SUPPLEMENTARY TABLE AND FIGURE LEGENDS

Table S1

Members of PE/PPE, and non-PE/PPE family found to be exactly similar and different between H_{37}Rv and H_{37}Ra strains of *Mycobacterium tuberculosis.* Members with * superscript are not annotated in H_{37}Ra, while members with $^{\#}$ superscript have been discontinued in NCBI database.

Table S2

List of PE/PPE proteins showing differences between H_{37}Rv and H_{37}Ra strains of *Mycobacterium tuberculosis.*

Table S3

Instability index, Aliphatic index and Gravy values of members of PE/PPE, and non-PE/PPE family found to be different between H_{37}Rv and H_{37}Ra strains of Mycobacterium tuberculosis

Figure S1

Gain or loss of globular domain as a function of variation between H_{37}Rv and H_{37}Ra as measured by GlobPlot analyses. Disorder propensity of the protein stretch is calculated by GlobPlot analyses to identify the globular domain which are shown in pink. Sequence alignment above the figure illustrates the amino acid sequence differences between H_{37}Rv and H_{37}Ra.
A: N-terminal extension in MRA_0313 leads to an additional globular domain.
B: N-terminal deletion in MRA_2113 leads to loss of globular domain.
C: Insertion in MRA_1102 leads to an additional globular domain.
D: MRA_3635 showed similarity to Rv3595c in the length and sequence of the globular domain.
E: MRA_3634 has a single globular domain which is different in sequence when compared with Rv3595c.
F: N-terminal extension in MRA_1156 leads to extension in already existing globular domain.
G: Insertions and substitutions in MRA_3950 result in extension of globular domain.
H: A single amino acid change of serine in H_{37}Rv to lysine in H_{37}Ra in PhoP (MRA_0767) had no effect on globular domain profile when compared to Rv0757.

Figure S2

Nucleotide variations between $H_{37}Rv$ and $H_{37}Ra$ result in gain, loss or both gain and loss of serine/threonine phosphorylation sites in the different proteins. The predictive phosphorylation site(s) in proteins is represented by blue circle (in the case of $H_{37}Rv$) or red dots (in case of $H_{37}Ra$). Overlap of blue and red circle indicates no gain or loss of phosphorylation sites in $H_{37}Rv$ and $H_{37}Ra$ proteins. Horizontal line represents the cutoff (threshold) above which it is considered as a putative phosphorylation site. The actual sequence of amino acids and the potential phosphorylation site (highlighted in red) is shown above the respective figures.

A: Deletion in MRA_0265 leads to loss of two serine phosphorylation site.
B: N-terminal deletion in MRA_0295 leads to loss of two serine phosphorylation sites.
C: N-terminal deletion in MRA_0763 leads to loss of one serine phosphorylation site.
D: N-terminal extension in MRA_0313 leads to gain of one threonine and three serine phosphorylation sites.
E: Insertion in MRA_2767 leads to gain of two serine phosphorylation sites.
F: N-terminal extension in MRA_1205 leads to gain of one serine phosphorylation site.
G: Deletion and substitutions in MRA_1102 lead to gain of four and loss of two serine phosphorylation sites.
H: Deletion in MRA_3428 leads to loss of one threonine phosphorylation site.
I: Deletion in MRA_2113 leads to loss of one serine phosphorylation site.
J: Substitution in MRA_0363 leads to gain of one serine phosphorylation site.
K: InDels and substitutions in MRA_1772 lead to loss of two and gain of one serine phosphorylation sites.
L: Deletion in MRA_3553 leads to loss of two serine phosphorylation sites.
M: Substitutions in MRA_0288 lead to loss three serine phosphorylation sites.
N: Substitution in MRA_0755 leads to a loss of one serine phosphorylation site.
O: Deletion in MRA_3384 leads to a loss of two threonine and thirteen serine phosphorylation sites.
P: Insertions and substitutions in MRA_0395 lead to loss of one and gain of three serine phosphorylation sites.
Q: Insertions and substitutions in MRA_0885 lead to gain of one and loss of one serine phosphorylation site.
R: Substitutions and deletions in MRA_1205A lead to gain of two and loss of two serine phosphorylation site positions.
S: Substitutions in MRA_3635 lead to gain of one serine and one threonine phosphorylation site.
T: Substitutions and deletions in MRA_3634 lead to loss of two and gain of seven serine phosphorylation sites.
U: PhoP in $H_{37}Ra$ (MRA_0767) has a single substitution which does not alter the number of Ser/Thr phosphorylation sites.

V: Substitutions in MRA_3950, SigM in H$_{37}$Ra result in gain of one and loss of two serine phosphorylation sites.
W: Mmpl13b in H$_{37}$Ra (MRA_1156) has an N-terminal extension which leads to gain of one serine phosphorylation site.

Table S1: Members of PE/PPE, and non-PE/PPE family found to be exactly similar and different between H$_{37}$Rv and H$_{37}$Ra strains of Mycobacterium tuberculosis

S. no.	Family	Members with no difference between H$_{37}$Rv and H$_{37}$Ra				Members different between H$_{37}$Rv and H$_{37}$Ra	
1	PE/PPE	Rv0096 (PPE1)	Rv2892c (PPE45)	Rv1386 (PE15)	Rv1651c (PE_PGRS30)	Rv0109 (PE_PGRS1)	Rv1450c (PE_PGRS27)
		Rv0280 (PPE3)	Rv3018c (PPE46)	Rv1430 (PE16)	Rv1768 (PE_PGRS31)	Rv0124 (PE_PGRS2)	Rv1759c (wag22)
		Rv0305c (PPE6)	Rv3125c (PPE49)	Rv1646 (PE17)	Rv1818c (PE_PGRS33)	Rv0256c (PPE2)	Rv1787 (PPE25)
		Rv0755c (PPE12)	Rv3135 (PPE50)	Rv1788 (PE18)	Rv1840c (PE_PGRS34)	Rv0278c (PE_PGRS3)	Rv1803c (PE_PGRS32)
		Rv0915c (PPE14)	Rv3136 (PPE51)	Rv1791 (PE19)	Rv1983 (PE_PGRS35)	Rv0279c (PE_PGRS4)	Rv1807 (PPE31)
		Rv1039c (PPE15)	Rv3159c (PPE53)	Rv1806 (PE20)	Rv2162c (PE_PGRS38)	Rv0286 (PPE4)	Rv1808 (PPE32)
		Rv1135c (PPE16)	Rv3425 (PPE57)	Rv2107 (PE22)	Rv2340c (PE_PGRS39)	Rv0304c (PPE5)	Rv1809 (PPE33)
		Rv1168c (PPE17)	Rv3426 (PPE58)	Rv2328 (PE23)	Rv2487c (PE_PGRS42)	Rv0354c (PPE7)	Rv2098c (PE_PGRS36)
		Rv1361c (PPE19)	Rv3429 (PPE59)	Rv2431c (PE25)	Rv2490c (PE_PGRS43)	Rv0355c (PPE8)	Rv2126c (PE_PGRS37)
		Rv1387 (PPE20)	Rv3478 (PPE60)	Rv2519 (PE26)	Rv2615c (PE_PGRS45)	Rv0387c (PPE9)	Rv2371 (PE_PGRS40)
						Rv0388c (PPE9)	Rv2396 (PE_PGRS41)

		Rv1548c (PPE21)	Rv3532 (PPE61)	Rv2769c (PE27)	Rv3345c (PE_PGRS50)	Rv0442c (PPE10)	Rv2408 (PE24)
		Rv1705c (PPE22)	Rv3533c (PPE62)	Rv3020c (esxS)	Rv3507 (PE_PGRS53)	Rv0453 (PPE11)	Rv2591 (PE_PGRS44)
		Rv1706c (PPE23)	Rv3539 (PPE63)	Rv3022A (PE29)	Rv3511 (PE_PGRS55)	Rv0532 (PE_PGRS6)	Rv2634c (PE_PGRS46)
		Rv1753c (PPE24)	Rv3558 (PPE64)	Rv3477 (PE31)	Rv3590c (PE_PGRS58)	Rv0578c (PE_PGRS7)	Rv2741 (PE_PGRS47)
		Rv1789 (PPE26)	Rv3621c (PPE65)	Rv3622c (PE32)	Rv3812 (PE_PGRS62)	Rv0742 (PE_PGRS8)	Rv2853 (PE_PGRS48)
		Rv1790 (PPE27)	Rv3738c (PPE66)	Rv3650 PE33	Rv3097c (lipY)	Rv0746 (PE_PGRS9)	Rv3021c/Rv3022c (PPE47/PPE48)
		Rv1800 (PPE28)	Rv3739c (PPE68)	Rv3746c (PE34)	Rv3822	Rv0747 (PE_PGRS10)	Rv3144c (PPE52)
		Rv1801 (PPE29)	Rv3873 (PPE68)	Rv3872 (PE35)	Rv0287 (esxG)	Rv0754 (PE_PGRS11)	Rv3343c (PPE54)
		Rv1802 (PPE30)	Rv3892c (PPE69)	Rv3893c (PE36)	Rv0378	Rv0833 (PE_PGRS13)	Rv3347c (PPE55)
		Rv1917c (PPE34)	Rv0151c (PE1)	Rv0297 (PE_PGRS5)	Rv1089* (PE10)	Rv0878c (PPE13)	Rv3350c (PPE56)
		Rv1918c (PPE35)	Rv0152c (PE2)	Rv0832 (PE_PGRS12)	Rv3344c* (PE_PGRS49)	Rv0977 (PE_PGRS16)	Rv3367 (PE_PGRS51)
		Rv2108 (PPE36)	Rv0159c (PE3)	Rv0834c (PE_PGRS14)	Rv3512* (PE_PGRS56)	Rv0978c (PE_PGRS17)	Rv3388 (PE_PGRS52)
		Rv2123 (PPE37)	Rv0160c (PE4)	Rv0872c (PE_PGRS15)	Rv3652* (PE_PGRS60)	Rv1068c (PE_PGRS20)	Rv3507 (PE_PGRS53)
		Rv2352c (PPE38)	Rv0285 (PE5)	Rv0980c (PE_PGRS18)	Rvnp02#	Rv1088 (PE9)	Rv3508 (PE_PGRS54)
		Rv2353c (PPE39)	Rv0335c (PE6)	Rv1067c (PE_PGRS19)	Rvnp03#	Rv1091 (PE_PGRS22)	Rv3511 (PE_PGRS55)

		Rv2356c (PPE40)	Rv0916c (PE7)	Rv1087 (PE_PGRS21)	Rv2099c[#] (PE21)	Rv1195 (PE13)	Rv3514 (PE_PGRS57)
		Rv2430c (PPE41)	Rv1040c (PE8)	Rv1243c (PE_PGRS23)	Rv3018A[#] (PE27A)	Rv1196 (PPE18)	Rv3595c (PE_PGRS59)
		Rv2608 (PPE42)	Rv1169c (PE11)	Rv1325c (PE_PGRS24)		Rv1396c (PE_PGRS25)	Rv3653 (PE_PGRS61)
		Rv2768c (PPE43)	Rv1172c (PE12)	Rv1452c (PE_PGRS28)		Rv1441c (PE_PGRS26)	
		Rv2770c (PPE44)	Rv1214c (PE14)	Rv1468c (PE_PGRS29)			
2	MCE	Rv0165c	Rv0586	Rv1963c	Rv3495c		
		Rv0166	Rv0587	Rv1964	Rv3496c		
		Rv0167	Rv0588	Rv1965	Rv3497c		
		Rv0168	Rv0589	Rv1966	Rv3498c		
		Rv0169	Rv0590	Rv1967	Rv3499c		
		Rv0170	Rv0590A	Rv1968	Rv3500c		
		Rv0171	Rv0591	Rv1969	Rv3501c		
		Rv0172	Rv0592	Rv1970			
		Rv0173	Rv0593	Rv1971			
		Rv0174	Rv0594	Rv3494c			
3	Mmpl	Rv0202c	Rv0507	Rv1522c	Rv2942	Rv1146	
		Rv0206c	Rv0676c	Rv1557	Rv3823c		
		Rv0402c	Rv1145	Rv2339			
		Rv0450c	Rv1183				

4	Sigma factors	Rv0182c	Rv1189	Rv2703	Rv3286c	Rv3911
		Rv0445c	Rv1221	Rv2710	Rv3328c	
		Rv0735	Rv2069	Rv3223c	Rv3414c	
5	TCCSs	Rv0260c	Rv0844c	Rv1032c	Rv3220c	Rv0757
		Rv0490	Rv0845	Rv1033c	Rv3245c	
		Rv0491	Rv0902c	Rv1626	Rv3246c	
		Rv0600c	Rv0903c	Rv2027c	Rv3764c	
		Rv0601c	Rv0981	Rv2884	Rv3765c	
		Rv0602c	Rv0982	Rv3132c		
		Rv0758	Rv1027c	Rv3133c		
		Rv0818	Rv1028c	Rv3143		

Table S2: List of PPE, PE and PE_PGRS proteins showing differences between $H_{37}Rv$ and $H_{37}Rv$ strains of Mycobacterium tuberculosis:

$H_{37}Rv$ gene product	$H_{37}Rv$ gene locus	$H_{37}Ra$ gene locus	Genetic Variations in $H_{37}Ra$	Amino acid length in $H_{37}Rv$/ $H_{37}Ra$	Protein Product Variation in $H_{37}Ra$
PPE2	Rv0256c	MRA_0265	Deletion	556/520	N-terminal shortened
PPE4	Rv0286	MRA_0295	Deletion	513/497	N-terminal shortened
PPE5	Rv0304c	MRA_0313	Insertion	2204/2373	N-terminal extended
PPE11	Rv0453	MRA_0458	Deletion	518/511	N-terminal shortened
PPE25	Rv1787	MRA_1801	Insertion	365/405	N-terminal extended, substitution
PPE31	Rv1807	MRA_1819	Insertion	399/403	N-terminal extended
PPE55	Rv3347c	MRA_3387	Deletion	3157/3145	N-terminal shortened
PE9	Rv1088	MRA_1099	Insertion	144/150	N-terminal extended
PE13	Rv1195	MRA_1205	Insertion	99/115	N-terminal extended, substitution
PE24	Rv2408	MRA_2433	Insertion	239/324	N-terminal extended, substitution
PE_PGRS8	Rv0742	MRA_0751	Deletion	175/172	N-terminal shortened, substitution
PE_PGRS11	Rv0754	MRA_0763	Deletion	584/581	N-terminal shortened, substitution
PE_PGRS25	Rv1396c	MRA_1405	Insertion	576/597	N-terminal extended
PE_PGRS26	Rv1441c	MRA_1449	Deletion	491/487	N-terminal shortened
PE_PGRS32	Rv1803c	MRA_1816	Insertion	639/650	N-terminal extended, substitution
PE_PGRS40	Rv2371	MRA_2394	Insertion	62/95	N-terminal extended
PE_PGRS44	Rv2591	MRA_2620	Insertion	543/553	N-terminal extended
PE_PGRS46	Rv2634c	MRA_2663	Deletion	778/766	N-terminal shortened
PE_PGRS48	Rv2853	MRA_2876	Deletion	615/614	N-terminal shortened, substitution
PE_PGRS61	Rv3653	MRA_3688	Insertion	195/242	N-terminal extended, substitution
Rv0387c	Rv0387c	MRA_0395	Insertion	244/443	N-terminal extended, substitution
PPE7	Rv0354c	MRA_0363	insertions	141/185	Insertions ,deletions and substitutions
PPE8	Rv0355c	MRA_0364	SNV	3300/3300	Substitution
PPE9	Rv0388c	MRA_0395	Insertions and SNV	180/443	Insertions , deletions and substitutions

