Electronic Supplementary Material (ESI) for Molecular BioSystems.

The nature of the conserved basic amino acid sequences found among 437 heparin binding proteins determined by network analysis

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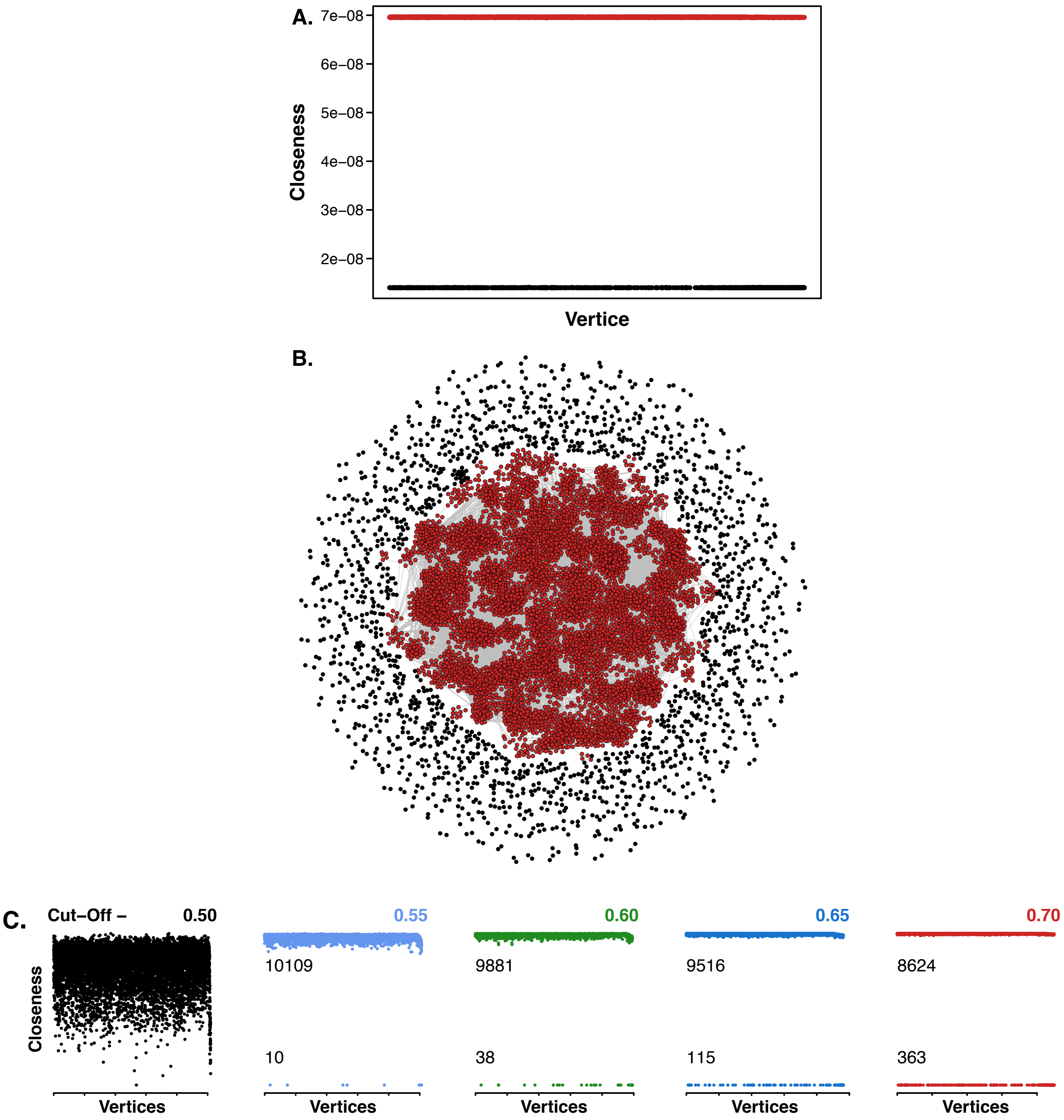
Supplementary Table 1. Amino acid classification used in the analyses.

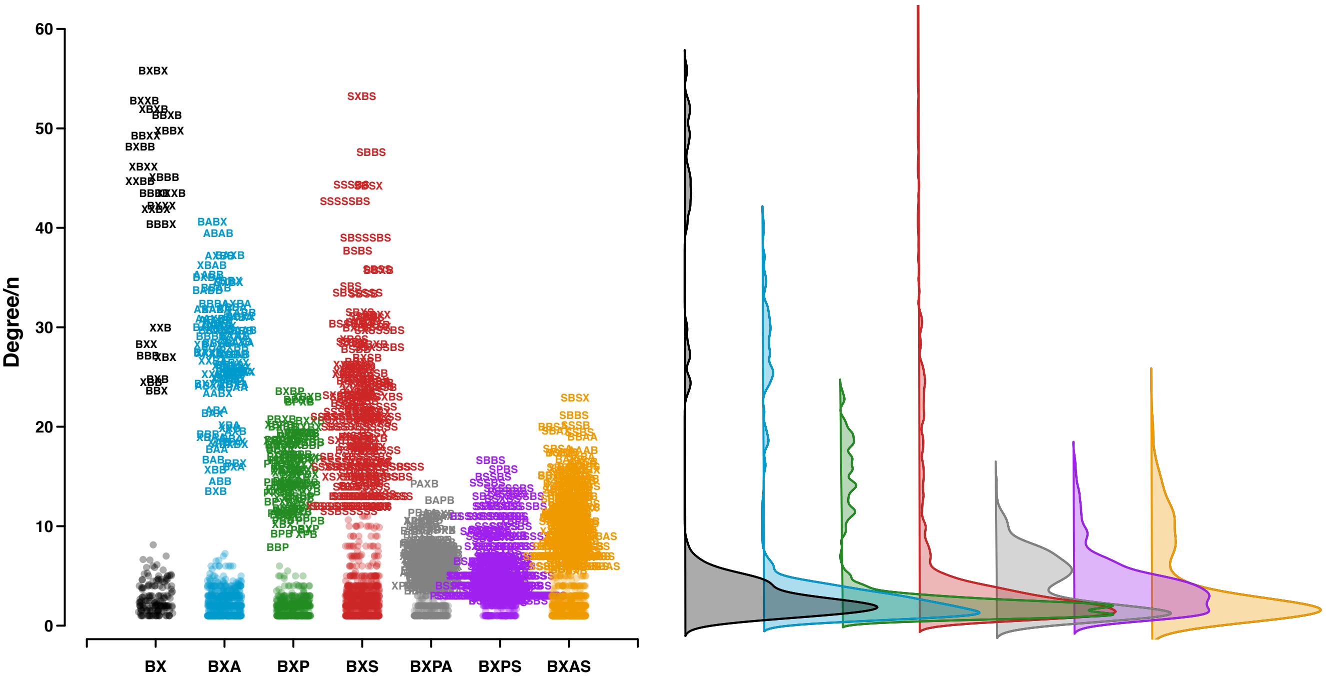
Basic	**B**	**-**	Arginine **R**	Lysine **K**	Histidine **H**	
Hydrophobic	**X**	**-**	Alanine **A**	Isoleucine **I**	Leucine **L**	Methionine **M**
			Tryptophan **W**	Tyrosine **Y**	Valine **V**	Phenylalanine **F**
Polar	**P**	**-**	Asparagine **N**	Glutamine **Q**	Serine **S**	Threonine **T**
Special	**S**	**-**	Cysteine **C**	Glycine **G**	Proline **P**	
Acidic	**A**	**-**	Aspartic Acid **D**	Glutamic Acid **E**		

Supplementary Table 2. *Properties of the* **HBS** *networks constructed from 437* **HEPbp***s, the parameter were extracted for networks containing* **BX** *amino acid sequences*. The table contains the basic network parameter: number of starting sequences, number of vertices, number of unique sequences, number of edges, network density, average degree, clustering coefficient - transtivity and the number of communities found the networks. These parameters are shown for networks constructed using different similarity cut-off values and then the closeness network parameter is used to remove dislocated vertices.

Cut-off	**0.5**	**0.55**	**0.6**	**0.65**	**0.7**	**0.75**	**0.8**	**0.85**	**0.9**	**0.95**	**1**
Whole Network											
No of starting sequences	10447	10447	10447	10447	10447	10447	10447	10447	10447	10447	10447
No of vertices	10203	10119	9919	9631	8987	8616	7763	5557	5509	5504	5504
No of unique sequences	5868	5784	5584	5296	4652	4281	3428	1222	1174	1169	1169
No of edges	2289358	740813	725326	539663	121007	120450	28099	23303	23265	23258	23258
Network density	0.044	0.014	0.015	0.012	0.003	0.003	0.001	0.002	0.002	0.002	0.002
Average degree	448.762	146.420	146.250	112.068	26.929	27.960	7.239	8.387	8.446	8.451	8.451
Clustering coefficient - transtivity	0.321	0.359	0.362	0.416	0.491	0.491	0.951	1.000	1.000	1.000	1.000
No of communities	37	114	393	631	566	463	1179	1191	1170	1169	1169
Closeness Selected Network Core											
No of starting sequences	na	10447	10447	10447	10447	10447	10447	10447	10447	10447	10447
No of vertices	na	10109	9881	9516	8624	8290	2411	68	68	68	68
No of unique sequences	na	5775	5552	5201	4348	4024	1977	2	2	2	2
No of edges	na	740808	725298	539568	120742	120215	4958	1473	1473	1473	1473
Network density	na	0.014	0.015	0.012	0.003	0.003	0.002	0.628	0.628	0.628	0.628
Average degree	na	146.564	146.807	113.402	28.001	29.002	4.113	43.324	43.324	43.324	43.324
Clustering coefficient - transtivity	na	0.359	0.362	0.416	0.491	0.491	0.441	1.000	1.000	1.000	1.000
No of communities	na	109	374	581	412	321	215	2	2	2	2



Supplementary Figure 1. *Determining the core of a* **HBS** *graph*. The core of the large HBS graphs was determined using the closeness centrality, this quantity is the reciprocal of the sum of distances between one vertex and all of the other vertices that make up the graph. As can be seen in panel **A**. the vertices that comprise the graph shown in panel **B**. are bivariate, the vertices with a greater closeness value (red) lying at the core of the graph, while the vertices with smaller closeness values (black) lie at the periphery of the graph. The effect of changing the graph similarity cut-off can be seen in panel **C**., as the number of dislocated, dissimilar, vertices increases as the similarity cut-off becomes more stringent.



Supplementary Figure 2. *Amino acid type analysis of the sequences found in the* **HBS** *networks*. Sequences were converted to there amino acid type, for example, the sequence **LLR** is converted to **XXB**, vertices with similar sequences were then combined and the ratio of the vertex degree to number was determined, the higher this value the more important the vertice is. The significant sequences, as determined by density analysis, can be found in **Supplementary Table 3**.

Supplementary Table 3. *A table containing the significant sequences found in* **Supplmentary Figure 2**. The significance of the vertices was measured by determining the ratio of the vertex degree to number, significant vertices were subsequently determined by using density analyses.

BX	BXA	BXP	BXS	BXPA	BXPS	BXAS
XXB	XXB	XXB	XXB	BXX	XXB	XBX
BXX	XBX	XBX	XBX	XXB	XBX	XXB
XBX	BXX	BXX	BXX	XBX	BXX	BXX
BXB	BBX	PXB	XBS	PXB	BXB	XBS
XBB	AXB	BXP	SBX	BXP	BXP	SBX
BBX	XBB	XBP	BSX	BPX	BXS	BSX
BBB	BXB	BPX	BXB	PBP	PXB	SXB
XBXX	BAX	PBX	XSB	PBX	XBP	XSB
BXXX	ABX	XPB	BXS	XBP	SBS	BXS
XXXB	XAB	BXB	XBB	BBX	XPB	AXB
XXBX	XBA	XBB	SXB	XPB	SBX	BBX
BXBX	BXA	PBP	BBX	PPB	SSB	SBS
XBXB	BBB	BPP	SBS	AXB	BSX	XBA
XBBX	BAB	PPB	BSS	XBB	BPX	XBB
XXBB	BBA	BBX	SSB	BPP	BPP	BXB
BXXB	ABB	PBB	SBB	ABX	XSB	XAB
BBXX	AAB	BBP	BSB	BAX	BSS	BXA
BXBB	ABA	BPB	BBB	BBP	XBS	BAX
XBBB	BAA	BBB	XBXX	BXB	XBB	BSS
BBXB	XBXX	BXXX	XXXB	XAB	SPB	ABX
BBBX	BXXX	XXXB	BXXX	XBA	PBX	SSB
BBBB	XXXB	XBXX	XXBX	BAP	SXB	ASB
	XXBX	XXBX	SXBX	PBB	PSB	BBS
	XBAX	XBXP	SBXX	APB	BBB	SBA
	XBXB	XBPX	SXBS	BPB	PBS	SAB
	BXBX	BXXP	XXBS	ABP	BPS	BSA
	XAXB	PXXB	XBSX	ABB	BBS	BBB
	XBBX	XXBP	BXBX	PAB	BPB	BSB
	ABXX	BPXX	SXXB	PBA	PBP	ABS
	BXXB	PXBX	XBBX	BBB	SBB	SBB
	XXBA	XPXB	XBXS	BAB	SBP	BBA
	XXAB	PBXX	XXBB	AAB	PBB	BAB
	BXXA	BXPX	XXSB	BAA	BBP	BAS
	BXAX	XXPB	BXXB	ABA	XXXB	AAB
	AXXB	XXBB	XBXB	XBXX	SXBS	ABA
	XXBB	XPBX	XSBX	PXXB	XBXX	BAA
	BAXX	BPPX	BXXS	BXXX	XXBX	ABB
	BBXX	BXBX	XSXB	XXXB	XPBX	XBXX
	AXBX	BXXB	BSXX	XBXP	XBXP	XXXB
	XBXA	BPXP	BBXX	BXXP	BXXP	BXXX

PTO.

BX	BXA	BXP	BXS	BXPA	BXPS	BXAS
	XABX	XBXB	BXSX	XXBX	SBXX	XXBX
	BXBB	PXBP	SBSX	XXBP	BXPX	XBAX
	AAXB	BBXX	SSXB	BPPX	BXXX	SXBX
	BBBB	PBXP	SSBS	XPPB	BPPX	SBXX
	BBXB	PPXB	BSXS	PXBP	BXXB	XAXB
	BXBA	XBBX	SXSB	XBPX	SXBX	XXBS
	AXBB	XBPP	BXSS	PBXX	BXBX	SXXB
	XBBB	XPPB	SBXS	XXPB	SPXB	XBSX
	BAAX	PBPX	XBSS	BPXX	BXXS	BXBX
	XAAB	XPBP	SBSS	PBPX	XBXB	XBBX
	BBBX	BPBX	XSBS	PBXP	PBXS	ABXX
	XABA	PXPB	SBXB	PPXB	SBXB	XSBX
	AXBA	BPXB	SBBX	BPXP	BPXP	XXSB
	XBBA	PPBP	BSSX	XXBB	XXBP	XXAB
	BXAA	BXPB	XSSB	AXBX	BXBS	XBXB
	BXAB	XPBB	XBBS	XPXB	XXPB	AXXB
	BABX	PXBB	SBBS	BXPX	XXBB	BXXB
	ABXA	BXBP	BBSX	BBXX	SXXB	SBSX
	BAXB	PPBX	BXSB	BXPA	SBXS	AXBX
	BBXA	BBXP	BXBS	XPBX	SBPS	BXXA
	AABX	PBXB	XBSB	BXXB	XPSB	XXBB
	ABXB	BXPP	SXBB	BAXX	PXXB	XBXS
	XABB	BPPP	BXBB	APXB	PBXX	SSXB
	AXAB	XBBB	SSBX	XBXA	XXBS	BXXS
	XBAB	XBBP	XSBB	AXXB	SPBS	XXBA
	ABBX	PBBX	BSXB	XXAB	SSBS	BSXX
	BBAX	PBPP	XBBB	XXBA	XBSS	BXSX
	XBAA	BBPX	BSBX	BXXA	XXSB	BXAX
	ABAX	BPBP	BBXS	ABXP	PXBX	SXSB
	BAXA	BBXB	SSSB	BPXB	XSXB	SBSS
	BBAB	XBPB	BBBB	BBXP	SBPP	BSXS
	BBBA	BPPB	SBSB	PPBP	BXPS	SXBS
	BABB	PPPB	BBBX	PXPB	BXPB	BXSS
	AAAB	PPBB	BBXB	XBBP	XPXB	XSXB
	AABA	BXBB	BSBS	PBXB	BXBP	BBXX
	AABB	PBBP	BBSS	BXPB	PPXB	BAXX
	ABAB	PBBB	BBSB	BXPP	BPXX	SBXS
	BABA	BBBX	BSSB	PXBX	SPSB	SSBS
	ABBB	BBPP	BSSS	BPBX	SBPX	XBXA
	ABAA	PBPB	BSBB	XBXB	BPBS	SBBX
	BAAA	BBBB	SBBB	PBPP	PBXB	XABX
	BBAA	BBPB	BBBS	XAXB	BXSB	AXSB
	ABBA	BBBP	SSBB	PXBB	PXBS	SAXB
	BAAB	BPBB	SSXBS	ABXX	XPBB	SABX
			BSXSS	XBPP	BSXS	XBSA
			SSSBS	BPPP	SBSS	SSBX
			XSSBS	BXBP	BBXS	XSBB
			SSBSX	AXPB	SSPB	XSBS
			BSXBS	BXAX	XSSB	BXBB
			BSSSS	BPPA	BSXP	SBXA
			SSSSB	XPBB	XBPX	BSSX
			BSSBS	ABPP	SPPB	AAXB
			BSBSX	BXBA	SXPB	SSSB
			BSBSS	PBBP	XPBP	BBXS
			SSBSB	BAPP	BXSX	XBBS
			BSSSSS	PPPB	XBXS	XSSB
			BSXSSS	BBPX	SBXP	AXBS
			SXBSSS	XPBP	XBBX	BSXB
			SXBSXSS	BXBX	BPXB	BSBX
			SXSSSBS	XBBX	XSBB	XBSS
			SXSSXBS	XAPB	BPPB	SBAX
			SXSSBSS	XPAB	XBSP	BBBB
			SSSSSBS	BBXB	XBSX	XABA
			SBSSBSS	XBAP	BSSX	SASB
			SSBSSSS	XPBA	PBSP	XASB
			SBSSSSS	BPBP	BXPP	SBSA
			SSXSSBS	BBBB	BPPP	BBSX
			SSSSXBS	XBPB	BPBP	XBSB
			SBSSXSS	ABXA	PBXP	AXBA
			SBSSSXS	BPPB	PPSB	BABX
			SXBSSSS	BABP	XBBB	BAAX
			SBSSSBS	XBAX	SBBS	AXBB
			SXBSXBS	PBAB	BSPS	BBXB
			SXBSSBS	BXBB	BBBX	SBAS
			SSBSSBS	PPBA	XBPP	XBAS
			XSXSSSBS	PBBB	PXPB	SBSB
			SSBSSSSS	BPXA	SBSX	XSAB
			SSSSSSBS	XAAB	PBSX	BXBS
			SSSSBSSB	AAXB	BSXX	BAXB
			SBSSSSSS	PPBX	BSPB	ABXB
			SSSSXSSXBS	AXBP	SXBP	XABB
			SBSSXSSSBS	APPB	XPBS	BSXA
			SBSSBSSSBS	PXBA	PSXB	ABSX
			SSSSBSSSSS	BAXP	BBSS	AABX
			SSXSSBSSSS	BAXB	PBPX	SXBB
			SSSSSSSSBS	BXAA	PPBP	SBBS
			BSSSSSSSBSS	XBBB	PPBX	BABS
			BSSSSSSSSSS	AXAB	SBBX	BBSS

PTO.

BX	BXA	BXP	BXS	BXPA	BXPS	BXAS
			SSSSSSSSXSB	BBAP	BPSB	BBAX
			XSSSSSSSSBSS	BXAP	BPSP	BXAB
			SSSSSXSSSSSSBS	BXAB	BSPX	BSAX
			XSBSSSSSSSSSSS	ABPX	BBPX	ASBX
				BAPX	BPXS	ABXA
				BPAX	SPBP	XBAB
				BBPB	BPPS	BAXA
				XBPA	SXSB	XAAB
				PXAB	XSBS	BBXA
				AABP	SPBB	BBBX
				BAPB	XSBX	SAAB
				AXBB	PBPS	SBAB
				ABAX	PBBB	ABAB
				PBBX	PSBP	BSSS
				PBXA	BPBB	AXAB
				XABX	SSXB	AAAB
				PBAX	PSBS	ABAS
				XABP	PBSS	XBBA
				PAXB	PSSB	BXSA
				PBPB	XBBP	ASXB
				AXBA	XBSB	BXSB
				PBPA	BBBB	ABAX
				BPAP	SBSB	SBBA
				PABX	XBPB	BXBA
				XBAA	BSBX	BSAB
				BPBA	PXBB	ASBS
				PBBA	BBXP	XBBB
				BBAB	SBPB	ABBX
				BBXA	PPPB	BBAS
				PABB	BPSX	BSBB
				BBPP	PXSB	BXAS
				XABA	XBBS	ABXS
				BAAX	BBXB	XABS
				PABP	BBPB	BSBA
				APBP	SBBP	BBSB
				BBBX	BSXB	BSSB
				AABX	BBPS	SBBB
				AABB	SSSB	BBBA
				PBAA	BPBX	SBXB
				BBPA	BSSS	BAXS
				BBBP	BBXX	BSAS
				PPBB	SBSP	BBAB
				ABPB	BXSP	SSBB
				XABB	BSSP	BASB
				BBAX	BBSP	SABS
				BAAP	BXBB	AASB
				BPBB	BSPBS	SABA
				ABBX	XSSBS	SXAB
				PAPB	BSXSS	ABBS
				ABXB	SSSBS	SSAB
				ABAA	BSXXS	BBBS
				PAAB	PSSBS	BABB
				APBX	BSXBS	XSBA
				ABBB	XSXBS	BASX
				PBAP	SPSSB	BSSA
				BAXA	XSBSS	AABB
				BABB	SBSXS	BASA
				BBBA	SBPSX	ABSB
				PABA	BSBBS	BSBS
				ABBP	SSXBS	SXBA
				XBAB	XXPBX	BXAA
				ABAP	SBXSX	ASAB
				BPAA	BSSBS	ABBB
				APBB	SXSSB	BASS
				BBAA	BSSPS	AABA
				BPAB	BSSSS	BAAA
				AAAB	SPSPB	SABB
				XBBA	BSPSS	ABSS
				PPAB	XSPBS	ASSB
				BAAB	SSBSS	SBAA
				AABA	BXSSB	AABS
				PBPPX	XBBSX	BBSA
				BBPPX	SPBPX	ABSA
				PBBPX	BSBSS	ASBA
				BPBXB	BSXPS	BSAA
				XBAXB	PSBSS	ABAA
				PBBXPBA	SSSSB	ASBB
				XPBPAAX	SSBPS	BABA
					SSBXS	SSBA
					PSXBS	BBAA
					SSSBSS	SSBSA
					SXSSSBS	SSSBS
					SXBSXSS	SSBSS
					SXSSXBS	BXSSS
					SPSSXBS	BSBSX
					SPPSPSB	AXBBS
					XSSSSBS	BSSBS
					XBXBSXX	SSBSABS

PTO.

BX	BXA	BXP	BXS	BXPA	BXPS	BXAS
					SSSSXBS	BSABSAS
					SSBSPBS	SSBSSSS
					SSBSXSS	SABSASS
					SPSSSBS	SSASSBS
					SPSSBBS	SBSSSBS
					SXBSSBS	SABSSBS
					SSBSSBS	SSSSBAS
					SSXBSPBS	SSBSAXS
					SSBSSSSS	BSABSASS
					SSSSBSSB	SSSSSSSBAS
					XSSBSXSS	SSSSASSBSS
					SSXSSPBS	SXSSAXSBAS
					BSSBSPBS	SSXSSBSSSS
					PSXBSPBS	SSSBSABSASS
					SSSXSXBS	BSSSSSSSBSS
					BSPSSSBS	XSSSSSSSSBSS
					BSSSSPBS	
					SSSSSSBS	
					SSPBSPBS	
					XSSSSSBS	
					SSSXSPBS	
					XSSXSSBS	
					XSBSSBSS	
					SXXSSPSSBS	
					SXSSXSSPBS	
					SXSSBSSPBS	
					SBSSXSSSBS	
					SBSSBSSSBS	
					SXBSXBSBBS	
					SBSSBSSPBS	
					SXBSXBSPBS	
					SBSSBSSBSS	
					SPSSPSSXBS	
					SSXSSXSSXBS	
					BSBSSSSSSSS	
					BSXXSXSSSBS	
					SSXSSXSSPBS	
					XSSBSSSSSBS	
					SSSSSSBSSPS	
					BSSPSSSSSSS	
					BSSSSSSSSSS	
					BSSXSPSSSBS	
					XSXSSXSSXBS	
					BSXSSXSSSPS	
					BSSSSBSSXSSX	
					SSXSSXSSXSSXBS	
					SSSSSXSSSSSSBS	
					BSSBSSSSSSSSXS	
					PSXSSXPSSSSSBS	
					SSSSSXSSXSSSBS	
					XSBSSSSSSSSSSS	
					SSSSSSSXPSXSSSBS	
					SSSSXSSXSSSSSSSSB	
					PSSSSPSSSPSSSSSBS	

Supplementary Table 4. *Influential sequences within the HEPbp basic amino acid containing sequence networks* - **Degree Centrality**. The table contains the significant sequences as determined by the degree centrality, the number of times that particular sequence appears in the network and the proteins that contain them. The vertices were considered significant if they were in the 99th percentile.

BX			**BXA**			**BXP**			**BXS**			**BXPA**			**BXPS**			**BXAS**		
Seq	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*
LLR	6	4F2	RARL	3	4F2	LRVL	4	4F2	GPKG	9	APOB	SYR	5	CAP7	GAKG	5	C1QA	GRCV	4	ANXA5
LRLV	5	APOB	LRLV	3	A2MG	RLKL	3	5NTD	GKG	8	ATS3	SVRT	3	COIA1	GTKG	4	C1QC	GRC	4	APLP1
LLRL	5	APOE	LLRL	3	AMBP	KLIK	2	A1BG	GLKG	7	C1QA	AAK	3	COJA1	GKG	2	CO1A1	LREV	3	APLP2
LRVL	5	AT1A1	LLR	3	APLP1	LRKA	2	ANXA6	GAKG	7	CCL28	TKTL	2	ECE1	GKKG	1	CO5A1	RARL	3	APOB
RLKL	3	ATS8	LRAL	3	APOB	SFK	2	APOB	GPRG	7	CFAB	SFK	2	ERBB2	GLPGPKG	1	CO5A3	ELLK	2	APOE
RARL	3	CAC1S	RRLA	3	APOE	SYR	2	ATPA	LLR	5	CHRD	SFR	2	FA12	KGAKG	1	CO9A1	GKCV	2	ATPA
LKK	3	CCD80	LREL	2	ATS8	SFR	2	ATRN	GRCV	5	CO1A1	RKAR	1	FBLN7	TGPKG	1	COBA2	GRRC	2	ATS1
KLLK	3	CEL	EKL	2	B4E216	RLVL	2	BMP3	LRG	4	CO1A2	SQRS	1	FBN1	PGPKG	1	CODA1	GGK	2	CAC1S
LRL	3	CHRD	ARKL	2	CAC1S	LSR	2	CAC1S	GLRG	4	CO3	LSYR	1	FBN2	GAPGPKG	1	CO1	YCR	2	CATG
RLRL	3	CO4A	ELKK	2	CCL4	LRAR	2	CAP7	GRG	3	CO3A1	SSYR	1	FGFR4	GLKG	1	HMGB1	LLR	2	CD1D
LAR	3	CO6A3	LVLK	2	CD1D	LSAR	2	CFAH	GLK	2	CO5A1	ESYR	1	HGF			MBL2	GCGK	2	CFAB
LLK	2	CO9	RRLL	2	CEL	LSRK	1	CO3	GGK	2	CO5A3	SEYR	1	HMGB1			Q9HCS8	LRLV	2	CLUS
KLLR	2	COBA2	RLRA	2	CHRD	SYRT	1	CO4A	GRC	2	CO6A3	ASYR	1	LAMA5			TSP1	VLRG	1	CO6A3
RLLR	2	COCA1	LKK	2	CO4A	KTSL	1	CO9	GCGK	2	CO8B	SFKT	1	LTBP1				LREL	1	CO7
LKRL	2	COMT	ELRK	2	CO6A3	LRVR	1	COBA2	LKL	1	COBA1	SVRS	1	PCOC2				KAKE	1	CO8B
LRKL	2	CO1	LRVL	2	CO7	KLKS	1	COCA1	GKKG	1	COBA2	QSYR	1	PCSK5				EKL	1	COBA2
LARL	2	CXCL6	LRLL	2	CO8B	KSLK	1	COMT	GGKG	1	COCA1	SEFK	1	PLMN				ELKK	1	COCA1
LALR	2	CYR61	LRL	2	COBA2	RKAR	1	CYR61	GARG	1	CODA1	SQLR	1	S4A4				LRG	1	COEA1
LKAA	2	DPP4	RVV	2	COCA1	LRK	1	DPP4	PGPKG	1	COEA1	SQR	1	TE				KPV	1	COPA1
LRAR	2	ENPP3	LKVK	1	COMT	KLKK	1	ENPP3	GVKG	1	COIA1	ISYR	1	TENX				LVLK	1	CSF2
LRRL	2	FA11	LKKL	1	CXCL6	KVTL	1	FA12	GKAL	1	COJA1	SAYR	1	TPA				EKLK	1	FBN1
LRAL	2	FGF4	EKE	1	CYR61	RLRL	1	FBN1	KPV	1	COLQ			TSP4				GPKG	1	FBN2
LKL	1	FGFP1	LKL	1	DCC	KLLR	1	FBN2	GIKG	1	CO1							DGK	1	FGFR3
KLV	1	FGFP3	LERL	1	DHB7	LRLR	1	FGFP1	GRPG	1	COPA1							GRGK	1	FST
KLK	1	FGFR2	LEKR	1	ERBB2	LKLR	1	FGFP3	KAVG	1	CSF2							GRPG	1	HFE
KAHL	1	FGFR3	LKAK	1	FA12	KLLK	1	FGFR1	GRV	1	ENPP1							GLKG	1	HGF
LRVR	1	FGFR4	ELR	1	FGF4	LLRK	1	FGFR4	GRRC	1	FBN1							GLRG	1	KALM
KALK	1	FSTL1	LELR	1	FGFR3	RLVK	1	IBP4	GARC	1	FBN2							GRCL	1	LAMA1
LKAK	1	HFE	ELKR	1	FGFR4	LRKL	1	IHH	GKCI	1	FCGRN							RLLR	1	LAMA5
LRLR	1	LAMA1	KVRV	1	FIBA	LSYR	1	IMPG2	KAGK	1	FINC							LRLA	1	LAMC2
LKLR	1	LAMA2	VAAK	1	FSTL1	ALK	1	INSR	GKLK	1	HMGB1							LKEK	1	MDR1
LLRK	1	LAMA3	EKLK	1	FURIN	LKLK	1	ITAM	GFKG	1	HPT							GRV	1	MDR3
LRV	1	LAMA4	LRLR	1	HFE	LALR	1	ITIH3	GRRG	1	LAMA1							GVGK	1	MET
LKLK	1	LAMA5	EEVK	1	IHH	LAR	1	LAMA1	YCR	1	LAMA2							ELRK	1	MRP6
KLL	1	LPHN2	LLRK	1	ITB3	KLAR	1	LAMA2	GLR	1	LAMA5							GPRP	1	V2
LRI	1	MET	LRV	1	KALM	RKLV	1	LAMA3	LKAL	1	LAMC2							GKLV	1	NOGG
KAF	1	MRP6	LKRL	1	LAMA1	SLK	1	LAMA4	GLRL	1	LDLR							GREV	1	PCSK5
KLKL	1	NOGG	LRIL	1	LAMA2	RKL	1	LAMA5	LRAV	1	MDR1							RGRR	1	PLMN
LRKV	1	OZF	KELK	1	LAMA3	LKAA	1	LTBP1	RGRC	1	MDR3							ARKL	1	PRDX4
KLVK	1	PEDF	RDRL	1	LAMA5	RSL	1	MRP6	GRP	1	MMP9							LRGL	1	PTC1
LKAL	1	PGS1	LARL	1	LIPC	KSL	1	NRTN	LRL	1	MOT1							GLR	1	PTPRC
LRAV	1	PLMN	LAR	1	LPHN2	KALR	1	OCLN	PRLG	1	NOGG							GKVV	1	RSPO3
RVRL	1	PRDX4	LLRE	1	MDR3	KAL	1	PCSK5	HFLV	1	PCSK5							ARL	1	S12A9
HFLV	1	PRELP	KEKV	1	MET	RVL	1	PERM	GRF	1	PCSK6							LHL	1	SLIT1
VVRV	1	PRG2	KLLR	1	MRP6	LSRL	1	PON1	GRCVC	1	PGBM							LRL	1	TAU
		S12A9	RLLR	1	V2	HSS	1	PRG2			PLMN							REV	1	TEN1
		S20A2	RKLV	1	NICA	SVRS	1	S12A9			POSTN							GRFD	1	TE
		S22AI	EKEK	1	NOGG	LKRK	1	S20A2			S12A9							LREG	1	TENX
		SCN5A	LRLA	1	OZF	LKSL	1	S39A4			SLIT1							GRLV	1	TRFE
		SHH	LKEK	1	PERM	LRRL	1	SHH			STIM1							LRGG	1	VWF
		SLIT1	LRI	1	PGS1	LRAL	1	SORT			TE									XDH
		SLIT2	ARLR	1	PLMN	RRLL	1	TE			TENX									
		STAB2	RRLR	1	PRDX4	LKKK	1	TENX			TSP1									
		STIM1	KELR	1	PRELP	LRA	1	TFR2			XDH									
		TEN1	VALR	1	PRG2	SQR	1	TRFE												
		TE	KAF	1	S12A9	QRV	1	VGFR1												
		TENX	LKRK	1	S20A2	LKAR	1	VGFR2												
		TFR2	LRKL	1	S22AI	NLRK	1													
		VGFR1	LEK	1	SCN5A	SKLK	1													
		VGFR2	LRKV	1	SEM5A	SRLR	1													
		WNT1	LRRL	1	SLIT1															
		XDH	LALR	1	SLIT2															
			ARL	1	SODE															
			LKAA	1	TEN1															
			LHE	1	TE															
			REV	1	TENX															
			VVRV	1	TGM2															
			EELR	1	THYG															
			RKVV	1	TRFL															
			ERL	1	VEGFB															

PTO.

BX			BXA			BXP			BXS			BXPA			BXPS			BXAS		
Seq	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*
			LEKK	1	VGFR1															
					XDH															
					ZNT1															
					ZPI															

Supplementary Table 5. *Influential sequences within the HEPbp basic amino acid containing sequence networks* - **Closeness Centrality**. The table contains the significant sequences as determined by the closeness centrality, the number of times that particular sequence appears in the network and the proteins that contain them. The vertices were considered significant if they were in the 99th percentile.

