Supplementary Information

Bioinformatics and molecular dynamics analyses of Ser/Thr motifs in transmembrane proteins Coral del Val, Stephen H. White, and Ana-Nicoleta Bondar

Supplementary Information contains:

- Figure legends
- Figures S1-S10
- Supplementary Information References

Figure legends

Figure S1. Examples of molecular transporters from data-α set that have significant number of Ser/Thr Signatures. (A) The AMPA subtype ionotropic glutamate receptor (3kg2, Sobolevsky et al, 2009). Chain A is shown as orange ribbons, and chains B-D as transparent ribbons. CA atoms of the Ser/Thr amino acids from chain A are shown as orange van der Waals spheres. (B) The full-length potassium channel KcsA (1f6g, Cortes et al, 2001). Chain A is shown in red, and chains B-D transparent pink. CA atoms of Ser/Thr in chain A are shown as green van der Waals spheres. In panels C-I, the protein is shown is orange, with CA atoms of the Ser/Thr groups as green van der Waals spheres. (C) The AHA2 P-type ATPase proton pump (3b8c, Pederson et al 2007). (D) The P-type ATP-ase Ca2+ pump (2agv_a, Obara et al, 2005). (E) The *Neurospora* proton pump (1mhs; Kühlbrandt et al 2002). (F) The ATP-gated P2X4 ion channel (3h9v, chain A, Kawate et al. 2009). (G) The KirBac3.4 potassium channel (Gulbis et al (pdb entry 1XL4). (H). The Wza translocon ((2j58_A; Dong et al 2006). (I) Mouse P-glycoprotein ABCB1 (3g5u,

chain A; Aller et al, 2009). (J) The arginine-agmatine antiporter (Fang et al 2009). The sequence used in the analysis was extracted from the 3hqk A pdb structure. To prepare the image, we used pdb 3ncy, which superseded 3hqk. (K) Aquaporin AQP1 (1J4N chainA; Sui et al 2001). (L) Bovine rhodopsin (3c9l, Stenkamp 2008). (M) The rat muscarinic M3 receptor (2amk; Li et al, 2005). (N) The ShuA transporter (3fhh, Brillet et al). (O) The hemophore receptor HasR (3csl, Krieg et al, 2009). (P) The outer membrane porin (2f1c, Subbarao et al 2006). (Q) The colicin I receptor from E. coli (Buchanan et al. 2007). Ser/Thr sidechains are shown as van der Waals spheres with carbon atoms colored cyan, oxygen - red, and nitrogen - blue. (R) N. europaea Rh50 protein from Lupo et al. 2007. In the left-hand image, all Ser/Thr sidechains are depicted; the right-hand panel highlights three transmembrane helices (shown in orange) with their Ser/Thr content. (S) Ser/Thr amino acids of bacteriorhodopsin. Ser/Thr sidechains other than the three pairs of consecutive Thr groups (Thr46/Thr47, Thr89/Thr90, and Thr141/Thr142) are shown as van der Waals spheres colored in green. The Asp96 sidechain is depicted as purple van der Waals spheres, and retinal with the Lys216 sidechain as black bonds. The structure of bacteriorhodopsin was taken from Belrhali et al, 1999. In left-hand panel, helix B is highlighted in dark blue; in the right-hand panel, three TM helices (shown in orange) and their Ser/Thr content are highlighted, with remaining TM helices and loops shown in transparent gray.

Figure S2. Percentage data- α sequences that contain specific Signatures. The specific signature assessed is indicated for each of the Panels A-F. At least one motif is present in 20-30% of the data set. The presence of 2 Signatures can also be significant: 17% of the proteins have two SxxT motifs (panel B). Detailed analyses of the data- α Signatures is given in Figures S3-S8.

Figure S3. Data- β sequences that contain specific Signatures. 21-25% of the sequences have at least one Signature. See Figures S9-S14 for detailed analyses of data- β Signatures.

Figure S4. Summary of the statistical analyses of the sequences in data- α and data- β .

Figure S5. Summary of the Shapiro test.

Figures S6. Number of Signatures per chain in data- α . In Panels A-S, the histogram gives the number and type of a specific Signature present in each chain of data- α . Only chains with at least one Signature are included in the histogram. The insets give the color scheme used for each Signature subset.

Figures S7. Number of Signatures per chain in data- β . See legend of Figure S6 above for a brief description of how the histograms from panels A-F were computed.

Figures S8-S9. Hierarchichal clustering of Signatures counts per sequence. Columns correspond to the signatures analyzed (TxxT, SxxxS, TT, ST, SxxT, SS, TxxxT, SxxS). All counts were normalized between 0 and 1 for each Signature (see main Text). The clustering method used was complete linkage using the Euclidean distance as similarity measure. The colors indicate the cluster to which the sequences belong according to the clustering procedure described in the main text. The number of records used is 291 in Figure S8 (data- α), and 48 in Figure S9 (data- β). The sequences are identified according to the pdb ID and the chain used in the analysis. The numbers under each Signature type indicates the number of Signatures for that particular sequence. For example, sequences 1a91_A and 1afo_A have no Signatures.

Figure S10. C α -rmsd profiles for peptides in Sim1 (panel A), Sim2 (panel B), Sim3 (panel C), and Sim4 (panel D). For the peptide in Sim1, the total rmsd profile is decomposed into the rmsd for the transmembrane part, and the N- and C-termini (amino acid residues 1-4 and 21-27, respectively. All rmsd values are reported in Å and were computed relative to the starting coordinates of the peptides.



