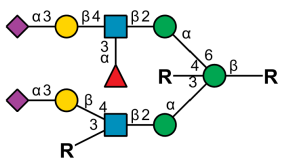
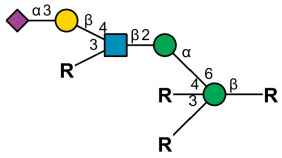
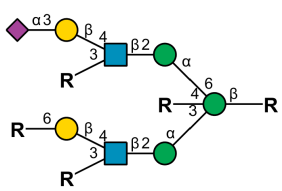
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	40
0			-0.02	32

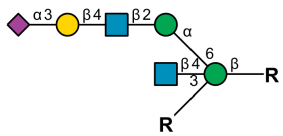
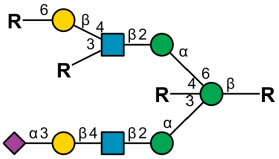
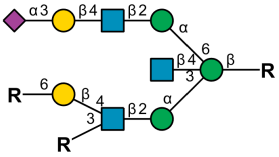
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

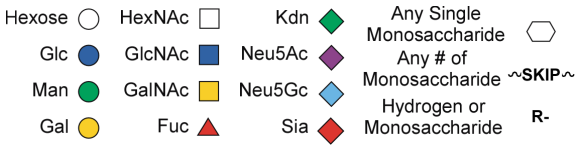


List of Fine-Specificity NR41637 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A3	Sialyl Lewis X a3 Sialyl Type 2 LacNAc (94%)		1.00	4	<0.001
A5*	a3 Sialyl Galactose Terminal N-Glycan N-Acetyl Glucosamine (90%)		0.73	5	<0.001
A0*			0.55	10	<0.001
A2*			0.35	9	<0.001

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A4			0.34	3	0.190
A6	a3 Sialyl Type 2 LacNAc Terminal beta-Galactose (92%)		0.04	6	1.000
A1	a3 Sialyl Type 2 LacNAc Terminal beta-Galactose (90%)		0.01	3	1.000
0	Non-Binders (100%)		0.00	32	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

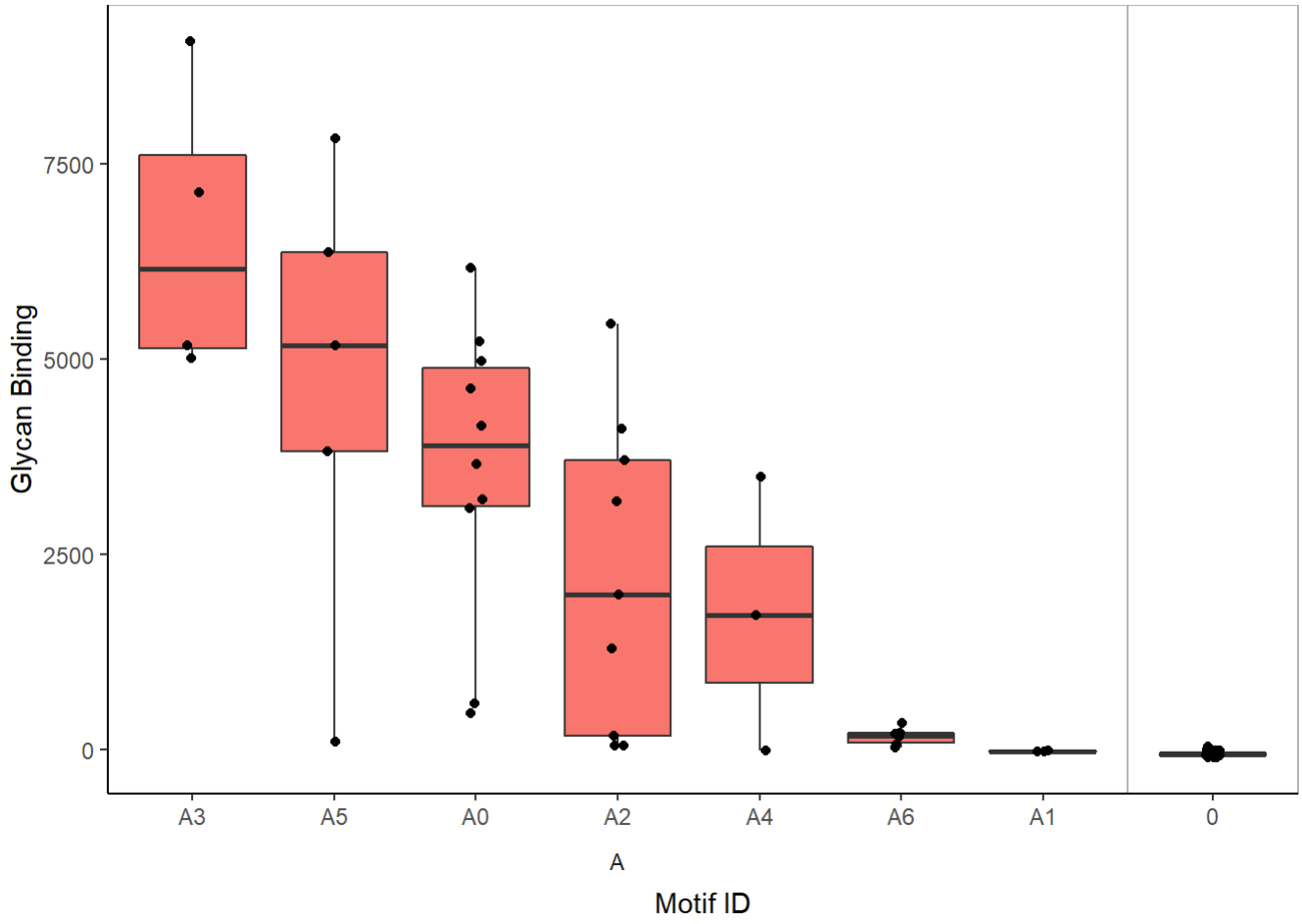


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

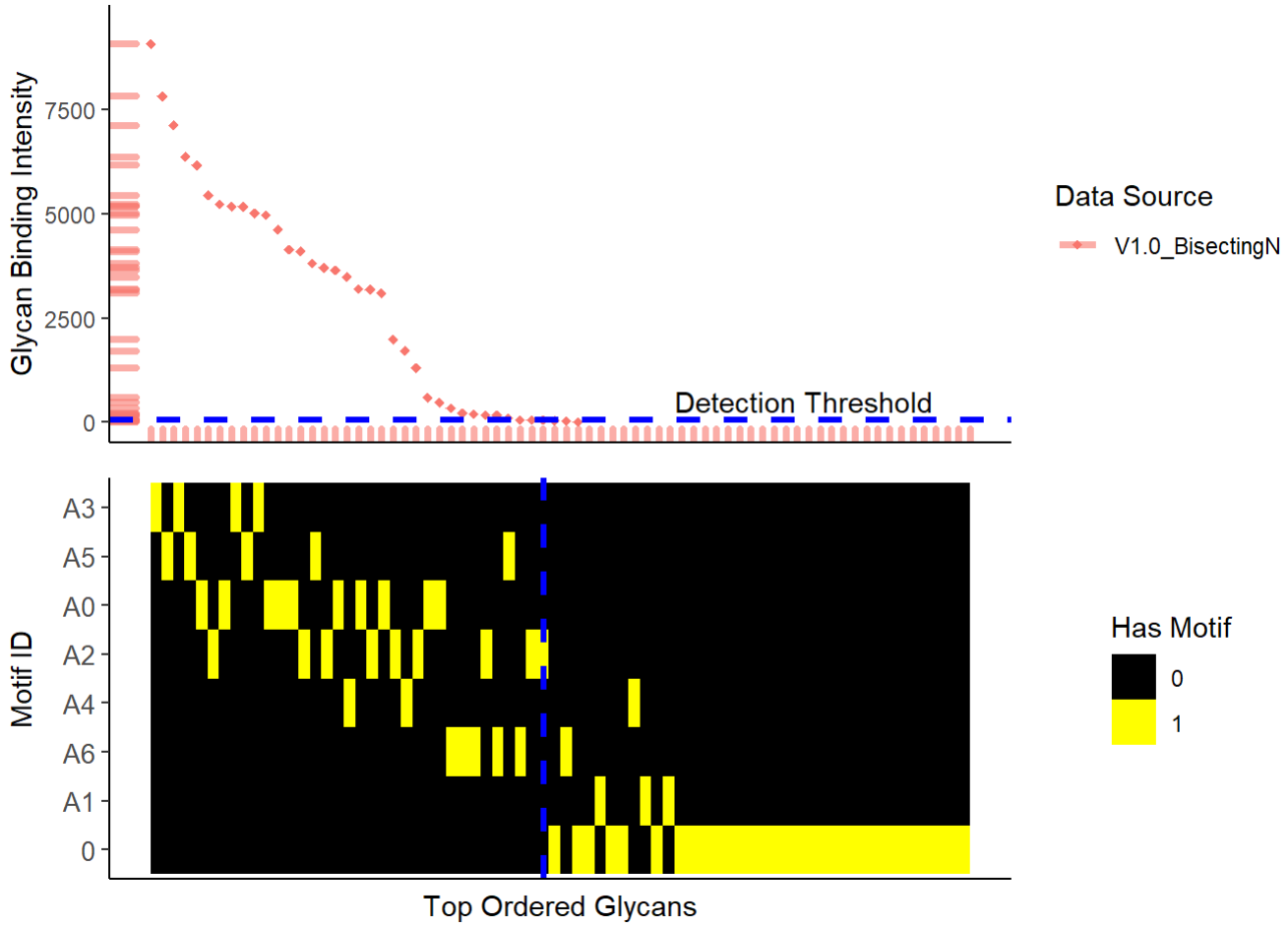
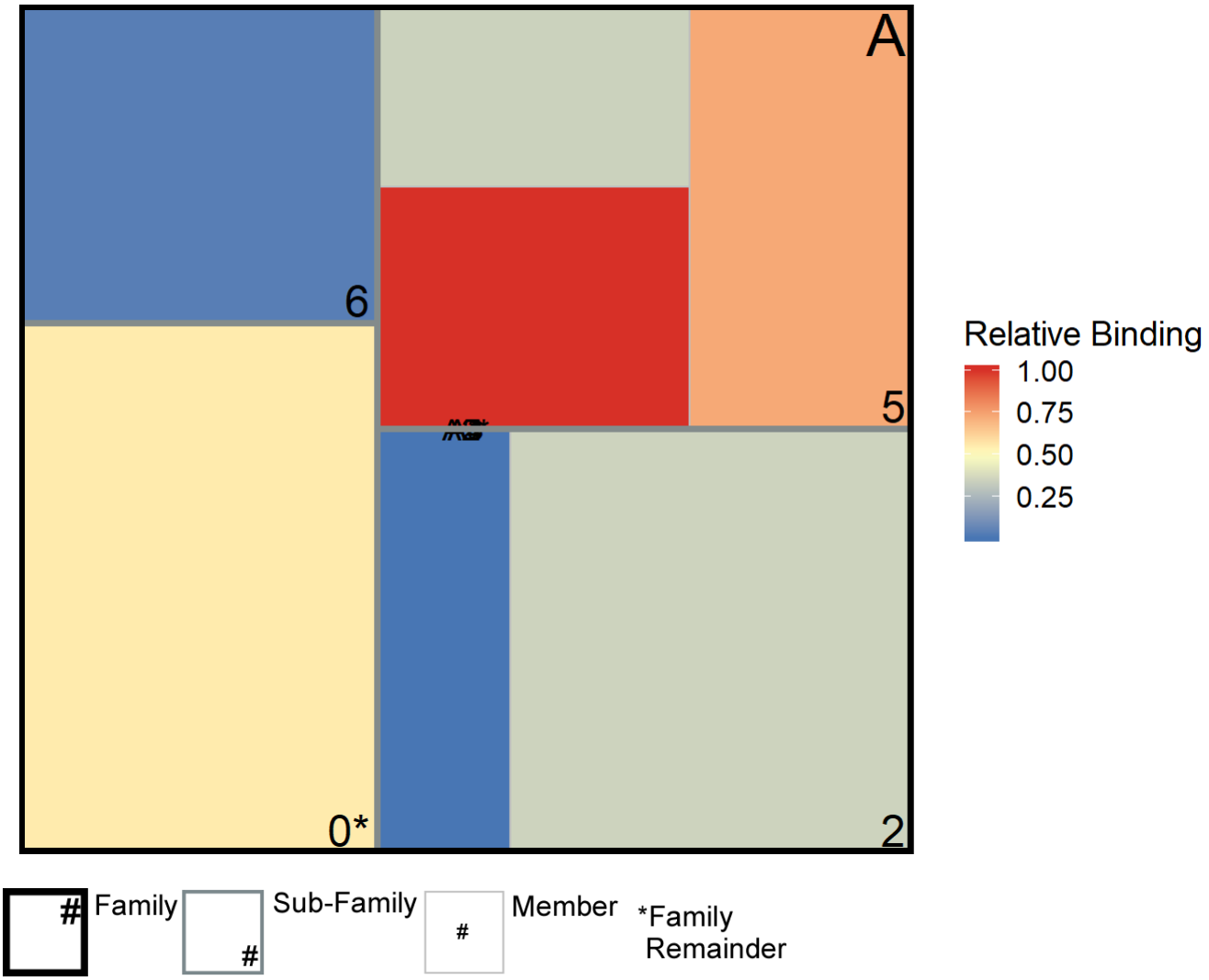