BX			BXA			BXP			BXS			BXPA			BXPS			BXAS		
Seq	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*
LRL	22	A2MG	LLR	20	AGRP	LRK	10	A1BG	GRG	14	ABP1	RKR	3	ARGI1	KLK	3	ARGI1	LRG	8	AAMP
LKL	19	ABP1	LRL	15	APOA5	LLR	8	ALDR	GKL	13	ALDR	RAR	2	ATS8	KLQ	2	ATRN	EKL	5	APOA5
RKL	19	AGRP	RKL	11	APOB	LKL	7	APOA5	LRG	13	ANXA3	RSSR	2	CAC1S	GKG	2	C1QA	KEK	4	APOB
LRK	15	ALDR	LEK	10	AT2B1	KLR	5	APOB	LRL	10	APOB	RKNR	2	CAP7	KLKS	1	CC134	GKL	4	AT2B1
LRVL	5	ANXA3	LRK	6	ATS3	LRL	5	ASIP	LKL	8	AT2B1	RKKR	1	CATG	GKKG	1	CFAB	ELK	4	ATPA
LKRL	2	APOA5	LRKK	2	BACE1	LRVL	4	B4E216	GLKG	7	ATPA	RKVS	1	CCL21	GLKG	1	CO4A	LREV	3	BACE1
LRKL	2	APOB	LRKA	2	CAC1S	KLS	4	BACE1	GKG	6	ATRN	RTVS	1	CO5A3	KLKP	1	CO1	LRLV	2	BMP6
LRVK	1	ATRN	RKRL	2	CEL	RLRS	2	CCD80	GLRG	4	ATS3	RKAR	1	COBA2	GLKP	1	HMGB1	LRLL	2	CATG
LKLK	1	ATS3	RLRK	2	CFAH	KLRL	1	CCL1	GLKL	3	BACE1	RESR	1	COMT	KLKA	1	ITB1	LRK	2	CFAB
		ATS8	ELRK	2	CHRD	SKRK	1	CFAH	LRGL	2	C1QA	RKDR	1	CRLD2	KLKQ	1	MDR3	GRLL	1	CO4A
		B4E216	LRLV	2	CO3	RLRL	1	CHRD	GKGL	2	CAC1S	RLRK	1	EF5	KLRQ	1	V2	GKVL	1	CO5A3
		BACE1	LKRV	2	CO4A	RLRK	1	CO2A1	GRVL	1	CADH8	RSAR	1	ELN	GKRG	1	POSTN	GRVL	1	CO7
		CCD80	LKAK	1	CO5	KLLR	1	CO3	LRGK	1	CCL28	LLRK	1	FGF12			STAB2	LRGK	1	COCA1
		CF015	KLLK	1	CO5A3	LRLR	1	CO4A	GKKG	1	CFAB	RYRS	1	FGFR3			TFR2	LRKK	1	COIA1
		CFAH	LLRK	1	CO6A3	LKLR	1	CO5A3	RKRL	1	CFAH	RRS	1	GP182			THRB	EKLK	1	CSF2
		CHRD	RLEK	1	COCA1	LLRK	1	CO9	GKAL	1	CHRD	RKRK	1	IBP3			TSP1	GRGK	1	DHB7
		CO2A1	LKRL	1	COMT	RLVK	1	COBA2	GRRL	1	CO1A2	RLRS	1	IBP5				GRRL	1	FBN1
		CO3	KELK	1	CTGF	RKRK	1	COCA1	GRGL	1	CO3	RLRQ	1	INSR				GLRG	1	FBN2
		CO5	RKRK	1	CYR61	LRKL	1	COIA1	GRKL	1	CO4A	RLR	1	LAMA5				KELK	1	FGF8
		CO6A3	RKEK	1	DCC	LKLK	1	COJA1	LKRL	1	CO5	RLVS	1	LIPE				LKLV	1	FGF9
		COBA2	KLLR	1	DHB7	KLSR	1	COMP	LRRL	1	CO5A3	RKSR	1	LIPL				EKLV	1	FGF20
		CYR61	LKEK	1	DHB13	KALR	1	COMT	GKLK	1	CO6A3	RKAK	1	MOT8				GRKC	1	FGFP1
		DHB13	LRKE	1	ECE1	LKRK	1	CYR61	GKRL	1	COCA1	RTRS	1	PCFT				GREK	1	FIBA
		DPP4	LKRK	1	ECM2	LKLT	1	DPP4	GRRG	1	COEA1	RARS	1	ROBO1				ELRK	1	ITAM
		ECM2	LRKL	1	ELN	LRRL	1	EF1	GLRK	1	COIA1	RSAK	1	S22A1				GEKL	1	ITB1
		ENPP3	LRKV	1	FA10	LKLS	1	ELN	GKLV	1	COMP	RVVS	1	SCN5A				GKLV	1	ITB3
		FA10			FA11			ENPP3	LRVL	1	CO1	RVRS	1	SEM5A				GREV	1	LAMA1
		FA11			FA12			FGFP1	LKAL	1	COPA1			SEM5B				LRGL	1	LAMC2
		FGFP1			FGFP1			FGFR3	GLRL	1	CSF2			SOST				LRKI	1	LPHN2
		FGFR4			FSTL1			HRG	GKLL	1	DPP4			TGM2				LRKC	1	V2
		HRG			HEP2			IMPG2	GKRG	1	FA9			VGFR1				GRLV	1	NCAM1
		IIGP5			HRG			INSR			FA12									PECA1
		INSR			IIGP5			ITA5			FBN1									PERM
		ITA1			ITAV			ITB1			FBN2									POSTN
		ITAM			ITIH3			ITIH3			FCGRN									PRDX4
		ITAV			LAMA1			LAMA2			FGF8									PTC1
		ITIH3			LAMA3			LAMA4			FGF16									PTPRC
		LAMA1			LAMA5			LAMA5			FGFR4									S20A2
		LAMA2			LGR4			LPHN2			FINC									S22A1
		LAMA3			LIFR			V2			FURIN									SFRP1
		LAMA4			LIPE			NET1			GHR									SLIT1
		LAMA5			LPHN2			PAI1			HMGB1									SLIT2
		LGR4			MET			PERM			ITA1									TENX
		LIPE			MOT8			PGBM			ITAM									TRFE
		MDR1			V2			PGS1			ITAV									TRFL
		MMP9			NICA			PIGR			ITB1									VGFR2
		V2			NOGG			PRDX4			ITIH3									VWF
		PAI1			PAIRB			PRG2			LAMA1									XDH
		PAIRB			PCSK5			RL29			LAMA2									
		PGBM			PEDF			ROBO1			LAMA5									
		PGS1			PERM			S12A9			LGR4									
		PIGR			PGBM			S22A1			LIFR									
		PRDX4			PGS1			SFRP1			LPHN2									
		PRELP			PIGR			TENX			MMP9									
		PSN1			PLGF			THYG			MRP6									
		RL29			PLMN			TIMP3			V2									
		ROBO1			PRDX4			VGFR1			PCSK6									
		RSPO4			PRELP			ZNT1			PDIA1									
		S12A9			PSN1						PGBM									
		S22A1			RL29						PGS1									

PTO.

BX			BXA			BXP			BXS			BXPA			BXPS			BXAS		
Seq	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*
		S22AI			S12A9						PIGR									
		SFRP1			S22A1						POSTN									
		SLIT1			S22AI						PRDX4									
		SLIT2			SAMP						PRELP									
		TE			SCN5A						PTC1									
		TENX			TE						S12A9									
		TIMP3			TENX						S20A2									
		TRFE			THYG						SLIT1									
		TRFL			TNFA						SLIT2									
		TSP2			TRFE						SORT									
		VGFR1			TRFL						STIM1									
		VTDB			TSP2						TE									
		VWF			VWF						TENX									
		ZNT1			XDH						THRB									
											TSP1									
											TSP2									
											TSP4									
											ZNT1									

Supplementary Table 6. *Influential sequences within the HEPbp basic amino acid containing sequence networks* - **Betweenness Centrality**. The table contains the significant sequences as determined by the betweenness centrality, the number of times that particular sequence appears in the network and the proteins that contain them. The vertices were considered significant if they were in the 99th percentile.

BX			BXA			BXP			BXS			BXPA			BXPS			BXAS		
Seq	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*
KALR	2	AMRP	LEKR	2	APOB	LSRK	1	5NTD	LRGL	2	4F2	ASTR	1	ATS1	KLKS	1	ATRN	GPKG	2	A1BG
LKRL	2	ANGT	ELRK	2	APOE	VKRK	1	ANXA2	RLKL	1	APLP1	RKVS	1	ATS8	GKKG	1	C1QA	LRLV	2	ABCBB
LRKL	2	APLP2	LHLV	1	APOH	KLRL	1	APOB	LPKG	1	APOB	RTVS	1	CAC1S	GLPGPKG	1	C1QC	KAVK	1	APLP1
RLHL	1	APOB	ARLK	1	AT2B1	LRVR	1	AT1B1	LRVR	1	ATPA	RESR	1	CATG	PRG	1	CO6	RGEK	1	APOB
LHLK	1	APOE	REVK	1	ATRN	RFKL	1	ATPA	GRVL	1	BACE1	DSSR	1	CCD80	PGAKG	1	COBA1	ELRP	1	AT1B3
HRIL	1	AT2B1	KLAV	1	ATS3	KLIK	1	ATS8	LRGK	1	C1QA	RKDR	1	CCL21	LKLR	1	COCA1	LHLV	1	BACE1
AVLK	1	ATP7B	RFRL	1	ATS8	KSFR	1	BMP3	GKKG	1	CADH8	KESR	1	CHRD	RLLR	1	CO1	GKEV	1	CEL
LRVR	1	ATPA	VRLV	1	B4E216	RKVS	1	CAP7	VRLH	1	CC134	TAER	1	CO5A3	GLKG	1	FGF16	LRGK	1	CFAH
ARLK	1	ATS8	LERL	1	CAC1S	KSLK	1	CBPD	KALR	1	CCD80	RLRK	1	COBA1	GSPR	1	ITB1	KALE	1	CO1A1
KLAV	1	CAC1S	KALK	1	CBPD	RKAR	1	CCL1	LRVK	1	CCL8	RHVS	1	COBA2	KLKP	1	MDR3	VKEK	1	CO3A1
RKIL	1	CAP7	KRLV	1	CEL	FSLR	1	CD47	KRGK	1	CCL11	RSAR	1	COMP	GLKP	1	POSTN	GPAGPRGPPG	1	CO5A1
AKLK	1	CBPD	EDRK	1	CFAH	SKRK	1	CEL	KLAK	1	CCL13	RKDN	1	COMT	KLKQ	1	PTPRC	GPPGKDG	1	CO6
KALK	1	CC134	VKLV	1	CO2	RKAV	1	CFAH	KLGK	1	CCL19	LLRK	1	ELN	KVKQ	1	TENX	GAEK	1	CO6A3
KRLV	1	CCD80	LKAK	1	CO3	TKAL	1	CO3	LRGR	1	CO1A1	RKRK	1	ENPP3	GSLR	1	TFR2	GEKG	1	CO7
RKAR	1	CCL11	VKEK	1	CO4A1	KLKK	1	CO4A	GPGGPPGPKG	1	CO3A1	KAER	1	FBN2	KLRQ	1	THRB	EKLK	1	CO9
VKLV	1	CEL	KALH	1	CO4A	KVTL	1	CO6A3	GPAGPRGPPG	1	CO4A2	SRED	1	FGFR3	GKRG	1		KGEK	1	COBA2
LRVK	1	CFAB	LRKF	1	CO6A3	RLRL	1	CO8G	GKPGPPG	1	CO4A	RLRS	1	GTR2				GPRGP	1	COCA1
KLAK	1	CO2	LELR	1	CO7	TRAL	1	CO9	GVKG	1	CO5	TALR	1	INHBA				GRGK	1	CODA1
LKAK	1	CO4A1	KVRV	1	COBA2	AHLT	1	COBA2	GGRG	1	CO5A1	TKLR	1	ITA5				KGEKG	1	COPA1
VRKA	1	COBA2	VAVK	1	COCA1	KLLR	1	COCA1	RKRL	1	CO5A3	SALR	1	ITAM				GRPG	1	CRLD2
KALH	1	COCA1	EKLK	1	COEA1	LRLR	1	COMT	ALKR	1	CO6A3	SKLS	1	LIFR				GPRGPPG	1	CSF2
LRKF	1	COMT	LRLR	1	COMT	LKLR	1	CYR61	GKPGP	1	CO9	VAER	1	LIPL				GLKG	1	DHB7
LRLR	1	CYR61	KLLK	1	CTGF	KLLK	1	ECE1	GPKG	1	CO9A1	SRLS	1	MMP9				KLRG	1	FBN2
LKLR	1	ECE1	LLLK	1	CYR61	LLRK	1	ENPP3	RGAR	1	COBA2	VAEH	1	MOT8				GLRG	1	FGFP1
LLRK	1	ECM2	LLRK	1	DCC	RLVK	1	FGF5	GLPGLKG	1	COCA1	RLVS	1	OCLN				KELK	1	HFE
RLVK	1	ENPP3	RLEK	1	DHB7	LRAK	1	FGFP1	GKAL	1	CODA1	RAAK	1	PCSK5				GRCV	1	IL3
LRAK	1	ERBB2	LKRL	1	ECE1	LRKL	1	GHR	GKRC	1	COEA1	SVRS	1	PDIA6				LKLV	1	ITB1
VARL	1	FA11	LRIL	1	ECM2	KRLA	1	GTR2	GHKG	1	COPA1	QRLT	1	ROBO1				RLLR	1	LAMA1
RILH	1	FGF5	KDLR	1	ELN	LKLK	1	IBP4	GLRGLPG	1	CRLD2	RKSR	1	SLIT2				RAVK	1	LAMC2
KILH	1	FGF6	KELK	1	ENPP3	QRLK	1	IL12B	GKLR	1	FA12	SHLR	1	TRFE				GRKC	1	V2
KRLA	1	FGF11	LVRK	1	ERBB2	FSKL	1	IMPG2	LKLR	1	FCGRN	NLRK	1					LKEK	1	PAIRB
RVKR	1	FGF18	VARL	1	FA11	KLAR	1	ITAV	GRGK	1	GHR							GREK	1	PCSK5
KVRL	1	FGFP1	RKRK	1	FA12	KSKR	1	ITB3	PGPPGLPGPPGPKG	1	HGF							LPRP	1	PEBP1
VRIK	1	GDNF	RLEA	1	FGF4	KLSR	1	LAMA1	GIKG	1	IL2							ELRK	1	PGBM
LKLK	1	GHR	LREL	1	FGF11	SHRA	1	LAMA3	GRPG	1	IL6							LRKE	1	PRDX4
KILK	1	GTR2	RILH	1	FGF18	KILA	1	LAMA5	GPRGPPG	1	IL12B							GPRP	1	PTC1
VRVR	1	IL6	VLKD	1	FIBA	AKVR	1	LIS1	KLRG	1	IMPG2							GPPKG	1	PTPRC
VKAK	1	INSR	KILH	1	FSTL1	LKAA	1	MDR1	AHC	1	ITIH3							GPRC	1	Q8IV69
ALRK	1	ITA1	RDRL	1	HFE	RKVK	1	MMP14	GRGL	1	LAMA1							GKLV	1	RSPO3
LRHF	1	ITB1	LARL	1	IBP4	KLFR	1	OCLN	RGRG	1	LAMA2							GREV	1	S12A9
VKLK	1	ITIH3	KVRL	1	IBP6	KALR	1	PECA1	RLKG	1	LAMA3							KEVK	1	SLIT1
AKLR	1	KALM	VRIK	1	IHH	RTLS	1	PERM	GYRG	1	LAMA4							KKGK	1	SLIT2
ARAL	1	LAMA1	KEKV	1	IMPG2	RTLK	1	PLBL1	LKPL	1	LAMA5							ARKL	1	TEN1
LRLA	1	LAMA3	KLLR	1	ITA1	KAVK	1	PON1	ALRK	1	LAMC2							LRGL	1	TE
RIRK	1	LAMA5	RLLR	1	ITAM	LRAV	1	POSTN	RVRG	1	LCAP							LRKI	1	TRFE
KLFR	1	LTBP1	VDRK	1	ITAV	LSRL	1	RSPO3	GKVG	1	LGR4							PRGI	1	VGFR1
KLHV	1	LYAM1	LRRE	1	ITB1	RVTL	1	S12A9	GRKL	1	LIFR							PKDL	1	VWF
ARLR	1	MBL2	RKLV	1	KALM	LKRK	1	S20A2	LKAA	1	LIPE							LREG	1	XDH
VLRL	1	MDR3	KDRL	1	LAMA1	VLRK	1	SLIT2	RGRL	1	LIPL							GFHV	1	ZPI
AAKH	1	MMP14	LEKL	1	LAMA5	NLVK	1	SORT	LRGV	1	MBL2							GRLV	1	WNT1
IRKI	1	NET1	ELKL	1	LGR4	LKSL	1	STAB2	RGPG	1	MDR3							LRGG	1	
RKAL	1	NICA	KERL	1	LIFR	KSLH	1	STIM1	VKVP	1	MOT1							GRKV	1	

PTO.

BX			BXA			BXP			BXS			BXPA			BXPS			BXAS		
Seq	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*	*Seq*	*No.*	*Prot*
RRLR	1	NRG1	KLEV	1	MDR3	SKSL	1	TFR2	HLKG	1	NCAM1							LAKE	1	
KLKV	1	PCFT	AKLR	1	MET	RLSR	1	THYG	LKRL	1	NRP1							GRLG	1	
KLKI	1	PCSK6	LRLA	1	V2	LRAL	1	TRFE	GARC	1	PCFT									
VALR	1	PEDF	LKEK	1	OCLN	SHLR	1	VGFR1	RKLV	1	PCSK5									
HLVK	1	PERM	ARKI	1	PAIRB	HSSR	1	VWF	LRIL	1	PCSK6									
KLVR	1	PGS1	ARKA	1	PCSK6	LKKK	1		GKIL	1	PGBM									
RLAK	1	PLBL1	ARLR	1	PEDF	LRTL	1		LLKI	1	PIGR									
KLKL	1	POSTN	RVKD	1	PERM	KVHL	1		RGLG	1	PPIB									
RKLR	1	PRELP	VAER	1	PGS1	LKAR	1		GLRGL	1	PTC1									
VLRK	1	RSPO1	RRLR	1	PON2	LKKA	1		RKAL	1	RL29									
ILKL	1	SCN5A	IKDL	1	POSTN	NLRK	1		RRLR	1	S22A7									
VRKL	1	SEM5B	KLRE	1	PRELP	SKLK	1		KAGK	1	SCN5A									
LRKV	1	SHH	KELR	1	PRG2	LKLS	1		HARV	1	SEM5A									
LARK	1	SLIT2	RAAK	1	PSN1	SRLR	1		AHCM	1	SHH									
KRVL	1	STIM1	LRKE	1	RL29	VRVK	1		KLVR	1	SLIT1									
LHVL	1	TENX	RLAK	1	ROBO1				GPRP	1	SLIT2									
VLLR	1	TFR1	KLAR	1	SCN5A				GKLK	1	STIM1									
KLVK	1	TFR2	LKRK	1	SEM5A				GKRL	1	TE									
LRKI	1	THRB	LRKL	1	THYG				GFKG	1	TENX									
LKAL	1	THYG	RLKA	1	TPA				VLKP	1	TFR2									
RVRL	1	TPA	KDLK	1	TRFL				GLRK	1	THRB									
KAVL	1	VGFR1	VRKL	1	VEGFB				KPLK	1	THYG									
LKAR	1	VGFR2	LRKV	1	VWF				GKLV	1	TRFL									
AKAL	1	VTNC	LHLR	1					LKGV	1	TSP3									
VKVR	1	VWF	RALH	1					RLLV	1	UROK									
HFLR	1		KFLR	1					RLPK	1	VEGFB									
HVLK	1		DLRK	1					RGIR	1	VWF									
HLYK	1		ELRD	1					KLVK	1										
KLVL	1		KRVL	1					LRVL	1										
KAVR	1		RKRV	1					GLR	1										
VRVK	1		AFLK	1					LRKI	1										
			RERL	1					LKAL	1										
			RDEK	1					GLRL	1										
			RKVV	1					LRAV	1										
			LRVA	1					LRAL	1										
									LRGP	1										
									GKRG	1										
									GKRP	1										
									LKLA	1										
									LKAV	1										
									GFGK	1										
									RKVV	1										
									KRPG	1										
									GRLV	1										

Supplementary Table 7. The total number of amino acid sequences found in the HEPbp **BX** HBS network expressed as there amino acid type, *i.e*, **B** (basic) and **X** (hydropathic). Sequences ranging in length between 3 and 7 amino acids with a total degree (Tot deg) greater than one were included the table.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
XXB	1068	31993	*XBXX*	402	18546	*XBXXX*	147	677	*BXXXXX*	21	30	*XXXXBXX*	17	52
BXX	1015	28746	*BXXX*	369	15583	*XXBXX*	140	666	*XBXXXX*	15	32	*XXXXXXB*	9	17
XBX	1003	27074	*XXXB*	359	15615	*BXXXX*	122	629	*XXXXXB*	14	19	*XXBXXXX*	7	20
BXB	393	9736	*XXBX*	303	12691	*XXXBX*	121	443	*XXBXXX*	13	20	*XXXXBXB*	7	24
XBB	350	8568	*BXBX*	155	8653	*XXXXB*	113	433	*XBXXXB*	11	23	*BXBXXXX*	7	20
BBX	342	8077	*XBXB*	150	7790	*BXXBX*	61	307	*XXXXBX*	10	24	*XXBXXBX*	7	16
BBB	144	3906	*XBBX*	143	7118	*XXBBX*	58	292	*BXXXXB*	9	13	*BXXXXXX*	7	16
			XXBB	136	6081	*XBXXB*	55	366	*XXXBXB*	8	15	*BXBBXXX*	6	15
			BXXB	133	7017	*XBBXX*	52	304	*XBBXXX*	8	11	*XXBBXXX*	6	11
			BBXX	124	6107	*BXXXB*	49	224	*XXXBXX*	8	17	*BBXXXXX*	5	10
			BXBB	53	2553	*BXBXX*	49	219	*XXBXBX*	7	11	*XXXBXBX*	5	9
			XBBB	52	2344	*XXBXB*	47	206	*BXXXBX*	7	11	*XXXXXBX*	5	12
			BBXB	48	2463	*XBXBX*	42	185	*BBXBXB*	6	12	*XXXXBBX*	5	33
			BBBX	44	1776	*BBXXX*	42	190	*BXBXBX*	6	9	*XBXXXBX*	5	14
			BBBB	41	1782	*XXXBB*	31	128	*BBXXXX*	5	12	*XXXBXXX*	4	10
						BXBBX	22	103	*XBXXBX*	5	9	*XBXBBXX*	4	10
						XXBBB	22	84	*BXBXXX*	5	9	*XXBXBXX*	4	11
						XBBXB	20	117	*BBXBXX*	5	19	*XXBBXXB*	4	11
						XBXBB	19	89	*XBXXBB*	4	6	*XBXXXXX*	4	8
						BBBXXB	18	95	*BBBBBB*	4	16	*XXXBBXB*	4	12
						BBXBX	17	56	*XXBBXX*	4	10	*XXBXXXB*	3	6
						BXXBB	17	50	*BXXBXX*	4	5	*BXXBXXX*	3	6
						XBBBX	15	78	*BBXXXB*	4	7	*BXXXBXB*	3	9
						BBBXX	13	61	*BXBBXX*	4	10	*XXXXXBB*	3	6
						BXBXB	12	34	*XBBXXB*	4	6	*XXXBXXB*	3	7
						BBBBB	8	65	*XBXBXX*	4	5	*XBXXBXX*	3	14
						BXBBB	8	37	*XXXXBB*	3	6	*XBXBXXB*	3	11
						BBBXB	8	49	*XXBBBX*	3	5	*XBXBXBX*	3	7
						BBBBX	7	32	*BXXBXB*	3	7	*XBBXXXX*	3	8
						BBXBB	5	28	*XBBBXX*	2	3	*BBXBXXX*	3	6
						XBBBB	5	19	*XXBXXB*	2	3	*BXXXXXB*	3	5
									BXBXXB	2	4	*XXBXBXB*	3	4
									XXXBBX	2	2	*XBXBXXX*	2	3
									BXXBBX	2	2	*XBBXBXX*	2	10
									XBBXBX	2	3	*XBBXBBX*	2	6
									XXBBXB	2	2	*XBXXXXB*	2	5
									BBBXXX	2	4	*BXXBXBX*	2	8
												BBXBBXX	2	3
												BXXXBXX	2	4
												BBXBXXB	2	4
												BXBXXBB	2	3
												XXXBXBB	2	2
												BBBXXXX	2	3
												BXBXXXB	2	6
												BXXXXBX	2	6
												XXXXBBB	2	4
												BXBXXBX	2	5

Supplementary Table 8. The significant communities found in the HEPbp **BX** HBS network.

Com1	Entr.	0.135	0.302	1.254	2.300	2.454	2.115	1.244	0.517	0.145	0.048	
	Cons. Seq.	-	-	-	-	**A**	**A**	**K**	-	-	-	
	Cons. Seq. (BX)	-	-	-	-	**X**	**X**	**B**	-	-	-	
	-	182	178	148	87	0	0	0	172	182	184	
	A	1	3	9	41	93	89	32	6	0	0	
	F	0	1	3	3	12	16	0	3	1	0	
	H	0	0	1	0	2	1	2	0	0	0	
	I	0	1	4	8	13	24	0	1	0	0	
	K	0	0	1	2	18	44	136	0	1	0	
	L	0	0	4	6	5	3	10	1	1	1	
	M	0	0	1	1	4	2	2	1	0	0	
	R	0	2	0	5	1	1	2	0	0	0	
	V	2	0	12	25	23	3	1	0	0	0	
	W	0	0	0	2	7	1	0	0	0	0	
	Y	0	0	2	5	7	1	0	1	0	0	
Com3	Entr.	0.034	0.393	1.590	2.810	1.884	0.329	2.689	1.370	0.366	0.048	
	Cons. Seq.	-	-	-	**L**	**L**	**R**	-	-	-	-	
	Cons. Seq. (BX)	-	-	-	**X**	**X**	**B**	-	-	-	-	
	-	932	893	701	269	5	0	448	745	898	931	
	A	0	4	29	98	97	1	55	20	4	1	
	F	0	2	28	38	45	0	28	13	3	1	
	H	0	1	8	31	19	11	24	9	2	0	
	I	0	2	13	31	13	0	60	27	2	0	
	K	0	4	34	55	10	28	52	12	6	0	
	L	1	17	61	277	622	0	72	39	6	1	
	M	0	2	6	15	22	0	13	2	4	0	
	R	2	4	21	45	0	892	91	25	7	1	
	V	0	3	16	56	42	0	49	28	1	0	
	W	0	2	5	2	14	0	14	5	1	0	
	Y	0	1	13	18	46	3	29	10	1	0	
Com4	Entr.	0.011	0.030	0.069	0.844	2.409	3.078	2.848	2.349			
	Cons. Seq.	-	-	-	-	-	**V**	**K**	**K**			
	Cons. Seq. (BX)	-	-	-	-	-	**X**	**B**	**B**			
	-	1072	1070	1066	951	582	1	1	1			
	A	0	0	0	12	16	57	51	48			
	F	0	0	0	1	40	107	105	112			
	H	0	0	0	2	10	27	33	21			
	I	0	0	1	33	83	144	88	144			
	K	0	2	3	17	77	211	407	559			
	L	0	0	0	13	40	54	94	10			
	M	0	0	0	5	15	19	14	34			
	R	0	0	0	17	58	144	90	88			
	V	1	1	2	15	109	225	124	23			
	W	0	0	0	0	9	18	5	5			
	Y	0	0	1	7	34	66	61	28			
Com5	Entr.	0.014	0.120	0.499	2.144	0.311	2.686	2.826	1.892	0.514	0.075	
	Cons. Seq.	-	-	-	-	**R**	**L**	**L**	-	-	-	
	Cons. Seq. (BX)	-	-	-	-	**B**	**X**	**X**	-	-	-	
	-	789	780	743	486	6	2	123	511	739	784	
	A	1	4	8	56	0	66	84	39	10	0	
	F	0	0	5	13	1	40	31	10	3	0	
	H	0	0	1	18	0	5	32	28	2	0	
	I	0	4	11	37	0	53	27	12	1	0	
	K	0	0	4	27	22	43	18	13	0	0	
	L	0	1	6	19	0	359	314	118	13	2	
	M	0	0	0	5	0	21	15	0	2	0	
	R	0	0	2	17	757	71	41	12	2	1	
	V	0	1	7	75	1	76	71	22	16	3	
	W	0	0	0	4	0	12	9	8	1	0	
	Y	0	0	3	33	3	42	25	17	1	0	
Com6	Entr.	0.013	0.235	1.214	2.827	0.628	3.110	2.774	0.981	0.218	0.025	0.013
	Cons. Seq.	-	-	-	-	**R**	**A**	-	-	-	-	-
	Cons. Seq. (BX)	-	-	-	-	**B**	**X**	-	-	-	-	-
	-	887	865	729	345	0	33	370	763	868	886	887
	A	0	3	40	103	17	211	83	29	5	0	0
	F	0	0	21	128	1	88	50	16	1	0	0
	H	0	5	10	22	32	22	18	3	1	0	0
	I	0	1	13	38	0	164	71	16	3	0	0
	K	0	1	0	20	39	55	44	15	2	1	0
	L	0	1	9	11	0	24	9	0	0	0	1
	M	0	0	13	17	0	22	13	2	1	0	0
	R	1	9	33	101	799	56	76	12	3	0	0
	V	0	3	10	35	0	155	118	28	4	0	0
	W	0	0	3	24	0	18	20	0	0	1	0
	Y	0	0	7	44	0	40	16	4	0	0	0

Com8	Entr.	1.782	2.626	1.599	1.477	0.395	0.250							
	Cons. Seq.	**-**	**F**	**F**	**H**	**-**	**-**							
	Cons. Seq. (BX)	**-**	**X**	**X**	**B**	**-**	**-**							
	-	26	2	0	7	45	46							
	A	0	7	0	6	2	0							
	F	11	15	30	2	0	2							
	H	6	9	9	32	0	0							
	I	3	5	2	1	0	0							
	K	0	1	0	0	0	0							
	L	0	2	5	0	0	0							
	M	0	0	2	0	1	0							
	V	2	7	0	0	0	0							
Com10	Entr.	0.269	1.262	0.984	0.090	2.354	1.776	0.358						
	Cons. Seq.	**-**	**-**	**L**	**H**	**L**	**-**	**-**						
	Cons. Seq. (BX)	**-**	**-**	**X**	**B**	**X**	**-**	**-**						
	-	85	71	8	0	0	58	84						
	A	0	0	0	0	6	10	1						
	F	1	2	2	0	0	0	0						
	H	1	4	5	87	20	1	0						
	I	0	2	1	0	0	0	0						
	K	0	0	0	0	0	3	0						
	L	1	2	72	0	25	7	1						
	M	0	0	0	0	5	2	1						
	R	0	2	0	0	0	0	0						
	V	0	1	0	1	25	4	1						
	W	0	1	0	0	6	3	0						
	Y	0	3	0	0	1	0	0						
Com11	Entr.	0.017	0.034	0.050	0.108	1.053	2.547	0.447	0.017	0.763	2.898	2.745	0.827	0.378
	Cons. Seq.	**-**	**-**	**-**	**-**	**-**	**-**	**K**	**-**	**-**	**L**	**L**	**-**	**-**
	Cons. Seq. (BX)	**-**	**-**	**-**	**-**	**-**	**-**	**B**	**-**	**-**	**X**	**X**	**-**	**-**
	-	639	638	637	633	541	322	3	639	568	49	158	562	612
	A	0	1	1	2	1	19	28	1	23	155	111	30	1
	F	0	0	0	2	15	31	0	0	5	60	35	3	1
	H	0	0	0	0	1	12	2	0	6	17	14	3	2
	I	0	0	0	0	13	24	0	0	2	31	32	2	2
	K	0	1	1	2	7	59	597	0	0	28	10	4	1
	L	1	0	0	0	36	75	0	0	28	195	192	25	8
	M	0	0	1	1	10	29	0	0	3	25	14	3	1
	R	0	0	0	0	2	2	10	0	0	4	10	1	1
	V	0	0	0	0	3	10	0	0	1	32	53	6	9
	W	0	0	0	0	4	26	0	0	0	2	8	0	0
	Y	0	0	0	0	7	31	0	0	4	42	3	1	2
Com13	Entr.	0.335	0.401	1.507	1.089	1.261	2.587	1.767	0.246	0.090				
	Cons. Seq.	**-**	**-**	**K**	**K**	**K**	**K**	**-**	**-**	**-**				
	Cons. Seq. (BX)	**-**	**-**	**B**	**B**	**B**	**B**	**-**	**-**	**-**				
	-	84	83	0	0	0	21	51	85	87				
	A	1	2	8	3	4	5	7	0	0				
	F	0	0	2	0	1	4	3	0	0				
	I	0	0	3	1	1	3	3	0	0				
	K	0	0	65	72	69	33	20	2	1				
	L	0	2	1	2	3	11	0	0	0				
	M	2	0	2	0	0	1	0	0	0				
	R	1	0	5	7	5	4	0	0	0				
	V	0	0	1	2	5	1	0	1	0				
	W	0	0	0	1	0	0	0	0	0				
	Y	0	1	1	0	0	5	4	0	0				
Com18	Entr.	0.242	0.621	2.447	2.021	0.000	1.321							
	Cons. Seq.	**-**	**-**	**-**	**A**	**H**	**F**							
	Cons. Seq. (BX)	**-**	**-**	**-**	**X**	**B**	**X**							
	-	48	45	15	0	0	22							
	A	0	2	6	21	0	0							
	F	0	0	1	8	0	24							
	H	0	0	5	1	50	4							
	L	2	2	15	14	0	0							
	M	0	0	1	0	0	0							
	V	0	1	1	1	0	0							
	Y	0	0	6	5	0	0							

Com23	Entr.	0.064	0.385	1.701	2.581	2.693	0.933	1.706	0.740	
	Cons. Seq.	**-**	**-**	**-**	**L**	**L**	**K**	**-**	**-**	
	Cons. Seq. (BX)	**-**	**-**	**-**	**X**	**X**	**B**	**-**	**-**	
	-	583	558	420	70	2	2	419	528	
	A	0	1	34	103	54	6	11	2	
	F	0	1	12	28	18	3	5	5	
	H	1	2	12	15	13	12	9	4	
	I	0	1	5	9	27	0	8	1	
	K	0	6	20	82	86	502	24	21	
	L	3	16	49	235	249	0	50	8	
	M	0	0	6	2	10	0	4	4	
	R	0	1	6	1	4	22	4	0	
	V	0	0	8	17	59	8	7	3	
	W	0	0	1	4	23	0	11	0	
	Y	0	1	14	21	42	32	35	11	
Com25	Entr.	0.047	0.047	0.503	1.383	1.660	2.299	2.172	1.158	0.394
	Cons. Seq.	**-**	**-**	**-**	**-**	**H**	**H**	**L**	**-**	**-**
	Cons. Seq. (BX)	**-**	**-**	**-**	**-**	**B**	**B**	**X**	**-**	**-**
	-	193	193	179	149	0	0	0	151	184
	A	0	0	6	16	22	3	4	1	0
	F	0	0	0	0	1	37	21	1	1
	H	0	0	2	2	134	62	8	0	2
	I	0	0	0	2	2	0	2	0	1
	K	0	0	0	2	4	0	3	0	0
	L	0	0	7	10	5	48	107	27	5
	M	0	0	0	1	0	0	5	3	0
	R	0	0	0	1	12	5	1	1	0
	V	1	1	0	5	3	33	13	4	0
	W	0	0	0	0	0	0	1	0	0
	Y	0	0	0	6	11	6	29	6	1
Com26	Entr.	0.747	1.705	1.271	0.839	1.992	0.474			
	Cons. Seq.	-	K	K	R	-	-			
	Cons. Seq. (BX)	-	B	B	B	-	-			
	-	53	19	2	0	25	55			
	F	2	0	0	0	1	0			
	H	0	0	3	0	23	0			
	K	0	29	43	12	1	0			
	L	0	1	0	0	0	0			
	M	2	0	0	1	2	4			
	R	0	2	11	47	1	0			
	V	0	0	0	0	3	1			
	W	2	9	1	0	0	0			
	Y	1	0	0	0	4	0			
Com29	Entr.	0.994	1.666	1.259	2.243	2.517	1.284	0.645		
	Cons. Seq.	**-**	**-**	**K**	**V**	**V**	**-**	**-**		
	Cons. Seq. (BX)	**-**	**-**	**B**	**X**	**X**	**-**	**-**		
	-	304	248	1	0	20	285	327		
	A	4	11	13	6	4	2	4		
	F	5	9	11	2	31	3	1		
	H	1	3	1	0	7	7	1		
	I	1	3	1	19	18	6	2		
	K	10	34	284	83	20	6	6		
	L	17	20	20	47	47	20	6		
	M	0	0	0	9	24	1	0		
	R	0	1	2	12	4	1	0		
	V	15	29	22	169	177	25	12		
	W	0	0	0	6	5	1	0		
	Y	2	1	4	6	2	2	0		
Com32	Entr.	0.034	0.675	1.816	2.982	1.886	0.211	1.398	0.379	0.094
	Cons. Seq.	**-**	**-**	**-**	**V**	**V**	**R**	**-**	**-**	**-**
	Cons. Seq. (BX)	**-**	**-**	**-**	**X**	**X**	**B**	**-**	**-**	**-**
	-	285	260	195	27	0	0	212	272	283
	A	0	5	24	40	42	0	5	0	0
	F	0	1	5	11	13	1	21	2	1
	H	0	0	1	12	8	0	0	0	0
	I	0	0	5	15	5	0	4	0	0
	K	0	1	10	21	0	1	2	1	0
	L	0	3	4	3	6	0	3	4	0
	M	0	1	5	4	6	3	2	0	0
	R	1	2	8	31	16	279	1	1	0
	V	0	9	25	99	183	2	34	6	2
	W	0	0	1	6	5	0	2	0	0
	Y	0	4	3	17	2	0	0	0	0