PPE10	Rv0442c	MRA_0447	SNV	487/487	Substitution
PPE13	Rv0878c	MRA_0885	SNV	443/448	C-terminal extended
PPE18	Rv1196	MRA_1205A	SNV	391/339	Insertions and deletions
PPE32	Rv1808	MRA_1820	SNV	409/409	No change
PPE33	Rv1809	MRA_1821	SNV	468/468	No change
PPE47/ PPE48	Rv3021c/ Rv3022c	MRA_3052	SNVs	435/435	Substitution
PPE52	Rv3144c	MRA_3177	SNV	409/409	Substitution
PPE54	Rv3343c	MRA_3384	SNV, Deletions, insertion	2523/1947	Deletion in mid
PPE56	Rv3350c	MRA_3390	Insertion	3716/3674	N-terminal shortened, substitution
PE_PGRS1	Rv0109	MRA_0115	SNV	496/496	Substitution
PE_PGRS2	Rv0124	MRA_0131	SNV	487/487	Substitution
PE_PGRS3	Rv0278c	MRA_0287	SNV	957/957	Substitution
PE_PGRS4	Rv0279c	MRA_0288	SNVs	837/837	Substitutions
PE_PGRS6	Rv0532	MRA_0539	SNVs	594/594	Substitutions
PE_PGRS7	Rv0578c	MRA_0585	SNVs	1306/1306	Substitutions
PE_PGRS9	Rv0746	MRA_0754	SNVs	783/783	Substitutions
PE_PGRS10	Rv0747	MRA_0755	SNVs	801/801	Substitutions
PE_PGRS13	Rv0833	MRA_0841a	SNVs	749/749	Substitutions
PE_PGRS16	Rv0977	MRA_0984	SNVs	923/923	Substitutions
PE_PGRS17	Rv0978	MRA_0985	SNVs	331/331	No change
PE_PGRS20	Rv1068c	MRA_1078	SNVs	463/463	Substitution
PE_PGRS22	Rv1091	MRA_1102	SNV, insertion	853/579	C-terminal shortened
PE_PGRS27	Rv1450c	MRA_1459	SNVs	1329/1398	Insertions
PE_PGRS36	Rv2098c	MRA_2113	Insertions	491/349	Insertions ,deletions and substitutions
PE_PGRS37	Rv2126c	MRA_2140A	SNV	256/256	No change
PE_PGRS41	Rv2396	MRA_2420	SNV	361/361	Substitutions
PE_PGRS47	Rv2741	MRA_2767	SNV, insertion	525/559	N-terminal extended , Substitution

PE_PGRS51	Rv3367	MRA_3407	SNV, Insertion	588/591	Insertions
PE_PGRS52	Rv3388	MRA_3428	SNV, Insertion, deletion	731/582	Insertions, deletions substitutions
PE_PGRS53	Rv3507	MRA_3547	SNV	1381/1381	Substitution
PE_PGRS54	Rv3508	MRA_3548	SNV, Insertion, deletion	1901/1545	Insertions, deletions substitutions
PE_PGRS55	Rv3511	MRA_3551	SNV, insertion	714/717	Insertions, substitutions
PE_PGRS57	Rv3514	MRA_3553	SNV, Insertion, deletion	1489/1211	Insertions, deletions substitutions
PE_PGRS59	Rv3595c	MRA_3634	Deletion	439/232	Insertions, deletions substitutions
		MRA_3635		439/238	Substitutions, deletion
Wag22	Rv1759c	MRA_1772	insertion	914/156	5' insertion, 3' deletion

Table S3: Instability index, aliphatic index and Gravy values of members of PE/PPE, and non-PE/PPE family found to be different between H_{37}Rv and H_{37}Ra strains of Mycobacterium tuberculosis.

Gene name	H37Rv gene locus	H37Ra gene locus	Instability index		Aliphatic index		GRAVY values	
			H37Rv	H37Ra	H37Rv	H37Ra	H37Rv	H37Ra
PPE2	Rv0256c	MRA_0265	43.73	43.29	86.62	86.23	0.191	0.187
PPE4	Rv0286	MRA_0295	37.75	35.66	86.69	86.52	0.284	0.278
PPE5	Rv0304c	MRA_0313	8.86	10.11	80.62	82.31	0.169	0.198
PPE11	Rv0453	MRA_0458	39.9	39.9	85.41	84.85	0.167	0.15
PPE25	Rv1787	MRA_1801	31.72	34.76	84.49	81.46	0.337	0.257
PPE31	Rv1807	MRA_1819	40.5	39.22	84.76	83.95	0.4	0.286
PPE7	Rv0354c	MRA_0363	22.85	13.86	61.63	69.62	0.17	0.155
PPE9	Rv0388c	MRA_0395	40.69	45.5	75.22	84.09	-0.007	0.261
	Rv0387c		56.31		88.69		0.3	
PPE10	Rv0442c	MRA_0447	29.94	29.94	75.59	75.59	0.062	0.062
PPE8	Rv0355c	MRA_0364	14.28	14.24	72.43	72.93	-0.004	-0.003
PPE13	Rv0878c	MRA_0885	19.33	20.65	74.7	74.73	0.023	-0.017
PPE18	Rv1196	MRA_1205A	22.04	23.29	64.95	65.19	0.161	0.158
PPE47	Rv3021c	MRA_3052	26.18	25.5	112.94	112.71	0.881	0.881
PPE52	Rv3144c	MRA_3177	33.62	34.22	78.83	78.83	0.253	0.254
PPE54	Rv3343c	MRA_3384	22.94	24.79	95.81	96.87	0.419	0.43
PPE55	Rv3347c	MRA_3387	18.34	18.07	91.34	91.25	0.323	0.323
PPE56	Rv3350c	MRA_3390	14.55	14.11	92.33	92.66	0.348	0.345

PE9	Rv1088	MRA_1099	64.3	62.28	70.76	70.75	-0.283	-0.295
PE13	Rv1195	MRA_1205	41.93	39.63	82.42	90.35	0.593	0.627
PE24	Rv2408	MRA_2433	34.42	40.4	95.31	83.89	0.07	-0.163
PE_PGRS8	Rv0742	MRA_0751	18.29	15.88	90.4	90.29	0.668	0.644
PE_PGRS11	Rv0754	MRA_0763	22.13	21.43	94.9	94.89	0.399	0.39
PE_PGRS25	Rv1396c	MRA_1405	15.74	15.48	53.45	55.33	-0.085	-0.051
PE_PGRS26	Rv1441c	MRA_1449	20	19.18	50.43	50.25	-0.093	-0.098
PE_PGRS32	Rv1803c	MRA_1816	17	18.1	54.71	54.23	-0.122	-0.146
PE_PGRS40	Rv2371	MRA_2394	24.41	31.63	113.61	92.53	0.808	0.325
PE_PGRS44	Rv2591	MRA_2620	22.04	23.39	64.95	65.19	0.161	0.158
PE_PGRS46	Rv2634c	MRA_2663	17.15	16.21	56.89	55.74	0.074	0.051
PE_PGRS48	Rv2853	MRA_2876	15.91	16.3	55.04	54.5	-0.089	-0.095
PE_PGRS51	Rv3367	MRA_3407	16.65	16.43	52.55	52.28	-0.202	-0.208
PE_PGRS52	Rv3388	MRA_3428	12.15	12.05	51.42	55.27	-0.076	-0.001
PE_PGRS53	Rv3507	MRA_3547	10.81	10.9	37.22	37.22	-0.289	-0.289
PE_PGRS54	Rv3508	MRA_3548	14.71	16.07	43.01	45.48	-0.126	-0.071
PE_PGRS55	Rv3511	MRA_3551	20.12	20.01	48.5	48.3	-0.204	-0.205
PE_PGRS57	Rv3514	MRA_3553	11.57	12.04	36.15	40.36	-0.183	-0.109
PE_PGRS61	Rv3653	MRA_3688	8.2	16.77	61.85	66.07	0.194	0.189
PE_PGRS1	Rv0109	MRA_0115	16.71	16.12	64.74	64.74	0.161	0.17
PE_PGRS2	Rv0124	MRA_0131	20.55	20.55	65.46	65.85	0.149	0.154
PE_PGRS3	Rv0278c	MRA_0287	23.02	23.2	60.46	60.46	0.095	0.099

PE_PGRS4	Rv0279c	MRA_0288	13.61	13.85	60.01	59.55	0.181	0.179
PE_PGRS6	Rv0532	MRA_0539	26.59	26.65	61.95	61.78	0.08	0.081
PE_PGRS7	Rv0578c	MRA_0585	10.75	10.75	39.09	39.09	-0.299	-0.3
PE_PGRS9	Rv0746	MRA_0754	18.35	19.36	70.33	70.72	0.318	0.332
PE_PGRS10	Rv0747	MRA_0755	16.66	17.42	62.08	62.08	0.244	0.254
PE_PGRS13	Rv0833	MRA_0841A	19.98	19.89	54.39	54.39	0.24	0.24
PE_PGRS16	Rv0977	MRA_0984	22.2	22.06	62.68	62.88	0.021	0.023
PE_PGRS20	Rv1068c	MRA_1078	13.79	13.34	51.1	51.73	-0.183	-0.173
PE_PGRS22	Rv1091	MRA_1102	16.39	42.66	50.08	53.58	-0.062	-0.311
PE_PGRS27	Rv1450c	MRA_1459	12.2	12.39	41.22	41.57	-0.265	-0.25
PE_PGRS36	Rv2098c	MRA_2113	25.47	29.02	61.41	56.33	-0.024	-0.171
PE_PGRS41	Rv2396	MRA_2420	22.45	23.13	76.29	76.29	0.318	0.326
PE_PGRS47	Rv2741	MRA_2767	16.97	20.23	58.63	60.64	0.149	0.11
PE_PGRS59	Rv3595c	MRA_3634	18.80	46.65	60.75	89.96	0.035	0.459
		MRA_3635		33.63		82.86		0.282
Wag22	Rv1759c	MRA_1772	16.41	25.39	56.09	82.37	0.171	0.063
mmpl13b	Rv1146	MRA_1156	41.39	41.04	108.53	107.52	0.461	0.508
sigM	Rv3911	MRA_3950	50.93	42.7	74.46	88.27	-0.535	-0.253
phoP	Rv0757	MRA_0767	36.18	36.18	98.99	100.57	-0.191	-0.172

Figure S1-A

```
MRA_0313         MANTGNINTGAFISGNHSNGLLWRGDNQGLIDLAIGVDIPEIPIVSVDVNIPIHIPITASFTDIVYSGLDLPPNTAVTVIFFGPVDIDP
Rv0304c          -----------------------------------------------------------------------------------------

MRA_0313         FTVPVIRITGPTPVVMVGGPTTAINIGATVVVDAINIPIIHIPATPGFGNSTGGLSSGFFNSGAGSASGFGNFGGAASGF170==2373
Rv0304c          --------------------------------------------------------------------------------001==2204
```

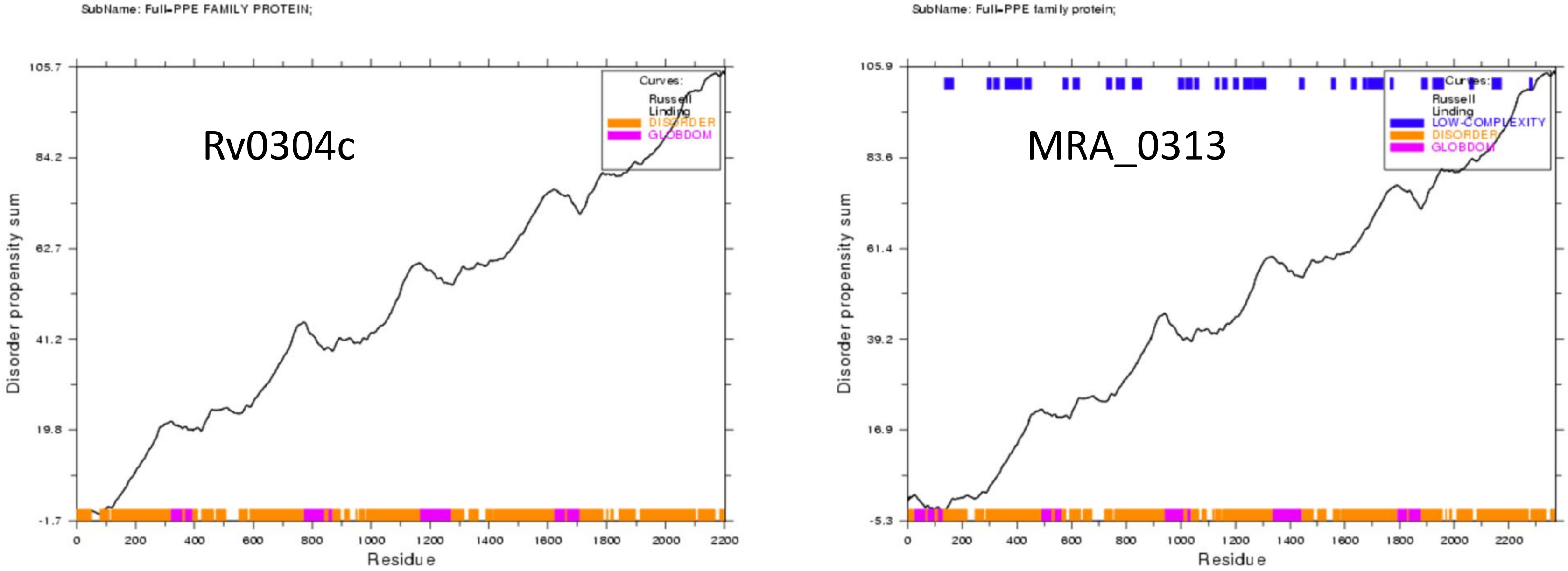


Figure S1-B

```
MRA_2113        ------------------------------------------------------------------------------M02=322WRQRW
Rv2098c         MSFVIASPEALLAAATDLAAIRSTIRAANAAAAVPTTGALAPAADEVSAGIAALFGAQAQSYQAVSAQAAAFHDRFVQL80=400GGSGG
                                                                                              :******  .

MRA_2113        ---------------PTAACGTATVAPAGPPAKGG--------------------------------------------------PA
Rv2098c         NGGVWYGNGGAGGAAGQGGPGMNTTSPGGPGGVGGHGGTAILFGDGGAGGAGAAGGPGTPDGAAGPGGSGGTGGLLFGVPGPSGPDG
                                     .. *  *.:*.** . **                                               .
```

