A. Supplemental

The coding of the variables used in **Model 1a** and **Model 1b** and **Model 2** is shown in Table S1B. The reference group is denoted by the coding value of 0. The reference ligand was none and thus its value for this variable is shown as 0 in Table S1B. Three other classes of ligand were analyzed in this model: *oligoethylene glycol linker (OEG),* monosaccharide *glucose (Glc),* and monosaccharide *mannose (Man).* Similarly, adsorbed glycoconjugates were the reference group for the modalities of display and 1μm beads at a surface area ratio of 1x to that of flat well surface adsorbed and 1.0 μg/ml soluble modalities were the other modalities compared in the model. In **Model 2** the reference group was any donor tested with a BSA conjugate with no ligand, presented from a well surface adsorbed modality.

Finally, for **Model 1a** and **b** and **Model 2** the variable *donor* was included in the analysis to account for the repeated measures of each donor across conjugates and to help limit the large inter-donor variability that is seen with primary donors. The reference donor was chosen at random and because all other factors control for donor in their calculation of beta no influence on the calculated coefficients or their significance was seen when changing between reference donors. Thus, the reference group was any donor with a conjugate that had no ligand and was adsorbed to the well of a plate.

Table S 1A: List of general linear model (GLM) continuous variables and their statistics. These factors indicate that both the inflammatory maturation factor (IMF) and tolerogenic maturation factor (TMF) are appropriate for analysis with parametric models such as a GLM and ANOVA.

	IMF	TMF
Number of Measures*	96	93
Mean	0.9705	0.1081
Standard Dev.	0.5833	0.1414
Minimum	0.273	-0.107
Maximum	3.309	0.735
Skewness	1.552	1.952
Kurtosis	2.656	5.821

*Three donors fell below the detection limit of the assay and were not included in the dataset.

Table S 1B: List of categorical variables, their coding in the Models 1a/1b and Model 2, and the frequency of occurrence of each variable. OEG represents all conjugates covalently modified with oligoethylene glycol with three repeats of the ethylene glycol. Glc represents all conjugates covalently modified with glucose-OEG_2-SH. Man represents all conjugates covalently modified with mannose-OEG_2-SH.

Variable	Sub Category	Code	Count
Ligand			
	None	0	24
	OEG	1	24
	Glc	2	24
	Man	3	24
Modality			
	Adsorbed	0	48
	1 um Bead	1	24
	Soluble (1ug/ml)	2	24
Donor			
	1-20	0-19	96

Table S 2: Pairwise comparisons between all 1 µm bead surface area ratios (altered by increase the number of beads per well) for dendritic cell IMF. The table shows the P value when comparing the indicated surface area ratios. Results indicate that all but 0.2x and 1.0x and 25x and 5x surface area ratios are statistically different from each other.

Surface Area Ratio	0.2x	1.0x	5.0x	25.0x
0.2x		0.8146	0.0002	0.0006
1.0x	0.8146		0.004	0.0092
5.0x	0.0002	0.004		0.9928
25.0x	0.0006	0.0092	0.9928	