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

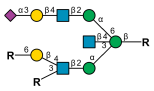
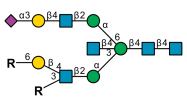
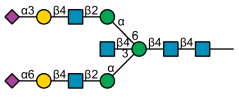
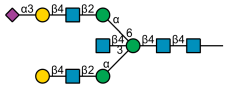
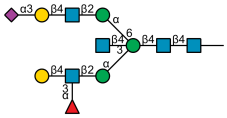


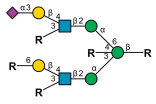
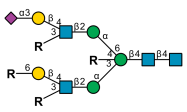
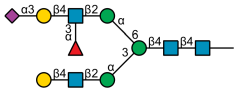
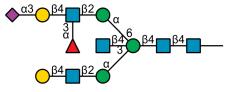
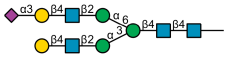
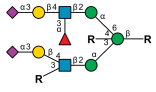
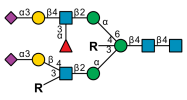
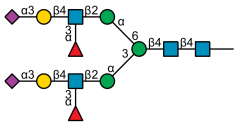
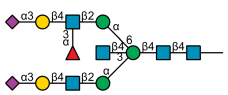
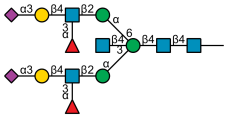
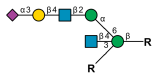
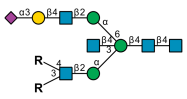
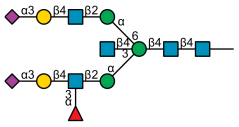
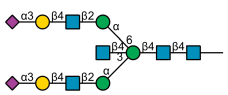
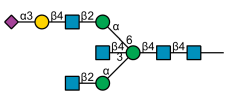
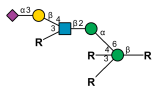
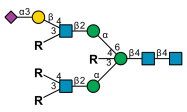
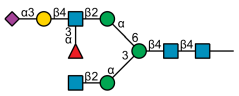
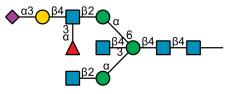
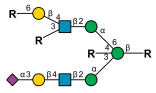
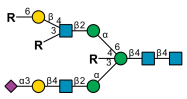
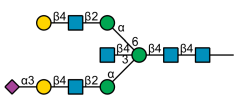
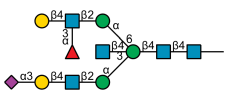
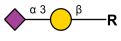
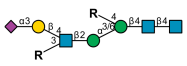
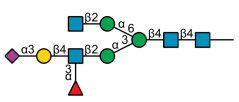
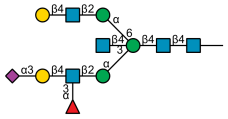
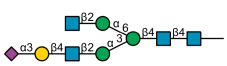
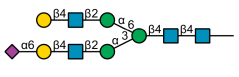
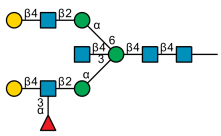
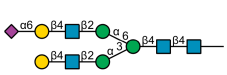
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

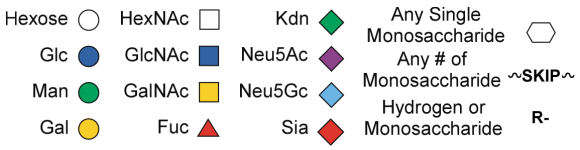
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				16		27		17

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A2				66		30		63
A3				42		33		6
A4				18		3		23
A5				62		26		59
A6				12		67		32
A0				47		15		44
0				49		14		64

Key:



All Concentration Plots:

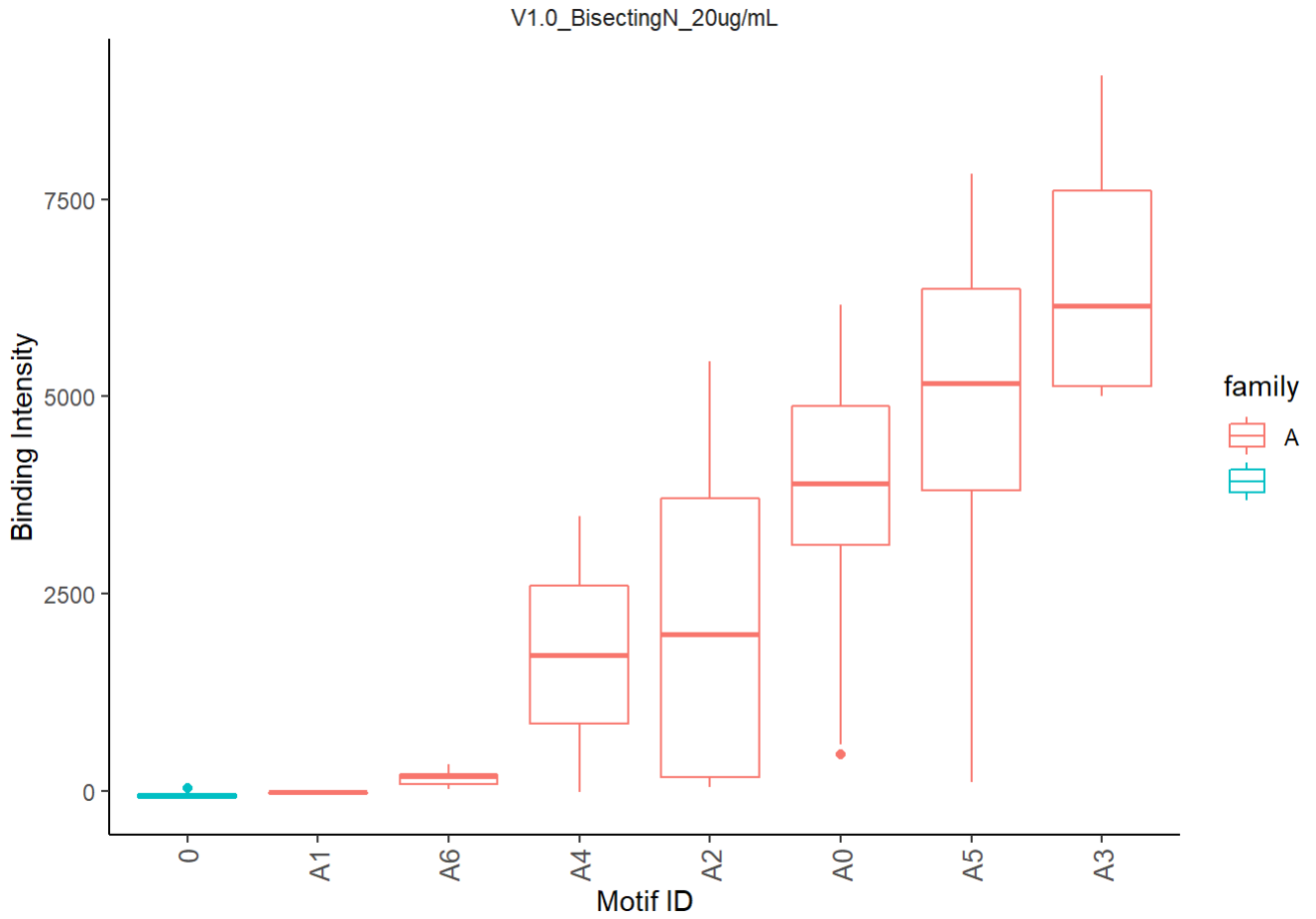
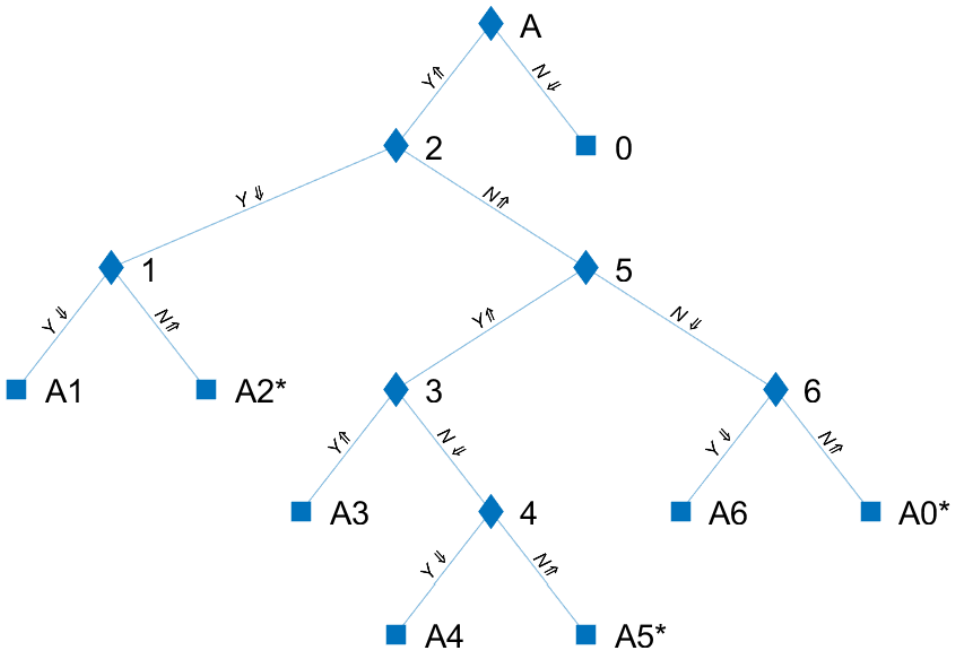


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



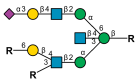
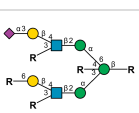
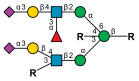
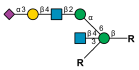
*Motif matches the remaining glycans not matched by earlier motifs in the model.

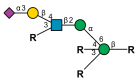
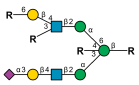
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

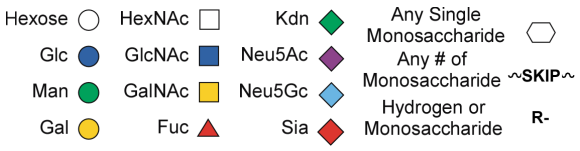
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f3f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3)(<3f4f6f>GlcNAcB1-4)<2f>ManB
A2*		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<2f3f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f>ManB
A3		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f>ManB
A4		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f4f6f>GlcNAcB1-4)<2f>ManB

Motif ID	Motif Graphic	Motif Text
A5*		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
A6		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<2f3f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6)<2f>ManB
A0*		<6f8f>Neu5AcA2-3<2f4f6f>GalB
0		Non-Binders

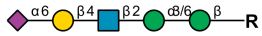
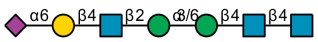
Key:



NR42486 (CR32_H1)

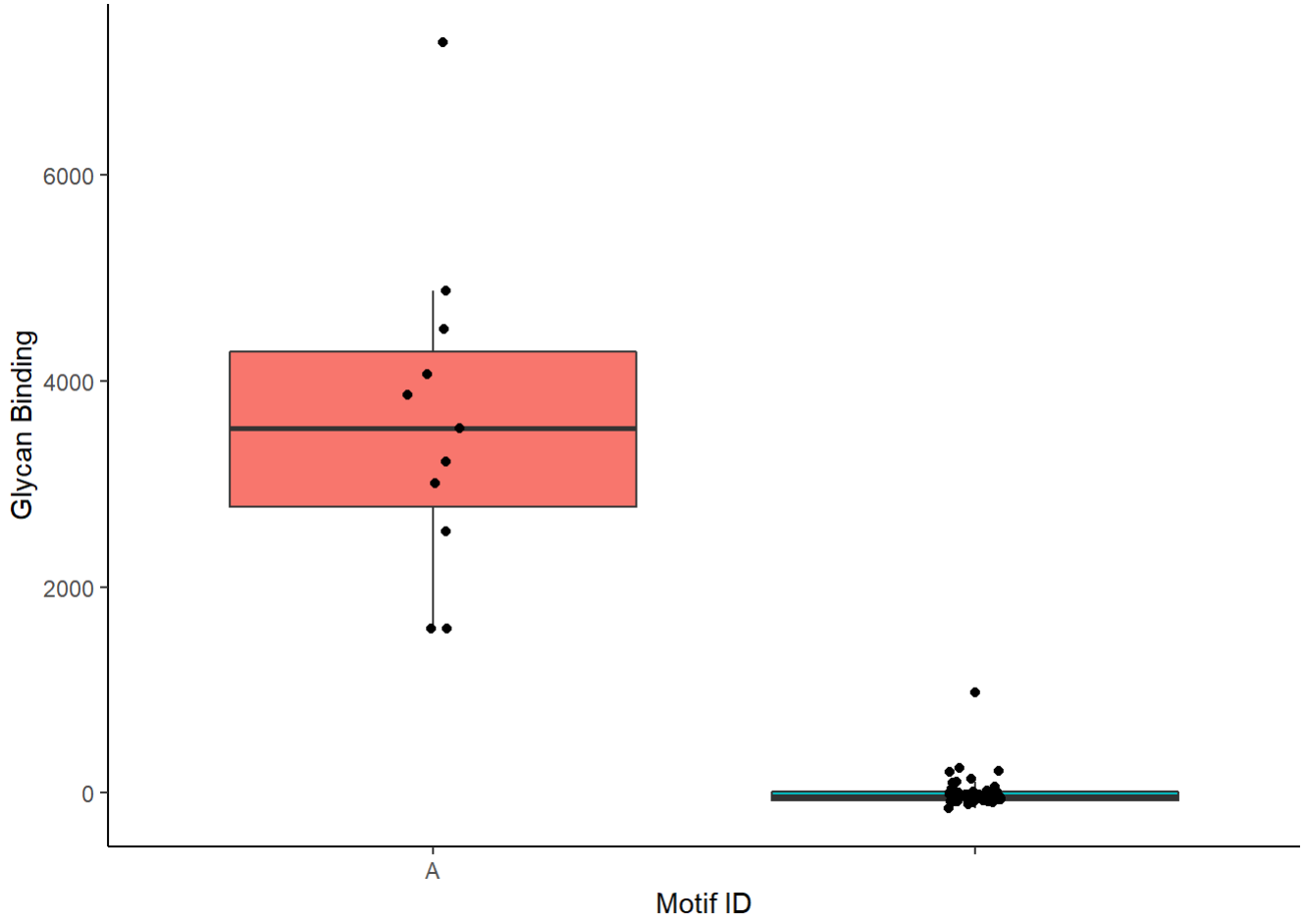
Automated Analysis report for NR42486 evaluated at 20 ug/mL