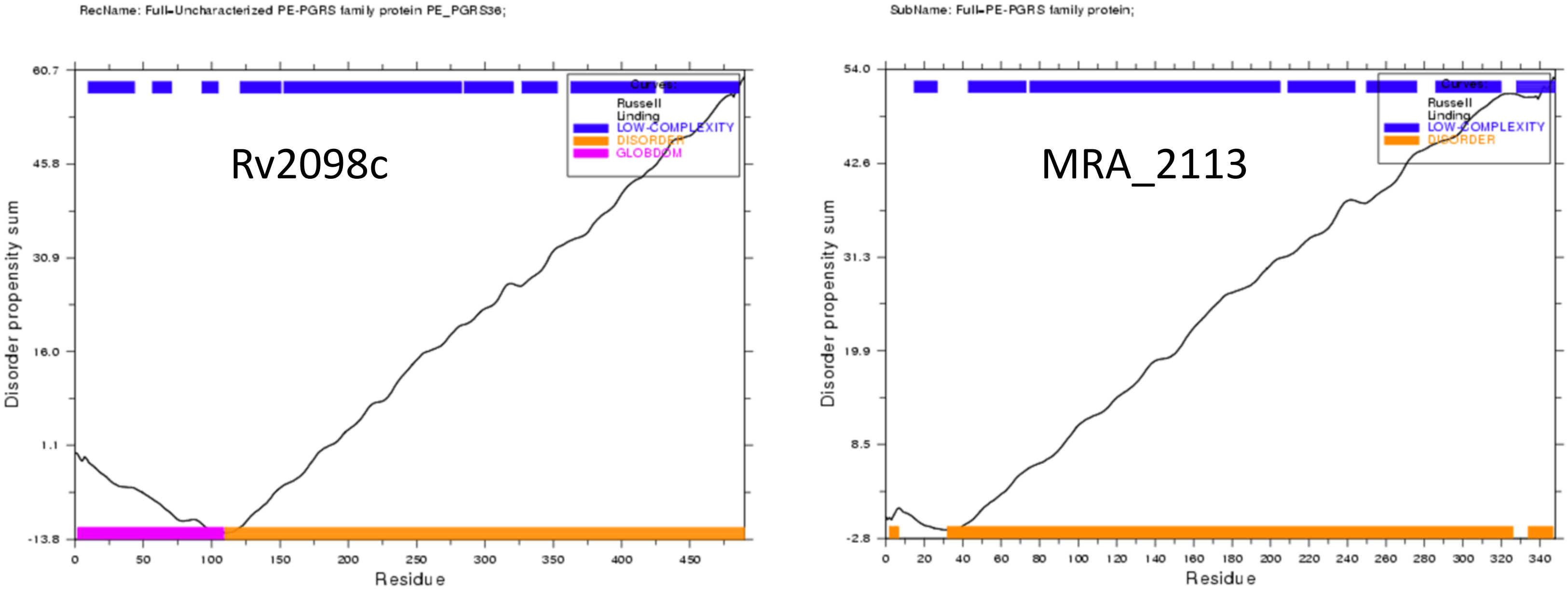


Figure S1-C

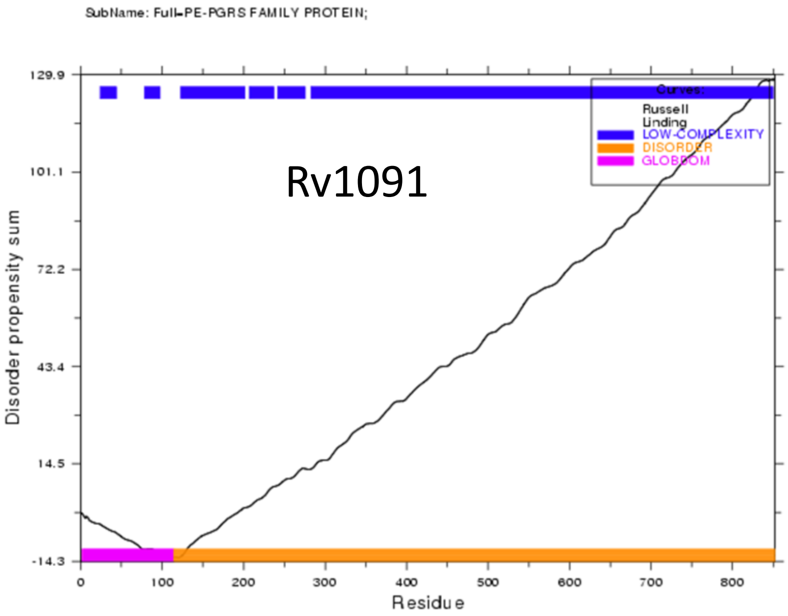
```
MRA_1102        1=470S500RGRRPRRVAVRRWRGWRERRGRGRRRRRRPSRRWRRERRQWRQRRQWRQWRQRRHRGVAVRQR------------------
Rv1091          1=470G500GAAGPA--------GWLFGDGGAG-----------------------------GNGGAAAAGGAGGQAGGGGGNGGNGGNG
                *****.*** .  *         **    * .                               : *.*.

MRA_1102        ------------------------------------------------------------------------------------------
Rv1091          GNGGNGGNGATGGWLYGNGGAGGQGATAGAGGAGANGVSSTNGGGTGGNGGIGGTGGSGGAGGNAGLLGVGGAGGHGASGGAGDRGGAGG
                    : *.*.

MRA_1102        ------------------------------------------------------------------------------------------
Rv1091          TGFISSDGGAGGDGGDGGNGGAGGTGGLLFGAGGNGGPGGSGGAADIGGNGGAGNGGGTDGNGGNGGSGGGAGSGGDGGGAGGNGAWLFG

MRA_1102        -----------------------------------------------------------------------------------------
Rv1091          NGGAGGGGGKGGNGAGGGLGGGSFGLPGLNGSGGDGGDGGNGAPGGVLYGNGGAGGQGSSGGIGGPGATGGAGGKGGDGGDAQLIGDGG

MRA_1102        ---------RGRRPG---------------RHRRSRRSRR
Rv1091          NGGNGGAGGTGGTPGPGGPGGSGGLGGLLFGQTGTAGVSP
                          *  **                :  :
```



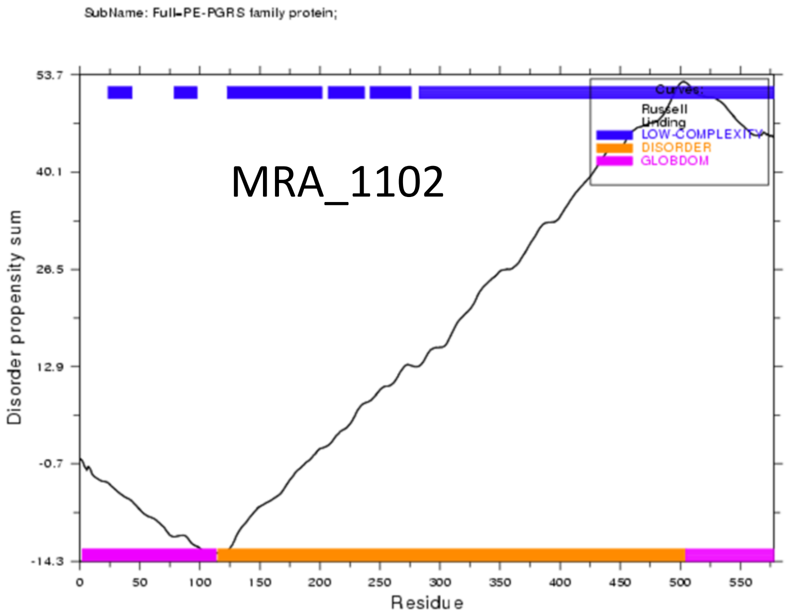
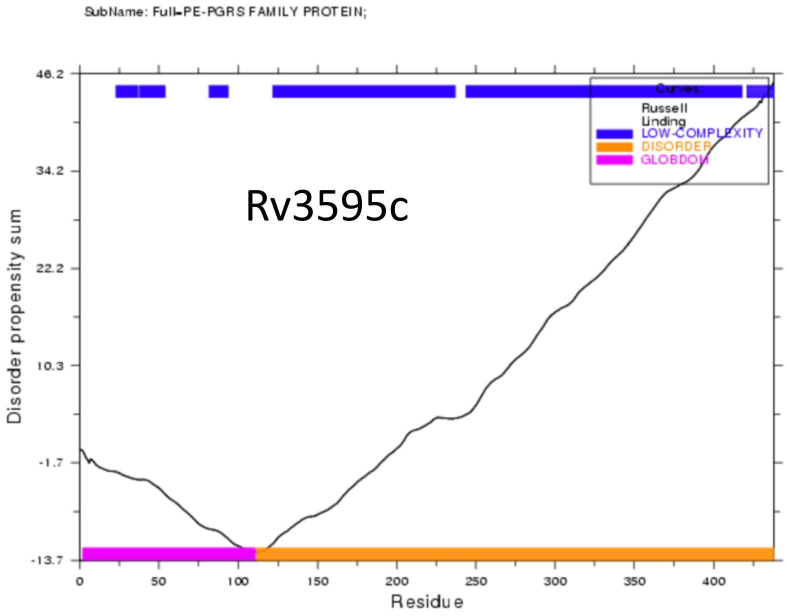


Figure S1-D

```
MRA_3635        1=162TADP-------------------------------------------------------------------------VVPA-------
Rv3595c         1=162NGGSGGAGGAGAAGGSGGQGGLLYGNGGAGGNGGAATIPGGNGGAGGAGGNAWLFGNGGAGGLGAAGAAGAAGVNPLTVPAGQGSMGN
                *****....                                                                         .***

MRA_3635        --EPVRPAGPADKAGCCTATA------------------------------------------------------------------------
Rv3595c         NGEPGGPGQPGTEFGQTGGTGGTGGTGLSVGGTGGTGGTGGTGGAGGSGGRGGLLVGDGGAGGIGGTGGEGGIGARGGTGGQGGMGGAGQPGV
                  **  *. *. : *   .*.

MRA_3635        ----------------------------------------------ARAATAGRRLSPAATAAPVVPAATRGYSATVGPGG-SARPARRVPPGSTP
Rv3595c         GGDAGDGGNGGIGGDGGAGGDGGAGGAGGAGGLFGVSGSSGLGGAAGSGGNGGGGGEPGVAGSPGVGPAGRGGDGNLGQFGPEGAPGQPGQPGQPG
                       . ....* .*....:* * .* ** ....:* * .. *.: **..
```



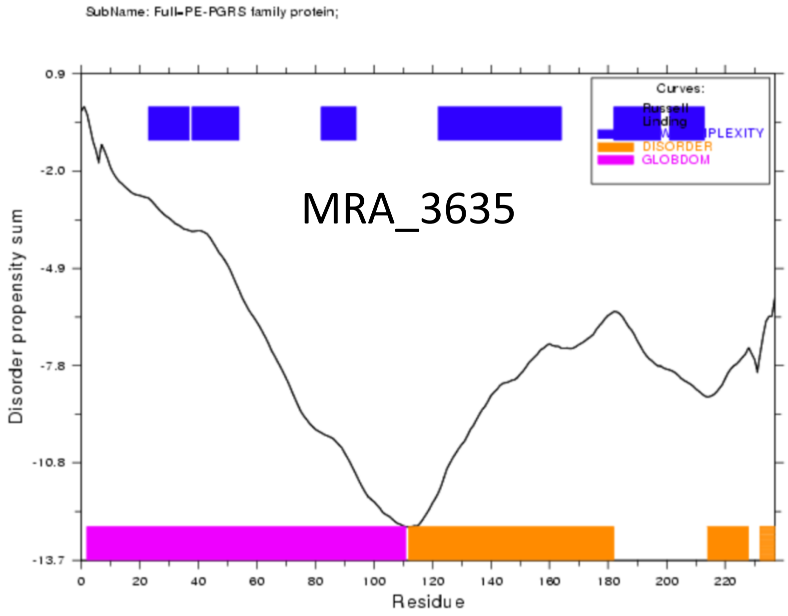


Figure S1-E

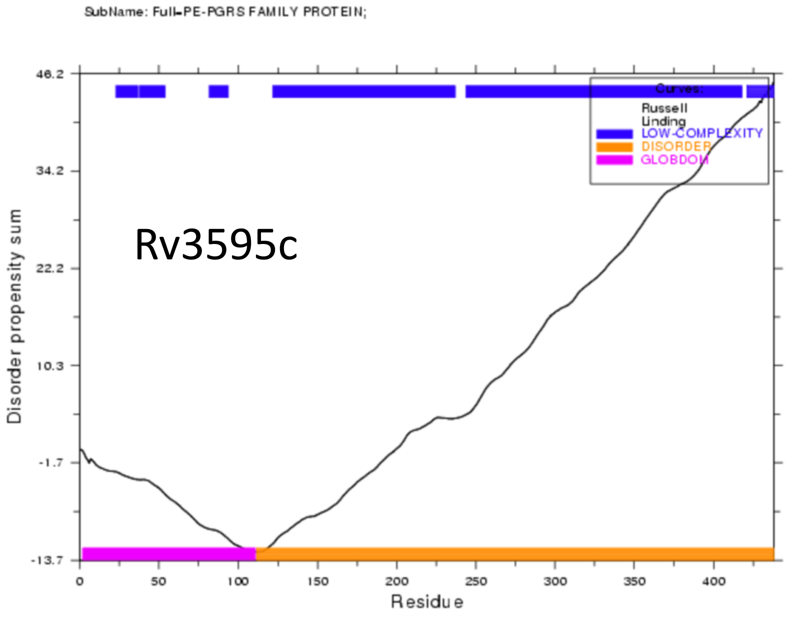
```
MRA_3634        ------------------------MNRADPASQAPSSGKPVAP----------------------------------------------------
Rv3595c         MSFVIAVPEFLSAAATDLANLGSTISAANAAASIPTTGVLAAGADDVSAAIAALFGAHAQAYQTISAQAATFHAQFVQTLSAGAGAYANAEAANV
                                        :. *:.*:. *::*  .*

MRA_3634        ----------VALAVLACPLAGPA-GPAAPGGPAGPAALAVGVGSWSATA--AQVASGAQGAKAASAPGAAPAVRAEWAAPGNQA----------
Rv3595c         QQSLLNAINAPTQALLGRPLIGDGADGTAPGQNGGAGGLLYGNGGNGAAGVNAGIAGGSGGAAGLIGNGGSGGAGGAGAAGGSGGQGGLLYGNGG
                           : *:*. ** * . . :***  .*...*  * *. .*:.  * :*.*: ** .  . *.: .. .  ** *. .

MRA_3634        -------------------------------------------------------------------------LGVTLVTGVTAGSAVTAAP---
Rv3595c         AGGNGGAATIPGGNGGAGGAGGNAWLFGNGGAGGLGAAGAAGAAGVNPLTVPAGQGSMGNNGEPGGPGQPGTEFGQTGGTGGTGGTGLSVGGTGG
                                                                                         :* *  ** *.*:.::..

MRA_3634        -----------------------------AETAARAARAARAACSASPVAPGWAVPPVAGVMAGAV---------------------VSPVWPAP
Rv3595c         TGGTGGTGGAGGSGGRGGLLVGDGGAGGIGGTGGEGGIGARGGTGGQGGMGGAGQPGVGGDAGDGGNGGIGGDGGAGGDGGAGGAGGAGGLFGVS
                                             . *..... .**.. ...    * . * *.*  ...                      .. :: ..


MRA_3634        RALGLRAVAATATSASS----ALKVHP-ASPASRASPVDIVAAGPSA-PRRLLEQLPSVTGPVEALARVEFCGQGVDLIAELG
Rv3595c         GSSGLGGAAGSGGNGGGGGEPGVAGSPGVGPAGRGGDGNLGQFGPEGAPGQP------------------------GQPGQPG
                 : ** ..*.:. ....    .:   * ..**.*..  ::   **.. * :                         .  .: *
```



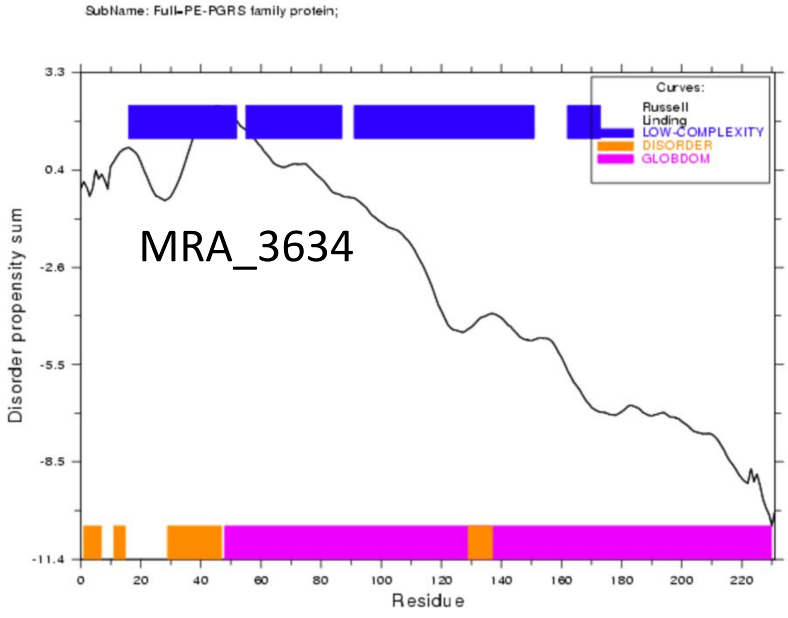
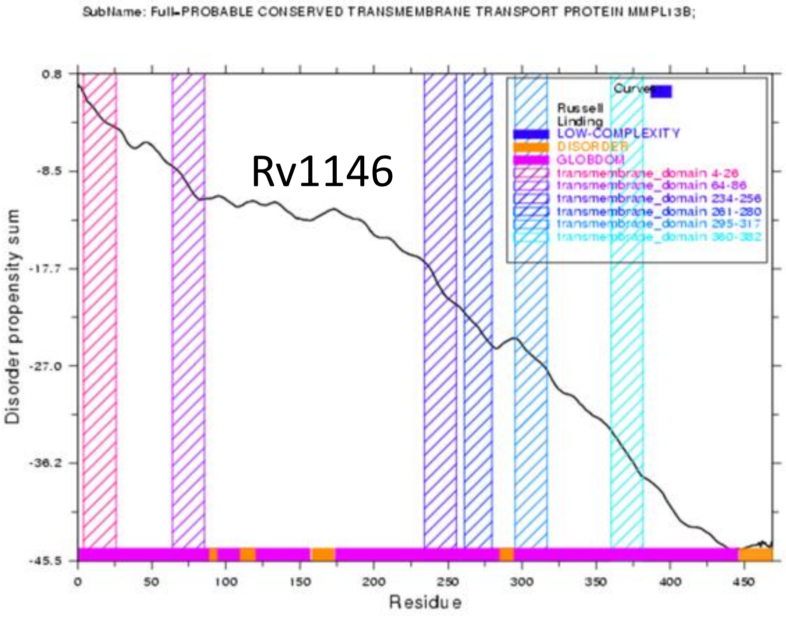


Figure S1-F

```
MRA_1156         MFSAVTVALSMSATALFPMYFLKSFAYAGV31==499
RV1146           -----------------------------M02==470
                                              :*******
```