Figure S1- part1, panels A-I



Figure S1- part 2, panels J-P



Figure S1 – part 3, panels Q-S



Figure S2



Figure S3

Figure S4-A

Alpha value (for confidence interval)	0.02				
Variable #1 (TT)					
Count	291 Skewness	2.28			
Mean	0.76 Skewness Standard Error	0.14			
Mean LCL	0.6 Kurtosis	10.01			
Mean UCL	0.92 Kurtosis Standard Error	0.28			
Variance	1.31 Alternative Skewness (Fisher's)	2.29			
Standard Deviation	1.14 Alternative Kurtosis (Fisher's)	7.15			
Mean Standard Error	0.07 Coefficient of Variation	1.5			
Minimum	0.E+0 Mean Deviation	0.85			
Maximum	7. Second Moment	1.31			
Range	7. Third Moment	3.4			
Sum	221. Fourth Moment	17.06			
Sum Standard Error	19.49 <i>Median</i>	0.E+0			
Total Sum Squares	547. Median Error	0.			
Adjusted Sum Squares	378.58 Percentile 25% (Q1)	0.E+0			
Geometric Mean	1.19 Percentile 75% (Q2)	1.			
Harmonic Mean	2.99 /QR	1.			
Mode	0.E+0 MAD	0.E+0			

Alpha value (for confidence interval)	0.02						
Variable #1 (ST)							
Count	291 Skewness 2.2	27					
Mean	0.89 Skewness Standard Error 0.1	4					
Mean LCL	0.71 Kurtosis 10	.2					
Mean UCL	1.07 Kurtosis Standard Error 0.2	28					
Variance	1.74 Alternative Skewness (Fisher's) 2.2	28					
Standard Deviation	1.32 Alternative Kurtosis (Fisher's) 7.3	35					
Mean Standard Error	0.08 Coefficient of Variation 1.4	18					
Minimum	0.E+0 Mean Deviation 0.9	94					
Maximum	9. Second Moment 1.7	73					
Range	9. Third Moment 5.1	8					
Sum	259. Fourth Moment 30.6	6					
Sum Standard Error	22.5 Median 0.E+	-0					
Total Sum Squares	735. Median Error 0.0)1					
Adjusted Sum Squares	504.48 Percentile 25% (Q1) 0.E+	-0					
Geometric Mean	1.24 Percentile 75% (Q2)	1.					
Harmonic Mean	2.96 IQR	1.					
Mode	0.E+0 MAD 0.E+	-0					

Alpha value (for confidence interval)	0.02	
	Variable #1 (SS)	
Count	291 Skewness	2.11
Mean	1.17 Skewness Standard Error	0.14
Mean LCL	0.95 Kurtosis	8.77
Mean UCL	1.4 Kurtosis Standard Error	0.28
Variance	2.68 Alternative Skewness (Fisher's)	2.12
Standard Deviation	1.64 Alternative Kurtosis (Fisher's)	5.89
Mean Standard Error	0.1 Coefficient of Variation	1.4
Minimum	0.E+0 Mean Deviation	1.19
Maximum	10. Second Moment	2.67
Range	10. Third Moment	9.22
Sum	341. Fourth Moment	62.61
Sum Standard Error	27.93 Median	1.
Total Sum Squares	1,177. Median Error	0.01
Adjusted Sum Squares	777.41 Percentile 25% (Q1)	0.E+0
Geometric Mean	1.37 Percentile 75% (Q2)	2.
Harmonic Mean	2.93 IQR	2.
Mode	0.E+0 MAD	1.

Alpha value (for confidence interval)		0.02		
	Va	iriable #	1 (TT)	
Count		48	Skewness	0.97
Mean		1.94	Skewness Standard Error	0.34
Mean LCL		1.29	Kurtosis	3.16
Mean UCL		2.58	Kurtosis Standard Error	0.63
Variance		3.42	Alternative Skewness (Fisher's)	1.
Standard Deviation		1.85	Alternative Kurtosis (Fisher's)	0.32
Mean Standard Error		0.27	Coefficient of Variation	0.95
Minimum		0.E+0	Mean Deviation	1.44
Maximum		7.	Second Moment	3.35
Range		7.	Third Moment	5.94
Sum		93.	Fourth Moment	35.51
Sum Standard Error		12.82	Median	1.5
Total Sum Squares		341.	Median Error	0.05
Adjusted Sum Squares		160.81	Percentile 25% (Q1)	1.
Geometric Mean		1.75	Percentile 75% (Q2)	3.
Harmonic Mean		2.34	IQR	2.
Mode	#N/A		MAD	1.5

Alpha value (for confidence interval)	0.02		
	Variable #	1 (ST)	
Count	48	Skewness	1.36
Mean	1.9	Skewness Standard Error	0.34
Mean LCL	1.31	Kurtosis	4.97
Mean UCL	2.48	Kurtosis Standard Error	0.63
Variance	2.86	Alternative Skewness (Fisher's)	1.41
Standard Deviation	1.69	Alternative Kurtosis (Fisher's)	2.33
Mean Standard Error	0.24	Coefficient of Variation	0.89
Minimum	0.E+0	Mean Deviation	1.3
Maximum	8.	Second Moment	2.8
Range	8.	Third Moment	6.4
Sum	91.	Fourth Moment	39.05
Sum Standard Error	11.72	Median	1.
Total Sum Squares	307.	Median Error	0.04
Adjusted Sum Squares	134.48	Percentile 25% (Q1)	1.
Geometric Mean	1.64	Percentile 75% (Q2)	3.
Harmonic Mean	1.76	IQR	2.
Mode	1.	MAD	1.

Alpha value (for confidence interval)	0.02	
	Variable #1 (SS)	
Count	48 Skewness	1.75
Mean	2.33 Skewness Standard Error	0.34
Mean LCL	1.59 Kurtosis	7.13
Mean UCL	3.08 Kurtosis Standard Error	0.63
Variance	4.61 Alternative Skewness (Fisher's)	1.8
Standard Deviation	2.15 Alternative Kurtosis (Fisher's)	4.73
Mean Standard Error	0.31 Coefficient of Variation	0.92
Minimum	0.E+0 Mean Deviation	1.6
Maximum	11. Second Moment	4.5
Range	11. Third Moment	16.78
Sum	112. Fourth Moment	145.23
Sum Standard Error	14.88 Median	2
Total Sum Squares	478. Median Error	0.0
Adjusted Sum Squares	216.67 Percentile 25% (Q1)	1
Geometric Mean	1.9 Percentile 75% (Q2)	3
Harmonic Mean	1.92 /QR	2
Mode	1. MAD	1

Figure S4-B

ALPHA Chains					
Variable #1 (Count SxxxS)					
Count	291	Skewness	1.81268		
Mean	1.05498	Skewness Standard Error	0.14237		
Mean LCL	0.86905	Kurtosis	7.07353		
Mean UCL	1.24091	Kurtosis Standard Error	0.28183		
Variance	1.83835	Alternative Skewness (Fisher's)	1.82209		
Standard Deviation	1.35586	Alternative Kurtosis (Fisher's)	4.1653		
Mean Standard Error	0.07948	Coefficient of Variation	1.28519		
Minimum	0.E+0	Mean Deviation	0.97472		
Maximum	8.	Second Moment	1.83203		
Range	8.	Third Moment	4.49489		
Sum	307.	Fourth Moment	23.74108		
Sum Standard Error	23.12917	Median	1.		
Total Sum Squares	857.	Median Error	0.00584		
Adjusted Sum Squares	533.12027	Percentile 25% (Q1)	0.E+0		
Geometric Mean	1.29781	Percentile 75% (Q2)	2.		
Harmonic Mean	2.53724	IQR	2.		
Mode	0.E+0	MAD	1.		