List of Primary NR42486 Motifs

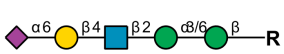
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1	11
0			0	61

Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

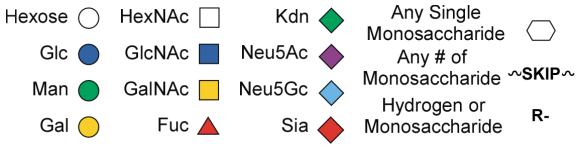
Boxplot of Primary Motifs



List of Fine-Specificity NR42486 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0			1	11	<0.001
0	Non-Binders (100%)		0	61	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

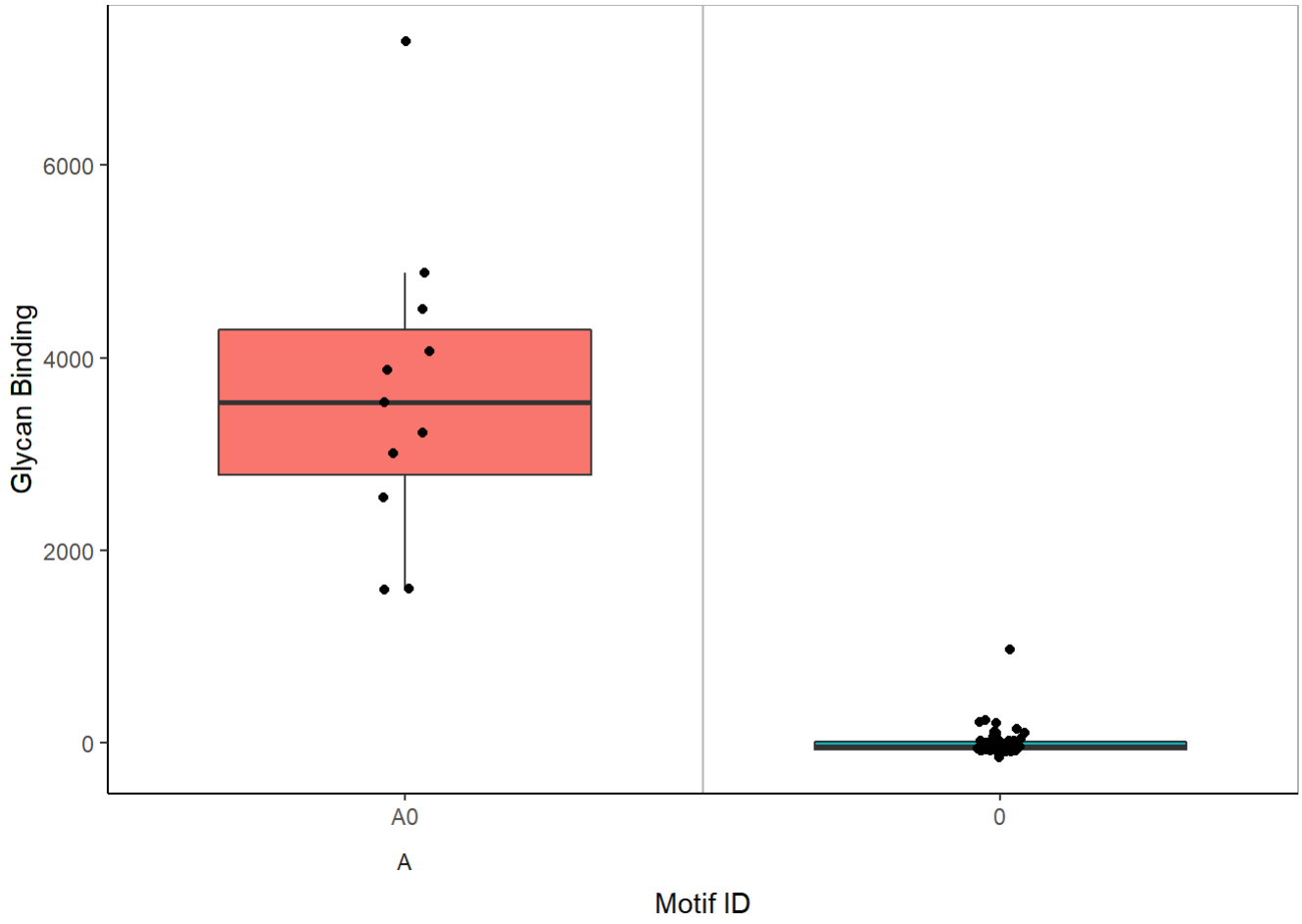


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

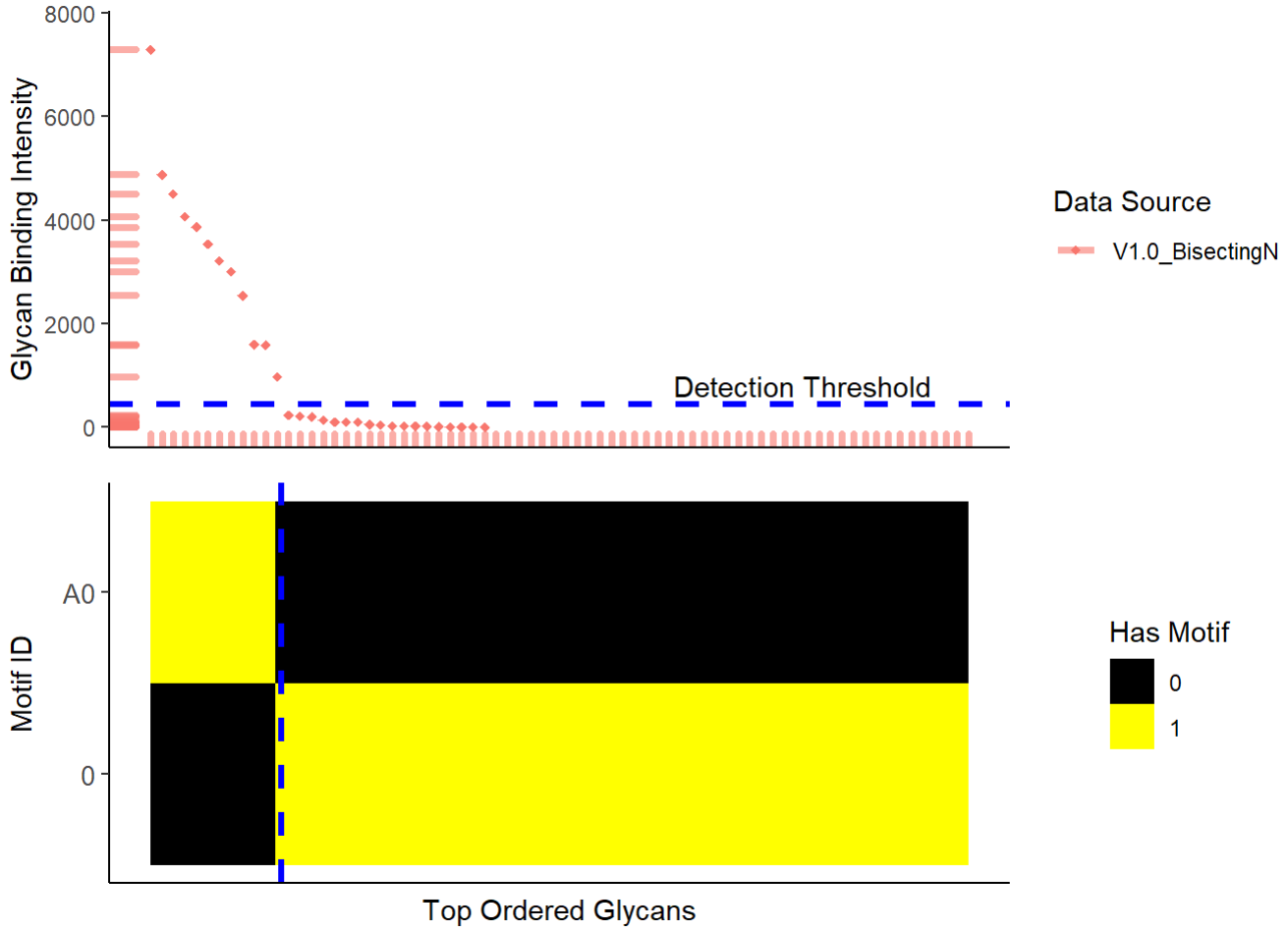
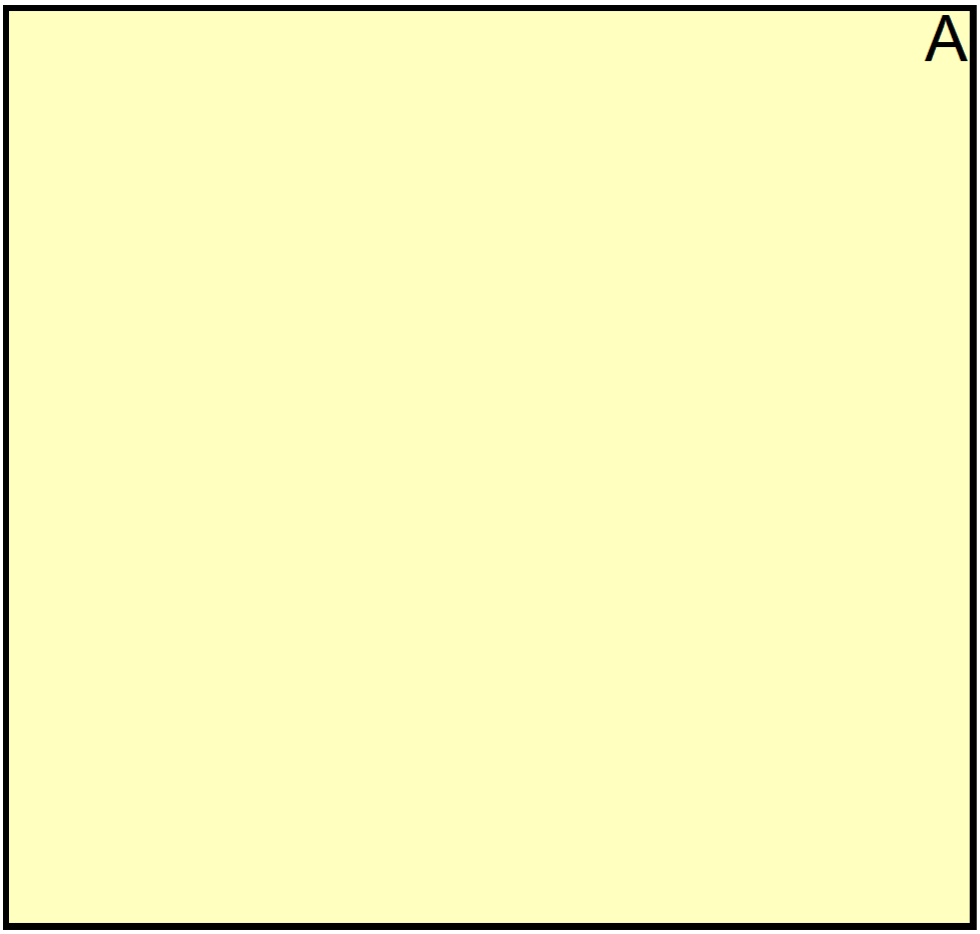