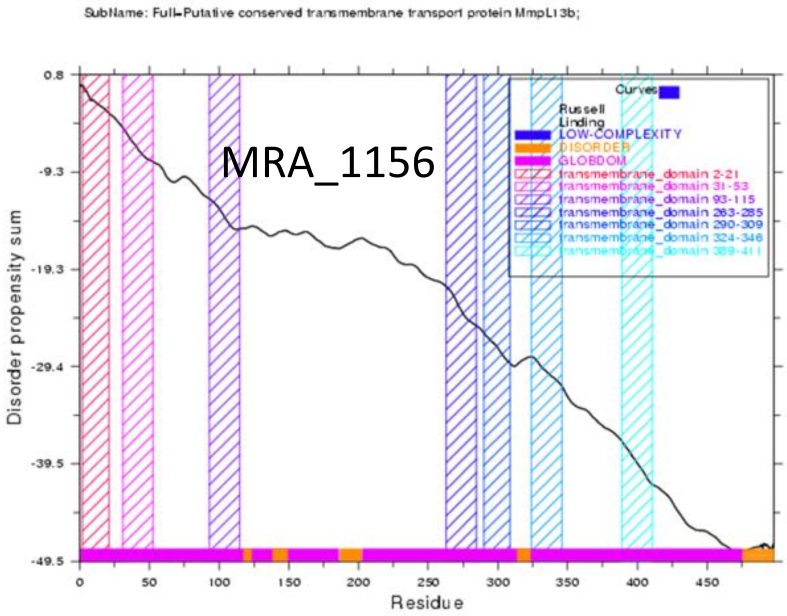
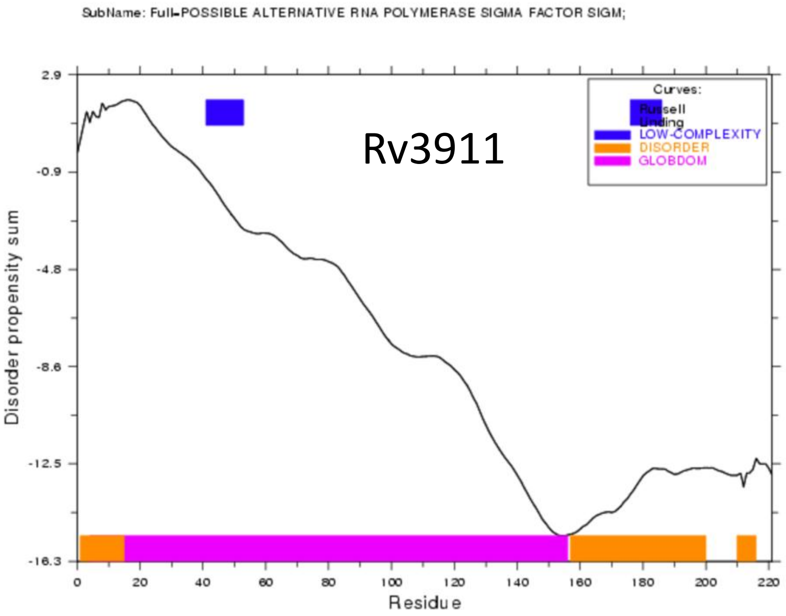


Figure S1-G

```
MRA_3950        MQGYSIADTARMLGVAEGTVKSRC--------------------------ARARARLARLLGYLNTGVNIRR
Rv3911          MQGYSIADTRPDAGRGRGHRQEPLRPGAGPPSAAAGLSQHRGEHPALTPLPVRRSIDPRARRYPTSGYCHRA
                *********    * ..*  :.                            .  *:  .*   * .:*   *
```



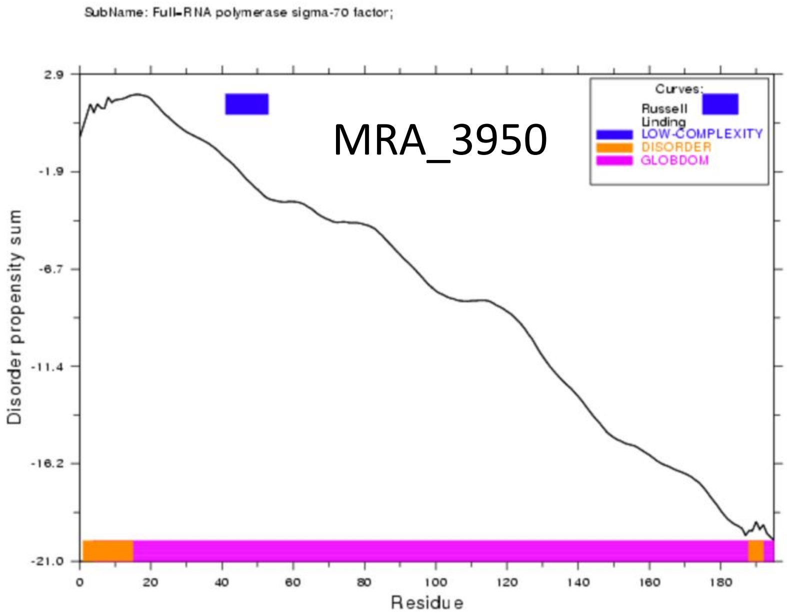
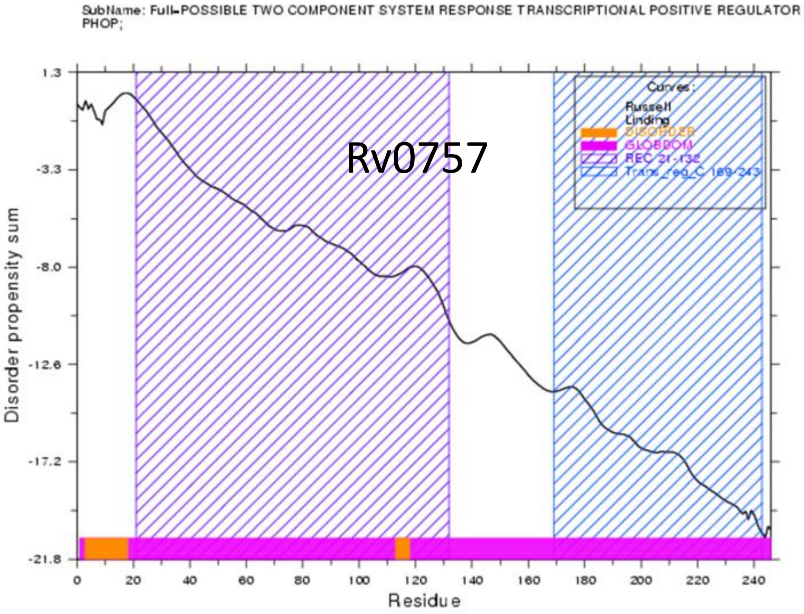


Figure S1-H

```
MRA_0767        1==200HVWRYDFGGDVNVVESYVLYLRRKIDTGEKRLLHTLRGVGYVLREPR
Rv0757          1==200HVWRYDFGGDVNVVESYVSYLRRKIDTGEKRLLHTLRGVGYVLREPR
                ************************ ****************************
```


SubName: Full=POSSIBLE TWO COMPONENT SYSTEM RESPONSE TRANSCRIPTIONAL POSITIVE REGULATOR PHOP;

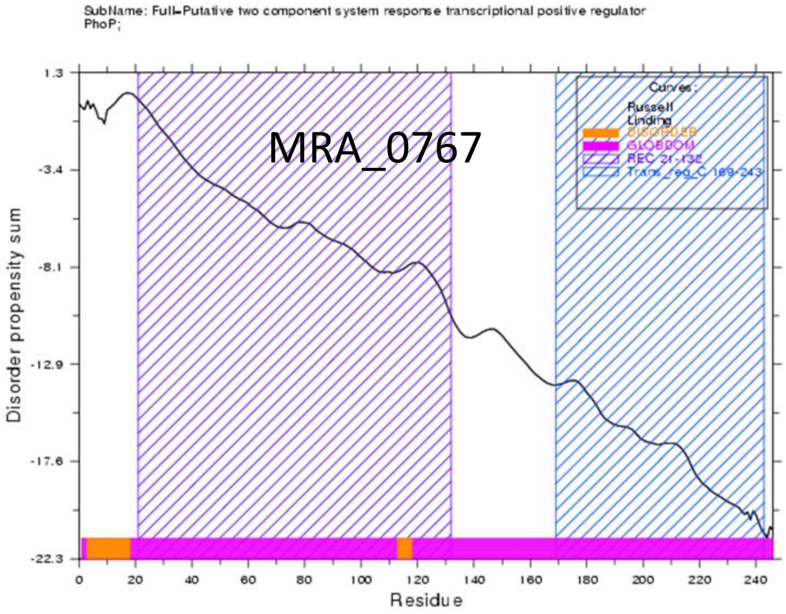

SubName: Full=Putative two component system response transcriptional positive regulator PhoP;

Figure S2-A

```
MRA_0265         ------------------------------------1 M 2=============520
Rv0256c          1 MTAPIWMASPPEVHSALLSSGPGPGPLLVSAEGWHSL 38============520
                                                         :  ****************
```

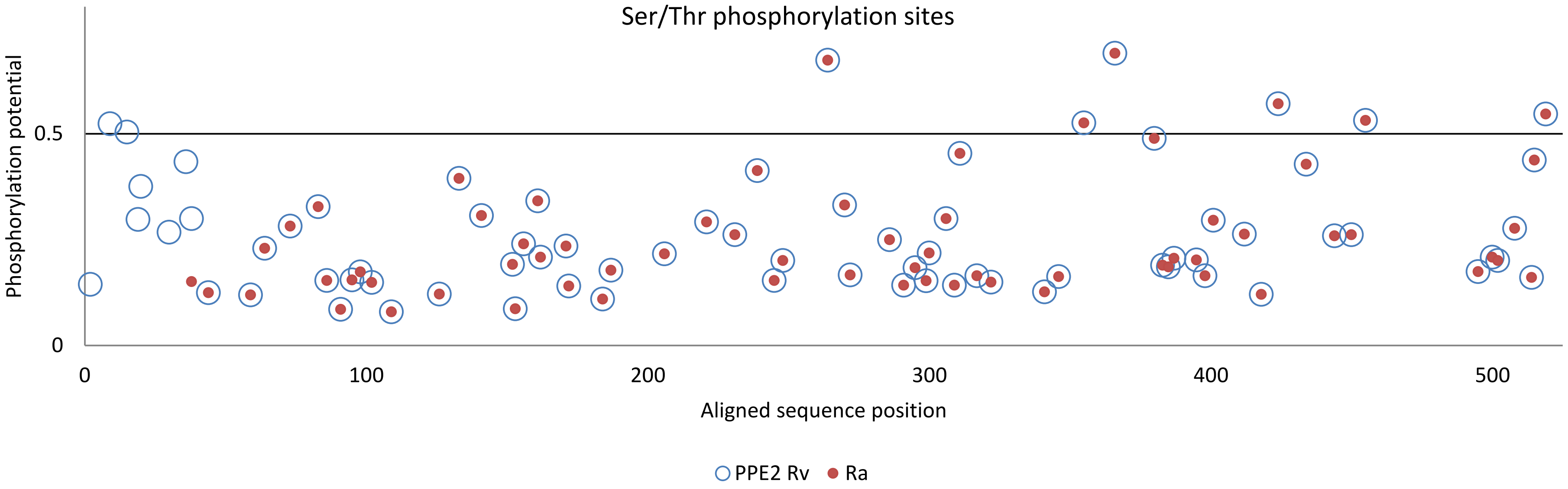


Figure S2-B

```
MRA_0295        ---------------- 1M2 ===============================497
Rv0286c        1MAAPIWMASPPEVHSAL18===============================513
                                : ***********************************
```

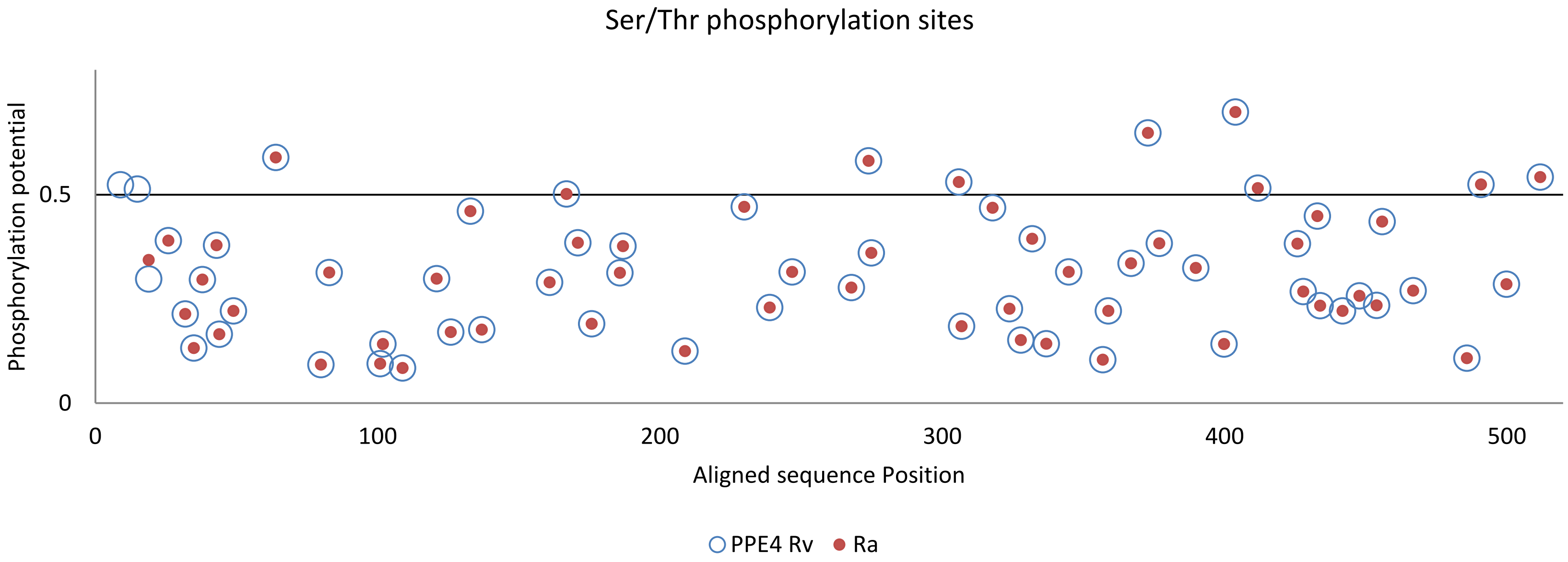


Figure S2-C

```
MRA_0763        ---M2===========================================581
Rv0754          MSFV5===========================================584
                   :***********************************************
```

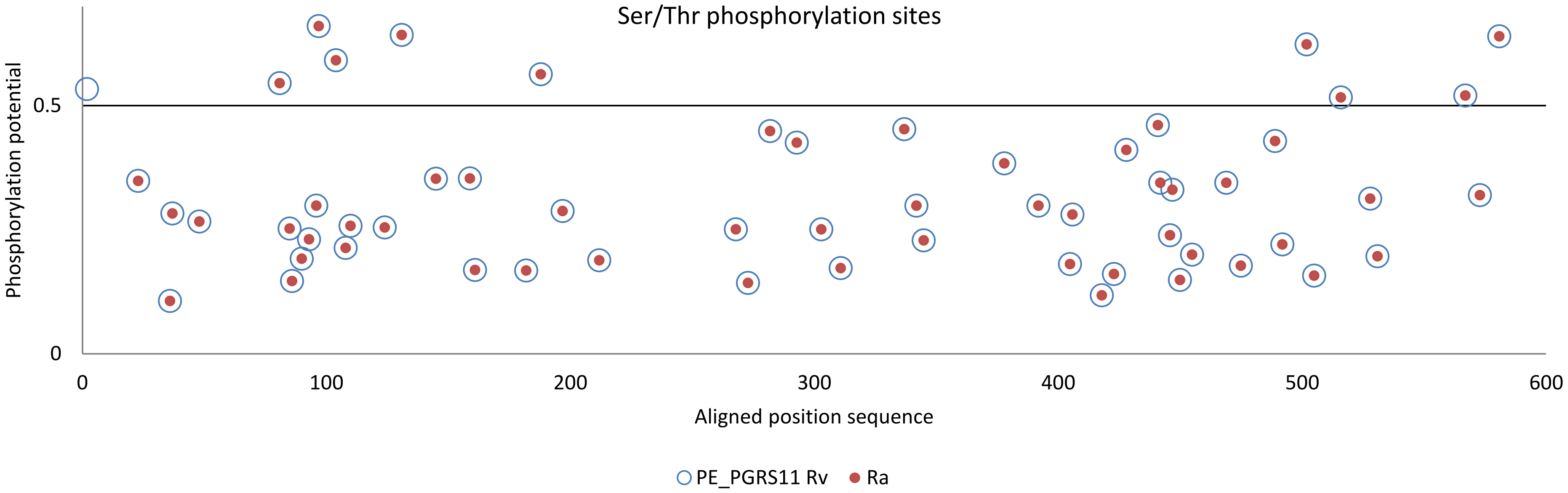


Figure S2-D

```
MRA_0313      MANTGNINTGAFISGNHSNGLLWRGDNQGLIDLAIGVDIPEIPIVSVDVNIPIHIPITASFTDIVYSGLDLPPNTAVTVIFFGPVDIDP
Rv0304c       -----------------------------------------------------------------------------------------


MRA_0313      FTVPVIRITGPTPVVMVGGPTTAINIGATVVVDAINIPIIHIPATPGFGNSTGGLSSGFFNSGAGSASGFGNFGGAASGF170==2373
Rv0304c       --------------------------------------------------------------------------------001==2204
```