	Variable a	#2 (Count SxxS)	
Count	291	Skewness	1.65303
lean	0.93471	Skewness Standard Error	0.14237
ean LCL	0.74797	Kurtosis	5.3019
ean UCL	1.12144	Kurtosis Standard Error	0.28183
riance	1.85434	Alternative Skewness (Fisher's)	1.66161
andard Deviation	1.36174	Alternative Kurtosis (Fisher's)	2.36286
ean Standard Error	0.07983	Coefficient of Variation	1.45686
nimum	0.E+0	Mean Deviation	1.02143
ximum	6.	Second Moment	1.84797
nge	6.	Third Moment	4.15263
m	272.	Fourth Moment	18.10598
m Standard Error	23.22959	Median	0.E+0
al Sum Squares	792.	Median Error	0.00586
justed Sum Squares	537.75945	Percentile 25% (Q1)	0.E+0
ometric Mean	1.27831	Percentile 75% (Q2)	1.
armonic Mean	3.25564	IQR	1.
ode	0.E+0	MAD	0.E+0

	variable	#3 (Count SXXT)	
Count	291	Skewness	2.02538
Mean	1.05498	Skewness Standard Error	0.14237
Mean LCL	0.85788	Kurtosis	8.72826
Mean UCL	1.25209	Kurtosis Standard Error	0.28183
Variance	2.06593	Alternative Skewness (Fisher's)	2.03589
Standard Deviation	1.43734	Alternative Kurtosis (Fisher's)	5.84882
Mean Standard Error	0.08426	Coefficient of Variation	1.36243
Minimum	0.E+0	Mean Deviation	1.05379
Maximum	9.	Second Moment	2.05883
Range	9.	Third Moment	5.98326
Sum	307.	Fourth Moment	36.99726
Sum Standard Error	24.5191	Median	1.
Total Sum Squares	923.	Median Error	0.00619
Adjusted Sum Squares	599.12027	Percentile 25% (Q1)	0.E+0
Geometric Mean	1.32682	Percentile 75% (Q2)	2.
Harmonic Mean	2.96146	IQR	2.
Mode	0.E+0	MAD	1.

Variable #4 (Count SxxxT)					
Count	291	Skewness	2.04607		
Mean	0.7354	Skewness Standard Error	0.14237		
Mean LCL	0.58205	Kurtosis	8.28952		
Mean UCL	0.88874	Kurtosis Standard Error	0.28183		
Variance	1.25043	Alternative Skewness (Fisher's)	2.05668		
Standard Deviation	1.11823	Alternative Kurtosis (Fisher's)	5.40245		
Mean Standard Error	0.06555	Coefficient of Variation	1.52058		
Minimum	0.E+0	Mean Deviation	0.84912		
Maximum	7.	Second Moment	1.24614		
Range	7.	Third Moment	2.84621		
Sum	214.	Fourth Moment	12.87241		
Sum Standard Error	19.07553	Median	0.E+0		
Total Sum Squares	520.	Median Error	0.00482		
Adjusted Sum Squares	362.62543	Percentile 25% (Q1)	0.E+0		
Geometric Mean	1.18858	Percentile 75% (Q2)	1.		
Harmonic Mean	3.19396	IQR	1.		
Mode	0.E+0	MAD	0.E+0		

BETA CHAINS						
	Variable #1 (Count SxxxS)					
Count	48	Skewness	0.51381			
Mean	2.1875	Skewness Standard Error	0.33592			
Mean LCL	1.5435	Kurtosis	2.21899			
Mean UCL	2.8315	Kurtosis Standard Error	0.63196			
Variance	3.43218	Alternative Skewness (Fisher's)	0.53054			
Standard Deviation	1.85261	Alternative Kurtosis (Fisher's)	-0.73269			
Mean Standard Error	0.2674	Coefficient of Variation	0.84691			
Minimum	0.E+0	Mean Deviation	1.55208			
Maximum	6.	Second Moment	3.36068			
Range	6.	Third Moment	3.16553			
Sum	105.	Fourth Moment	25.06156			
Sum Standard Error	12.83529	Median	2.			
Total Sum Squares	391.	Median Error	0.04837			
Adjusted Sum Squares	161.3125	Percentile 25% (Q1)	1.			
Geometric Mean	1.9517	Percentile 75% (Q2)	3.			
Harmonic Mean	2.55319	IQR	2.			
Mode	0.E+0	MAD	1.			

	Variable a	#2 (Count SxxS)	
Count	48	Skewness	1.61804
Mean	1.79167	Skewness Standard Error	0.33592
Mean LCL	1.26007	Kurtosis	7.27672
Mean UCL	2.32326	Kurtosis Standard Error	0.63196
Variance	2.33865	Alternative Skewness (Fisher's)	1.67071
Standard Deviation	1.52927	Alternative Kurtosis (Fisher's)	4.89434
Mean Standard Error	0.22073	Coefficient of Variation	0.85354
Minimum	0.E+0	Mean Deviation	1.06771
Maximum	8.	Second Moment	2.28993
Range	8.	Third Moment	5.60692
Sum	86.	Fourth Moment	38.15754
Sum Standard Error	10.59506	Median	2.
Total Sum Squares	264.	Median Error	0.03993
Adjusted Sum Squares	109.91667	Percentile 25% (Q1)	1.
Geometric Mean	1.68553	Percentile 75% (Q2)	2.
Harmonic Mean	2.0623	IQR	1.
Mode	2.	MAD	1.