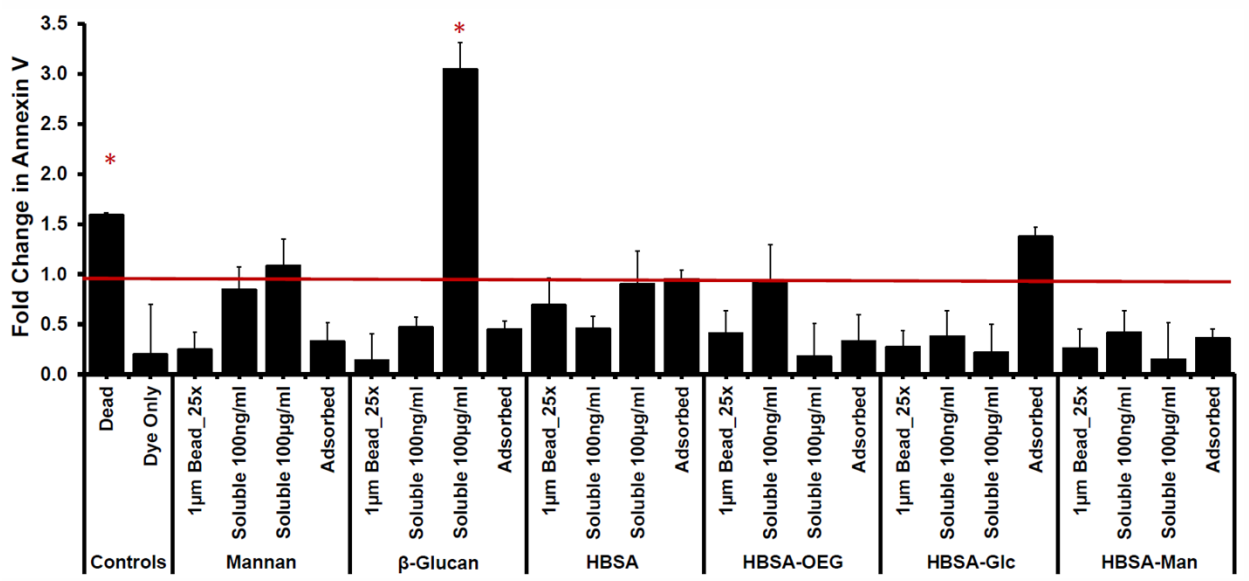

Figure S1: DC apoptosis as measured by Annexin V-FITC Binding. The average fold change over untreated cells is shown. Positive control (dead) and 100 µg/ml β-glucan showed a statistical increase in fold change of Annexin V binding. N=3 donors. Error bars represent standard error, red line indicates mean iDC response, * indicates statistical difference from iDC.

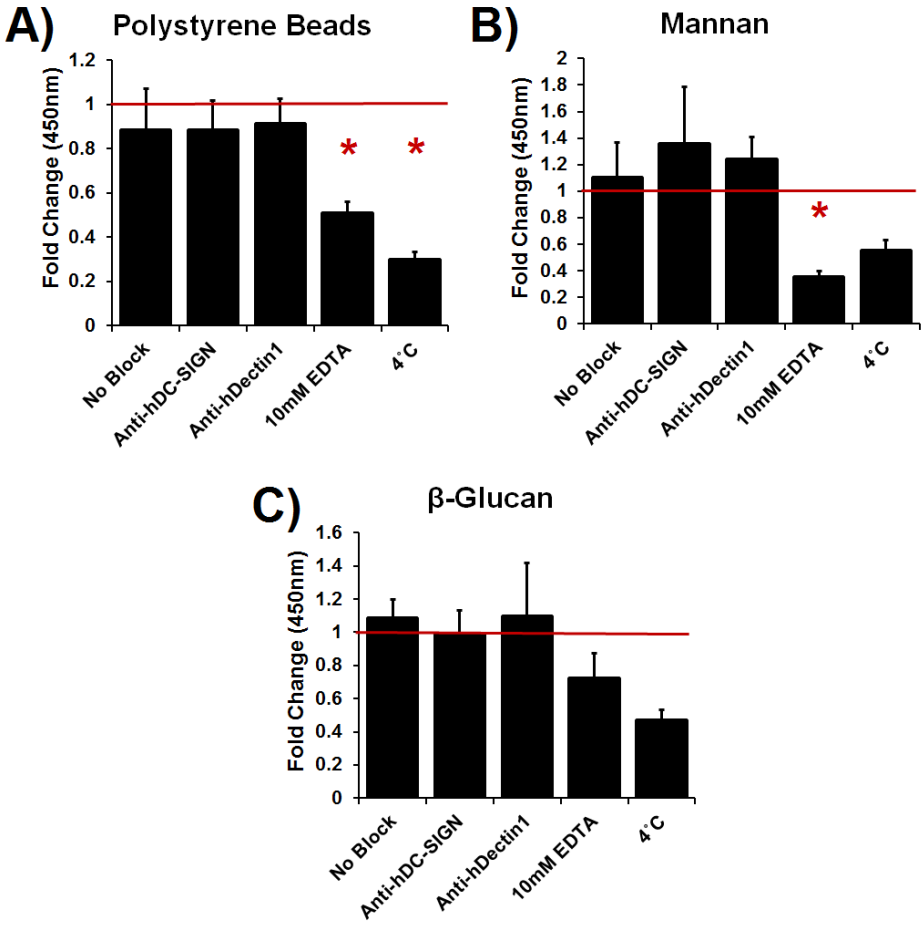

Figure S2: Quantification of phagocytosed 1 µm fluorescent beads with no conjugate (A), mannan (B), or β-glucan (C) coated fluorescent beads in the presence of CLR blocking antibodies, EDTA, or 4°C treatment. Data is fold change over isotype control treated DCs. N=4 donors. Error bars represent standard error, red line indicates mean isotype control treated cells' internalization of beads fluorescence, * indicates statistical difference from isotype control treated cells.