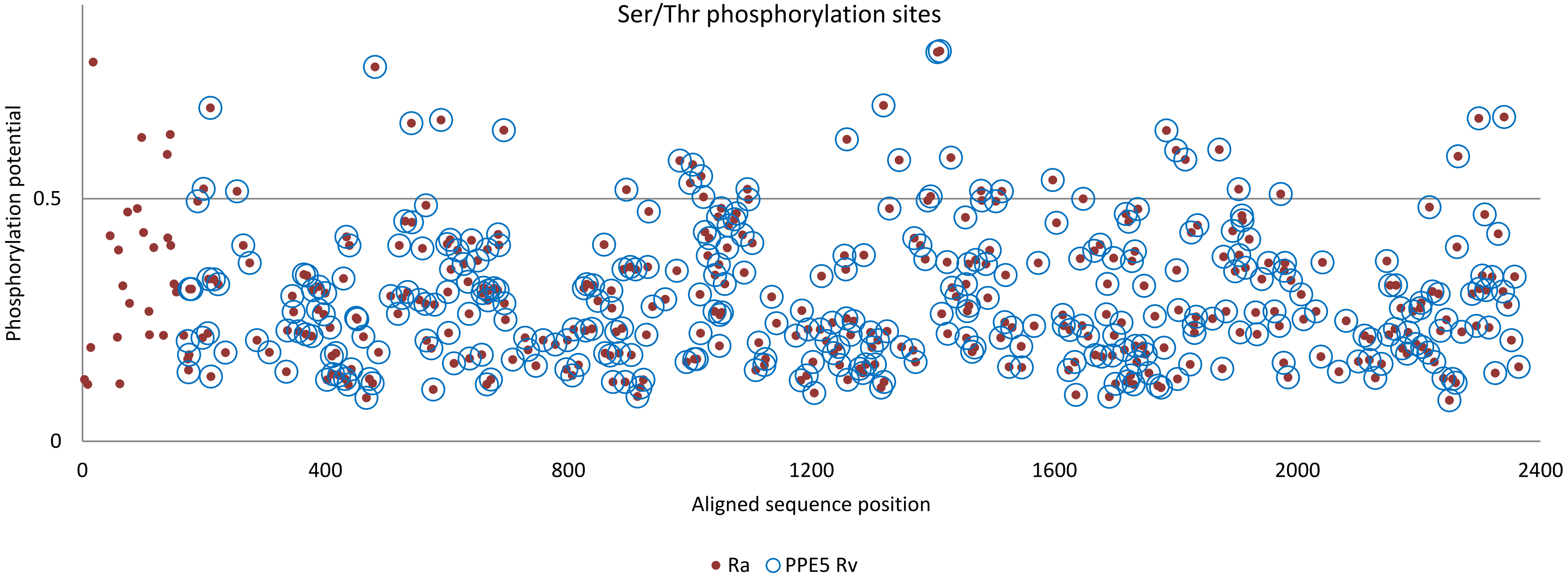


Figure S2-E

```
MRA_2767         MHRLGRYTIPMHSLEGELAILGRHDGLWRVWRSQ1==304G306==559
Rv2741           ----------------------------------1==270S272==525
                                                   ******.********
```

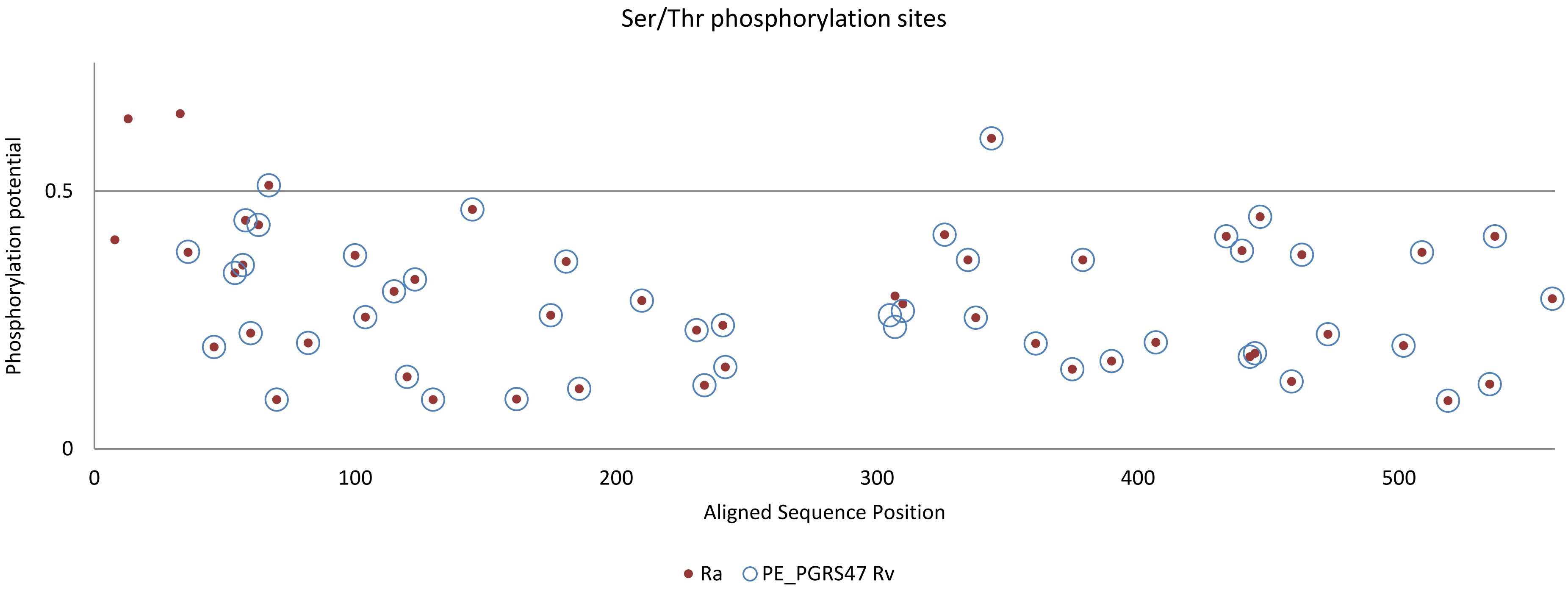


Figure S2-F

```
MRA_1205        MIVPVRVLGPFEDGVHVS=============================115
Rv1195          ----------------MS==============================99
                                :*********************************
```

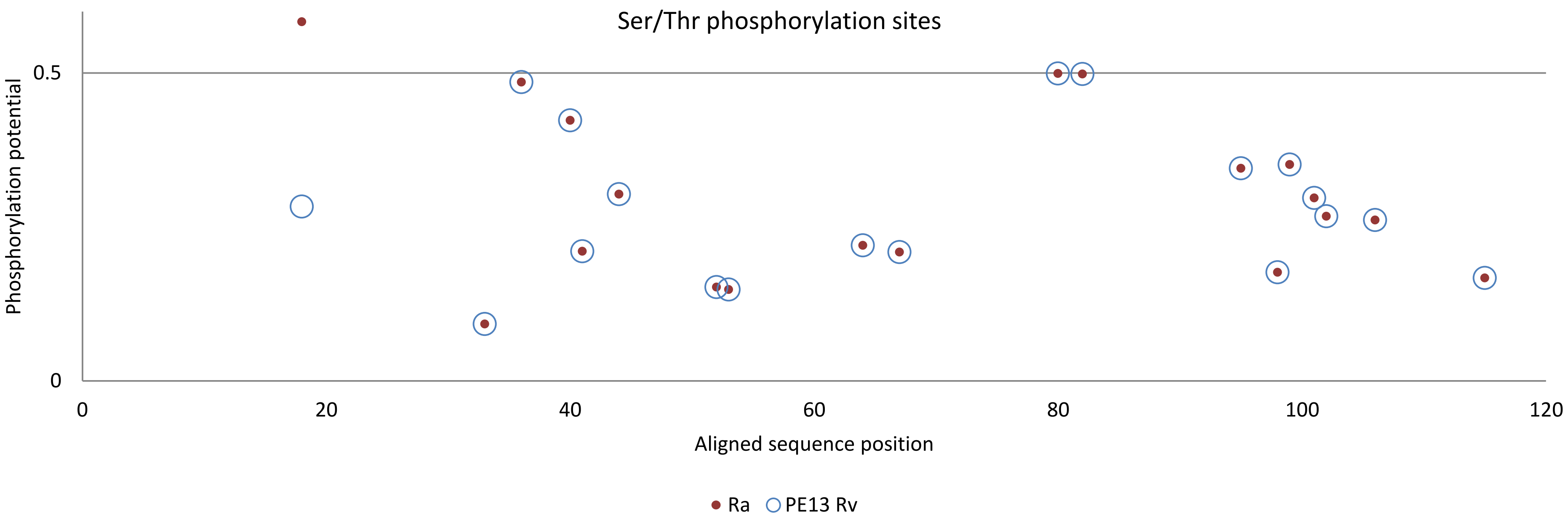


Figure S2-G

```
MRA_1102        1=470S500RGRRPRRVAVRRWRGWRERRGRGRRRRRRPSRRWRRERRQWRQRRQWRQWRQRRHRGVAVRQR------------------
Rv1091          1=470G500GAAGPA--------GWLFGDGGAG-----------------------------GNGGAAAAGGAGGQAGGGGGNGGNGGNG
                *****.*** .  *         **    * .                               : *.*.

MRA_1102        ------------------------------------------------------------------------------------------
Rv1091          GNGGNGGNGATGGWLYGNGGAGGQGATAGAGGAGANGVSSTNGGGTGGNGGIGGTGGSGGAGGNAGLLGVGGAGGHGASGGAGDRGGAGG
                    : *.*.

MRA_1102        ------------------------------------------------------------------------------------------
Rv1091          TGFISSDGGAGGDGGDGGNGGAGGTGGLLFGAGGNGGPGGSGGAADIGGNGGAGNGGGTDGNGGNGGSGGGAGSGGDGGGAGGNGAWLFG

MRA_1102        -----------------------------------------------------------------------------------------
Rv1091          NGGAGGGGGKGGNGAGGGLGGGSFGLPGLNGSGGDGGDGGNAPGGVLYGNGGAGGQGSSGGIGGPGATGGAGGKGGDGGDAQLIGDGG

MRA_1102        ---------RGRRPG---------------RHRRSRRSRR
Rv1091          NGGNGGAGGTGGTPGPGGPGGSGGLGGLLFGQTGTAGVSP
                          *  **                : :
```

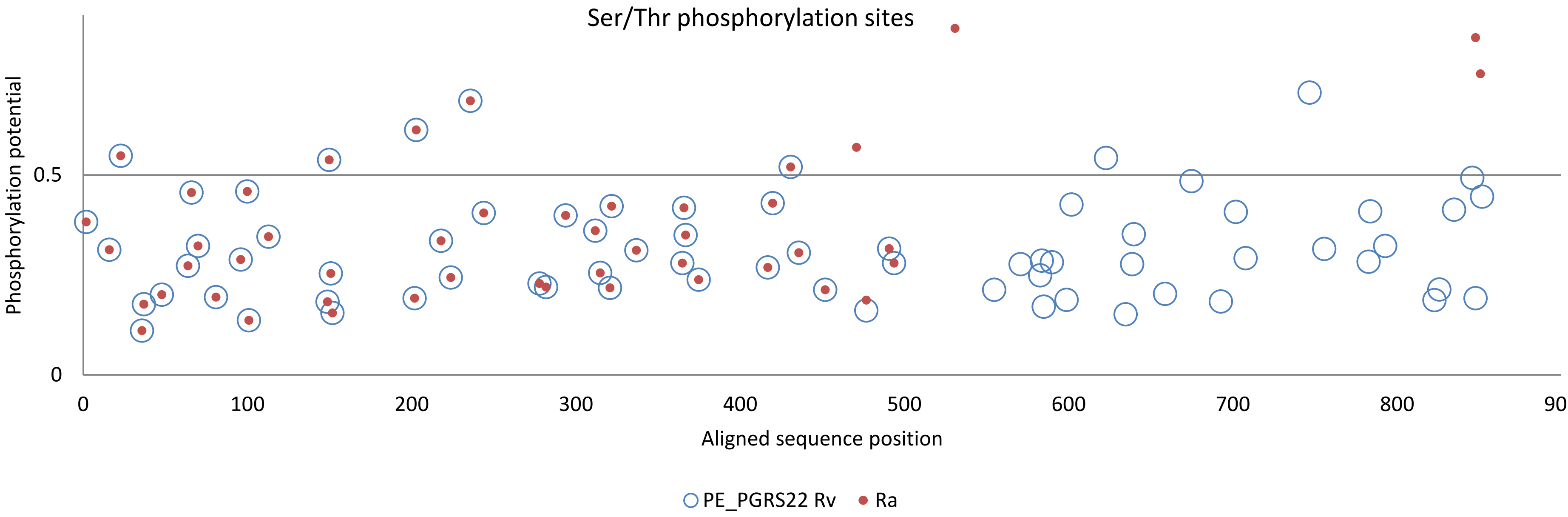


Figure S2-H

```
MRA_3428        1==444---------------------------------------------------------------------------
Rv3388          1==444AGGNGGAGGAGGQLYGNGGDGGNGGAGGANIAGGNGSDGGAAGHGGAGGSARLIGAGGHGGDGGAGGNTAGRRAD
                ******

MRA_3428        --------------------------------------------------------------------------445==582
Rv3388          AIAGTGGDGGNGGNGGLLSGNAGAGGHGGAGGSSTATTTTGTPPTGATGGNGGNGGAGGTAGFTGSGGIGGNGG594==731
                                                                      *******
```

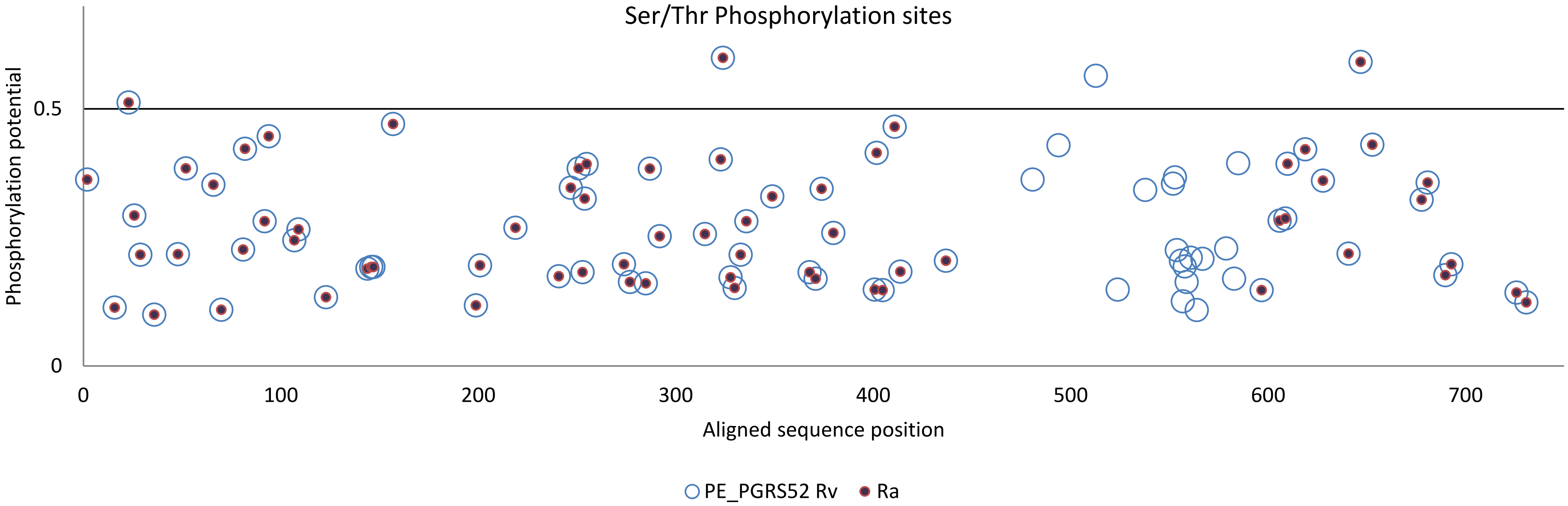


Figure S2-I

```
MRA_2113        ------------------------------------------------------------------------------M02=322WRQRW
Rv2098c         MSFVIASPEALLAAATDLAAIRSTIRAANAAAAVPTTGALAPAADEVSAGIAALFGAQAQSYQAVSAQAAAFHDRFVQL80=400GGSGG
                                                                              :******  .

MRA_2113        ---------------PTAACGTATVAPAGPPAKGG--------------------------------------------------PA
Rv2098c         NGGVWYGNGGAGGAAGQGGPGMNTTSPGGPGGVGGHGGTAILFGDGGAGGAGAAGGPGTPDGAAGPGGSGGTGGLLFGVPGPSGPDG
                                     .. *  *.:*.** . **                                               .
```