	Variable	#3 (Count SxxT)	
Count	48	Skewness	0.39149
Mean	2.02083	Skewness Standard Error	0.33592
Mean LCL	1.48668	Kurtosis	2.37423
Mean UCL	2.55499	Kurtosis Standard Error	0.63196
Variance	2.36126	Alternative Skewness (Fisher's)	0.40423
Standard Deviation	1.53664	Alternative Kurtosis (Fisher's)	-0.55998
Mean Standard Error	0.22179	Coefficient of Variation	0.7604
Minimum	0.E+0	Mean Deviation	1.27517
Maximum	6.	Second Moment	2.31207
Range	6.	Third Moment	1.37632
Sum	97.	Fourth Moment	12.69179
Sum Standard Error	10.64615	Median	2.
Total Sum Squares	307.	Median Error	0.04012
Adjusted Sum Squares	110.97917	Percentile 25% (Q1)	1.
Geometric Mean	1.85415	Percentile 75% (Q2)	3.
Harmonic Mean	2.23776	IQR	2.
Mode	1.	MAD	1.

Variable #4 (Count SxxxT)								
Count	48	Skewness	0.81957					
Mean	2.4375	Skewness Standard Error	0.33592					
Mean LCL	1.74262	Kurtosis	3.05187					
Mean UCL	3.13238	Kurtosis Standard Error	0.63196					
Variance	3.99601	Alternative Skewness (Fisher's)	0.84625					
Standard Deviation	1.999	Alternative Kurtosis (Fisher's)	0.19395					
Mean Standard Error	0.28853	Coefficient of Variation	0.8201					
Minimum	0.E+0	Mean Deviation	1.60677					
Maximum	8.	Second Moment	3.91276					
Range	8.	Third Moment	6.34326					
Sum	117.	Fourth Moment	46.72326					
Sum Standard Error	13.84949	Median	2.					
Total Sum Squares	473.	Median Error	0.0522					
Adjusted Sum Squares	187.8125	Percentile 25% (Q1)	1.					
Geometric Mean	2.08915	Percentile 75% (Q2)	4.					
Harmonic Mean	2.41192	IQR	3.					
Mode	2.	MAD	1.					

Figure S4-C

Variable #5 (Count TxxxT)								
Count	291	Skewness	1.92348					
Mean	0.76976	Skewness Standard Error	0.14237					
Mean LCL	0.61001	Kurtosis	7.10462					
Mean UCL	0.92951	Kurtosis Standard Error	0.28183					
Variance	1.35715	Alternative Skewness (Fisher's)	1.93346					
Standard Deviation	1.16497	Alternative Kurtosis (Fisher's)	4.19694					
Mean Standard Error	0.06829	Coefficient of Variation	1.51342					
Minimum	0.E+0	Mean Deviation	0.87821					
Maximum	6.	Second Moment	1.35249					
Range	6.	Third Moment	3.02544					
Sum	224.	Fourth Moment	12.99594					
Sum Standard Error	19.87287	Median	0.E+0					
Total Sum Squares	566.	Median Error	0.00502					
Adjusted Sum Squares	393.57388	Percentile 25% (Q1)	0.E+0					
Geometric Mean	1.20018	Percentile 75% (Q2)	1.					
Harmonic Mean	3.15618	IQR	1.					
Mode	0.E+0	MAD	0.E+0					

	Variable #	#6 (Count TxxT)					
Count	291	Skewness	2.17813				
Mean	0.73196	Skewness Standard Error	0.14237				
Mean LCL	0.58947	Kurtosis	10.10485				
Mean UCL	0.87444	0.87444 Kurtosis Standard Error					
Variance	1.07963	Alternative Skewness (Fisher's)	2.18943				
Standard Deviation	1.03905	Alternative Kurtosis (Fisher's)	7.24936				
Mean Standard Error	0.06091	Coefficient of Variation	1.41955				
Minimum	0.E+0	Mean Deviation	0.77975				
Maximum	7.	Second Moment	1.07592				
Range	7.	Third Moment	2.43082				
Sum	213.	Fourth Moment	11.69741				
Sum Standard Error	17.72491	Median	0.E+0				
Total Sum Squares	469.	Median Error	0.00448				
Adjusted Sum Squares	313.09278	Percentile 25% (Q1)	0.E+0				
Geometric Mean	1.15955	Percentile 75% (Q2)	1.				
Harmonic Mean	2.68385	IQR	1.				
Mode	0.E+0	MAD	0.E+0				

		5	
	Variable #	5 (Count TxxxT)	
Count	48	Skewness	0.77054
Mean	2.58333	Skewness Standard Error	0.33592
Mean LCL	1.81827	Kurtosis	2.8654
Mean UCL	3.3484	Kurtosis Standard Error	0.63196
Variance	4.84397	Alternative Skewness (Fisher's)	0.79563
Standard Deviation	2.2009	Alternative Kurtosis (Fisher's)	-0.01352
Mean Standard Error	0.31767	Coefficient of Variation	0.85196
Minimum	0.E+0	Mean Deviation	1.77431
Maximum	8.	Second Moment	4.74306
Range	8.	Third Moment	7.95949
Sum	124.	Fourth Moment	64.46166
Sum Standard Error	15.2483	Median	2.
Total Sum Squares	548.	Median Error	0.05747
Adjusted Sum Squares	227.66667	Percentile 25% (Q1)	1.
Geometric Mean	2.1615	Percentile 75% (Q2)	4.
Harmonic Mean	2.54964	IQR	3.
Mode	#N/A	MAD	1.

	Variable	#6 (Count TxxT)	
Count	48	Skewness	0.75555
Mean	2.	Skewness Standard Error	0.33592
Mean LCL	1.33501	Kurtosis	2.4013
Mean UCL	2.66499	Kurtosis Standard Error	0.63196
Variance	3.65957	Alternative Skewness (Fisher's)	0.78014
Standard Deviation	1.913	Alternative Kurtosis (Fisher's)	-0.52986
Mean Standard Error	0.27612	Coefficient of Variation	0.9565
Minimum	0.E+0	Mean Deviation	1.625
Maximum	6.	Second Moment	3.58333
Range	6.	Third Moment	5.125
Sum	96.	Fourth Moment	30.83333
Sum Standard Error	13.25366	Median	1.
Total Sum Squares	364.	Median Error	0.04995
Adjusted Sum Squares	172.	Percentile 25% (Q1)	1.
Geometric Mean	1.75824	Percentile 75% (Q2)	3.
Harmonic Mean	2.2695	IQR	2.
Mode	1.	MAD	1.