Com35	Entr.	0.061	0.061	0.169	1.960	2.367	2.234	0.149	0.465	0.061
	Cons. Seq.	**-**	**-**	**-**	**-**	**L**	**L**	**H**	**-**	**-**
	Cons. Seq. (BX)	**-**	**-**	**-**	**-**	**X**	**X**	**B**	**-**	**-**
	-	139	139	137	86	0	0	0	131	139
	A	0	1	1	9	26	15	0	5	0
	F	1	0	0	5	16	5	0	0	0
	H	0	0	0	1	0	0	137	1	0
	I	0	0	0	2	8	24	0	1	0
	K	0	0	0	0	0	0	0	1	0
	L	0	0	0	9	45	50	0	0	0
	M	0	0	0	4	4	4	0	0	0
	R	0	0	0	0	2	2	3	0	0
	V	0	0	2	19	38	40	0	0	0
	Y	0	0	0	5	1	0	0	1	1
Com37	Entr.	1.452	2.827	2.335	0.608	1.572	0.210	0.210		
	Cons. Seq.	**-**	**I**	**I**	**R**	**-**	**-**	**-**		
	Cons. Seq. (BX)	**-**	**X**	**X**	**B**	**-**	**-**	**-**		
	-	76	17	0	0	79	104	104		
	A	9	18	2	0	4	0	0		
	F	0	0	0	2	3	0	1		
	H	1	4	17	0	5	0	0		
	I	15	22	47	2	8	2	0		
	K	1	0	0	0	0	0	0		
	L	2	13	3	2	0	1	2		
	M	0	2	7	2	3	0	0		
	R	2	18	12	98	2	0	0		
	V	1	0	0	0	1	0	0		
	W	0	12	2	1	1	0	0		
	Y	0	1	17	0	1	0	0		
Com40	Entr.	0.135	1.116	0.000	2.045	1.484	1.462	0.715	0.135	
	Cons. Seq.	**-**	**-**	**H**	**A**	**A**	**-**	**-**	**-**	
	Cons. Seq. (BX)	**-**	**-**	**B**	**X**	**X**	**-**	**-**	**-**	
	-	52	38	0	0	6	36	46	52	
	A	1	12	0	24	38	10	5	1	
	H	0	0	53	0	1	0	0	0	
	I	0	0	0	1	1	0	0	0	
	K	0	0	0	6	2	0	1	0	
	L	0	1	0	3	0	2	0	0	
	M	0	0	0	0	0	1	0	0	
	R	0	0	0	14	4	3	0	0	
	V	0	0	0	5	1	0	0	0	
	W	0	2	0	0	0	0	0	0	
	Y	0	0	0	0	0	1	1	0	
Com42	Entr.	0.998	1.722	2.666	2.289	0.798				
	Cons. Seq.	**I**	**H**	**H**	**-**	**-**				
	Cons. Seq. (BX)	**X**	**B**	**B**	**-**	**-**				
	-	1	0	0	47	74				
	A	11	7	5	3	0				
	F	0	0	1	0	0				
	H	0	51	28	9	6				
	I	68	3	10	4	0				
	K	4	2	4	4	1				
	L	0	19	17	7	0				
	M	1	0	1	1	0				
	R	0	1	0	0	0				
	V	0	0	14	6	2				
	W	0	2	4	1	1				
	Y	0	0	1	3	1				
Com74	Entr.	0.056	0.382	0.571	2.435	2.511	1.735	0.478		
	Cons. Seq.	**-**	**-**	**K**	**I**	**I**	**-**	**-**		
	Cons. Seq. (BX)	**-**	**-**	**B**	**X**	**X**	**-**	**-**		
	-	155	148	0	0	0	99	143		
	A	0	0	0	18	17	2	0		
	F	0	2	0	7	2	2	0		
	H	0	0	0	7	8	2	1		
	I	0	0	2	74	69	33	11		
	K	0	1	143	21	19	5	1		
	L	0	1	1	1	2	2	0		
	M	1	4	7	11	10	0	0		
	R	0	0	2	8	21	6	0		
	V	0	0	1	0	0	0	0		
	W	0	0	0	0	1	1	0		
	Y	0	0	0	9	7	4	0		

Com98	Entr.	0.983	0.000	1.022	1.494	1.705	0.401
	Cons. Seq.	-	H	L	A	-	-
	Cons. Seq. (BX)	-	B	X	X	-	-
	-	39	0	0	1	29	44
	A	1	0	6	30	3	0
	H	3	47	0	0	0	0
	I	2	0	3	8	2	1
	L	0	0	37	7	9	2
	M	2	0	1	0	0	0
	V	0	0	0	0	1	0
	W	0	0	0	1	3	0

Supplementary Table 9. The total number of amino acid sequences found in the **HEPbp BXA HBS** network expressed as there amino acid type, i.e, **B** (basic), **X** (hydropathic) and **A** (acidic). Sequences ranging in length between 3 and 7 amino acids with a total degree (Tot deg) greater than one were included the table.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
XXB	626	12420	*XBXX*	242	7299	*XBXXX*	76	241	*XBXXXB*	8	17	*XXXXBXX*	8	20
XBX	622	11363	*BXXX*	221	5743	*BXXXX*	65	277	*XBXXXX*	5	8	*XXBBXAX*	6	16
BXX	598	11049	*XXXB*	198	5423	*XXBXX*	64	236	*BXXXBX*	4	9	*BXBBXXX*	4	8
BBX	227	3707	*XXBX*	174	4340	*XXXBX*	57	157	*XXABXX*	4	5	*XXXXBBX*	4	26
AXB	200	3914	*XBAX*	94	2655	*XXXXB*	55	136	*XBBXXX*	4	5	*XXAAXBB*	3	6
XBB	197	3085	*XBXB*	90	2689	*BXXBX*	43	178	*BXXXXB*	4	9	*XBXXXBA*	3	9
BXB	193	2614	*BXBX*	86	2970	*XXBXB*	27	83	*BXXBXB*	4	7	*BXBAXXX*	3	6
BAX	168	3585	*XAXB*	79	2154	*XBXXB*	27	141	*XAXAXB*	3	8	*BAXXXXB*	3	13
ABX	158	2883	*XBBX*	79	2740	*XBXAX*	26	91	*BXXXAA*	3	6	*XXXABXB*	3	4
XAB	154	2845	*ABXX*	78	2064	*XXXAB*	25	60	*BABXXX*	3	5	*XXAXBXX*	3	3
XBA	152	3065	*BXXB*	76	2090	*XXBAX*	25	113	*XAXBXX*	3	6	*BXXXXXX*	3	6
BXA	135	2159	*XXBA*	75	1999	*XBBXX*	25	113	*XBXXAA*	3	8	*BBBXXXX*	3	3
BBB	95	1827	*XXAB*	72	1845	*BXBXX*	23	69	*XBXXXA*	3	5	*BXBAXBX*	2	3
BAB	88	1469	*BXXA*	72	1752	*XXABX*	23	91	*AAXABA*	3	5	*XXBXXXA*	2	2
BBA	70	1316	*BXAX*	71	1811	*AXXBX*	22	73	*XXAXXB*	3	3	*BXBXBXA*	2	4
ABB	60	873	*AXXB*	68	1942	*XBXXA*	22	69	*AXXXBX*	3	3	*AXBXXXX*	2	3
AAB	56	1376	*XXBB*	68	1720	*XAXXB*	21	62	*BXXXXX*	3	3	*AXXABXX*	2	4
ABA	51	1106	*BAXX*	66	1811	*BAXXX*	21	87	*BXBXBX*	2	2	*XBXXAXA*	2	8
BAA	50	887	*BBXX*	64	1993	*XBXBX*	20	58	*AXBXXX*	2	3	*XBXBXXB*	2	6
			AXBX	64	1623	*AXBXX*	20	74	*BXBXXX*	2	3	*BXXAXXX*	2	3
			XBXA	62	1506	*XBAXX*	19	46	*XBBAAX*	2	3	*XXBAAXB*	2	7
			XABX	43	1068	*XXBBX*	19	54	*XXBABX*	2	2	*XXXXAXB*	2	4
			BXBB	34	952	*XXAXB*	18	44	*XXXXBA*	2	3	*XBXXXAB*	2	3
			AAXB	33	1019	*XABXX*	18	63	*BBBBBB*	2	6	*BXBXXXX*	2	4
			BBBB	31	881	*BXXXB*	18	39	*XBXXAX*	2	7	*AXXXXXB*	2	4
			BBXB	31	921	*BXXAX*	18	61	*XXBXXX*	2	3	*XXXXXBB*	2	3
			BXBA	30	1051	*ABXXX*	16	49	*XBAXBX*	2	2	*XXXXXXB*	2	2
			AXBB	28	1042	*XXXBB*	15	44	*BBXXAB*	2	4	*BXXXBXX*	2	3
			XBBB	28	763	*XXBXA*	15	41	*XBBXBA*	2	3	*XBXXXXA*	2	6
			BAAX	27	788	*BXAXX*	15	34	*XXXXXB*	2	3	*XBXXBXX*	2	8
			XAAB	27	828	*BXBBX*	14	52	*XBXAXB*	2	2	*BXXAXXB*	2	4
			BBBX	26	757	*XAXBX*	14	39	*AXBBXX*	2	2	*AXBAXXB*	2	5
			XABA	26	827	*XBAXB*	13	60	*XXXBXB*	2	5	*XXBXXXX*	2	5
			AXBA	25	810	*XBBXA*	12	31	*XBAXXB*	2	3	*XBXXXAA*	2	4
			XBBA	25	652	*BBXXX*	11	37	*AXAXBB*	2	2	*XBXXXXX*	2	3
			BXAA	25	639	*XXXBA*	11	41	*BXBXAX*	2	5	*XAXXBXX*	2	6
			BXAB	24	698	*BXXXA*	11	28	*BXBAXX*	2	3	*XXXXAAB*	2	4
			BABX	23	934	*BBXXB*	10	38	*BXBBXX*	2	5	*BAXBXXX*	2	6
			ABXA	23	555	*XBBXB*	10	40	*BXXAAX*	2	3	*XBBXXXX*	2	6
			BAXB	22	819	*AXXBB*	10	48	*BXXBXX*	2	3	*BBXXABX*	2	6
			BBXA	21	551	*BBBXX*	10	28	*XXXXBX*	2	2	*BBXBXXX*	2	3
			AABX	21	491	*XBXBB*	9	22	*XBABXX*	2	3	*ABBXABX*	2	4
			ABXB	21	646	*XABXB*	9	28	*BBXXXA*	2	6	*XXXAXBA*	2	6
			XABB	20	629	*AXXBA*	9	25	*XBAXBA*	2	2	*BXXBXBX*	2	5
			AXAB	19	519	*XAXBA*	9	43	BXXAXX	2	5	XXXXBBB	2	3
			XBAB	19	689	*XXBBB*	9	24	*BBXXAX*	2	3			
			ABBX	18	446	*BXBXA*	9	32	*XXABBX*	2	2			
			BBAX	18	460	*AAXXB*	8	25	*ABXBAX*	2	3			
			XBAA	17	322	*XAXBB*	8	28	*XAXXXB*	2	2			
			ABAX	17	541	*BAXBX*	8	35	*XXBBXA*	2	4			
			BAXA	17	484	*XABAX*	8	58	*XAABXX*	2	4			
			BBAB	13	442	*BXBBB*	8	24	*BBAXBX*	2	3			
			BBBA	11	356	*AXXXB*	8	19						
			BABB	11	371	*BXBXB*	8	17						
			AAAB	10	297	*AXBBX*	8	28						
			AABA	10	252	*XBABA*	7	46						
			AABB	10	353	*ABBXX*	7	20						
			ABAB	9	355	*BABXX*	7	27						
			BABA	9	279	*AXBXA*	7	21						
			ABBB	9	267	*AXBXB*	7	14						
			ABAA	8	192	*BAAXX*	7	21						
			BAAA	6	182	*XBXAB*	7	18						
			BBAA	6	155	*BAXAA*	6	25						
			ABBA	5	160	*BXXBA*	6	15						
			BAAB	4	120	*XAAXB*	6	18						
						BXBAX	6	27						
						BAXAX	6	16						
						BXXBB	6	8						
						BBXXA	6	11						

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
						ABAXB	6	23						
						AXBAX	6	20						
						BXABX	6	13						
						XBAAX	6	25						
						BAXXA	6	14						
						ABXBX	6	13						
						BAABX	5	12						
						BXAAX	5	17						
						BBBBX	5	17						
						XXABA	5	9						
						XXBBA	5	17						
						BBXAX	5	16						
						BAXBB	5	14						
						BAAXB	5	14						
						XAXAB	5	9						
						BBAXX	5	14						
						ABXXA	5	8						
						BXAXB	5	22						
						XBAXA	5	10						
						AAXBX	4	11						
						AABXX	4	14						
						BABAX	4	11						
						BXABA	4	13						
						XBBAX	4	11						
						BXXAB	4	7						
						BAXXB	4	4						
						BBBXB	4	17						
						XABAB	4	18						
						BXXAA	4	13						
						AXABX	4	17						
						BBXBX	4	14						
						BXBAB	4	16						
						XBXAA	4	15						
						AAABX	4	9						
						ABXBA	4	14						
						XBXBA	4	11						
						AABBX	4	11						
						ABXAX	4	15						
						AXBBB	4	5						
						BAAXA	4	9						
						XXABB	3	7						
						XXAAB	3	4						
						BBBBB	3	17						
						ABAXX	3	8						
						AXABB	3	12						
						AXABA	3	8						
						AXBAA	3	9						
						BXBBA	3	11						
						XABBA	3	3						
						XAABB	3	11						
						BXAAB	3	9						
						BAAAX	3	11						
						ABBBA	3	9						
						ABXXB	3	6						
						XBBBB	3	5						
						AABXB	3	8						
						XAABX	3	5						
						BABXA	3	8						
						XABBX	3	14						
						ABABX	3	6						
						BBAXB	3	6						
						XBBBX	3	13						
						BAXAB	2	3						
						ABBXA	2	3						
						AAXBB	2	6						
						XBBBA	2	4						
						AAAXB	2	12						
						ABXAB	2	7						
						XXBAB	2	7						
						BAXBA	2	12						
						XBABX	2	5						
						XBABB	2	4						
						AXBAB	2	9						
						BXAXA	2	9						
						AAABB	2	7						

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
						ABBXB	2	6						
						AXXAB	2	9						
						XXBAA	2	3						
						BBXAB	2	7						
						ABXBB	2	4						
						BBABB	2	6						
						BBXAA	2	3						
						ABBBX	2	5						
						ABAAX	2	4						

Supplementary Table 10. The significant communities found in the HEPbp **BXA** HBS network.

Com1	Entr.	0.680	2.244	2.283	0.954	1.420					
	Cons. Seq.	-	-	**F**	**R**	**Y**					
	Cons. Seq. (BXA)	-	-	**X**	**B**	**X**					
	-	44	17	0	0	16					
	A	0	16	8	0	0					
	D	4	1	0	1	1					
	E	0	1	0	0	0					
	F	0	0	23	0	0					
	H	1	0	5	4	0					
	I	0	1	0	0	0					
	L	0	0	0	1	0					
	M	1	9	2	0	1					
	R	0	0	2	42	0					
	V	0	4	7	0	1					
	W	0	1	3	1	1					
	Y	0	0	0	1	30					
Com3	Entr.	0.013	0.024	0.809	2.290	2.579	3.165	2.911	0.050	0.037	0.037
	Cons. Seq.	-	-	-	-	**K**	**K**	**V**	-	-	-
	Cons. Seq. (BXA)	-	-	-	-	**B**	**B**	**X**	-	-	-
	-	848	847	747	415	0	1	6	845	846	846
	A	0	0	1	23	57	100	107	1	0	2
	D	0	0	4	21	47	58	26	0	0	0
	E	0	0	5	34	56	86	85	0	0	0
	F	0	0	7	13	23	34	42	0	0	0
	H	0	0	3	10	13	12	2	0	0	0
	I	0	0	4	18	22	20	29	0	0	0
	K	0	0	56	234	433	202	19	0	1	0
	L	0	0	1	24	72	138	219	0	2	0
	M	0	0	1	2	9	13	10	0	0	0
	R	0	0	0	2	6	10	4	2	0	0
	V	1	0	15	26	74	124	233	1	0	1
	W	0	0	1	9	10	17	13	0	0	0
	Y	0	2	4	18	27	34	54	0	0	0
Com7	Entr.	0.031	0.046	0.529	1.944	3.089	2.686	0.031	2.276	0.987	0.221
	Cons. Seq.	-	-	-	-	**L**	**L**	**R**	-	-	-
	Cons. Seq. (BXA)	-	-	-	-	**X**	**X**	**B**	-	-	-
	-	709	708	665	475	145	0	0	423	614	694
	A	0	0	1	8	24	35	0	32	10	3
	D	1	1	4	15	29	21	0	8	1	0
	E	0	0	3	45	80	46	1	72	11	2
	F	0	0	2	18	35	45	0	18	13	2
	H	0	0	2	9	16	19	0	15	5	1
	I	0	0	3	13	26	33	0	17	8	0
	K	0	0	2	20	19	16	1	13	0	0
	L	0	1	19	70	223	360	0	57	25	7
	M	0	0	0	6	14	12	0	13	2	1
	R	1	1	1	12	36	39	709	6	1	1
	V	0	0	7	17	48	26	0	25	15	0
	W	0	0	1	0	7	8	0	2	0	0
	Y	0	0	1	3	9	51	0	10	6	0
Com8	Entr.	0.632	1.968	2.446	3.044	2.098	0.586	0.443			
	Cons. Seq.	-	-	**A**	**R**	**R**	-	-			
	Cons. Seq. (BXA)	-	-	**X**	**B**	**B**	-	-			
	-	363	235	7	0	0	368	374			
	A	15	77	193	66	0	2	0			
	D	1	7	19	22	12	4	2			
	E	1	8	26	40	19	5	0			
	F	1	4	9	2	20	3	4			
	H	0	2	3	8	11	1	1			
	I	2	5	7	8	7	2	2			
	K	3	12	26	36	14	0	0			
	L	4	0	8	27	47	6	10			
	M	2	7	5	3	7	0	0			
	R	1	0	8	117	245	0	1			
	V	3	33	82	47	0	1	1			
	W	0	4	3	7	5	1	0			
	Y	0	2	0	13	9	3	1			

Com9	Entr.	0.011	0.669	2.556	3.321	3.328	1.587	0.668	0.197	0.108	
	Cons. Seq.	-	-	-	**L**	**K**	**K**	-	-	-	
	Cons. Seq. (BXA)	-	-	-	**X**	**B**	**B**	-	-	-	
	-	1087	995	534	9	0	1	1000	1066	1077	
	A	0	11	53	115	101	58	17	3	1	
	D	0	5	51	97	60	22	6	1	3	
	E	0	11	105	164	135	40	9	1	0	
	F	0	3	21	47	51	26	11	4	0	
	H	1	3	17	35	25	9	8	1	0	
	I	0	4	29	54	64	25	5	1	1	
	K	0	1	19	87	235	825	0	1	1	
	L	0	34	156	249	178	33	16	8	3	
	M	0	3	10	22	38	12	2	0	1	
	R	0	2	5	18	26	17	2	0	0	
	V	0	14	71	135	111	5	5	2	0	
	W	0	1	4	16	21	3	6	0	0	
	Y	0	1	13	40	43	12	1	0	1	
Com12	Entr.	0.015	0.044	0.785	2.742	3.044	2.243	2.997	0.053	0.029	0.029
	Cons. Seq.	-	-	-	-	**K**	**K**	**K**	-	-	-
	Cons. Seq. (BXA)	-	-	-	-	**B**	**B**	**B**	-	-	-
	-	755	753	683	359	2	2	4	752	754	754
	A	0	0	8	25	50	37	26	0	1	0
	D	0	0	7	20	38	37	127	0	0	0
	E	0	0	6	46	92	63	109	0	0	0
	F	0	0	5	19	23	33	66	0	0	0
	H	0	0	1	11	7	3	25	0	0	0
	I	1	0	14	45	80	37	72	2	0	0
	K	0	1	12	103	273	461	231	2	0	1
	L	0	0	2	12	23	20	15	0	1	0
	M	0	0	2	9	11	10	31	0	0	0
	R	0	1	5	45	44	5	7	0	0	0
	V	0	0	6	33	63	13	2	0	0	0
	W	0	0	2	17	10	12	4	0	0	0
	Y	0	1	3	12	40	23	37	0	0	1
Com13	Entr.	0.013	0.703	2.476	3.035	2.745	2.964	0.013	0.026	0.036	
	Cons. Seq.	-	-	-	**R**	**R**	**R**	-	-	-	
	Cons. Seq. (BXA)	-	-	-	**B**	**B**	**B**	-	-	-	
	-	879	802	481	2	1	1	879	878	877	
	A	0	2	13	16	16	17	0	0	0	
	D	0	9	45	82	71	124	0	0	0	
	E	0	1	14	27	36	78	0	0	0	
	F	0	5	23	90	65	67	0	0	0	
	H	0	1	5	18	23	12	0	0	0	
	I	0	7	30	54	84	124	0	1	0	
	K	1	10	43	123	86	97	0	1	2	
	L	0	7	33	43	10	2	0	0	0	
	M	0	0	14	7	9	12	0	0	0	
	R	0	24	112	308	401	280	0	0	0	
	V	0	6	23	54	47	33	0	0	1	
	W	0	1	7	10	7	10	0	0	0	
	Y	0	5	37	46	24	23	1	0	0	
Com16	Entr.	0.015	0.459	1.749	0.815	3.130	3.098	2.297	0.817	0.109	0.069
	Cons. Seq.	-	-	-	**R**	**L**	**L**	-	-	-	-
	Cons. Seq. (BXA)	-	-	-	**B**	**X**	**X**	-	-	-	-
	-	739	701	528	2	6	59	423	661	732	735
	A	0	4	6	3	63	81	51	14	0	0
	D	0	1	23	3	56	35	23	3	0	0
	E	1	9	46	23	91	102	32	6	1	2
	F	0	9	26	0	31	26	9	4	0	1
	H	0	2	7	25	9	26	15	2	0	0
	I	0	0	7	0	40	22	9	2	1	0
	K	0	1	9	30	22	20	14	3	0	0
	L	0	2	3	1	246	259	109	20	2	2
	M	0	0	5	0	6	4	4	3	0	0
	R	0	4	5	649	80	52	13	3	0	0
	V	0	4	56	4	53	18	12	17	3	0
	W	0	1	4	0	17	10	5	1	1	0
	Y	0	2	15	0	20	26	21	1	0	0

Com18	Entr.	0.371	0.371	0.813	2.173	1.690	1.547	0.942	0.778
	Cons. Seq.	**-**	**-**	**-**	**-**	**H**	**F**	**L**	**-**
	Cons. Seq. (BXA)	**-**	**-**	**-**	**-**	**B**	**X**	**X**	**-**
	-	56	56	49	27	0	0	0	52
	A	1	1	8	14	10	3	0	0
	D	0	0	0	1	0	0	0	0
	E	0	0	0	1	0	0	0	1
	F	0	0	0	0	1	35	3	1
	H	0	0	1	6	38	12	0	0
	I	0	0	0	0	2	0	1	1
	K	1	0	0	0	1	0	1	0
	L	0	0	1	7	4	9	49	3
	M	0	0	0	0	0	0	5	1
	R	0	1	0	1	3	0	0	0
	V	1	1	0	0	0	0	0	0
	Y	0	0	0	2	0	0	0	0
Com20	Entr.	0.894	2.326	0.086	2.455	2.588	1.414	0.423	
	Cons. Seq.	**-**	**-**	**H**	**A**	**A**	**-**	**-**	
	Cons. Seq. (BXA)	**-**	**-**	**B**	**X**	**X**	**-**	**-**	
	-	81	49	0	0	18	71	85	
	A	1	12	0	37	33	9	8	
	D	1	2	0	12	17	2	0	
	E	1	7	0	0	3	3	0	
	F	1	4	0	13	1	1	0	
	H	0	0	92	0	0	0	0	
	I	0	0	0	0	1	0	0	
	K	0	2	1	6	7	1	0	
	L	0	2	0	5	1	1	0	
	M	3	0	0	0	0	1	0	
	R	2	2	0	14	4	3	0	
	V	0	1	0	6	8	0	0	
	W	3	11	0	0	0	0	0	
	Y	0	1	0	0	0	1	0	
Com25	Entr.	0.367	1.905	0.074	1.930	2.662	1.775	0.525	
	Cons. Seq.	**-**	**-**	**H**	**L**	**A**	**-**	**-**	
	Cons. Seq. (BXA)	**-**	**-**	**B**	**X**	**X**	**-**	**-**	
	-	107	68	0	0	8	75	104	
	A	0	6	0	7	33	7	0	
	D	1	0	0	2	13	3	2	
	E	0	3	0	25	16	2	1	
	F	1	1	0	0	0	0	0	
	H	0	0	111	0	6	0	0	
	I	1	2	0	4	8	4	1	
	K	0	3	1	0	0	2	1	
	L	1	1	0	63	26	14	3	
	M	0	1	0	1	0	0	0	
	R	0	0	0	8	0	0	0	
	V	1	23	0	1	1	2	0	
	W	0	2	0	0	1	3	0	
	Y	0	2	0	1	0	0	0	
Com29	Entr.	0.755	1.839	2.172	2.144	0.276	0.484		
	Cons. Seq.	**-**	**-**	**E**	**I**	**H**	**-**		
	Cons. Seq. (BXA)	**-**	**-**	**A**	**X**	**B**	**-**		
	-	37	26	0	0	0	39		
	A	1	0	0	0	0	0		
	D	0	0	1	1	0	1		
	E	1	3	19	5	0	0		
	F	0	1	1	0	0	0		
	H	0	1	0	0	40	0		
	I	0	0	2	18	0	1		
	K	1	3	8	1	0	0		
	L	0	0	0	0	0	1		
	M	0	0	0	3	2	0		
	R	0	0	1	2	0	0		
	V	0	6	9	12	0	0		
	W	2	2	1	0	0	0		

Com32	Entr.	0.172	1.404	2.359	0.000	0.172	1.404	0.560
	Cons. Seq.	-	-	**L**	**H**	-	-	**F**
	Cons. Seq. (BXA)	-	-	**X**	**B**	-	-	**X**
	-	38	28	3	0	38	28	1
	A	0	0	1	0	1	2	0
	D	0	2	0	0	0	4	0
	F	0	0	5	0	0	2	35
	H	0	0	0	39	0	0	3
	I	0	0	1	0	0	0	0
	K	0	0	0	0	0	3	0
	L	0	2	13	0	0	0	0
	V	1	3	11	0	0	0	0
	Y	0	4	5	0	0	0	0
Com42	Entr.	0.648	2.259	2.086	2.871	1.439		
	Cons. Seq.	-	-	**K**	**E**	**I**		
	Cons. Seq. (BXA)	-	-	**B**	**A**	**X**		
	-	152	81	0	0	0		
	A	0	2	0	2	0		
	D	0	14	15	39	43		
	E	0	3	14	40	13		
	F	3	9	11	1	2		
	H	1	1	1	6	0		
	I	0	1	13	31	108		
	K	12	45	102	19	0		
	L	0	2	2	8	2		
	M	1	5	4	1	0		
	R	1	0	0	13	1		
	V	0	3	3	0	0		
	W	0	0	0	1	1		
	Y	0	4	5	9	0		
Com48	Entr.	1.194	2.043	0.000	2.204	2.024	0.422	
	Cons. Seq.	-	**L**	**H**	**D**	-	-	
	Cons. Seq. (BXA)	-	**X**	**B**	**A**	-	-	
	-	74	11	0	3	53	88	
	A	0	1	0	5	13	1	
	D	0	0	0	35	7	0	
	E	3	1	0	0	0	0	
	F	2	2	0	3	2	0	
	H	0	11	94	0	0	0	
	I	0	1	0	0	1	0	
	L	8	55	0	25	8	0	
	M	0	0	0	1	0	0	
	V	2	2	0	21	9	4	
	W	0	2	0	1	0	0	
	Y	5	8	0	0	1	1	
Com49	Entr.	0.152	0.896	0.855	2.030	2.908	2.367	1.037
	Cons. Seq.	-	-	**R**	**A**	**A**	-	-
	Cons. Seq. (BXA)	-	-	**B**	**X**	**X**	-	-
	-	173	150	4	1	2	96	146
	A	1	16	14	107	70	25	6
	D	0	3	0	1	1	1	0
	E	1	0	1	3	2	1	0
	F	0	1	0	10	12	7	0
	H	0	0	1	0	0	3	6
	I	0	1	0	15	18	9	5
	K	0	0	4	3	7	9	3
	L	0	0	1	3	4	0	0
	M	0	1	0	1	9	2	0
	R	0	2	151	17	18	5	0
	V	1	0	0	15	16	12	10
	W	0	1	0	0	12	2	0
	Y	0	1	0	0	5	4	0
Com57	Entr.	1.739	0.000	1.294	2.330	1.730	0.129	
	Cons. Seq.	-	**E**	**E**	**R**	-	-	
	Cons. Seq. (BXA)	-	**A**	**A**	**B**	-	-	
	-	31	0	0	4	35	55	
	A	1	0	0	0	0	0	
	D	0	0	1	0	0	0	
	E	17	56	38	1	0	0	
	F	1	0	0	6	0	0	
	H	0	0	14	4	0	0	
	I	1	0	1	1	2	0	
	K	0	0	1	1	3	0	
	L	1	0	0	4	2	0	
	R	1	0	1	30	11	1	
	V	3	0	0	4	2	0	
	W	0	0	0	1	0	0	
	Y	0	0	0	0	1	0	

Com58	Entr.	0.742	1.296	1.202	1.056	1.907	0.159	
	Cons. Seq.	**-**	**F**	**F**	**K**	**-**	**-**	
	Cons. Seq. (BXA)	**-**	**X**	**X**	**B**	**-**	**-**	
	-	38	8	0	0	17	42	
	E	2	0	0	1	0	0	
	F	0	31	32	0	0	0	
	H	0	0	0	0	1	0	
	I	0	1	0	0	1	0	
	K	1	0	7	28	1	0	
	L	0	1	2	0	0	0	
	M	0	1	0	0	0	0	
	R	1	0	1	14	9	0	
	V	0	1	1	0	14	1	
	Y	1	0	0	0	0	0	
Com59	Entr.	0.162	1.030	0.000	0.324	2.640	1.753	0.437
	Cons. Seq.	**-**	**-**	**H**	**V**	**L**	**-**	**-**
	Cons. Seq. (BXA)	**-**	**-**	**B**	**X**	**X**	**-**	**-**
	-	41	32	0	0	8	24	39
	A	0	5	0	0	2	1	0
	D	0	0	0	0	1	0	0
	E	0	0	0	0	2	0	0
	H	0	0	42	0	6	1	0
	I	0	0	0	0	1	0	1
	K	0	0	0	0	0	1	0
	L	0	0	0	1	13	11	2
	M	1	5	0	0	0	1	0
	V	0	0	0	40	0	0	0
	W	0	0	0	0	1	0	0
	Y	0	0	0	1	8	3	0
Com64	Entr.	0.839	2.418	2.619	2.908	1.629	0.123	0.117
	Cons. Seq.	**-**	**-**	**R**	**R**	**V**	**-**	**-**
	Cons. Seq. (BXA)	**-**	**-**	**B**	**B**	**X**	**-**	**-**
	-	283	161	0	0	0	313	313
	A	1	7	11	4	0	0	0
	D	1	10	9	7	4	0	2
	E	2	16	27	16	8	0	0
	F	2	1	1	4	26	1	0
	H	3	5	14	13	0	0	0
	I	3	10	19	8	15	1	0
	K	4	2	7	28	7	0	0
	L	5	9	9	29	1	0	0
	M	0	5	8	12	2	1	1
	R	4	63	155	100	18	0	1
	V	7	15	38	81	229	1	0
	W	0	0	1	8	3	0	0
	Y	2	13	18	7	4	0	0
Com75	Entr.	0.436	2.327	2.696	2.619	0.000	0.509	
	Cons. Seq.	**-**	**-**	**L**	**L**	**H**	**-**	
	Cons. Seq. (BXA)	**-**	**-**	**X**	**X**	**B**	**-**	
	-	124	66	3	0	0	121	
	A	1	15	20	23	0	2	
	D	0	0	8	17	0	0	
	E	0	11	12	7	0	0	
	F	1	4	11	6	0	0	
	H	0	1	0	0	131	0	
	I	1	2	8	6	0	0	
	K	1	0	0	0	0	0	
	L	1	12	51	52	0	0	
	M	0	2	0	1	0	1	
	R	0	0	1	0	0	6	
	V	2	16	15	11	0	0	
	W	0	0	1	7	0	0	
	Y	0	2	1	1	0	1	
Com83	Entr.	1.565	1.892	0.889	1.335	0.661		
	Cons. Seq.	**-**	**F**	**H**	**I**	**-**		
	Cons. Seq. (BXA)	**-**	**X**	**B**	**X**	**-**		
	-	12	0	0	10	25		
	D	0	0	0	0	1		
	E	1	3	0	1	0		
	F	0	10	0	0	0		
	H	0	0	22	1	0		
	I	0	0	5	16	1		
	R	12	8	0	0	0		
	W	0	0	0	0	1		
	Y	3	7	1	0	0		

Com101	Entr.	0.566	1.091	1.192	2.117	2.175	0.296
	Cons. Seq.	**-**	**I**	**H**	**L**	**-**	**-**
	Cons. Seq. (BXA)	**-**	**X**	**B**	**X**	**-**	**-**
	-	42	7	0	0	19	45
	A	0	0	0	8	1	0
	D	0	0	0	0	2	1
	F	0	0	1	0	0	0
	H	1	0	32	14	15	1
	I	4	36	2	0	0	0
	K	0	0	0	3	4	0
	L	0	2	12	16	3	0
	W	0	2	0	6	0	0
	Y	0	0	0	0	3	0
Com120	Entr.	0.546	0.000	0.365	1.862	1.960	1.265
	Cons. Seq.	**-**	**H**	**-**	**-**	**V**	**V**
	Cons. Seq. (BXA)	**-**	**B**	**-**	**-**	**X**	**X**
	-	33	0	34	18	0	0
	A	1	0	1	9	2	0
	D	1	0	0	0	2	2
	E	0	0	0	1	2	3
	H	0	36	0	0	0	0
	I	0	0	0	0	11	5
	K	0	0	1	0	0	0
	L	0	0	0	1	0	0
	R	1	0	0	0	0	0
	V	0	0	0	6	17	26
	Y	0	0	0	1	2	0
Com326	Entr.	0.754	0.659	0.410	0.000	0.835	
	Cons. Seq.	**-**	**A**	**A**	**H**	**-**	
	Cons. Seq. (BXA)	**-**	**X**	**X**	**B**	**-**	
	-	26	3	0	0	25	
	A	4	27	29	0	0	
	D	0	0	0	0	1	
	E	1	0	0	0	0	
	H	0	0	0	31	0	
	I	0	0	0	0	5	
	K	0	0	1	0	0	
	V	0	0	1	0	0	
	W	0	1	0	0	0	