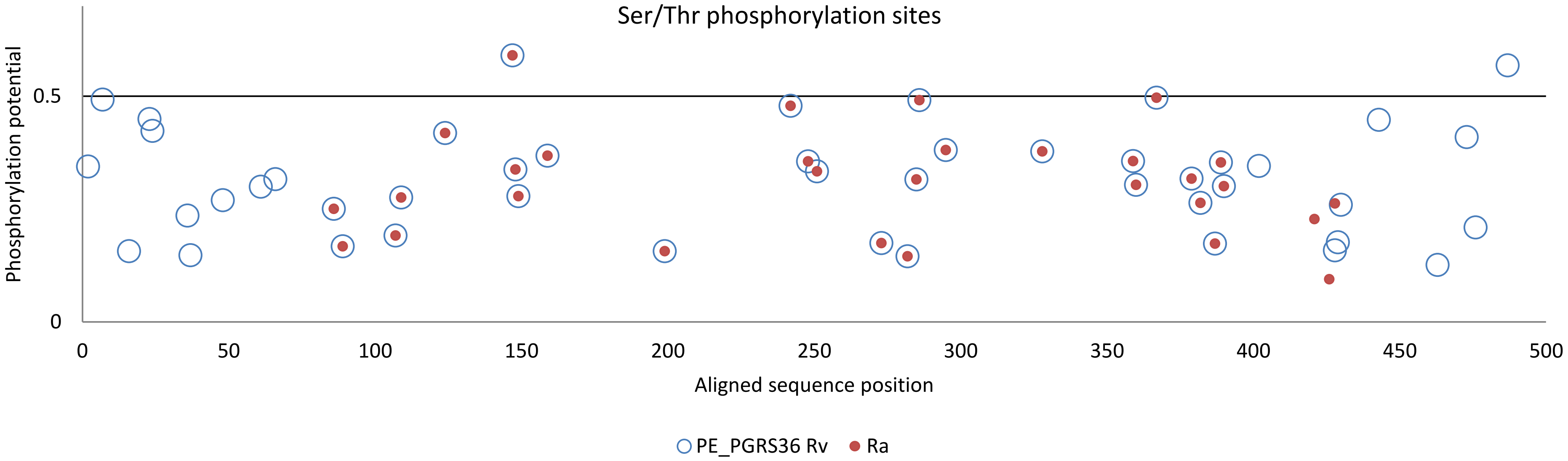


Figure S2-J

```
MRA_0363        MRV4=127NSGFQNFGNLLSGWANLGNTVSGFYNTSMLDLATQALISGFGNHGARLSGILNNGSGP
Rv0354c         M--2=125IR------------------------------------------ASKTSATCCRAGRT
                *  *****                                            .:: *.   ... .
```

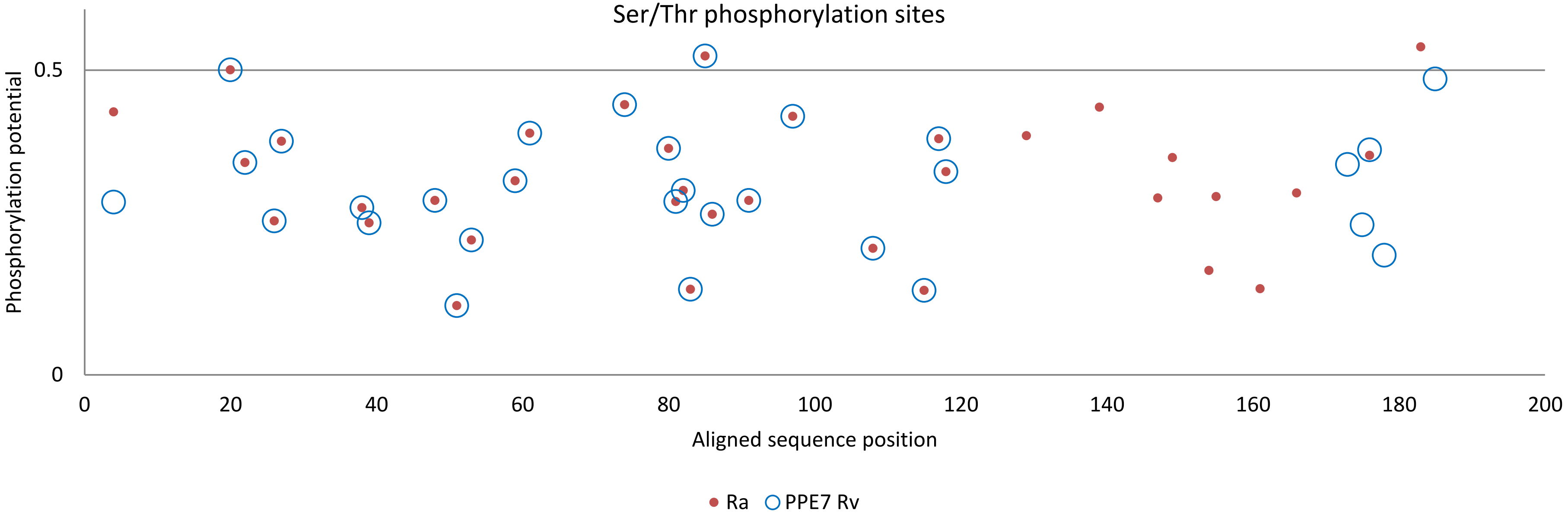


Figure S2-K

```
MRA_1772        MEHRLGRLPAHTLIGTDSPGAEASWVVGITWWSAVVGGFQ41=175RLCGRRGRR---------------------------------------------
Rv1759c         ----------------------------------------01==85AYAAAEAAAVTPLLNSINAPVLAATGRPLIGNGANGAPGTGANGGDAGWLIGNG
                                                        ******  .. ..

MRA_1772        ----------------------------------------------------------------------------------------------------
Rv1759c         GAGGSGAKGANGGAGGPGGAAGLFGNGGAGGAGGTATANNGIGGAGGAGGSAMLFGAGGAGGAGGAATSLVGGIGGTGGTGGNAGMLAGAAGAGGAGGFS

MRA_1772        ----------------------------------------------------------------------------------------------------
Rv1759c         FSTAGGAGGAGGAGGLFTTGGVGGAGGQGHTGGAGGAGGAGGLFGAGGMGGAGGFGDHGTLGTGGAGGDGGGGGLFGAGGDGGAGGSGLTTGGAAGNGGN

MRA_1772        ----------------------------------------------------------------------------------------------------
Rv1759c         AGTLSLGAAGGAGGTGGAGGTVFGGGKGGAGGAGGNAGMLFGSGGGGGTGGFGFAAGGQGGVGGSAGMLSGSGGSGGAGGSGGPAGTAAGGAGGAGGAPG

MRA_1772        -------------------------------------------------------------------------RD-------------------------
Rv1759c         LIGNGGNGGNGGESGGTGGVGGAGGNAVLIGNGGEGGIGALAGKSGFGGFGGLLLGADGYNAPESTSPWHNLQQDILSFINEPTEALTGRPLIGNGDSGT
                                                                                        :*

MRA_1772        ----------------------------------------------------------------------------------------------------
Rv1759c         PGTGDDGGAGGWLFGNGGNGGAGAAGTNGSAGGAGGAGGILFGTGGAGGAGGVGTAGAGGAGGAGGSAFLIGSGGTGGVGGAATTTGGVGGAGGNAGLLI

MRA_1772        ----------------------------------------------------------------------------------------------------
Rv1759c         GAAGLGGCGGGAFTAGVTTGGAGGTGGAAGLFANGGAGGAGGTGSTAGGAGGAGGAGGLYAHGGTGGPGGNGGSTGAGGTGGAGGPGGLYGAGGSGGAGG

MRA_1772        -----------------------------AAAQLDQRAR-------------------------------------------------------------
Rv1759c         HGGMAGGGGGVGGNAGSLTLNASGGAGGSGGSSLSGKAGAGGAGGSAGLFYGSGGAGGNGGYSLNGTGGDGGTGGAGQITGLRSGFGGAGGAGGASDTGA
                                             ..:.*. :*

MRA_1772        -----------------------------------------------------------------PGRYRPSADR
Rv1759c         GGNGGAGGKAGLYGNGGDGGAGGDGATSGKGGAGGNAVVIGNGGNGGNAGKAGGTAGAGGAGGLVLGRDGQHGLT
                                                                                  **    .
```

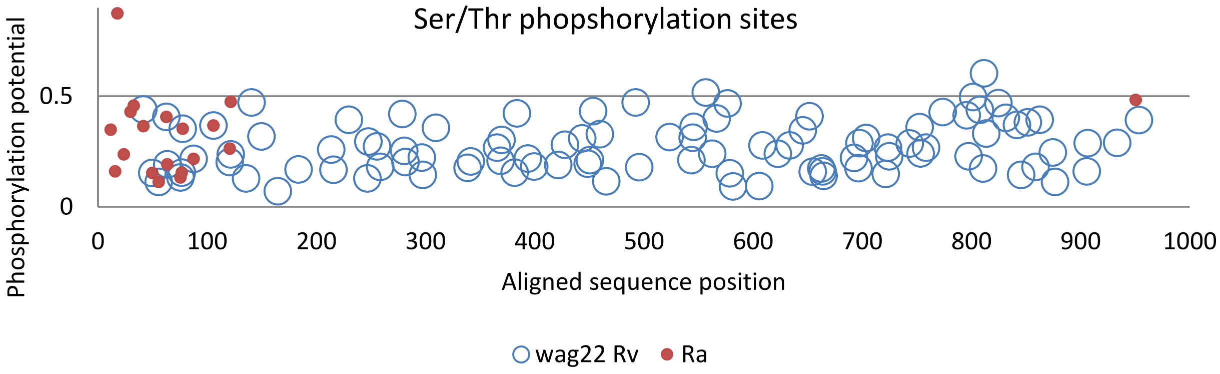


Figure S2-L

```
MRA_3553        1=57L59===653--------------------------------------------------------------------------------
Rv3514          1=57F59===653KAGGSSSAGGTNSSGSAGGTGRQSGTGGAGGAGADNPTGIGGTGGDGGTGGAAGAGGAGGAAGTGGTGGMIGTTGNAGVG
                ****:********

MRA_3553        654=723V725=768AGGAGGAGGSSGAGSTNGSGGAGGTGGQGG799==965----------------------------------------
Rv3514          734=803I805=848---AGGSGGSSCAGGTNGSGGAGGTCGQVV876=1042AGGAGGKGGAGGSSGAGGTNGSGGAGGAGGQGGAGGAGIS
                *******:*******   ***:**** **.********** **  ********

MRA_3553        ---------------------------------------------------------------------------------------------
Rv3514          FSNGSNGGTGGTGGVGGTGGDGGNAGTGAGDPGKGGTGGTGGTGGSGGAGGSGGANFNGGTGGTGGTGGTGGKGGMGGIAGDGGPGGDGGNAG

MRA_3553        --------------------------------------------------------------------AGGAGGKGGAGGNAGTGGAIGSGAG
Rv3514          VGGKGGTNGNGGSGGTGGTGGAGGNAGAGGLANTGGTAGNAGIGGDGGQGGNGGQGDSGSGLGGQPGFAGGPGGKGGAGGNAGTGGTNGSGAG
                                                                                    ***.**************: *****

MRA_3553        GAGVQCGAGGAGISFSNVSNGGTGGTGGVGGTGGGGGIAGTGAADPGKGGTGGTAGTGGSGGSGGSGGANLYGGTGGTGGTGGTS1076=1211
Rv3514          GAGGQGGAGGAGISFSNGSNGGTGGTGGVGGTGGDGGNAGTGAGDPGKGGTGGTGGTGGSGGAGGSGGANFNGGTGGTGGTGGTG1354=1489
                *** * *********** ****************.** *****.**********.*******:*******: ************.*********
```

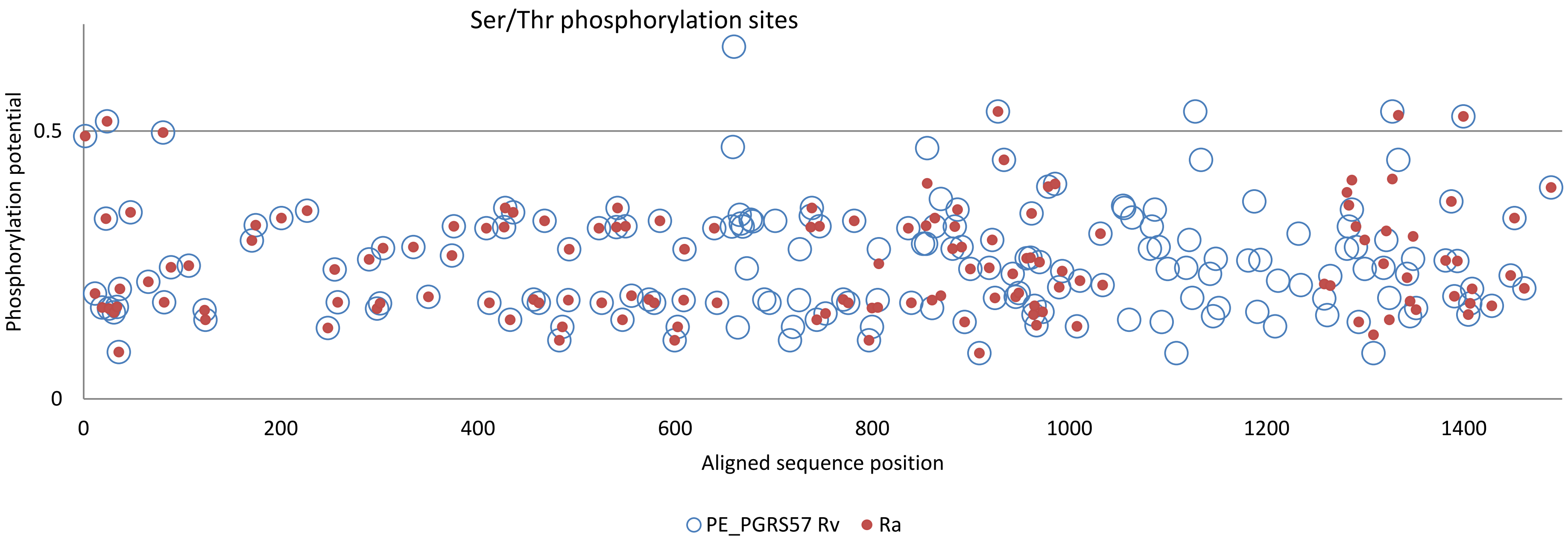


Figure S2-M

```
MRA_0288        1=324S326=351G353=371S373=776KKGDGGAGGFGAGTGGYGGVGG799==837
Rv0279c         1=324N326=351C353=371I373=776NGGDGGAGGFGADTGGNSSSVP799==837
                *****.******* ***************: **********.*** ..   ********
```