		Alnha	chaine		Reta (haine
Cinnoturo		BUILDING				
aigilature	>	Ъ	Normal Distribution	8	٩	Normal Distribution
SxxxS	0.7575	2.20E-16	No	0.9046	0.0008876	No
SxxS	0.7193	2.20E-16	No	0.8342	8.48E-06	No
SxxT	0.7368	2.20E-16	No	0.9215	0.003362	No
SxxxT	0.6908	2.20E-16	No	0.9062	0.001001	No
TxxxT	0.6951	2.20E-16	No	0.9068	0.001051	No
TxxT	0.703	2.20E-16	No	0.8591	3.83E-05	No

if the p-value is less than the chosen alpha level (0.05), then the null hypothesis is rejected

Figure S5



Figure S6-A





Figure S6-C



Figure S6-D









Figure S6-H



Figure S6-I



Figure S6-J



Figure S6-K



Figure S6-L





Figure S6-N











Figure S7-A











Figure S7-F

Data- β , SxxS Signatures



Figure S8-A

Sequences	Cluster	тт	ST	SS	TxxT	TxxxT	SxxxT	SxxxS	SxxT	SxxS
1a91_A	1	0	0	0	0	0	0	0	0	0
1afo_A	1	0	0	0	0	0	0	0	0	0
1aig_H	1	0	1	1	1	0	0	0	0	0
1aig_L	1	0	0	0	1	1	1	0	1	0
1ar1_B	1	0	0	1	4	0	0	0	0	0
1b9u_A	1	0	0	0	0	0	0	0	0	0
1ba4_A	1	0	0	0	0	0	0	0	0	0
1be3_K	1	0	0	0	0	0	0	1	0	0
1bzk_A	1	0	0	0	0	0	1	0	1	0
1c17_M	1	0	0	0	0	1	0	1	0	2
1c51_B	1	0	0	0	0	0	0	0	0	0
1dx7_A	1	0	0	0	1	0	0	1	0	0
1et2_S	1	0	1	1	4	1	1	0	1	1
1eys_M	1	0	0	0	1	1	0	1	0	0
1f6g_A	1	2	0	0	4	0	0	0	1	0
1fft_C	1	0	1	1	4	1	1	4	1	0
1fx8_A	1	2	2	0	1	0	1	0	0	2
1ijd_B	1	0	0	0	0	0	0	0	0	0
1izl_A	1	3	2	2	1	0	0	4	1	1
1jb0_F	1	1	0	0	0	0	1	0	0	0
1jb0_l	1	0	0	0	0	0	0	1	0	0
1jb0_K	1	2	0	0	1	1	0	0	0	0
1jb0_L	1	0	1	2	0	0	0	4	1	0
1jb0_M	1	0	1	0	0	0	0	0	0	0
1jb0_X	1	0	0	0	0	0	1	0	0	0
1jdm_A	1	0	0	0	0	0	0	0	0	0
1kqf_B	1	0	1	0	1	1	0	1	0	1
1kqf_C	1	0	0	0	1	0	0	0	0	2
1kyk_A	1	0	0	1	0	0	0	0	0	0

Figure	S8-B
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1 7v_A	1	0	2	0	0	0	1	0	0	0
1lbn_A	1	0	0	0	0	0	0	1	1	0
1lgh_A	1	0	1	0	0	0	0	0	0	0
1m0k_A	1	2	2	0	0	0	0	1	0	0
1m56_D	1	0	0	0	0	0	1	0	0	0
1nw0_A	1	0	2	0	0	0	0	0	0	0
1oed_B	1	1	0	0	0	1	0	4	3	1
1oed_C	1	0	4	2	1	0	0	9	1	0
1orq_C	1	1	0	1	1	0	0	4	1	2
1p7b_A	1	1	1	3	1	0	1	4	2	1
1pb2_A	1	2	1	1	1	1	0	9	3	1
1pb4_D	1	2	1	1	0	1	0	1	1	2
1prc_H	1	0	0	0	0	0	0	1	1	1
1pw4_A	1	0	0	2	1	0	0	1	0	2
1q90_A	1	0	0	0	0	0	0	0	1	0
1q90_L	1	0	0	0	0	0	0	0	0	0
1q90_M	1	0	0	0	1	0	0	0	0	0
1q90_N	1	0	0	0	0	0	0	1	0	0
1qle_C	1	1	0	0	0	1	0	0	0	0
1rh5_A	1	1	1	2	1	0	1	1	0	1
1rh5_B	1	1	0	0	0	0	0	0	0	0
1rh5_C	1	0	0	0	0	1	0	0	0	0
1rkl_A	1	0	1	0	0	0	1	0	0	1
1s6e_A	1	0	2	0	1	0	0	4	3	2
1spf_A	1	0	0	0	0	0	0	0	0	0
1sr1_A	1	1	0	1	1	1	0	1	0	1
1upe_A	1	0	2	2	1	0	1	4	0	1
1vry_A	1	2	0	1	1	1	0	0	0	1
1waz_A	1	0	0	0	0	0	0	0	1	0
1wrg_A	1	0	0	1	0	0	0	0	1	0