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map



Relative Binding

1

Family

Sub-Family

Member

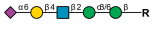
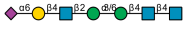
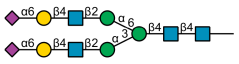
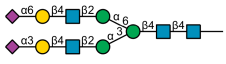
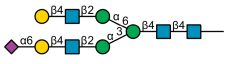
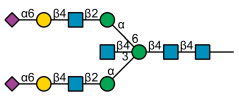
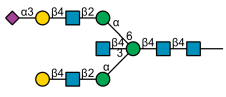
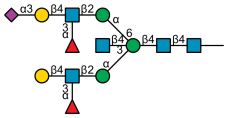
*Family Remainder

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

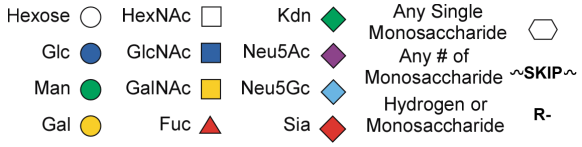
Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A0				40		67		49
0				4		27		36

Key:



All Concentration Plots:

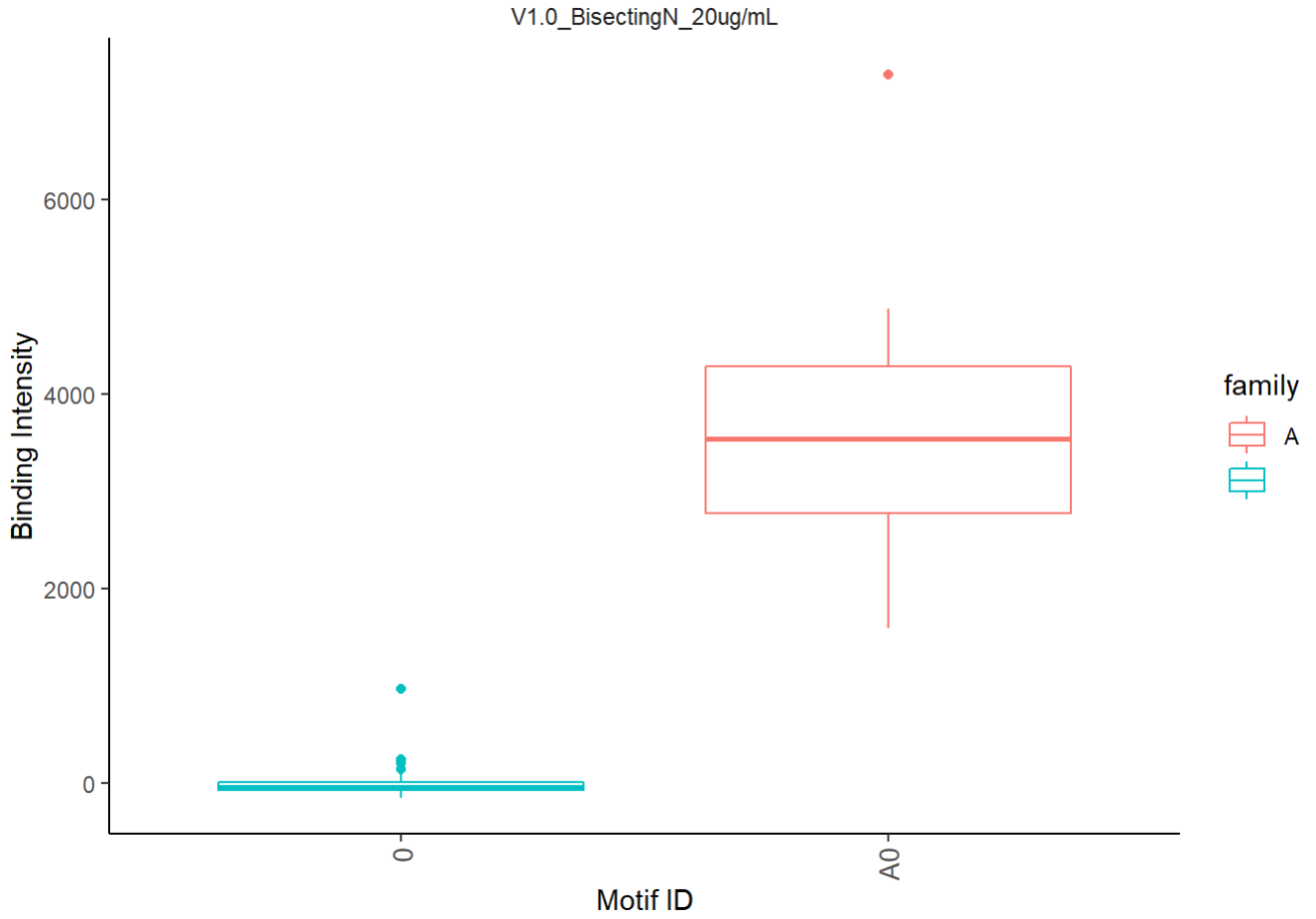
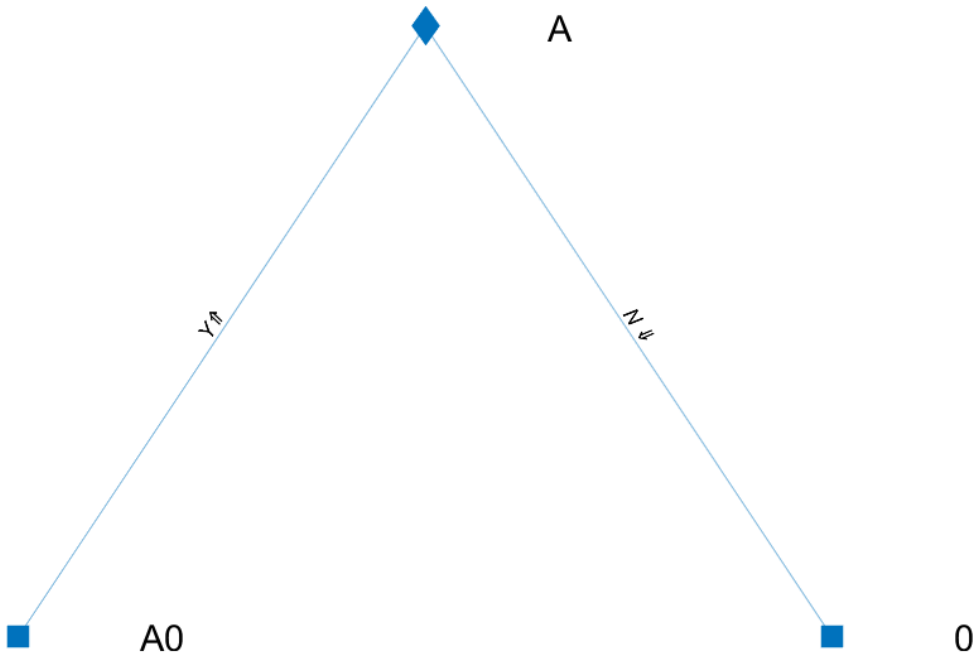


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



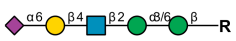
*Motif matches the remaining glycans not matched by earlier motifs in the model.

Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

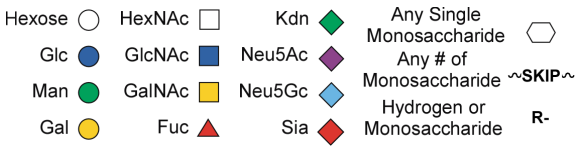
Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A0		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-<3or6><2f4f>ManB
0		Non-Binders

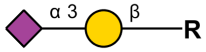
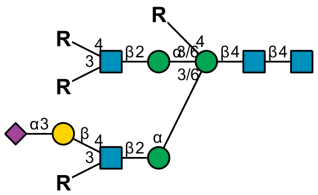
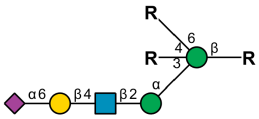
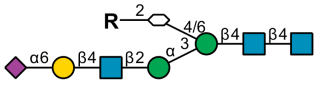
Key:



NR44365 (A1_H7)

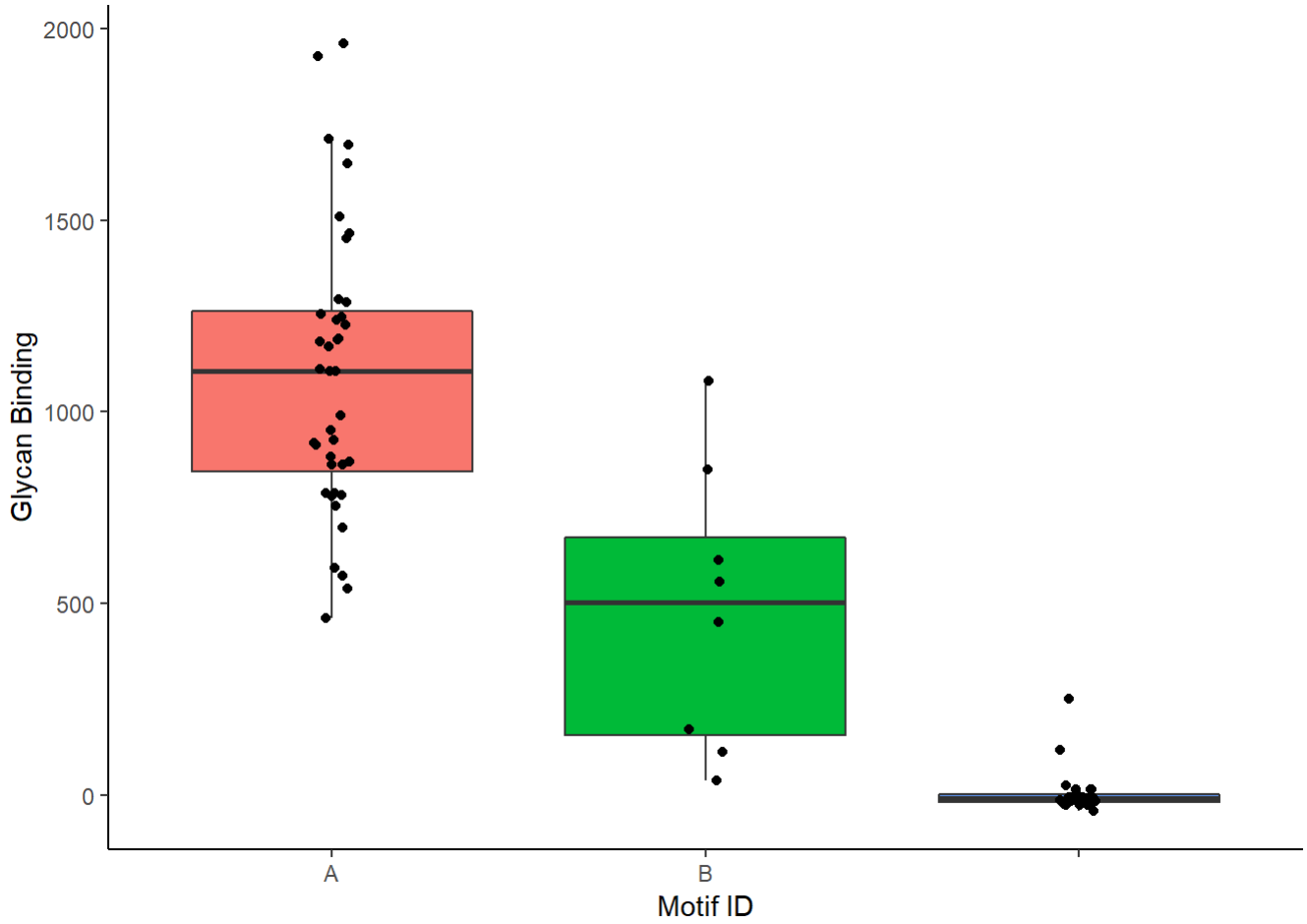
Automated Analysis report for NR44365 evaluated at 20 ug/mL

List of Primary NR44365 Motifs

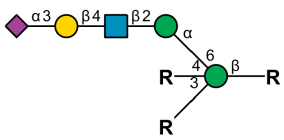
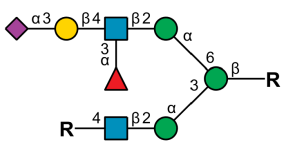
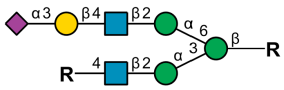
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1.00	40
B			0.49	8
0			0.01	24

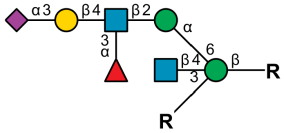
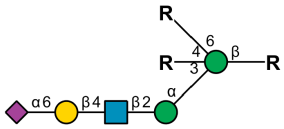
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

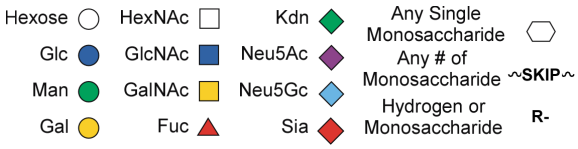


List of Fine-Specificity NR44365 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A2*	a3 Sialyl Type 2 LacNAc Bisecting N-Glycan (90%)		1.00	8	<0.001
A3			0.92	4	<0.001
A0*			0.74	18	<0.001
A1			0.72	4	<0.001