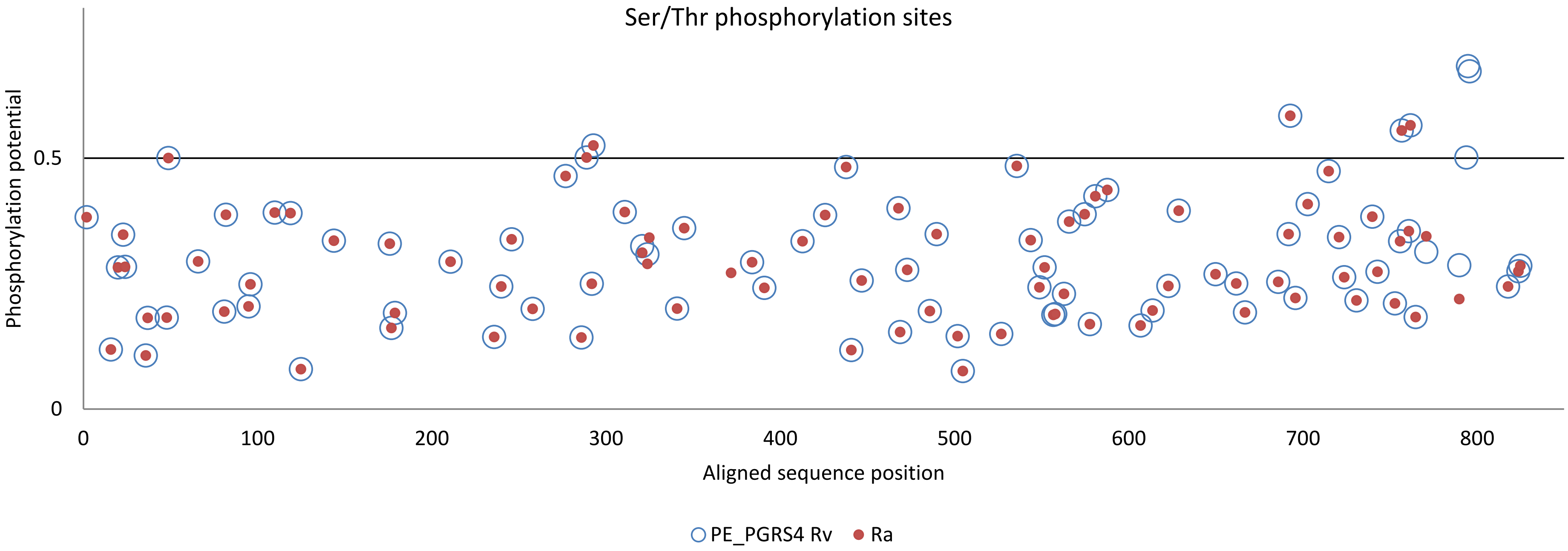


Figure S2-N

```
MRA_0755         1=====224GEG228======294RSVGDG301=========801
Rv0747           1=====224RER228======294KSVGDS301=========801
                 ********* * ************:****.***************
```

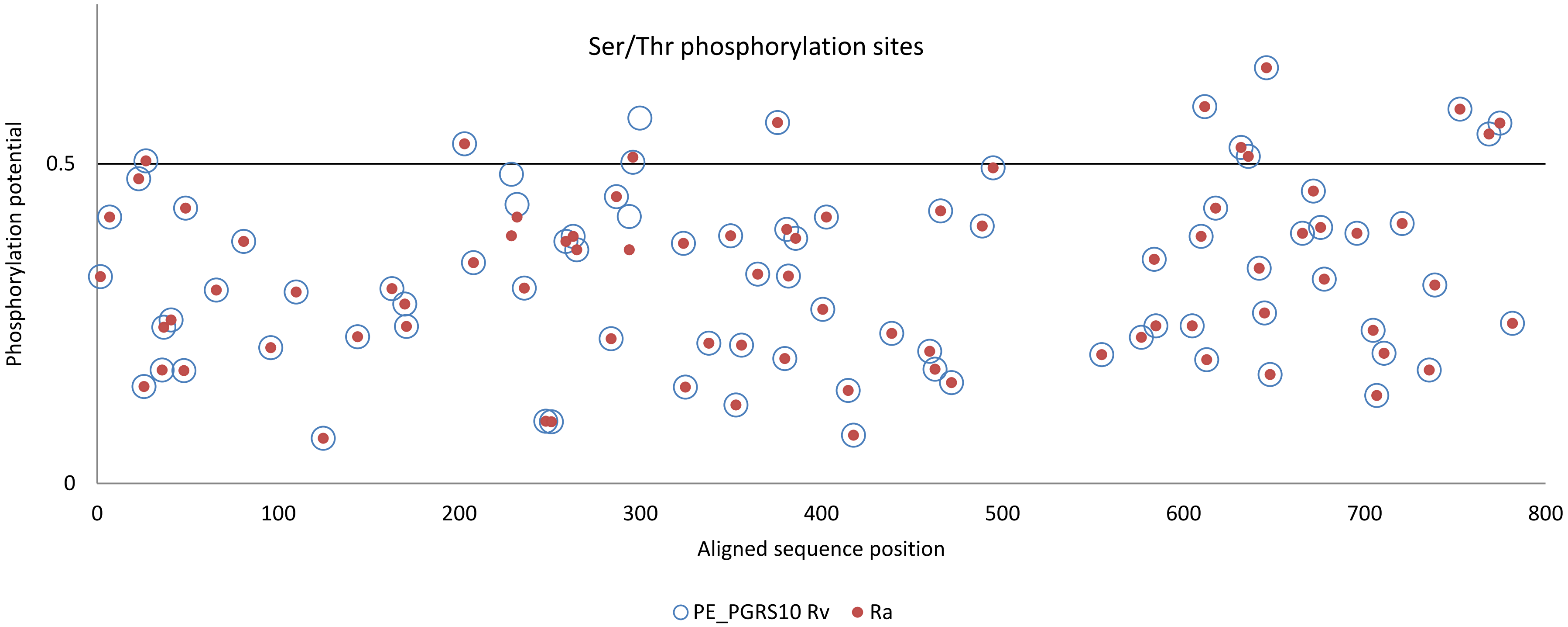


Figure S2-O

```
MRA_3384     1=1518----------------------------------------------------------------------------------------------
Rv3343c      1=1518GSYNTGIGNSGIASTGLFNAGGFNTGVVNAGSYNTGSFNAGQANTGGFNPGSVNTGWLNTGDINTGVANSGDVNTGAFISGNYSNGAFWRGDYQ
             ******

MRA_3384     ----------------------------------------------------------------------------------------------------
Rv3343c      GLLGFSYRPAVLPQTPFLDLTLTGGLGSVVIPAIDIPAIRPEFSANVAIDSFTVPSIPIPQIDLAATTVSVGLGPITVPHLDIPRVPVTLNYLFGSQPGG

MRA_3384     ----------------------------------------------------------------------------------------------------
Rv3343c      PLKIGPITGLFNTPIGLTPLALSQIVIGASSSQGTITAFLANLPFSTPVVTIDEIPLLASITGHSEPVDIFPGGLTIPAMNPLSINLSGGTGAVTIPAIT

MRA_3384     ----------------------------------------------------------------------------------------------------
Rv3343c      IGEIPFDLVAHSTLGPVHILIDLPAVPGFGNTTGAPSSGFFNSGAGGVSGFGNVGAMVSGGWNQAPSALLGGGSGVFNAGTLHSGVLNFGSGMSGLFNTS

MRA_3384     ----------------------------------------------------------------------------------------------------
Rv3343c      VLGLGAPALVSGLGSVGQQLSGLLASGTALHQGLVLNFGLADVGLGNVGLGNVGDFNLGAGNVGGFNVGGGNIGGNNVGLGNVGWGNFGLGNSGLTPGLM

MRA_3384     ----------------------------------------------------------------------------------1519==========1947
Rv3343c      GLGNIGFGNAGSYNFGLANMGVGNIGFANTGSGNFGIGLTGDNLTGFGGFNTGSGNVGLFNSGTGNVGFFNSGTGNWGVFNS2095==========2523
                                                                                               ******************
```

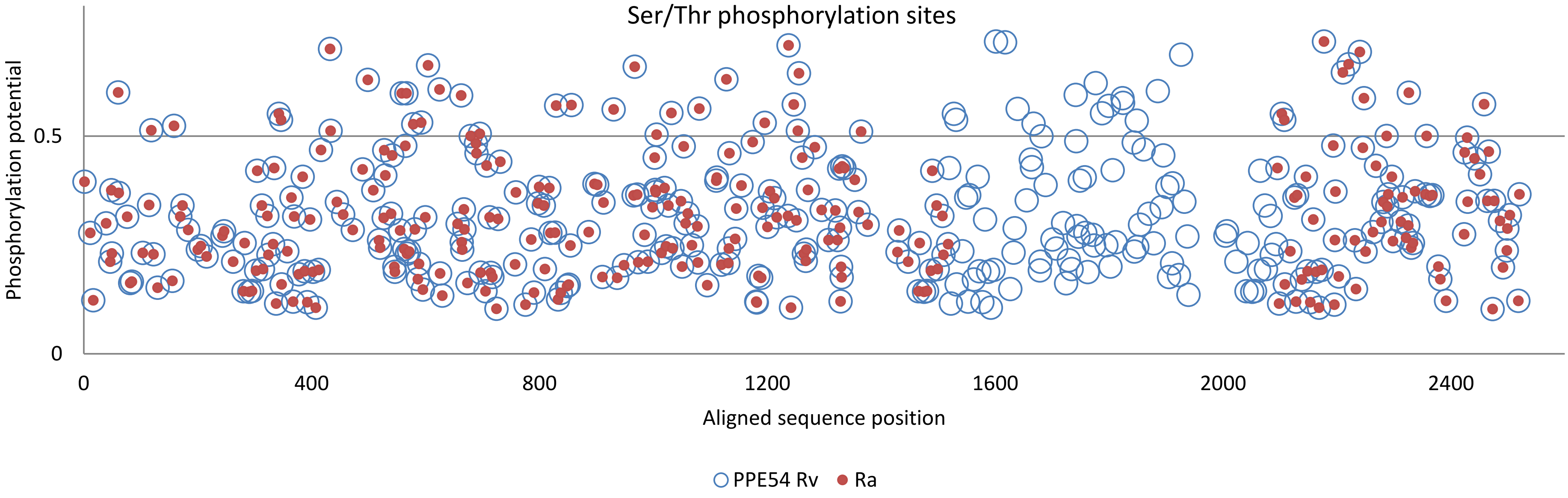


Figure S2-P

```
MRA_0395        1=118SLVK123=137AQYGEMWAQDIVAMEGYAGASAAASQLPPFTPPPATTSGAGSLSDAAATAAQAVVPAAAATDVSLLPTLQ
Rv0388c         1=118SLVQ123=137THYGEMWAHDILAMDGYAGASGAASQLRR---SPAT----------------------------------
                ********:*******::******:**:**:******.*****     .***

MRA_0395        SFLPPPFDAIPNPIEDLDVLVAAAVAVAAGSLGVSAAQLGEIYRHDVVDEAQKAPHCPAESDQTPAGAAGDGDLPEVGGRVTSPPQ
Rv0388c         ------------------------------------------------------------GDHQ-------------RG-------
                                                                            .*:               *

MRA_0395        PPVAALTGYSANIGGLSVPHSWNLPPAVRQVAAMFPGATPMYMTGSSDGSYAGLAAAGLAGTGLAGLAARGGSAPTPAAAAPAGA
Rv0388c         -------------------------------------------------------------------------------------

MRA_0395        GGAGPAATRPAAQQTPAVPAAAAGSAIPGLPPGLPPGVVANLAATLAAIPGATIIVVPPSPNANQ
Rv0388c         -------------------------------------------------------------RVAE
                                                                             .. :
```

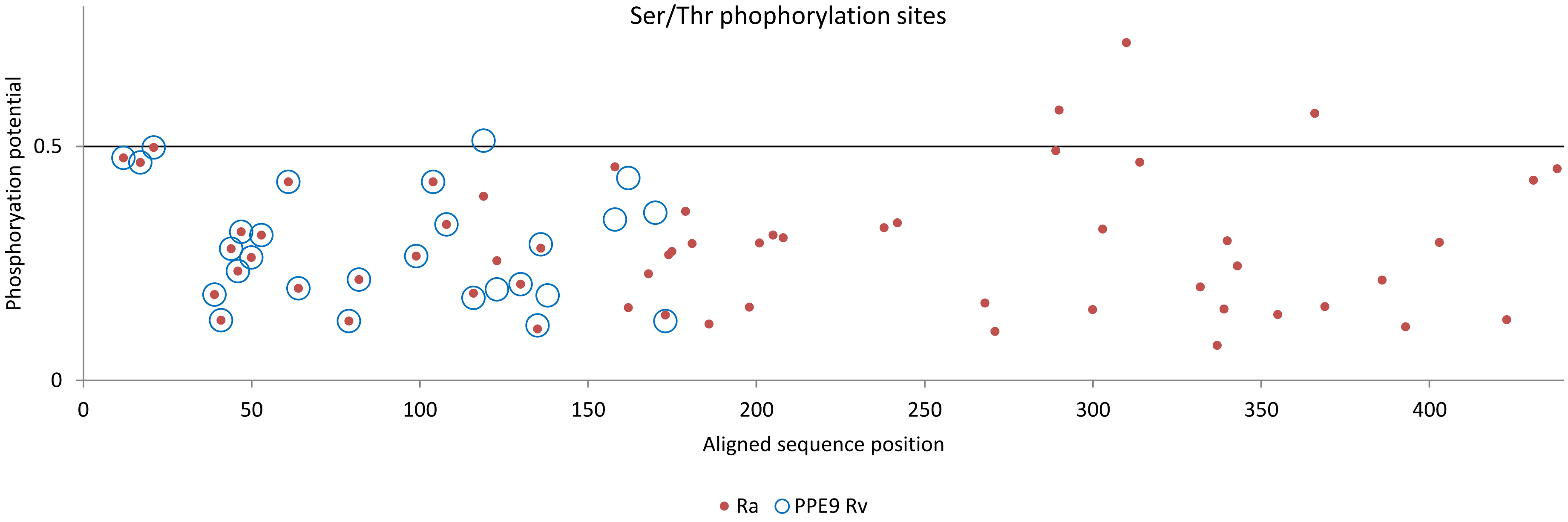


Figure S2-Q

```
MRA_0885        1==========================435PKKSREQRVRENL
Rv0878c         1==========================435QKK-----VGNSG
                *****************************  **      * :.
```

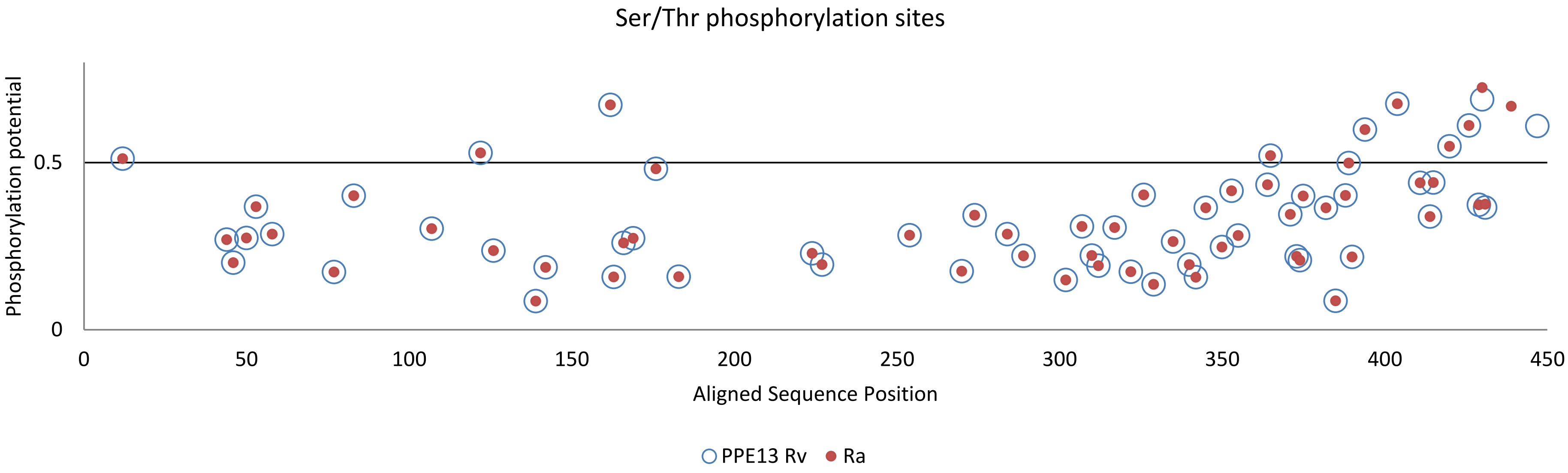


Figure S2-R

```
MRA_1205A       1=307TWVGRPRSVRCRC--------------------------------------------------------RRPGPRPTRQSPRRRGCR
Rv1196          1=307N-LGRAASVGSLSVPQAWAAANQAVTPAARALPLTSLTSAAERGPGQMLGGLPVGQMGARAGGGLSGVLRVPPRPYVM-PH-SPAAG
                *****. :**. ** . .                                                        *  ***     *:    .
```