Fiqure	S8-C
	~ ~ ~

1xio_A	1	2	1	1	4	0	2	0	1	0
1y8s_A	1	0	3	1	4	1	0	0	3	1
1yew_C	1	1	0	0	1	2	0	0	1	0
1zas_A	1	0	0	0	0	0	0	1	1	0
1zc7_A	1	0	2	1	4	1	0	0	1	1
1zza_A	1	1	0	0	0	1	0	0	1	0
2a06_E	1	2	1	3	1	1	2	9	0	3
2a06_G	1	0	0	0	1	0	0	0	0	0
2a06_W	1	0	1	0	0	1	0	0	0	0
2acz_C	1	0	0	1	0	0	2	1	0	1
2acz_D	1	0	0	0	0	1	1	0	1	1
2akh_X	1	0	0	1	1	0	0	0	0	1
2akh_Y	1	1	1	2	1	1	0	1	2	1
2akh_Z	1	2	0	0	1	1	0	0	1	0
2aui_A	1	0	0	0	0	0	0	1	0	0
2axt_E	1	1	1	0	0	0	1	0	0	0
2axt_F	1	0	0	0	1	0	0	0	0	0
2axt_H	1	1	1	0	0	0	0	0	0	0
2axt_l	1	0	0	0	0	1	0	0	0	0
2axt_K	1	0	0	0	0	0	0	0	0	0
2axt_T	1	0	0	0	0	0	0	0	0	0
2b0x_A	1	1	2	2	1	1	2	4	2	2
2b2f_A	1	1	2	3	0	0	2	0	0	1
2b6s_A	1	0	2	1	0	0	1	4	0	0
2b76_C	1	1	1	0	0	1	0	0	0	0
2b76_D	1	0	0	0	1	0	0	0	0	0
2bg9_E	1	1	2	1	1	1	0	1	3	0
2bl2_A	1	1	0	0	0	0	0	1	0	1
2c3e_A	1	0	0	0	0	0	0	1	0	0
2cpb_A	1	0	0	0	0	0	0	1	0	1

	Fi	qure	S8-D	1
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2d2c_A	1	0	0	1	0	0	1	0	1	0
2d2c_B	1	1	0	0	1	0	0	0	0	0
2d2c_D	1	1	0	0	1	1	0	0	0	0
2d2c_E	1	0	0	0	0	0	0	0	0	0
2d2c_F	1	0	0	0	0	0	0	0	0	0
2d2c_G	1	0	0	0	0	0	0	0	0	0
2d57_A	1	1	1	2	1	0	2	1	2	2
2dyr_l	1	0	1	0	0	0	0	0	0	0
<mark>2evu_</mark> A	1	1	0	1	0	0	1	1	1	1
2f93_A	1	2	0	1	1	0	0	1	0	1
2f95_B	1	0	1	0	0	0	0	1	2	0
2fbw_C	1	1	0	2	0	1	0	9	1	1
2fbw_D	1	0	0	1	0	0	1	1	1	0
2fkw_A	1	1	0	0	0	0	0	0	1	0
<mark>2fyn_</mark> A	1	1	1	0	4	0	0	4	2	0
<mark>2fyn_</mark> B	1	1	0	0	1	1	1	0	1	0
2fyn_C	1	1	0	1	0	0	0	1	0	0
2h8a_A	1	0	1	1	0	1	0	0	2	0
2hac_A	1	0	0	0	0	0	0	0	0	0
2ibz_G	1	0	0	0	0	0	0	1	1	0
2ibz_l	1	0	0	1	1	1	1	0	0	1
2ic8_A	1	0	0	0	0	0	0	1	0	0
<mark>2j7a_C</mark>	1	0	1	0	0	0	0	1	0	0
<mark>2jo1_</mark> A	1	0	1	1	0	0	0	0	0	0
<mark>2jow_</mark> A	1	0	0	0	1	0	0	0	0	1
<mark>2jp3_</mark> A	1	0	1	1	0	1	0	0	1	0
<mark>2jwa_</mark> A	1	0	0	0	0	0	0	1	1	1
2k1k_A	1	0	0	0	0	0	1	1	0	0
2k37_A	1	0	0	0	0	0	0	1	0	0
2k73_A	1	0	0	0	0	1	1	0	0	0

Figure S8-E

2k9j_B	1	0	0	0	0	0	0	0	0	0
2k9p_A	1	0	2	1	0	0	0	1	4	1
2k9y_A	1	0	0	0	0	0	0	1	0	0
2ka1_A	1	0	0	0	0	0	0	1	0	0
2kb7_P	1	0	1	0	0	0	0	0	0	0
2kdc_A	1	1	0	1	1	1	0	0	0	0
2ki9_A	1	1	0	0	0	0	1	0	1	0
2kih_A	1	0	0	1	0	0	0	1	0	1
2kix_A	1	0	0	1	0	0	0	1	0	1
2klu_A	1	0	0	0	0	0	1	0	0	1
2knc_A	1	0	0	0	0	0	0	0	0	0
2kns_A	1	0	0	3	0	0	0	1	0	1
2kog_A	1	0	1	0	1	0	1	0	0	1
2ksd_A	1	0	0	0	0	0	0	0	0	0
2kse_A	1	1	1	1	0	0	0	0	0	0
2ksf_A	1	0	0	0	0	0	2	0	0	0
2nq2_A	1	0	1	1	0	0	0	9	2	0
2nr9_A	1	0	0	0	0	1	0	0	1	0
2nrg_A	1	0	0	0	0	1	0	0	0	0
2oar_A	1	0	1	1	4	2	0	0	1	1
2oau_A	1	1	1	3	1	1	0	0	0	0
2pno_A	1	1	0	0	0	0	1	0	0	0
2q67_A	1	1	1	0	4	0	1	0	2	1
2q7m_A	1	1	2	0	4	1	1	1	0	0
2qfi_A	1	0	0	0	1	0	0	1	1	1
2rdd_B	1	0	0	0	0	0	0	0	0	1
2rh1_A	1	1	0	3	1	1	1	4	3	1
2v4h_A	1	0	0	2	0	0	0	1	0	0
2vpw_C	1	0	0	0	0	0	1	0	0	0
2w1p_A	1	1	0	0	0	0	0	0	1	0