Supplementary Table 11. The total number of amino acid sequences found in the **HEPbp BXS HBS** network expressed as there amino acid type, i.e, **B** (basic), **X** (hydropathic) and **S** (special). Sequences ranging in length between 3 and 7 amino acids with a total degree (Tot deg) greater than one were included the table.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
XXB	526	9927	*XBXX*	205	5249	*XXBXX*	65	244	*SBXXXX*	9	28	*SXBSXSS*	9	168
XBX	500	8147	*XXXB*	195	4746	*XBXXX*	59	210	*XBXXXX*	7	12	*XXXXBXX*	8	25
BXX	495	7898	*BXXX*	178	3709	*XXXBX*	49	120	*BSXSSX*	6	39	*SXSSSBS*	7	208
XBS	247	4697	*XXBX*	148	3684	*BXXXX*	46	152	*SBSBSX*	6	15	*SXSSXBS*	6	139
SBX	235	4119	*SXBX*	91	2347	*XXXXB*	42	115	*XBXXXB*	5	13	*SXXBSXX*	5	17
BSX	202	3105	*SBXX*	87	2720	*XBXXB*	34	138	*BSSSSS*	5	82	*SXXBXBX*	5	10
BXB	189	2954	*SXBS*	82	4364	*XXBBX*	34	125	*BXXXXX*	5	7	*XXXXSXB*	4	10
XSB	188	2708	*XXBS*	82	2153	*XXBSX*	33	153	*BBBBBB*	4	12	*SXSSBSS*	4	83
BXS	187	2633	*XBSX*	80	2044	*SBXXX*	32	125	*XXBXXX*	4	4	*XXXXBXB*	4	14
XBB	160	2237	*BXBX*	75	2290	*XBBXX*	28	126	*SBBSXX*	4	16	*SBXXXXS*	4	5
SXB	154	2856	*SXXB*	74	1735	*XSBXX*	26	76	*XXXXBX*	4	13	*XXXXXXB*	4	8
BBX	141	1679	*XBBX*	72	1820	*XBXXS*	25	85	*SBBXSX*	4	15	*SBBXSSX*	3	6
SBS	138	4710	*XBXS*	71	1645	*BXXXB*	23	72	*SSXBSS*	4	13	*XXBSXSS*	3	12
BSS	104	1954	*XXBB*	70	1659	*XXXBS*	22	47	*BSXBSX*	4	9	*SBXBXXX*	3	6
SSB	98	2175	*XXSB*	68	1582	*BXXBX*	20	50	*SXBXXX*	4	5	*SBSBSBS*	3	8
BBS	70	928	*BXXB*	68	2057	*XBSXX*	19	61	*XBXXSB*	4	6	*XSXXBXB*	3	10
SBB	69	990	*XBXB*	67	2051	*BXBXX*	19	46	*XXBSXX*	4	13	*SSSSSBS*	3	128
BSB	67	943	*XSBX*	64	1374	*XXBXB*	18	59	*XSXBXX*	4	5	*SBSSBSS*	3	46
BBB	60	1082	*BXXS*	60	1226	*SXXBX*	18	46	*XXXXXB*	4	6	*XXBXXBX*	3	5
			XSXB	59	1126	*XBXBX*	17	55	*XXXBXX*	4	6	*SBSBSXX*	3	11
			BSXX	57	1007	*SXXXB*	17	46	*XSSXBX*	3	5	*XBXXXXX*	3	6
			BBXX	55	1354	*BXXXS*	17	34	*XBSXXX*	3	5	*XSBXXSX*	3	7
			BXSX	54	1179	*XSXXB*	16	56	*BSXSSS*	3	53	*BXXXXXX*	3	6
			SBSX	50	2211	*SSXBS*	16	333	*BXXXBX*	3	5	*XXXSBXX*	3	3
			SSXB	47	1057	*SXBXX*	16	51	*XSBXBX*	2	2	*XXBBXXX*	3	7
			SSBS	45	3826	*SBXXS*	16	54	*SXSXBX*	2	3	*XXBSXBX*	3	11
			BSXS	42	870	*SBXSX*	15	63	*XXXSBX*	2	4	*XSSXXBX*	2	3
			SXSB	42	1100	*XSXBS*	15	107	*XXSSXB*	2	5	*XXSBSXX*	2	3
			BXSS	41	779	*BBXXX*	15	55	*BBXBXB*	2	3	*XXBXSXX*	2	2
			SBXS	40	1261	*BSXSS*	14	185	*BSXXSB*	2	3	*XSSXBXX*	2	7
			XBSS	39	1124	*SXBSX*	14	76	*XBXXSX*	2	4	*SBSSXXS*	2	7
			SBSS	38	1362	*SSSBS*	14	621	*XXBXXS*	2	4	*XBXSXXX*	2	3
			XSBS	36	882	*XSXBX*	14	35	*SBSXSS*	2	6	*XXXBXBX*	2	3
			SBXB	35	991	*SBSXS*	14	149	*SXXXBX*	2	2	*BBXXXXX*	2	4
			SBBX	34	970	*BSXSX*	13	28	*SXXBXX*	2	2	*SBXXBXS*	2	5
			BSSX	33	638	*XBXSX*	13	34	*XXXBSS*	2	3	*XSBXSXS*	2	5
			XSSB	27	482	*SBSXX*	13	38	*BXBBBS*	2	4	*SXXBSXB*	2	7
			XBBS	27	838	*BXSXX*	13	37	*XBSXSS*	2	2	*SBXSXXX*	2	3
			SBBS	26	1238	*XSSBS*	12	292	*XSBXXS*	2	4	*SXXBXXB*	2	7
			BBSX	26	641	*XSBXS*	12	39	*SSSSXB*	2	3	*BXXBXSB*	2	4
			BXSB	26	700	*XBSXS*	12	35	*XXBXBX*	2	5	*SSBXXXX*	2	8
			BXBS	25	749	*SBBXX*	12	44	*XSXXBS*	2	2	*SSBSXXB*	2	3
			XBSB	25	602	*XXXSB*	12	47	*BXXXXS*	2	2	*SBXSXXS*	2	10
			SXBB	24	682	*XXBSS*	12	40	*SSSBSX*	2	4	*XXBXXXX*	2	7
			BXBB	24	603	*SBXBX*	12	34	*SXSBBX*	2	3	*SBXXXXX*	2	5
			SSBX	24	519	*BXBSX*	12	28	*SSSBXB*	2	4	*XBXBXXB*	2	7
			XSBB	23	594	*BSXXX*	11	17	*SXXBXB*	2	2	*SBXXSXX*	2	3
			BSXB	23	610	*SSBSX*	11	132	*XSSBSS*	2	10	*XXXSXBX*	2	4
			XBBB	23	481	*XXBSB*	11	40	*BSSSSX*	2	15	*XBXSXBX*	2	2
			BSBX	21	631	*BSXBS*	11	163	*XBXSXX*	2	3	*BXSXXSS*	2	3
			BBXS	20	471	*SXBBX*	11	37	*BSSBSX*	2	5	*BBSBXXS*	2	5
			SSSB	20	508	*XSSXB*	11	26	*XXBSXB*	2	8	*XBXBBXX*	2	3
			BBBB	19	466	*BSSSS*	11	187	*BSXXSS*	2	7	*BXBXBSX*	2	10
			SBSB	18	601	*BSSXX*	11	40	*XSSXSB*	2	3	*SBSSSSX*	2	9
			BBBX	18	390	*XXXBB*	11	24	*XBXXBX*	2	3	*XSSXXBS*	2	9
			BBXB	17	608	*BSBXX*	10	36	*SBBSBS*	2	5	*XBXXBXX*	2	7
			BSBS	13	490	*BSXXS*	10	44	*SXXXBS*	2	2	*XBXBSXX*	2	5
			BBSS	13	322	*XXSBX*	10	17	*BSBXXS*	2	3	*XXSBXXX*	2	3
			BBSB	11	287	*BXXSX*	10	30	*BSXXXX*	2	4	*XBBXXXS*	2	2
			BSSB	11	269	*XBBBX*	10	39	*XBBXSX*	2	4	*XXBSXXB*	2	7
			BSSS	11	246	*SBSSX*	10	42	*BSXBXX*	2	5	*SSBSSSS*	2	46
			BSBB	10	278	*XBXSS*	10	22	*SBSSXS*	2	9	*SSBSXSS*	2	14
			SBBB	9	203	*XSSBX*	9	21	*BXXSXS*	2	2	*SSSSBXS*	2	14
			BBBS	8	181	*SSBSS*	9	91	*XSBBXX*	2	2	*XBXXXBX*	2	4
			SSBB	7	218	*SSSSB*	9	135	*SBSSXX*	2	8	*XSXXBSX*	2	2
						XSBSS	9	56	*XSXBXS*	2	2	*XBXXXBS*	2	5
						SXSSB	9	89	*XXXBXB*	2	5	*SBSSSSS*	2	67
						SXXSB	9	21	*BBBXXX*	2	4	*SXBSXXX*	2	2
						SXBSS	9	76	*XBXBXX*	2	2	*SXSSXXB*	2	4
						SSXSB	9	47	*SSSSBS*	2	8	*SXXBBBB*	2	6
						BSXBX	9	27				*XXXXSBX*	2	5

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
						BXXSS	9	21				*BXXSXBS*	2	3
						SBXXB	9	27				*XBSXXXX*	2	2
						BBXBX	9	23				*XSXBXXX*	2	2
						XXBBS	9	24				*XSXXBXX*	2	10
						XSBBX	9	26						
						BXSSX	8	30						
						BSSBS	8	243						
						BBXXS	8	26						
						XXBXS	8	22						
						SSBXS	8	36						
						XXSBS	8	19						
						SXBSB	8	21						
						XSBXB	8	23						
						XXSXB	8	27						
						XBBSX	7	19						
						XBXBB	7	19						
						SXXBS	7	17						
						SSXBX	7	12						
						XSXBB	7	20						
						BBBXB	7	29						
						SXSXB	7	16						
						SXBXB	7	14						
						XBSBS	7	19						
						BXBBX	7	18						
						SSBXX	7	20						
						BBSXX	7	13						
						BSBXS	7	25						
						XSXSB	6	15						
						SXSBX	6	16						
						BXBSS	6	23						
						BSSXS	6	36						
						XSBSX	6	13						
						SBXSB	6	22						
						BBXSX	6	20						
						XBSXB	6	20						
						BSXSB	6	19						
						SBBSX	6	16						
						XXSSB	6	18						
						BXXBB	6	11						
						BBXXB	6	22						
						XXSBB	6	8						
						XBBXB	5	10						
						BXXSB	5	19						
						SBBSB	5	19						
						BSBBS	5	25						
						SBSBS	5	22						
						XBSBB	5	12						
						SSBBS	5	49						
						BXXBS	5	13						
						SSXXB	5	10						
						XBBXS	5	12						
						SSSXB	5	18						
						BSBSX	4	72						
						XSBBS	4	14						
						XBXBS	4	4						
						SSXBB	4	9						
						SBBXS	4	12						
						BBSSB	4	19						
						BXSBS	4	6						
						XSSBB	4	7						
						SBSSS	4	27						
						BXSSS	4	24						
						SBBBX	4	11						
						BBXBS	4	10						
						BXBXS	4	10						
						XBBSS	4	8						
						BBXSS	4	9						
						BBSXB	4	7						
						BBBBX	4	8						
						BSXXB	4	8						
						XBSSS	3	9						
						SBSBX	3	9						
						BXSSB	3	15						
						BXSXB	3	5						

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
						BSSSX	3	6						
						SXSBS	3	7						
						BBBBB	3	19						
						SBSSB	3	9						
						SBSSB	3	9						
						BBXBB	3	11						
						XBBBB	3	7						
						XSBBB	3	8						
						SBXBS	3	3						
						BBBXX	3	8						
						SXXBB	3	10						
						XSBSB	3	8						
						BBBSS	3	7						
						SXBBS	3	18						
						XBXSB	3	10						
						BBSBB	2	6						
						BBSSX	2	6						
						SXSBB	2	3						
						XBSSX	2	3						
						BBBXS	2	6						
						SSBXB	2	10						
						BBSSS	2	6						
						SBBBB	2	6						
						BSBXB	2	6						
						SSSBX	2	8						
						XBSBX	2	3						
						SBBXB	2	9						
						BBBBS	2	4						
						XBBBS	2	8						
						BXBBS	2	5						
						SBBSS	2	10						
						BXBBB	2	2						
						BXSXS	2	4						
						XXBBB	2	4						
						SXBXS	2	4						
						BXBXB	2	3						
						XSSSB	2	8						

Supplementary Table 12. The significant communities found in the HEPbp **BXS** HBS network.

Com1	Entr.	0.463	1.965	3.126	3.060	0.371	1.969	0.602	0.058				
	Cons. Seq.	-	-	**V**	**V**	**K**	-	-	-				
	Cons. Seq. (BXS)	-	-	**X**	**X**	**B**	-	-	-				
	-	318	224	42	3	0	229	313	335				
	A	8	24	61	50	0	3	1	1				
	C	0	2	2	7	0	5	1	0				
	F	1	5	16	34	0	16	4	0				
	G	2	1	0	8	0	2	0	0				
	H	0	3	5	5	3	4	0	0				
	I	2	7	31	66	1	8	1	0				
	K	1	2	14	11	321	24	2	1				
	L	1	5	6	37	0	14	4	0				
	M	1	2	3	3	0	8	1	0				
	P	1	9	7	1	6	13	2	0				
	R	0	10	19	7	5	0	2	0				
	V	2	34	98	90	0	3	0	0				
	W	0	3	13	5	0	3	4	0				
	Y	0	6	20	10	1	5	2	0				
Com2	Entr.	0.083	0.083	0.857	2.223	2.264	3.139	2.332	0.028	0.221	0.138	0.110	0.443
	Cons. Seq.	-	-	-	-	**K**	**L**	**L**	-	-	-	-	-
	Cons. Seq. (BXS)	-	-	-	-	**B**	**X**	**X**	-	-	-	-	-
	-	357	357	317	196	0	0	0	359	351	355	356	341
	A	0	0	1	2	0	3	2	0	0	1	1	1
	C	0	0	0	2	2	16	9	0	0	0	0	0
	F	1	1	7	14	22	25	8	0	0	0	0	0
	G	0	1	5	3	2	48	29	0	3	0	0	5
	H	0	0	0	4	10	7	4	0	0	0	1	1
	I	1	0	9	5	5	10	26	1	1	1	0	1
	K	0	0	12	80	209	81	1	0	0	0	0	0
	L	0	1	2	17	42	82	183	0	3	1	1	2
	M	0	0	0	12	18	12	5	0	1	0	0	0
	P	0	0	4	4	12	32	73	0	0	1	1	3
	R	0	0	1	5	8	21	3	0	1	0	0	2
	V	0	0	2	3	2	0	1	0	0	1	0	0
	W	0	0	0	2	6	3	9	0	0	0	0	0
	Y	1	0	0	11	22	20	7	0	0	0	0	4
Com3	Entr.	0.242	1.432	3.050	2.745	0.092	2.846	1.500	0.269	0.040			
	Cons. Seq.	-	-	-	**L**	**R**	-	-	-	-			
	Cons. Seq. (BXS)	-	-	-	**X**	**B**	-	-	-	-			
	-	514	415	168	7	0	247	414	511	525			
	A	0	14	26	28	1	28	7	1	0			
	C	0	7	15	28	0	12	7	2	0			
	F	1	7	37	26	0	13	12	1	0			
	G	3	33	50	34	0	34	15	7	0			
	H	0	2	4	13	2	11	7	0	0			
	I	1	5	20	21	0	33	12	0	0			
	K	1	9	13	11	2	27	7	2	0			
	L	1	16	120	271	0	11	4	2	1			
	M	0	2	2	1	0	0	2	0	0			
	P	0	6	17	28	0	20	12	1	0			
	R	1	2	11	18	522	14	3	0	0			
	V	2	3	25	15	0	54	20	0	1			
	W	1	1	7	10	0	9	1	0	0			
	Y	2	5	12	16	0	14	4	0	0			
Com4	Entr.	0.042	0.042	0.042	0.084	0.686	2.116	2.046	2.380	2.042	0.349	0.247	
	Cons. Seq.	-	-	-	-	-	-	**K**	**V**	**V**	-	-	
	Cons. Seq. (BXS)	-	-	-	-	-	-	**B**	**X**	**X**	-	-	
	-	219	219	219	218	199	125	0	1	1	211	213	
	A	1	0	0	1	2	4	17	18	17	2	0	
	C	0	0	0	0	0	2	3	1	5	0	0	
	F	0	0	0	0	1	5	10	15	7	1	0	
	G	0	0	1	0	0	3	1	7	21	0	2	
	H	0	0	0	0	0	2	0	0	0	0	0	
	I	0	0	0	0	0	1	2	0	1	0	0	
	K	0	0	0	0	5	45	132	57	0	0	0	
	L	0	1	0	1	7	14	21	19	26	1	4	
	M	0	0	0	0	0	0	1	1	2	0	0	
	P	0	0	0	0	1	5	6	1	0	0	0	
	R	0	0	0	0	1	3	0	2	0	1	0	
	V	0	0	0	0	4	9	24	93	131	2	1	
	W	0	0	0	0	0	0	0	0	8	0	0	
	Y	0	0	0	0	0	2	3	5	1	2	0	

Com13	Entr.	0.136	2.415	0.664	2.086	2.645	1.622	0.232	
	Cons. Seq.	**-**	**-**	**K**	**I**	**I**	**-**	**-**	
	Cons. Seq. (BXS)	**-**	**-**	**B**	**X**	**X**	**-**	**-**	
	-	103	51	5	0	28	72	102	
	A	0	12	6	14	14	6	0	
	C	0	6	0	2	1	0	0	
	F	0	9	0	10	5	2	0	
	I	0	12	0	62	34	14	1	
	K	0	4	93	6	2	5	0	
	L	0	0	0	1	2	0	0	
	M	0	0	0	4	2	1	1	
	P	2	8	0	3	10	4	0	
	R	0	0	1	1	0	0	1	
	V	0	1	0	1	1	0	0	
	W	0	1	0	0	0	0	0	
	Y	0	1	0	1	6	1	0	
Com14	Entr.	0.206	0.000	2.431	2.989	0.589	2.404		
	Cons. Seq.	**-**	**H**	**P**	**P**	**-**	**-**		
	Cons. Seq. (BXS)	**-**	**B**	**S**	**S**	**-**	**-**		
	-	72	0	0	0	68	36		
	A	0	0	0	4	0	6		
	C	0	0	4	4	0	1		
	F	0	0	5	5	1	1		
	G	0	0	7	15	1	6		
	H	1	74	1	4	0	3		
	I	1	0	2	4	1	0		
	K	0	0	0	1	0	1		
	L	0	0	3	9	1	5		
	M	0	0	0	0	0	1		
	P	0	0	34	17	0	13		
	R	0	0	1	0	0	0		
	V	0	0	15	11	2	1		
	Y	0	0	2	0	0	0		
Com15	Entr.	1.346	2.621	2.901	1.074	2.737	0.720	0.109	0.109
	Cons. Seq.	**-**	**P**	**P**	**R**	**-**	**-**	**-**	**-**
	Cons. Seq. (BXS)	**-**	**S**	**S**	**B**	**-**	**-**	**-**	**-**
	-	127	29	0	1	54	143	158	158
	A	6	23	19	12	28	3	0	0
	C	0	1	8	1	2	1	1	0
	F	0	0	2	1	0	0	0	0
	G	3	1	3	1	3	4	0	0
	H	0	2	12	1	4	0	0	0
	I	3	6	19	3	5	1	0	1
	K	3	6	8	2	6	0	1	0
	L	2	6	4	0	6	7	0	1
	M	0	1	0	0	0	0	0	0
	P	3	70	57	5	25	0	0	0
	R	1	2	21	133	24	1	0	0
	V	4	5	6	0	0	0	0	0
	W	0	4	1	0	0	0	0	0
	Y	8	4	0	0	3	0	0	0
Com16	Entr.	0.081	0.864	2.037	3.251	3.459	2.968	1.458	
	Cons. Seq.	**-**	**-**	**R**	**V**	**R**	**-**	**-**	
	Cons. Seq. (BXS)	**-**	**-**	**B**	**X**	**B**	**-**	**-**	
	-	445	384	161	21	29	153	351	
	A	0	18	9	74	32	33	16	
	C	0	2	0	4	24	19	1	
	F	1	1	2	4	18	13	3	
	G	3	0	4	26	21	12	14	
	H	0	0	3	2	8	4	2	
	I	0	1	5	39	18	14	11	
	K	0	0	60	53	53	15	2	
	L	0	0	0	5	5	4	2	
	M	0	0	4	8	10	10	1	
	P	0	0	2	68	35	7	8	
	R	0	0	187	15	98	84	7	
	V	0	14	9	97	67	68	24	
	W	0	0	2	5	2	1	2	
	Y	0	29	1	28	29	12	5	

Com20	Entr.	0.084	0.084	0.598	1.341	2.534	2.743	1.253	0.749	0.252
	Cons. Seq.	**-**	**-**	**-**	**R**	**R**	**I**	**P**	**-**	**-**
	Cons. Seq. (BXS)	**-**	**-**	**-**	**B**	**B**	**X**	**S**	**-**	**-**
	-	94	94	87	41	0	0	16	84	92
	A	0	1	2	2	0	15	1	4	0
	C	0	0	0	0	11	15	7	0	0
	F	0	0	1	1	5	5	1	0	1
	G	1	0	3	0	4	21	0	0	0
	H	0	0	0	1	0	7	0	0	0
	I	0	0	0	0	3	25	1	4	1
	K	0	0	0	0	0	0	0	0	1
	L	0	0	0	0	1	1	0	1	0
	M	0	0	0	0	6	0	0	0	0
	P	0	0	0	0	17	2	69	0	0
	R	0	0	1	49	42	3	0	0	0
	V	0	0	1	0	3	1	0	1	0
	W	0	0	0	1	3	0	0	0	0
	Y	0	0	0	0	0	0	0	1	0
Com21	Entr.	0.681	1.593	2.764	1.490	0.453	1.437			
	Cons. Seq.	**-**	**C**	**V**	**R**	**-**	**-**			
	Cons. Seq. (BXS)	**-**	**S**	**X**	**B**	**-**	**-**			
	-	53	0	0	0	56	38			
	A	0	0	0	0	0	1			
	C	2	40	0	0	1	0			
	F	0	0	3	19	1	0			
	G	4	10	5	0	0	0			
	H	0	0	1	0	0	0			
	I	1	4	9	0	0	0			
	K	0	1	12	3	0	3			
	L	0	0	0	1	0	0			
	M	0	1	8	1	0	0			
	R	0	1	9	35	0	16			
	V	0	3	13	1	2	1			
	Y	0	0	0	0	0	1			
Com22	Entr.	0.531	2.221	0.593	1.953	2.832	1.835	0.075	0.075	
	Cons. Seq.	**-**	**-**	**R**	**A**	**A**	**-**	**-**	**-**	
	Cons. Seq. (BXS)	**-**	**-**	**B**	**X**	**X**	**-**	**-**	**-**	
	-	100	52	1	1	19	71	108	108	
	A	0	12	0	60	36	14	0	1	
	C	0	1	0	3	0	0	0	0	
	F	6	19	0	25	5	4	0	0	
	G	0	0	2	0	2	6	0	0	
	H	0	0	0	1	6	2	0	0	
	I	0	2	3	11	22	6	0	0	
	K	0	1	2	0	0	0	0	0	
	L	0	2	0	0	3	2	0	0	
	M	1	0	0	0	2	0	0	0	
	P	0	0	0	2	0	0	0	0	
	R	1	17	100	0	6	0	0	0	
	V	1	1	1	0	3	1	0	0	
	W	0	2	0	3	1	0	1	0	
	Y	0	0	0	3	4	3	0	0	
Com24	Entr.	1.077	1.834	1.903	2.092	0.382	0.382			
	Cons. Seq.	**-**	**-**	**L**	**A**	**H**	**-**			
	Cons. Seq. (BXS)	**-**	**-**	**X**	**X**	**B**	**-**			
	-	25	14	0	0	0	32			
	A	0	0	11	17	0	0			
	C	0	0	0	0	1	0			
	F	0	0	1	4	0	0			
	G	0	2	5	5	0	0			
	H	0	0	0	4	32	0			
	I	6	2	0	1	1	0			
	K	0	0	0	3	0	0			
	L	3	14	15	0	0	0			
	M	0	0	1	0	0	0			
	V	0	1	1	0	0	1			
	W	0	1	0	0	0	1			

Com25	Entr.	0.126	0.126	0.942	2.113	1.457	1.893	0.000	0.251								
	Cons. Seq.	-	-	-	-	**A**	**A**	**R**	-								
	Cons. Seq. (BXS)	-	-	-	-	**X**	**X**	**B**	-								
	-	57	57	49	26	0	0	0	56								
	A	0	1	0	6	41	34	0	0								
	C	0	0	0	0	1	1	0	0								
	F	0	0	0	1	0	12	0	0								
	G	1	0	1	1	0	4	0	0								
	H	0	0	0	1	1	0	0	0								
	I	0	0	0	0	0	2	0	0								
	K	0	0	2	6	8	1	0	0								
	L	0	0	4	16	5	2	0	0								
	M	0	0	0	0	1	0	0	0								
	P	0	0	1	0	0	0	0	0								
	R	0	0	0	0	0	2	58	1								
	V	0	0	1	0	1	0	0	0								
	W	0	0	0	1	0	0	0	0								
	Y	0	0	0	0	0	0	0	1								
Com26	Entr.	0.017	0.017	0.034	0.034	0.913	2.533	3.121	0.031	0.034	3.013	2.268	0.017	0.196	0.192	0.051	0.048
	Cons. Seq.	-	-	-	-	-	-	**L**	-	-	**K**	**K**	-	-	-	-	-
	Cons. Seq. (BXS)	-	-	-	-	-	-	**X**	-	-	**B**	**B**	-	-	-	-	-
	-	631	631	630	630	552	305	15	630	630	13	2	631	615	616	629	629
	A	0	1	0	0	8	34	59	0	0	32	3	0	1	1	1	0
	C	0	0	0	0	0	7	3	0	0	3	12	0	0	0	0	0
	F	0	0	0	0	4	12	19	0	0	14	11	0	0	0	0	0
	G	0	0	1	0	8	16	25	0	1	40	24	0	0	0	0	0
	H	0	0	0	0	4	16	19	0	0	7	10	0	0	0	0	0
	I	0	0	0	0	9	20	37	0	0	14	33	0	0	0	0	2
	K	0	0	1	0	4	27	80	2	0	187	378	0	15	13	1	0
	L	1	0	0	1	32	132	229	0	1	168	75	1	0	2	1	1
	M	0	0	0	0	1	5	7	0	0	7	14	0	0	0	0	0
	P	0	0	0	0	4	32	59	0	0	56	6	0	0	0	0	0
	R	0	0	0	0	3	1	16	0	0	16	26	0	0	0	0	0
	V	0	0	0	0	1	6	29	0	0	36	4	0	1	0	0	0
	W	0	0	0	0	0	4	7	0	0	9	8	0	0	0	0	0
	Y	0	0	0	1	2	15	28	0	0	30	26	0	0	0	0	0
Com31	Entr.	0.109	0.953	1.679	1.670	1.664	1.377	0.218									
	Cons. Seq.	-	-	**R**	**R**	**R**	**R**	-									
	Cons. Seq. (BXS)	-	-	**B**	**B**	**B**	**B**	-									
	-	68	56	29	0	0	0	67									
	A	0	1	0	1	0	1	0									
	C	0	0	0	1	0	0	0									
	F	0	0	3	1	0	2	0									
	G	0	0	1	0	0	0	0									
	H	0	0	0	0	1	0	0									
	I	0	0	1	6	17	1	0									
	K	0	0	1	2	1	1	0									
	L	0	0	1	5	2	0	0									
	M	0	0	0	0	1	0	0									
	P	0	1	0	1	0	0	1									
	R	1	9	32	49	41	51	0									
	V	0	2	1	2	6	7	1									
	W	0	0	0	1	0	6	0									
Com32	Entr.	0.292	2.194	0.979	1.985	1.305											
	Cons. Seq.	-	**C**	**K**	**G**	**C**											
	Cons. Seq. (BXS)	-	**S**	**B**	**S**	**S**											
	-	46	12	0	0	18											
	A	0	0	7	3	0											
	C	1	22	0	11	27											
	G	0	0	0	16	0											
	H	1	0	0	0	0											
	I	0	1	0	0	0											
	K	0	2	38	16	2											
	L	0	1	0	0	1											
	M	0	1	1	2	0											
	P	0	1	2	0	0											
	R	0	1	0	0	0											

	W	0	7	0	0	0				
Com34	Entr.	0.436	0.614	1.419	0.233	2.503	2.376	1.220	0.510	
	Cons. Seq.	-	-	-	**R**	**G**	**G**	-	-	
	Cons. Seq. (BXS)	-	-	-	**B**	**S**	**S**	-	-	
	-	88	85	56	2	6	21	65	86	
	A	0	0	0	0	1	3	0	0	
	C	0	0	0	0	4	1	1	0	
	F	0	1	0	0	0	1	0	0	
	G	0	0	2	0	40	44	24	6	
	H	0	0	0	0	1	0	0	0	
	I	3	2	31	1	8	0	0	0	
	L	0	0	0	0	0	1	1	0	
	M	0	0	1	0	0	1	0	0	
	P	0	0	0	0	12	3	1	0	
	R	2	0	1	91	1	3	1	0	
	V	1	1	0	0	17	11	1	1	
	W	0	5	1	0	0	4	0	1	
	Y	0	0	2	0	4	1	0	0	
Com35	Entr.	0.105	0.274	2.341	3.315	1.813	2.736	1.821	0.128	0.044
	Cons. Seq.	-	-	**K**	**K**	**K**	**A**	-	-	-
	Cons. Seq. (BXS)	-	-	**B**	**B**	**B**	**X**	-	-	-
	-	467	457	160	31	0	115	324	465	470
	A	0	0	4	58	38	169	30	1	0
	C	1	3	2	18	2	0	2	0	1
	F	0	0	21	21	9	22	23	0	0
	G	0	1	8	31	11	23	2	1	0
	H	0	0	0	1	6	5	5	0	0
	I	0	1	1	15	7	7	3	0	0
	K	2	6	190	134	333	66	31	5	1
	L	1	0	29	38	10	14	34	0	0
	M	0	3	12	2	3	12	5	0	0
	P	0	0	8	44	15	4	1	0	0
	R	0	0	23	38	21	20	3	0	0
	V	1	1	8	23	12	9	5	0	0
	W	0	0	0	3	0	1	1	0	0
	Y	0	0	6	15	5	5	3	0	0
Com38	Entr.	0.579	1.484	0.813	1.619	3.116	1.920	0.338		
	Cons. Seq.	-	-	**G**	**H**	**H**	-	-		
	Cons. Seq. (BXS)	-	-	**S**	**B**	**B**	-	-		
	-	91	73	3	0	11	64	94		
	A	0	1	0	0	6	5	3		
	C	0	6	3	2	0	0	0		
	F	0	0	0	1	0	0	0		
	G	3	8	86	2	17	6	2		
	H	1	4	0	69	20	6	0		
	I	0	1	0	2	7	2	0		
	K	0	0	0	0	2	0	0		
	M	1	0	0	0	5	8	0		
	P	0	2	0	2	5	2	0		
	R	0	0	5	9	19	0	0		
	V	2	0	0	1	3	5	0		
	W	0	0	2	0	0	0	0		
	Y	1	4	0	11	4	1	0		
Com43	Entr.	0.162	2.074	1.027	0.891	2.947	1.295	0.093		
	Cons. Seq.	-	-	**H**	**L**	**G**	-	-		
	Cons. Seq. (BXS)	-	-	**B**	**X**	**S**	-	-		
	-	82	47	0	0	14	63	83		
	A	2	10	4	4	14	0	0		
	C	0	2	0	0	0	0	0		
	F	0	1	0	0	1	0	0		
	G	0	0	1	1	17	3	0		
	H	0	13	70	0	4	0	0		
	I	0	5	0	6	6	0	0		
	K	0	0	1	0	1	0	0		
	L	0	3	0	71	9	10	1		
	M	0	2	0	0	0	0	0		
	P	0	1	2	0	14	5	0		
	R	0	0	5	0	0	0	0		
	V	0	0	0	0	0	1	0		

	Y	0	0	1	2	4	2	0							
Com46	Entr.	0.244	0.439	0.562	1.818	0.625	2.998	1.755	0.224	2.457	1.899	0.196	1.279	0.369	0.330
	Cons. Seq.	-	-	-	-	**G**	**P**	**P**	**G**	**P**	**K**	**G**	-	-	-
	Cons. Seq. (BXS)	-	-	-	-	**S**	**S**	**S**	**S**	**S**	**B**	**S**	-	-	-
	-	96	90	90	60	8	0	0	0	2	2	3	77	93	93
	A	0	0	1	7	0	13	5	0	4	3	0	1	0	0
	C	0	0	0	0	0	0	1	0	0	0	0	0	0	0
	F	0	0	0	0	0	6	0	0	4	0	0	0	0	0
	G	0	9	0	2	88	9	3	96	1	1	96	0	0	6
	H	0	0	0	0	0	1	2	0	11	0	0	3	0	0
	I	0	0	0	6	0	4	1	0	0	1	0	0	0	0
	K	1	0	5	2	0	9	10	0	4	47	0	8	5	0
	L	0	0	0	0	1	13	3	0	11	1	0	3	0	0
	M	1	0	0	0	0	0	1	0	1	0	0	0	0	0
	P	1	0	3	19	0	31	69	2	51	30	0	5	0	0
	R	0	0	0	2	2	7	3	0	7	14	0	2	1	0
	V	0	0	0	1	0	3	1	1	2	0	0	0	0	0
	Y	0	0	0	0	0	3	0	0	1	0	0	0	0	0
Com47	Entr.	0.331	2.036	1.145	0.629	0.000	1.777	0.111							
	Cons. Seq.	-	-	**L**	**L**	**R**	-	-							
	Cons. Seq. (BXS)	-	-	**X**	**X**	**B**	-	-							
	-	65	37	0	0	0	48	67							
	A	0	2	2	0	0	3	0							
	C	1	0	0	1	0	2	0							
	F	0	0	0	1	0	0	0							
	G	1	1	0	2	0	0	0							
	H	1	2	2	0	0	1	0							
	I	0	0	1	0	0	3	0							
	K	0	0	1	0	0	0	0							
	L	0	16	53	62	0	3	1							
	M	0	1	9	1	0	0	0							
	P	0	4	0	0	0	2	0							
	R	0	2	0	0	68	0	0							
	V	0	3	0	0	0	1	0							
	W	0	0	0	0	0	2	0							
	Y	0	0	0	1	0	3	0							
Com52	Entr.	0.331	1.643	1.973	0.648	2.665	2.231	0.541	0.110						
	Cons. Seq.	-	-	**G**	**R**	**C**	-	-	-						
	Cons. Seq. (BXS)	-	-	**S**	**B**	**S**	-	-	-						
	-	225	164	7	0	1	132	220	233						
	A	0	2	8	0	5	4	0	0						
	C	0	1	0	0	91	14	4	2						
	F	0	3	17	0	20	7	0	1						
	G	8	37	143	1	0	1	2	0						
	H	0	2	0	4	0	1	0	0						
	I	1	5	0	0	2	3	0	0						
	K	0	3	2	6	9	10	2	0						
	L	1	4	5	4	4	3	0	0						
	M	0	2	0	0	1	1	0	0						
	P	0	0	5	0	49	7	2	0						
	R	1	11	41	215	20	6	3	0						
	V	0	1	4	2	22	44	1	0						
	W	0	1	3	0	0	0	0	0						
	Y	0	0	1	4	12	3	2	0						
Com54	Entr.	0.173	1.833	2.887	2.302	0.237	1.106	0.528	0.087						
	Cons. Seq.	-	-	**L**	**L**	**H**	-	-	-						
	Cons. Seq. (BXS)	-	-	**X**	**X**	**B**	-	-	-						
	-	90	62	18	0	1	61	85	91						
	A	0	4	12	5	0	0	0	0						
	C	1	0	0	0	0	0	0	0						
	F	0	2	0	0	0	0	0	0						
	G	0	1	0	9	0	28	2	1						
	H	0	0	5	1	89	0	1	0						
	I	0	0	0	3	0	2	0	0						
	K	0	0	1	7	0	0	1	0						
	L	0	5	20	47	0	0	0	0						
	M	0	3	1	3	0	1	0	0						
	P	0	0	3	3	2	0	3	0						
	R	1	3	11	0	0	0	0	0						
	V	0	7	16	14	0	0	0	0						

	Y	0	5	5	0	0	0	0	0		
Com56	Entr.	0.416	2.048	1.952	2.678	0.000	0.748				
	Cons. Seq.	**-**	**-**	**G**	**L**	**H**	**-**				
	Cons. Seq. (BXS)	**-**	**-**	**S**	**X**	**B**	**-**				
	-	48	23	0	0	0	45				
	A	0	0	3	11	0	2				
	C	0	1	0	0	0	1				
	F	0	0	2	4	0	0				
	G	1	10	24	4	0	0				
	H	0	3	0	0	51	0				
	I	0	3	7	9	0	0				
	L	1	0	0	15	0	0				
	M	0	0	0	0	0	2				
	P	1	11	14	2	0	0				
	V	0	0	0	3	0	1				
	W	0	0	1	0	0	0				
	Y	0	0	0	3	0	0				
Com60	Entr.	0.302	0.955	2.741	0.302	2.829	2.977	1.548	0.185	0.035	0.017
	Cons. Seq.	**-**	**-**	**-**	**R**	**L**	**L**	**-**	**-**	**-**	**-**
	Cons. Seq. (BXS)	**-**	**-**	**-**	**B**	**X**	**X**	**-**	**-**	**-**	**-**
	-	593	537	299	0	2	143	469	602	612	613
	A	3	10	42	1	34	3	0	0	0	0
	C	0	0	7	0	19	16	11	1	0	0
	F	0	9	13	2	24	17	6	1	0	0
	G	3	10	41	0	84	37	14	0	0	1
	H	0	1	1	3	10	6	4	0	0	0
	I	1	8	41	0	39	23	9	3	1	0
	K	0	5	9	14	13	19	7	0	0	0
	L	6	14	45	1	276	205	46	4	0	0
	M	0	2	6	1	2	10	1	0	0	0
	P	0	3	17	0	38	33	10	0	0	0
	R	2	5	30	591	22	58	14	0	1	0
	V	5	9	43	1	26	21	10	2	0	0
	W	1	0	5	0	4	1	3	1	0	0
	Y	0	1	15	0	21	22	10	0	0	0
Com62	Entr.	0.169	1.689	0.336	0.550	1.745	1.710				
	Cons. Seq.	**-**	**-**	**L**	**H**	**L**	**-**				
	Cons. Seq. (BXS)	**-**	**-**	**X**	**B**	**X**	**-**				
	-	39	24	0	0	2	26				
	A	0	0	0	0	0	1				
	C	0	0	0	3	0	0				
	F	0	2	0	0	0	0				
	G	0	0	0	0	1	0				
	H	0	9	1	36	16	1				
	I	0	0	1	0	0	0				
	K	0	0	0	0	0	2				
	L	1	1	38	1	18	6				
	P	0	1	0	0	0	0				
	V	0	0	0	0	1	3				
	W	0	0	0	0	2	1				
	Y	0	3	0	0	0	0				
Com63	Entr.	0.411	0.589	1.400	2.231	2.039	2.285	0.736			
	Cons. Seq.	**-**	**-**	**C**	**R**	**K**	**-**	**-**			
	Cons. Seq. (BXS)	**-**	**-**	**S**	**B**	**B**	**-**	**-**			
	-	70	68	11	0	1	30	65			
	A	1	2	0	3	0	0	0			
	C	1	0	53	0	1	0	0			
	F	0	1	0	0	0	1	0			
	G	0	0	1	7	0	1	1			
	H	0	1	0	0	8	1	0			
	I	0	0	0	1	0	0	0			
	K	1	0	0	14	37	1	0			
	L	0	0	0	1	0	0	0			
	M	0	0	3	0	3	7	2			
	P	0	0	3	17	15	23	5			
	R	1	1	3	30	9	0	0			
	V	0	0	0	0	0	6	0			