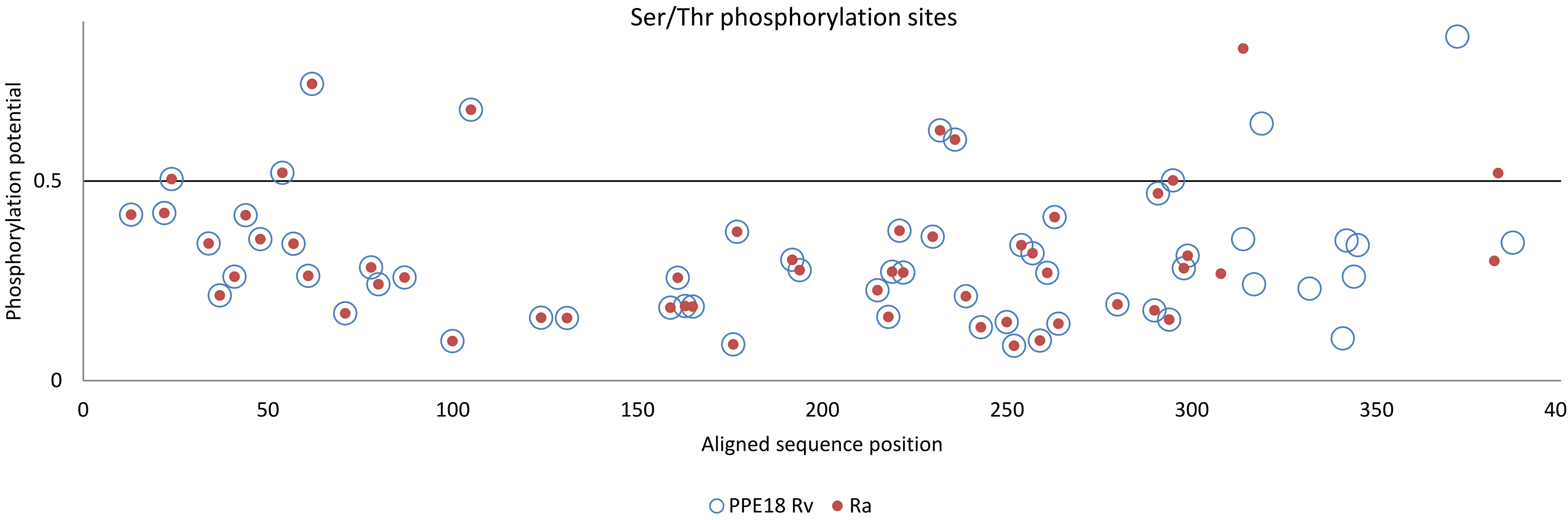


Figure S2-S

```
MRA_3635        1=162TADP-------------------------------------------------------------------------VVPA-------
Rv3595c         1=162NGGSGGAGGAGAAGGSGGQGGLLYGNGGAGGNGGAATIPGGNGGAGGAGGNAWLFGNGGAGGLGAAGAAGAAGVNPLTVPAGQGSMGN
                *****....                                                                         .***

MRA_3635        --EPVRPAGPADKAGCCTATA------------------------------------------------------------------------
Rv3595c         NGEPGGPGQPGTEFGQTGGTGGTGGTGLSVGGTGGTGGTGGTGGAGGSGGRGGLLVGDGGAGGIGGTGGEGGIGARGGTGGQGGMGGAGQPGV
                  **  *. *. : *   .*.

MRA_3635        ----------------------------------------------ARAATAGRRLSPAATAAPVVPAATRGYSATVGPGG-SARPARRVPPGSTP
Rv3595c         GGDAGDGGNGGIGGDGGAGGDGGAGGAGGAGGLFGVSGSSGLGGAAGSGGNGGGGGEPGVAGSPGVGPAGRGGDGNLGQFGPEGAPGQPGQPGQPG
                       . ....*  .*....:* * .* ** ....:* * .. *.:  **..
```

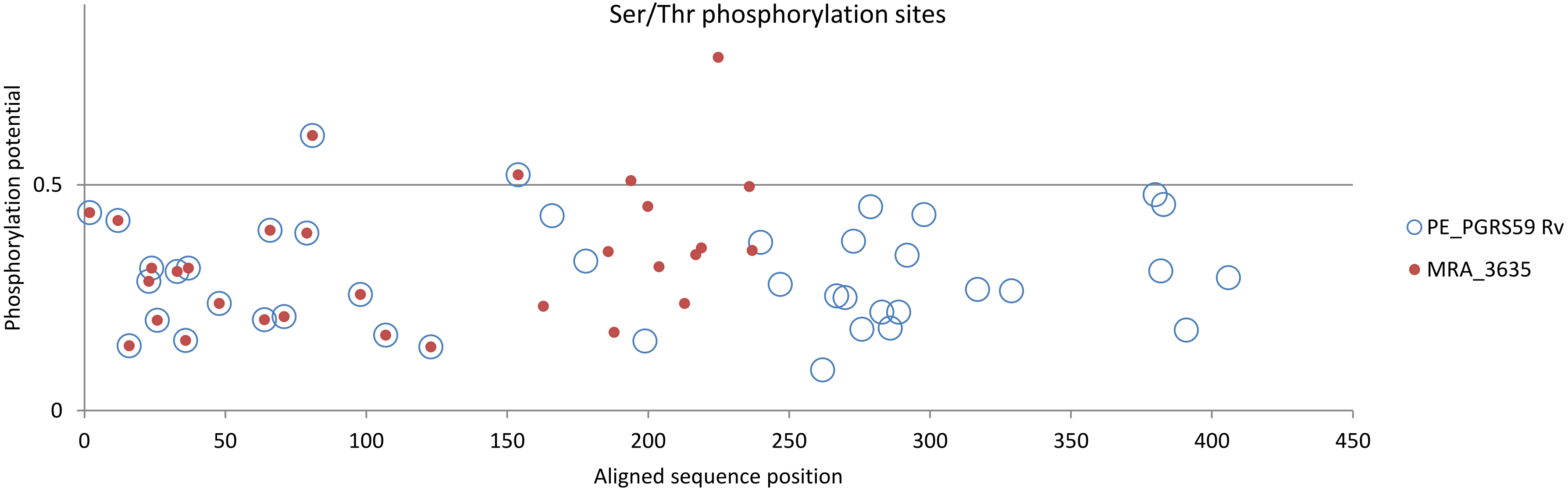


Figure S2-T

```
MRA_3634        ------------------------MNRADPASQAPSSGKPVAP----------------------------------------------------
Rv3595c         MSFVIAVPEFLSAAATDLANLGSTISAANAAASIPTTGVLAAGADDVSAAIAALFGAHAQAYQTISAQAATFHAQFVQTLSAGAGAYANAEAANV
                                        :. *:.*:. *::*  .*

MRA_3634        ----------VALAVLACPLAGPA-GPAAPGGPAGPAALAVGVGSWSATA--AQVASGAQGAKAASAPGAAPAVRAEWAAPGNQA----------
Rv3595c         QQSLLNAINAPTQALLGRPLIGDGADGTAPGQNGGAGGLLYGNGGNGAAGVNAGIAGGSGGAAGLIGNGGSGGAGGAGAAGGSGGQGGLLYGNGG
                           : *:*. ** * . . :***  .*...*  * *. .*:.  * :*.*: ** .  . *.: .. .  ** *. .

MRA_3634        -------------------------------------------------------------------------LGVTLVTGVTAGSAVTAAP---
Rv3595c         AGGNGGAATIPGGNGGAGGAGGNAWLFGNGGAGGLGAAGAAGAAGVNPLTVPAGQGSMGNNGEPGGPGQPGTEFGQTGGTGGTGGTGLSVGGTGG
                                                                                         :* *  ** *.*:.::..

MRA_3634        -----------------------------AETAARAARAARAACSASPVAPGWAVPPVAGVMAGAV---------------------VSPVWPAP
Rv3595c         TGGTGGTGGAGGSGGRGGLLVGDGGAGGIGGTGGEGGIGARGGTGGQGGMGGAGQPGVGGDAGDGGNGGIGGDGGAGGDGGAGGAGGAGGLFGVS
                                             . *..... .**.. ...    * . * *.*  ...                      .. :: ..


MRA_3634        RALGLRAVAATATSASS----ALKVHP-ASPASRASPVDIVAAGPSA-PRRLLEQLPSVTGPVEALARVEFCGQGVDLIAELG
Rv3595c         GSSGLGGAAGSGGNGGGGGEPGVAGSPGVGPAGRGGDGNLGQFGPEGAPGQP------------------------GQPGQPG
                 : ** ..*.:. ....    .:   * ..**.*..  ::   **.. * :                         .  .: *
```

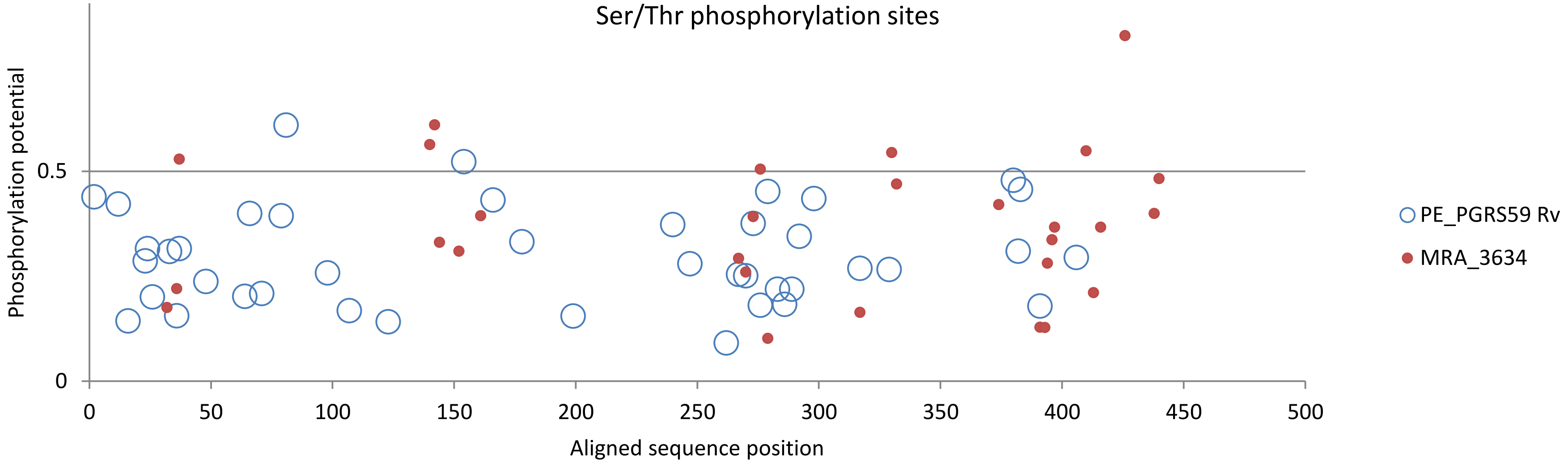


Figure S2-U

```
MRA_0767        1==200HVWRYDFGGDVNVVESYVLYLRRKIDTGEKRLLHTLRGVGYVLREPR
Rv0757          1==200HVWRYDFGGDVNVVESYVSYLRRKIDTGEKRLLHTLRGVGYVLREPR
                ************************ ****************************
```

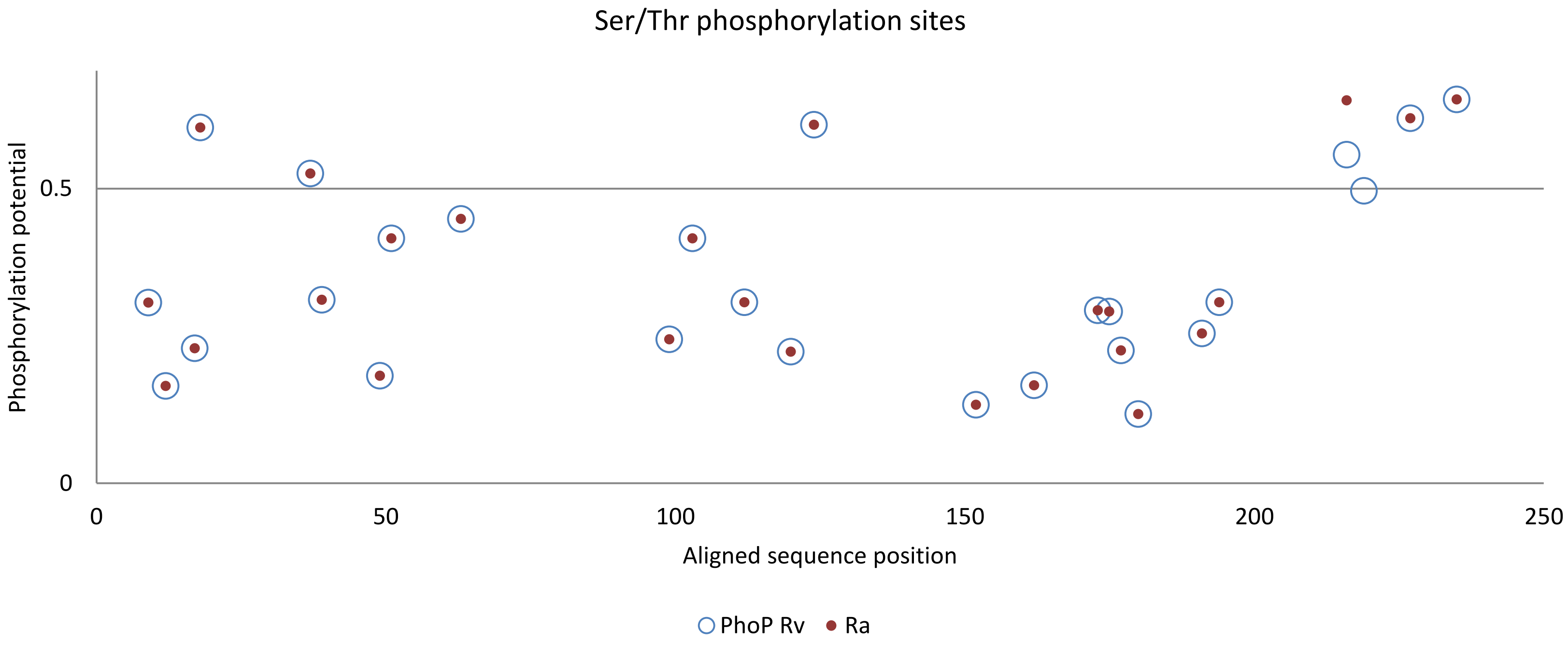


Figure S2-V

```
MRA_3950        1=====159ARMLGVAEGTVKSRC-------------------------ARARARLARLLGYLNTGVNIRR
Rv3911          1=====159RPDAGRGRGHRQEPLRPGAGPPSAAAGLSQHRGEHPALTPLPVRRSIDPRARRYPTSGYCHRA
                *********    * ..*  :.                            .  *:  .*   * .:*   *
```

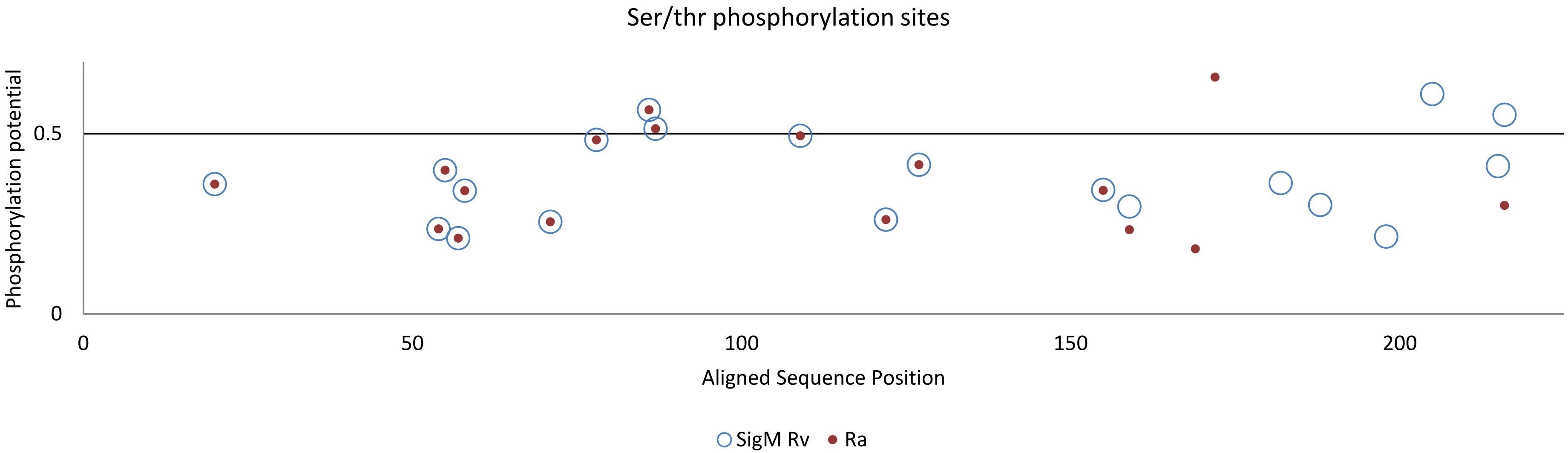


Figure S2-W

```
MRA_1156        MFSAVTVALSMSATALFPMYFLKSFAYAGV 31=================499
RV1146          -----------------------------M 02=================470
                                             :   ********************
```