Figure S	38-F	1
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2w83_C	1	0	0	0	0	0	0	0	0	0
2wgm_A	1	0	2	0	0	0	0	0	0	0
<mark>2wsc_1</mark>	1	0	0	2	1	0	0	4	0	3
<mark>2wsc_H</mark>	1	2	0	1	0	0	1	1	2	1
2wsc_l	1	0	1	0	0	0	0	0	0	0
<mark>2wsc_J</mark>	1	0	1	0	0	0	0	0	0	0
<mark>2wsc_K</mark>	1	3	1	2	1	1	1	4	2	2
<mark>2yvx_</mark> A	1	0	0	3	0	2	0	0	1	1
<mark>2z73_</mark> A	1	1	1	1	0	0	1	4	3	1
<mark>2z9a_A</mark>	1	0	0	1	0	0	0	1	0	1
<mark>2zjs_</mark> E	1	0	0	0	1	0	0	0	0	0
<mark>2zjs_</mark> Y	1	0	0	0	0	1	0	1	1	0
<mark>2zw3_</mark> A	1	0	2	1	4	0	1	0	1	1
3a0b_J	1	0	0	1	0	0	0	0	0	0
3a0b_L	1	0	0	1	0	0	0	0	0	0
3a0b_M	1	0	0	1	0	0	0	1	0	0
3a0b_Z	1	0	0	0	0	0	0	0	0	0
<mark>3a3y_</mark> B	1	2	0	2	1	0	0	4	1	1
<mark>3a3y_G</mark>	1	0	0	0	0	0	1	0	0	0
3a7k_A	1	1	3	3	1	1	0	1	2	1
3abl_B	1	2	1	3	9	1	2	0	0	2
3abl_D	1	0	1	1	0	0	0	1	0	1
3abl_G	1	0	0	0	0	1	0	1	0	0
3abl_J	1	0	0	0	0	0	0	0	0	0
<mark>3abl_K</mark>	1	0	0	0	0	0	0	0	1	0
3abl_L	1	0	0	0	0	0	0	0	0	0
3abl_M	1	0	0	1	0	0	0	0	0	0
3b4r_A	1	0	1	0	0	0	0	0	0	0
3b5d_A	1	1	1	0	0	0	1	0	2	1
3beh_A	1	3	2	2	1	1	1	4	2	2

rigure so-G	Figure	S8-G
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3bvd_B	1	1	1	0	1	1	0	0	0	0
3bvd_C	1	0	0	0	0	0	0	0	0	0
<mark>3bz1_X</mark>	1	0	0	1	0	0	1	0	0	1
<mark>3bz1_y</mark>	1	0	0	0	0	0	0	0	0	0
3c02_A	1	1	1	2	0	0	1	16	0	0
3c1g_A	1	0	0	1	1	1	1	0	2	0
3chx_B	1	2	1	0	1	0	1	1	0	0
3cn5_A	1	0	0	1	1	1	0	4	2	0
3cp1_A	1	0	0	0	0	0	0	1	0	0
3cx5_D	1	2	0	1	1	1	0	0	1	0
3d31_C	1	0	0	2	0	0	0	9	1	1
3ddl_A	1	0	2	2	4	0	1	4	0	1
<mark>3dhw_</mark> A	1	0	0	0	1	2	0	0	0	0
<mark>3din_</mark> D	1	0	0	0	0	0	0	1	0	1
<mark>3din_</mark> E	1	0	0	0	0	0	1	0	0	1
3dl8_C	1	0	0	0	0	0	0	1	0	0
3dl8_E	1	1	1	0	1	0	0	0	1	0
<mark>3dww_</mark> A	1	0	1	1	0	0	1	1	0	0
<mark>3e7k_</mark> A	1	0	0	0	1	0	0	0	2	1
<mark>3eam_</mark> A	1	0	2	0	1	1	1	0	1	0
3egw_C	1	2	0	1	0	0	0	0	1	0
<mark>3eh3_</mark> A	1	0	2	0	1	2	0	4	3	2
<mark>3fh6_G</mark>	1	1	1	1	0	0	0	0	0	0
3hd7_B	1	0	1	1	0	0	1	1	0	1
3hgc_A	1	1	1	2	4	1	0	1	3	1
<mark>3jyc_</mark> A	1	3	1	1	4	1	0	1	2	0
<mark>3k3f_</mark> A	1	2	2	0	1	1	0	1	2	1
3k69_A	1	0	0	0	0	2	1	1	0	0
3kcu_A	1	1	1	0	1	1	1	0	1	1
3llq_A	1	0	2	1	1	0	2	0	0	1

Figure	S8-H

1dop_D	2	1	1	1	4	2	0	1	2	0
1fft_A	2	2	1	1	1	2	2	1	0	0
1kad_A	2	1	4	0	4	3	0	4	2	0
105w_A	2	0	1	1	0	3	1	1	1	0
1suk_A	2	3	1	1	4	3	2	4	2	1
2a0d_A	2	2	4	5	0	3	0	4	2	1
2a65_A	2	1	0	1	4	3	0	0	2	0
2bs2_C	2	1	1	2	1	2	0	1	1	0
2gfp_A	2	1	1	2	0	2	0	1	3	0
2hyd_A	2	3	2	0	4	1	2	1	2	1
2iub_A	2	1	1	3	1	3	2	1	2	1
2j58_A	2	3	1	0	0	1	2	1	4	0
2jln_A	2	1	4	1	16	2	2	1	1	0
2r6g_F	2	6	1	3	4	4	3	0	3	1
2vl0_A	2	1	1	1	1	2	0	1	2	0
2wpr_A	2	4	0	0	4	2	1	0	1	0
2wsc_A	2	6	1	3	4	3	1	4	3	2
3c9l_A	2	5	1	0	1	3	1	1	2	0
3chx_A	2	2	2	1	9	2	1	1	0	1
3det_A	2	1	1	1	0	2	0	1	2	0
3h9v_A	2	2	1	3	1	3	2	4	6	0
3kbc_A	2	0	0	2	0	4	1	0	4	0
3kp9_A	2	2	0	1	4	3	0	0	3	0
1fft_B	3	1	0	0	1	1	2	25	1	0
1j4n_A	3	2	0	3	0	0	3	9	5	2
1lnq_A	3	0	3	0	1	0	2	1	2	0
1lvi_A	3	0	2	2	1	1	5	9	4	4
1p49_A	3	1	3	3	4	2	3	4	2	2
1pb4_C	3	1	0	1	0	1	2	1	1	0
1xl4_A	3	1	0	2	25	0	2	4	2	2