	W	0	0	0	0	0	2	0									
	Y	0	1	0	1	0	2	1									
Com69	Entr.	0.434	1.797	2.617	2.007	0.000	1.145										
	Cons. Seq.	**-**	**-**	**V**	**V**	**R**	**-**										
	Cons. Seq. (BXS)	**-**	**-**	**X**	**X**	**B**	**-**										
	-	134	92	4	0	0	117										
	A	2	17	37	17	0	2										
	C	0	1	1	0	0	11										
	F	0	3	10	1	0	1										
	G	1	5	6	31	0	2										
	H	0	0	1	0	0	0										
	I	0	2	3	8	0	1										
	K	0	0	3	4	0	0										
	L	3	4	18	4	0	2										
	M	0	1	2	1	0	1										
	P	0	0	2	0	0	0										
	R	0	0	0	0	142	1										
	V	1	16	53	75	0	1										
	W	1	1	2	1	0	0										
	Y	0	0	0	0	0	3										
Com76	Entr.	0.029	0.029	0.081	0.116	1.442	2.133	3.075	1.130	0.058	0.140	0.647	0.818	0.738	0.604	0.081	0.029
	Cons. Seq.	**-**	**-**	**-**	**-**	**-**	**G**	**P**	**K**	**-**	**-**	**-**	**G**	**-**	**-**	**-**	**-**
	Cons. Seq. (BXS)	**-**	**-**	**-**	**-**	**-**	**S**	**S**	**B**	**-**	**-**	**-**	**S**	**-**	**-**	**-**	**-**
	-	337	337	335	334	261	111	1	1	336	333	311	23	307	313	335	337
	A	0	0	0	1	7	9	41	0	0	0	3	4	3	3	0	0
	C	0	0	0	0	0	4	13	0	0	0	3	8	2	1	0	0
	F	0	0	0	0	1	5	7	0	0	0	2	0	1	1	0	0
	G	1	0	2	1	8	160	34	1	0	1	5	295	1	0	0	0
	H	0	0	0	0	1	1	7	2	0	0	0	3	1	0	0	0
	I	0	0	0	0	4	9	25	0	0	0	2	0	2	5	0	0
	K	0	0	0	1	9	1	8	208	0	0	2	0	0	2	0	1
	L	0	0	0	0	3	7	27	0	1	0	2	1	3	6	2	0
	M	0	0	0	0	4	3	13	1	0	0	0	0	1	2	0	0
	P	0	0	1	0	27	7	121	1	1	0	5	2	10	1	0	0
	R	0	1	0	0	8	8	13	123	0	2	0	1	1	0	0	0
	V	0	0	0	1	5	13	25	0	0	1	0	0	3	3	1	0
	W	0	0	0	0	0	0	2	1	0	0	0	1	1	0	0	0
	Y	0	0	0	0	0	0	1	0	0	1	3	0	2	1	0	0
Com96	Entr.	0.382	1.863	1.431	2.059	0.804	0.191										
	Cons. Seq.	**-**	**-**	**K**	**I**	**G**	**-**										
	Cons. Seq. (BXS)	**-**	**-**	**B**	**X**	**S**	**-**										
	-	32	15	0	0	3	33										
	A	0	0	0	0	1	0										
	C	0	0	0	10	0	0										
	F	0	1	1	0	0	0										
	G	0	0	0	2	29	0										
	I	0	0	1	13	0	0										
	K	0	4	23	7	0	0										
	L	0	0	0	1	0	0										
	M	0	1	0	0	0	0										
	P	0	0	0	0	1	0										
	R	0	0	3	0	0	0										
	V	0	0	0	1	0	1										
	W	1	1	0	0	0	0										
	Y	1	12	6	0	0	0										
Com97	Entr.	0.382	1.172	2.543	1.438	1.277	1.763										
	Cons. Seq.	**-**	**-**	**R**	**H**	**G**	**Y**										
	Cons. Seq. (BXS)	**-**	**-**	**B**	**B**	**S**	**X**										
	-	32	27	6	0	0	11										
	A	0	1	6	0	0	0										
	F	0	0	2	2	2	0										
	G	0	1	0	1	24	5										
	H	0	1	3	25	0	0										
	I	0	0	0	0	2	0										
	K	0	0	0	2	0	0										
	M	0	0	1	0	0	0										
	P	0	0	0	2	0	0										
	R	0	3	10	2	0	0										
	V	1	0	0	0	6	3										

	Y	1	1	6	0	0	15			
Com101	Entr.	0.790	0.860	0.689	1.789	1.637				
	Cons. Seq.	**-**	**I**	**K**	**K**	**-**				
	Cons. Seq. (BXS)	**-**	**X**	**B**	**B**	**-**				
	-	29	0	0	0	25				
	A	0	1	0	0	1				
	C	0	2	0	2	0				
	I	9	32	0	0	0				
	K	0	0	31	19	3				
	L	0	3	0	0	0				
	M	0	0	0	1	0				
	P	0	0	0	6	1				
	R	0	0	7	0	0				
	V	0	0	0	10	5				
	W	0	0	0	0	3				
Com110	Entr.	0.156	0.156	0.745	1.881	1.437	0.700	2.343	0.819	0.359
	Cons. Seq.	**-**	**R**	**G**	**L**	**P**	**G**	**-**	**-**	**-**
	Cons. Seq. (BXS)	**-**	**B**	**S**	**X**	**S**	**S**	**-**	**-**	**-**
	-	43	0	4	0	0	0	18	38	41
	A	0	0	0	4	1	0	4	0	0
	C	0	0	0	0	1	0	0	0	0
	F	0	0	0	3	0	0	0	1	0
	G	0	0	38	1	1	38	1	3	0
	H	0	0	0	0	2	0	0	0	0
	I	0	0	1	0	1	0	0	0	0
	K	0	0	1	0	0	2	1	1	0
	L	0	1	0	19	1	0	0	0	0
	M	0	0	0	0	1	0	0	0	0
	P	0	0	0	16	34	4	11	1	3
	R	0	43	0	0	2	0	4	0	0
	V	1	0	0	0	0	0	4	0	0
	Y	0	0	0	1	0	0	1	0	0
Com114	Entr.	0.024	1.106	1.113	2.579	3.344	3.006	0.778	0.071	0.048
	Cons. Seq.	**-**	**-**	**G**	**K**	**K**	**-**	**-**	**-**	**-**
	Cons. Seq. (BXS)	**-**	**-**	**S**	**B**	**B**	**-**	**-**	**-**	**-**
	-	427	365	36	2	21	155	386	425	426
	A	0	2	4	10	16	7	3	0	0
	C	0	2	1	16	26	35	3	0	1
	F	0	4	0	23	13	4	0	0	0
	G	1	4	354	25	25	29	2	0	1
	H	0	5	4	16	19	3	1	0	0
	I	0	7	3	19	34	50	6	0	0
	K	0	10	7	230	143	61	6	1	0
	L	0	0	0	5	25	23	6	1	0
	M	0	3	4	7	9	6	0	0	0
	P	0	4	1	5	42	12	3	1	0
	R	0	5	6	8	8	7	3	0	0
	V	0	8	6	43	27	27	8	0	0
	W	0	0	2	3	10	5	1	0	0
	Y	0	9	0	16	10	4	0	0	0
Com122	Entr.	0.383	1.934	1.739	1.675	0.327	0.680	0.141		
	Cons. Seq.	**-**	**-**	**K**	**G**	**P**	**-**	**-**		
	Cons. Seq. (BXS)	**-**	**-**	**B**	**S**	**S**	**-**	**-**		
	-	47	26	0	0	3	44	49		
	C	0	2	1	1	0	0	0		
	F	0	0	0	1	0	0	0		
	G	0	0	0	26	0	0	0		
	I	0	0	1	0	0	0	0		
	K	2	14	34	0	0	0	0		
	L	0	0	2	0	0	1	0		
	M	0	0	0	3	0	4	0		
	P	0	2	3	2	47	0	0		
	R	0	2	1	0	0	0	0		
	V	0	2	6	17	0	1	1		

	W	1	0	1	0	0	0	0
	Y	0	2	1	0	0	0	0
Com132	Entr.	0.480	1.181	1.915	0.000	2.187	0.179	1.401
	Cons. Seq.	**-**	**-**	**F**	**H**	**L**	**-**	**-**
	Cons. Seq. (BXS)	**-**	**-**	**X**	**B**	**X**	**-**	**-**
	-	34	23	5	0	0	36	22
	A	1	0	1	0	0	0	1
	C	0	0	0	0	3	0	0
	F	0	2	18	0	0	0	0
	G	2	12	10	0	0	1	0
	H	0	0	0	37	0	0	0
	I	0	0	1	0	4	0	0
	L	0	0	0	0	19	0	11
	M	0	0	0	0	5	0	0
	P	0	0	0	0	3	0	3
	R	0	0	0	0	1	0	0
	Y	0	0	2	0	2	0	0
Com153	Entr.	0.187	0.000	1.423	1.515	1.300	0.422	
	Cons. Seq.	**-**	**R**	**L**	**A**	**-**	**-**	
	Cons. Seq. (BXS)	**-**	**B**	**X**	**X**	**-**	**-**	
	-	34	0	0	0	19	32	
	A	0	0	0	20	14	3	
	F	0	0	1	0	0	0	
	H	0	0	0	1	0	0	
	I	0	0	0	0	1	0	
	K	1	0	1	2	1	0	
	L	0	0	25	11	0	0	
	M	0	0	5	0	0	0	
	R	0	35	0	1	0	0	
	V	0	0	2	0	0	0	
	W	0	0	1	0	0	0	
Com179	Entr.	0.589	1.956	2.717	1.064	1.111	0.191	
	Cons. Seq.	**-**	**-**	**P**	**C**	**-**	**K**	
	Cons. Seq. (BXS)	**-**	**-**	**S**	**S**	**-**	**B**	
	-	62	41	8	0	54	2	
	A	0	1	0	0	0	0	
	C	1	11	1	55	0	0	
	F	0	1	0	4	0	0	
	G	1	1	0	0	0	0	
	H	0	0	7	0	1	0	
	I	0	1	1	0	0	0	
	K	0	5	13	0	0	66	
	L	0	0	0	0	1	0	
	M	0	1	1	2	1	0	
	P	3	5	20	0	7	0	
	R	1	1	1	0	0	0	
	V	0	0	12	5	4	0	
	Y	0	0	4	2	0	0	

Supplementary Table 13. The total number of amino acid sequences found in the **HEPbp BXP HBS** network expressed as there amino acid type, i.e, **B** (basic), **X** (hydropathic) and **P** (polar). Sequences ranging in length between 3 and 7 amino acids with a total degree (Tot deg) greater than one were included the table.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
XXB	317	3628	*BXXX*	109	1766	*BXXXX*	36	102	*PXBPXX*	4	16	*BXXPBPP*	4	16
XBX	293	2986	*XXXB*	107	1515	*XXBXX*	30	82	*XBXPPP*	3	6	*XBXXXXP*	4	19
BXX	281	3202	*XBXX*	106	1654	*XXPXB*	26	59	*BBXBXX*	3	12	*PBXBBPB*	3	7
PXB	237	3189	*XXBX*	91	1230	*XBXXX*	22	41	*XXBXXP*	3	7	*XXXXPPB*	2	4
BXP	209	2040	*XBXP*	80	1230	*XPXBX*	21	39	*XXBPXP*	3	4	*BXBXXXX*	2	5
XBP	195	2128	*XBPX*	77	1212	*XXXXB*	20	31	*XBXXXX*	2	2	*XPXXBPX*	2	3
BPX	165	2037	*BXXP*	77	1205	*XXBPX*	19	49	*PXPBXP*	2	2	*XBBXBBX*	2	4
PBX	159	1537	*PXXB*	74	1349	*PXPXB*	17	40	*BBXPXP*	2	2	*XXXXXBX*	2	4
XPB	155	1427	*XXBP*	69	1083	*XPXXB*	17	44	*XXBPPB*	2	4	*PXXBPXX*	2	7
BXB	145	1664	*BPXX*	62	773	*BXXBX*	16	42	*PBXXPB*	2	4	*BBXPBPX*	2	6
XBB	119	1395	*PXBX*	58	826	*XBPXX*	15	30	*PXPBXB*	2	4	*XXBPPXB*	2	5
PBP	112	1303	*XPXB*	56	1088	*XPBXX*	15	30	*XBPXXB*	2	3	*XXBBXXB*	2	5
BPP	111	1284	*PBXX*	55	764	*BXXXP*	15	34	*XXXBXX*	2	3	*XXXXPBB*	2	6
PPB	111	1258	*BXPX*	54	871	*BXPXX*	14	28	*XXPXBX*	2	2	*XBPPPXP*	2	4
BBX	104	1150	*XXPB*	53	678	*XBXXP*	14	39	*BXPXPX*	2	3			
PBB	74	785	*XXBB*	51	970	*XBXPX*	13	23	*XXBXXX*	2	2			
BBP	60	473	*XPBX*	50	706	*PXXXB*	13	22	*XBXXXP*	2	7			
BPB	58	536	*BPPX*	48	810	*BXPXP*	12	31	*XBBPPX*	2	4			
BBB	47	525	*BXBX*	48	959	*XBPXP*	12	26	*PBXXBX*	2	3			
			BXXB	46	949	*XXBXP*	11	26						
			BPXP	46	824	*BXXPX*	11	26						
			XBXB	44	1013	*BPXXP*	11	22						
			PXBP	44	841	*PXXPB*	11	16						
			BBXX	42	745	*BXBXP*	11	19						
			PBXP	40	665	*XXXBX*	11	18						
			PPXB	39	583	*BXXPB*	10	25						
			XBBX	39	661	*BXBXX*	10	29						
			XBPP	38	459	*PBPXX*	10	26						
			XPPB	37	534	*PXXBX*	10	29						
			PBPX	36	673	*BBXXX*	10	24						
			XPBP	34	475	*XXBBB*	10	23						
			BPBX	31	472	*PXBXX*	10	30						
			PXPB	31	398	*PBPPX*	10	30						
			BPXB	28	630	*XXPBX*	10	23						
			PPBP	28	408	*BBXXB*	9	22						
			BXPB	27	522	*XPBXP*	9	19						
			XPBB	26	447	*XXXBP*	9	18						
			PXBB	25	461	*XXBXB*	8	18						
			BXBP	24	566	*XBXBB*	8	24						
			PPBX	24	331	*XXPPB*	8	17						
			BBXP	24	403	*PBXPX*	8	18						
			PBXB	23	478	*XPBBX*	8	14						
			BXPP	23	322	*XXBBX*	8	33						
			BPPP	23	391	*BPXXX*	8	15						
			XBBB	20	372	*XBPPP*	8	18						
			XBBP	19	345	*XBXXB*	8	19						
			PBBX	19	314	*XXBPP*	7	12						
			PBPP	19	274	*BXXXB*	7	18						
			BBPX	18	284	*PXBPX*	7	15						
			BPBP	18	348	*BBPXX*	7	16						
			BBXB	18	345	*BXBPX*	7	23						
			XBPB	18	364	*XPXPB*	7	10						
			BPPB	17	316	*XBPPX*	7	13						
			PPPB	17	179	*BPPXX*	7	17						
			PPBB	16	214	*XBXBP*	7	13						
			BXBB	15	300	*XXXPB*	6	8						
			PBBP	14	228	*BXPBX*	6	10						
			PBBB	13	240	*PXBXP*	6	11						
			BBBX	13	185	*XBBXB*	6	14						
			BBPP	12	142	*PXPBX*	6	24						
			PBPB	11	214	*XBXBX*	6	20						
			BBBB	10	182	*XPXBP*	6	17						
			BBPB	8	138	*BPBXX*	6	13						
			BBBP	7	91	*XBBXX*	6	16						
			BPBB	7	159	*BXXBP*	6	16						
						XBPBX	6	10						
						BXXPP	5	12						
						XPBPX	5	11						
						XPBPP	5	10						

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
						XPBXB	5	7						
						XBBXP	5	11						
						BBBBB	5	8						
						XXPBB	5	10						
						BBXXP	5	12						
						PPXXB	5	8						
						XPPBP	5	11						
						PBXXB	5	7						
						BXPPX	5	10						
						XXBBP	5	12						
						XXXBB	5	15						
						XPPXB	5	12						
						XPPBX	5	11						
						XPXBB	5	9						
						PPPBP	5	10						
						XBXPB	5	6						
						XXBPB	4	22						
						XBBPP	4	7						
						PBBPX	4	10						
						PXBBX	4	10						
						PBPXB	4	10						
						PBXXP	4	5						
						PBXBB	4	7						
						BPPPX	4	9						
						BXBPB	4	8						
						PBBPP	4	10						
						BBXBX	4	9						
						PBBXX	4	9						
						PPBPB	4	5						
						PBXXX	4	7						
						XBXPP	4	11						
						PPBPX	4	5						
						PBXBX	3	6						
						PPBXP	3	7						
						PBPBP	3	5						
						PXBBP	3	4						
						XBBBX	3	5						
						XBPXB	3	6						
						BBPBB	3	18						
						XBBPX	3	8						
						XXPBP	3	4						
						BPBXP	3	6						
						BPXBX	3	15						
						PPBXX	3	6						
						BPXPP	3	7						
						XPBBP	3	11						
						BBPXP	3	10						
						BBPPX	3	11						
						BXBBX	3	12						
						XBBBP	3	8						
						BBBXX	3	7						
						BXPXB	3	6						
						PXPBP	3	7						
						BBXBP	3	5						
						BBXPX	3	7						
						PBPPP	3	5						
						XPPPB	3	5						
						BXXBB	3	5						
						PPXBX	3	5						
						PBXBP	3	6						
						BPXXB	3	8						
						XPBBB	2	2						
						PXBBB	2	3						
						BXPPP	2	2						
						PPPXB	2	3						
						PPBXB	2	2						
						BPPXP	2	5						
						BPBBP	2	4						
						BPPBX	2	4						
						BBBPB	2	3						
						PXPBB	2	2						
						PBPBB	2	2						
						BXPBP	2	2						
						XBBBB	2	5						

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
						PBBXP	2	3						
						BBPBP	2	2						
						BXBBP	2	2						
						XBPPB	2	3						
						BPXBB	2	5						
						PPBBX	2	6						
						BPPBB	2	4						
						BPPPP	2	5						

Supplementary Table 14. The significant communities found in the HEPbp **BXP** HBS network.

Com1	Entr.	0.512	2.411	3.091	3.171	2.313	0.194	0.119		
	Cons. Seq.	-	-	**R**	**R**	**R**	-	-		
	Cons. Seq. (BXP)	-	-	**B**	**B**	**B**	-	-		
	-	289	160	0	0	0	301	304		
	A	0	6	12	9	12	0	2		
	F	1	6	5	0	6	0	0		
	H	0	1	0	1	3	0	0		
	I	0	8	12	16	13	1	0		
	K	0	0	5	12	15	1	0		
	L	1	1	2	5	3	0	0		
	M	0	2	7	6	3	0	0		
	N	0	8	20	30	15	0	1		
	Q	1	0	5	11	8	0	0		
	R	3	30	77	91	184	0	0		
	S	3	33	62	35	1	0	0		
	T	3	28	40	20	2	0	0		
	V	5	22	47	52	30	4	1		
	W	1	0	8	8	3	1	0		
	Y	1	3	6	12	10	0	0		
Com3	Entr.	0.613	2.278	2.257	1.816	2.012				
	Cons. Seq.	-	-	**F**	**R**	**I**				
	Cons. Seq. (BXP)	-	-	**X**	**B**	**X**				
	-	62	31	0	0	10				
	A	4	16	1	0	0				
	F	0	2	22	0	0				
	H	0	0	0	3	1				
	I	0	10	18	4	39				
	K	1	3	6	14	9				
	M	0	0	1	0	4				
	Q	0	0	1	8	2				
	R	2	3	18	39	3				
	S	0	0	0	1	1				
	T	0	1	0	0	0				
	V	0	1	0	0	0				
	Y	0	2	2	0	0				
Com4	Entr.	0.022	0.378	2.330	2.675	2.966	3.263	0.940	0.089	0.022
	Cons. Seq.	-	-	-	**K**	**K**	**L**	-	-	-
	Cons. Seq. (BXP)	-	-	-	**B**	**B**	**X**	-	-	-
	-	464	445	189	10	3	9	404	461	464
	A	0	1	13	26	20	40	5	0	0
	F	0	0	11	11	8	15	1	0	0
	H	0	5	1	3	3	3	1	0	0
	I	0	0	3	8	16	12	1	1	0
	K	1	2	157	175	141	52	16	1	0
	L	0	4	36	142	128	154	16	0	1
	M	0	4	10	4	5	6	1	0	0
	N	0	0	2	5	22	12	5	0	0
	Q	0	0	6	14	13	31	0	0	0
	R	0	0	1	8	20	22	0	0	0
	S	0	0	0	15	42	50	8	1	0
	T	0	1	23	30	30	24	1	0	0
	V	0	1	2	3	9	23	4	0	0
	W	0	1	3	4	1	3	0	0	0
	Y	0	1	8	7	4	9	2	1	0

Com6	Entr.	0.049	0.499	2.539	2.970	2.314	2.773	0.136	0.147
	Cons. Seq.	-	-	-	A	K	K	-	-
	Cons. Seq. (BXP)	-	-	-	X	B	B	-	-
	-	181	170	81	0	0	1	179	179
	A	0	4	41	60	26	39	0	0
	F	0	0	1	5	8	0	2	0
	H	0	0	1	0	0	2	0	0
	I	0	1	8	13	3	3	0	0
	K	1	0	0	38	97	54	0	0
	L	0	1	3	6	16	5	0	0
	M	0	0	2	0	0	2	0	0
	N	0	0	1	2	8	5	0	1
	Q	0	0	7	13	5	1	0	0
	R	0	0	8	10	0	2	0	0
	S	0	1	7	7	0	4	0	0
	T	0	0	1	1	9	33	1	1
	V	0	4	18	15	8	27	0	1
	W	0	0	2	10	2	4	0	0
	Y	0	1	1	2	0	0	0	0
Com11	Entr.	1.243	0.415	0.095	1.822	3.114	1.984	0.705	
	Cons. Seq.	**-**	**-**	**R**	**A**	**A**	**-**	**-**	
	Cons. Seq. (BXP)	**-**	**-**	**B**	**X**	**X**	**-**	**-**	
	-	61	77	0	0	5	45	74	
	A	0	0	0	53	25	10	1	
	F	10	0	0	1	1	2	1	
	H	0	0	0	0	9	3	0	
	I	0	1	0	3	9	1	1	
	K	0	0	0	0	1	0	0	
	L	0	0	0	4	3	0	0	
	M	0	1	0	0	2	2	0	
	N	0	0	0	1	1	0	0	
	Q	0	3	0	1	3	0	0	
	R	1	0	81	6	0	0	2	
	S	0	0	1	11	5	0	0	
	T	0	0	0	2	3	1	1	
	V	0	0	0	0	14	17	2	
	W	3	0	0	0	0	0	0	
	Y	7	0	0	0	1	1	0	
Com12	Entr.	0.858	2.171	3.027	2.595	0.000			
	Cons. Seq.	**-**	**-**	**V**	**L**	**K**			
	Cons. Seq. (BXP)	**-**	**-**	**X**	**X**	**B**			
	-	72	36	0	0	0			
	A	2	2	6	5	0			
	F	1	0	0	0	0			
	H	0	1	1	0	0			
	I	1	9	17	7	0			
	K	0	0	1	0	82			
	L	0	1	5	32	0			
	M	1	1	6	5	0			
	N	0	0	2	15	0			
	Q	3	22	17	1	0			
	R	0	0	3	2	0			
	S	1	0	2	1	0			
	V	1	9	19	12	0			
	W	0	0	2	0	0			
	Y	0	1	1	2	0			
Com17	Entr.	0.774	2.598	3.010	2.939	0.931	0.072	0.072	
	Cons. Seq.	**-**	**-**	**L**	**V**	**K**	**-**	**-**	
	Cons. Seq. (BXP)	**-**	**-**	**X**	**X**	**B**	**-**	**-**	
	-	204	114	0	0	0	227	227	
	A	1	7	10	9	1	0	0	
	F	1	6	8	4	1	0	0	
	H	0	2	0	0	1	0	0	
	I	2	1	1	5	3	0	0	
	K	0	8	14	40	198	0	0	
	L	10	29	60	42	0	0	2	
	M	0	2	4	0	0	0	0	
	N	0	15	23	6	4	2	0	
	Q	1	3	2	16	12	0	0	
	R	1	6	11	1	0	0	0	
	S	2	11	20	23	1	0	0	
	T	1	4	14	13	6	0	0	
	V	6	21	59	65	1	0	0	
	W	0	0	1	0	1	0	0	
	Y	0	0	2	5	0	0	0	

Com21	Entr.	0.373	1.567	2.968	2.455	0.276	2.717	1.265	0.268	
	Cons. Seq.	-	-	-	**L**	**R**	-	-	-	
	Cons. Seq. (BXP)	-	-	-	**X**	**B**	-	-	-	
	-	406	319	130	3	0	218	350	412	
	A	1	6	22	29	0	22	4	0	
	F	1	15	22	20	0	3	4	1	
	H	0	4	12	4	2	9	3	0	
	I	0	8	8	17	0	15	8	1	
	K	1	1	3	6	14	24	8	2	
	L	6	36	124	249	0	20	8	1	
	M	0	0	10	4	0	2	0	2	
	N	2	6	19	6	0	9	2	0	
	Q	0	0	1	11	1	10	2	1	
	R	1	3	13	6	407	41	16	2	
	S	3	7	19	21	0	11	2	0	
	T	2	6	17	14	0	8	7	0	
	V	0	6	18	22	0	13	8	2	
	W	0	0	1	4	0	1	1	0	
	Y	1	7	5	8	0	18	1	0	
Com25	Entr.	0.629	2.489	2.459	2.960	2.823	0.170	0.078	0.052	0.047
	Cons. Seq.	-	-	**R**	**L**	**L**	-	-	-	-
	Cons. Seq. (BXP)	-	-	**B**	**X**	**X**	-	-	-	-
	-	353	175	0	0	1	377	381	382	382
	A	6	14	23	20	19	0	0	0	0
	F	0	7	6	14	19	1	0	0	0
	H	0	0	3	7	2	0	0	0	0
	I	1	9	16	22	19	0	1	0	0
	K	2	2	10	27	11	0	0	0	0
	L	5	14	39	106	184	3	0	1	0
	M	0	2	2	5	1	0	0	0	0
	N	0	2	0	1	6	1	0	0	0
	Q	0	5	12	15	30	0	0	0	0
	R	9	101	208	106	6	0	1	1	0
	S	2	13	16	5	22	1	0	0	0
	T	1	9	15	9	25	0	0	0	0
	V	4	21	31	43	24	0	1	0	2
	W	1	5	1	2	8	0	0	0	0
	Y	0	5	2	2	7	1	0	0	0
Com32	Entr.	0.351	1.679	2.570	2.414	0.697	0.900			
	Cons. Seq.	-	-	**Q**	**Q**	**R**	-			
	Cons. Seq. (BXP)	-	-	**P**	**P**	**B**	-			
	-	53	27	0	0	0	48			
	F	0	0	5	1	2	3			
	H	0	0	0	0	0	1			
	I	0	1	3	0	0	0			
	K	0	3	2	0	1	0			
	L	0	0	7	13	1	2			
	M	0	0	1	2	0	0			
	N	0	0	0	0	0	1			
	Q	2	20	21	20	2	0			
	R	0	0	0	6	50	0			
	S	1	0	0	1	0	1			
	T	0	5	12	10	0	0			
	V	0	0	4	0	0	0			
	W	0	0	0	3	0	0			
	Y	0	0	1	0	0	0			
Com33	Entr.	1.645	1.882	0.476	2.245	1.665	0.365			
	Cons. Seq.	-	**L**	**H**	**V**	-	-			
	Cons. Seq. (BXP)	-	**X**	**B**	**X**	-	-			
	-	28	5	0	4	26	40			
	A	1	8	1	0	0	0			
	H	1	0	40	3	1	0			
	I	8	3	0	0	0	0			
	L	2	23	0	0	1	0			
	N	0	0	1	0	1	0			
	Q	0	0	0	2	0	0			
	S	0	0	0	14	8	3			
	T	0	4	1	3	0	0			
	V	2	0	0	16	6	0			
	W	1	0	0	0	0	0			
	Y	0	0	0	1	0	0			

Com34	Entr.	1.646	2.285	1.871	2.247	2.514	0.221	0.221	
	Cons. Seq.	**-**	**Q**	**R**	**V**	**V**	**-**	**-**	
	Cons. Seq. (BXP)	**-**	**P**	**B**	**X**	**X**	**-**	**-**	
	-	46	20	0	4	12	66	66	
	F	3	0	0	0	2	0	0	
	H	0	0	1	1	0	0	0	
	I	1	0	0	0	0	0	0	
	K	0	0	2	2	0	0	0	
	L	1	1	0	1	6	1	1	
	M	0	1	0	0	0	0	0	
	N	0	2	2	0	2	1	0	
	Q	6	22	21	1	1	0	1	
	R	4	16	34	16	0	0	0	
	S	0	0	0	0	2	0	0	
	T	0	4	2	6	13	0	0	
	V	7	1	6	32	27	0	0	
	W	0	1	0	0	1	0	0	
	Y	0	0	0	5	2	0	0	
Com37	Entr.	0.057	0.770	2.788	2.749	1.573	2.872	0.171	0.171
	Cons. Seq.	**-**	**-**	**-**	**K**	**K**	**K**	**-**	**-**
	Cons. Seq. (BXP)	**-**	**-**	**-**	**B**	**B**	**B**	**-**	**-**
	-	151	136	69	0	1	1	149	149
	A	0	3	1	3	0	16	0	1
	F	0	1	10	5	6	6	0	0
	H	0	0	6	3	2	0	0	0
	I	0	4	6	7	0	3	0	1
	K	0	4	20	62	102	57	0	0
	L	0	1	4	3	0	0	0	0
	M	0	0	0	0	1	6	0	0
	N	0	0	7	8	2	20	1	0
	Q	0	1	4	6	0	4	0	0
	R	0	0	1	2	0	0	0	0
	S	0	1	8	5	2	7	1	0
	T	0	1	11	37	29	23	1	0
	V	0	0	1	5	7	3	0	1
	W	0	0	0	1	0	2	0	0
	Y	1	0	4	5	0	4	0	0
Com39	Entr.	0.480	2.178	2.149	1.636	0.842			
	Cons. Seq.	**-**	**-**	**K**	**K**	**F**			
	Cons. Seq. (BXP)	**-**	**-**	**B**	**B**	**X**			
	-	34	18	0	0	1			
	A	0	1	0	0	0			
	F	0	2	0	1	31			
	H	0	0	0	1	0			
	I	0	0	0	1	0			
	K	0	5	16	26	0			
	N	2	0	1	2	0			
	Q	0	0	0	1	4			
	R	0	6	4	0	0			
	S	1	4	10	0	0			
	T	0	0	1	0	0			
	V	0	0	0	4	0			
	W	0	1	4	0	0			
	Y	0	0	1	1	1			
Com43	Entr.	0.322	1.543	1.135	2.146	3.154	2.200	0.768	
	Cons. Seq.	**-**	**-**	**R**	**S**	**S**	**-**	**-**	
	Cons. Seq. (BXP)	**-**	**-**	**B**	**P**	**P**	**-**	**-**	
	-	182	143	0	0	25	95	168	
	A	0	2	1	8	21	2	1	
	F	1	3	1	2	0	0	1	
	H	0	4	4	3	1	1	0	
	I	1	5	0	0	2	0	0	
	K	1	0	0	0	1	2	0	
	L	0	1	2	1	27	15	5	
	M	0	0	2	2	4	4	0	
	N	0	1	0	12	7	1	1	
	Q	0	4	6	7	8	4	0	
	R	1	1	157	23	29	11	1	
	S	2	13	11	109	43	47	9	
	T	1	7	2	20	15	5	0	
	V	0	0	1	1	4	1	1	
	W	0	0	0	0	0	1	2	
	Y	0	5	2	1	2	0	0	

Com46	Entr.	0.595	2.397	3.002	3.288	2.999	0.065	0.046
	Cons. Seq.	**-**	**-**	**K**	**K**	**K**	**-**	**-**
	Cons. Seq. (BXP)	**-**	**-**	**B**	**B**	**B**	**-**	**-**
	-	409	226	0	0	0	438	439
	A	5	22	43	40	21	0	0
	F	1	13	32	48	5	0	0
	H	0	4	10	13	8	0	0
	I	1	12	25	31	9	0	0
	K	10	88	163	119	114	2	0
	L	1	0	3	12	25	1	0
	M	1	1	1	5	2	0	0
	N	1	4	28	17	18	0	0
	Q	0	2	2	1	2	0	1
	R	3	21	45	65	111	0	0
	S	5	27	51	37	51	0	0
	T	1	8	9	14	16	0	0
	V	2	5	14	23	51	0	1
	W	0	2	2	2	0	0	0
	Y	1	6	13	14	8	0	0
Com48	Entr.	0.380	2.379	2.577	2.053	1.032		
	Cons. Seq.	**-**	**-**	**A**	**S**	**K**		
	Cons. Seq. (BXP)	**-**	**-**	**X**	**P**	**B**		
	-	71	39	0	0	0		
	A	2	11	22	8	0		
	F	1	2	0	0	1		
	H	0	2	0	0	3		
	I	0	1	7	0	0		
	K	0	0	0	14	61		
	Q	0	1	8	4	0		
	R	0	3	4	0	0		
	S	0	3	17	30	0		
	T	0	6	12	19	0		
	V	0	1	0	0	0		
	W	0	0	0	0	5		
	Y	1	6	5	0	5		
Com58	Entr.	1.209	2.270	2.187	0.988	1.852		
	Cons. Seq.	**-**	**A**	**A**	**R**	**-**		
	Cons. Seq. (BXP)	**-**	**X**	**X**	**B**	**-**		
	-	37	9	0	0	23		
	A	3	18	19	0	0		
	F	1	0	1	0	0		
	I	2	3	1	0	2		
	K	0	0	1	0	1		
	L	0	1	0	0	0		
	M	0	0	0	0	2		
	N	3	4	6	0	0		
	Q	0	1	0	9	16		
	R	1	11	11	36	1		
	S	0	0	0	0	2		
	T	0	0	8	1	0		
	W	0	0	0	1	0		
Com64	Entr.	0.611	1.819	2.423	2.718	0.459		
	Cons. Seq.	**-**	**-**	**H**	**H**	**L**		
	Cons. Seq. (BXP)	**-**	**-**	**B**	**B**	**X**		
	-	41	19	0	0	0		
	A	0	0	0	2	1		
	F	0	1	3	8	0		
	H	1	18	20	11	0		
	I	1	3	1	0	1		
	L	0	1	5	8	42		
	N	0	0	1	1	0		
	R	0	0	2	0	0		
	S	0	3	9	3	0		
	T	1	0	0	8	0		
	V	0	0	3	4	1		
	W	1	0	0	0	0		
	Y	0	0	1	0	0		

Com66	Entr.	1.861	0.391	2.225	2.317	0.812		
	Cons. Seq.	**-**	**K**	**S**	**Q**	**-**		
	Cons. Seq. (BXP)	**-**	**B**	**P**	**P**	**-**		
	-	17	0	0	11	33		
	I	0	0	2	7	1		
	K	1	36	0	0	0		
	M	11	0	0	1	0		
	N	0	0	1	0	0		
	Q	0	0	11	14	4		
	R	0	3	8	3	0		
	S	2	0	14	0	0		
	T	8	0	2	1	0		
	V	0	0	1	1	0		
	W	0	0	0	0	1		
	Y	0	0	0	1	0		
Com69	Entr.	0.714	0.472	2.853	2.752	2.050	0.625	
	Cons. Seq.	**-**	**K**	**S**	**S**	**-**	**-**	
	Cons. Seq. (BXP)	**-**	**B**	**P**	**P**	**-**	**-**	
	-	101	0	0	0	55	100	
	A	2	0	10	2	2	0	
	F	1	0	11	14	9	0	
	H	1	0	0	4	1	0	
	I	4	0	2	4	5	0	
	K	0	104	8	2	0	0	
	L	0	0	0	1	0	0	
	M	0	0	0	1	0	0	
	N	0	0	0	3	0	2	
	R	0	4	1	1	0	0	
	S	1	0	30	49	28	8	
	T	1	0	22	7	0	0	
	V	0	0	19	10	11	2	
	W	0	1	4	1	0	0	
	Y	1	3	5	13	1	0	
Com80	Entr.	0.672	1.997	2.239	1.376	0.000	1.103	0.389
	Cons. Seq.	**-**	**-**	**S**	**L**	**H**	**-**	**-**
	Cons. Seq. (BXP)	**-**	**-**	**P**	**X**	**B**	**-**	**-**
	-	44	27	4	1	0	38	46
	A	1	1	0	0	0	0	0
	F	2	2	1	0	0	1	0
	H	0	0	0	0	49	0	0
	I	0	0	2	10	0	0	0
	L	1	9	14	33	0	0	0
	M	0	0	1	0	0	1	0
	N	0	0	0	0	0	0	2
	Q	0	2	2	0	0	0	0
	R	0	0	1	0	0	0	1
	S	0	5	22	4	0	0	0
	T	0	0	0	1	0	7	0
	V	0	3	2	0	0	0	0
	Y	1	0	0	0	0	2	0
Com83	Entr.	0.191	1.822	1.890	1.641	0.970		
	Cons. Seq.	**-**	**V**	**V**	**K**	**S**		
	Cons. Seq. (BXP)	**-**	**X**	**X**	**B**	**P**		
	-	33	12	0	0	5		
	F	0	2	0	0	0		
	H	0	0	2	3	0		
	I	0	0	1	2	0		
	K	1	1	13	20	0		
	L	0	0	0	8	1		
	Q	0	0	1	0	1		
	S	0	2	0	0	27		
	T	0	0	1	0	0		
	V	0	16	15	0	0		
	W	0	1	0	1	0		
	Y	0	0	1	0	0		