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A4	Sialyl Lewis X Bisecting N-Glycan (93%)		0.52	6	<0.001
B0			0.37	8	<0.001
0	Non-Binders (100%)		0.00	24	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

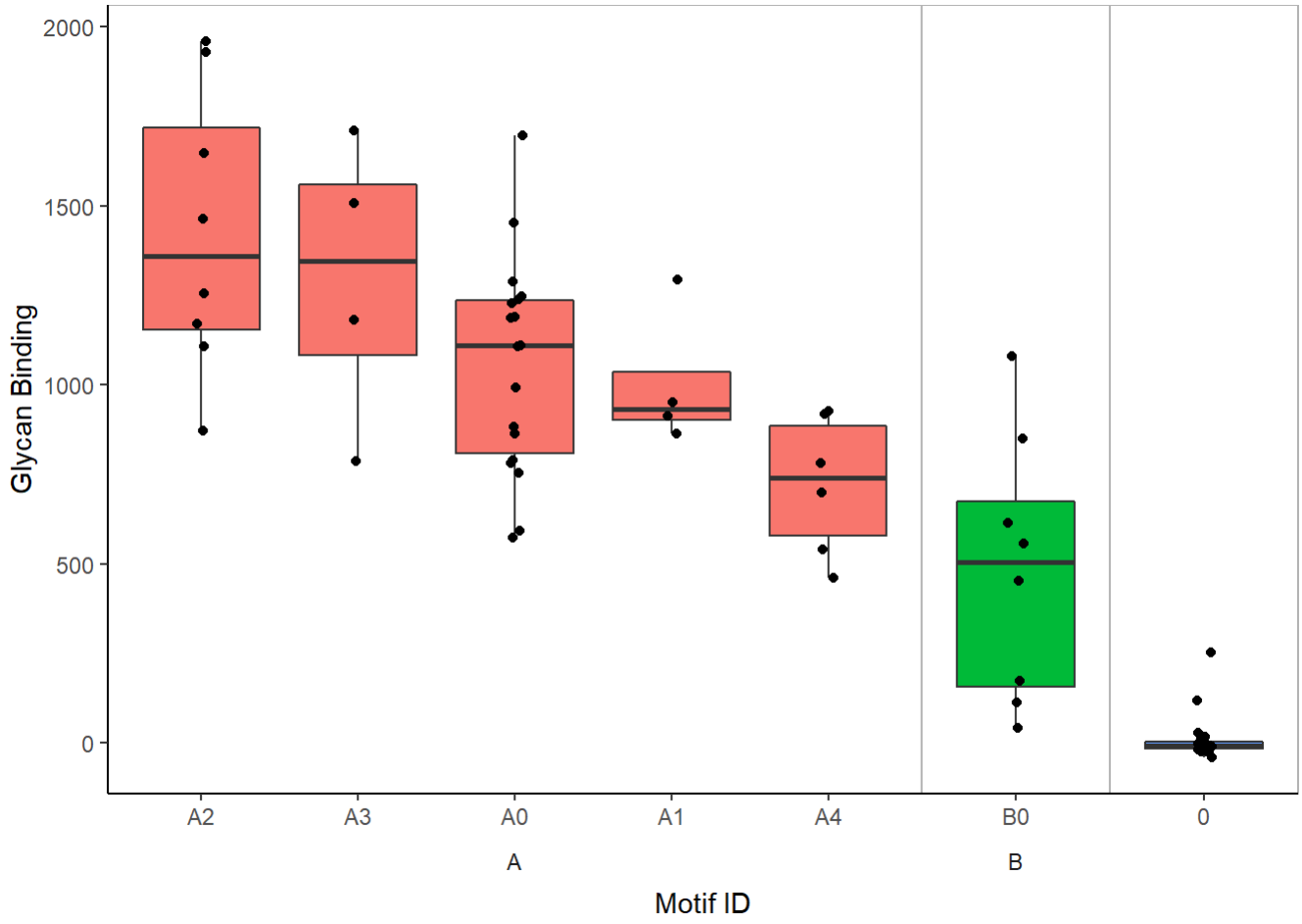


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

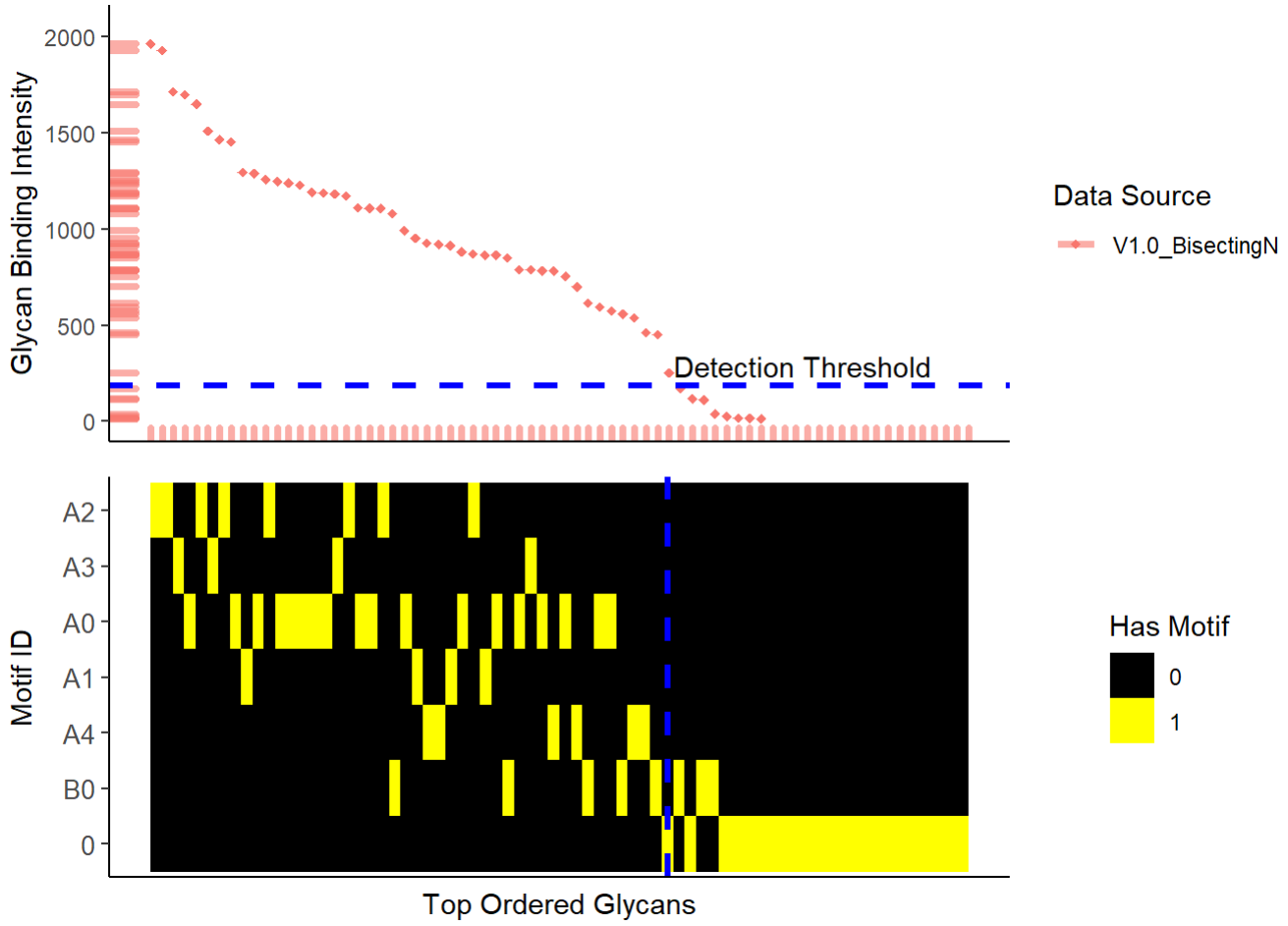


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

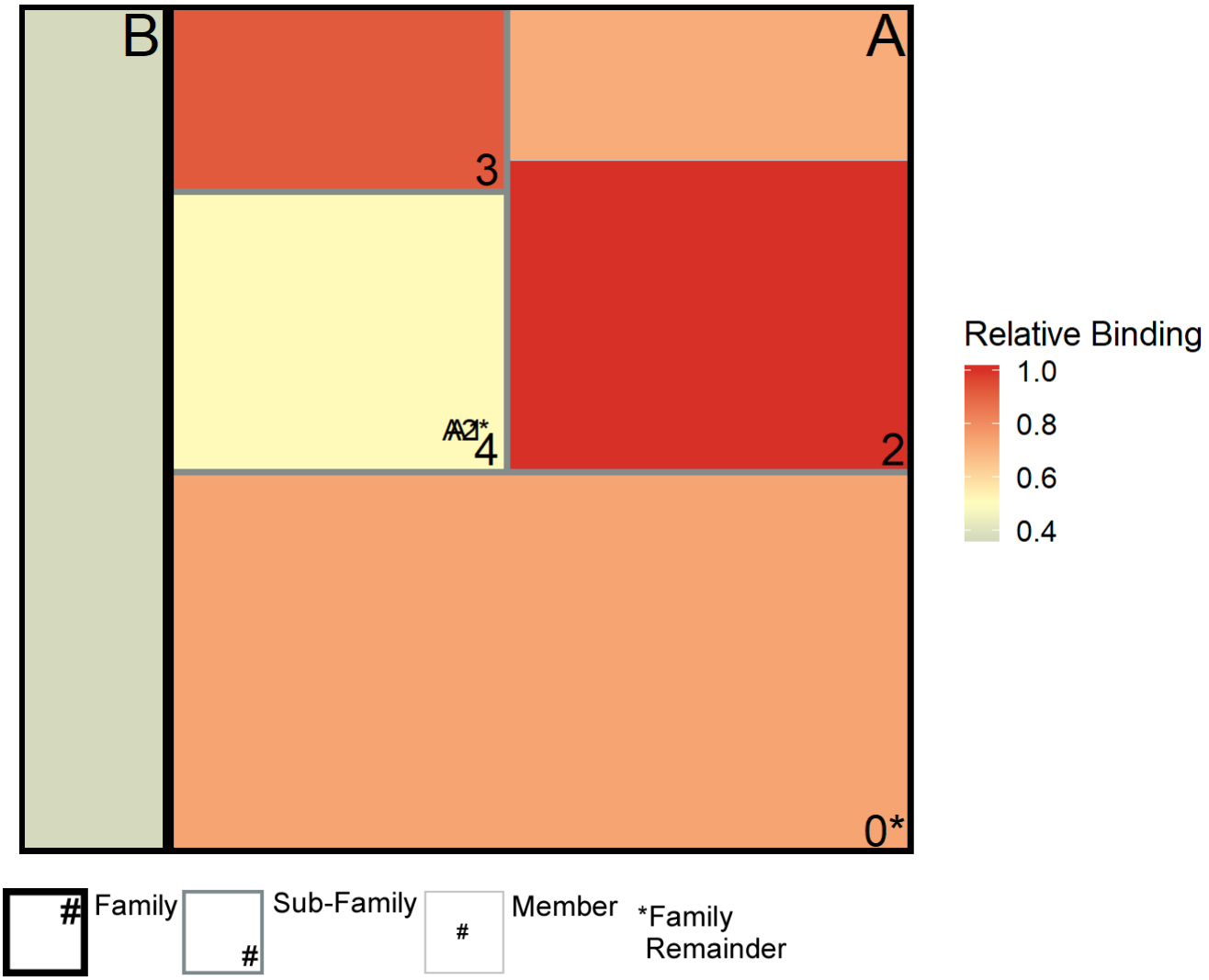


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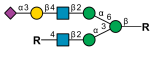
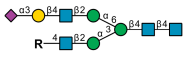
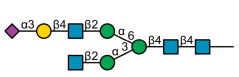
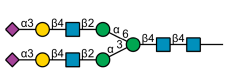
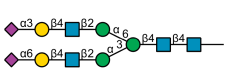
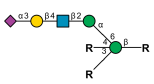
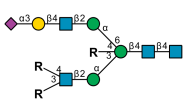
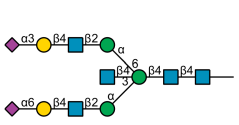
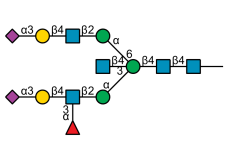
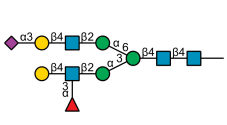
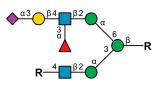
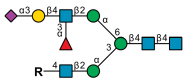
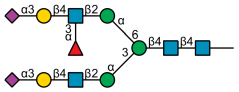
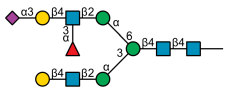
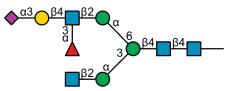
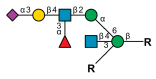
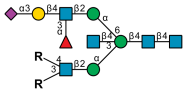
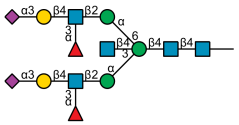
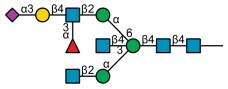
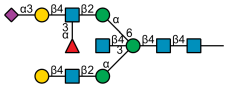
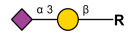
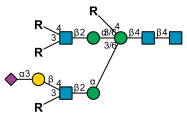
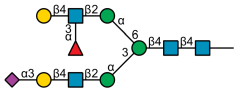
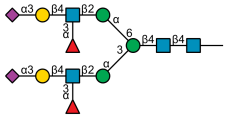
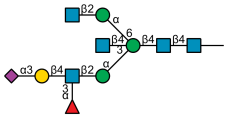
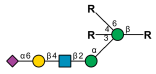
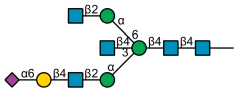
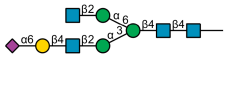
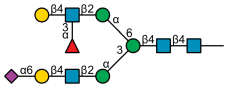
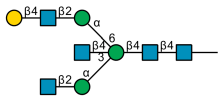
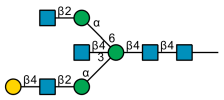
Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