									Fi	gure S8-I
1y36_A	3	2	2	3	0	3	2	1	2	3
1yg7_A	3	0	0	1	1	1	3	9	0	0
1yo9_L	3	1	0	5	1	0	3	9	4	2
1zti_A	3	1	2	4	9	2	2	9	0	4
2ac6_A	3	0	3	4	4	1	2	9	1	3
2bg9_A	3	0	3	3	0	1	2	4	2	3
2bmn_A	3	1	0	1	1	1	2	0	0	0
2cfp_A	3	1	0	2	0	0	3	1	3	3
2f75_A	3	1	1	5	1	0	4	9	3	1
2g2a_A	3	0	0	5	0	0	3	1	2	0
2iil	3	1	3	2	1	2	1	9	2	3
2ik3	3	2	3	1	1	2	2	1	2	3
2wsc_2	3	2	5	3	4	1	2	25	2	3
2wvy_A	3	0	1	3	9	0	4	1	3	3
3b9w_A	3	3	0	0	16	1	2	4	4	2
3dtu_A	3	2	3	2	0	2	4	9	0	4
3hqk_A	3	1	2	4	0	1	2	1	1	2
3ixz_B	3	1	2	0	0	0	4	1	1	0
1bcc_C	4	0	0	2	16	3	2	1	1	2
1mhs_A	4	3	2	4	9	3	1	9	2	4
1y9c_A	4	1	1	0	1	4	1	4	1	2
1z8e_A	4	2	3	2	1	2	0	4	6	3
1zcd_A	4	1	0	2	0	0	0	4	1	4
2axt_B	4	2	0	3	1	1	0	0	2	3
2axt_C	4	2	0	5	1	0	3	0	0	4
2gfz_A	4	0	3	2	1	1	1	9	2	4
2iqp_A	4	0	1	2	0	2	0	4	1	3
2jiz_G	4	1	1	3	0	1	1	9	2	3
2r9r_B	4	2	4	5	9	4	1	4	3	4
2wcd A	4	3	0	2	1	3	0	9	1	2

rigure so	3-J
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2wit_A	4	2	4	2	0	4	2	9	3	4
2wsc_3	4	0	0	3	0	0	1	4	1	3
2wsc_F	4	0	0	6	1	1	0	1	0	2
3b8c_A	4	1	3	2	9	3	2	16	5	2
3dh4_A	4	2	2	2	1	2	1	9	3	5
3fwl_A	4	2	2	2	9	3	1	16	3	3
3g67_A	4	0	0	2	0	2	0	4	2	3
3gi8_C	4	0	1	2	1	0	0	4	0	5
3hd6_A	4	0	2	3	4	0	1	4	1	3
1kpw_A	5	0	4	5	0	1	2	9	4	5
1oz5_A	5	2	3	8	1	0	3	36	2	3
2he6	5	1	1	5	9	2	1	36	2	5
2wsc_G	5	0	2	7	0	0	1	36	1	3
3b5w_A	5	1	4	6	9	0	3	16	3	6
2g1x_A	6	1	3	3	9	6	5	16	2	3
2gif_A	6	3	7	7	4	6	1	16	2	4
3ixz_A	7	2	4	3	4	4	5	1	8	3
3kg2_A	7	2	6	3	1	3	5	16	9	6
2agv_A	8	7	5	4	49	6	2	36	5	3
2amk_A	8	5	2	9	36	3	2	36	2	4
3g5u_A	9	6	9	5	1	2	3	64	5	6
1u5n_A	10	9	6	10	4	5	7	16	7	6

Figure S9

Data-b	Cluster	SS	ST	TT	SxxxS	SxxS	SxxT	ТхххТ	ТххТ	SxxxT
1mm4_A	1	0	1	1	0	0	0	2	0	0
2f1c_X	1	0	1	1	0	0	0	2	1	1
2k0l_A	1	0	1	0	2	0	0	0	1	1
3hw9_A	1	0	1	0	0	0	2	3	1	1
1fw2_A	1	1	0	0	2	1	1	0	0	1
1orm_A	1	1	1	1	2	0	1	2	0	1
1tlw_A	1	1	2	0	1	1	1	1	0	0
2erv_A	1	1	1	0	0	0	1	1	0	1
2f1t_A	1	1	0	2	1	1	0	2	2	0
2qom_A	1	1	1	0	2	3	1	1	1	1
2wjq_A	1	1	0	1	1	2	2	1	1	2
3emo_C	1	1	2	1	0	2	1	1	0	2
3fid_A	1	1	0	0	1	1	1	1	1	2
1yc9_A	1	2	2	1	2	1	1	0	0	1
204v_A	1	3	1	2	0	1	0	0	1	3
3dwn_A	1	3	1	3	0	2	2	3	1	4
1h6s_1	1	4	1	3	0	1	1	0	1	2
1uxf_A	1	4	2	1	0	0	0	3	2	5
1uun_A	2	0	1	2	2	0	3	0	0	0
1e54_A	2	1	3	0	0	2	3		1	2
2por	2	1	1	2	1	2	2	2	0	1
1aOs_P	2	2	3	2	1	3	2	1	1	2
2odj_A	2	2	0	3	1	1	4	1	1	0
1i78_A	2	3	1	2	1	2	3	1	0	1
3emn X	2	3		1	0	2	4	0	3	0
7ahl A	2	3	2	2	1	2	3	2	4	2
3dwo X	3	2	1	1	3	1	0	5	1	4
2qdz_A	3	1	2	0	3	2	3	4	0	4
3bry_A	3	4	1	1	3	2	0	6	3	2
1mpr_A	3	3	5	2	3	3	3	3	1	4
3kvn_X	3	1	4	0	4	5	1	3	1	2
1p4t_A	3	2	1	0	5	2	0	0	0	2
1tqq_A	4	3	2	5	6	3	3	3	2	5
2guf_A	4	3	3	4	5	1	4	6	4	2
1k24_A	4	4	1	2	5	3	2	3	4	2
1kmo A	4	4	4	2	5	2	4	4	3	0
1wp1 A	4	1	1	3	3	0	3	3	3	3
1uyn X	4	0	4	1	3	2	2	4	3	2
2iah_A	4	4	3	1	3	1	3	3	6	5
3jty A	4	1	1	0	3	2	2	1	3	2
2grx A	5	5	0	4	1	2	5	3	4	8
2hdf_A	5	7	1	4	4	2	6	8	4	7
1fep_A	6	2	5	6	2	4	4	8	6	6
1xkw A	6	1	4	7	6	1	4	5	6	3
3efm A	6	1	2	5	6	2	3	7	6	5
1v36_A	7	5	8	3	4	3	1	4	5	6
3csl A	8	7	4	5	4	8	4	6	3	4
3fhh_A	8	11	5	6	3	5	1	5	5	4



Figure S10

Supplementary Information References

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