Com98	Entr.	0.318	1.485	0.159	2.163	1.772	1.435	0.159
	Cons. Seq.	-	-	K	I	T	-	-
	Cons. Seq. (BXP)	-	-	B	X	P	-	-
	-	41	30	0	0	4	30	42
	A	0	0	0	9	12	7	1
	F	0	1	0	0	0	1	0
	H	0	1	0	1	0	0	0
	I	0	0	0	16	0	0	0
	K	0	3	42	1	0	0	0
	M	0	0	0	0	0	1	0
	N	1	6	0	0	0	0	0
	R	0	0	1	0	0	0	0
	S	0	0	0	1	0	0	0
	T	0	0	0	12	22	3	0
	V	1	2	0	0	1	0	0
	Y	0	0	0	3	4	1	0
Com99	Entr.	0.330	1.627	0.000	1.062	1.755	1.368	
	Cons. Seq.	-	-	R	N	T	-	
	Cons. Seq. (BXP)	-	-	B	P	P	-	
	-	39	26	0	0	5	31	
	A	0	0	0	0	0	1	
	H	0	1	0	0	0	0	
	I	0	0	0	0	10	4	
	L	1	1	0	0	0	1	
	M	0	2	0	0	0	0	
	N	0	0	0	29	3	0	
	R	0	3	41	10	0	0	
	T	0	0	0	2	22	1	
	V	1	8	0	0	0	1	
	Y	0	0	0	0	1	2	
Com100	Entr.	0.409	0.082	2.259	2.948	2.322	0.632	
	Cons. Seq.	-	K	V	T	-	-	
	Cons. Seq. (BXP)	-	B	X	P	-	-	
	-	93	0	0	0	45	89	
	A	0	0	2	0	0	0	
	F	1	0	0	4	0	1	
	H	1	1	4	7	1	0	
	I	0	0	1	8	9	2	
	K	0	97	1	1	1	0	
	L	1	0	4	22	17	1	
	M	0	0	0	6	3	0	
	N	0	0	35	0	0	0	
	Q	0	0	0	7	2	0	
	R	0	0	5	1	1	0	
	S	0	0	1	4	0	0	
	T	0	0	5	27	16	4	
	V	0	0	39	11	3	0	
	W	1	0	1	0	0	1	
	Y	1	0	0	0	0	0	
Com113	Entr.	0.281	1.705	1.967	0.330	2.181	0.281	
	Cons. Seq.	-	I	Y	K	T	-	
	Cons. Seq. (BXP)	-	X	X	B	P	-	
	-	39	14	0	0	7	39	
	F	0	1	0	0	0	0	
	H	0	0	2	0	0	0	
	I	2	20	8	0	0	0	
	K	0	0	3	39	1	0	
	M	0	4	10	0	5	0	
	N	0	0	0	1	3	0	
	Q	0	2	0	1	0	0	
	R	0	0	0	0	1	0	
	T	0	0	0	0	21	2	
	V	0	0	0	0	1	0	
	Y	0	0	18	0	2	0	

Com120	Entr.	0.131	2.034	2.388	0.000	0.670	0.625
	Cons. Seq.	-	-	V	R	T	-
	Cons. Seq. (BXP)	-	-	X	B	P	-
	-	54	34	0	0	0	48
	A	0	1	0	0	0	0
	F	0	1	1	0	0	0
	I	0	2	1	0	2	1
	K	0	1	0	0	0	0
	L	0	0	0	0	2	0
	N	0	1	0	0	0	0
	Q	0	0	1	0	0	0
	R	0	0	0	55	0	0
	S	0	6	15	0	0	0
	T	0	5	11	0	49	6
	V	0	2	16	0	0	0
	W	0	0	2	0	0	0
	Y	1	2	8	0	2	0
Com125	Entr.	0.851	1.828	1.788	1.984	1.344	
	Cons. Seq.	-	T	A	R	K	
	Cons. Seq. (BXP)	-	P	X	B	B	
	-	37	5	0	0	17	
	A	2	2	20	7	0	
	F	0	0	0	1	0	
	I	0	0	2	0	0	
	K	1	0	0	14	23	
	L	0	1	0	0	0	
	N	1	12	0	1	0	
	Q	0	0	2	0	0	
	R	0	1	2	18	2	
	S	0	0	1	0	0	
	T	2	22	16	0	1	
	V	0	0	0	1	0	
	W	0	0	0	1	0	
Com161	Entr.	0.709	2.103	1.225	0.618	2.021	0.758
	Cons. Seq.	**-**	**-**	**K**	**V**	**N**	**-**
	Cons. Seq. (BXP)	**-**	**-**	**B**	**X**	**P**	**-**
	-	29	17	0	0	0	30
	F	0	0	0	1	0	0
	I	0	1	1	0	1	1
	K	4	8	22	0	2	1
	L	0	1	0	0	0	0
	N	0	1	0	3	15	0
	Q	0	0	0	0	8	0
	R	1	1	0	0	0	1
	S	0	0	1	0	1	0
	V	0	4	10	30	7	1
	W	0	1	0	0	0	0

Supplementary Table 15. The total number of amino acid sequences found in the **HEPbp BXPA HBS** network expressed as there amino acid type, i.e, **B** (basic), **X** (hydropathic), **P** (polar) and **A** (acidic). Sequences ranging in length between 3 and 7 amino acids with a total degree (Tot deg) greater than one were included the table.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
BXX	95	465	XBXX	39	231	XXPXB	7	9	XXPBPA	2	3	PABXPPA	2	4
XXB	93	478	PXXB	36	290	BXXXX	6	9	XPBAAX	2	4	XXBAXPA	2	3
XBX	85	320	BXXX	34	227	PBPPX	5	20				XXBBXAX	2	5
PXB	84	879	XXXB	31	195	XXBPX	5	6						
BXP	78	405	XBXP	29	181	PBXBB	4	6						
BPX	64	357	BXXP	29	219	BXXPX	4	6						
PBP	58	457	XXBX	26	126	XXXAB	4	7						
PBX	56	256	XXBP	26	157	BXXXA	3	5						
XBP	53	292	BPPX	25	147	BXAXB	3	4						
BBX	46	221	XPPB	25	140	BAXAA	3	8						
XPB	43	167	PXBP	23	250	PXXXB	3	3						
PPB	41	297	XBPX	22	132	PBPXX	3	8						
AXB	38	188	PBXX	21	121	BXXBX	3	6						
XBB	35	139	XXPB	21	97	PXBXP	3	3						
BPP	35	177	BPXX	20	97	XAXXB	3	4						
ABX	32	161	PBPX	20	193	BXPXP	3	3						
BAX	32	149	PBXP	17	169	PXBXX	3	7						
BBP	31	142	PPXB	17	163	BXBXA	3	8						
BXB	31	142	BPXP	17	125	BAXXX	2	3						
XAB	27	109	XXBB	16	109	BXXXP	2	3						
XBA	26	111	AXBX	16	94	PBBPP	2	4						
BAP	25	131	XPXB	16	169	BBPPX	2	7						
PBB	24	93	BXPX	16	96	XXPAB	2	3						
APB	21	121	BBXX	15	116	XXBPP	2	3						
BPB	21	91	BXPA	15	58	BXBXP	2	2						
BXA	20	65	XPBX	15	73	BBXXB	2	4						
ABP	19	85	BXXB	14	98	XXBPB	2	6						
ABB	18	79	BAXX	14	81	AXBXX	2	5						
PAB	17	85	APXB	13	104	XABPX	2	3						
PBA	17	91	XBXA	13	80	BXBAB	2	6						
BBB	16	100	AXXB	13	84	PBXXB	2	2						
BAB	13	66	XXAB	13	85	APPBX	2	2						
BPA	10	30	XXBA	13	72	BBBBB	2	2						
AAB	9	57	BXXA	13	63	XPXXB	2	3						
BAA	9	46	ABXP	13	74	XBXBB	2	3						
BBA	6	18	BPXB	12	101	XBXBP	2	2						
ABA	6	27	BBXP	12	135	XABXX	2	2						
			PPBP	12	124	XABAB	2	3						
			PXPB	12	69	ABBXX	2	2						
			XBBP	11	71	XAPBP	2	2						
			PBXB	11	91	BAXPA	2	6						
			BXPB	11	78	PABPX	2	5						
			BXPP	11	77	BBXXP	2	3						
			PXBX	11	55	PXBPX	2	4						
			BPBX	11	69	PBXAA	2	3						
			XBXB	11	73	XBPXP	2	3						
			PBPP	11	70	XBXXX	2	2						
			XAXB	11	87	XXPBB	2	2						
			PXBB	10	86	PPPBP	2	4						
			ABXX	10	71	PXPBP	2	3						
			XBPP	10	60	PPBPB	2	2						
			BPPP	9	56	XBXXP	2	4						
			BXBP	9	100	XBBXA	2	5						
			AXPB	9	50	XBPPX	2	6						
			BXAX	9	36	PPBPX	2	3						
			BPPA	9	65	XXXBX	2	2						
			XPBB	9	51									
			ABPP	9	44									
			BXBA	9	56									
			PBBP	8	57									
			BAPP	8	59									
			PPPB	8	32									
			BBPX	8	59									
			XPBP	8	53									
			BXBX	8	50									
			XBBX	8	64									
			XAPB	7	41									
			XPAB	7	36									
			BBXB	7	64									

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
			XBAP	7	50									
			XPBA	7	41									
			BPBP	7	40									
			BBBB	7	67									
			XBPB	6	27									
			ABXA	6	36									
			BPPB	6	44									
			BABP	6	46									
			XBAX	6	29									
			PBAB	6	39									
			BXBB	6	44									
			PPBA	6	46									
			PBBB	6	49									
			BPXA	6	33									
			XAAB	6	27									
			AAXB	6	44									
			PPBX	6	31									
			AXBP	6	39									
			APPB	6	52									
			PXBA	6	47									
			BAXP	6	43									
			BAXB	6	49									
			BXAA	6	32									
			XBBB	6	45									
			AXAB	6	32									
			BBAP	6	58									
			BXAP	5	25									
			BXAB	5	39									
			ABPX	5	28									
			BAPX	5	39									
			BPAX	5	28									
			BBPB	5	50									
			XBPA	5	20									
			PXAB	5	36									
			AABP	5	43									
			BAPB	5	63									
			AXBB	5	38									
			ABAX	5	28									
			PBBX	5	38									
			PBXA	5	34									
			XABX	5	21									
			PBAX	5	33									
			XABP	4	24									
			PAXB	4	57									
			PBPB	4	31									
			AXBA	4	24									
			PBPA	4	14									
			BPAP	4	15									
			PABX	4	24									
			XBAA	4	17									
			BPBA	4	24									
			PBBA	4	31									
			BBAB	4	32									
			BBXA	4	14									
			PABB	4	32									
			BBPP	4	24									
			XABA	4	16									
			BAAX	4	32									
			PABP	4	39									
			APBP	4	33									
			BBBX	3	25									
			AABX	3	23									
			AABB	3	19									
			PBAA	3	34									
			BBPA	3	11									
			BBBP	3	21									
			PPBB	3	17									
			ABPB	3	15									
			XABB	3	26									
			BBAX	3	19									
			BAAP	3	16									
			BPBB	3	22									
			ABBX	3	19									
			PAPB	3	12									
			ABXB	3	16									

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
			ABAA	3	15									
			PAAB	3	15									
			APBX	3	14									
			ABBB	3	16									
			PBAP	2	14									
			BAXA	2	10									
			BABB	2	9									
			BBBA	2	8									
			PABA	2	7									
			ABBP	2	14									
			XBAB	2	15									
			ABAP	2	15									
			BPAA	2	12									
			APBB	2	21									
			BBAA	2	13									
			BPAB	2	13									

Supplementary Table 16. The significant communities found in the HEPbp **BXPA** HBS network.

Com2	Entr.	1.302	0.154	2.467	2.380	1.259			
	Cons. Seq.	**-**	**R**	**D**	**S**	**-**			
	Cons. Seq. (BXPA)	**-**	**B**	**A**	**P**	**-**			
	-	32	0	0	3	33			
	A	1	0	0	1	1			
	D	9	0	13	3	0			
	E	0	1	0	0	0			
	H	0	0	7	1	0			
	I	0	0	7	7	1			
	K	0	0	0	0	1			
	L	1	0	0	1	0			
	N	0	0	1	0	0			
	R	1	44	0	0	0			
	S	1	0	10	22	8			
	T	0	0	6	3	0			
	V	0	0	1	0	0			
	Y	0	0	0	4	1			
Com7	Entr.	0.051	0.845	2.305	0.373	2.928	3.409	2.177	0.446
	Cons. Seq.	**-**	**-**	**-**	**R**	**S**	**-**	**-**	**-**
	Cons. Seq. (BXPA)	**-**	**-**	**-**	**B**	**P**	**-**	**-**	**-**
	-	173	153	104	0	10	39	106	163
	A	0	4	2	0	20	18	2	0
	D	0	1	0	0	3	6	1	0
	E	0	0	2	0	1	8	2	0
	F	0	1	1	0	4	8	9	0
	H	0	0	4	0	0	0	1	0
	I	0	2	3	0	0	0	0	0
	K	0	1	1	2	26	8	5	1
	L	0	0	8	0	8	8	5	0
	M	0	0	3	0	0	2	1	0
	N	0	0	3	1	2	6	1	0
	Q	0	0	1	1	4	4	1	0
	R	0	1	0	166	10	18	20	4
	S	0	7	16	2	68	34	13	5
	T	0	0	11	0	2	7	3	1
	V	0	4	5	2	12	4	0	0
	W	0	0	0	0	1	0	0	0
	Y	1	0	10	0	3	4	4	0
Com8	Entr.	1.619	3.019	2.866	2.375	0.487			
	Cons. Seq.	**K**	**N**	**E**	**E**	**-**			
	Cons. Seq. (BXPA)	**B**	**P**	**A**	**A**	**-**			
	-	0	0	0	26	69			
	A	1	12	3	0	0			
	D	0	6	4	0	0			
	E	6	14	24	27	2			
	F	0	0	0	1	0			
	H	13	3	1	0	0			
	I	0	2	0	0	1			
	K	48	10	4	0	0			
	L	4	6	3	2	0			
	M	0	0	0	2	0			
	N	0	16	0	0	1			
	Q	0	1	10	3	0			
	R	1	3	8	5	1			
	S	0	1	5	1	0			
	T	0	0	12	3	0			
	V	1	0	0	4	0			

Com9	Entr.	0.349	2.949	3.643	3.267	1.584	0.409	0.256
	Cons. Seq.	**-**	**-**	**S**	**L**	**R**	**-**	**-**
	Cons. Seq. (BXPA)	**-**	**-**	**P**	**X**	**B**	**-**	**-**
	-	197	93	3	3	0	196	200
	A	1	5	17	10	2	0	0
	D	0	0	7	1	0	0	0
	E	0	16	24	11	9	3	1
	F	1	8	8	5	0	2	0
	H	0	3	2	4	2	0	0
	I	0	2	3	2	0	0	0
	K	0	8	6	8	14	1	1
	L	1	15	20	54	1	1	1
	M	0	2	3	0	0	0	0
	N	0	3	11	3	11	0	1
	Q	0	2	0	6	1	1	0
	R	0	13	29	44	152	1	0
	S	4	12	31	20	4	0	2
	T	0	15	21	3	4	0	0
	V	2	6	14	5	6	1	0
	W	0	0	5	3	0	0	0
	Y	0	3	2	24	0	0	0
Com10	Entr.	0.656	2.408	2.744	0.892	2.804	0.746	0.091
	Cons. Seq.	**-**	**-**	**R**	**V**	**S**	**-**	**-**
	Cons. Seq. (BXPA)	**-**	**-**	**B**	**X**	**P**	**-**	**-**
	-	78	32	0	0	13	77	85
	A	0	1	0	3	4	0	0
	D	0	1	2	0	0	0	0
	E	2	1	2	0	0	2	0
	F	0	0	4	0	0	0	0
	H	0	3	9	0	0	0	0
	I	2	2	1	0	0	0	0
	K	0	7	19	1	3	0	0
	L	1	2	2	2	7	1	0
	M	0	0	0	1	0	0	0
	N	0	2	1	0	16	0	0
	Q	0	0	0	0	1	0	0
	R	2	30	29	1	1	2	1
	S	0	1	0	0	26	1	0
	T	1	4	8	2	5	0	0
	V	0	0	9	75	10	2	0
	W	0	0	0	1	0	0	0
	Y	0	0	0	0	0	1	0
Com11	Entr.	0.286	2.412	3.085	2.778	2.562		
	Cons. Seq.	**-**	**-**	**S**	**K**	**K**		
	Cons. Seq. (BXPA)	**-**	**-**	**P**	**B**	**B**		
	-	103	46	0	0	0		
	A	0	4	6	5	1		
	D	0	0	3	13	21		
	E	0	1	7	14	20		
	F	0	0	2	8	0		
	H	0	0	1	1	0		
	I	0	3	7	5	12		
	K	1	2	8	37	35		
	L	1	5	8	0	0		
	M	0	0	2	0	0		
	N	0	1	2	1	4		
	Q	0	0	0	1	0		
	R	0	5	15	19	1		
	S	2	30	38	2	0		
	T	0	8	7	1	10		
	V	0	1	1	0	3		
	Y	0	1	0	0	0		

Com13	Entr.	0.164	2.644	2.537	3.028	0.411	0.606
	Cons. Seq.	**-**	**-**	**A**	**V**	**K**	**-**
	Cons. Seq. (BXPA)	**-**	**-**	**X**	**X**	**B**	**-**
	-	81	34	0	0	3	76
	A	2	11	30	19	0	1
	D	0	5	5	1	0	0
	E	0	12	20	3	1	0
	F	0	1	0	1	0	2
	I	0	1	12	7	0	0
	K	0	6	1	2	78	0
	L	0	0	0	4	0	0
	M	0	0	0	7	0	0
	N	0	0	6	5	0	0
	Q	0	9	3	0	0	0
	R	0	1	0	3	0	0
	S	0	1	2	0	0	2
	T	0	1	0	9	0	1
	V	0	1	4	22	1	1
Com21	Entr.	2.647	1.731	2.732	2.063	0.424	
	Cons. Seq.	**K**	**K**	**K**	**S**	**-**	
	Cons. Seq. (BXPA)	**B**	**B**	**B**	**P**	**-**	
	-	13	0	0	11	53	
	A	1	2	5	0	1	
	D	7	4	2	1	0	
	E	6	0	0	0	0	
	F	1	3	5	4	0	
	I	12	5	1	1	0	
	K	14	38	23	7	0	
	L	0	1	1	0	0	
	N	0	0	4	1	0	
	Q	1	0	1	0	0	
	R	0	0	1	0	0	
	S	0	0	6	30	3	
	T	0	4	8	2	0	
	V	2	0	0	0	0	
Com26	Entr.	2.212	0.834	2.822	2.544	0.505	
	Cons. Seq.	**S**	**K**	**L**	**-**	**-**	
	Cons. Seq. (BXPA)	**P**	**B**	**X**	**-**	**-**	
	-	2	0	0	19	50	
	A	12	0	1	1	0	
	D	0	0	1	1	0	
	E	0	1	2	5	0	
	F	9	1	3	0	0	
	H	0	1	1	0	0	
	I	1	0	0	0	0	
	K	0	48	5	1	0	
	L	0	0	23	9	1	
	Q	0	0	5	8	0	
	R	0	0	1	1	0	
	S	17	2	8	10	4	
	T	0	0	1	0	0	
	V	14	2	0	0	0	
	W	0	0	1	0	0	
	Y	0	0	3	0	0	
Com30	Entr.	0.758	2.974	2.540	2.562	0.262	
	Cons. Seq.	**K**	**A**	**L**	**-**	**-**	
	Cons. Seq. (BXPA)	**B**	**X**	**X**	**-**	**-**	
	-	0	0	0	15	43	
	A	0	11	3	1	0	
	D	0	7	3	0	0	
	E	2	0	2	5	0	
	F	0	5	1	0	0	
	H	0	0	1	0	0	
	I	5	2	0	0	0	
	K	38	8	0	2	0	
	L	0	4	16	7	0	
	M	0	0	1	0	0	
	N	0	1	0	0	0	
	Q	0	1	0	0	0	
	S	0	0	2	2	0	
	T	0	0	14	10	2	
	V	0	4	2	0	0	
	W	0	2	0	0	0	
	Y	0	0	0	3	0	

Com37	Entr.	3.139	2.555	1.994	1.958	0.480		
	Cons. Seq.	**S**	**R**	**R**	**-**	**-**		
	Cons. Seq. (BXPA)	**P**	**B**	**B**	**-**	**-**		
	-	3	0	0	36	63		
	D	0	1	0	0	0		
	E	1	0	1	1	0		
	F	2	0	0	0	0		
	I	9	8	0	0	1		
	K	4	0	3	1	0		
	L	0	1	0	0	0		
	N	8	0	0	0	0		
	Q	4	4	7	4	0		
	R	2	28	33	2	1		
	S	20	8	0	0	0		
	T	3	5	19	19	3		
	V	8	10	2	2	0		
	W	0	0	0	1	0		
	Y	4	3	3	2	0		
Com43	Entr.	0.341	2.494	2.061	2.500	2.034		
	Cons. Seq.	**-**	**-**	**K**	**K**	**L**		
	Cons. Seq. (BXPA)	**-**	**-**	**B**	**B**	**X**		
	-	55	23	0	0	0		
	A	0	1	2	0	1		
	D	0	0	1	1	0		
	E	0	9	3	0	0		
	F	1	0	0	2	5		
	H	0	0	0	1	0		
	I	0	0	0	1	1		
	K	0	6	33	20	1		
	L	0	2	0	3	32		
	M	0	1	1	0	0		
	N	0	1	1	6	7		
	Q	0	0	2	0	0		
	S	0	0	2	12	2		
	T	2	12	12	12	9		
	W	0	2	1	0	0		
	Y	0	1	0	0	0		
Com47	Entr.	0.181	1.022	2.977	0.000	2.338	2.280	0.919
	Cons. Seq.	**-**	**-**	**-**	**R**	**L**	**-**	**-**
	Cons. Seq. (BXPA)	**-**	**-**	**-**	**B**	**X**	**-**	**-**
	-	71	61	20	0	0	24	62
	A	0	3	14	0	19	4	2
	D	2	2	4	0	1	0	0
	E	0	0	0	0	0	1	0
	F	0	0	1	0	7	14	5
	I	0	0	1	0	0	1	0
	K	0	0	0	0	1	0	0
	L	0	2	10	0	29	24	2
	N	0	0	1	0	0	2	1
	Q	0	0	1	0	10	0	0
	R	0	0	0	73	1	0	0
	S	0	0	3	0	2	0	0
	T	0	2	9	0	3	2	1
	V	0	3	6	0	0	0	0
	W	0	0	0	0	0	1	0
	Y	0	0	3	0	0	0	0
Com49	Entr.	0.453	2.783	2.337	2.321	2.115		
	Cons. Seq.	**-**	**N**	**K**	**K**	**-**		
	Cons. Seq. (BXPA)	**-**	**P**	**B**	**B**	**-**		
	-	91	0	0	0	37		
	A	2	8	0	0	0		
	D	0	2	0	3	4		
	E	1	6	8	6	0		
	F	0	1	1	1	0		
	H	0	0	0	1	0		
	I	0	2	2	0	0		
	K	1	6	41	48	36		
	L	0	27	24	4	0		
	N	2	30	2	0	0		
	Q	0	0	0	10	4		
	R	0	8	12	19	5		
	S	0	1	0	1	1		
	T	0	0	0	3	9		
	V	0	5	4	1	1		
	Y	0	1	3	0	0		

Supplementary Table 17. The total number of amino acid sequences found in the **HEPbp BXPS HBS** network expressed as there amino acid type, i.e, **B** (basic), **X** (hydropathic), **P** (polar) and **S** (special). Sequences ranging in length between 3 and 7 amino acids with a total degree (Tot deg) greater than one were included the table.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
XXB	48	201	*XXXB*	21	78	*BSPBS*	8	48	*SSXBSS*	2	4	*SXSSSBS*	5	69
XBX	32	131	*SXBS*	19	229	*XSSBS*	7	93				*SXBSXSS*	3	14
BXX	28	99	*XBXX*	19	92	*BSXSS*	6	39				*SXSSXBS*	3	33
BXB	25	115	*XXBX*	16	76	*XXBXX*	6	12				*SPSSXBS*	2	19
BXP	24	85	*XPBX*	15	51	*SSSBS*	5	72						
BXS	22	96	*XBXP*	14	52	*BSXXS*	4	12						
PXB	22	72	*BXXP*	13	60	*PSSBS*	4	54						
XBP	21	96	*SBXX*	12	63	*BSXBS*	4	51						
SBS	19	167	*BXPX*	12	53	*XSXBS*	4	30						
XPB	19	57	*BXXX*	12	44	*SPSSB*	4	24						
SBX	18	70	*BPPX*	11	47	*XSBSS*	4	17						
SSB	16	51	*BXXB*	11	60	*XXSSB*	4	6						
BSX	16	47	*SXBX*	11	50	*XBXXX*	4	6						
BPX	15	55	*BXBX*	11	57	*SBSXS*	3	9						
BPP	14	57	*SPXB*	10	64	*SBPSX*	3	10						
XSB	13	40	*BXXS*	10	36	*BSBBS*	3	18						
BSS	13	47	*XBXB*	10	62	*SSXBS*	3	29						
XBS	13	50	*PBXS*	10	27	*BXXPB*	2	2						
XBB	13	53	*SBXB*	9	82	*BPBXX*	2	2						
SPB	12	57	*BPXP*	9	49	*XBXPS*	2	3						
PBX	12	35	*XXBP*	9	41	*XXPBX*	2	6						
SXB	11	32	*BXBS*	9	59	*XPBXX*	2	2						
BBX	11	22	*XXPB*	9	39	*XXXXB*	2	3						
PSB	9	31	*XXBB*	9	47	*XBPSX*	2	3						
BBB	9	35	*SXXB*	9	38	*SBXSX*	2	5						
BSP	9	19	*SBXS*	8	71	*BSSBS*	2	30						
PBS	9	57	*SBPS*	8	80	*SXSSB*	2	6						
PPB	9	18	*XPSB*	8	36	*BSSPS*	2	8						
BPS	8	19	*PXXB*	8	56	*BSSSS*	2	12						
BBS	8	19	*PBXX*	7	29	*BXXBP*	2	4						
BPB	7	20	*XXBS*	7	24	*XXPSB*	2	3						
PBP	7	23	*SPBS*	7	110	*BXBPX*	2	3						
SBB	6	20	*SSBS*	7	67	*SPBXX*	2	2						
BSB	4	8	*XBSS*	7	30	*BPPXX*	2	4						
SBP	4	29	*XXSB*	7	20	*XBXBP*	2	2						
PBB	3	8	*PXBX*	7	28									
BBP	3	11	*XSXB*	7	19									
			SBPP	6	56									
			BXPS	6	28									
			BXPB	6	33									
			XBPS	6	14									
			XPXB	6	23									
			BXBP	6	58									
			PPXB	6	27									
			BPXX	6	21									
			SPSB	5	40									
			SBPX	5	24									
			BPBS	5	24									
			PBXB	5	33									
			BXSB	5	28									
			PXBS	5	15									
			XPBB	5	24									
			BSXS	4	17									
			PBPP	4	9									
			SBSS	4	32									
			BBXS	4	15									
			SSPB	4	11									
			XSSB	4	18									
			BSXP	4	11									
			XBPX	4	28									
			SPPB	4	17									
			SXPB	4	11									
			SPBX	4	7									
			XPBP	4	19									
			BXSX	4	12									
			XBXS	4	20									
			SBXP	4	22									
			XBBX	4	15									
			BPXB	3	20									

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
			XSBB	3	12									
			BPPB	3	11									
			XBSP	3	20									
			XBSX	3	17									
			BSSX	3	12									
			PBSP	3	20									
			BXPP	3	18									
			BPPP	3	12									
			BPBP	3	8									
			PBXP	3	12									
			PXBP	3	7									
			PPSB	3	9									
			XBBB	3	17									
			SBBS	3	50									
			BSPS	3	12									
			BBBX	3	14									
			XBPP	3	13									
			PXPB	3	14									
			BXSS	3	7									
			SBSX	3	27									
			PPBB	3	5									
			PBSX	3	10									
			BSXX	3	16									
			BSPB	3	9									
			SXBP	2	13									
			XPBS	2	7									
			PSXB	2	7									
			BBSS	2	11									
			PBPX	2	9									
			PPBP	2	5									
			XSBP	2	4									
			PPBX	2	5									
			SBBX	2	7									
			BPSB	2	7									
			BPSP	2	10									
			BSPX	2	8									
			BBPX	2	10									
			BPXS	2	10									
			SPBP	2	5									
			BPPS	2	6									
			SXSB	2	9									
			XSBS	2	8									
			SPBB	2	7									
			XSBX	2	10									
			PBPS	2	12									
			PBBB	2	8									
			PSBP	2	13									
			BPBB	2	8									
			SSXB	2	8									
			PSBS	2	6									
			PBSS	2	7									
			PSSB	2	7									
			XBBP	2	13									
			XBSB	2	6									
			BBBB	2	11									
			SBSB	2	9									
			XBPB	2	21									
			BSBX	2	5									
			PXBB	2	6									
			BBXP	2	9									
			SBPB	2	8									
			PPPB	2	5									
			BSBB	2	4									

Supplementary Table 18. The significant communities found in the HEPbp **BXPS** HBS network.

Com5	Entr.	1.295	0.989	2.682	2.344	0.127	2.212	1.273	0.127	0.831	0.554	0.485
	Cons. Seq.	-	**G**	-	**P**	**G**	**P**	**K**	**G**	-	-	-
	Cons. Seq. (BXPS)	-	**S**	-	**S**	**S**	**S**	**B**	**S**	-	-	-
	-	45	25	25	0	0	1	0	1	49	51	51
	A	2	0	4	7	0	2	2	0	1	1	0
	F	0	0	5	1	0	3	0	0	0	0	0
	G	1	32	1	1	56	2	0	56	0	0	6
	H	0	0	0	0	0	1	0	0	0	0	0
	I	1	0	4	0	0	1	0	0	0	0	0
	K	0	0	0	2	0	1	40	0	0	5	0
	L	0	0	3	1	0	2	0	0	2	0	0
	M	0	0	0	2	0	0	0	0	0	0	0
	N	0	0	0	1	0	1	0	0	0	0	0
	P	3	0	7	33	0	36	0	0	4	0	0
	Q	0	0	2	1	0	0	2	0	0	0	0
	R	3	0	0	2	1	0	12	0	0	0	0
	S	0	0	3	2	0	3	0	0	1	0	0
	T	1	0	0	1	0	1	1	0	0	0	0
	V	1	0	3	3	0	3	0	0	0	0	0
Com13	Entr.	1.130	2.360	2.113	1.795	2.095	0.323					
	Cons. Seq.	-	-	**L**	**G**	**R**	-					
	Cons. Seq. (BXPS)	-	-	**X**	**S**	**B**	-					
	-	20	10	1	2	9	32					
	A	0	2	2	0	0	0					
	F	0	0	1	0	0	0					
	G	0	8	1	20	7	0					
	H	0	0	0	1	0	0					
	I	0	0	0	0	1	0					
	L	0	3	13	4	0	2					
	P	1	3	4	6	6	0					
	R	13	8	12	0	11	0					
	W	0	0	0	1	0	0					
Com16	Entr.	0.101	0.101	1.623	0.891	2.815	2.021	1.468				
	Cons. Seq.	-	-	-	**G**	**K**	**K**	**G**				
	Cons. Seq. (BXPS)	-	-	-	**S**	**B**	**B**	**S**				
	-	75	75	50	10	0	0	9				
	A	0	1	7	0	18	1	1				
	C	0	0	0	0	0	1	0				
	F	0	0	0	0	2	0	1				
	G	1	0	0	62	6	3	54				
	K	0	0	11	0	21	45	8				
	L	0	0	0	0	1	0	0				
	M	0	0	0	0	0	1	1				
	N	0	0	1	0	2	2	0				
	P	0	0	5	1	3	15	0				
	Q	0	0	0	0	4	1	1				
	R	0	0	0	0	4	0	0				
	S	0	0	0	0	0	3	1				
	T	0	0	1	3	14	2	0				
	V	0	0	1	0	1	2	0				
Com17	Entr.	1.758	1.878	2.881	2.346	0.612						
	Cons. Seq.	**K**	**V**	**L**	-	-						
	Cons. Seq. (BXPS)	**B**	**X**	**X**	-	-						
	-	0	0	0	13	28						
	A	1	4	4	3	0						
	G	5	0	0	0	0						
	H	0	0	3	0	0						
	K	19	8	5	2	1						
	L	0	0	7	8	1						
	M	1	0	1	0	0						
	N	0	3	1	1	0						
	S	0	0	1	1	0						
	T	3	0	3	2	0						
	V	2	15	6	1	0						
	W	0	0	0	0	1						
	Y	0	1	0	0	0						

Com18	Entr.	0.063	0.189	1.623	2.264	2.076	2.844	2.477
	Cons. Seq.	**-**	**-**	**-**	**K**	**L**	**K**	**-**
	Cons. Seq. (BXPS)	**-**	**-**	**-**	**B**	**X**	**B**	**-**
	-	134	132	98	16	0	2	72
	A	0	0	2	5	8	8	4
	C	0	0	1	2	0	0	4
	F	0	0	1	1	2	2	1
	G	0	1	4	5	0	0	0
	H	0	0	0	0	0	3	0
	I	0	0	0	0	1	6	3
	K	0	1	2	80	5	59	12
	L	1	0	16	4	83	18	7
	M	0	0	2	1	3	0	0
	N	0	0	0	0	2	1	0
	P	0	1	0	1	16	4	13
	Q	0	0	1	1	5	5	6
	R	0	0	4	5	0	9	4
	S	0	0	1	7	8	10	7
	T	0	0	1	6	2	7	2
	W	0	0	0	0	0	1	0
	Y	0	0	2	1	0	0	0

Com27	Entr.	1.145	1.839	1.773	0.000	1.197	0.242
	Cons. Seq.	**-**	**L**	**L**	**R**	**L**	**-**
	Cons. Seq. (BXPS)	**-**	**X**	**X**	**B**	**X**	**-**
	-	19	2	0	0	11	24
	A	0	0	1	0	0	0
	F	0	0	3	0	0	0
	H	0	1	0	0	1	0
	K	0	0	0	0	0	1
	L	3	15	12	0	13	0
	N	0	0	1	0	0	0
	Q	2	3	0	0	0	0
	R	0	0	0	25	0	0
	S	0	1	8	0	0	0
	V	1	3	0	0	0	0

Com30	Entr.	1.701	2.343	0.402	0.795
	Cons. Seq.	**C**	**I**	**F**	**K**
	Cons. Seq. (BXPS)	**S**	**X**	**X**	**B**
	-	6	0	0	0
	C	14	0	0	0
	F	0	0	23	0
	I	3	8	0	0
	K	1	6	0	19
	N	0	4	2	0
	R	1	4	0	6
	T	0	1	0	0
	V	0	2	0	0

Com49	Entr.	0.391	1.040	1.843	2.862	1.791
	Cons. Seq.	**-**	**G**	**R**	**S**	**-**
	Cons. Seq. (BXPS)	**-**	**S**	**B**	**P**	**-**
	-	36	0	0	1	19
	G	0	31	0	6	6
	K	0	4	8	1	0
	L	0	0	0	1	0
	M	0	2	4	0	0
	N	0	0	0	2	0
	P	0	0	2	1	0
	Q	0	0	0	4	11
	R	0	0	21	8	0
	S	3	2	4	12	2
	T	0	0	0	2	0
	W	0	0	0	1	0
	Y	0	0	0	0	1

Com60	Entr.	0.455	0.827	3.324	2.070	0.968
	Cons. Seq.	**G**	**R**	**C**	**C**	**-**
	Cons. Seq. (BXPS)	**S**	**B**	**S**	**S**	**-**
	-	1	0	2	4	21
	A	0	0	3	0	0
	C	0	0	5	10	2
	G	25	1	0	0	0
	I	0	0	3	0	0
	K	0	1	0	0	0
	L	1	0	2	5	0
	P	0	2	1	0	0
	Q	0	0	2	0	0
	R	0	23	3	0	0
	T	0	0	2	1	0
	V	0	0	3	7	4
	Y	0	0	1	0	0