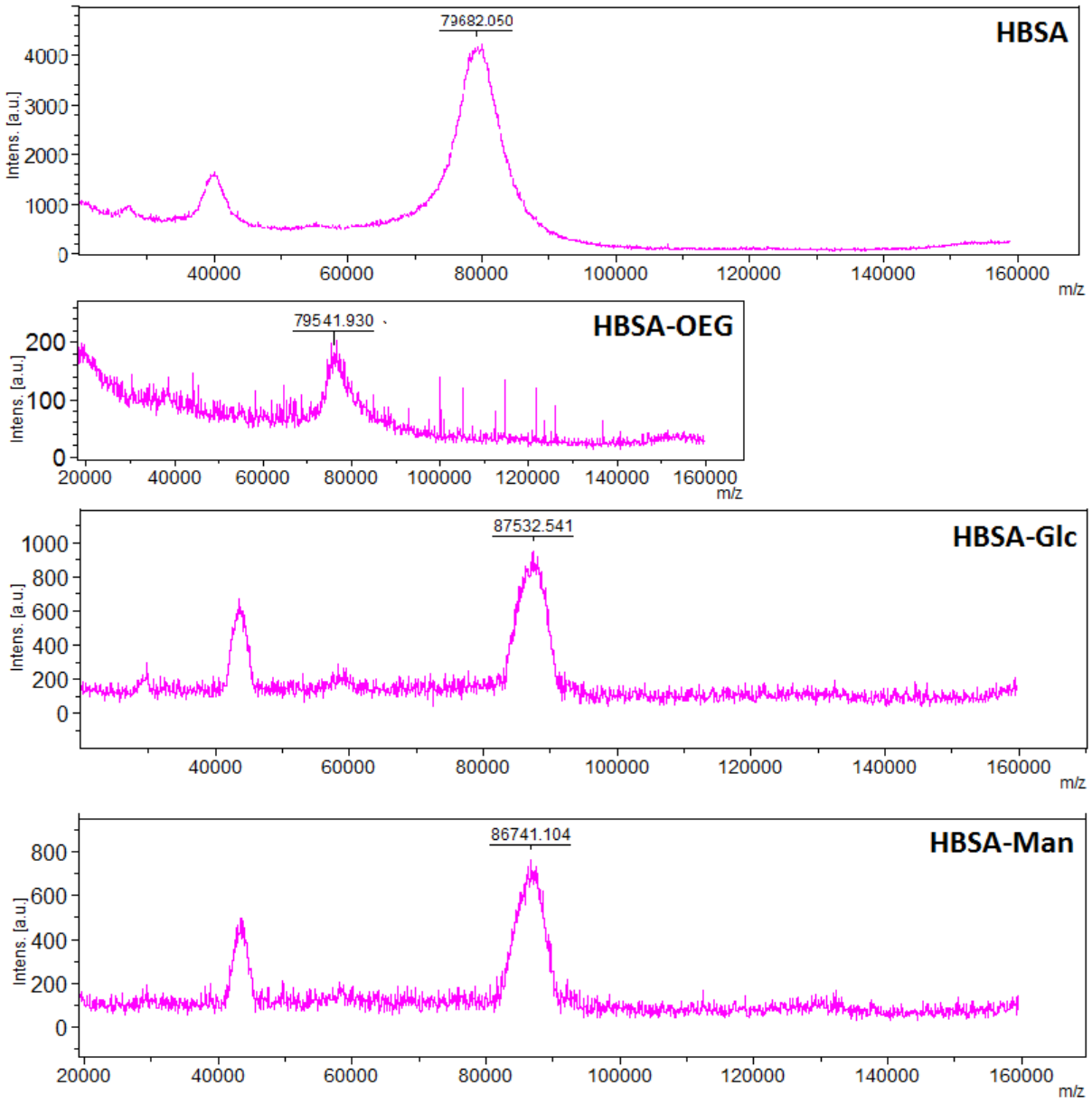

Figure S3: MALDI-TOF spectra of conjugates. No cross-linking between conjugates was seen. A half expected mass peak is seen in each of the spectra due to ion cleavage of the BSA protein.