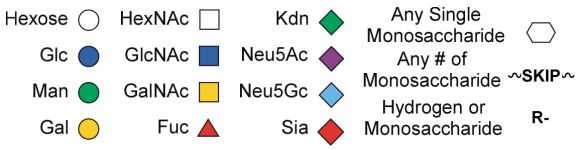
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A1				59		39		52
A2				16		18		53

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A3				69		66		62
A4				6		26		30
A0				68		42		11
B0				9		45		70
0				60		22		7

Key:



All Concentration Plots:

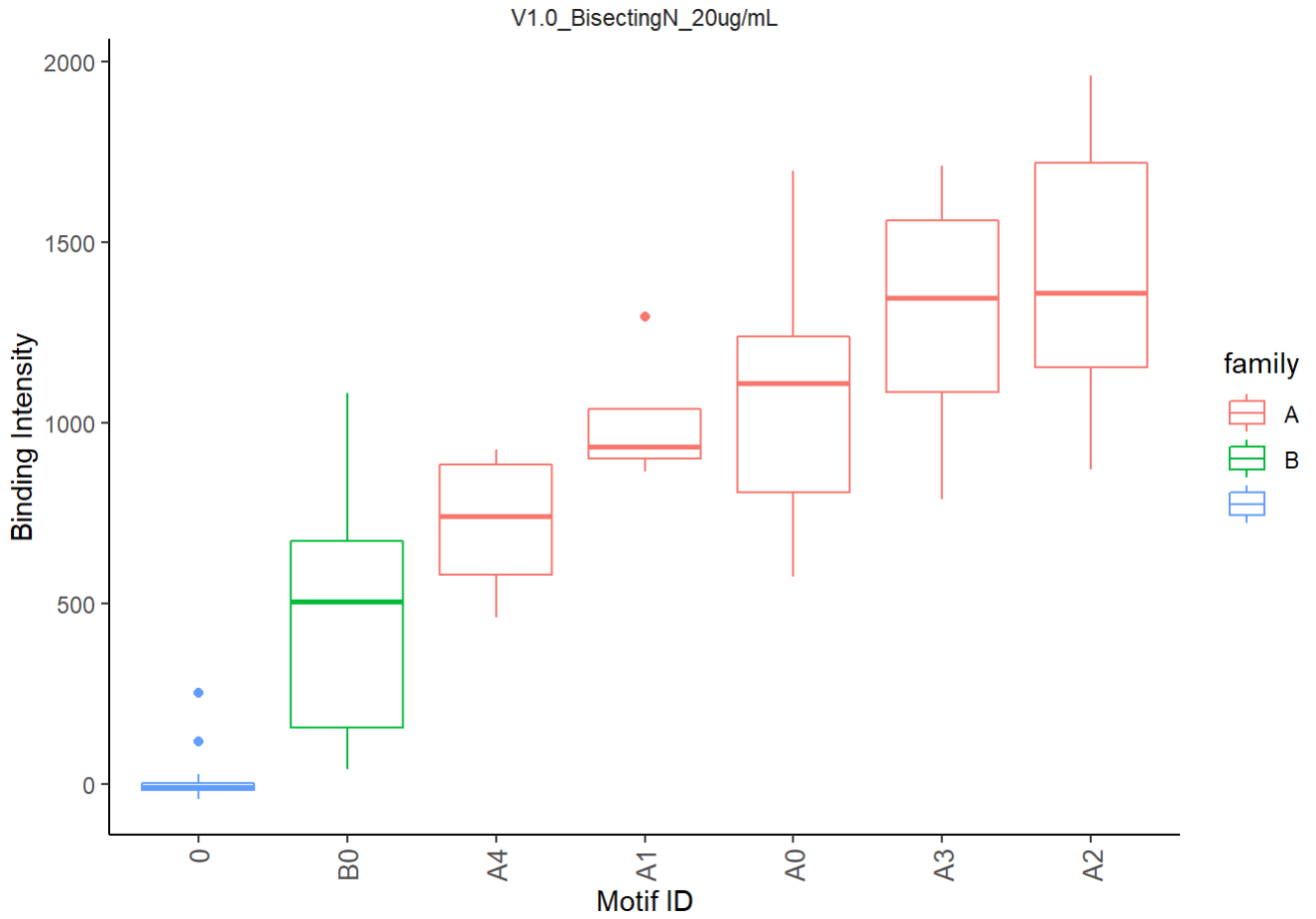
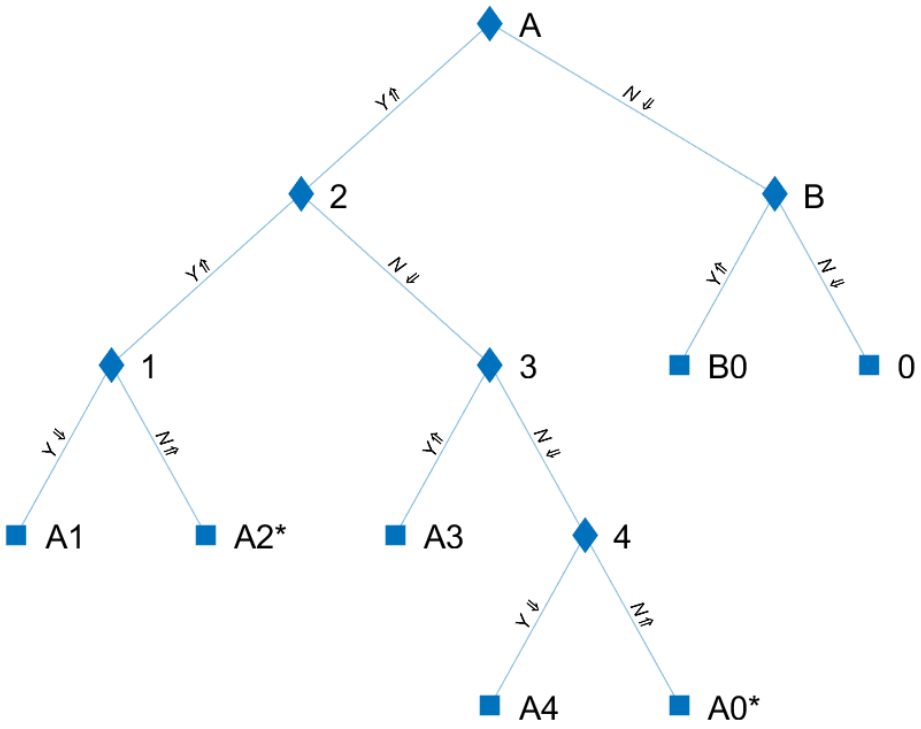


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



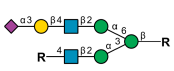
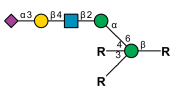
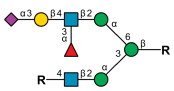
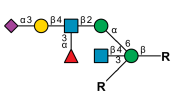
*Motif matches the remaining glycans not matched by earlier motifs in the model.

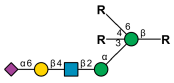
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

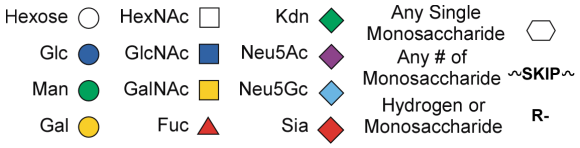
No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f4f>ManB
A2*		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-6<2f>ManB
A3		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f4f>ManB
A4		<6f8f>Neu5AcA2-3<2f4f6f>GalB1-4(<2f3f4f>FucA1-3)<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f4f6f>GlcNAcB1-4)<2f>ManB

Motif ID	Motif Graphic	Motif Text
A0*		<6f8f>Neu5AcA2-3<2f4f6f>GalB
B0		<6f8f>Neu5AcA2-6<2f3f4f>GalB1-4<3f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
0		Non-Binders

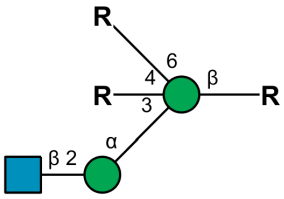
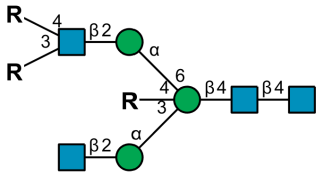
Key:



RatDCIR2_DeepSearch2

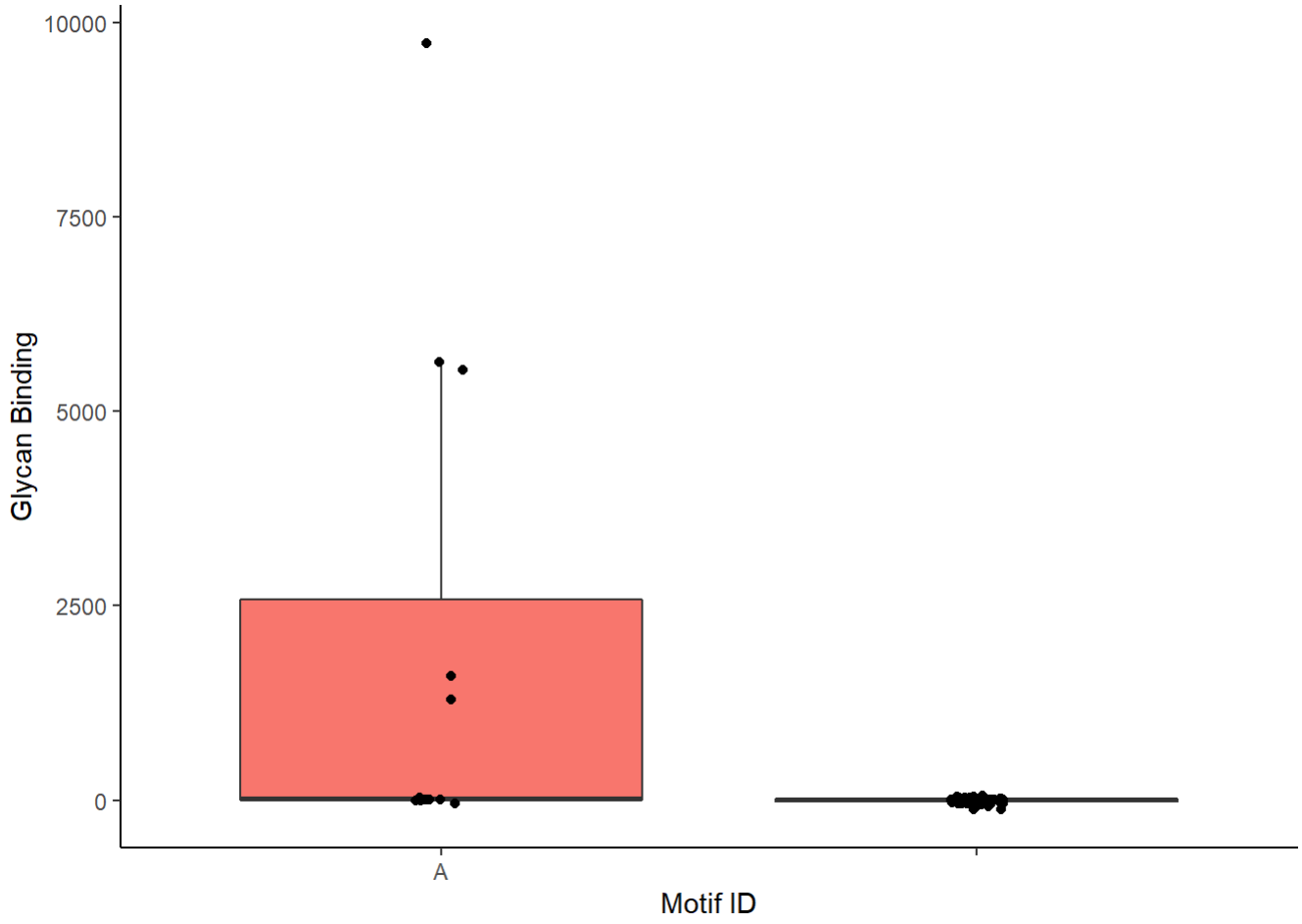
Automated Analysis report for RatDCIR2_DeepSearch2 evaluated at 20 ug/mL

List of Primary RatDCIR2_DeepSearch2 Motifs

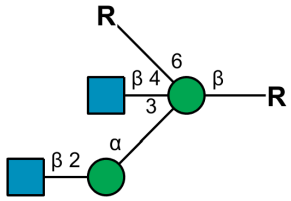
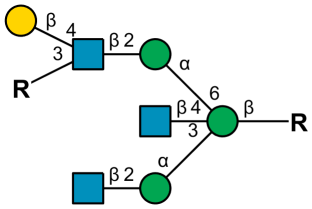
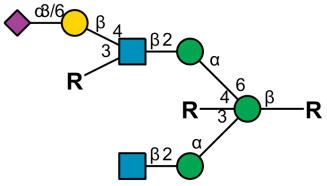
Primary Motif ID	Primary Motif Minimal Structure	Primary Motif Complete Structure	Relative Binding	Number of Glycans
A			1	12
0			0	60

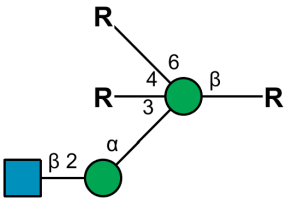
Minimal and complete motif definitions match the same set of glycans defined in the array. Components found in the complete motif but excluded in the minimal motif are not tested by the array. Monosaccharide identities and subsitution intolerance may or may not have been tested by the array, they are retained from the complete motif for readability.