Supplementary Table 19. The total number of amino acid sequences found in the **HEPbp BXAS HBS** network expressed as there amino acid type, i.e, **B** (basic), **X** (hydropathic), **A** (acidic) and **S** (Special). Sequences ranging in length between 3 and 7 amino acids with a total degree (Tot deg) greater than one were included the table.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
XBX	237	2005	*XBXX*	87	1113	*BXXXX*	21	64	*XASXBS*	2	3	*ABSAXXS*	3	13
XXB	213	2035	*XXXB*	81	932	*XXBXX*	16	42	*AXBBXX*	2	3	*XXBASAX*	2	2
BXX	188	1456	*BXXX*	80	779	*XBXXX*	12	29	*BBBBBB*	2	4	*XXXXBXX*	2	4
XBS	106	852	*XXBX*	61	580	*SBXXX*	11	28	*BXBXAX*	2	4	*BXXBXSB*	2	4
SBX	101	960	*XBAX*	48	664	*SBXXS*	11	29	*SSSBSX*	2	4	*AXXABXX*	2	4
BSX	89	605	*SXBX*	44	471	*XBXXB*	10	30	*SBBSBS*	2	4	*XXXXBBX*	2	8
SXB	74	602	*SBXX*	43	648	*BXXBX*	10	25	*BSBXXS*	2	4	*XBXBXXB*	2	4
XSB	73	586	*XAXB*	37	387	*XXBAX*	10	25				*BBSBXXS*	2	8
BXS	72	444	*XXBS*	35	400	*XSBXX*	10	20				*SSBSABS*	2	14
AXB	69	587	*SXXB*	35	427	*XBBXX*	9	25				*SXSSBSS*	2	10
BBX	66	396	*XBSX*	35	416	*XXABX*	9	18				*SXBSABS*	2	10
SBS	64	757	*BXBX*	33	487	*XXXXB*	9	19				*SXBSXSS*	2	11
XBA	63	528	*XBBX*	33	395	*XXBBX*	9	18				*BXXXXXX*	2	3
XBB	61	406	*ABXX*	32	350	*SSBSX*	8	38						
BXB	59	327	*XSBX*	31	289	*SXBSX*	7	19						
XAB	57	450	*XXSB*	30	373	*AXBXX*	7	16						
BXA	51	364	*XXAB*	30	322	*XBXAX*	7	14						
BAX	49	541	*XBXB*	29	374	*SBSXS*	7	32						
BSS	45	421	*AXXB*	28	318	*XSXBX*	6	10						
ABX	43	370	*BXXB*	27	316	*BSABS*	6	30						
SSB	38	486	*SBSX*	26	596	*XBXXA*	6	13						
ASB	34	332	*AXBX*	26	282	*BXXXS*	6	8						
BBS	34	236	*BXXA*	26	340	*AXXBX*	6	17						
SBA	32	263	*XXBB*	26	235	*XBSXS*	6	17						
SAB	32	250	*XBXS*	26	243	*XXBSX*	6	8						
BSA	31	222	*SSXB*	26	271	*BXSSX*	5	6						
BBB	29	258	*BXXS*	25	202	*BXXAX*	5	10						
BSB	28	195	*XXBA*	25	253	*XBSXA*	5	18						
ABS	28	184	*BSXX*	24	165	*XBAXS*	5	10						
SBB	27	198	*BXSX*	24	198	*XXAXB*	5	9						
BBA	25	222	*BXAX*	24	268	*SSBSA*	5	36						
BAB	24	182	*SXSB*	23	340	*SABSA*	5	24						
BAS	23	168	*SBSS*	22	351	*XXXBS*	5	7						
AAB	19	174	*BSXS*	22	197	*SBAXX*	5	12						
ABA	18	137	*SXBS*	22	306	*XXBXB*	5	9						
BAA	17	114	*BXSS*	21	168	*SXBSA*	5	20						
ABB	12	69	*XSXB*	21	203	*SXBXX*	5	12						
			BBXX	19	189	*XBXBX*	5	9						
			BAXX	19	203	*XBAXX*	5	11						
			SBXS	18	214	*AXBBX*	5	16						
			SSBS	18	350	*XBAAX*	5	10						
			XBXA	18	198	*SBSSX*	5	18						
			SBBX	17	266	*SXABS*	4	8						
			XABX	16	209	*XSXSB*	4	8						
			AXSB	16	197	*SXSXB*	4	6						
			SAXB	15	152	*BXBSX*	4	7						
			SABX	14	181	*SXBSS*	4	15						
			XBSA	14	148	*XSSBX*	4	7						
			SSBX	13	108	*XBXSA*	4	6						
			XSBB	13	146	*BXXXB*	4	10						
			XSBS	13	155	*BSXXX*	4	5						
			BXBB	13	142	*BXAXX*	4	5						
			SBXA	13	175	*SSBXS*	4	9						
			BSSX	12	108	*XABXX*	4	9						
			AAXB	12	166	*SBBXX*	4	9						
			SSSB	12	242	*SBXSB*	4	6						
			BBXS	11	130	*XSBBX*	4	7						
			XBBS	11	155	*XXXBB*	4	8						
			XSSB	11	103	*SSXBX*	4	7						
			AXBS	11	159	*SBSXX*	4	7						
			BSXB	11	121	*BSXBX*	4	8						
			BSBX	11	158	*XXXAB*	4	8						
			XBSS	11	144	*SBXSX*	4	7						
			SBAX	10	196	*XBXAS*	4	4						
			BBBB	10	92	*XXXBX*	4	7						
			XABA	10	104	*XAXXB*	3	3						
			SASB	10	105	*SXXXB*	3	3						
			XASB	10	104	*XXBAS*	3	6						
			SBSA	9	160	*XBSBB*	3	7						

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
			BBSX	9	98	*XAXBX*	3	5						
			XBSB	9	117	*BSBXX*	3	8						
			AXBA	9	105	*XBXBS*	3	3						
			BABX	9	141	*BXASS*	3	4						
			BAAX	9	99	*XAXSB*	3	4						
			AXBB	9	157	*SXSBX*	3	4						
			BBXB	9	131	*XXXBA*	3	4						
			SBAS	8	95	*BXAXS*	3	4						
			XBAS	8	88	*BXXSB*	3	9						
			SBSB	8	112	*XSBSS*	3	4						
			XSAB	8	92	*BSXXS*	3	5						
			BXBS	8	86	*XXBSB*	3	7						
			BAXB	8	134	*BABXX*	3	6						
			ABXB	8	90	*SXBSB*	3	8						
			XABB	8	68	*SXBBX*	3	5						
			BSXA	8	72	*XBBSA*	3	8						
			ABSX	8	67	*BXBSS*	3	8						
			AABX	7	45	*SSSBS*	3	20						
			SXBB	7	72	*SSBSS*	3	17						
			SBBS	7	148	*BXBSA*	3	6						
			BABS	7	86	*XSXXB*	3	5						
			BBSS	7	106	*SASSB*	3	8						
			BBAX	7	81	*SXXSB*	3	5						
			BXAB	7	54	*BXBXX*	3	5						
			BSAX	7	106	*XBXXS*	3	8						
			ASBX	7	61	*BBBXB*	3	7						
			ABXA	7	60	*BXXSS*	3	4						
			XBAB	7	114	*BSASX*	3	3						
			BAXA	7	64	*SBBSA*	3	7						
			XAAB	6	95	*SSXSB*	3	3						
			BBXA	6	67	*XXSXB*	3	5						
			BBBX	6	58	*XAXBA*	3	8						
			SAAB	6	73	*XBAXB*	3	8						
			SBAB	6	80	*XASXB*	3	5						
			ABAB	6	80	*XXBSA*	3	5						
			BSSS	6	65	*XBSAX*	3	9						
			AXAB	6	73	*XBSBS*	3	5						
			AAAB	6	106	*BBAXX*	3	6						
			ABAS	6	65	*BSSSS*	3	14						
			XBBA	6	70	*ABASX*	3	9						
			BXSA	6	62	*SXXBX*	3	4						
			ASXB	6	68	*XXABS*	3	6						
			BXSB	6	42	*BASXX*	3	4						
			ABAX	6	79	*XXBSS*	3	9						
			SBBA	6	82	*SSSXB*	3	4						
			XBAA	6	31	*BBXAS*	2	2						
			BXBA	6	71	*BBBBX*	2	3						
			BSAB	6	86	*XBSXX*	2	2						
			ASBS	6	51	*XXSBB*	2	2						
			XBBB	6	61	*AXXBB*	2	4						
			ABBX	5	43	*XXSBX*	2	3						
			BBAS	5	62	*XSBSX*	2	4						
			BSBB	5	87	*SBSSS*	2	4						
			BXAS	5	45	*SAXSB*	2	8						
			ABXS	5	76	*XAXBS*	2	3						
			XABS	5	54	*ABXAX*	2	6						
			BSBA	5	39	*XASBX*	2	3						
			BBSB	5	49	*AXXSB*	2	2						
			BSSB	5	67	*ABSBX*	2	4						
			SBBB	5	49	*XXABB*	2	4						
			BBBA	5	64	*BBSSB*	2	6						
			SBXB	5	43	*SBXBX*	2	2						
			BAXS	5	40	*BABSX*	2	4						
			BSAS	4	33	*SBASX*	2	2						
			BBAB	4	36	*SAABS*	2	5						
			SSBB	4	62	*XBSXB*	2	2						
			BASB	4	59	*AXXBA*	2	4						
			SABS	4	64	*XXXSB*	2	5						
			AASB	4	66	*XXBBA*	2	6						
			SABA	4	49	*BSXSX*	2	2						
			SXAB	4	58	*BXSAA*	2	2						
			ABBS	4	56	*BASBX*	2	5						
			SSAB	4	31	*ASBXS*	2	4						
			BAAS	3	14	*AXABB*	2	3						
			BBBS	3	42	*XSBXB*	2	4						

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Cont.

3 aa seq	no	Tot deg	4 aa seq	no	Tot deg	5 aa seq	no	Tot deg	6 aa seq	no	Tot deg	7 aa seq	no	Tot deg
			BABB	3	34	*BBSAX*	2	2						
			XSBA	3	26	*BBXXB*	2	10						
			BASX	3	27	*BXBBX*	2	4						
			BSSA	3	24	*SASBX*	2	2						
			AABB	3	39	*XASBS*	2	3						
			BASA	3	36	*XSBAX*	2	5						
			ABSB	3	36	*SXBXB*	2	5						
			BSBS	3	31	*AAXXB*	2	5						
			SXBA	3	51	*XXBXA*	2	4						
			BXAA	3	23	*ASXBS*	2	10						
			ASAB	2	21	*AXBAB*	2	4						
			ABBB	**2**	**24**	*SAAXB*	**2**	**3**						
			BASS	**2**	**20**	*SXAAB*	**2**	**4**						
			AABA	**2**	**17**	*SSBAB*	**2**	**4**						
			BAAA	**2**	**21**	*SSSSB*	**2**	**5**						
			SABB	2	16	*BSASS*	2	10						
			ABSS	2	20	*BXSSS*	2	15						
			ASSB	2	12	*XSBSA*	2	4						
			SBAA	2	16	*XBBXA*	2	3						
						BBXSX	2	6						
						ASSXB	2	3						
						BXXXA	2	3						
						BXBXS	2	3						
						XASBB	2	2						
						BXBBB	2	2						
						ABXXX	2	2						
						ASBXX	2	3						
						BBBXX	2	5						
						BXSSA	2	2						
						SSXXB	2	2						
						XBASX	2	4						
						BXXAS	2	3						
						XSAXB	2	8						
						XBBXS	2	3						
						BAXXA	2	3						
						SSBXX	2	7						
						XBXSS	2	2						
						BSBXS	2	5						
						XBAXA	2	2						

Supplementary Table 20. The significant communities found in the HEPbp **BXAS** HBS network.

Com1	Entr.	0.020	0.282	1.784	3.059	1.129	3.671	2.570	1.099	
	Cons. Seq.	-	-	-	**G**	**R**	**R**	-	-	
	Cons. Seq. (BXAS)	-	-	-	**S**	**B**	**B**	-	-	
	-	513	498	363	66	0	30	274	440	
	A	0	1	4	4	2	22	10	4	
	C	0	0	2	15	4	73	16	7	
	D	0	1	3	6	9	11	24	9	
	E	0	1	2	18	7	15	16	4	
	F	0	2	7	24	3	21	8	2	
	G	0	7	46	195	2	71	66	14	
	H	0	0	2	4	6	10	5	1	
	I	0	1	8	9	4	47	15	1	
	K	0	0	8	17	10	18	2	1	
	L	0	0	5	5	1	17	12	2	
	M	0	0	1	4	0	6	0	1	
	P	0	1	22	51	30	44	10	12	
	R	1	1	32	37	431	78	21	6	
	V	0	1	4	7	1	38	30	6	
	W	0	0	2	3	0	6	3	1	
	Y	0	0	3	49	4	7	2	3	
Com2	Entr.	0.296	1.222	2.442	2.463	1.946	1.209	0.342		
	Cons. Seq.	-	-	-	**K**	**P**	**C**	-		
	Cons. Seq. (BXAS)	-	-	-	**B**	**S**	**S**	-		
	-	45	36	18	2	0	15	44		
	A	0	1	0	0	0	0	0		
	C	0	1	2	9	0	29	0		
	D	0	0	0	2	0	0	0		
	E	0	0	2	0	5	3	0		
	F	0	0	0	1	0	0	0		
	G	0	1	0	2	9	0	0		
	H	0	0	0	3	0	0	0		
	I	0	0	0	0	1	0	0		
	K	0	6	8	23	12	0	3		
	L	1	0	1	0	0	0	0		
	M	0	0	0	1	0	0	0		
	P	0	2	10	2	20	0	0		
	V	1	0	0	0	0	0	0		
	W	0	0	2	1	0	0	0		
	Y	0	0	4	1	0	0	0		
Com3	Entr.	0.042	0.042	0.678	2.768	3.552	3.397	1.092	1.129	0.206
	Cons. Seq.	-	-	-	-	**L**	**L**	**R**	-	-
	Cons. Seq. (BXAS)	-	-	-	-	**X**	**X**	**B**	-	-
	-	431	431	398	213	20	0	2	364	423
	A	0	0	4	29	37	29	8	3	0
	C	0	0	2	9	16	25	0	10	4
	D	0	0	4	16	37	22	5	7	0
	E	0	0	3	38	59	39	8	1	1
	F	0	0	1	5	15	19	0	2	0
	G	0	0	8	21	26	47	2	19	1
	H	0	0	2	5	2	5	2	0	0
	I	0	0	1	6	10	10	12	13	3
	K	0	0	0	10	14	10	8	3	0
	L	0	2	1	44	97	122	7	3	1
	M	0	0	0	3	6	1	2	3	0
	P	2	0	4	14	17	32	9	0	0
	R	0	0	3	9	49	43	368	1	0
	V	0	0	0	2	15	15	0	0	0
	W	0	0	1	6	12	3	0	2	0
	Y	0	0	1	3	1	11	0	2	0

Com4	Entr.	0.033	0.033	0.274	2.945	3.515	3.304	2.301	1.036
	Cons. Seq.	**-**	**-**	**-**	**-**	**L**	**K**	**K**	**-**
	Cons. Seq. (BXAS)	**-**	**-**	**-**	**-**	**X**	**B**	**B**	**-**
	-	654	654	637	288	17	0	0	566
	A	0	0	0	8	33	45	7	1
	C	0	0	0	13	3	10	25	1
	D	0	1	2	27	71	35	20	7
	E	0	0	1	41	73	70	32	2
	F	0	0	1	9	16	16	10	13
	G	0	0	3	35	29	25	62	12
	H	0	0	0	6	5	10	2	1
	I	0	0	1	15	18	4	10	4
	K	0	0	0	27	101	188	400	22
	L	0	0	4	98	145	86	16	6
	M	1	0	0	2	8	6	4	6
	P	0	1	2	21	33	58	25	1
	R	0	0	1	27	37	42	7	0
	V	1	0	4	23	40	49	23	5
	W	0	0	0	7	11	5	2	7
	Y	0	0	0	9	16	7	11	2
Com5	Entr.	0.452	2.523	3.023	2.311	3.024	0.342	0.176	
	Cons. Seq.	**-**	**-**	**K**	**K**	**I**	**-**	**-**	
	Cons. Seq. (BXAS)	**-**	**-**	**B**	**B**	**X**	**-**	**-**	
	-	137	68	0	0	5	140	144	
	A	0	5	14	2	3	0	1	
	C	0	0	1	0	0	0	0	
	D	0	3	10	13	9	0	0	
	E	0	1	5	5	4	2	0	
	F	2	7	5	4	29	4	0	
	G	0	2	1	14	24	0	0	
	H	0	1	6	0	0	0	0	
	I	6	29	16	10	43	0	1	
	K	0	5	50	83	8	0	0	
	L	0	2	4	5	10	0	0	
	M	0	2	5	0	2	0	0	
	P	0	2	3	1	2	0	1	
	R	0	0	0	7	1	1	0	
	V	2	18	25	2	1	0	0	
	Y	0	2	2	1	6	0	0	
Com7	Entr.	0.176	0.176	1.081	1.536	1.742	1.622	0.790	0.867
	Cons. Seq.	**-**	**-**	**-**	**-**	**V**	**L**	**K**	**-**
	Cons. Seq. (BXAS)	**-**	**-**	**-**	**-**	**X**	**X**	**B**	**-**
	-	37	37	31	24	0	0	0	33
	C	0	0	0	0	0	9	0	0
	E	0	0	0	1	0	0	0	0
	F	0	0	0	0	0	0	0	1
	G	0	0	1	0	0	0	0	0
	H	0	0	0	1	0	0	0	1
	I	0	0	1	0	0	0	0	1
	K	0	0	0	0	0	0	29	0
	L	0	0	3	6	9	19	0	0
	M	0	0	0	0	0	0	0	1
	P	0	0	0	0	2	0	0	0
	R	1	0	1	0	0	0	9	1
	V	0	1	1	6	17	1	0	0
	Y	0	0	0	0	10	9	0	0
Com8	Entr.	0.705	2.132	2.185	0.325	3.063	2.158	0.770	
	Cons. Seq.	**-**	**-**	**I**	**R**	**-**	**-**	**-**	
	Cons. Seq. (BXAS)	**-**	**-**	**X**	**B**	**-**	**-**	**-**	
	-	87	51	16	0	29	60	87	
	A	0	2	0	0	0	0	0	
	C	0	0	2	0	0	0	0	
	D	0	2	1	0	2	0	0	
	E	0	0	0	0	2	3	0	
	F	0	2	0	0	8	3	0	
	G	0	0	0	4	16	5	0	
	H	0	0	0	0	8	0	1	
	I	2	7	48	0	0	0	0	
	K	0	0	0	1	1	0	0	
	L	1	11	19	0	8	6	2	
	M	1	0	0	0	0	2	0	
	P	0	0	5	0	6	3	2	
	R	0	1	1	94	5	5	1	
	V	8	21	5	0	2	3	0	
	W	0	1	2	0	0	0	0	
	Y	0	1	0	0	12	9	6	

Com19	Entr.	0.361	1.901	2.838	2.350	0.381	1.338	0.665	0.133	0.229		
	Cons. Seq.	-	-	**G**	**G**	**H**	-	-	-	-		
	Cons. Seq. (BXAS)	-	-	**S**	**S**	**B**	-	-	-	-		
	-	51	29	9	4	0	40	48	53	52		
	A	0	0	1	8	0	0	0	0	0		
	C	0	2	3	1	0	0	0	0	0		
	F	0	0	0	0	0	2	0	0	0		
	G	1	10	12	26	4	7	3	0	0		
	H	0	4	11	0	50	0	0	0	0		
	I	0	0	1	4	0	0	1	0	2		
	K	0	1	0	0	0	0	0	1	0		
	L	0	0	0	1	0	0	0	0	0		
	P	2	8	7	7	0	2	0	0	0		
	V	0	0	4	2	0	2	2	0	0		
	Y	0	0	6	1	0	1	0	0	0		
Com21	Entr.	0.014	0.014	0.122	0.014	0.054	0.231	2.955	2.959	3.596	3.064	0.693
	Cons. Seq.	-	-	-	-	-	-	**K**	**K**	**K**	-	-
	Cons. Seq. (BXAS)	-	-	-	-	-	-	**B**	**B**	**B**	-	-
	-	781	781	773	781	778	763	6	1	1	322	719
	A	0	0	1	0	2	1	76	64	69	34	5
	C	0	0	0	0	0	0	31	12	28	16	0
	D	0	0	0	0	0	0	13	28	57	33	5
	E	0	0	0	0	1	1	62	51	87	48	5
	F	0	1	0	0	0	2	10	15	7	3	3
	G	0	0	2	0	0	5	94	34	33	19	5
	H	0	0	0	0	0	1	4	12	37	6	0
	I	0	0	1	0	0	0	9	21	55	45	7
	K	0	0	2	0	0	2	325	348	140	62	4
	L	0	0	0	0	0	0	6	40	97	77	9
	M	0	0	1	0	0	0	10	4	11	11	1
	P	0	0	1	1	1	2	61	61	30	29	3
	R	0	0	1	0	0	0	22	7	16	9	4
	V	0	0	0	0	0	5	28	49	88	56	9
	W	1	0	0	0	0	0	3	2	6	3	2
	Y	0	0	0	0	0	0	22	33	20	9	1
Com22	Entr.	0.391	0.172	1.368	2.692	2.043	0.799					
	Cons. Seq.	-	**R**	**A**	**A**	-	-					
	Cons. Seq. (BXAS)	-	**B**	**X**	**X**	-	-					
	-	36	0	0	1	22	34					
	A	0	1	27	11	5	2					
	C	3	0	0	0	0	0					
	D	0	0	0	1	1	0					
	F	0	0	7	6	2	0					
	G	0	0	0	1	0	1					
	I	0	0	1	3	3	0					
	K	0	0	0	3	2	0					
	M	0	0	1	1	0	0					
	P	0	0	0	0	0	1					
	R	0	38	0	1	0	0					
	V	0	0	3	11	4	1					
Com27	Entr.	0.603	2.724	3.070	3.070	0.743	0.364					
	Cons. Seq.	-	-	**G**	**G**	**K**	-					
	Cons. Seq. (BXAS)	-	-	**S**	**S**	**B**	-					
	-	114	53	0	0	0	119					
	A	0	1	3	2	3	3					
	C	0	0	9	19	6	0					
	D	0	1	1	0	0	0					
	E	0	9	6	0	0	0					
	F	0	4	17	7	0	0					
	G	5	26	42	30	0	0					
	H	0	1	0	4	0	0					
	I	0	3	13	28	1	1					
	K	1	2	0	11	110	0					
	L	0	0	4	4	0	0					
	M	0	1	3	6	0	1					
	P	3	2	2	3	0	0					
	R	0	7	5	1	5	0					
	V	1	8	13	9	0	0					
	W	0	1	0	1	0	1					
	Y	1	6	7	0	0	0					

Com29	Entr.	0.254	0.831	0.472	2.441	3.143	2.403	0.472
	Cons. Seq.	**-**	**-**	**R**	**L**	**P**	**-**	**-**
	Cons. Seq. (BXAS)	**-**	**-**	**B**	**X**	**S**	**-**	**-**
	-	55	49	0	0	4	29	53
	A	0	1	0	1	0	0	0
	C	1	0	0	1	3	3	0
	D	0	0	0	0	1	0	0
	F	0	0	0	0	6	4	2
	G	0	1	0	0	5	5	0
	H	1	0	2	1	1	0	0
	I	0	0	0	0	2	3	0
	K	0	0	0	0	0	1	1
	L	0	0	1	18	4	0	0
	P	0	2	0	17	15	4	0
	R	0	0	53	3	1	0	0
	V	0	0	0	9	10	6	1
	W	0	0	1	6	5	2	0
	Y	0	4	0	1	0	0	0
Com45	Entr.	0.401	2.567	2.739	1.519	0.149	0.149	
	Cons. Seq.	**-**	**-**	**L**	**L**	**H**	**-**	
	Cons. Seq. (BXAS)	**-**	**-**	**X**	**X**	**B**	**-**	
	-	44	17	0	0	0	46	
	A	1	9	7	0	0	0	
	C	0	0	0	1	0	0	
	E	0	4	7	5	1	0	
	F	0	4	2	1	0	0	
	H	0	0	0	0	46	0	
	K	2	1	2	0	0	0	
	L	0	7	16	33	0	0	
	P	0	0	0	1	0	0	
	R	0	2	6	0	0	0	
	V	0	3	3	1	0	1	
	W	0	0	3	5	0	0	
	Y	0	0	1	0	0	0	
Com46	Entr.	0.915	2.521	2.299	2.282	0.172	0.172	
	Cons. Seq.	**-**	**-**	**D**	**G**	**K**	**-**	
	Cons. Seq. (BXAS)	**-**	**-**	**A**	**S**	**B**	**-**	
	-	33	18	0	0	0	38	
	C	0	1	1	1	0	0	
	D	2	2	22	6	0	0	
	E	1	2	5	1	0	0	
	F	0	0	1	0	0	0	
	G	0	0	2	15	0	0	
	H	0	0	1	1	0	0	
	K	0	0	0	0	38	0	
	L	0	4	1	1	0	1	
	M	0	3	3	12	1	0	
	P	0	4	1	0	0	0	
	R	1	1	0	1	0	0	
	V	2	4	1	0	0	0	
	Y	0	0	1	1	0	0	
Com48	Entr.	0.557	2.100	2.369	1.078	0.408	0.426	0.151
	Cons. Seq.	**-**	**-**	**V**	**V**	**R**	**-**	**-**
	Cons. Seq. (BXAS)	**-**	**-**	**X**	**X**	**B**	**-**	**-**
	-	42	26	0	0	2	42	45
	A	0	3	11	11	0	0	0
	C	0	1	0	0	1	4	0
	D	0	0	0	0	0	0	1
	E	0	0	0	1	0	0	0
	F	0	1	3	0	0	0	0
	G	0	1	0	0	0	0	0
	H	0	1	4	0	0	0	0
	I	0	1	1	0	0	0	0
	K	0	0	2	0	0	0	0
	L	2	2	5	0	0	0	0
	M	0	0	1	0	0	0	0
	R	0	0	0	1	43	0	0
	V	1	9	19	33	0	0	0
	W	1	1	0	0	0	0	0

Com49	Entr.	0.050	0.780	2.635	0.074	3.314	3.214	1.848	0.360
	Cons. Seq.	-	-	-	**R**	**L**	**L**	-	-
	Cons. Seq. (BXAS)	-	-	-	**B**	**X**	**X**	-	-
	-	405	368	186	0	2	93	278	391
	A	1	5	37	0	40	22	17	4
	C	0	1	8	0	14	5	2	1
	D	0	1	13	0	24	13	5	2
	E	0	5	6	1	65	41	16	1
	F	1	5	10	0	8	6	2	0
	G	0	0	9	0	12	21	9	0
	H	0	1	1	0	2	2	3	0
	I	0	2	1	0	16	11	5	0
	K	0	0	2	0	15	5	1	1
	L	0	4	69	1	113	101	44	1
	M	0	0	3	0	6	7	1	1
	P	0	5	24	0	13	4	0	0
	R	0	3	0	404	11	19	2	0
	V	0	3	33	1	55	47	19	3
	W	0	0	3	0	7	0	1	1
	Y	0	4	2	0	4	10	2	1
Com70	Entr.	0.715	2.259	2.242	0.934	1.759	1.122	0.336	
	Cons. Seq.	-	-	**P**	**R**	**A**	-	-	
	Cons. Seq. (BXAS)	-	-	**S**	**B**	**X**	-	-	
	-	35	15	0	0	7	32	38	
	A	0	0	1	6	25	4	1	
	C	0	0	0	0	0	1	0	
	D	0	0	1	0	1	0	0	
	E	1	0	1	0	2	0	0	
	F	0	0	1	1	1	0	1	
	H	0	0	5	1	1	0	0	
	K	1	3	4	0	0	0	0	
	L	0	0	0	0	0	1	0	
	P	0	7	18	0	3	1	0	
	R	0	8	0	32	0	1	0	
	V	3	6	9	0	0	0	0	
	W	0	1	0	0	0	0	0	
Com80	Entr.	2.014	0.847	1.994	2.478	0.651			
	Cons. Seq.	**L**	**H**	**L**	**L**	-			
	Cons. Seq. (BXAS)	**X**	**B**	**X**	**X**	-			
	-	8	0	0	13	46			
	A	0	0	2	9	2			
	C	0	0	0	2	1			
	D	0	0	14	6	0			
	E	3	0	0	1	0			
	F	0	0	0	0	1			
	G	0	0	0	1	0			
	H	0	42	11	0	0			
	K	1	4	0	0	0			
	L	28	5	21	16	0			
	M	1	0	0	0	0			
	P	5	0	0	0	0			
	V	0	0	2	3	1			
	W	0	0	1	0	0			
	Y	5	0	0	0	0			

Supplementary Table 21. Conserved basic amino acid containing sequences found in FGF-3. The regions in green and blue are the peptides identified by the mass spectrometry ‘protect and label’ method, where the blue highlighted lysines are the residues that bind to heparin/HS (Y. Li, C. Sun, E. A. Yates, C. Jiang, M. C. Wilkinson and D. G. Fernig, Open Biol., 2016, 6, 150275.). In this circumstance the method performs poorly, of the 7 lysines identified by Li *et al.* 5 are indentifies through conservation with only one of those being represented in multiple amino acid subsets. One caveat is that the mass spectrometry ‘protect and label’ method only identifies lysines and not arginines, which are highly conserved in FGF-3.

AA no	22	23	24	25	26	27	28	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64
FGF3	**G**	**A**	**R**	**L**	**R**	**R**	**D**	**G**	**V**	**Y**	**E**	**H**	**L**	**G**	**G**	**A**	**P**	**R**	**R**	**R**	**K**	**L**	**Y**	**C**	**A**	**T**	**K**	**Y**	**H**	**L**	**Q**	**L**	**H**	**P**	**S**	**G**	**R**	**V**
BX seq	-	A	R	L	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Y	H	L	-	-	-	-	-	-	-	-
BXP seq	-	A	R	L	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	V
BXS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Y	H	L	-	L	H	P	-	G	R	V
BXA seq	-	-	-	-	-	-	-	-	V	Y	E	H	L	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Y	H	L	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	V
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Y	H	L	-	L	H	P	-	G	R	V

AA no	65	66	84	85	86	87	88	89	90	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	119	120	121	122	123	131	132	133
FGF3	N	G	G	I	V	A	I	R	G	G	R	Y	L	A	M	N	K	R	G	R	L	Y	A	S	E	H	Y	S	A	E	E	R	I	H	E	S	R	L
BX seq	-	-	-	I	V	A	I	R	-	-	R	Y	L	A	M	-	-	-	-	R	L	Y	A	-	-	-	-	-	-	-	-	R	I	H	-	-	R	L
BXP seq	N	-	-	I	V	A	I	R	-	-	-	-	-	-	-	-	-	-	-	R	L	Y	A	S	-	H	Y	S	A	-	-	R	I	H	-	-	-	-
BXS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	R	G	R	L	Y	A	-	-	-	-	-	-	-	-	R	I	H	-	-	R	L
BXA seq	-	-	-	I	V	A	I	R	-	-	-	-	-	-	-	-	-	-	-	R	L	Y	A	-	E	H	Y	-	-	-	-	-	-	-	-	-	R	L
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H	Y	S	A	-	-	R	I	H	-	-	-	-
BXPA seq	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	R	G	R	L	Y	A	-	-	-	-	-	-	-	-	-	-	-	-	-	R	L

AA no	134	135	136	140	141	142	143	144	145	146	147	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177
FGF3	Y	R	T	T	P	G	A	R	R	Q	P	R	L	W	Y	V	S	V	N	G	K	G	R	P	R	R	G	F	K	T	R	R	T	Q	K	S	S	L
BX seq	Y	R	-	-	-	-	A	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	A	R	R	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	Y	R	-	-	P	G	A	R	R	-	-	-	-	-	-	-	-	-	-	G	K	G	R	P	R	R	G	F	K	-	-	-	-	-	-	-	-	-
BXA seq	Y	R	-	-	-	-	A	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	A	R	R	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	Y	R	-	-	P	G	A	R	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
													-	-	-	-	-	-	-	-	x	-	-	-	-	-	-	-	x	-	-		-	-	x	-	-	-

AA no	178	179	180	181	182	183	184	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219
FGF3	F	L	P	R	V	L	D	E	M	V	R	Q	L	Q	S	G	L	P	R	P	P	G	K	G	V	Q	P	R	R	R	R	Q	K	Q	S	P	D	N
BX seq	-	-	-	R	V	L	-	-	M	V	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	R	R	R	-	-	-	-	-	-	-
BXP seq	-	-	-	R	V	L	-	-	M	V	R	Q	L	Q	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	-	-	M	V	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	R	R	R	R	-	-	-	-	-	-	-
BXA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	R	R	R	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	L	P	R	P	P	G	K	G	V	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	220	221	222	223	224	225	226	227	228	229	230	231	232	235	236	237	238	239
FGF3	L	E	P	S	H	V	Q	A	S	R	L	G	S	E	A	S	A	H
BX seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	S	A	H
BXS seq	-	-	-	-	-	-	-	-	-	R	L	G	-	-	-	-	-	-
BXA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	R	L	G	-	-	-	-	-	-

Supplementary Table 22. Conserved basic amino acid containing sequences found in FGF-4. The regions in green and blue are the peptides identified by the mass spectrometry ‘protect and label’ method, where the blue highlighted lysines are the residues that bind to heparin/HS (Y. Li, C. Sun, E. A. Yates, C. Jiang, M. C. Wilkinson and D. G. Fernig, Open Biol., 2016, 6, 150275.). All of lysines, apart from one K183, are found in conserved sequences in FGF-4, with all of the found lysines expect K65 appearing in multiple amino acid subsets.

AA no	*44*	*45*	*46*	*47*	*48*	*49*	*50*	*51*	*52*	*53*	*54*	*55*	*56*	*57*	*58*	*59*	*61*	*62*	*63*	*64*	*65*	*66*	*67*	*68*	*69*	*70*	*71*	*72*	*73*	*74*	*75*	*76*	*77*	*78*	*79*	*80*	*81*	*82*
FGF4	E	R	R	W	E	S	L	V	A	L	S	L	A	R	L	P	A	A	Q	P	K	E	A	A	V	Q	S	G	A	G	D	Y	L	L	G	I	K	R
BX seq	-	R	R	W	-	-	-	-	-	-	-	L	A	R	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	K	R
BXP seq	-	R	R	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	-	R	R	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXA seq	-	-	-	-	-	-	-	-	-	-	-	L	A	R	L	-	-	-	-	-	K	E	A	A	V	-	-	-	-	-	-	-	-	-	-	I	K	R
BXPS seq	-	R	R	W	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	*83*	*84*	*85*	*86*	*87*	*88*	*93*	*94*	*95*	*96*	*97*	*106*	*107*	*108*	*109*	*110*	*111*	*120*	*121*	*122*	*123*	*124*	*125*	*126*	*127*	*136*	*137*	*138*	*139*	*140*	*141*	*142*	*143*	*144*	*145*	*146*	*147*	*148*
FGF4	L	R	R	L	Y	C	G	F	H	L	Q	G	A	H	A	D	T	P	V	E	R	G	V	V	S	F	V	A	M	S	S	K	G	K	L	Y	G	S
BX seq	L	R	R	L	Y	-	-	F	H	L	-	-	A	H	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	L	Y	-	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	A	H	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	L	Y	-	-
BXS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	G	V	V	-	-	-	-	-	-	-	K	G	K	L	Y	G	-
BXA seq	L	R	R	L	Y	-	-	F	H	L	-	-	A	H	A	D	-	-	V	E	R	-	-	-	-	-	-	-	-	-	-	-	-	K	L	Y	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	E	R	-	-	-	-	-	-	-	-	-	-	-	-	K	L	Y	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	G	K	L	Y	G	-

AA no	*154*	*155*	*156*	*157*	*158*	*159*	*160*	*161*	*162*	*163*	*164*	*165*	*166*	*167*	*168*	*169*	*170*	*171*	*172*	*173*	*174*	*175*	*176*	*177*	*178*	*179*	*180*	*181*	*182*	*183*	*184*	*185*	*186*	*187*	*188*	*189*	*190*	*191*
FGF4	E	C	T	F	K	E	I	L	L	P	N	N	Y	N	A	Y	E	S	Y	K	Y	P	G	M	F	I	A	L	S	K	N	G	K	T	K	K	G	N
BX seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y	K	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	-	T	F	K	-	-	-	-	-	-	-	-	-	-	-	-	S	Y	K	Y	-	-	-	-	-	-	-	-	-	-	-	K	T	K	K	-	N
BXS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	K	G	-
BXA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y	K	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	C	T	F	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	T	K	K	-	N
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	K	G	-

AA no	*192*	*193*	*194*	*195*	*196*	*197*	*198*	*199*	*200*	*201*	*202*	*203*	*204*
FGF4	R	V	S	P	T	M	K	V	T	H	F	L	P
BX seq	-	-	-	-	-	M	K	V	-	H	F	L	-
BXP seq	R	V	S	-	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	M	K	V	-	-	-	-	-
BXA seq	-	-	-	-	-	M	K	V	-	H	F	L	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	R	V	S	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	M	K	V	-	-	-	-	-

Supplementary Table 23. Conserved basic amino acid containing sequences found in FGF-6. The regions in green and blue are the peptides identified by the mass spectrometry 'protect and label' method, where the blue highlighted lysines are the residues that bind to heparin/HS (Y. Li, C. Sun, E. A. Yates, C. Jiang, M. C. Wilkinson and D. G. Fernig, Open Biol., 2016, 6, 150275.). All of lysines, apart from one K185, are found in conserved sequences in FGF-6, with all of the found lysines appearing in multiple amino acid subsets.

AA no	51	52	53	54	55	56	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91
FGF6	S	R	G	W	G	T	R	S	R	A	G	L	A	G	E	I	A	G	V	N	W	E	S	G	Y	L	V	G	I	K	R	Q	R	R	L	Y	C	N
BX seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	K	R	-	R	R	L	Y	-	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	-	R	G	W	G	-	-	-	R	A	G	L	A	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	R	L	Y	C	-
BXA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	K	R	-	R	R	L	Y	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	R	G	W	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	95	96	97	98	99	103	104	105	106	107	108	109	110	111	112	113	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143
FGF6	G	F	H	L	Q	D	G	R	I	S	G	T	H	E	E	N	T	V	E	R	G	V	V	S	L	F	G	V	R	S	A	L	F	V	A	M	N	S
BX seq	-	F	H	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	-	R	I	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	G	R	I	-	-	-	-	-	-	-	-	-	-	R	G	V	V	-	L	F	G	V	R	-	-	-	-	-	-	-	-	-
BXA seq	-	F	H	L	-	-	-	-	-	-	-	-	H	E	E	-	-	V	E	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	R	I	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	H	E	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199
FGF6	K	G	R	L	Y	A	T	P	S	F	Q	E	E	C	K	F	R	E	Y	I	A	L	S	K	Y	G	R	V	K	R	G	S	K	V	S	P	I	M
BX seq	-	-	R	L	Y	A	-	-	-	-	-	-	-	-	K	F	R	-	-	-	-	-	-	-	-	-	R	V	K	R	-	-	-	-	-	-	-	-
BXP seq	-	-	R	L	Y	A	T	-	-	-	-	-	-	-	K	F	R	-	-	-	-	-	-	-	-	-	R	V	K	R	-	S	K	V	S	-	-	-
BXS seq	K	G	R	L	Y	A	-	-	-	-	-	-	-	C	K	F	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXA seq	-	-	R	L	Y	A	-	-	-	-	-	-	-	-	K	F	R	E	-	-	-	-	-	-	-	-	R	V	K	R	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	C	K	F	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	V	K	R	-	S	K	V	S	-	-	-
BXAS seq	K	G	R	L	Y	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	200	201	202	203	204	205	206	207	208
FGF6	T	V	T	H	F	L	P	R	I
BX seq	-	-	-	H	F	L	-	-	-
BXP seq	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	-	-	-
BXA seq	-	-	-	H	F	L	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-

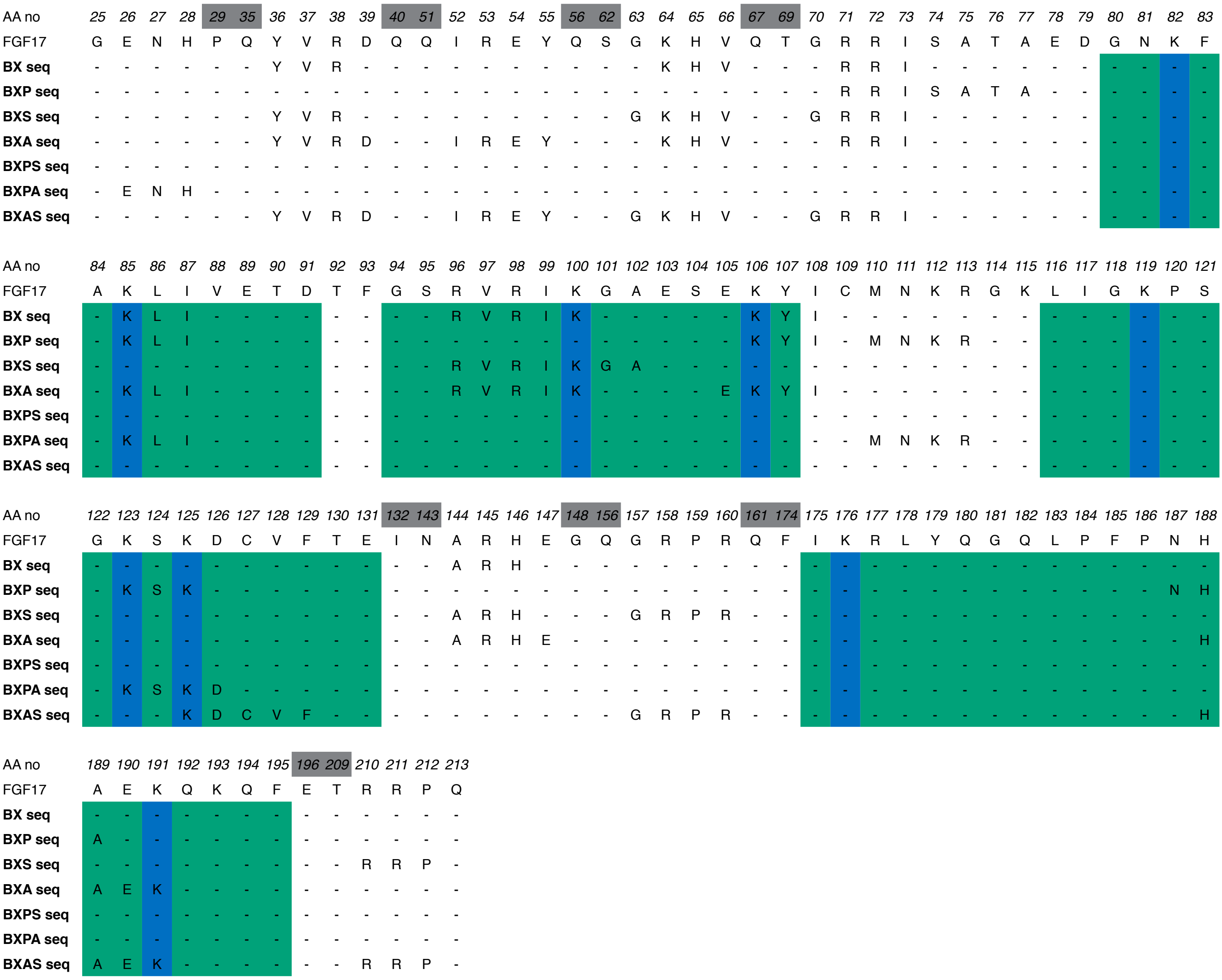
Supplementary Table 24. Conserved basic amino acid containing sequences found in FGF-10. The regions in green and blue are the peptides identified by the mass spectrometry ‘protect and label’ method, where the blue highlighted lysines are the residues that bind to heparin/HS (Y. Li, C. Sun, E. A. Yates, C. Jiang, M. C. Wilkinson and D. G. Fernig, Open Biol., 2016, 6, 150275.). All of lysines, apart from one K87 and K191, are found in conserved sequences in FGF-4, with all of the found lysines expect K183 appearing in multiple amino acid subsets.

AA no	*64*	*65*	*66*	*67*	*68*	*69*	*76*	*77*	*78*	*79*	*80*	*81*	*82*	*83*	*84*	*85*	*86*	*87*	*88*	*89*	*91*	*92*	*93*	*94*	*95*	*96*	*97*	*98*	*99*	*100*	*101*	*102*	*103*	*104*	*105*	*119*	*120*	*121*
FGF10	G	R	H	V	R	S	D	V	R	W	R	K	L	F	S	F	T	K	Y	F	K	I	E	K	N	G	K	V	S	G	T	K	K	E	N	G	V	V
BX seq	-	R	H	V	R	-	-	V	R	W	R	K	L	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	V
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	V	S	-	T	K	K	-	-	-	-	-
BXS seq	-	-	-	-	-	-	-	V	R	W	R	K	L	F	-	-	-	-	-	-	-	-	-	-	-	G	K	V	-	-	-	-	-	-	-	-	-	-
BXA seq	-	R	H	V	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	K	E	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	V	S	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	K	V	-	-	-	K	K	E	-	-	-	-

AA no	*122*	*123*	*124*	*125*	*126*	*130*	*131*	*132*	*133*	*134*	*135*	*136*	*137*	*138*	*139*	*140*	*141*	*142*	*143*	*144*	*145*	*146*	*147*	*149*	*150*	*151*	*152*	*153*	*154*	*174*	*175*	*176*	*177*	*178*	*179*	*180*	*181*	*182*
FGF10	A	V	K	A	I	Y	Y	L	A	M	N	K	K	G	K	L	Y	G	S	K	E	F	N	D	C	K	L	K	E	R	Q	M	Y	V	A	L	N	G
BX seq	A	V	K	A	I	-	-	-	-	-	-	-	-	-	K	L	Y	-	-	-	-	-	-	-	-	K	L	K	-	-	-	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	L	Y	-	-	-	-	-	-	-	-	K	L	K	-	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	-	-	-	-	-	K	K	G	K	L	Y	G	-	-	-	-	-	-	C	K	L	K	-	-	-	-	-	-	-	-	-	G
BXA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	L	Y	-	-	K	E	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	K	L	K	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	L	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	K	K	G	K	L	Y	G	-	K	E	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	*183*	*184*	*185*	*186*	*187*	*188*	*189*	*190*	*191*	*192*	*193*	*194*	*195*	*196*	*197*	*198*	*199*	*200*	*201*	*202*	*203*	*204*	*205*	*206*	*207*	*208*
FGF10	K	G	A	P	R	R	G	Q	K	T	R	R	K	N	T	S	A	H	F	L	P	M	V	V	H	S
BX seq	-	-	-	-	-	-	-	-	-	-	R	R	K	-	-	-	A	H	F	L	-	M	V	V	H	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	K	G	A	P	R	R	G	-	-	-	R	R	K	-	-	-	-	-	-	-	-	-	-	-	-	-
BXA seq	-	-	-	-	-	-	-	-	-	-	R	R	K	-	-	-	A	H	F	L	-	M	V	V	H	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	R	R	K	-	-	-	-	-	-	-	-	-	-	-	-	-

Supplementary Table 25. Conserved basic amino acid containing sequences found in FGF-17. The regions in green and blue are the peptides identified by the mass spectrometry 'protect and label' method, where the blue highlighted lysines are the residues that bind to heparin/HS (Y. Li, C. Sun, E. A. Yates, C. Jiang, M. C. Wilkinson and D. G. Fernig, Open Biol., 2016, 6, 150275.). Six of the nine heparin interacting lysines are identified through conservation, K85, K100, K106, K123, K125 and K191, all of which are found in multiple amino acid subsets.



AA no	25	26	27	28	29	35	36	37	38	39	40	51	52	53	54	55	56	62	63	64	65	66	67	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83
FGF17	G	E	N	H	P	Q	Y	V	R	D	Q	Q	I	R	E	Y	Q	S	G	K	H	V	Q	T	G	R	R	I	S	A	T	A	E	D	G	N	K	F
BX seq	-	-	-	-	-	-	Y	V	R	-	-	-	-	-	-	-	-	-	-	K	H	V	-	-	-	R	R	I	-	-	-	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	R	I	S	A	T	A	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	Y	V	R	-	-	-	-	-	-	-	-	-	G	K	H	V	-	-	G	R	R	I	-	-	-	-	-	-	-	-	-	-
BXA seq	-	-	-	-	-	-	Y	V	R	D	-	-	I	R	E	Y	-	-	-	K	H	V	-	-	-	R	R	I	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	E	N	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	Y	V	R	D	-	-	I	R	E	Y	-	-	G	K	H	V	-	-	G	R	R	I	-	-	-	-	-	-	-	-	-	-

AA no	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121
FGF17	A	K	L	I	V	E	T	D	T	F	G	S	R	V	R	I	K	G	A	E	S	E	K	Y	I	C	M	N	K	R	G	K	L	I	G	K	P	S
BX seq	-	K	L	I	-	-	-	-	-	-	-	-	R	V	R	I	K	-	-	-	-	-	K	Y	I	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	K	L	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	Y	I	-	M	N	K	R	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	-	-	-	-	-	-	R	V	R	I	K	G	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXA seq	-	K	L	I	-	-	-	-	-	-	-	-	R	V	R	I	K	-	-	-	-	E	K	Y	I	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	K	L	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	N	K	R	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	122	123	124	125	126	127	128	129	130	131	132	143	144	145	146	147	148	156	157	158	159	160	161	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188
FGF17	G	K	S	K	D	C	V	F	T	E	I	N	A	R	H	E	G	Q	G	R	P	R	Q	F	I	K	R	L	Y	Q	G	Q	L	P	F	P	N	H
BX seq	-	-	-	-	-	-	-	-	-	-	-	-	A	R	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	K	S	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	H
BXS seq	-	-	-	-	-	-	-	-	-	-	-	-	A	R	H	-	-	-	G	R	P	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXA seq	-	-	-	-	-	-	-	-	-	-	-	-	A	R	H	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	K	S	K	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	K	D	C	V	F	-	-	-	-	-	-	-	-	-	-	G	R	P	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H

AA no	189	190	191	192	193	194	195	196	209	210	211	212	213
FGF17	A	E	K	Q	K	Q	F	E	T	R	R	P	Q
BX seq	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	A	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	-	-	-	R	R	P	-
BXA seq	A	E	K	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	A	E	K	-	-	-	-	-	-	R	R	P	-

Supplementary Table 26. Conserved basic amino acid containing sequences found in FGF-20. The regions in green and blue are the peptides identified by the mass spectrometry ‘protect and label’ method, where the blue highlighted lysines are the residues that bind to heparin/HS (Y. Li, C. Sun, E. A. Yates, C. Jiang, M. C. Wilkinson and D. G. Fernig, Open Biol., 2016, 6, 150275.). All of lysines, apart from one K186, are found in conserved sequences in FGF-20, with all of the found lysines expect K171 appearing in multiple amino acid subsets.

AA no	*23*	*24*	*25*	*26*	*27*	*28*	*38*	*39*	*40*	*41*	*42*	*43*	*44*	*45*	*46*	*47*	*48*	*49*	*50*	*56*	*57*	*58*	*59*	*60*	*61*	*62*	*63*	*64*	*65*	*66*	*67*	*68*	*69*	*70*	*71*	*72*	*73*	*74*
FGF20	S	H	F	L	L	P	G	E	R	R	S	A	A	E	R	S	A	R	G	Q	L	A	H	L	H	G	I	L	R	R	R	Q	L	Y	C	R	T	G
BX seq	-	H	F	L	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	A	H	L	H	-	I	L	R	R	R	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	-	-	R	R	S	A	A	-	R	S	A	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	Y	C	R	-	G
BXA seq	-	H	F	L	L	-	-	E	R	R	-	A	A	E	R	-	-	-	-	-	L	A	H	L	H	-	I	L	R	R	R	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	A	A	E	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	Y	C	R	-	G

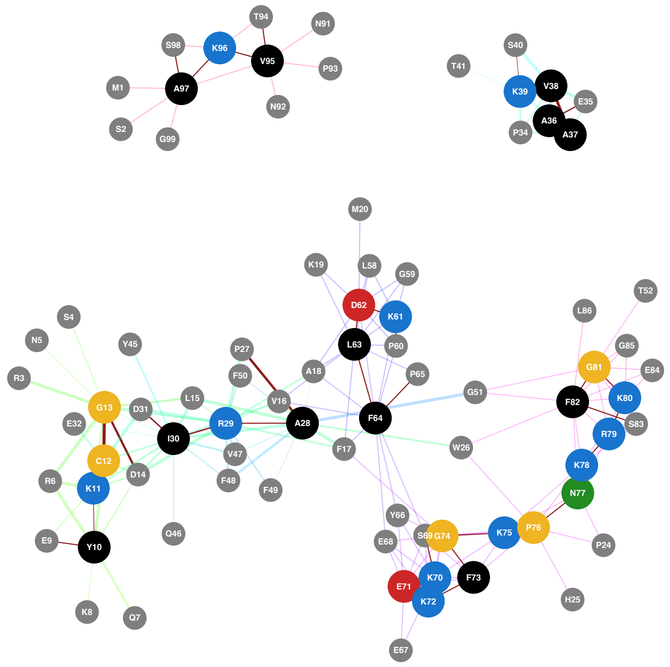
AA no	*75*	*76*	*77*	*78*	*87*	*88*	*89*	*90*	*91*	*92*	*93*	*94*	*95*	*96*	*106*	*107*	*108*	*109*	*110*	*111*	*112*	*113*	*114*	*115*	*117*	*118*	*119*	*120*	*121*	*122*	*123*	*124*	*125*	*126*	*127*	*128*	*129*	*130*
FGF20	F	H	L	Q	G	T	R	Q	D	H	S	L	F	G	G	L	V	S	I	R	G	V	D	S	L	Y	L	G	M	N	D	K	G	E	L	Y	G	S
BX seq	F	H	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	T	R	Q	-	H	S	L	F	-	-	L	V	S	I	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	F	H	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	R	G	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXA seq	F	H	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	N	D	K	-	-	-	-	-	S
BXAS seq	F	H	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	R	G	V	D	-	-	-	-	-	-	-	D	K	G	E	L	Y	G	-

AA no	*131*	*132*	*133*	*134*	*135*	*136*	*137*	*138*	*139*	*140*	*141*	*142*	*154*	*155*	*156*	*157*	*158*	*159*	*160*	*161*	*162*	*163*	*164*	*165*	*166*	*167*	*168*	*169*	*170*	*171*	*172*	*173*	*174*	*175*	*176*	*177*	*178*	*179*
FGF20	E	K	L	T	S	E	C	I	F	R	E	Q	N	I	Y	K	H	G	D	T	G	R	R	Y	F	V	A	L	N	K	D	G	T	P	R	D	G	A
BX seq	-	-	-	-	-	-	-	I	F	R	-	-	-	I	Y	K	H	-	-	-	-	R	R	Y	F	V	A	L	-	-	-	-	-	-	-	-	-	-
BXP seq	-	K	L	T	S	-	-	I	F	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXS seq	-	-	-	-	-	-	C	I	F	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	A
BXA seq	E	K	L	-	-	-	-	I	F	R	E	-	-	I	Y	K	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	K	L	T	S	-	C	I	F	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	T	P	R	-	-	-
BXPA seq	E	K	L	T	S	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	E	K	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	D	G	-	-	-	-	-	-

AA no	*180*	*181*	*182*	*183*	*184*	*185*	*186*	*187*	*188*	*189*	*190*	*197*	*198*	*199*	*200*	*201*	*202*	*203*	*204*	*205*	*206*	*207*	*208*	*209*	*210*	*211*
FGF20	R	S	K	R	H	Q	K	F	T	H	F	P	E	R	V	P	E	L	Y	K	D	L	L	M	Y	T
BX seq	-	-	K	R	H	-	-	-	-	-	-	-	-	-	-	-	-	L	Y	K	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	Y	K	-	-	-	-	-	-
BXS seq	R	-	K	R	H	-	-	-	-	-	-	-	-	R	V	P	-	L	Y	K	-	-	-	-	-	-
BXA seq	-	-	K	R	H	-	-	-	-	-	-	-	E	R	V	-	-	-	-	-	-	-	-	-	-	-
BXPS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	R	V	P	-	L	Y	K	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	E	R	V	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	K	R	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

AA no	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	27	28	29	30	31	34	35	36	37	38	39	40	60	61	62	63	64	65	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	93	94	95	96	97	98	99	123	124	125	126	127	128	136
HDGF	*Q*	*K*	*E*	*Y*	*K*	*C*	*G*	*D*	*L*	*V*	*F*	*A*	*K*	*M*	*K*	*G*	*P*	*A*	*R*	*I*	*D*	*P*	*E*	*A*	*A*	*V*	*K*	*S*	*P*	*K*	*D*	*L*	*F*	*P*	*S*	*K*	*E*	*K*	*F*	*G*	*K*	*P*	*N*	*K*	*R*	*K*	*G*	*F*	*S*	*P*	*T*	*V*	*K*	*A*	*S*	*G*	*G*	*D*	*K*	*K*	*G*	*N*	*E*
BX seq	-	-	-	-	-	-	-	-	L	V	F	A	K	M	K	-	-	A	R	I	-	-	-	A	A	V	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	R	K	-	-	-	-	-	V	K	A	-	-	-	-	-	-	-	-	-
BXP seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	R	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	K	R	K	-	-	-	-	T	V	K	A	S	-	-	-	-	-	-	-	-
BXS seq	-	-	-	Y	K	C	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	A	V	K	-	-	-	-	-	-	-	-	-	-	K	F	G	K	P	-	K	R	K	G	F	-	-	-	V	K	A	-	-	-	-	K	K	G	-	-
BXS seq	-	K	E	Y	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	A	A	V	K	-	-	K	D	L	F	-	-	K	E	K	F	-	-	-	-	K	R	K	-	-	-	-	-	V	K	A	-	-	-	D	K	K	-	-	-
BXPS seq	-	-	-	Y	K	C	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	D	L	F	-	-	-	-	-	-	-	-	-	N	K	R	K	-	-	-	-	-	-	-	-	-	-	-	D	K	K	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	E	K	F	G	K	P	-	K	R	K	G	F	-	-	-	V	K	A	-	-	-	-	-	-	-	-	-

AA no	137	138	139	140	141	142	143	144	145	146	147	148	149	165	166	167	168	169	170	171	172	173	174	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	206	207	208	209	210	211	212	223	224	225	226	227	230	231	232	233	234	235	236	237	238	239
HDGF	*G*	*K*	*L*	*V*	*I*	*D*	*E*	*P*	*A*	*K*	*E*	*K*	*N*	*S*	*P*	*K*	*R*	*P*	*K*	*E*	*A*	*E*	*N*	*T*	*L*	*E*	*V*	*E*	*R*	*P*	*L*	*P*	*M*	*E*	*V*	*E*	*K*	*N*	*S*	*T*	*P*	*S*	*G*	*R*	*G*	*P*	*P*	*Q*	*E*	*A*	*T*	*K*	*E*	*E*	*A*	*P*	*G*	*I*	*R*	*D*	*H*	*E*	*S*
BX seq	-	K	L	V	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXP seq	-	K	L	V	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	N	S	T	-	-	-	-	-	-	-	-	-	A	T	K	-	-	-	-	-	-	-	-	-	-	-
BXS seq	G	K	L	V	I	-	-	P	A	K	-	-	-	-	P	K	R	P	K	-	-	-	-	-	-	-	-	-	R	P	L	P	M	-	-	-	-	-	-	-	-	-	G	R	G	P	P	-	-	-	-	-	-	-	A	P	G	I	R	-	-	-	-
BXA seq	-	-	-	-	-	-	-	-	A	K	E	K	-	-	-	-	-	-	K	E	A	E	-	-	L	E	V	E	R	-	-	-	M	E	V	E	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	R	D	H	E	-
BXPS seq	-	-	-	-	-	-	-	P	A	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXPA seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
BXAS seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	R	G	P	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



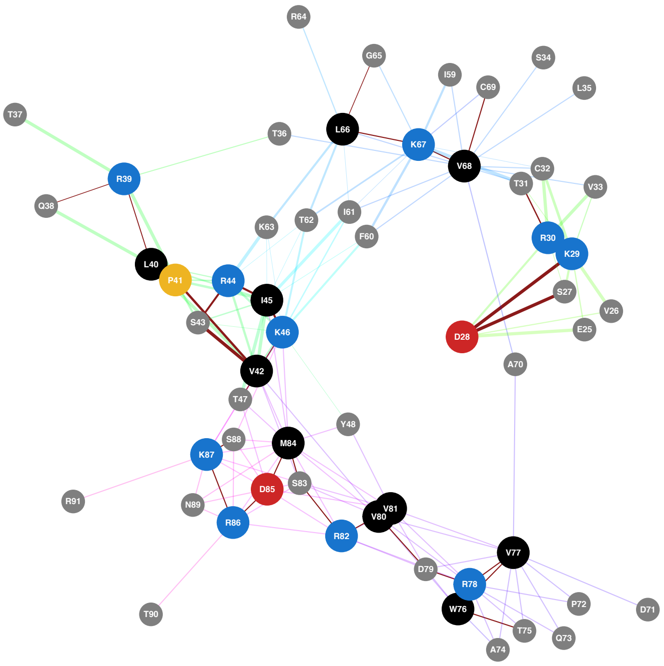
Supplementary Figure 3. *Conserved basic amino acid containing sequences found in Hepatoma-derived growth factor (HDGF)*. The table shows the sequences found for the different amino acid combinations. As a further selection criterion, an amino acid was only considered to be significant if it arose at least twice in the different amino acid groups, e.g., R79 appears in all but one of the amino acid subsets. Amino acid residues that were found experimentally to bind to HS/heparin are shown in blue. The conserved amino acids are illustrated on the molecular structure of HDGF. This structure was also represented as a network, the vertices of the network are the αC positions. In the network conserved basic amino acid containing residues are shown along with any amino acid that is less than 0.8 nm away, the approximate length of a HS/heparin disaccharide. This reductionist view illustrates how the small basic amino acid containing sequences in unison can form an extended heparin-binding domain.

Solution NMR analysis of Hepatoma-derived Growth Factor indicated that it had a primary heparin binding site and then possibly a minor binding site at the proteins N-terminal. The primary HBS is comprised of lysines 19, 61, 72, 78 and 80 as well as arginine 79, the secondary site which resides in the flexible N-terminus of the molecule is formed of arginines 2 and 6 and Lysines 8 and 11 [S. C. Sue, J. Y. Chen, S. C. Lee, W. G. Wu and T. H. Huang, J. Mol. Biol., 2004, 343, 1365–1377.]. The similarity analysis found all the members of the proposed principal binding site apart from lysine 19, this amino acid was found by the analysis, but it only appeared once, in the BX group of amino acids. Of the minor binding site only K11 was found to be significantly conserved, while K8 appeared once in the BXA amino acid group analysis. The network representation of HDGFs HBS highlights how the conserved basic amino acid containing sequences could come together to form the principal HBS, with the conserved sequence ${}_{28}\mathrm{ARI}_{30}$ (green labelled amino acid in the table) linking the primary and secondary HBSs together.

XCL1

AA no	27	28	29	30	31	32	38	39	40	41	42	43	44	45	46	47	54	55	56	57	58	59	60
XCL1	*S*	*D*	*K*	*R*	*T*	*C*	*Q*	*R*	*L*	*P*	*V*	*S*	*R*	*I*	*K*	*T*	*S*	*L*	*R*	*A*	*V*	*I*	*F*
bx seq	-	-	-	-	-	-	-	-	-	-	-	-	R	I	K	-	-	-	-	-	-	-	-
bxp seq	-	-	K	R	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bxs seq	-	-	-	-	-	-	-	R	L	P	V	-	R	I	K	-	-	-	-	-	-	-	-
bxa seq	-	D	K	R	-	-	-	-	-	-	-	-	R	I	K	-	-	L	R	A	V	I	F
bxps seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bxpa seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bxas seq	-	D	K	R	-	-	-	R	L	P	V	-	R	I	K	-	-	-	-	-	-	-	-

AA no	61	62	63	64	65	66	67	68	69	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92
XCL1	*I*	*T*	*K*	*R*	*G*	*L*	*K*	*V*	*C*	*T*	*W*	*V*	*R*	*D*	*V*	*V*	*R*	*S*	*M*	*D*	*R*	*K*	*S*	*N*	*T*	*R*	*N*
bx seq	-	-	-	-	-	L	K	V	-	-	W	V	R	-	V	V	R	-	-	-	-	-	-	-	-	-	-
bxp seq	-	-	-	-	-	L	K	V	-	-	-	-	-	-	V	V	R	S	M	-	-	-	-	-	-	-	-
bxs seq	-	-	-	-	-	-	-	-	-	-	W	V	R	-	V	V	R	-	-	-	-	-	-	-	-	-	-
bxa seq	I	-	-	-	-	L	K	V	-	-	-	-	-	-	-	-	-	-	M	D	R	K	-	-	-	-	-
bxps seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bxpa seq	-	-	-	-	-	L	K	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
bxas seq	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	D	R	K	-	-	-	-	-



Supplementary Figure 4. *Conserved basic amino acid containing sequences found in Chemokine (C motif) ligand (XCL1) (lymphotactin)*. The table shows the sequences found for the different amino acid combinations. As a further selection criterion, an amino acid was only considered to be significant if it arose at least twice in the different amino acid groups, e.g., K46 appears in all but one of the amino acid subsets. Amino acid residues that were found experimentally to bind to HS/heparin are shown in blue. The conserved amino acids are illustrated on the molecular structure of XCL1. This structure was also represented as a network, the vertices of the network are the αC positions. In the network conserved basic amino acid containing residues are shown along with any amino acid that is less than 0.8 nm away, the approximate length of a HS/heparin disaccharide. This reductionist view illustrates how the small basic amino acid containing sequences in unison can form an extended heparin-binding domain.

The following amino acids were identified as interacting with heparin, R39, R44, K46, K63, R64, K67, R78, R86, K87, and R91 [F. C. Peterson, E. S. Elgin, T. J. Nelson, F. Zhang, T. J. Hoeger, R. J. Linhardt and B. F. Volkman, J. Biol. Chem., 2004, 279, 12598–12604.]. Further use of site-directed mutagenesis identified R44 and R64 as the high affinity residues. All but three of these amino acids were identified by the similarity method employed in this manuscript, these are K63, R64 and R70. The method was able to identify 1 of the high affinity binding residues and 70 percent of the total interacting residues.

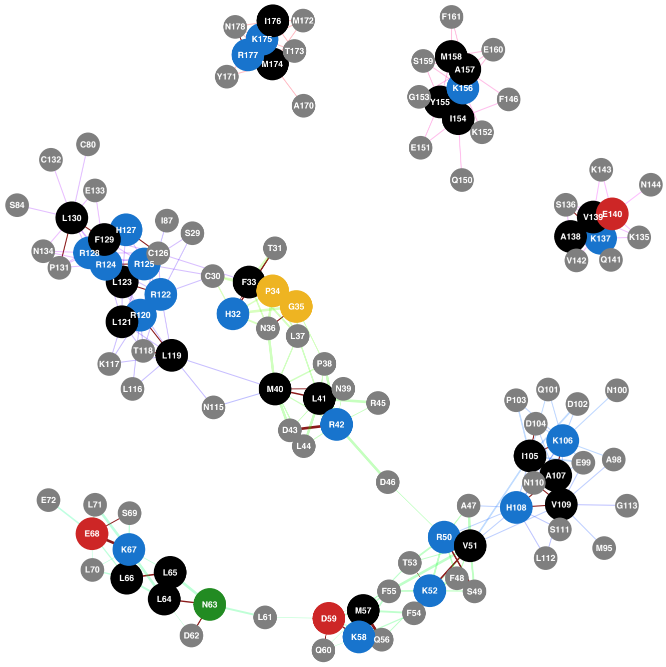
AA no	30	31	32	33	34	35	36	37	38	39	40	41	42	43
IL10	*C*	*T*	*H*	*F*	*P*	*G*	*N*	*L*	*P*	*N*	*M*	*L*	*R*	*D*
bx seq	.	.	.	.	.	.	.	.	.	.	M	L	R	.
bxp seq	.	T	H	F	.	.	.	.	.	N	M	L	R	.
bxs seq	.	.	H	F	P	G	.	.	.	.	M	L	R	.
bxa seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxps seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxpa seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxas seq	.	.	H	F	P	G	.	.	.	.	.	.	.	.

AA no	49	50	51	52	53	56	57	58	59	60	62	63	64	65	66	67	68	69
IL10	*S*	*R*	*V*	*K*	*T*	*Q*	*M*	*K*	*D*	*Q*	*D*	*N*	*L*	*L*	*L*	*K*	*E*	*S*
bx seq	.	R	V	K	.	.	.	.	.	.	.	.	L	L	L	K	.	.
bxp seq	.	.	.	.	.	.	.	.	.	.	.	N	L	L	L	K	.	.
bxs seq	.	R	V	K	.	.	.	.	.	.	.	.	L	L	L	K	.	.
bxa seq	.	R	V	K	.	.	M	K	D	.	.	.	L	L	L	K	E	.
bxps seq	.	.	.	.	.	.	.	.	.	.	.	N	L	L	L	K	.	.
bxpa seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxas seq	.	R	V	K	.	.	M	K	D	.	.	.	L	L	L	K	E	.

AA no	70	71	72	73	74	75	76	104	105	106	107	108	109	110	118
IL10	*L*	*L*	*E*	*D*	*F*	*K*	*G*	*D*	*I*	*K*	*A*	*H*	*V*	*N*	*T*
bx seq	.	.	.	.	.	.	.	.	I	K	A	H	V	.	.
bxp seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxs seq	.	.	.	.	.	.	.	.	I	K	A	H	V	.	.
bxa seq	L	L	E	D	F	K	.	.	.	.	.	.	.	.	.
bxps seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxpa seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxas seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.

AA no	119	120	121	122	123	124	125	126	127	128	129	130	131	134	135	136
IL10	*L*	*R*	*L*	*R*	*L*	*R*	*R*	*C*	*H*	*R*	*F*	*L*	*P*	*N*	*K*	*S*
bx seq	L	R	L	R	L	R	R	.	H	R	F	L	.	.	.	.
bxp seq	.	.	.	.	.	.	.	.	H	R	F	L	.	.	.	.
bxs seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxa seq	L	R	L	R	L	R	R	.	H	R	F	L	.	.	.	.
bxps seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxpa seq	.	.	.	.	.	.	.	.	H	R	F	L	.	.	.	.
bxas seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.

AA no	137	138	139	140	141	153	154	155	156	157	158	159	173	174	175	176	177	178
IL10	*K*	*A*	*V*	*E*	*Q*	*G*	*I*	*Y*	*K*	*A*	*M*	*S*	*T*	*M*	*K*	*I*	*R*	*N*
bx seq	K	A	V	.	.	.	I	Y	K	A	M	.	.	M	K	I	R	.
bxp seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxs seq	K	A	V	.	.	.	.	.	.	.	.	.	.	M	K	I	R	.
bxa seq	K	A	V	E	.	.	I	Y	K	A	M	.	.	M	K	I	R	.
bxps seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxpa seq	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
bxas seq	K	A	V	E	.	.	.	.	.	.	.	.	.	M	K	I	R	.



Supplementary Figure 5. *Conserved basic amino acid containing sequences found in Interleukin-10 (IL-10).* The table shows the sequences found for the different amino acid combinations. As a further selection criterion, an amino acid was only considered to be significant if it arose at least twice in the different amino acid groups, e.g., K137 appears in all but one of the amino acid subsets. Amino acid residues that were found experimentally to bind to HS/heparin are shown in blue. The conserved amino acids are illustrated on the molecular structure of IL-10. This structure was also represented as a network, the vertices of the network are the αC positions. In the network conserved basic amino acid containing residues are shown along with any amino acid that is less than 0.8 nm away, the approximate length of a HS/heparin disaccharide. This reductionist view illustrates how the small basic amino acid containing sequences in unison can form an extended heparin-binding domain.

By NMR it was determined that IL-10 interacts with heparin via a binding site that is comprised of resides in helix D and the adjacent DE loop 39. The residues involved in the interaction are arginines 120, 121, 124, 125 and lysines 135 and 137 [G. Kunze, S. Köhling, A. Vogel, J. Rademann, D. Huster, S. Ko, A. Vogel and D. Huster, J. Biol. Chem., 2016, 291, 3100–3113]. The analyses shown in this manuscript identifies all of these residues except lysine 135, in particular the analyses identifies a domain comprised of 8 basic amino acids, arginines 42, 120, 122, 124, 125, 128 and 127 and histidines 32 and 127.

Supplementary Table 27. The 329 proteins identifed from the human proteome that have the highest number of conserved basic amino acid containing sequences. These are proteins that appeared in the 99TH percentile, it is a unique list of the proteins found in the amino acid subsets. The proteins are identified by their UNIPROT entry name.

Predicted HBPs
ABCAC, ABCAD, ACACA, ACACB, AKAP9, ANK2, ANK3, APOB, ASCC3, ASH1L, ASPM, ATM, ATR, BIRC6, BPTF, BRCA2, BRWD1, CABIN, CAC1A, CAC1B, CAC1C, CAC1D, CAC1E, CAC1S, CE042, CE290, CENPE, CFA46, CFA54, CHD3, CHD4, CHD5, CHD6, CHD7, CHD8, CHD9, CKAP5, CO6A3, COCA1, DESP, DJC13, DMD, DMXL1, DMXL2, DNHD1, DOC10, DOC11, DOCK3, DOCK6, DPOE1, DPOLQ, DPOLZ, DYH10, DYH1, DYH11, DYH12, DYH14, DYH17, DYH2, DYH3, DYH5, DYH6, DYH7, DYH8, DYH9, DYHC1, DYHC2, DYSF, DYST, EP400, EPG5, FAT1, FAT2, FAT3, FAT4, FRAS1, FRY, FRYL, FSIP2, GCN1L, GPR98, HD, HEAT1, HECD4, HELZ2, HERC1, HERC2, HMCN1, HMCN2, HTR5B, HUWE1, HYDIN, IF172, INT1, IQGA3, ITPR1, ITPR2, ITPR3, JHD2C, K0100, K1109, KALRN, KMT2A, KMT2B, KMT2C, KMT2D, KNTC1, LAMA1, LAMA2, LAMA3, LAMA5, LRBA, LRP2, LRRK2, LYST, MACF1, MDN1, MINT, MRO2A, MTOR, MUC16, MXRA5, MYCB2, MYH10, MYO10, MYO15, MYO5A, MYO5B, MYO7A, MYO7B, MYO9A, MYO9B, MYOF, NBAS, NBEA, NBEL1, NBEL2, NEBU, NF1, NIPBL, NPA1P, OBSCN, PCLO, PCNT, PIEZ1, PIEZ2, PK1L1, PKD1, PKDRE, PKHD1, PKHL1, PLEC, PRKDC, PRP8, RBP2, RGPD3, RN213, RRP5, RTTN, RYR1, RYR2, RYR3, SACS, SETX, SMG1, SPEG, SPTB2, SPTN2, SPTN4, SPTN5, SRCAP, STAR9, SYNE1, SYNE2, SZT2, TEN1, TEP1, TITIN, TRIO, TRNK1, TRPM6, TRRAP, UBP24, UBP34, UBR4, UNC80, USH2A, USP9X, USP9Y, UTP20, UTRO, VP13A, VP13B, VP13C, VP13D, WDFY3, WDFY4, WDR87, XIRP2, ZFHX3, ZFHX4, ZZEF1, ALMS1, ANR11, ATRX, CE350, CENPF, CMYA5, CNTRL, CO6A5, CP250, CRBG3, CTRO, DOCK1, EVPL, GOGA4, GOGB1, LRP1, LRP1B, MGAP, MY18B, MYH1, MYH11, MYH13, MYH15, MYH2, MYH3, MYH4, MYH6, MYH7, MYH7B, MYH8, MYH9, MYOME, PEPL, SPEF2, SPTA1, SPTB1, SPTN1, TNC18, U520, APC, BD1L1, BSN, C2CD3, CC168, CE295, DOCK9, DOP1, FA8, GVIN1, IGS10, KI67, MY18A, NAV2, PCX1, PDZD2, PGBM, PTN13, TEN3, TEN4, TEX15, TPR, UN13C, UNC79, ZDBF2, ZEP1, ZN292, ZN462, ATS9, BAHC1, CELR1, CELR3, CSMD1, CSMD2, CSMD3, EMAL5, EYS, FAS, FBN1, FLNB, FLNC, FREM2, MAST4, MEGF8, NSD1, OTOF, SSPO, STAB1, STAB2, SVEP1, TEN2, TENX, TF3C1, THYG, VWF, ZAN, ZN469, AKP13, ANR12, ANR26, BDP1, DAPLE, GRDN, MYH14, NUMA1, SETD2, SVIL, UBR5, ZN318, AHNK2, APC2, CELR2, CHD2, CO6A6, ESPL1, HECD1, NAV3, PLCE1, RAI1, ZC3H1, ZFHX2, DIDO1, EMAL6, MAP1A, NCOR2, PRC2C, SMHD1, ZEP3