Boxplot of Primary Motifs

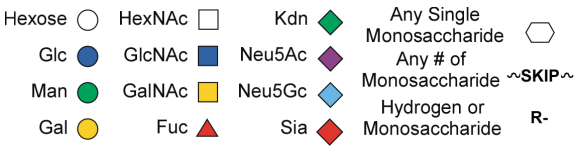


List of Fine-Specificity RatDCIR2_DeepSearch2 Motifs

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A3*			1.00	1	<0.001
A2	Terminal N-Glycan N-Acetyl Glucosamine Terminal Type 2 LacNAc (94%)		0.57	2	<0.001
A1	Terminal N-Glycan N-Acetyl Glucosamine 5-Acetyl Neuramic Acid (92%)		0.11	6	<0.001

Motif ID	Nearest Common Name (Accuracy%**)	Motif Graphic Structure	Relative Binding	Number of Glycans	P-Value***
A0*	Terminal N-Glycan N-Acetyl Glucosamine Terminal beta-Galactose (90%)		0.00	3	1.000
0	Non-Binders (100%)		0.00	60	NA

Key:



See Symbol Nomenclature for Glycans (SNFG) for complete key: https://www.ncbi.nlm.nih.gov/glycans/snfg.html (https://www.ncbi.nlm.nih.gov/glycans/snfg.html)

*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

**Accuracy describes the consistency between common-name definition of the motif and the formal, text-based definition of the motif, in terms of percent agreement in the glycans containing the two motifs. Common Name label definitions given here (http://carbogrove.org/MotifLabels.php).

***P-Value refers to difference from Non-Binders with multiple testing correction (Dunnet's Test)

Motifs with a red motif ID fail to show a logistic response to protein concentration in the range of concentrations analyzed. These motifs may be nonbinding motifs (motifs which define nonbinding exceptions) or simply fail to fit. Nonbinding motifs are determined based on concentration dependent response when available or the average binding of non-motif glycans otherwise.

Boxplot of Fine-Specificity Motifs

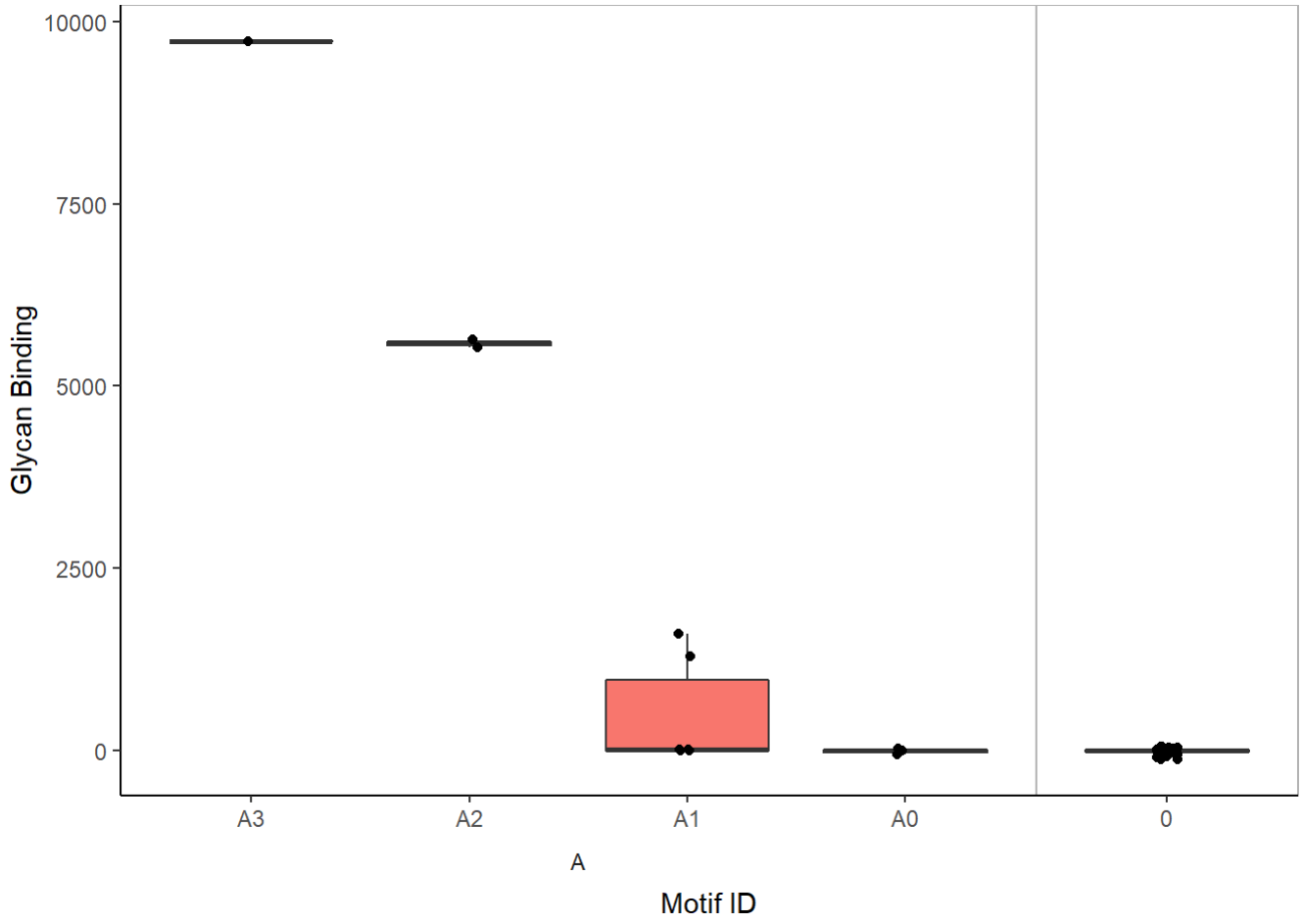


Figure 1. Glycan binding grouped by motif and motif family. Individual glycans are given as points on the plot.

Motif Intensity Map

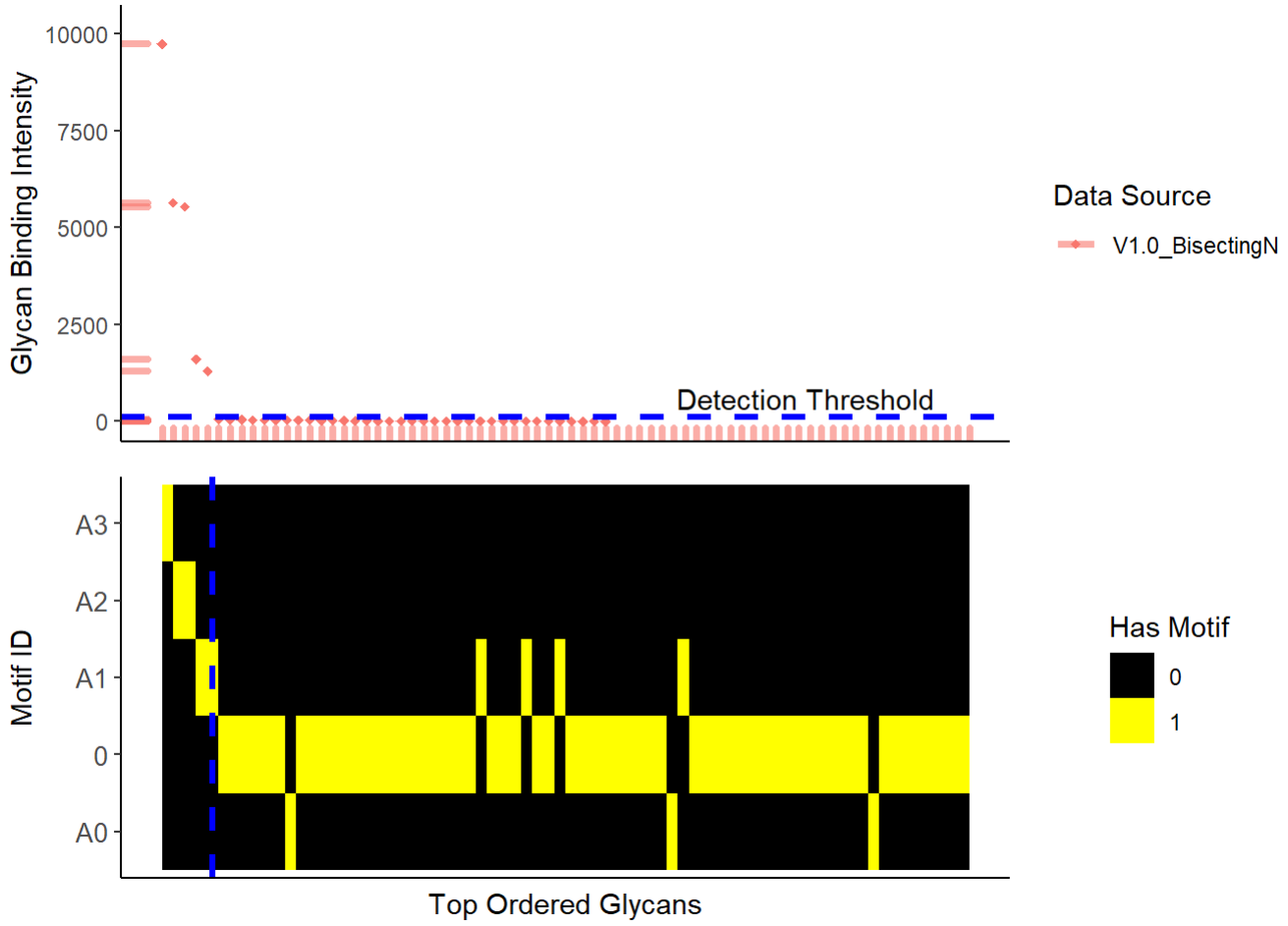
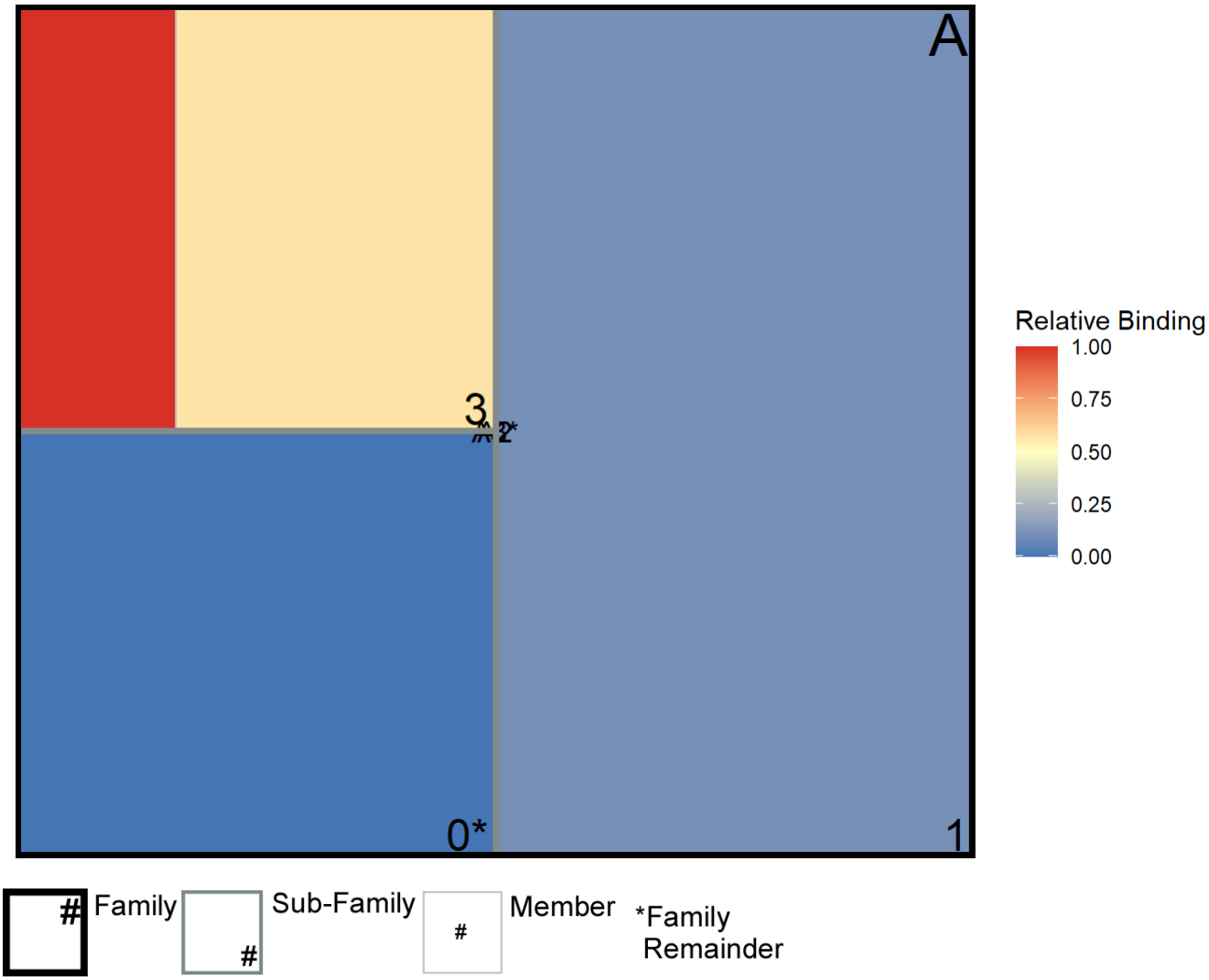


Figure 2. Glycan intensity and motif distribution plot. The top half of the plot presents the observed glycan binding intensity of various glycans used in the array over their rank binding intensity; only the top glycans are shown. The second plot indicates the position of glycans containing the various motifs in the top plot with a yellow tick.

Motif Family Membership Map

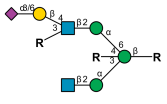
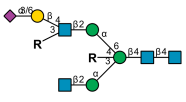
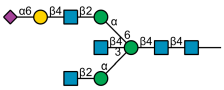
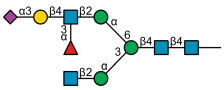
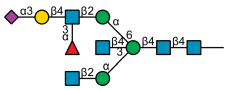


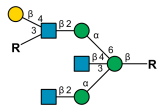
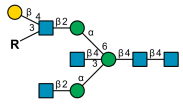
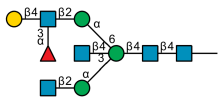
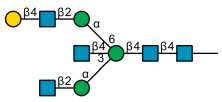
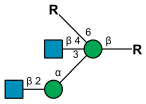
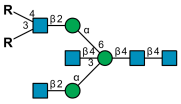
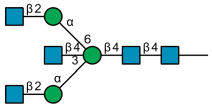
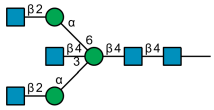
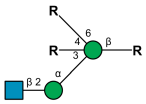
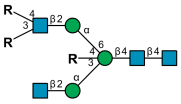
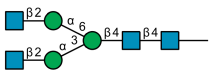
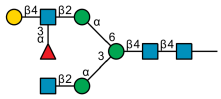
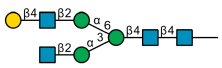
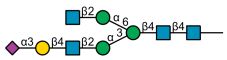
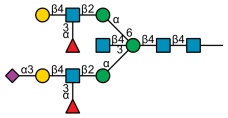
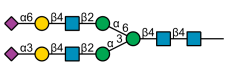
*Motif indicates the remaining glycans not matched by motifs which are a subset. Motif definition needs to be taken in the context of the model.

Figure 3. Treemap of glycan binding grouped by motif and family structure. The model structure can be represented as nested boxes where box size is proportional to the number of glycans with the motif and color changes with change in average relative binding of glycans with the motif. Only three layers of data splitting are included here, though further splitting may be possible.

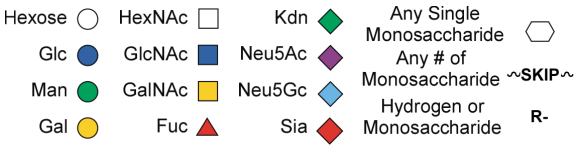
Detailed Model Breakdown

Motif Glycan Examples:

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan	Moderate Glycan	Lowest Glycan
A1			 24	 62	 26

Motif ID	Motif Minimal Graphic	Motif Complete Graphic	Highest Glycan		Moderate Glycan		Lowest Glycan	
A2				25				22
A3				1				1
A0				37		61		58
0				44		21		67

Key:



All Concentration Plots:

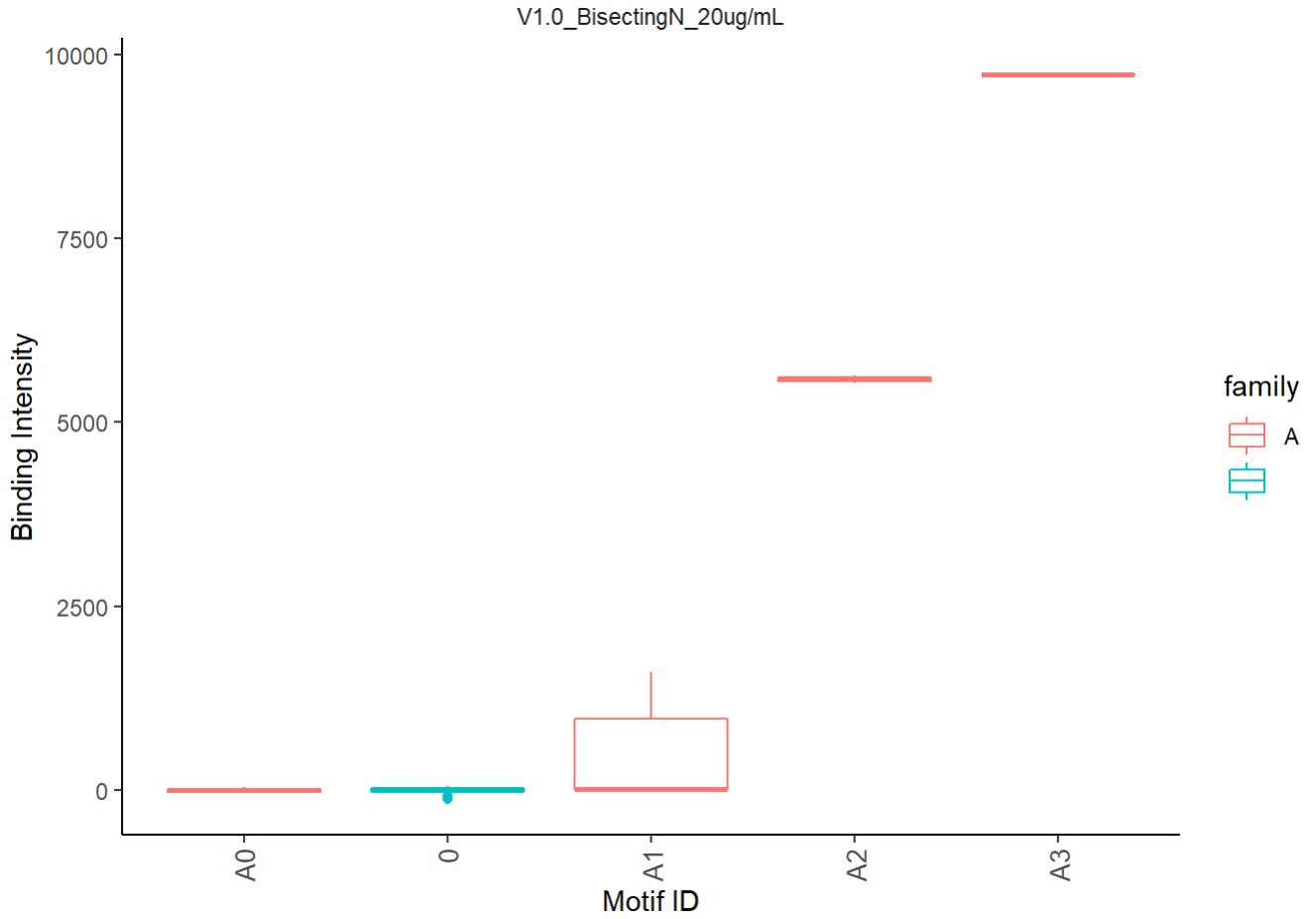
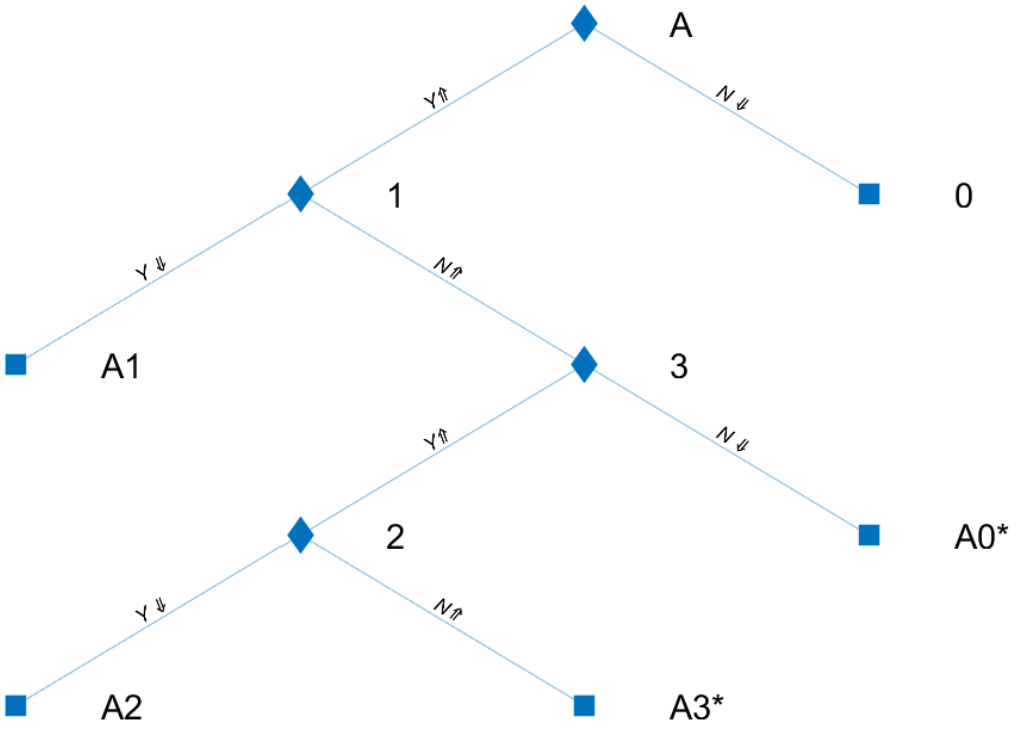


Figure 4. Boxplots of glycan binding grouped by motif for each dataset in the model. Motifs are listed in ascending average binding intensity (for the selected concentration) and colored by family.

Model Structure:



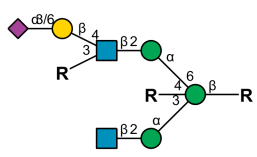
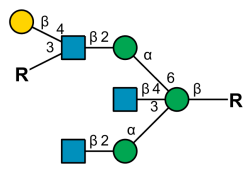
*Motif matches the remaining glycans not matched by earlier motifs in the model.

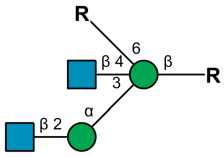
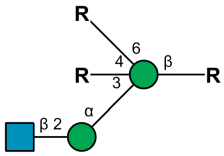
Figure 5. Tree representation of the regression tree model trained on array data. Data flows through the tree (top-down) and is split by the various motifs. The motif used the split the data at each point has the id “family+split number” except when further split. In the case of futher splits the id of the motif used to split the data is denoted with an asterisk.

Curve Fitting:

No curves were fit for model

Motif Text Structures:

Motif ID	Motif Graphic	Motif Text
A1		<6f8f>Neu5AcA2-<3or6><2f4f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3)<2f>ManB
A2		<2f3f4f6f>GalB1-4<6f>GlcNAcB1-2<3f4f6f>ManA1-6(<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3)(<3f4f6f>GlcNAcB1-4)<2f>ManB

Motif ID	Motif Graphic	Motif Text
A3*		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3(<3f4f6f>GlcNAcB1-4)<2f>ManB
A0*		<3f4f6f>GlcNAcB1-2<3f4f6f>ManA1-3<2f>ManB
0		Non-Binders

Key: