

Peak Area	iCV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM				CarT		RajIB	Ascor	MOWSE	Sequence
<10	0										
10	2										
20	4										
40	6										
60	8										
70	10										
80	12										
90	14										
>100	>16										
		Protein Name	Gene	Phosphosites							
		14-3-3 epsilon YWHAE		S210					13.4	57.0	K.AAFDDAAIELDTLSEESYK.D
		14-3-3 epsilon YWHAE		T208					9.1	53.4	K.AAFDDAAIELDTLSEESYK.D
		14-3-3 Eta YWHAH		S46					37.7	36.8	R.NLLSVAYK.N
		14-3-3 theta YWHAQ		S230					16.9	27.8	R.DNLTLWTSDSAGEECDAAEGAEN.-
		14-3-3 theta YWHAQ		S232					15.3	38.5	R.DNLTLWTSDSAGEECDAAEGAEN.-
		14-3-3 zeta YWHAZ		S207					24.1	93.9	K.TAFDEAIAELDTLSEESYK.D
		14-3-3 zeta YWHAZ		T205					10.2	43.5	K.TAFDEAIAELDTLSEESYK.D
		3 Phosphoinositide dependent protein kinase 1	PDPK1	S241					57.2	129.2	R.ANSFVGTAAQVYSPPELTK.S
		3 Phosphoinositide dependent protein kinase 1	PDPK1	T245					9.2	38.2	R.ANSFVGTAAQVYSPPELTK.S
		5 azacytidine Induced 1 CEP131		S89					10.1	59.8	R.SGSPPRPTPTDFLMFEGSPSGK.K
		5 azacytidine Induced 1 CEP131		S87S105					11.3	35.9	R.SGSPRPTPTDFLMFEGSPSGK.K
		CEP131		S89S105					3.2	32.4	R.SGSPPRPTPTDFLMFEGSPSGKK.R
		5 azacytidine Induced 1 CEP131		T96S105					9.8	15.7	R.SGSPRPTPTDFLMFEGSPSGKK.R
		5 azacytidine Induced 1 CEP131		T93					9.2	37.1	R.SGSPRPTPTDFLMFEGSPSGK.K
		5 azacytidine Induced 1 CEP131		T96S107					9.6	21.5	R.SGSPRPTPTDFLMFEGSPSGKK.R
		5'-3' exoribonuclease 2 XRN2		S448					46.9	26.4	R.NSPGSQVASNPR.Q
		5'-3' exoribonuclease 2 XRN2		S499S501					100.0	105.2	R.KAEDSDSEPEEDNVR.L
		5'-3' exoribonuclease 2 XRN2		T478					15.2	59.4	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S473					8.4	133.5	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S482					-0.2	19.5	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S471					2.3	86.7	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S475					6.0	63.6	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S471S473					12.3	79.6	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S475T478					3.2	79.5	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S473S475					11.4		R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S471S475					2.4	90.4	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S470S471					11.3	38.1	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		T478S479					13.6	11.8	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S470					7.4	25.7	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5'-3' exoribonuclease 2 XRN2		S471T478					5.4	73.1	R.MQNNSSPSISPNTSFTSDGSPPLGGIK.R
		5', 3'-Nucleotidase, cytosolic NT5C		S182					51.2	58.2	R.LLSWSDNWRE
		6-phosphofructo-2 kinase/fructose-2,6- bisphosphatase 2	PFKFB2	S466					51.2	50.9	R.RNSFTPLSSSNTIR.R
		6-phosphofructo-2 kinase/fructose-2,6- bisphosphatase 2	PFKFB2	S482					9.0	14.5	R.NYVSGSRPLKPLSLR.A
		6-phosphofructo-2 kinase/fructose-2,6- bisphosphatase 2	PFKFB2	S483					24.1	33.3	R.NYVSGSRPLKPLSLR.A
		6-phosphofructo-2 kinase/fructose-2,6- bisphosphatase 2	PFKFB2	S486S493					37.9	18.0	R.NYSVGSRLKPLSLR.A
		6-phosphofructo-2 kinase/fructose-2,6- bisphosphatase 2	PFKFB2	S483S493					13.0	21.2	R.NYVSGSRPLKPLSLR.A
		6-phosphofructo-2 kinase/fructose-2,6- bisphosphatase 2	PFKFB2	S486					16.1	33.2	R.NYSVGSRLKPLSLR.A
		6-phosphofructo-2 kinase/fructose-2,6- bisphosphatase 2	PFKFB2	S482S493					8.3	14.2	R.NYVSGSRPLKPLSLR.A
		60S ribosomal protein L22-like 1 RPL22L1		S117					12.1	40.6	R.YFQISQDEDESSED.-
		7-dehydrocholesterol reductase DHCR7		S14					46.8	13.8	K.SLDGVTNDR.T
		A kinase anchor protein 11 AKAP11		S1337S1340					10.6	23.5	K.YPSCESVTDEYAGHLQILK.Q
		A kinase anchor protein 11 AKAP11		Y1335S1340					23.9	58.3	K.YPSCESVTDEYAGHLQILK.Q
		A kinase anchor protein 11 AKAP11		S1242					-0.5	22.1	R.SVSPFLNPSDENLK.T
		A kinase anchor protein 2 AKAP2		S383					17.8	82.0	R.DALGDSLQVPVSPSTTSSR.C
		A kinase anchor protein 2 AKAP2		S951					33.6	63.1	R.TLSMIEEIR.A
		A kinase anchor protein 2 AKAP2		S979					39.3	31.6	R.QVLQSTQSPR.T
		A kinase anchor protein 2 AKAP2		T949					10.6	60.7	R.TLSMIEEIR.A
		A kinase anchor protein 2 AKAP2		S385					7.8	47.0	R.DALGDSLQVPVSPSTTSSR.C
		A kinase anchor protein 2 AKAP2		T1012					1.6	12.1	K.VKPPPSPTTEGSPLODLAPEEAAGTQRPK.N
		A kinase anchor protein 2 AKAP2		S1016					18.4	13.2	K.VKPPPSPTTEGSPLODLAPEEAAGTQRPK.N
		A kinase anchor protein 2 AKAP2		S862					13.4	12.9	R.DGAEQQGPEATVEEAFAAGSEKPSMFEPPQVSSPVQEK.R
		A kinase anchor protein 2 AKAP2		T837					16.3		R.DGAEQQGPEATVEEAFAAGSEKPSMFEPPQVSSPVQEK.R
		A kinase anchoring protein 13 AKAP13		S2732					19.8	56.2	K.SGSLDELSVSPK.R
		A kinase anchoring protein 13 AKAP13		S1880					104.4	85.5	R.SAVLLVDATTPIFANR.R
		A kinase anchoring protein 13 AKAP13		S1931S1936					14.4	22.5	K.FLSHSTDNLN.I
		A kinase anchoring protein 13 AKAP13		S1559					9.9	16.7	R.SLSPFRR.H
		A kinase anchoring protein 13 AKAP13		S1910					5.1	28.6	K.SVSIQINITGVGNDENMSNTWK.F
		A kinase anchoring protein 13 AKAP13		S1931S1933					14.7	17.6	K.FLSHSTDNLN.I
		A kinase PRKA anchor protein 8 like AKAPBL		S297S300S302					1.7	68.6	R.TDCSDNSDSDNDEGTEGATEGLEGTEAVEK.G
		A kinase PRKA anchor protein 8 like AKAPBL		S297S302T308					2.4	40.3	R.TDCSDNSDSDNDEGTEGATEGLEGTEAVEK.G
		A_Raf ARAF		S299					9.8	27.1	R.DSGYYWEVPPSEVQLLK.R
		A_Raf ARAF		T213					-0.3	41.3	R.STSTPNVHMVSTTAPMDSNLIQLTGQSFSTDAAGSR.G

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				CarT	RajiB			Ascor	MOWSE	Sequence	
Protein Name	Gene	Phosphosites									
A_Raf	ARAF	S212						11.5	39.9	R.S*TSPNVHMVSTTAPMDSNLQLTGQSFSTDAAGSR.G	
ABL Interactor 1	ABI1	S231						11.4	24.0	R.TA\$*LNQRPR.T	
Absent in melanoma 1	CRYBG1	T20						-0.1	44.5	K.ST*DSPGADAELPESA.R.D	
Acetyl-CoA carboxylase alpha	ACACA	S117						22.5	62.3	R.SMS*\$GLHLVK.Q	
Acetyl-CoA carboxylase alpha	ACACA	S62						10.9	61.9	R.FIIGSV\$*EDNSEDEISNLVK.L	
Acetyl-CoA carboxylase alpha	ACACA	S60S66						46.7	105.3	R.FIIG\$*VSEDN\$*EDEISNLVK.L	
Acetyl-CoA carboxylase alpha	ACACA	S62S66						41.9	115.7	R.FIIGSV\$*EDN\$*EDEISNLVK.L	
Acetyl-CoA carboxylase alpha	ACACA	S60S62						20.5	14.2	R.FIIG\$*V\$*EDNSEDEISNLVK.L	
Acetyl-CoA carboxylase alpha	ACACA	T1249S1253						6.5	11.6	R.MSFSSNLNHYGMT*HVA\$*VSDVLLDNSFTPPCQR.M	
Acetyl-CoA carboxylase alpha	ACACA	S87S90						3.1	38.3	K.EGSL\$*PA\$*VGSDTLSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S85S87S90						1.2	43.1	K.EG\$*L\$*PA\$*VGSDTLSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S85S87S93						5.4	32.8	K.EG\$*L\$*PASVG\$*DTLSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S1296						7.4	11.5	R.IFDEVMGCFDS\$*PPOSPTTFPEAGHTSLYDEDKVPR.D	
Acetyl-CoA carboxylase alpha	ACACA	S1296T1302						22.2	70.5	R.IFDEVMGCFDS\$*PPOSPT*TFPEAGHTSLYDEDKVPR.D	
Acetyl-CoA carboxylase alpha	ACACA	S1296S1300						26.0	52.8	R.IFDEVMGCFDS\$*PPQS\$*PTTFPEAGHTSLYDEDKVPR.D	
Acetyl-CoA carboxylase alpha	ACACA	S1294S1296							46.6	R.IFDEVMGCF\$*DS\$*PPOSPTTFPEAGHTSLYDEDKVPR.D	
Acetyl-CoA carboxylase alpha	ACACA	S85S87						7.3	43.4	K.EG\$*L\$*PASVGSDTLSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S85S90						12.2	63.9	K.EG\$*LSPA\$*VGSDTLSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S85S87S90T95						5.1	57.3	K.EG\$*L\$*PAS*VGSDT*LSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S87S90S93S97						5.0	44.5	K.EGSL\$*PA\$*VG\$*DTL\$*DLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S66						9.1	74.6	R.FIIGSVSEDN\$*EDEISNLVK.L	
Acetyl-CoA carboxylase alpha	ACACA	S60						5.5	69.1	R.FIIG\$*VSEDNSEDEISNLVK.L	
Acetyl-CoA carboxylase alpha	ACACA	S1253S1255						2.2	24.5	R.MSFSSNLNHYGMTHVA\$*V\$*DVLLDNSFTPPCQR.M	
Acetyl-CoA carboxylase alpha	ACACA	S1238T1249						2.5	24.2	R.M\$*FSSNLNHYGMT*HVASV\$*VSDVLLDNSFTPPCQR.M	
Acetyl-CoA carboxylase alpha	ACACA	Y1246S1255						10.0	58.8	R.MSFSSNLNHY*GMTHVASV\$*DVLLDNSFTPPCQR.M	
Acetyl-CoA carboxylase alpha	ACACA	Y1246T1249						3.3	12.8	R.MSFSSNLNHY*GMT*HVASV\$*VSDVLLDNSFTPPCQR.M	
Acetyl-CoA carboxylase alpha	ACACA	S1238S1240						2.2	23.7	R.M\$*F\$*SNLNHYGMTHVASV\$*VSDVLLDNSFTPPCQR.M	
Acetyl-CoA carboxylase alpha	ACACA	S1300T1302						27.8	17.3	R.IFDEVMGCFSDSPQ\$*PT*TFPEAGHTSLYDEDKVPR.D	
Acetyl-CoA carboxylase alpha	ACACA	S1294T1302						11.9	38.0	R.IFDEVMGCF\$*DSPPOSPT*TFPEAGHTSLYDEDK.V	
	ACACA	S1294S1300						6.4	20.2	R.IFDEVMGCF\$*DSPPOS\$*PTTFPEAGHTSLYDEDK.V	
Acetyl-CoA carboxylase alpha	ACACA	S85T95						6.1	21.3	K.EG\$*LSPASVGSDT*LSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S87S90S93						5.8	36.6	K.EGSL\$*PA\$*VG\$*DTLSDLGISSLQDGLALHIR.S	
Acetyl-CoA carboxylase alpha	ACACA	S85S87S93T95						17.0	71.4	K.EG\$*L\$*PASVG\$*DT*LSDLGISSLQDGLALHIR.S	
Acetylserotonin methyltransferase-like	ASMTL	S239						66.0	120.0	K.HDSIPAADTFEDLS\$*DVEGGGSEPTQR.D	
Acetylserotonin methyltransferase-like	ASMTL	T234						16.5	13.0	K.HDSIPAADT*FEDLSDVEGGGSEPTQR.D	
Acheron	FAM27E3	S247S248						100.0	28.2	R.RIS*\$R.G	
TRAF3-interacting JNK-activating modulator	TRAF3IP3	S110						100.0	30.6	R.RIS*\$SPR.E	
ACINUS	ACIN1	T563						18.4	41.9	R.RASHT*LLPSHR.L	
ACINUS	ACIN1	S1004						71.2	36.0	R.TAQVPS*PPR.G	
ACINUS	ACIN1	S490						121.6	70.3	K.AES\$*PAEKVPEESVLPLVK.S	
ACINUS	ACIN1	T408						7.9	58.3	K.ASLVALPEQT*ASEEETPPPLLTKE	
ACINUS	ACIN1	T408T414						12.4	27.7	K.ASLVALPEQT*ASEEET*PPPLLTKE	
ACINUS	ACIN1	S386S388						32.4	24.1	K.SKS\$*PS\$*PPRL	
ACINUS	ACIN1	S729						100.0	29.5	R.LQPERGS*PK.K	
ACINUS	ACIN1	S605						35.1	25.1	R.SH\$*PLR.S	
ACINUS	ACIN1	S898						61.4	57.3	R.IS\$*EDETER.N	
ACINUS	ACIN1	S710						46.5	54.6	R.RLS\$*QPESAEKH	
ACINUS	ACIN1	S655S657						60.8	48.6	K.\$*L\$*PGVSR.D	
ACINUS	ACIN1	S478S482						26.4	48.8	R.ELLVSQHTVQLVGGL\$*PLS\$*PSDTKA	
ACINUS	ACIN1	S478S481						24.0	60.3	R.ELLVSQHTVQLVGGL\$*PLS\$*SPSDTKA	
ACINUS	ACIN1	S216						16.9	63.3	K.SSSISEEKGS\$*DDEKPR.K	
ACINUS	ACIN1	S895						44.6	24.2	K.SLIPDIKPLAQEAVDLHADD\$*RISEETER.N	
ACINUS	ACIN1	S467T470S478							47.2	R.C*LVSDNTLVVGL\$*EDSEEDTVACSDVVECEV.DLVV.S	
ACINUS	ACIN1	S1329S1331T1						100.0	20.2	R.\$*RS\$*T*PVRDR.G	
ACINUS	ACIN1	S166S169						14.0	20.5	R.EAAELEE\$*AES\$*EDEMIIHPEGVASLLPPDFQSSLERPELELSR.	
ACINUS	ACIN1	S1331T1332						10.4	23.9	R.SRS\$*T*PVRDR.G	
ACINUS	ACIN1	S603						24.6	27.8	R.\$*HSPLR.S	
ACINUS	ACIN1	S561						25.8	32.8	R.RAS\$*HTLLPSHR.L	
ACINUS	ACIN1	S240S243						61.8	39.1	K.L\$*EG\$*QPAEEEEQDETPSR.N	
ACINUS	ACIN1	S410						2.2	67.7	K.ASLVALPEQT\$*EEETPPPLLTKE	
ACINUS	ACIN1	S410T414						3.8	22.7	K.ASLVALPEQT\$*EEET*PPPLLTKE	
ACINUS	ACIN1	S1284						100.0	12.9	K.RREH\$*R.E	

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				5	6	5	6			
<div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> </div>										
	ACINUS	ACIN1	S365					9.1	24.9	K.TT <b>S</b> *PLEEEER.E
	ACINUS	ACIN1	S657S661					8.4	12.4	K.SL <b>S</b> *PGV <b>S</b> *R.D
	ACINUS	ACIN1	S478					24.4	17.0	R.ELLVSGHTVQLVGGL <b>S</b> *PLSSPSDTK.A
	ACINUS	ACIN1	S210					11.9	42.3	K.SSSIS <b>S</b> *EEKGSDSDEKPR.K
	Actin alpha, cardiac muscle	ACTB	Y242					-0.3	93.2	R.S <b>Y</b> *ELPDGQVITIGNER.F
	Actin binding LIM protein 1	ABLIM1	S452					13.8	76.7	R.ST <b>S</b> *QGSINSPVYSR.H
	Actin binding LIM protein 1	ABLIM1	S655					25.4	24.1	K.TA <b>S</b> *LPGYGR.N
	Actin binding LIM protein 1	ABLIM1	S431					25.3	80.5	R.TL <b>S</b> *PTPSAEGYQDV.R.D
	Actin binding LIM protein 1	ABLIM1	S185					98.4	40.1	R.S <b>S</b> *PQHFRPDQGINIYR.K
	Actin binding LIM protein 1	ABLIM1	S352					9.8	53.6	R.T <b>S</b> *SESIYSRPGSSIPGSPGHTIYAK.V
	Actin binding LIM protein 1	ABLIM1	S352S367					16.1	35.1	R.T <b>S</b> *SESIYSRPGSSIPG <b>S</b> *PGHTIYAK.V
	Actin binding LIM protein 1	ABLIM1	S367					38.4	24.9	R.TSSESIYSRPGSSIPG <b>S</b> *PGHTIYAK.V
	Actin binding LIM protein 1	ABLIM1	S353					1.3	32.2	R.T <b>S</b> *ESIYSRPGSSIPGSPGHTIYAK.V
	Actin binding LIM protein 1	ABLIM1	S353S367					13.8	21.9	R.T <b>S</b> *ESIYSRPGSSIPG <b>S</b> *PGHTIYAK.V
	Actin filament associated protein	AFAP1	S342S343					6.5	24.0	K.KKPSTDEQ <b>T</b> <b>S</b> * <b>S</b> *AEEDVPTCGYLVNLSNSR.W
	Actin gamma 1	ACTB	S232					28.2	12.3	K.LCYVALDFEQEMATA <b>S</b> *SSSLEK.S
	Actin-bundling protein with BAIAP2 homoloov	MTSSL1	S639T643						13.1	K.RL <b>S</b> *LPNT <b>S</b> *AWGSPPEAAGYPGAGAEDEQQOALANRHS <b>S</b> *LVEKL
	Actin-bundling protein with BAIAP2 homoloov	MTSSL1	S639S673					10.1	12.0	K.RL <b>S</b> *LPNTAWGSPPEAAGYPGAGAEDEQQOALANRHS <b>S</b> *LVEKL
	Actin-like 6A	ACTL6A	S233					100.0	34.2	R.EG <b>S</b> *PANWK.R
	Activating transcription factor 1	PKP4	S63					13.9	19.2	R.RP <b>S</b> *YR.K
	Activating transcription factor 2	ATF2	T69T71					16.4	37.6	R.NDSVIVADQ <b>T</b> *P <b>T</b> *PTR.F
	Active BCR related Gene	ABR	T30S33					15.3	49.0	K.VLEDEDVFLLEECELG <b>T</b> <b>S</b> *P <b>S</b> *PGSGSPFLVAVK.V
	Active BCR related Gene	ABR	S33					10.3	45.3	K.VLEDEDVFLLEECELGTP <b>S</b> *P <b>S</b> *PGSGSPFLVAVK.V
	Activity dependent neuroprotector	ADNP	S953S955					100.0	64.8	K.LMHNA <b>S</b> *D <b>S</b> *EVDQDDVVEWK.D
	Activity dependent neuroprotector	ADNP	S1058						57.7	R.L <b>S</b> *NPQIEWQNSTIDSEGEQFDNMTDGVAEPMHGLAGVK.L
	Activity dependent neuroprotector	ADNP	S1071					7.4	69.1	R.LSNPQIEWQNSTID <b>S</b> *EDGEQFDNMTDGVAEPMHGLAGVK.L
	Activity dependent neuroprotector	ADNP	S1067					7.7	23.4	R.LSNPQIEWQ <b>N</b> <b>S</b> *TIDSEGEQFDNMTDGVAEPMHGLAGVK.L
	Activity dependent neuroprotector	ADNP	T1068S1071					3.5	42.7	R.LSNPQIEWQ <b>N</b> <b>S</b> *TID <b>S</b> *EDGEQFDNMTDGVAEPMHGLAGVK.L
	Activity dependent neuroprotector	ADNP	S1058S1067						14.8	R.L <b>S</b> *NPQIEWQ <b>N</b> <b>S</b> *TIDSEGEQFDNMTDGVAEPMHGLAGVK.L
	Activity dependent neuroprotector	ADNP	T1068					4.2	61.0	R.LSNPQIEWQ <b>N</b> <b>S</b> *TIDSEGEQFDNMTDGVAEPMHGLAGVK.L
	ADAM17	ADAM17	S791					58.9	35.5	K.S <b>S</b> *FEDLTDHPVTR.S
	AP3D1	S632S634S636						100.0	27.0	K.KVPVPEGLDDAWINEPL <b>S</b> *D <b>S</b> *E <b>S</b> *EDERPR.A
	Adaptin, delta	AP3D1	S758S759						17.2	R. M <b>S</b> *E <b>H</b> *GTSENFENADAVVIVVITCEMBEIAI DQENFVFNDAINQV.D.A
	Adducin 1 alpha	ADD2	S757					13.9	23.5	K.FRTP <b>S</b> *FLKK.S
	Adducin 1 alpha	ADD1	S431					15.8	69.7	K.YSDVEVPASVTGYSFASDGDSG <b>T</b> <b>S</b> *PLR.H
	Adducin 1 alpha	ADD1	S358					39.1	91.8	R.SP <b>G</b> <b>S</b> *PVGEGTGSPPKWQIQEQEFALMR.M
	Adducin 1 alpha	ADD1	T364					18.1	15.5	R.SP <b>G</b> <b>S</b> *PVGEG <b>T</b> <b>S</b> *GSPPKWQIQEQEFALMR.M
	Adducin 1 alpha	ADD1	S358S366					14.9	82.6	R.SP <b>G</b> <b>S</b> *PVGEG <b>T</b> <b>S</b> *PPKWQIQEQEFALMR.M
	Adducin 1 alpha	ADD1	S465					17.0	48.3	R.GDEASEEQNG <b>S</b> *PK.S
	Adducin 1 alpha	ADD1	S423S436					-0.2	21.7	K.YSDVEVPASVTGYSFAS <b>S</b> *DGDSG <b>T</b> <b>S</b> *PLR <b>S</b> *FQK.Q
	Adducin 1 alpha	ADD1	S355S366					12.0	58.6	R.S <b>S</b> *PGSPVGEG <b>T</b> <b>S</b> *PPKWQIQEQEFALMR.M
	Adducin 1 alpha	ADD1	S355S358					17.2	48.3	R.S <b>S</b> *PG <b>S</b> *PVGEGTGSPPKWQIQEQEFALMR.M
	Adducin 1 alpha	ADD1	S355T364					11.8	14.2	R.S <b>S</b> *PGSPVGEG <b>T</b> <b>S</b> *GSPPKWQIQEQEFALMR.M
	Adducin 1 alpha	ADD1	S512					6.5	22.1	K.EDGHR <b>T</b> <b>S</b> *TSAVPNLFVPLNTNPK.E
	Adducin 1 alpha	ADD1	S700T702T706						14.5	K. CECALURD <b>S</b> *Q <b>T</b> *C <b>A</b> D <b>T</b> *C <b>A</b> <b>S</b> *E <b>C</b> D <b>A</b> D <b>A</b> D <b>A</b> D <b>A</b> CECAAD <b>A</b> AD <b>A</b> VE <b>C</b> A <b>A</b> D <b>A</b> D
	Adducin 1 alpha	ADD1	S436					2.0	16.6	K.YSDVEVPASVTGYSFASDGDSG <b>T</b> <b>S</b> *PLR <b>S</b> *FQK.Q
	Adducin 1 alpha	ADD1	T511					-6.1	23.6	K.EDGHR <b>T</b> <b>S</b> *TSAVPNLFVPLNTNPK.E
	Adducin 1 alpha	ADD1	S366					6.6	45.8	R.SP <b>G</b> <b>S</b> *PVGEG <b>T</b> <b>S</b> *PPKWQIQEQEFALMR.M
	Adducin 1 alpha	ADD1	T364S366					2.3	59.4	R.SP <b>G</b> <b>S</b> *PVGEG <b>T</b> <b>S</b> *PPKWQIQEQEFALMR.M
	Adducin 3	ADD3	S673S677S681					19.2	21.3	K.IEEVL <b>S</b> *PEG <b>S</b> *PSK <b>S</b> *PSK.K
	Adducin 3	ADD3	S402S423					30.4	56.8	R.HK <b>S</b> *DVEIPATVTFSPEDDT <b>V</b> <b>S</b> *PLK.Y
	Adducin 3	ADD3	S423					23.1	55.1	K.SDVEIPATVTFSPEDDT <b>V</b> <b>S</b> *PLK.Y
	Adducin 3	ADD3	S677S681					6.9	10.9	K.IEEVLS <b>P</b> <b>E</b> <b>G</b> <b>S</b> *PSK <b>S</b> *PSK.K
	Adducin 3	ADD3	S461					21.2	26.1	R.NGET <b>S</b> *PR.T
	Adducin 3	ADD3	S42					100.0	21.1	R.NM <b>S</b> *PDLR.Q
	Adducin 3	ADD3	T460						13.7	R.NGET <b>S</b> *SPR.T
	Adducin 3	ADD3	S600					3.5	46.6	R.KQQGLEDAEQELLSDDASSV <b>S</b> Q <b>I</b> <b>S</b> Q <b>T</b> <b>S</b> *PQNVPEK.L
	Adducin 3	ADD3	S585						33.0	R.KQQGLEDAEQELL <b>S</b> *DDASSV <b>S</b> Q <b>I</b> <b>S</b> Q <b>T</b> <b>S</b> *PQNVPEK.L
	Adenosine deaminase, RNA specific	ADAR	S825					100.0	34.1	R.S <b>S</b> *PEADPK.T
	Adenosine deaminase, RNA specific	ADAR	S614					37.8	75.0	K.S <b>S</b> *PVTTL <b>E</b> CMHKL
	Adenosine monophosphate deaminase 2	AMPD2	S190					-0.3	32.1	K.TD <b>S</b> *DSDLQLY.E
	Adenylyl cyclase-associated protein	CAP1	S308					16.4	54.9	R.SGPKPFSAPKPQ <b>T</b> <b>S</b> *PSPK.R

Peak Area		%CV		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM													

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Alsin ALS2		S1462				13.1	35.3	R.S <sup>+</sup> ESPEPGYVVTSSGLLPVLLPRL
		Alsin ALS2		Y1469				0.2	28.0	R.SESPEPGY <sup>+</sup> VVTSSGLLPVLLPRL
		Amida TFPT		S252				20.6	48.1	K.LLPYPTLASPAS <sup>+</sup> D.-
		Amida TFPT		S249S252				31.0	44.2	K.LLPYPTLAS <sup>+</sup> PAS <sup>+</sup> D.-
		Amida TFPT		T246S252				8.3	41.5	K.LLPYPT <sup>+</sup> LASPAS <sup>+</sup> D.-
		Amida TFPT		Y244S252				8.9	47.2	K.LLPY <sup>+</sup> PTLASPAS <sup>+</sup> D.-
		Amida TFPT		Y244T246				5.7	26.0	K.LLPY <sup>+</sup> PT <sup>+</sup> LASPASD.-
		AMP deaminase 3 AMPD3		S112T130				9.8	12.4	K.GPPAAS <sup>+</sup> PAMSP <sup>+</sup> TPPVGTGATSLPT <sup>+</sup> PAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S112T119				1.2	44.8	K.GPPAAS <sup>+</sup> PAMSP <sup>+</sup> TT <sup>+</sup> PVVGTGATSLTPAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S116T118				6.1	40.6	K.GPPAAS <sup>+</sup> PAMS <sup>+</sup> PT <sup>+</sup> TPVGTGATSLTPAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S116T123				4.1	31.5	K.GPPAAS <sup>+</sup> PAMS <sup>+</sup> PTTPPVV <sup>+</sup> TGATSLTPAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S116S127				-1.7	26.0	K.GPPAAS <sup>+</sup> PAMS <sup>+</sup> PTTPPVVTGATSL <sup>+</sup> PTAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S112T118				4.9	40.7	K.GPPAAS <sup>+</sup> PAMSP <sup>+</sup> TPVVGTGATSLTPAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S112T123				6.2	38.4	K.GPPAAS <sup>+</sup> PAMSP <sup>+</sup> TPPVV <sup>+</sup> TGATSLTPAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S112S116				0.5	32.8	K.GPPAAS <sup>+</sup> PAMS <sup>+</sup> PTTPPVVTGATSLTPAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		T119S127				-1.7	36.2	K.GPPAAS <sup>+</sup> PAMSPT <sup>+</sup> TPVVTGATSL <sup>+</sup> PTAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S112S127				1.9	23.6	K.GPPAAS <sup>+</sup> PAMISPTTPVVTGATSL <sup>+</sup> PTAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		T118T123				4.5	25.9	K.GPPAAS <sup>+</sup> PAMSP <sup>+</sup> TPPVV <sup>+</sup> TGATSLTPAPYAMPEFQR.V
		AMP deaminase 3 AMPD3		S116T119				12.2	38.2	K.GPPAAS <sup>+</sup> PAMS <sup>+</sup> PTT <sup>+</sup> PVVGTGATSLTPAPYAMPEFQR.V
		Amphiphysin II BIN1		S302S305				6.2	74.2	K.SP <sup>+</sup> S <sup>+</sup> QS <sup>+</sup> SLPAVVETFPATVNGTVEGSGAGRL
		Amphiphysin II BIN1		S300S305				12.6	70.3	K.S <sup>+</sup> PSQS <sup>+</sup> SLPAVVETFPATVNGTVEGSGAGRL
		Amphiphysin II BIN1		S302S304				4.3	55.0	K.SP <sup>+</sup> S <sup>+</sup> Q <sup>+</sup> SLPAVVETFPATVNGTVEGSGAGRL
		Amphiphysin II BIN1		S304S305				5.4	50.4	K.SPQS <sup>+</sup> S <sup>+</sup> SLPAVVETFPATVNGTVEGSGAGRL
		Amphiphysin II BIN1		S302				1.8	35.7	K.SP <sup>+</sup> QS <sup>+</sup> SLPAVVETFPATVNGTVEGSGAGRL
		Amphiphysin II BIN1		S300S304				4.8	28.2	K.S <sup>+</sup> PSQ <sup>+</sup> SLPAVVETFPATVNGTVEGSGAGRL
		AMPK alpha 1 PRKAA1		T355				26.0	29.5	K.DFYLAT <sup>+</sup> SPDSELDHILTRPHER.V
		AMPK alpha 1 PRKAA1		S508				10.2	27.4	R.SDS <sup>+</sup> DAEAQK.S
		AMPK beta 2 PRKAB2		S183				12.6	61.5	R.DLS <sup>+</sup> SPPPGYGQEMYAFR.S
		AMPK beta1 PRKAB1		S108				137.2	42.4	R.S <sup>+</sup> HNNFVAILDLPEGEHQYK.F
		Amyotrophic lateral sclerosis 2 FAM117B chromosome region, candidate 13		S170S173				8.3	86.7	R.SQSVS <sup>+</sup> PTS <sup>+</sup> FLTISNEGSESPCSADOLLVDPR.D
		Amyotrophic lateral sclerosis 2 FAM117B chromosome region, candidate 13		S170T176				6.7	50.0	R.SQSVS <sup>+</sup> PTSLT <sup>+</sup> ISNEGSESPCSADOLLVDPR.D
		Anaphase promoting complex subunit 5 ANAPC5		S195				100.0	49.2	K.EELDVS <sup>+</sup> VR.E
		Anaphase promoting complex, subunit 1 ANAPC1		S688				24.1	58.1	R.NDFEGSL <sup>+</sup> S <sup>+</sup> PVIAPK.K
		Anaphase promoting complex, subunit 1 ANAPC1		S547S564				32.9	26.2	K.LLGS <sup>+</sup> LDEVLLSPVPELRDS <sup>+</sup> K.L
		Anaphase promoting complex, subunit 1 ANAPC1		S51S60				25.4	63.5	R.QLQPASELWS <sup>+</sup> DGAAGLVGS <sup>+</sup> LOEVTIHEK.Q
		Anaphase promoting complex, subunit 1 ANAPC1		S50S60				25.9	47.5	R.QLQPASELWS <sup>+</sup> SDGAAGLVGS <sup>+</sup> LOEVTIHEK.Q
		Anaphase promoting complex, subunit 1 ANAPC1		S547S563				42.3	31.7	K.LLGS <sup>+</sup> LDEVLLSPVPELRDS <sup>+</sup> SK.L
		Anaphase promoting complex, subunit 1 ANAPC1		S547S555				100.0	40.3	K.LLGS <sup>+</sup> LDEVLLS <sup>+</sup> PVPELR.D
		Anaphase promoting complex, subunit 3 CDC27		S364				52.0	78.0	R.EVTPILAQTQSSGPQTSTTPQVL <sup>+</sup> S <sup>+</sup> PTTISPPNALPR.R
		Anaphase promoting complex, subunit 3 CDC27		T343					44.1	R.EV <sup>+</sup> T <sup>+</sup> PILAQTQSSGPQTSTTPQVLPTTISPPNALPR.R
		Anaphase promoting complex, subunit 4 ANAPC4		S777				34.6		K.IKEEVL <sup>+</sup> SEEAENQQAGAAALAPEIVK.V
		Anaphase promoting complex, subunit 8 CDC23		S588				23.4	19.8	R.RVS <sup>+</sup> PLNLSVTP.-
		Androgen induced proliferation inhibitor PDS5B		S1358				45.3	105.4	R.AES <sup>+</sup> PESSAESTQSTPQK.G
		Androgen induced proliferation inhibitor PDS5B		S1358T1370				31.2	70.7	R.AES <sup>+</sup> PESSAESTQS <sup>+</sup> T <sup>+</sup> PQK.G
		PDS5B		S1283				100.0	51.4	R.LKEDILENEEQNS <sup>+</sup> PPKK.G
		Androgen induced proliferation inhibitor PDS5B		S1182				11.5	24.3	R.LDSSEMDHS <sup>+</sup> ENEDYTMSSPLPGKK.S
		Androgen induced proliferation inhibitor PDS5B		S1176				-1.8	18.3	R.LDS <sup>+</sup> SEMDHSENYDTMSSPLPGK.K
		Androgen induced proliferation inhibitor PDS5B		T1381				20.3	21.5	K.T <sup>+</sup> PSPSQPK.K
		Androgen induced proliferation inhibitor PDS5B		S1166				22.5	84.9	R.METVSNASSSSNPS <sup>+</sup> PGR.I
		Androgen induced proliferation inhibitor PDS5B		S1358S1369				24.2	19.5	R.AES <sup>+</sup> PESSAESTQS <sup>+</sup> TPQK.G
		Androgen induced proliferation inhibitor PDS5B		S1165				15.8	44.5	R.METVSNASSSSNPS <sup>+</sup> SPGR.I
		Androgen induced proliferation inhibitor PDS5B		S1176S1177					43.2	R.LDS <sup>+</sup> S <sup>+</sup> EMDHSENYDTMSSPLPGKK.S
		Androgen induced proliferation inhibitor PDS5B		S1383				39.8	33.2	K.TPS <sup>+</sup> PSQPK.K
		Anillin actin binding protein ANLN		S97S99				9.3	30.7	K.SCS <sup>+</sup> PS <sup>+</sup> PVSPQVQQAADTISDSVAVPASLLGMR.R
		Anillin actin binding protein ANLN		S95S97				8.5	35.6	K.S <sup>+</sup> CS <sup>+</sup> PSPVSPQVQQAADTISDSVAVPASLLGMR.R
		Anillin actin binding protein ANLN		S97S102				10.8	20.9	K.SCS <sup>+</sup> PSPV <sup>+</sup> S <sup>+</sup> PQVQQAADTISDSVAVPASLLGMR.R
		Anion exchange protein (Fragment) SLCA47		S258				13.9	41.2	R.NGILASPQS <sup>+</sup> APGNLDNSK.S
		Anion exchange protein (Fragment) SLCA47		S743				33.2	33.8	K.YSVOPS <sup>+</sup> IVNISDEMAKT
		Ankyrin 2 ANK2		T3844				6.8	51.8	R.KT <sup>+</sup> SLVIVESADNQPETCER.L
		Ankyrin 2 ANK2		S3845				8.0	18.5	R.KT <sup>+</sup> S <sup>+</sup> LVIVESADNQPETCER.L
		Ankyrin repeat and BTB/POZ domain-ABTB2 containing protein 2		S67				14.6	68.5	R.HNS <sup>+</sup> WDTVNTVLPEDPEVADLFSR.C
		Ankyrin repeat and BTB/POZ domain-ABTB2 containing protein 2		S29				14.0	24.7	R.S <sup>+</sup> LSLSSK.S

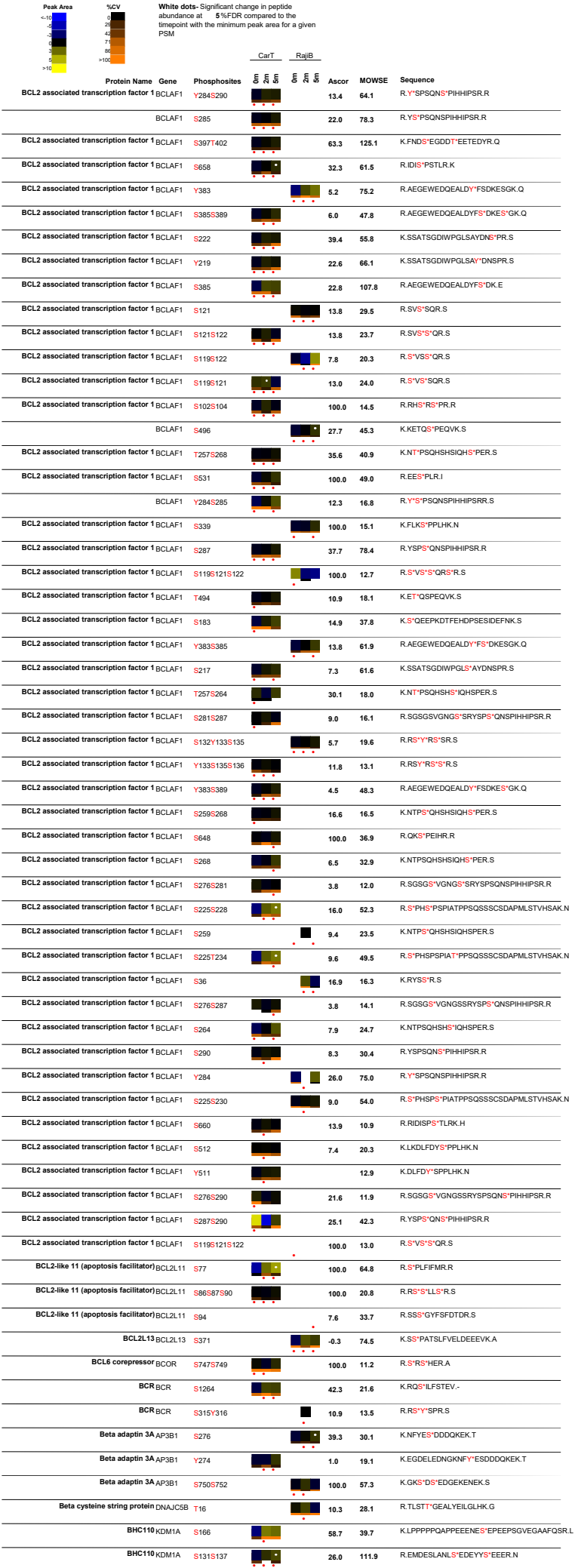
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajIB		Ascor	MOWSE	Sequence
		5	6	5	6					
Ankyrin repeat and KH domain containing 1 ANKHD1										
		S95						12.1	90.8	R.TGGGGGASG <sup>S</sup> DEDEVSEVSFLDQEDLDNPVLK.T
Ankyrin repeat and KH domain containing 1 ANKHD1										
		T86						-1.2	13.2	R.TGGGGGASGSDDEVSEVSFLDQEDLDNPVLK.T
Ankyrin repeat and KH domain containing 1 ANKHD1										
		S93						6.0	51.3	R.TGGGGGAS <sup>S</sup> GSDEVSEVSFLDQEDLDNPVLK.T
Ankyrin repeat domain 11 ANKRD11										
		S1792						18.9	13.0	R.SV <sup>S</sup> VDIR.R
Ankyrin repeat domain 28 ANKRD28										
		S1048						5.2	43.7	R.NEPSSYCSFNNIGGEQEYLYTDVDELND <sup>S</sup> SETY.-
Ankyrin repeat domain 28 ANKRD28										
		T1040						0.7	27.1	R.NEPSSYCSFNNIGGEQEYLYTDVDELNDSDSETY.-
Ankyrin repeat domain 28 ANKRD28										
		Y1037						12.6	38.4	R.NEPSSYCSFNNIGGEQEYLYTDVDELNDSDSETY.-
Ankyrin repeat domain protein 17 ANKRD17										
		T5							63.9	K.ATVPVAAATAAEGEGSPPAVAAGPPAAAEVGGVGSSRA
Ankyrin repeat domain protein 17 ANKRD17										
		S19						9.9	35.8	K.ATVPVAAATAAEGEG <sup>S</sup> PPAVAAAGPPAAAEVGGVGSSRA
Ankyrin repeat domain protein 17 ANKRD17										
		S2041S2047						5.9	18.2	K.EHYPV <sup>S</sup> SPSPS <sup>S</sup> PPAQPGGVSR.N
Anti silencing function 1B ASF1B										
		S198						100.0	24.0	K.GLGLPGCIPGLPEN <sup>S</sup> MDCI.-
Anti-silencing function 1A ASF1A										
		S166						25.9	63.3	K.LEDAESS <sup>N</sup> NPNQLSLSTDALPSASK.G
Anti-silencing function 1A ASF1A										
		S165						48.3	57.1	K.LEDAES <sup>S</sup> SNPNQLSLSTDALPSASK.G
Antigen identified by monoclonal antibody MKI67 Ki-67										
		S2002						100.0	25.0	R.LKIS <sup>L</sup> LGK.V
Antigen identified by monoclonal antibody MKI67 Ki-67										
		S584						29.9	84.7	K.AQSLVISPPAP <sup>S</sup> PR.K
Antigen identified by monoclonal antibody MKI67 Ki-67										
		S357						48.5	56.9	K.TPVQYS <sup>S</sup> QQQNS <sup>S</sup> PQK.H
Antigen identified by monoclonal antibody MKI67 Ki-67										
		S352						5.1	25.7	K.TPVQYS <sup>S</sup> QQQNSPQK.H
Antigen identified by monoclonal antibody MKI67 Ki-67										
		S1131						20.0	30.3	K.S <sup>S</sup> PPPEVDPTSTK.Q
Antigen identified by monoclonal antibody MKI67 Ki-67										
		S2223						37.2	38.9	R.S <sup>S</sup> PODPVGTPTIFKQSK.R
Antisense ERCC1 CD3EAP										
		S126S136						42.7	42.6	R.ILEGPQQLS <sup>S</sup> GSPLQIPAS <sup>S</sup> PPQIIPGLRPR.F
Antisense ERCC1 CD3EAP										
		S124S136						26.1	16.9	R.ILEGPQQS <sup>S</sup> LSGSLQIPAS <sup>S</sup> PPQIIPGLRPR.F
Antisense ERCC1 CD3EAP										
		S128S136						34.5	52.1	R.ILEGPQQLSGS <sup>S</sup> PLQIPAS <sup>S</sup> PPQIIPGLRPR.F
Antisense ERCC1 CD3EAP										
		S124S126							35.5	R.ILEGPQQS <sup>S</sup> LS <sup>S</sup> GSPLQIPASPPQIIPGLRPR.F
AP2 associated kinase 1 AAK1										
		T620S624						12.5	25.9	K.VGSLT <sup>S</sup> PPSS <sup>S</sup> PK.T
AP2 associated kinase 1 AAK1										
		S623S624						12.2	24.6	K.VGSLTFPS <sup>S</sup> <sup>S</sup> PK.T
AP2 associated kinase 1 AAK1										
		T640						13.8	48.5	R.ILSDVT <sup>T</sup> HSAVFGVPASK.S
AP2 associated kinase 1 AAK1										
		T653						-0.3	83.5	K.ST <sup>S</sup> QLLQAAAEASLNK.S
AP2 associated kinase 1 AAK1										
		S637						61.2	65.4	R.ILS <sup>S</sup> DVTHSAVFGVPASK.S
AP47 AP1M1										
		T154						16.2	37.3	K.LETGAPRPPATV <sup>T</sup> NAVSWR.S
AP47 AP1M1										
		T152T154						34.9	29.3	K.LETGAPRPPATV <sup>T</sup> NAVSWR.S
APBB2 APBB2										
		S123						53.8	21.5	K.NLS <sup>S</sup> PTAVINITSEK.L
APC APC										
		S2837							16.8	K.RHSGS <sup>S</sup> YLVTSV.-
APC APC										
		S780						36.4	41.0	K.ALEAELDAQHLSSETFDNIDNLS <sup>S</sup> PK.A
APG4 autophagy 4 homolog B ATG4B										
		S383						60.5	48.6	R.FFDS <sup>S</sup> EDEFEILSL.-
Apoptosis antagonizing transcription factor AATF										
		S203						107.9	48.8	R.AGRNRS <sup>S</sup> EDDGVMTFSSVK.V
Apoptosis antagonizing transcription factor AATF										
		S320S321						10.1	31.4	R.YLVDGTPKNAGSEE <sup>S</sup> <sup>S</sup> EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF										
		T310S316S321						12.0	23.7	R.YLVDGT <sup>S</sup> KPNAGS <sup>S</sup> EEIS <sup>S</sup> EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF										
		S316S320S321						28.0	66.1	R.YLVDGTPKNAGS <sup>S</sup> EEIS <sup>S</sup> <sup>S</sup> EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF										
		T310S316S320						9.7	17.1	R.YLVDGT <sup>S</sup> KPNAGS <sup>S</sup> EEIS <sup>S</sup> SEDELVEEK.K
Apoptosis antagonizing transcription factor AATF										
		T310S320S321						3.9	22.9	R.YLVDGT <sup>S</sup> KPNAGSEEIS <sup>S</sup> <sup>S</sup> EDDELVEEK.K
Apoptosis antagonizing transcription factor AATF										
		Y305T310S316						9.0	34.5	R.Y <sup>L</sup> LVDGT <sup>S</sup> KPNAGS <sup>S</sup> EEISSEDELVEEK.K
Apoptosis antagonizing transcription factor AATF										
		S169S170S178						100.0	49.0	K.GMDLGS <sup>S</sup> <sup>S</sup> EEEEDES <sup>S</sup> GMEEGDDAEDS <sup>S</sup> QGES <sup>S</sup> EEDR.A
Apoptosis antagonizing transcription factor AATF										
		T310S321						20.0	11.6	R.YLVDGT <sup>S</sup> KPNAGSEEIS <sup>S</sup> EDDELVEEK.K
Apoptosis inhibitor 5 API5										
		S462						13.9	69.4	R.ASEDTT <sup>S</sup> GSPPKK.S
Apoptosis inhibitor 5 API5										
		S464						7.8	46.1	R.ASEDTTGS <sup>S</sup> PPKK.S
Apoptotic chromatin condensation inducer ACIN1 in the nucleus (Fragment)										
		S125						3.4	30.2	K.EAVVDLHADD <sup>S</sup> RISEDETER.N
Apoptotic chromatin condensation inducer ACIN1 in the nucleus (Fragment)										
		S128						9.2	24.2	K.EAVVDLHADD <sup>S</sup> SRIS <sup>S</sup> EDETER.N
Aprataxin APTX										
		S132						22.2	42.2	R.S <sup>S</sup> GNSDSIER.D
ANP32B										
		T244						100.0	28.3	R.ET <sup>S</sup> DDEGEDD.-
Arachidonate 12-oxidoeductase ALOX12										
		S246						10.2	27.2	R.RST <sup>S</sup> LPSRL
Arachidonate 12-oxidoeductase ALOX12										
		S244						15.4	13.3	R.RS <sup>S</sup> TSLPSRL
Arf-GAP with dual PH domain-containing ADAP1 orotein 1 (Fragment)										
		S71						100.0	14.7	K.IAP <sup>S</sup> ER.K
Arginine/serine-rich collod-coil 2 RSRC2										
		S216S218T220						100.0	17.4	R.S <sup>S</sup> LS <sup>S</sup> RT <sup>S</sup> PS <sup>S</sup> PPFFR.G
Arginine/serine-rich collod-coil 2 RSRC2										
		S32						10.9	43.7	K.EQSEVS <sup>S</sup> V <sup>S</sup> PR.A
Arginine/serine-rich collod-coil 2 RSRC2										
		S41						6.5	11.7	K.HHY <sup>S</sup> RS
Arginine/serine-rich collod-coil 2 RSRC2										
		S30S32						10.5	14.7	K.EQSEVS <sup>S</sup> V <sup>S</sup> PR.A
Arginine/serine-rich collod-coil 2 RSRC2										
		Y40							17.0	K.HHY <sup>S</sup> RS
Arginine/serine-rich splicing factor 10 TRA2B										
		S39						26.3	27.8	R.S <sup>S</sup> KEDSRRS
Arginine/serine-rich splicing factor 10 TRA2B										
		T201						32.0	33.5	K.RPHT <sup>T</sup> PTPGYMGRTPTYGSSR.R
Arginine/serine-rich splicing factor 10 TRA2B										
		T201Y213						17.1	23.8	K.RPHT <sup>T</sup> PTPGYMGRTPTY <sup>T</sup> GSSR.R
Arginine/serine-rich splicing factor 10 TRA2B										
		T201T212						8.5	22.2	K.RPHT <sup>T</sup> PTPGYMGRTPT <sup>T</sup> YGSSR.R
Arginine/serine-rich splicing factor 10 TRA2B										
		S29T33						100.0	17.6	K.S <sup>S</sup> ARHT <sup>T</sup> PAR.S

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Protein Name	Gene	Phosphosites							
Arginine/serine-rich splicing factor 10	TRA2B	T69					13.9	34.7	R.RH <sup>Y</sup> T.R.S
Arginine/serine-rich splicing factor 10	TRA2B	S95S97S99					33.8	34.5	R.RH <sup>S</sup> *H <sup>S</sup> *H <sup>S</sup> *PMSTR.R
Arginine/serine-rich splicing factor 10	TRA2B	S95S97					14.9	38.8	R.RH <sup>S</sup> *H <sup>S</sup> *HSPMSTR.R
Arginine/serine-rich splicing factor 10	TRA2B	S95S99					13.7	21.8	R.RH <sup>S</sup> *HSH <sup>S</sup> *PMSTR.R
Arginine/serine-rich splicing factor 10	TRA2B	S97S99					7.3	25.6	R.RHSH <sup>S</sup> *H <sup>S</sup> *PMSTR.R
Arginine/serine-rich splicing factor 10	TRA2B	T201Y207					16.1	25.4	K.RPHT <sup>T</sup> PTPGI <sup>Y</sup> *MGRPTYGSSR.R
Arginine/serine-rich splicing factor 10	TRA2B	T201S215					11.8	19.8	K.RPHT <sup>T</sup> PTPGIYMG <sup>R</sup> PTYGS <sup>S</sup> *R.R
Arginine/serine-rich splicing factor 10	TRA2B	S97S102T103					15.3	18.6	R.RHSH <sup>S</sup> *HSPMS <sup>T</sup> *RR.R
Arginine/serine-rich splicing factor 10	TRA2B	T203Y207					19.0	25.8	K.RPHTPT <sup>T</sup> PGI <sup>Y</sup> *MGRPTYGSSR.R
Arginine/serine-rich splicing factor 10	TRA2B	T201T203					10.4	23.5	K.RPHT <sup>T</sup> PT <sup>T</sup> PGIYMG <sup>R</sup> PTYGSSR.R
Arginine/serine-rich splicing factor 10	TRA2B	S43					-0.2	19.7	R.SKED <sup>S</sup> *RR.S
Arginine/serine-rich splicing factor 10	TRA2B	T203T212					3.9	17.4	K.RPHTPT <sup>T</sup> PGIYMG <sup>R</sup> PT <sup>T</sup> YGSSR.R
Arginine/serine-rich splicing factor 10	TRA2B	S102T103					21.5	17.3	R.RHSHSHSPMS <sup>T</sup> *T.R.R
Arginine/serine-rich splicing factor 10	TRA2B	S97S99S102					3.3	12.6	R.RRSH <sup>S</sup> *H <sup>S</sup> *PMS <sup>T</sup> *R.R
Arginine/serine-rich splicing factor 10	TRA2B	S39S43					100.0	15.1	R. <sup>S</sup> *KED <sup>S</sup> *RR.S
Arginine/serine-rich splicing factor 10	TRA2B	Y207					8.9	11.9	K.RPHTPTPGI <sup>Y</sup> *MGRPTYGSSR.R
Arginine/serine-rich splicing factor 10	TRA2B	Y68					24.6		R.RH <sup>Y</sup> *T.R.S
ARID1B	ARID1B	S1550					32.1	52.4	R.MS <sup>T</sup> *PSKSPFLPSMK.M
ARL6IP4	ARL6IP4	S252					90.9	108.6	R. <sup>S</sup> *AGEEEDGPVL <sup>T</sup> DEQK.S
Armadillo repeat containing 1	ARMC1	S120					24.9	61.9	K.LLASEIYDILQSSNMADGDS <sup>F</sup> *FNEMNSR.R
ARPP-21	ARPP21	S383					15.1	76.2	K.TAS <sup>F</sup> *FGGITVLTR.G
ARPP-21	ARPP21	S138					35.2	46.6	K.DCS <sup>T</sup> *QEYTDSTGIDLHEFLINTLK.N
ARPP19	ENSA	S62					35.2	66.6	K.YFDS <sup>T</sup> *GDYNMAK.A
Arsenite resistance protein 2	SRRT	S67					100.0	23.0	R.ERF <sup>S</sup> *PPR.H
Arsenite resistance protein 2	SRRT	T544					26.7	58.1	R.TQLWASEPG <sup>T</sup> *PPLTSLPSQNPILK.N
Arsenite resistance protein 2	SRRT	S74					100.0	29.1	R.HEL <sup>S</sup> *PPQKR.M
ASH1L	ASH1L	S1162S1170					25.4	23.5	R.RL <sup>S</sup> *PPTLLPN <sup>S</sup> *PSHLSELTSLK.E
ASH2 like	ASH2L	S623					100.0	28.0	R. <sup>S</sup> *PPWEP.-
ASK1	MAP3K5	S1029S1033					12.1	14.7	R.TLFLGIPDENFEDHS <sup>T</sup> *APPS <sup>T</sup> *PEEK.D
AT hook DNA binding motif containing 1	AHDC1	S846S849					29.5	53.6	R.SLDS <sup>T</sup> *DD <sup>S</sup> *SLLDFALSASRPESR.K
AT hook DNA binding motif containing 1	AHDC1	S842S849					13.3	39.4	R. <sup>S</sup> *LLDSDD <sup>S</sup> *SLLDFALSASRPESR.K
AT hook DNA binding motif containing 1	AHDC1	S842S846					5.0	15.4	R. <sup>S</sup> *LLDS <sup>T</sup> *DDSSDLLDFALSASRPESR.K
AT hook transcription factor	AKNA	S1170S1173					13.1	60.5	R.LS <sup>T</sup> *LS <sup>S</sup> *ESELPSLPFSEK.S
AT hook transcription factor	AKNA	S534S537					9.7	44.4	R.GDL <sup>S</sup> *PS <sup>S</sup> *LTSMPTLGWL <sup>T</sup> PENR.D
AT hook transcription factor	AKNA	S534T539					2.2	23.3	R.GDL <sup>S</sup> *PSSL <sup>T</sup> *SMTPLGWL <sup>T</sup> PENR.D
AT hook transcription factor	AKNA	S1172S1173					16.5	79.9	R.LSL <sup>S</sup> *S <sup>T</sup> *ESELPSLPFSEK.S
AT hook transcription factor	AKNA	T539					6.0	29.2	R.GDLSPSSL <sup>T</sup> *SMTPLGWL <sup>T</sup> PENR.D
AT hook transcription factor	AKNA	S1170S1175					3.5	19.7	R.LS <sup>T</sup> *LSSE <sup>S</sup> *ELPSLPFSEK.S
AT hook transcription factor	AKNA	S534					11.0	86.6	R.GDL <sup>S</sup> *PSSL <sup>T</sup> *SMTPLGWL <sup>T</sup> PENR.D
AT hook transcription factor	AKNA	S540					4.8	38.7	R.GDLSPSSL <sup>T</sup> *MPTLGWL <sup>T</sup> PENR.D
AT hook transcription factor	AKNA	S534S536					1.4	21.6	R.GDL <sup>S</sup> *PS <sup>T</sup> *SLTSMPTLGWL <sup>T</sup> PENR.D
AT hook transcription factor	AKNA	S536					-0.2	42.5	R.GDLSP <sup>S</sup> *SLTSMPTLGWL <sup>T</sup> PENR.D
AT rich interactive domain 1A	ARID1A	S1600					16.7	52.4	R.TS <sup>T</sup> *PSKSPFLHSGMK.M
AT rich interactive domain 1A	ARID1A	S696					53.8	80.1	R.GP <sup>S</sup> *PSPVGSPASVAQSR.S
AT rich interactive domain 1A	ARID1A	S1754						78.3	K.VS <sup>T</sup> *SPAPMEGEEEEELGPK.L
AT rich interactive domain 1A	ARID1A	S1600S1602					12.8	24.1	R.TS <sup>T</sup> *PS <sup>T</sup> *KSPFLHSGMK.M
AT rich interactive domain 1A	ARID1A	S363					31.6	74.8	R.SH4PMS <sup>T</sup> *PGSSGGGGQPLAR.T
AT rich interactive domain 1A	ARID1A	S789					15.6	35.7	R.NPQMPOYSSPOPGS <sup>T</sup> *ALS <sup>T</sup> PR.Q
AT rich interactive domain 1A	ARID1A	S772					3.5	25.9	R.NPQMPOYSSPOPGSALS <sup>T</sup> *PR.Q
AT rich interactive domain 3A	ARID3A	S77S81S88					100.0	58.3	R.AAAAGLHPAS <sup>T</sup> *PGGS <sup>T</sup> *EDGPPGS <sup>T</sup> *EEEDAAR.E
ATAD2	ATAD2	S327					45.3	61.5	R.KPNIFYSGPAS <sup>T</sup> *PARPR.Y
ATAD2	ATAD2	Y750					4.3	70.8	K.TLDSDISCPLES <sup>T</sup> DLAY <sup>T</sup> *SDDDVPSVYENGLSQK.S
ATAD2	ATAD2	S746Y750					51.4	47.3	K.TLDSDISCPLES <sup>T</sup> *DLAY <sup>T</sup> *SDDDVPSVYENGLSQK.S
ATAD2	ATAD2	S746S757					7.3	51.5	K.TLDSDISCPLES <sup>T</sup> *DLAYSDDDVPS <sup>T</sup> *VYENGLSQK.S
ATAD2	ATAD2	Y750S751					29.7	52.7	K.TLDSDISCPLES <sup>T</sup> DLAY <sup>T</sup> *S <sup>T</sup> *DDDVPSVYENGLSQK.S
ATAD2	ATAD2	Y750S757					8.2	33.4	K.TLDSDISCPLES <sup>T</sup> DLAY <sup>T</sup> *SDDDVPS <sup>T</sup> *VYENGLSQK.S
ATAD2	ATAD2	S757					13.8	45.8	K.TLDSDISCPLES <sup>T</sup> DLAYSDDDVPS <sup>T</sup> *VYENGLSQK.S
ATAD2	ATAD2	S746					1.2	40.6	K.TLDSDISCPLES <sup>T</sup> *DLAYSDDDVPSVYENGLSQK.S
ATAD2	ATAD2	S751					4.6	40.5	K.TLDSDISCPLES <sup>T</sup> DLAYS <sup>T</sup> *DDDVPSVYENGLSQK.S
Ataxin 10	ATXN10	S12					100.0	47.1	R.LS <sup>T</sup> *GVMVPAPIQLEALR.A
Ataxin 2	ATXN2	S848S850S865					5.8	14.3	K.DSFIENS <sup>T</sup> *SS <sup>T</sup> *NCTSGSSKPNSPSIS <sup>T</sup> *PSILSNT <sup>T</sup> EHK.R
Ataxin 2	ATXN2	S667					-0.3	82.2	R.TS <sup>T</sup> *PSGGTWSVSVSGVPR.L





Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		0	2	4	6	8	10			
<10	0									
10	2									
20	4									
30	6									
40	8									
50	10									
60	12									
70	14									
80	16									
90	18									
>100	20									
Protein Name	Gene	Phosphosites								
Autoantigen RCD8	EDC4	S734						0.5	29.7	R.SPDVIS*SASTALSQDIPEIASEALSR.G
Autoantigen RCD8	EDC4	S729S735						21.7	38.3	R.S*PDVISS*ASTALSQDIPEIASEALSR.G
Autoantigen RCD8	EDC4	T727S741						6.4	18.7	R.T*RSPDVISSASTALS*QDIPEIASEALSR.G
Autophagy related 9 homolog A	ATG9A	S761						7.6	67.9	R.SA\$*YPCAAPRPGAPETTALHGGFQR.R
Autophagy related 9 homolog A	ATG9A	S828						100.0	23.1	R.HPEPVPPEG\$*EDELPPQVHKV.-
B cell CLL/lymphoma 9 like	BCL9L	S1480						11.7	29.3	R.SV\$*LDSQMGYLPAPGGMANLPF.-
B cell CLL/lymphoma 9 like	BCL9L	S934						7.2	44.4	K.S*PTLSQVHSPLVTSPSANLK.S
B cell CLL/lymphoma 9 like	BCL9L	S750						54.7	53.0	R.GLL\$*PPMGQSGLR.E
B cell CLL/lymphoma 9 like	BCL9L	S1478						10.0	32.8	R.S*VSLDSQMGYLPAPGGMANLPF.-
B cell lymphoma 6 protein	BCL6	S307S308						100.0	31.9	K.EEERP\$*S*EDEIALHFEPNAPLNR.K
B-lymphocyte cell-surface antigen B1	MS4A1	S253						6.1	38.6	K.EEVVGLTETS*\$SQPK.N
B-lymphocyte cell-surface antigen B1	MS4A1	S7						51.9	75.4	R.N\$*VNGTFPAEPMK.G
	MS4A1	S225						101.1	64.7	K.S*NIVLSAEKK.E
B-lymphocyte cell-surface antigen B1	MS4A1	T252S254						11.5	53.6	K.EEVVGLTET*\$SQPK.N
	MS4A1	S36						-0.1	64.2	R.MS\$*LVGPTQSFFMR.E
B-lymphocyte cell-surface antigen B1	MS4A1	S35S36						68.1	86.9	R.M\$*S*LVGPTQSFFMR.E
B-lymphocyte cell-surface antigen B1	MS4A1	S295						30.5	26.4	K.NEEDIEIPIQEEEEETETNFPPEPPDQEQESSPIEND\$*SP.-
B-lymphocyte cell-surface antigen B1	MS4A1	S25						100.0	37.0	K.GPIAMQ\$*GPKPLFR.R
	MS4A1	S35						27.6	61.6	R.RM\$*SLVGPTQSFFMR.E
B-lymphocyte cell-surface antigen B1	MS4A1	S288						4.6	18.6	K.NEEDIEIPIQEEEEETETNFPPEPPDQEQ\$*SPIENDSSP.-
B-lymphocyte cell-surface antigen B1	MS4A1	T252S253						9.3	29.7	K.EEVVGLTET*\$SQPK.N
B-lymphocyte cell-surface antigen B1	MS4A1	T275						6.1	23.1	K.NEEDIEIPIQEEEEET*ETNFPPEPPDQEQESSPIENDSSP.-
B-lymphocyte cell-surface antigen B1	MS4A1	S254						7.2	35.6	K.EEVVGLTETS*\$QPK.N
B-lymphocyte cell-surface antigen B1	MS4A1	T250T252						14.6	33.9	K.EEVVGLT*ET*\$SQPK.N
B-lymphocyte cell-surface antigen B1	MS4A1	T252						0.5	30.7	K.EEVVGLTET*\$SQPK.N
B-lymphocyte cell-surface antigen B1	MS4A1	T250S254						3.5	26.1	K.EEVVGLTETS*\$QPK.N
B-lymphocyte cell-surface antigen B1	MS4A1	S253S254						8.9	39.1	K.EEVVGLTETS*\$QPK.N
B-lymphocyte cell-surface antigen B1	MS4A1	S35S43						-0.5	24.3	R.RM\$*SLVGPTQ\$*FFMIR.E
B-lymphocyte cell-surface antigen B1	MS4A1	S289						5.5	12.0	K.NEEDIEIPIQEEEEETETNFPPEPPDQEQ\$*SPIENDSSP.-
B-Raf	BRAF	S446						92.2	50.0	R.RD\$*SDWEIPDGGQITVGQRI
	BRAF	S365						23.6	77.7	R.SS\$*APNVHINTIEPVNIDDLIR.D
B-Raf	BRAF	S364						-0.3	52.5	R.S\$*SAPNVHINTIEPVNIDDLIR.D
B-Raf	BRAF	S447						9.0	55.0	R.RD\$*\$DWEIPDGGQITVGQRI
B-Raf	BRAF	T753						70.5	53.2	K.T*PIQAGGYGAFPVH.-
B-Raf	BRAF	S729						9.5	42.8	R.SA\$*EPSLNR.A
B-Raf	BRAF	S363						1.8	39.8	R.DR\$*SSAPNVHINTIEPVNIDDLIR.D
B-Raf	BRAF	T373						-5.3	17.5	R.SSSAPNVHINT*IEPVNIDDLIR.D
Baculoviral IAP repeat containing protein 6	BIRC6	S452						18.4	42.4	K.LEGSDSDLLED\$*DSEHSR.S
Baculoviral IAP repeat containing protein 6	BIRC6	T4689S4691T46						28.9	12.6	R.GT*P\$*GT*\$QSSR.E
Baculoviral IAP repeat containing protein 6	BIRC6	S421						12.0	80.7	K.FEINAYDPAIVQQLSGDPSSGVDS*RR
Basic leucine zipper and W2 domains 1	BZW1	S345						22.6	92.9	K.NAEES*\$ESEAEEGD.-
Basic leucine zipper and W2 domains 1	BZW1	S345S347						100.0	62.9	K.NAEES*\$ES*\$EAEEGD.-
	BZW2	S412S414						100.0	48.7	K.FVEWLQNAEES*\$ES*\$EGEEN.-
Basic transcription factor 3	BTTF3	S158						15.8	52.9	K.QLTEMLPSILNQLGADS*LTSLR.R
BAT2 domain containing 1	PRRC2C	S878						25.7	47.1	R.S*\$VEDVRPH+HTDANNQSACFEAPDQK.T
BAT2 domain containing 1	PRRC2C	S1248S1249						3.1	42.3	R.SE\$*\$DFEVVPK.R
BAT2 domain containing 1	PRRC2C	S1542						15.3	14.3	R.S*\$FSSQRPVDR.Q
BAT2 domain containing 1	PRRC2C	S1246S1249						7.4	35.0	R.\$*ES\$*DFEVVPK.R
BAT2 domain containing 1	PRRC2C	S1246S1248						5.5	37.7	R.\$*ES*\$DFEVVPK.R
BAT2 domain containing 1	PRRC2C	S2105						100.0	21.7	K.LPDL\$*PVENK.E
Bcl 2 related proline rich protein	BCL2L12	S242						16.9	35.2	R.L\$*SDSFAR.L
BCL11A	BCL11A	S625S630						23.8	59.8	K.LLLQ\$*PSSL\$*PFSK.R
BCL2 antagonist of cell death	BAD	S118						53.1	28.4	R.RM\$*DEFVDSFKK.G
BCL2 antagonist of cell death	BAD	S99						100.0	39.6	R.S*APPNLWAAQR.Y
BCL2 associated athanogene 2	BAG2	S19						-0.4	34.4	R.S\$*SMADR.S
BCL2 associated athanogene 2	BAG2	S20						9.6	14.3	R.SS\$*MADR.S
BCL2 associated transcription factor 1	BCLAF1	S177						100.0	33.3	K.AEGEPQEE\$*PLK.S
BCL2 associated transcription factor 1	BCLAF1	S285S287						16.4	36.3	R.Y\$*P\$*QNSPIHIPSRR.S
BCL2 associated transcription factor 1	BCLAF1	S287S297						12.4	17.4	R.YSP\$*QNSPIHIPS*RR.S
BCL2 associated transcription factor 1	BCLAF1	Y284S287						17.6	29.0	R.Y*SP\$*QNSPIHIPSRR.S
BCL2 associated transcription factor 1	BCLAF1	S285S290						19.5	52.6	R.Y\$*P\$QNS*PIHIPSRR.S
BCL2 associated transcription factor 1	BCLAF1	S397						55.7	87.2	K.QKFND\$*EGDDTEEDYR.Q



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		Protein Name	Gene	Phosphosites						
		BHC110	KDM1A	Y136S137				9.9	32.9	R.EMDESLANLSEDEYY* <b>S</b> *EEER.N
		BHC110	KDM1A	S126S137				12.5	50.2	R.EMDE <b>S</b> *LANLSEDEYY* <b>S</b> *EEER.N
		BHC110	KDM1A	S126S131				4.4	11.3	R.EMDE <b>S</b> *LANL <b>S</b> *EDEYYEEER.N
		BHC110	KDM1A	S849				14.7	19.3	R.QATPGVPAQ <b>S</b> *PSM.-
		BHC80	PHF21A	T446S455				19.3	25.6	K.YNAVLGFGAL <b>T</b> <b>P</b> *SPQSSHPD <b>S</b> *PENEK.T
		BHC80	PHF21A	T446S451				5.7	27.6	K.YNAVLGFGAL <b>T</b> <b>P</b> *SPQ <b>S</b> *HPD <b>S</b> PENEK.T
		BHC80	PHF21A	T446S450				4.3	25.5	K.YNAVLGFGAL <b>T</b> <b>P</b> *SPQ <b>S</b> *SHPD <b>S</b> PENEK.T
		BHC80	PHF21A	S447S455				19.2	15.8	K.YNAVLGFGAL <b>T</b> <b>P</b> <b>S</b> *PQSSHPD <b>S</b> *PENEK.T
		BIG1	ARFGEF1	S1569				73.2	39.7	K. <b>S</b> *VDIHDSIQPR.S
		BIG1	ARFGEF1	Y662S670				4.3	67.9	R.Y*GSLNSL <b>S</b> *TSSSGIGSYSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S664S678				3.0	97.6	R.YG <b>S</b> *LNSLESTSSSGIG <b>S</b> *YSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S664S670				7.6	98.1	R.YG <b>S</b> *LNSL <b>S</b> *TSSSGIGSYSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S667S670				6.0	47.8	R.YGSLN <b>S</b> *L <b>S</b> *TSSSGIGSYSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S664S667				3.7	92.9	R.YG <b>S</b> *LNS*L <b>E</b> STSSSGIGSYSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S664S680				0.4	88.4	R.YG <b>S</b> *LNSLESTSSSGIG <b>S</b> * <b>T</b> QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S678Y679				-4.5	33.2	R.YGSLNSLESTSSSGIG <b>S</b> * <b>Y</b> * <b>T</b> QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S664S674				2.0	92.8	R.YG <b>S</b> *LNSLEST <b>S</b> <b>S</b> *GIGSYSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S664Y679				4.7	66.8	R.YG <b>S</b> *LNSLESTSSSGIG <b>S</b> * <b>Y</b> * <b>T</b> QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S670S673T681				4.9	17.0	R.YGSLNSL <b>S</b> * <b>T</b> <b>S</b> *SGIGSY <b>T</b> *QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	Y662S667				3.6	53.0	R.Y*GSLN <b>S</b> *L <b>E</b> STSSSGIGSYSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S678S680				4.6	38.2	R.YGSLNSLESTSSSGIG <b>S</b> * <b>Y</b> <b>S</b> * <b>T</b> QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S670T671				5.1	31.5	R.YGSLNSL <b>S</b> * <b>T</b> *SSSGIGSYSTQMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S670S673S680				6.2	19.5	R.YGSLNSL <b>S</b> * <b>T</b> <b>S</b> *SGIG <b>S</b> * <b>T</b> QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S670S672S678				6.2	36.2	R.YGSLNSL <b>S</b> * <b>T</b> <b>S</b> *SSGIG <b>S</b> * <b>Y</b> <b>T</b> QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S670T671S678				5.2	20.8	R.YGSLNSL <b>S</b> * <b>T</b> *SSSGIG <b>S</b> * <b>Y</b> * <b>T</b> QMSGTDNPEQFEVLK.Q
		BIG1	ARFGEF1	S664T671				2.5	70.1	R.YG <b>S</b> *LNSL <b>S</b> * <b>T</b> *SSSGIGSYSTQMSGTDNPEQFEVLK.Q
		BIN2	BIN2	S458				7.8	48.4	R.ASLGTGT <b>A</b> <b>S</b> *PR.T
		BIN2	BIN2	S357				24.4	35.4	R.AK <b>S</b> *QEEVLPSSTTPSPGGALSPSGQPS <b>S</b> ATEVLR.T
		BIN2	BIN2	S273S277				10.3	32.4	R.TATV <b>S</b> *PL <b>T</b> <b>S</b> *PTSPSTLSLK.S
		BIN2	BIN2	S259				67.1	35.7	R. <b>S</b> *LVISPPVR.T
		BIN2	BIN2	T454				8.4	35.4	R.ASLG <b>T</b> *GTASPR.T
		Bin3, bicoid-interacting 3, homolog	MEPCE	S254				39.4	31.1	K.DITDPLSLNTCTDEGHVVL <b>A</b> <b>S</b> *PLK.T
		Bin3, bicoid-interacting 3, homolog	MEPCE	S330				12.4	71.1	R.DEV <b>S</b> *PLPSALQGP <b>S</b> GLSAPPAASVISAP <b>S</b> SSSR.H
		Bin3, bicoid-interacting 3, homolog	MEPCE	S334				7.7	52.6	R.DEV <b>S</b> PLP <b>S</b> *ALQGP <b>S</b> GLSAPPAASVISAP <b>S</b> SSSR.H
		Bin3, bicoid-interacting 3, homolog	MEPCE	S342				-0.3	42.8	R.DEV <b>S</b> PLPSALQGP <b>S</b> <b>S</b> *LSAPPAASVISAP <b>S</b> SSSR.H
		Block of proliferation 1	BOP1	S126S127				91.4	114.9	R.IGDEY <b>A</b> ED <b>S</b> * <b>S</b> *DEEDIR.N
		Block of proliferation 1	BOP1	Y122S126				6.3	27.6	R.IGDEY <b>A</b> ED <b>S</b> *SDEEDIR.N
		Block of proliferation 1	BOP1	S126T135				10.5	17.8	R.IGDEY <b>A</b> ED <b>S</b> *SDEEDIR <b>T</b> *VGNVPLEWYDDFHVGYDLDGR.R
		BLOS3	BLOC153	T63S65				73.4	48.2	R.VAGEAA <b>E</b> <b>T</b> *D <b>S</b> *EPEPEPEPTAAPR.D
		BMP2 inducible protein kinase	BMP2K	S949				35.1	68.7	K.S <b>E</b> <b>S</b> *NEDLFGLVFDEITGSQQQK.V
		BMP2 inducible protein kinase	BMP2K	S947				10.0	108.7	K. <b>S</b> * <b>S</b> ESNEDLFGLVFDEITGSQQQK.V
		BMS1	BMS1	S639				3.1	33.4	K.LGPQN <b>F</b> ID <b>T</b> <b>S</b> *DIENLLKEEDYKEEN <b>D</b> SK.E
		BMS1 like ribosome assembly protein	BMS1	T638					58.0	K.LGPQN <b>F</b> ID <b>T</b> *SDIENLLK.E
		Bone marrow stromal cell derived ubiquitin like	UBL7 like	S230				123.4	59.2	R.DMPGGFL <b>F</b> EGL <b>S</b> *DDEDDFHPNTR.S
		BPY2 interacting protein 1	MAP1S	T782					71.6	R. ADGI <b>DA</b> ECT <b>DD</b> TVSEEE <b>DI</b> ENGGID <b>GI</b> AD <b>AA</b> AN <b>DE</b> TE <b>DE</b> GV
		BPY2 interacting protein 1	MAP1S	T638S640				36.2	38.8	R. <b>T</b> <b>P</b> <b>S</b> *PESH <b>R</b> .S
		BPY2 interacting protein 1	MAP1S	S731				-0.4	14.7	R.S <b>A</b> <b>S</b> *PHDVDLCLVSPCFEHRK.A
		BPY2 interacting protein 1	MAP1S	S657				26.0	29.5	R.LSL <b>S</b> *PLR.G
		BPY2 interacting protein 1	MAP1S	S729				5.5	29.2	R. <b>S</b> *ASPHDVDLCLVSPCFEHRK
		BPY2 interacting protein 1	MAP1S	S759				25.4	34.7	K.AVPMAPAP <b>S</b> *PGSSNDSSAR.S
		Branched chain alpha-ketoacid dehydroenase kinase	BCKDK	T32				-0.3	44.2	R. <b>S</b> * <b>T</b> ATDTHH <b>V</b> EMAR.E
		Branched chain alpha-ketoacid dehydroenase kinase	BCKDK	S31				7.4	13.1	R. <b>S</b> * <b>T</b> ATDTHH <b>V</b> EMAR.E
		Branched chain keto acid dehydrogenase E1. aloha polypeptide	BCKDHA E1. aloha polypeptide	Y353				7.1	11.1	R.SVDEVN <b>Y</b> *WDKQDHPISRL
		Branched chain keto acid dehydrogenase E1. aloha polypeptide	BCKDHA E1. aloha polypeptide	S347				90.2	61.3	R. <b>S</b> * <b>V</b> DEVN <b>Y</b> WDK.Q
		Branched chain keto acid dehydrogenase E1. aloha polypeptide	BCKDHA E1. aloha polypeptide	S337				26.0	87.6	R.IGH <b>H</b> <b>S</b> * <b>T</b> SDSSAYR.S
		BRCA1	BRCA1	S1217S1218				36.9	79.7	K.KLESSEENL <b>S</b> * <b>S</b> *EDEELPCFQHLLFGK.V
		BRCA1	BRCA1	S1189S1191				24.7	47.8	R. <b>S</b> * <b>P</b> <b>S</b> *PFTHTHLAQGYR.R
		BRCA1	BRCA1	S1189T1194				19.1	30.9	R. <b>S</b> *PS <b>P</b> <b>F</b> <b>T</b> HTHLAQGYR.R
		BRCA1	BRCA1	S1212S1218				3.5	10.8	K.L <b>E</b> <b>S</b> *EENL <b>S</b> *EDEELPCFQHLLFGK.V
		BRCA1	BRCA1	S1189				20.5	51.1	R. <b>S</b> *PS <b>P</b> <b>F</b> <b>T</b> HTHLAQGYR.R
		BRCA1	BRCA1	S1211S1212S12				100.0	30.1	K.KL <b>E</b> <b>S</b> * <b>S</b> *EENL <b>S</b> * <b>S</b> *EDEELPCFQHLLFGK.V
		BRCA2 and CDKN1A interacting protein	BCCIP	S42				100.0	79.8	R.DEEEEKEVE <b>N</b> EDDD <b>S</b> *DKEK.D

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
<10	0	Protein Name	Gene	Phosphosites					
10-20	1-2	BRCA2 and CDKN1A interacting protein	BCCIP	S112S115			8.9	39.9	K.QTDV <b>S</b> *ED <b>S</b> *NDDMDEDEVFGFISLNLTER.K
20-30	3-4	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	S218S227			40.9	39.0	R.ELEKPIQSK <b>PQ</b> <b>S</b> *P <b>VIQ</b> AAV <b>S</b> *PK.F
30-40	5-6	Brefeldin A-inhibited guanine nucleotide-exchange protein 2	ARFGEF2	S227			71.3	66.7	R.ELEKPIQSK <b>PQ</b> SP <b>VIQ</b> AAV <b>S</b> *PK.F
40-50	7-8	BRG1 associated factor 180 KD	PBRM1	S10S14			15.1	58.3	R.AT <b>S</b> *P <b>SS</b> <b>S</b> *VSGDFDDGH <b>S</b> VSTPGPSR.K
50-60	9-10	BRG1 associated factor 180 KD	PBRM1	S10S12S13S14			10.9	39.3	R.AT <b>S</b> *P <b>S</b> * <b>S</b> * <b>S</b> *VSGDFDDGH <b>S</b> VSTPGPSR.K
60-70	11-12	BRG1 associated factor 180 KD	PBRM1	S371S375T377			7.4	26.6	R.YEEGES*EA <b>S</b> *IT* <b>S</b> FM <b>D</b> VSNPFYQLYD <b>T</b> VR.S
70-80	13-14	BRG1 associated factor 180 KD	PBRM1	S371S375S378			12.0	68.0	R.YEEGES*EA <b>S</b> *IT <b>S</b> *FMDVSNPFYQLYD <b>T</b> VR.S
80-90	15-16	BRG1 associated factor 180 KD	PBRM1	S375T377S378			6.8	10.9	R.YEEGE <b>SEAS</b> <b>S</b> *IT <b>S</b> *FMDVSNPFYQLYD <b>T</b> VR.S
90-100	17-18	BRG1 associated factor 180 KD	PBRM1	S383S355			9.3	84.8	R.LSAITMALQY <b>S</b> * <b>ES</b> *EEDAALAAAR.Y
100-110	19-20	BRG1 associated factor 180 KD	PBRM1	Y3S1S353			9.8	45.1	R.LSAITMALQY* <b>G</b> <b>S</b> *ESEEDAALAAAR.Y
110-120	21-22	BRG1 associated factor 180 KD	PBRM1	T9S10S12S14			5.0	14.5	R.AT* <b>S</b> *P <b>S</b> * <b>S</b> <b>S</b> *VSGDFDDGH <b>S</b> VSTPGPSR.K
120-130	23-24	BRG1 associated factor 180 KD	PBRM1	S10S13S14S16			6.4	31.9	R.AT <b>S</b> *P <b>SS</b> * <b>S</b> * <b>V</b> <b>S</b> *GDFDDGH <b>S</b> VSTPGPSR.K
130-140	25-26	PBRM1	S375T377				2.7	63.3	R.YEEGE <b>SEAS</b> <b>S</b> *IT* <b>S</b> FM <b>D</b> VSNPFYQLYD <b>T</b> VR.S
140-150	27-28	PBRM1	S371S375				3.6	50.9	R.YEEGES*EA <b>S</b> *IT <b>S</b> FM <b>D</b> VSNPFYQLYD <b>T</b> VR.S
150-160	29-30	BRG1 associated factor 180 KD	PBRM1	T346Y351			4.3	12.0	R.LSAITMALQY* <b>G</b> SESEEDAALAAAR.Y
160-170	31-32	BRG1 associated factor 180 KD	PBRM1	Y366S371			4.4	63.2	R.Y*EEGES*EAESIT <b>S</b> FM <b>D</b> VSNPFYQLYD <b>T</b> VR.S
170-180	33-34	BRG1 associated factor 180 KD	PBRM1	Y366T377			3.9	13.2	R.Y*EEGE <b>SEAS</b> IT* <b>S</b> FM <b>D</b> VSNPFYQLYD <b>T</b> VR.S
180-190	35-36	BRG1 associated factor 180 KD	PBRM1	S178			10.3	54.4	K.GEADDEDD <b>EDG</b> DNQ <b>T</b> VT <b>EG</b> <b>S</b> *PAYLK.E
190-200	37-38	BRG1 associated factor 180 KD	PBRM1	S343T346			2.8	43.1	R.L <b>S</b> *A <b>IT</b> *MALQY <b>G</b> SESEEDAALAAAR.Y
200-210	39-40	BRG1 associated factor 180 KD	PBRM1	T346S353			6.7	23.4	R.LSAITMALQY <b>G</b> <b>S</b> *ESEEDAALAAAR.Y
210-220	41-42	BRG1 associated factor 180 KD	PBRM1	Y3S1S355			6.5	51.5	R.LSAITMALQY* <b>G</b> SE <b>S</b> *EEDAALAAAR.Y
220-230	43-44	BRG1 associated factor 180 KD	PBRM1	S177			18.0	40.1	K.GEADDEDD <b>EDG</b> DNQ <b>T</b> VT <b>EG</b> <b>S</b> *SPAYLK.E
230-240	45-46	BRG1 associated factor 180 KD	PBRM1	S371T377			8.4	78.0	R.YEEGES*EAESIT* <b>S</b> FM <b>D</b> VSNPFYQLYD <b>T</b> VR.S
240-250	47-48	BRG1 associated factor 180 KD	PBRM1	S371S383			4.5	41.8	R.YEEGES*EAESIT <b>S</b> FM <b>D</b> V <b>S</b> *NPFYQLYD <b>T</b> VR.S
250-260	49-50	BRG1 associated factor 180 KD	PBRM1	S375S378			6.3	12.8	R.YEEGE <b>SEAS</b> <b>S</b> *IT <b>S</b> *FMDVSNPFYQLYD <b>T</b> VR.S
260-270	51-52	Bromo adjacent homology domain containing 1	BAHD1	S121			100.0	106.3	R.L <b>S</b> *LNAELNLLLER.E
270-280	53-54	Bromodomain adjacent to zinc finger BAZ1A domain 1A	S820				58.5	76.8	R.NSTADIS <b>I</b> GEER.E
280-290	55-56	Bromodomain adjacent to zinc finger BAZ1A domain 1A	S420				45.1	40.5	K.IAEQDSYFFPD <b>PPT</b> FI <b>S</b> *PANLR
290-300	57-58	Bromodomain adjacent to zinc finger BAZ1A domain 1A	T731				28.9	22.4	K.ELDQDM <b>V</b> *T <b>E</b> EDDP <b>G</b> SHKR.G
300-310	59-60	Bromodomain adjacent to zinc finger BAZ1A domain 1A	S1531				56.4	20.0	R.KRQ <b>S</b> *PEPSP <b>V</b> TLGR.R
310-320	61-62	Bromodomain adjacent to zinc finger BAZ1B domain 1B	S349				27.7	41.3	K.SLS <b>G</b> <b>S</b> *PLK.V
320-330	63-64	Bromodomain adjacent to zinc finger BAZ1B domain 1B	S1468				113.7	145.4	R.LAEDEGD <b>S</b> *EPA <b>V</b> GGQR.G
330-340	65-66	Bromodomain adjacent to zinc finger BAZ1B domain 1B	S708T710				3.5	64.2	R.SDVQEESE <b>G</b> <b>S</b> *D <b>T</b> *DNKDS*AAFEDNEVQDEFLEK.L
340-350	67-68	Bromodomain adjacent to zinc finger BAZ1B domain 1B	T710S716				4.0	64.3	R.SDVQEESE <b>GS</b> <b>T</b> *DNK <b>D</b> <b>S</b> *AAFEDNEVQDEFLEK.L
350-360	69-70	Bromodomain adjacent to zinc finger BAZ1B domain 1B	S70S708				2.9	40.0	R.SDVQEE <b>S</b> *EG <b>S</b> *DTDNKDSAAFEDNEVQDEFLEK.L
360-370	71-72	Bromodomain and PHD finger containing 1	BRPF1	S238			14.1	36.5	R.KTE <b>G</b> <b>V</b> <b>S</b> *PIQ <b>E</b> IF <b>Y</b> LMDR.L
370-380	73-74	Bromodomain containing 1	BRD1	S105S1055			17.4	36.6	R.VHGEPT <b>S</b> *DL <b>S</b> *DID.-
380-390	75-76	Bromodomain containing 4	BRD4	S1117			100.0	26.7	K.IH <b>S</b> *PIIR.S
390-400	77-78	BRD4	S1064S1083				13.9	10.7	R.EAP <b>S</b> *PLM <b>H</b> <b>S</b> PMQ <b>S</b> QFQSL <b>TH</b> <b>S</b> *PPQ <b>Q</b> N <b>V</b> QPK.K
400-410	79-80	Bromodomain containing 4	BRD4	S1070S1083			24.3	23.2	R.EAP <b>S</b> PLM <b>H</b> <b>S</b> *PMQ <b>S</b> QFQSL <b>TH</b> <b>S</b> *PPQ <b>Q</b> N <b>V</b> QPK.K
410-420	81-82	Bromodomain containing 4	BRD4	S1064S1070S1			35.3	18.8	R.EAP <b>S</b> *PLM <b>H</b> <b>S</b> *PMQ <b>S</b> QFQSL <b>TH</b> <b>S</b> *PPQ <b>Q</b> N <b>V</b> QPK.K
420-430	83-84	Bromodomain containing 4	BRD4	T1080			21.4	27.0	R.EAP <b>S</b> PLM <b>H</b> PMQ <b>S</b> QFQSL <b>T</b> *HQ <b>S</b> PPQ <b>Q</b> N <b>V</b> QPK.K
430-440	85-86	Bromodomain containing 4	BRD4	S1078S1083			7.2	11.0	R.EAP <b>S</b> PLM <b>H</b> PMQ <b>S</b> QFQ <b>S</b> *L <b>TH</b> <b>S</b> *PPQ <b>Q</b> N <b>V</b> QPK.K
440-450	87-88	Bromodomain containing 4	BRD4	S1083			14.2	12.4	R.EAP <b>S</b> PLM <b>H</b> PMQ <b>S</b> QFQSL <b>TH</b> <b>S</b> *PPQ <b>Q</b> N <b>V</b> QPK.K
450-460	89-90	Bromodomain containing 8	BRD8	T264S268			27.8	45.1	K.AT*PP <b>P</b> <b>S</b> *PL <b>L</b> SELLK.K
460-470	91-92	Bromodomain containing 8	BRD8	T264			41.9	52.1	K.AT*PP <b>P</b> <b>S</b> PL <b>L</b> SELLK.K
470-480	93-94	Bromodomain containing 8	BRD8	S268S272			1.6	38.8	K.ATPP <b>P</b> <b>S</b> *PL <b>S</b> *ELLK.K
480-490	95-96	BTB POZ domain containing 14	NACC1	S140S151			2.5	21.0	K.V <b>S</b> SPSCDSQGLHAEAP <b>S</b> *SE <b>P</b> QSPVAQ <b>T</b> <b>S</b> *GW <b>P</b> ACSTPLPLVSR.
490-500	97-98	BTB POZ domain containing 14	NACC1	T150S151			6.9	21.7	K.V <b>S</b> SPSCDSQGLHAEAP <b>S</b> EPQSPVAQ <b>T</b> * <b>S</b> *GW <b>P</b> ACSTPLPLVSR.
500-510	99-100	BTB POZ domain containing 14	NACC1	S127S130			6.6	25.1	K.V <b>S</b> SP <b>S</b> *CD <b>S</b> *QGLHAEAP <b>S</b> EPQSPVAQ <b>T</b> SGW <b>P</b> ACSTPLPLVSR.
510-520	101-102	BTB POZ domain containing 14	NACC1	S124S125			28.6		K.V <b>S</b> * <b>S</b> *PSCDSQGLHAEAP <b>S</b> EPQSPVAQ <b>T</b> SGW <b>P</b> ACSTPLPLVSR.
520-530	103-104	BTB POZ domain containing 14	NACC1	S124			18.5		K.V <b>S</b> * <b>S</b> PS <b>C</b> DSQGLHAEAP <b>S</b> EPQSPVAQ <b>T</b> SGW <b>P</b> ACSTPLPLVSR.
530-540	105-106	BTB POZ domain containing 14	NACC1	S140S141			4.6	31.9	K.V <b>S</b> SPSCDSQGLHAEAP <b>S</b> * <b>S</b> *EPQSPVAQ <b>T</b> SGW <b>P</b> ACSTPLPLVSR.
540-550	107-108	BTBK	BTBK	S1045			44.5	59.3	R.DLQ <b>S</b> *PDFTTGFHSDKIEAK.V
550-560	109-110	BTBK	BTBK	S111S1116			9.0	24.5	R.IDTT <b>S</b> SASWVAG <b>S</b> *P <b>V</b> <b>S</b> *PPV <b>D</b> LR.T
560-570	111-112	BTBK	BTBK	Y996			6.5	19.2	R.SD <b>S</b> GGY <b>N</b> LS <b>D</b> IQSP <b>S</b> TGLLK.S
570-580	113-114	BTBK	BTBK	S111S1116			19.6	44.7	R.IDTT <b>S</b> SASWVAG <b>S</b> *F <b>S</b> P <b>V</b> <b>S</b> *PPV <b>D</b> LR.T
580-590	115-116	BTBK	BTBK	S992			5.1	22.6	R.SD <b>S</b> *SGGY <b>N</b> LS <b>D</b> IQSP <b>S</b> TGLLK.S
590-600	117-118	BTBK	BTBK	S993			8.0	23.3	R.SD <b>S</b> *GGY <b>N</b> LS <b>D</b> IQSP <b>S</b> TGLLK.S
600-610	119-120	BTBK	BTBK	T1102S1116			2.4	12.1	R.IDTT <b>S</b> SASWVAG <b>S</b> F <b>S</b> P <b>V</b> <b>S</b> *PPV <b>D</b> LR.T
610-620	121-122	BUB1	BUB1	S602			0.9	83.2	K.SPGDFT <b>S</b> *AAQLASTPFHK.L
620-630	123-124	BUB1	BUB1	T601			32.1	81.5	K.SPGDFT* <b>S</b> AAQLASTPFHK.L

Peak Area		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM																	
		CarT		RajiB															
	Protein Name	Gene	Phosphosites			Ascor	MOWSE	Sequence											
	BUB1	BUB1	S596			1.8	38.8	K.S <sup>PGDFT</sup> SAQAQLASTPFHK.L											
	Butyrate induced transcript 1	HACD3	S114			100.0	74.2	R.WLDE <sup>S</sup> DAEMEL.R											
	Bystin	BYSL	S98			110.5	96.3	R.MPQDGS <sup>D</sup> DEDEEWPTLEK.A											
	Bystin	BYSL	S167S170			13.1	52.2	K.QTEVETVMS <sup>E</sup> VS <sup>G</sup> GFPMQLDPR.V											
	Bystin	BYSL	S167			22.0	60.8	K.QTEVETVMS <sup>E</sup> VS <sup>G</sup> GFPMQLDPR.V											
	Bystin	BYSL	T164S170			7.0	15.0	K.QTEVET <sup>T</sup> VMSEVS <sup>G</sup> GFPMQLDPR.V											
	Bystin	BYSL	T164			12.8	23.7	K.QTEVET <sup>T</sup> VMSEVS <sup>G</sup> GFPMQLDPR.V											
	Bystin	BYSL	T160			6.7	22.6	K.QT <sup>E</sup> EVETVMSEVS <sup>G</sup> GFPMQLDPR.V											
	c-Mpl binding protein	LARP4	T601			9.5	89.2	R.AST <sup>T</sup> ASPCNNNINAATAVALQEPR.K											
	c-Mpl binding protein	LARP4	S603			15.8	65.4	R.ASTAS <sup>T</sup> PCNNNINAATAVALQEPR.K											
	c-Mpl binding protein	LARP4	S589			37.7	38.4	K.DGLNQTTIPV <sup>S</sup> PPSTTKPSR.A											
	c-Mpl binding protein	LARP4	S600			7.4	50.2	R.AS <sup>T</sup> ASPCNNNINAATAVALQEPR.K											
	c-Myb	MYB	S11S12			13.7	29.1	R.HSIYS <sup>S</sup> S <sup>S</sup> DEDDFEMCDHDYDGLLPK.S											
	c-Myc	MYC	T73S77			19.9	35.5	K.KFELLPT <sup>T</sup> PPLS <sup>S</sup> PSRR.S											
	c-Myc	MYC	S86			22.3	53.4	R.SGLCS <sup>S</sup> PSYVAVTFPSLR.G											
	c-Myc	MYC	T73S79			24.7	17.6	K.FELLPT <sup>T</sup> PPLSPS <sup>S</sup> RR.S											
	c-Src	SRC	S17			125.2	55.9	R.S <sup>S</sup> LEPAENVHGAGGAFPASQTSPKPSADGHR.G											
	C-X-C chemokine receptor type 5	CXCR5	S359			13.4	20.7	R.RS <sup>S</sup> LSSENASTLTTF.-											
	C/EBP induced protein	FAM117A	S213			100.0	71.6	R.S <sup>S</sup> LEGLNQEELEEVFK.E											
	C/EBP induced protein	FAM117A	S30S317S319			8.7	12.2	K.AS <sup>S</sup> SPGHFPAFLEDGS <sup>S</sup> PS <sup>S</sup> PVLAFAS <sup>S</sup> PRPNISYIFK.R											
	C10orf3 protein	CEP55	S428			14.0	115.0	K.S <sup>S</sup> PTAALNESLVECPK.C											
	C10orf3 protein	CEP55	T430			3.9	62.6	K.SP <sup>T</sup> AALNESLVECPK.C											
	C10orf47 protein	PROSER2	S311			153.9	37.8	R.AQVLATHIGHAGAFPAAGDAGEGAPGGGS <sup>S</sup> SPER.V											
	C10orf69 protein	ERLIN1	S323			25.4	37.9	R.ES <sup>S</sup> SLPSK.E											
	C10orf69 protein	ERLIN1	S324			13.9	38.2	R.ES <sup>S</sup> SLPSK.E											
	C10orf86 protein	NSMCE4A	S30S32			30.3	22.1	R.S <sup>S</sup> RS <sup>S</sup> PLSPR.S											
	C10orf86 protein	NSMCE4A	S63S72			4.9	28.6	R.EAPERPSLEDTEPSD <sup>S</sup> S <sup>S</sup> GOEMMDPAS <sup>S</sup> LEAEADQGLCLR.Q											
	C10orf86 protein	NSMCE4A	T58S61S72			5.1	33.6	R.EAPERPSLED <sup>T</sup> EP <sup>S</sup> S <sup>S</sup> DSGOEMMDPAS <sup>S</sup> LEAEADQGLCLR.Q											
	C11orf23 protein	PPP6R3	S537			100.0	131.5	R.IQQFDDGGS <sup>S</sup> DEEDIWEEK.H											
	C12orf5 protein	TIGAR	S159			8.0	53.4	K.EQFSQGS <sup>S</sup> NCLETSLAEIFPLGK.N											
	C12orf5 protein	TIGAR	S157			21.4	53.5	K.EQFSQGS <sup>S</sup> PSNCLETSLAEIFPLGK.N											
	C13orf3 protein	SKA3	S119			71.2	81.1	K.NSVHEQEAINS <sup>S</sup> DPELSNCENFQK.T											
	C13orf3 protein	SKA3	S155			67.1	66.1	R.S <sup>S</sup> PQLSDFGLER.Y											
	C13orf8 protein	CHAMP1	S476			100.0	49.3	R.GGS <sup>S</sup> PDLWK.S											
	C13orf8 protein	CHAMP1	S204S214			67.7	14.4	K.LAPVP <sup>S</sup> PEPQKPAPVS <sup>S</sup> PESVK.A											
	C13orf8 protein	CHAMP1	S627			16.9	79.1	K.DNQESS <sup>S</sup> DAELSSSEYIK.T											
	C13orf8 protein	CHAMP1	S44S452			40.6	53.2	R.KPSGS <sup>S</sup> PDLWKLS <sup>S</sup> PDQR.K											
	C13orf8 protein	CHAMP1	S308S319			54.2	34.0	R.RPAPAV <sup>S</sup> PGSWKGPPTS <sup>S</sup> PRPWK.S											
	C13orf8 protein	CHAMP1	S286			29.7	68.2	R.KPSPSES <sup>S</sup> PEPWKFFPAVSPEPR.R											
	C13orf8 protein	CHAMP1	S282			18.4	52.0	R.KPS <sup>S</sup> PSESPFWKFFPAVSPEPR.R											
	C13orf8 protein	CHAMP1	S282S297			56.8	29.6	R.KPS <sup>S</sup> PSESPFWKFFPAVS <sup>S</sup> PEPR.R											
	C13orf8 protein	CHAMP1	S282S284			68.9	34.2	R.KPS <sup>S</sup> PS <sup>S</sup> ESPEPWKFFPAVSPEPR.R											
	C13orf8 protein	CHAMP1	S282S286			21.7	40.8	R.KPS <sup>S</sup> PSES <sup>S</sup> PEPWKFFPAVSPEPR.R											
	C13orf8 protein	CHAMP1	S65S653			7.6	67.1	K.GQES <sup>S</sup> S <sup>S</sup> DQEQVDVESIDFSK.E											
	C13orf8 protein	CHAMP1	S651S653			49.6	130.4	K.GQES <sup>S</sup> S <sup>S</sup> DQEQVDVESIDFSK.E											
	C13orf8 protein	CHAMP1	S43S436			100.0	41.1	R.S <sup>S</sup> PAGS <sup>S</sup> PELR.K											
	C13orf8 protein	CHAMP1	S44S452			63.3	45.3	R.KPS <sup>S</sup> GSPDLWKL <sup>S</sup> PDQR.K											
	C13orf8 protein	CHAMP1	S284			20.3	70.1	R.KPSPS <sup>S</sup> ESPEPWKFFPAVSPEPR.R											
	C13orf8 protein	CHAMP1	S626			55.5	61.7	K.DNQES <sup>S</sup> SDAELSSSEYIK.T											
	C13orf8 protein	CHAMP1	S651S652			68.5	52.6	K.GQES <sup>S</sup> S <sup>S</sup> SDQEQVDVESIDFSK.E											
	C13orf8 protein	CHAMP1	S275			22.5	30.6	R.TTS <sup>S</sup> PEPR.K											
	C13orf8 protein	CHAMP1	S459			16.9	41.0	R.KTS <sup>S</sup> PASLDFPESQK.S											
	C13orf8 protein	CHAMP1	S445			5.9	38.5	R.KPSGS <sup>S</sup> PDLWK.L											
	C13orf8 protein	CHAMP1	S627S632			13.0	84.2	K.DNQESS <sup>S</sup> DAELS <sup>S</sup> SSEYIK.T											
	C13orf8 protein	CHAMP1	S427S432S436			100.0	13.0	R.KGPPLS <sup>S</sup> PEIRS <sup>S</sup> PAGS <sup>S</sup> PELR.K											
	C13orf8 protein	CHAMP1	S284S286			20.1	34.7	R.KPSPS <sup>S</sup> ES <sup>S</sup> PEPWKFFPAVSPEPR.R											
	C13orf8 protein	CHAMP1	S282S286S297			24.8	19.4	R.KPS <sup>S</sup> PSES <sup>S</sup> PEPWKFFPAVS <sup>S</sup> PEPR.R											
	C13orf8 protein	CHAMP1	T274			-0.2	28.9	R.TT <sup>S</sup> SPEPR.K											
	C13orf8 protein	CHAMP1	S627S633			8.7	79.5	K.DNQESS <sup>S</sup> DAELS <sup>S</sup> SSEYIK.T											
	C13orf8 protein	CHAMP1	S626S632			7.6	30.4	K.DNQES <sup>S</sup> SDAELS <sup>S</sup> SSEYIK.T											
	C13orf8 protein	CHAMP1	S311S319			24.9	29.0	R.RPAPAVSPGS <sup>S</sup> WKPGPTS <sup>S</sup> PRPWK.S											
	C13orf8 protein	CHAMP1	S626S627			4.1	30.2	K.DNQES <sup>S</sup> S <sup>S</sup> DAELSSSEYIK.T											

Peak Area	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
	Protein Name	Gene	Phosphosites						
	C13orf8 protein	CHAMP1	S286S297				49.6	26.6	R.KPSPSES*PEPWKPPFAVS*PEPR.R
	C13orf8 protein	CHAMP1	S626S633				12.4	48.2	K.DNQES*SDAELSS*SEYIK.T
	C14orf103 protein	ATG2B	S1018T1022				7.4	27.0	K.SAVHYDEESG*EEET*LOYFSTVDPNYR.S
	C14orf103 protein	ATG2B	S1016S1018				7.8	34.2	K.SAVHYDEES*GS*EEET*LOYFSTVDPNYR.S
	C14orf103 protein	ATG2B	S1016T1022				13.5	25.8	K.SAVHYDEES*GSEET*LOYFSTVDPNYR.S
	C14orf106 protein	MIS18BP1	T821S824				27.6	27.5	R.NTSNPVILEPET*EES*ENEFYIK.Q
	C14orf11 protein	EAPP	S109S111				48.4	67.9	R.YYDDIYFDS*DS*EDED.RA
	C14orf11 protein	EAPP	Y106S111				21.1	28.7	R.YYDDIY*FSDS*EDED.RA
	C14orf11 protein	EAPP	Y106S109				9.7	62.9	R.YYDDIY*FDS*DSEDED.RA
	C14orf11 protein	EAPP	S17S24S25S26				41.5	23.6	R.LPDDYDPYAVEEPS*DEEPALS*SS*EDEVDLLHGTDPQK.R
	NGDN		S142S143				131.4	103.2	K.LS*SS*EDEEDEAEDDQSEASGK.K
	C14orf133 protein	VIPAS39	S121				13.7	67.9	R.TRPGS*FQSLSDALSDTPAK.S
	C14orf133 protein	VIPAS39	T117				22.6	67.1	R.TRPGSFQSLSDALSDTPAK.S
	C14orf133 protein	VIPAS39	S124				7.3	31.3	R.TRPGSFQS*LSDALSDTPAK.S
	C14orf133 protein	VIPAS39	S93T104S105				8.2	12.8	R.NS*FSSYAQLPKPT*STYLS*SSFFR.G
	C14orf133 protein	VIPAS39	S95T104				13.1	16.7	R.NSFS*SYAQLPKPT*STYLS*SSFFR.G
	C14orf133 protein	VIPAS39	S93S95S96				15.2	16.4	R.NS*FS*SS*YAQLPKPTSTYLS*SSFFR.G
	C14orf133 protein	VIPAS39	S93S105				4.4	14.1	R.NS*FSSYAQLPKPTS*TYLS*SSFFR.G
	C14orf133 protein	VIPAS39	S93S96Y97				12.9	13.0	R.NS*FS*Y*YAQLPKPTSTYLS*SSFFR.G
	C14orf133 protein	VIPAS39	S93T104				20.3	22.6	R.NS*FSSYAQLPKPT*STYLS*SSFFR.G
	C14orf133 protein	VIPAS39	S96T104S105				12.9	13.6	R.NSFS*YAQLPKPT*STYLS*SSFFR.G
	C14orf171 protein	TMEM63C	S77S80				17.4	46.6	R.LALLIHD*SLTS*LIYGEQSEK.T
	C14orf171 protein	TMEM63C	S77T79				15.1	44.5	R.LALLIHD*SLT*SLIYGEQSEK.T
	C14orf35 protein	NAA30	S55				40.2	15.7	R.S*PAGGESATVAAK.G
	C14orf4 protein	IRF2BPL	S61S5639				6.8	12.6	R.TTPES*APQNGPSMAALMSVADTLGTAH*PK.D
	C18orf25 protein	C18orf25	S66S69				29.4	31.7	R.RDS*SES*QLASTESDKPTTGR.V
	C18orf25 protein	C18orf25	S67S69				8.6	11.4	R.RDS*ES*QLASTESDKPTTGR.V
	C19orf14 protein	WDR62	T1021S1022					23.6	R.FAT*SLPHFGCAGPTEDELSLPEGPSVPS*SLPQT*PEQEK.F
	C19orf14 protein	WDR62	S1228				16.8	157.1	R.SIS*LGDS*EGPIVATLAQPLR.R
	C19orf14 protein	WDR62	S1249				5.8	79.9	R.RPS*V*GELASLGQELQAITTAT*PSLDSEGG*EPALR.S
	C19orf14 protein	WDR62	S1248				29.8	55.1	R.RPS*V*GELASLGQELQAITTAT*PSLDSEGG*EPALR.S
	C19orf14 protein	WDR62	S1048T1053				24.3	15.7	R.FATSLPHFGCAGPTEDELSLPEGPSVPS*SLPQT*PEQEK.F
	C19orf14 protein	WDR62	S1248T1268				11.7	30.7	R.RPS*V*GELASLGQELQAITTAT*PSLDSEGG*EPALR.S
	C19orf14 protein	WDR62	S1249T1268				6.2	23.0	R.RPS*V*GELASLGQELQAITTAT*PSLDSEGG*EPALR.S
	C19orf14 protein	WDR62	S1255T1264				15.0	30.9	R.RPSSV*GELAS*LGQELQAITTAT*PSLDSEGG*EPALR.S
	C19orf14 protein	WDR62	S1248S1249				6.6	14.8	R.RPS*SS*V*GELASLGQELQAITTAT*PSLDSEGG*EPALR.S
	C1orf16 protein	SMG7	S520				34.0	60.2	K.ENLILQETS*VIESLAADGS*PGLK.S
	C1orf24 protein	FAM129A	S579T584				1.2	37.5	K.HNLFEDNMALPSES*VSSLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S577S581				2.9	37.7	K.HNLFEDNMALPSES*ESVS*SLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S577S592S596				7.9	24.5	K.HNLFEDNMALPSES*VSSSLTDLKPPT*GS*WQAS*PAR.R
	C1orf24 protein	FAM129A	S579S582				4.9	70.2	K.HNLFEDNMALPSES*VSS*SLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S579S581				3.6	48.5	K.HNLFEDNMALPSES*VS*SLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S581S592S596				10.2	30.8	K.HNLFEDNMALPSES*VS*SLTDLKPPT*GS*WQAS*PAR.R
	C1orf24 protein	FAM129A	S579T584T590				11.0	17.1	K.HNLFEDNMALPSES*VSSLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S577S582				1.8	13.8	K.KHNLFEDNMALPSES*ESVS*SLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	T584S592S596				9.9	45.6	K.HNLFEDNMALPSESVSSLT*DLKPPT*GS*WQAS*PAR.R
	C1orf24 protein	FAM129A	S579T590S596				15.9	25.5	K.HNLFEDNMALPSES*VSSSLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	T584T590S596				4.2	14.3	K.HNLFEDNMALPSESVSSLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S582T584T590				14.5	17.8	K.HNLFEDNMALPSESVS*SLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S581S582				1.9	25.2	K.HNLFEDNMALPSESVS*SLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S577S579				5.7	46.1	K.HNLFEDNMALPSES*ES*VSSLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S579T590				2.7	15.8	K.HNLFEDNMALPSES*VSSSLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S579S592S596				12.5	34.3	K.HNLFEDNMALPSES*VSSSLTDLKPPT*GS*WQAS*PAR.R
	C1orf24 protein	FAM129A	S579S581S592				2.0	17.2	K.HNLFEDNMALPSES*VS*SLTDLKPPT*GS*WQAS*PAR.R
	C1orf24 protein	FAM129A	S581T584T590				2.1	29.5	K.HNLFEDNMALPSESVS*SLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S577S579T590				1.2	14.7	K.HNLFEDNMALPSES*ES*VSSSLTDLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S582T584				3.6	30.7	K.HNLFEDNMALPSESVS*SLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S577T584T590				16.8	19.2	K.HNLFEDNMALPSES*ESVSSLT*DLKPPT*GSNQAS*PAR.R
	C1orf24 protein	FAM129A	S577T584S592				5.9	15.9	K.HNLFEDNMALPSES*ESVSSLT*DLKPPT*GS*WQAS*PAR.R
	C1orf35 protein	MMTAG2	S217T219				-0.4	13.2	R.RPAEATS*PT*SPERPR.H
	C1orf35 protein	MMTAG2	S216T219				7.7	13.6	R.RPAEATS*SP*PT*SPERPR.H
	C1orf52 protein	C1orf52	S158				4.3	65.7	R.LLPEGETLES*DDEKDEHTSK.K

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence	
<10 10 20 40 60 70 80 90 >100	0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100	Protein Name	Gene	Phosphosites	5 6 7 8	5 6 7 8				
		C1orf52 protein C1orf52	T155				50.1	50.4	R.LLPEGEET*LESDDKEHETSK.K	
		C20ORF1 protein TPX2	S486				100.0	39.3	K.S*PAFALK.N	
		C20ORF1 protein TPX2	S738				32.7	35.0	K.SSDQPLTVPV*S*PK.F	
		C20ORF121 protein TTPAL	S13S16				3.8	10.9	R.TSPS*VAS*LSENLPPPPPEPPGYVCSLTEDLVTK.A	
		C20ORF121 protein TTPAL	S11S16				2.6	13.5	R.TS*PSVAS*LSENLPPPPPEPPGYVCSLTEDLVTK.A	
		C20orf14 protein PRPF8	T27S5279				24.4	52.1	K.GYLT*DLNS*MPTHGGDINDIKK.A	
		C20orf14 protein PRPF8	T20S1212227T				9.0	18.1	R.QT*QFGLNT*PYPGNLNTYPYPGMT*PGLMT*PGTGELDMR.K	
		C20orf14 protein PRPF8	T27S1283				4.4	22.1	K.GYLT*DLNSMPT*HGGDINDIKK.A	
		C20orf6 protein ESF1	S153				18.8	49.4	K.FKIDSNIS*PK.K	
		C20orf6 protein ESF1	S663				95.5	77.6	K.ALAEFASEELPS*DVDLNDPYFAEEVK.Q	
		C20orf6 protein ESF1	S657				40.8	63.0	K.ALAEFAS*EEELPSDVLNDPYFAEEVK.Q	
		C20orf6 protein ESF1	S657S663				98.3	79.4	K.ALAEFAS*EEELPS*DVDLNDPYFAEEVK.Q	
		C20orf6 protein ESF1	T311S312T319				108.5	63.7	R.GKGNIE*T*S*SEDEDT*ADLFPEESGFHAWR.E	
		C20orf6 protein ESF1	S312S313T319				6.9	49.0	R.GKGNIE*T*S*SEDEDT*ADLFPEESGFHAWR.E	
		C20orf6 protein ESF1	T311S313T319				21.7	30.5	K.GNIE*T*SS*SEDEDT*ADLFPEESGFHAWR.E	
		C20orf6 protein ESF1	S75S77S79S82				21.9	51.1	R.FYDLS*DS*DS*NLS*GEDSK.A	
		C20orf6 protein ESF1	T311S312S313				15.9	23.2	R.GKGNIE*T*S*S*SEDEDTADLFPEESGFHAWR.E	
		C20orf6 protein ESF1	T311T319					43.9	R.GKGNIE*T*SSEDEDT*ADLFPEESGFHAWR.E	
		C20ORF77 protein RPRD18	S164				42.4	76.2	R.TFQQIEEEDDDYPGS*YSPDPSAGPLLTELIK.A	
		C20ORF77 protein RPRD18	Y161				6.6	46.7	R.TFQQIEEEDDDY*PGSYSPDPSAGPLLTELIK.A	
		C20ORF77 protein RPRD18	Y165				13.9	83.5	R.TFQQIEEEDDDYPGS*Y*SPDPSAGPLLTELIK.A	
		C20ORF77 protein RPRD18	T149					56.1	R.T*FQQIEEEDDDYPGSYSPDPSAGPLLTELIK.A	
		C20ORF77 protein RPRD18	S166					51.8	R.TFQQIEEEDDDYPGS*Y*S*PDPSAGPLLTELIK.A	
		C21orf66 protein PAXBP1	S557S563				13.5	83.5	K.MADHLEGLS*SDDDET*STDITNFLEK.D	
		C21orf66 protein PAXBP1	S557S558				22.5	97.5	K.MADHLEGLS*S*DDEET*STDITNFLEK.D	
		C21orf66 protein PAXBP1	S558T563				11.6	24.9	K.MADHLEGLS*S*DDEET*STDITNFLEK.D	
		C22orf5 protein TMEM184	S402S403				37.8	20.8	K.TLLLS*S*DDEF.-	
		C22orf9 protein KIAA0930	S309				35.2	63.4	R.NNRPAFFS*PSLKR.K	
		C22orf9 protein KIAA0930	S367				40.6	39.6	R.SLVGS*WLK.L	
		C4orf9 protein NOP14	T15S5157				25.5	26.0	K.HNDIVDS*SDAEDRG*T*LS*AELTAHFGGGGLLHK.K	
		C4orf9 protein NOP14	S146T155				6.5	12.2	K.HNDIVDS*SDAEDRG*T*LSAELTAHFGGGGLLHK.K	
		C4orf9 protein NOP14	S146T161				5.9	16.2	K.HNDIVDS*SDAEDRG*LSAEL*AAHFGGGGLLHK.K	
		C4orf9 protein NOP14	S148T155				4.3	13.1	K.HNDIVDS*S*DAEDRG*T*LSAELTAHFGGGGLLHK.K	
		NOP14	S146S148					35.3	K.HNDIVDS*S*DAEDRG*LSAELTAHFGGGGLLHKK.T	
		C4orf9 protein NOP14	S148S157				1.5	14.1	K.HNDIVDS*S*DAEDRG*LS*AELTAHFGGGGLLHK.K	
		C5orf3 protein FAM114A2	S145				37.0	66.1	K.ENENS*SPVAGAFGVFSTISTAVQSTGK.S	
		C5orf6 protein FAM53C	S232S236				15.7	18.5	R.RFS*LSPS*LGPQASR.F	
		C5orf6 protein FAM53C	S232S234				31.3	54.2	R.RFS*LS*PSLGPQASR.F	
		C6orf106 protein C6orf106	S209				9.1	14.9	R.LSQNSVNLSPS*S*HANLNVVITYSK.G	
		C6orf106 protein C6orf106	S206				20.0	72.8	R.LSQNSVNL*S*PSSHANLNVVITYSK.G	
		C6orf106 protein C6orf106	S202				1.2	14.2	R.LSQNS*VNLSPSSHANLNVVITYSK.G	
		C6orf111 protein PNISR	S290S304T309				24.3	58.0	R.SKFD*S*DEEEDTENVEAAS*SGKV*T*R.S	
		C6orf111 protein PNISR	T297S304T309				8.1	13.5	R.SKFDSD*DEEEDT*ENVEAAS*SGKV*T*R.S	
		C6orf111 protein PNISR	S290				18.8	61.5	R.SKFD*S*DEEEDTENVEAASSGK.V	
		C6orf111 protein PNISR	S290T309				11.8	55.2	R.SKFD*S*DEEEDTENVEAASSGKV*T*R.S	
		C6orf111 protein PNISR	S290S305				2.6	15.6	R.SKFD*S*DEEEDTENVEAAS*S*GKVTR.S	
		C6orf111 protein PNISR	S211				100.0	44.5	R.S*PIALPV.KQ	
		C6orf111 protein PNISR	S393S396				4.3	27.3	K.QLAQSSALASLTGLGGLGYGS*GDS*EDER.S	
		C6orf111 protein PNISR	S611S613				100.0	16.2	R.NR*S*PS*RER.R	
		C6orf111 protein PNISR	S672				100.0	35.9	R.S*IDKDR.K	
		C6orf111 protein PNISR	S601				15.7	14.5	R.SNRNS*IER.E	
		C6orf111 protein PNISR	S726				25.8	57.5	R.SGS*ISVK.I	
		C6orf111 protein PNISR	S670S672				100.0	22.9	R.S*RS*IDKDR.K	
		C6orf111 protein PNISR	T383S396				4.0	47.8	K.QLAQSSALASLT*GLGGLGYSGDS*EDER.S	
		C6orf111 protein PNISR	S290S304				11.7	26.9	R.SKFD*S*DEEEDTENVEAAS*SGK.V	
		C6orf111 protein PNISR	Y391S396				23.8	77.8	K.QLAQSSALASLTGLGGLGY*GSGDS*EDER.S	
		C6orf111 protein PNISR	S311S313T326				12.8	11.3	R.S*PS*PVPQEEHSDPEMT*EEKEYQMLLTK.M	
		C6orf111 protein PNISR	S290S304S305				25.9	47.6	R.SKFD*S*DEEEDTENVEAAS*S*GKV*T*R.S	
		PNISR	S311S313S321				73.6	29.8	R.S*PS*PVPQEEH*S*DPMEETEEKEYQMLLTK.M	
		C6orf111 protein PNISR	S724				20.3	47.3	R.S*GSISVK.I	
		C6orf113 protein ZUFSP	S253				20.2	16.1	R.RSEES*R.Q	
		C6orf32 protein RIPOR2	T522				10.8	59.9	R.LT*SAEVPMATDR.L	

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites				
		C6orf32 protein RIPOR2		S473			35.9	R.DN <sup>S</sup> GRAGAEU <sup>S</sup> LEMDVAEM <sup>S</sup> LEEESEAESE <sup>S</sup> VDEI <sup>S</sup> ITSEGNITV <sup>S</sup> Q
		C6orf32 protein RIPOR2		S19			18.0	R.S <sup>S</sup> QSFAGFSGLOER.R
		C6orf32 protein RIPOR2		S21			33.7	R.SQ <sup>S</sup> SFAGFSGLOER.R
		C6orf32 protein RIPOR2		S53S538			45.1	R.LLS <sup>S</sup> EGS <sup>S</sup> VGGESEGC.R.S
		C6orf32 protein RIPOR2		S344T350			15.7	R.RMSMY <sup>S</sup> SGTPT <sup>S</sup> PTFK.D
		C6orf32 protein RIPOR2		S523			13.9	R.LTS <sup>S</sup> AEVPMATDR.L
		C6orf32 protein RIPOR2		Y343T350			12.2	R.RMSMY <sup>S</sup> SGTPT <sup>S</sup> PTFK.D
		C7orf25 protein C7orf25		S208S210S212			65.4	R.GDIVAVNALLDHPELOP <sup>S</sup> ES <sup>S</sup> ES <sup>S</sup> DDEGFELLOVTR.V
		C8orf20 protein REEP4		S152			15.1	R.SFS <sup>S</sup> MODLR.S
		C8orf20 protein REEP4		S194T196S202			21.8	R.AGGLQDS <sup>S</sup> DT <sup>S</sup> EDECW <sup>S</sup> STEAVPRA
		C8orf20 protein REEP4		S150			10.5	R.S <sup>S</sup> FSMODLR.S
		C9orf25 protein FAM129A		T96S98			27.6	K.GYSSLDQSPDEKPLVALDT <sup>S</sup> DS <sup>S</sup> DDDFDMSR.Y
		C9orf42 protein FAM122A		S143S147			21.9	K.RIDFIPV <sup>S</sup> PAPS <sup>S</sup> PTR.G
		C9orf42 protein FAM122A		T47			34.7	R.SNSAPLIHGLSDT <sup>S</sup> SPVFQAEAPSAR.R
		C9orf42 protein FAM122A		S37			18.8	R.SNS <sup>S</sup> APLIHGLSDTSPVFQAEAPSAR.R
		C9orf42 protein FAM122A		S45			16.9	R.SNSAPLIHGLS <sup>S</sup> DTSPVFQAEAPSAR.R
		C9orf42 protein FAM122A		S143T149			20.9	K.RIDFIPV <sup>S</sup> PAPSP <sup>T</sup> R.G
		C9orf42 protein FAM122A		S270			48.0	K.VSTTTDSPV <sup>S</sup> PAQAAS <sup>S</sup> PFPIDELSSK.-
		C9orf42 protein FAM122A		S276			1.8	K.VSTTTDSPV <sup>S</sup> PAQAAS <sup>S</sup> PFPIDELSSK.-
		C9orf42 protein FAM122A		T263S270			4.2	K.VS <sup>T</sup> T <sup>T</sup> TDSPV <sup>S</sup> PAQAAS <sup>S</sup> PFPIDELSSK.-
		C9orf42 protein FAM122A		S267S270			-3.1	K.VSTTTDS <sup>S</sup> PV <sup>S</sup> PAQAAS <sup>S</sup> PFPIDELSSK.-
		C9orf42 protein FAM122A		S76			100.0	R.HGLLLPAS <sup>S</sup> PVR.M
		C9orf42 protein FAM122A		S189			-0.2	R.SQ <sup>S</sup> S <sup>S</sup> PINCIRPSVLGLK.R
		C9orf42 protein FAM122A		S35			26.2	R.S <sup>S</sup> NSAPLIHGLSDTSPVFQAEAPSAR.R
		C9orf42 protein FAM122A		S270S276			41.4	K.VSTTTDSPV <sup>S</sup> PAQAAS <sup>S</sup> PFPIDELSSK.-
		C9orf42 protein FAM122A		S267S276			-5.3	K.VSTTTDS <sup>S</sup> PV <sup>S</sup> PAQAAS <sup>S</sup> PFPIDELSSK.-
		C9orf42 protein FAM122A		S62			16.9	R.RN <sup>S</sup> STTFPSR.H
		C9orf42 protein FAM122A		S262S270			5.5	K.VS <sup>S</sup> T <sup>T</sup> TDSPV <sup>S</sup> PAQAAS <sup>S</sup> PFPIDELSSK.-
		C9orf55 protein DENND4C		S1089			16.9	R.STS <sup>S</sup> LSALVR.S
		C9orf55 protein DENND4C		S767S769			27.6	R.KSSTGS <sup>S</sup> IS <sup>S</sup> NVLFSTQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		S890			-0.3	R.SS <sup>S</sup> PVPEMLEESQELLEPPVDDVPK.T
		C9orf55 protein DENND4C		S899			1.8	R.SSPVPEMLEE <sup>S</sup> QELLEPPVDDVPK.T
		C9orf55 protein DENND4C		S769S774T775			8.1	R.KSSTGS <sup>S</sup> IS <sup>S</sup> NVLF <sup>S</sup> T <sup>T</sup> QDPVEDAVFGEATNLKK
		C9orf55 protein DENND4C		S764T765			8.8	R.KS <sup>S</sup> T <sup>T</sup> GSISNVLFSTQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		S1404T1415			17.8	R.SH <sup>S</sup> S <sup>S</sup> VGGPLQNDFT <sup>T</sup> QRPFHGISTVSLPNSLQEVDPGLK.R
		DENND4C		S763S764T765			5.4	R.KS <sup>S</sup> S <sup>T</sup> T <sup>T</sup> GSISNVLFSTQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		S763S764S774			2.8	R.KS <sup>S</sup> S <sup>S</sup> TGSISNVLF <sup>S</sup> TQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		S1404S1423S1			16.4	R.SH <sup>S</sup> S <sup>S</sup> VGGPLQNDFTQRPFHGISTVSLPNSLQEVDPGLK.R
		C9orf55 protein DENND4C		S1404T1415T14			10.9	R.SH <sup>S</sup> S <sup>S</sup> VGGPLQNDFT <sup>T</sup> QRPFHGISTVSLPNSLQEVDPGLK.R
		C9orf55 protein DENND4C		S763S769			16.5	R.KS <sup>S</sup> STGS <sup>S</sup> IS <sup>S</sup> NVLFSTQDPVEDAVFGEATNLKK
		C9orf55 protein DENND4C		S763S764			25.9	R.KS <sup>S</sup> S <sup>S</sup> TGSISNVLFSTQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		T765S769			6.6	R.KSST <sup>S</sup> GSIS <sup>S</sup> NVLFSTQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		T1088			-0.4	R.ST <sup>S</sup> LSALVR.S
		C9orf55 protein DENND4C		T765S769S774			9.0	R.KSST <sup>S</sup> GSIS <sup>S</sup> NVLF <sup>S</sup> TQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		S774T775			28.3	R.KSSTGSISNVLF <sup>S</sup> T <sup>T</sup> QDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		S763S767			2.0	R.KS <sup>S</sup> STGS <sup>S</sup> ISNVLFSTQDPVEDAVFGEATNLKK
		C9orf55 protein DENND4C		T765S767S769			9.5	R.KSST <sup>S</sup> GS <sup>S</sup> IS <sup>S</sup> NVLFSTQDPVEDAVFGEATNLKK
		C9orf55 protein DENND4C		S732S737			24.9	K.HSQP <sup>S</sup> PEPH <sup>S</sup> PTPEPAWGSSNK.V
		C9orf55 protein DENND4C		S1404S1423			25.3	R.SH <sup>S</sup> S <sup>S</sup> VGGPLQNDFTQRPFHGISTVSLPNSLQEVDPGLK.R
		C9orf55 protein DENND4C		S1404T1424S1			10.3	R.SH <sup>S</sup> S <sup>S</sup> VGGPLQNDFTQRPFHGIST <sup>S</sup> V <sup>S</sup> LPNSLQEVDPGLK.R
		C9orf55 protein DENND4C		T765S767			4.3	R.KSST <sup>S</sup> GS <sup>S</sup> ISNVLFSTQDPVEDAVFGEATNLKK.N
		C9orf55 protein DENND4C		S764S769			9.3	R.KS <sup>S</sup> S <sup>S</sup> TGSIS <sup>S</sup> NVLFSTQDPVEDAVFGEATNLKK
		C9orf55 protein DENND4C		T765S767S774			8.4	R.KSST <sup>S</sup> GS <sup>S</sup> ISNVLF <sup>S</sup> TQDPVEDAVFGEATNLKK
		C9orf55 protein DENND4C		S1404S1426			9.8	R.SH <sup>S</sup> S <sup>S</sup> VGGPLQNDFTQRPFHGIST <sup>S</sup> LPNSLQEVDPGLK.R
		C9orf78 C9orf78		S261			92.1	R.VGDTKEPEPERS <sup>S</sup> PPNR.K
		C9orf78 C9orf78		S15S17			68.5	R.RRGDS <sup>S</sup> ES <sup>S</sup> EDEQDSEVR.L
		C9orf88 protein FAM129B		S691S696			24.0	K.AAPEAS <sup>S</sup> SPPAS <sup>S</sup> PLQHLPGKA
		C9orf88 protein FAM129B		S641S646			8.7	K.QVVSVVQDEEVLGPFEEASPES <sup>S</sup> PPPAS <sup>S</sup> PDGVTEIR.G
		C9orf88 protein FAM129B		S692S696			26.1	K.AAPEAS <sup>S</sup> PPAS <sup>S</sup> PLQHLPGKA
		Calcipressin 1 RCAN1		S163S167			100.0	K.QFLIS <sup>S</sup> PPAS <sup>S</sup> PPVGWK.Q
		Calcium channel, voltage dependent, P/Q CACNA1A		S2457			6.6	R.S <sup>S</sup> PRTPRA
		Calcium regulated heat stable protein 1 CARHSP1		S52			33.6	R.TFS <sup>S</sup> ATVRA



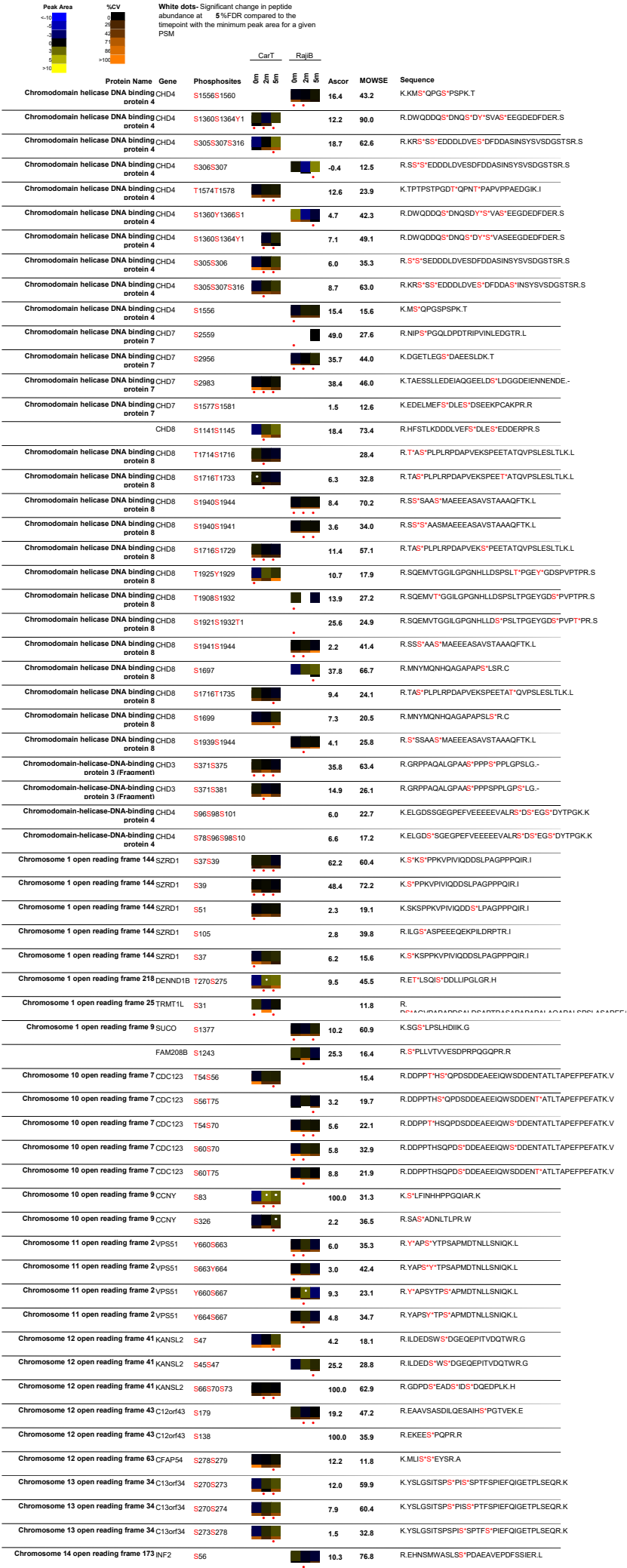
Peak Area	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM	Protein Name	Gene	Phosphosites	CarT		RajIB	Ascor	MOWSE	Sequence
		Calcium regulated heat stable protein 1	CARHSP1	S41				41.9	24.4	R.GNVVPS*PLPTRR.T
		Calcium regulated heat stable protein 1	CARHSP1	S146				-0.4	28.0	K.HETWSGHVIS* <b>S</b> -
		Calcium regulated heat stable protein 1	CARHSP1	S305S32S41				45.0	22.7	R.ERS* <b>PS</b> *PLRGNVPS*PLPTR.R
		Calcium regulated heat stable protein 1	CARHSP1	S305S32				100.0	31.8	R.ERS* <b>PS</b> *PLR.G
		Calcium regulated heat stable protein 1	CARHSP1	T50				3.5	13.8	R.TRT*FSATV.R.A
		Calcium regulated heat stable protein 1	CARHSP1	S305S41				23.1	27.5	R.ERS*PSPLRGNVPS*PLPTR.R
		Calcium/calmodulin dependent protein kinase IV	CAMK4	S360				100.0	47.9	R.DPS*PIQDGNEDMK.A
		Calmodulin regulated spectrin-associated protein 1	CAMAP1	S447				16.3	74.3	K.SPNS*HDSEPWTLTLR.Q
		Calmodulin regulated spectrin-associated protein 1	CAMAP1	S297				39.0	34.5	R.S*PQGQLDTSESKPDS*FFLEPLMPAVLKPAK.E
		Calmodulin regulated spectrin-associated protein 1	CAMAP1	S311				-2.7	36.1	R.SPOGQLDTSESKPDS*FFLEPLMPAVLKPAK.E
		Calmodulin regulated spectrin-associated protein 1	CAMAP1	S307				8.2	45.1	R.SPOGQLDTSES*KPDSFFLEPLMPAVLKPAK.E
		Calmodulin regulated spectrin-associated protein 1	CAMAP1	S444				15.0	80.1	K.S*PNSHDSEPWTLTLR.Q
		Calmodulin regulated spectrin-associated protein 1	CAMAP1	S450				0.2	29.1	K.SPNSHDS*EPWTLTLR.Q
		Calmodulin regulated spectrin-associated protein 1	CAMAP1	S460S462				183.2	72.5	R.QDS*DS*DVDIEAEHDFMGAEHPVVF.S.R.Y
		Calmodulin regulated spectrin-associated protein 1-like 1	CAMAP2	S404				-0.1	21.7	R.SS*SMSYVDGFIGTWPK.E
		Calnexin	CANX	S583				100.0	49.3	K.AEEDILNRS*PR.N
		Calnexin	CANX	T562S564				15.5	66.7	K.QKSDAEEDGGT* <b>VS</b> *QEEEDRKPK.A
		Calnexin	CANX	S554				28.6	66.4	K.QKS*DAEEDGGTVSQEEEDR.K
		Calnexin	CANX	S554T562				8.3	56.4	K.QKS*DAEEDGGT*VSQEEEDRKPK.A
		Calnexin	CANX	T562				6.5	37.7	K.QKSDAEEDGGT*VSQEEEDR.K
		Calnexin	CANX	S564				17.8	65.8	K.SDAEEDGGTVS*QEEEDR.K
		Calpastatin	CAST	S326				25.9	68.9	K.KEGITGPPADSSKPIGPDDAIDALSSDTCGS*PTAAGK.K
		Calpastatin	CAST	T299					63.0	K.KEGIT*GPPADSSKPIGPDDAIDALSSDTCGSPTAAGK.K
		Calpastatin	CAST	S449				-0.2	55.6	R.SES*ELIDELSEDFDR.S
		Calpastatin	CAST	T323				5.6	13.4	K.EGITGPPADSSKPIGPDDAIDALSSDFT*CGSPTAAGK.K
		CAP-GLY domain containing linker protein 1	CLIP1	S348				27.7	98.3	R.KIS*GTTALQEQALK.E
		CAP-GLY domain containing linker protein 1	CLIP1	S147				1.4	77.2	R.ATS*PLCTSTASMVSSSPSTPSNIPQKPSQPAK.E
		CAP-GLY domain containing linker protein 1	CLIP1	S195S200S204				20.3	55.8	K.TASES*ISNLS*EAGS*IK.K
		CAP-GLY domain containing linker protein 1	CLIP1	S200S204				26.7	67.7	K.TASESISNLS*EAGS*IK.K
		CAP-GLY domain containing linker protein 1	CLIP1	S147S160				-0.5	18.3	R.ATS*PLCTSTASMVSS*PSTPSNIPQKPSQPAK.E
		CAP-GLY domain containing linker protein 1	CLIP1	S147S158				3.6	20.5	R.ATS*PLCTSTASMVSS*PSTPSNIPQKPSQPAK.E
		CAP-GLY domain containing linker protein 1	CLIP1	S197S204				19.3	42.0	K.TASESIS*NLSEAGS*IK.K
		CAP-GLY domain containing linker protein 1	CLIP1	S195S197S204				2.8	24.2	K.TASES*IS*NLSEAGS*IK.K
		CapZ-interacting protein	RCSO1	S75				75.7	69.2	K.LQANLTFDPAALLPGAS*PK.S
		Carboxypeptidase D	CPD	T1368T1370				27.6	63.7	K.SLLSHEFQDET* <b>DT</b> *EETLYSSKH.-
		Cardiac lineage protein 1	HEXIM1	T236S237S252				1.9	35.3	K.SDDT* <b>S</b> *DDDFMEEGEEDGGS*DGMMGGDGEFLQR.D
		Cask-interacting protein 2	CASKIN2	S471				102.6	44.1	R.S*GEQIFTQDVRPEQLLEGK.D
		Cask-interacting protein 2	CASKIN2	T252				10.5	73.0	R.NT*YNGTALDIVNGFTTSQASR.E
		Cask-interacting protein 2	CASKIN2	S358				11.1	28.9	R.LPS*APTPLRPGFSR.T
		Cask-interacting protein 2	CASKIN2	Y253				16.9	68.8	R.NT*Y*NGTALDIVNGFTTSQASR.E
		CasL interacting molecule	MICAL1	S872S875S876				66.5	63.9	K.EEKES* <b>PF</b> * <b>S</b> *EEEEEDVPLDSVQEQALQTFAK.T
		CasL interacting molecule	MICAL1	S876				5.3	75.0	K.ESPFSS*EEEEEDVPLDSVQEQALQTFAK.T
		CasL interacting molecule	MICAL1	S875				12.3	81.1	K.ESPFSS*EEEEEDVPLDSVQEQALQTFAK.T
		CasL interacting molecule	MICAL1	S875S876				9.4	86.6	K.ESPFSS*EEEEEDVPLDSVQEQALQTFAK.T
		CasL interacting molecule	MICAL1	S872S875				29.7	56.5	K.EEKES* <b>PF</b> * <b>S</b> *EEEEEDVPLDSVQEQALQTFAK.T
		Caspase 2	CASP2	S157				39.9	48.3	K.LRLS*TDTEVHSLDNK.D
		Caspase 2	CASP2	T160				4.5	32.2	K.LRLSTD*TEVHSLDNK.D
		CASPR4	CNTNAP4	S520				22.4	23.9	R.LIS*ISGK.V
		Catalase	CAT	S515				1.9	30.5	K.NAHTFVQS*GSHLAAR.E
		Catenin alpha 1	CTNNA1	S641				49.2	74.8	R.TPEELDSS*DFETEDFV.R.S
		CBF1 interacting corepressor	CIR1	S202				28.3	104.9	R.NLTANDPSQOEYV* <b>E</b> *EGEEDPEVEFLK.S
		CBF1 interacting corepressor	CIR1	Y199				9.2	42.3	R.NLTANDPSQOEY*VASEGEEDPEVEFLK.S
		CBFA2	RUNX1	T41S48				41.4	45.1	R.RFT*PPSTALS*PGK.M
		CBFA2	RUNX1	S276S303				22.9	41.4	R.QIQPS*PPWSYDQSYQYLGSIASPSVHPATP*PGR.A
		CBFA2	RUNX1	S48				55.8	67.8	R.RFTPPSTALS*PGK.M
		CBFA2	RUNX1	S276S280					19.0	R.QIQPS*PPWS*YDQSYQYLGSIASPSVHPATPISPGR.A
		CBFA2	RUNX1	S239				7.7	18.5	R.TAMRVS*PHHPAPTNP.R.A
		CBFA2	RUNX1	S303				11.4	26.8	R.QIQSPPWYSYDQSYQYLGSIASPSVHPATP*PGR.A
		CBL	CBL	S619				60.9	28.3	R.HS*LPFSLPSQMEPRPDVRL.L
		CBP80	NCBP1	S22				19.1	66.1	R.KTS* <b>D</b> ANETEDHLESICK.V
		CBP80	NCBP1	T27				11.9	28.8	R.RKTSANET*EDHLESICK.V
		CC chemokine receptor type 7	CCR7	S367				17.8	26.5	R.RSSMS*VEAETTTTFSP.-

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		Protein Name	Gene	Phosphosites						
		CC chemokine receptor type 7	CCR7	S364				32.4	17.9	R.RS <sup>S</sup> SMSVEAETTTTFSF.-
		CC chemokine receptor type 7	CCR7	S365				14.7	35.7	R.RS <sup>S</sup> MSVEAETTTTFSF.-
		CCAAT binding factor	CEBPZ	S629				34.9	83.9	R.SQLDDHPES <sup>D</sup> DDEEFIDANDEDEMEK.F
		CCAAT binding factor	CEBPZ	T33				29.5	56.8	K.RPWRP <sup>E</sup> EAEVD <sup>D</sup> PDEDEDNT <sup>T</sup> SEANGFSLEEVL.R.L
		CCAAT binding factor	CEBPZ	S34				38.4	83.8	K.RPWRP <sup>E</sup> EAEVD <sup>D</sup> PDEDEDNTS <sup>T</sup> EAENGFSLEEVL.R.L
		CCAAT binding factor	CEBPZ	S973				24.6	54.8	R.NLND <sup>S</sup> SLFVSAEEFGHLLENMGSK.F
		CCAAT/Enhancer binding protein, beta	CEBPB	S229				12.1	26.7	R.AYLGYQAVPSGSSGSLSTSS <sup>S</sup> SSPFGT <sup>T</sup> PSPADAK.A
		CCAAT/Enhancer binding protein, beta	CEBPB	S228T235				10.9	15.5	R.AYLGYQAVPSGSSGSLSTSS <sup>S</sup> SSSPGT <sup>T</sup> PSPADAK.A
		CCAAT/Enhancer binding protein, beta	CEBPB	S218T235				9.0	23.2	R.AYLGYQAVPS <sup>S</sup> GSSGSLSTSSSSSPGT <sup>T</sup> PSPADAK.A
		CTCF		S609S610S612				18.4		K.ED <sup>S</sup> S <sup>S</sup> DS <sup>S</sup> ENAEPLD <sup>N</sup> DNEDEEPAVEIEPEPEQPVT <sup>T</sup> PAPPAK. V
		CCR4-NOT transcription complex, subunit 3	CNOT3	S473				41.9		K. CDMAAATGACGALGCGGMSGCGELIUBAIDGCSSTPESNA
		CCR4-NOT transcription complex, subunit 3	CNOT3	S506				14.6	34.0	K. CDMAAATGACGALGCGGMSGCGELIUBAIDGCSSTPESNA
		CCR4-NOT transcription complex, subunit 3	CNOT3	S358				13.1		K. ACGADSLNCSGTADYAAAIADADCSSTTGGPDSGSGGCG
		CCR4-NOT transcription complex, subunit 3	CNOT3	S507				5.3	47.8	K. CDMAAATGACGALGCGGMSGCGELIUBAIDGCSSTPESNA
		CD19	CD19	S499				13.9	106.5	R.EATSLGSQS <sup>S</sup> YEDMR.G
		CD19	CD19	S494S499				13.2	80.5	R.EAT <sup>S</sup> LGQS <sup>S</sup> YEDMR.G
		CD19	CD19	T493S497				27.3	68.6	R.EAT <sup>T</sup> SLGS <sup>S</sup> QSYEDMR.G
		CD19	CD19	Y531				-0.3	65.7	R.GQPGPNHEEDADS <sup>S</sup> YENMDNPDGPDPAWGGGR.M
		CD19	CD19	T493S494S499				6.0	53.2	R.EAT <sup>S</sup> SLGSQS <sup>S</sup> YEDMR.G
		CD19	CD19	S530					59.0	R.GQPGPNHEEDADS <sup>S</sup> YENMDNPDGPDPAWGGGR.M
		CD19	CD19	T493S497S499				11.3	56.2	R.EAT <sup>T</sup> SLGS <sup>S</sup> QSYEDMR.G
		CD19	CD19	S494S497				12.8	61.8	R.EAT <sup>S</sup> LG <sup>S</sup> QSYEDMR.G
		CD19	CD19	S494S497S499				9.7	55.8	R.EAT <sup>S</sup> LG <sup>S</sup> QSYEDMR.G
		CD19	CD19	T493S499				20.8	78.3	R.EAT <sup>T</sup> SLGSQS <sup>S</sup> YEDMR.G
		CD2 antigen binding protein 2	CD2BP2	S195				9.8	41.4	R.KGPGQPS <sup>S</sup> SPORL
		CD2BP2		S194					11.3	R.KGPGQPS <sup>S</sup> SPORLDR.L
		CD2 antigen binding protein 2	CD2BP2	S49				36.0	124.2	K.HSLDS <sup>S</sup> DEEEDDDGGSSK.Y
		CD2 associated protein	CD2AP	S233				7.9	51.8	R.TSS <sup>S</sup> SETEEKKPEKPLILQSLGPK.T
		CD2 associated protein	CD2AP	S458				78.4	69.9	K.S <sup>S</sup> VDFSLTVR.T
		CD2 associated protein	CD2AP	S86				25.8	45.6	R.IST <sup>T</sup> TYGLPAGGIQHPQTK.N
		CD2 associated protein	CD2AP	T87				12.6	50.0	R.IST <sup>T</sup> TYGLPAGGIQHPQTK.N
		CD2 associated protein	CD2AP	Y88				12.9	47.1	R.IST <sup>T</sup> YGLPAGGIQHPQTK.N
		CD28		S189				7.9	22.4	R.LLHS <sup>S</sup> DYMMNTPR.R
		CD28		Y191				11.1	26.5	R.LLHSD <sup>T</sup> YMMNTPR.R
		CD3 gamma	CD3G	T152				1.3	39.0	R.ASDKQT <sup>T</sup> LLPNDQLYQPLK.D
		CD3 gamma	CD3G	S148				4.4	22.2	R.AS <sup>S</sup> DKQTLLPNDQLYQPLK.D
		CD40	CD40	S272				100.0	37.7	R.IIS <sup>S</sup> VOER.Q
		CD5	CD5	S428				14.9	89.0	R.QWIGPTGMNQNS <sup>S</sup> FHR.N
		CD5	CD5	S482S483S485				16.6	34.6	R.SSMQPDNS <sup>S</sup> S <sup>S</sup> SDYDLHGAQR.L
		CD5	CD5	T421				2.6	84.9	R.QWIGPT <sup>T</sup> GMNQNSFHR.N
		CD5	CD5	S439				31.3	35.5	R.S <sup>T</sup> HAENPTASHVDNEYSQPPR.N
		CD5	CD5	S476S482				3.3	50.9	R.SS <sup>S</sup> MQPDNS <sup>S</sup> SDSDYDLHGAQR.L
		CD5	CD5	S476S482S483				2.8	34.0	R.SS <sup>S</sup> MQPDNS <sup>S</sup> S <sup>S</sup> SDYDLHGAQR.L
		CD7	CD7	S228				10.7	52.6	K.NSAACV <sup>V</sup> YEDMSH <sup>S</sup> R.C
		CD7	CD7	S226				-0.4	50.1	K.NSAACV <sup>V</sup> YEDMS <sup>S</sup> HSR.C
		CD74 antigen	CD74	S25				100.0	58.3	R.DLS <sup>S</sup> MNEQLPMLGR.R
		CD80 antigen	CD80	S284				100.0	20.5	R.LRRES <sup>S</sup> VRPV.-
		CDC 25B	CDC25B	S396				61.1	53.4	K.S <sup>T</sup> LCHDEIENLLSDHRE
		CDC 25B	CDC25B	S344				22.3	29.1	R.SP <sup>S</sup> MPCSVIRPIK.R
		CDC like kinase 3	CDCA5	S27				23.9	21.0	R.RSY <sup>S</sup> R.LL
		CDC like kinase 3	CDCA5	S25Y26				13.9	17.8	R.RS <sup>T</sup> Y <sup>S</sup> SR.LL
		CDC like kinase 3	CLK3	S49S51				30.5	13.0	R.S <sup>T</sup> RS <sup>S</sup> HDRLPYQR.R
		CDC2	CDK1	Y15				16.9	61.0	K.IGEGT <sup>T</sup> GVVYK.A
		CDC2	CDK1	T14Y15				50.2	60.6	K.IGEGT <sup>T</sup> YGVVYK.A
		CDC2 related protein kinase 7	CDK12	S274S276				46.0	38.2	R.RQ <sup>S</sup> S <sup>V</sup> SPPYKEPSAYQSSTR.S
		CDC2 related protein kinase 7	CDK12	S333S334				8.3	32.2	R.SS <sup>S</sup> S <sup>S</sup> PFLSK.R
		CDC2 related protein kinase 7	CDK12	S382S385				21.3	43.5	R.HS <sup>S</sup> SIS <sup>S</sup> PVRLPLNSSLGAELSR.K
		CDC2 related protein kinase 7	CDK12	S383S385				35.8	48.9	R.HSS <sup>S</sup> S <sup>S</sup> PVRLPLNSSLGAELSR.K
		CDC2 related protein kinase 7	CDK12	S681S685				126.6	39.6	R.HLLTDLPPELPGGDL <sup>S</sup> PPDS <sup>S</sup> PEPK.A
		CDC2 related protein kinase 7	CDK12	S301S303				38.3	25.5	R.S <sup>S</sup> VS <sup>S</sup> PYSR.R
		CDC2 related protein kinase 7	CDK12	Y892				5.8	23.0	R.LYNSEESRP <sup>T</sup> YTNK.V
		CDC2 related protein kinase 7	CDK12	S379S382S383				39.9	19.0	R.S <sup>T</sup> RHS <sup>S</sup> S <sup>S</sup> S <sup>S</sup> PVRLPLNSSLGAELSR.K

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		Protein Name	Gene	Phosphosites					
		CDK2 related protein kinase 7	CDK12	S77S78S80S84			7.9	26.2	K.DMGLVTPEAASLGTVIKPLVEYDD <b>S</b> * <b>DS</b> *DT <b>F</b> S*DDMAFK.L
		CDK2 related protein kinase 7	CDK12	V73S78T82S84			5.6	15.2	K.DMGLVTPEAASLGTVIKPLVEY*DD <b>IS</b> * <b>DS</b> DT* <b>F</b> S*DDMAFK.L
		CDK2 related protein kinase 7	CDK12	T57S62T65V73			4.1	16.4	K.DMGLVT*PEAAS* <b>L</b> GT*VIKPLVEY*DD <b>IS</b> SDSTFSDMAFK.L
		CDK2 related protein kinase 7	CDK12	S332S333			10.0	39.0	R. <b>S</b> * <b>S</b> *SPFLSK.R
		CDK2 related protein kinase 7	CDK12	S62T65S77S84			2.0	22.1	K.DMGLVTPEAAS* <b>L</b> GT*VIKPLVEYDD <b>IS</b> *SD <b>S</b> T <b>F</b> S*DDMAFK.L
		CDK2 related protein kinase 7	CDK12	S382S383			17.9	43.7	R. <b>HS</b> * <b>S</b> *ISPVRLPLNSSLGAELSR.K
		CDK2 related protein kinase 7	CDK12	S77S78T82S84			6.6	11.4	K.DMGLVTPEAASLGTVIKPLVEYDD <b>S</b> * <b>DS</b> DT* <b>F</b> S*DDMAFK.L
		CDK2 related protein kinase 7	CDK12	Y73S78S80T82			4.4	23.0	K.DMGLVTPEAASLGTVIKPLVEY*DD <b>IS</b> * <b>DS</b> *DT*FSDMAFK.L
		CDK2 related protein kinase 7	CDK12	S1083			11.2	61.4	K. <b>NS</b> * <b>S</b> *PAPPQAPGK.V
		CDK2 related protein kinase 7	CDK12	S383S393			12.2	29.3	R. <b>HS</b> * <b>S</b> *ISPVRLPL <b>N</b> *SLGAELSR.K
		CDK2 related protein kinase 7	CDK12	S681			40.0	35.8	R.HLLTDLPLPPELPGDGL <b>S</b> *PPDSPPEPK.A
		CDK2 related protein kinase 7	CDK12	T893			12.1	32.0	R.LYNSEESRPY <b>T</b> *NK.V
		CDK2 related protein kinase 7	CDK12	S276Y279			5.3	12.2	R.RQSV <b>S</b> *PPY*KEPSAYQSSTR.S
		CDK2 related protein kinase 7	CDK12	Y73S78S80S84			7.1	22.7	K.DMGLVTPEAASLGTVIKPLVEY*DD <b>IS</b> * <b>DS</b> *DT <b>F</b> S*DDMAFK.L
		CDK2 related protein kinase 7	CDK12	S62T65Y73S84			3.6	24.2	K.DMGLVTPEAAS* <b>L</b> GT*VIKPLVEY*DD <b>IS</b> SDST <b>F</b> S*DDMAFK.L
		CDC25C	CDC25C	S263			6.6	64.7	K.TV <b>S</b> *LCDITITQMLEEDSNQGHLDGFSK.V
		CDC26	CDC26	S42			48.1	47.6	K.QKEDVEVVGGS*DGEGAIGLSSDPK.S
		CDK42 effector protein 4	CDC42EP	S9			20.1	15.4	K.QLV <b>S</b> *SSVHSK.R
		CDC5	CDC5L	T373T377T396			18.1	12.6	R.ILOEAQNLMALT <b>N</b> VD <b>T</b> *PLKGGNLNPLHESD <b>SG</b> VT*PQR.Q
		CDCA5	CDCA5	S35			-0.2	36.2	K.SG <b>S</b> *ELPSILPEIWPK.T
		Cdk5 and Abl enzyme substrate 2	CABLES2	S105			5.5	38.5	R.TPAQGLL <b>S</b> *PTQVPTGLLDGQR.Q
		CDP-DAG synthase 2	CDS2	S33			49.2	65.4	K.VDGETAS* <b>D</b> SESR.A
		Cell death regulator Aven	AVEN	S94			6.9	76.2	R.REPGGWGAGASAPVED <b>S</b> *DAETYGEENDEQGNYSK.R
		Cell death regulator Aven	AVEN	T98			6.5	11.6	R.REPGGWGAGASAPVEDD <b>S</b> DA <b>T</b> *YGEENDEQGNYSK.R
		Cell division cycle 2 like 1	CDK11B	Y67			9.5	11.3	-MEITIRNSPY* <b>R</b> R
		Cell division cycle 2 like 1	CDK11B	T595			16.9	55.6	K.AY <b>T</b> *PVVTLWYRA
		Cell division cycle 2 like 1	CDK11B	S589T595			16.0	88.3	R.EYGS* <b>PL</b> KAY <b>T</b> *PVVTLWYRA
		Cell division cycle 2 like 1	CDK11B	Y587S589			24.9	67.4	R.EY* <b>G</b> <b>S</b> * <b>PL</b> KAYTPVVTLWYRA
		Cell division cycle 2 like 1	CDK11B	Y594T595			24.0	60.4	R.EYGSPLKAY <b>T</b> *PVVTLWYRA
		Cell division cycle 2 like 1	CDK11B	Y587Y594			10.6	57.7	R.EY*GSPLKAY*TPVVTLWYRA
		Cell division cycle 2 like 1	CDK11B	S589Y594			14.5	34.4	R.EYGS* <b>PL</b> KAY*TPVVTLWYRA
		Cell division cycle 2 like 1	CDK11B	Y587T595			12.3	59.2	R.EY*GSPLKAY <b>T</b> *PVVTLWYRA
		Cell division cycle 2 like 1	CDK11B	S65			16.1	20.5	-MEITIRNS* <b>P</b> YR.R
		Cell division cycle 2 like 2	CDK11B	S574			26.0	35.4	R.EYGS* <b>PL</b> K.A
		Cell division cycle 2 like 2	CDK11B	T736S737			73.0	26.9	K.RGT* <b>S</b> *SPRPEGGGLGYSQLGDDDLK.E
		Cell division cycle 2 like 2	CDK11A	T580			16.8	55.4	K.AY <b>T</b> *PVV <b>T</b> QWYRA
		Cell division cycle 2 like 2	CDK11B	S271			16.8	59.3	R.DLL <b>S</b> LOD <b>IS</b> * <b>D</b> SER.K
		Cell division cycle 2 like 2	CDK11A	Y579T580			16.6	76.2	R.EYGSPLKAY <b>T</b> *PVV <b>T</b> QWYRA
		Cell division cycle 2 like 2	CDK11A	Y572Y579			17.4	61.4	R.EY*GSPLKAY*TPVV <b>T</b> QWYRA
		Cell division cycle 2 like 2	CDK11B	S265S271			38.0	89.0	R.DLL <b>S</b> * <b>D</b> LQD <b>IS</b> * <b>D</b> SER.K
		Cell division cycle 2 like 2	CDK11B	S363S366T377			14.7		R. EPDREYVGSCEAEEDVAG <b>RT</b> *D <b>NS</b> *WITGAWNSD <b>SL</b> SELY
		Cell division cycle 2 like 2	CDK11B	S222			100.0	23.5	R. <b>S</b> *PPRPRL
		Cell division cycle 2 like 2	CDK11A	S574T580			11.2	74.9	R.EYGS* <b>PL</b> KAY <b>T</b> *PVV <b>T</b> QWYRA
		Cell division cycle 2 like 2	CDK11A	Y572T580			12.0	61.9	R.EY*GSPLKAY <b>T</b> *PVV <b>T</b> QWYRA
		Cell division cycle 2 like 2	CDK11A	Y572S574			13.5	20.6	R.EY* <b>G</b> <b>S</b> * <b>PL</b> KAYTPVV <b>T</b> QWYRA
		Cell division cycle 2 like 5	CDK13	T1056T1058			0.3	39.1	R.KDLSLGLDD <b>S</b> <b>R</b> <b>T</b> * <b>N</b> <b>T</b> *PQGVL <b>P</b> SSQLK.S
		Cell division cycle 2 like 5	CDK13	S437S439			20.0	57.7	R. <b>HS</b> * <b>S</b> * <b>S</b> *PSTLT <b>L</b> K.S
		Cell division cycle 2 like 5	CDK13	S1054T1056			5.9	32.7	R.KDLSLGLDD <b>S</b> <b>R</b> <b>T</b> * <b>N</b> <b>T</b> *PQGVL <b>P</b> SSQLK.S
		Cell division cycle 2 like 5	CDK13	S436S437			8.5	42.5	R. <b>HS</b> * <b>S</b> * <b>S</b> *PSTLT <b>L</b> K.S
		Cell division cycle 2 like 5	CDK13	S315S317			100.0	29.8	R. <b>S</b> * <b>L</b> <b>S</b> * <b>P</b> LGGR.D
		Cell division cycle 2 like 5	CDK13	S1054T1058			6.8	35.5	R.KDLSLGLDD <b>S</b> <b>R</b> <b>T</b> * <b>N</b> <b>T</b> *PQGVL <b>P</b> SSQLK.S
		Cell division cycle 2 like 5	CDK13	S315S317S325			31.4	13.4	R. <b>S</b> * <b>L</b> <b>S</b> * <b>P</b> LGGRDD <b>S</b> * <b>P</b> VSHRA
		Cell division cycle 2 like 5	CDK13	S383			32.1	11.4	R.GGDV <b>S</b> *PSPYSSSSWR.R
		Cell division cycle 2 like 5	CDK13	S436S439			13.4	45.5	R. <b>HS</b> * <b>S</b> <b>S</b> * <b>S</b> *PSTLT <b>L</b> K.S
		Cell division cycle and apoptosis regulator	CCAR1	S333			100.0	20.6	R.ER <b>S</b> * <b>P</b> QR.K
		Centaurin beta 1	ACAP1	T739			46.2	33.9	R.SHD <b>L</b> H <b>T</b> * <b>L</b> -
		Centaurin beta 5	ACAP3	T454S456				11.4	R.K <b>P</b> <b>T</b> * <b>A</b> <b>S</b> *SSRQDK.E
		Centaurin delta 2	ARAP1	S229			39.3	91.2	R.LFPEFD <b>S</b> * <b>D</b> YDEVPEEGPGAPAR.V
		Centaurin delta 2	ARAP1	Y231			22.6	19.6	R.LFPEFDSD <b>S</b> * <b>D</b> YDEVPEEGPGAPAR.V
		Centaurin delta 2	ARAP1	S1195			81.4	71.2	R. <b>S</b> * <b>V</b> AFTADPL <b>S</b> LLR.N
		Centromeric protein a	CENPA	S17S19			27.5	32.7	R.RR <b>S</b> * <b>S</b> * <b>P</b> TP <b>T</b> PGPSR.R
		Centromeric protein c1	CENPC	S316			52.5	33.3	R. <b>S</b> * <b>W</b> ITIPR.K

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		Protein Name	Gene	Phosphosites						
<10	0	Centromeric protein E	CENPE	S1259				17.8	22.5	R.RSVSEK.T
10-20	1	Centromeric protein E	CENPE	S1257				9.5	16.9	R.RSVSEK.T
20-30	2	Centromeric protein F	CENPF	S1651				8.9	29.9	R.LQLQLDLSR.S
30-40	3	Centrosomal protein 72kDa	CEP72	S237				60.5	27.6	R.HLLSPQLVGYQCQDGGK.Q
40-50	4	Centrosome protein 4	CEP135	S1125S1132				4.5	20.4	R.HGLATPPLSSTLRSPSHPEHR.N
50-60	5	Centrosome protein 4	CEP135	S439				9.6	14.6	R.DRSPSRLDTFLK.G
60-70	6	Centrosome protein 4	ELOA2	S1132S1134				28.7	40.3	R.SPSHSPHHR.N
70-80	7	Centrosome protein 4	CEP135	S1125S1126				0.8	13.2	R.HGLATPPLSSTLRSPSHPEHR.N
80-90	8	Centrosome protein 4	CEP135	T1127S1130				2.2	12.5	R.HGLATPPLSSTLRSPSHPEHR.N
90-100	9	Centrosome protein 4	CEP135	S439S441				100.0	14.7	R.RDRSPSR.RL
>100	10	Centrosome protein 4	CEP135	S441				7.9	13.3	R.DRSPSRDLDTFLK.G
		Centrosome protein 4	CEP135	S1130S1132				5.1	13.7	R.HGLATPPLSSTLRSPSHPEHR.N
		Centrosome protein 4	CEP135	T1127S1132				-0.2	16.6	R.HGLATPPLSSTLRSPSHPEHR.N
		Ceramide synthase 4	CERS4	S291S296S298				100.0	55.3	K.DIRSDVEESDSSEAAAAQEPLQK.N
		Ceramide synthase 4	CERS4	S291S296S298				14.7	37.9	R.SDVEESDSSEAAAAQEPLQK.N
		Ceramide synthase 4	CERS4	S291S299				24.7	18.4	K.DIRSDVEESDSSEAAAAQEPLQK.N
		Ceramide synthase 4	CERS4	S291S296S299				8.5	42.6	R.SDVEESDSSEAAAAQEPLQK.N
		Ceramide synthase 4	CERS4	S291S298				14.4	13.2	K.DIRSDVEESDSSEAAAAQEPLQK.N
		Ceramide synthase 4	CERS4	S291S296				14.1	11.7	K.DIRSDVEESDSSEAAAAQEPLQK.N
		Ceramide synthase 4	CERS4	S291S298S299				14.6	52.5	K.DIRSDVEESDSSEAAAAQEPLQK.N
		Cerebellar degeneration-related autoantigen 2		S311				10.9	53.4	R.SSETILSSLAGSDIVK.G
		Cerebellar degeneration-related autoantigen 2		S310				-0.2	45.7	R.SSETILSSLAGSDIVK.G
		Cerebral protein 11	TMCC3	S438				100.0	64.7	R.NKFGSADNIAHLK.D
		CGI-07 protein	NMD3	S468T470				48.4	38.5	R.DSAIPVESDTDDEGAPR.I
		CGI-07 protein	NMD3	T470				9.1	59.4	R.DSAIPVESDTDDEGAPR.I
		CGI-79 protein	RBMX2	S187				13.9	11.5	R.EVQAEQPSSSPR.R
		CGI-79 protein	RBMX2	S188				9.8	24.6	R.EVQAEQPSSSPR.R
		CGI115 protein	RRP15	S266S276S280				8.9	21.7	K.DWDKESDGPDSRPESASDSDT.-
		CGI115 protein	RRP15	S272S276S280				0.6	18.1	K.DWDKESDGPDDSRPESASDSDT.-
		Chemokine, CXC motif, receptor 4	CXCR4	S321S324				4.0	14.5	K.TSAQHALTSVSRGS.SLK.I
		Chemokine, CXC motif, receptor 4	CXCR4	T318S319S324				12.1	15.5	K.TSAQHALTSVSRGS.SLK.I
		Chemokine, CXC motif, receptor 4	CXCR4	S347				5.8	46.9	K.RGQHSSVSTESESSFHSS.-
		Chemokine, CXC motif, receptor 4	CXCR4	S324S325				31.3	32.1	K.TSAQHALTSVSRGS.SLK.I
		Chemokine, CXC motif, receptor 4	CXCR4	T311S312				2.1	12.4	K.TSAQHALTSVSRGSSLK.I
		CHERP	CHERP	S813S815S817				47.5	83.2	R.SRSRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S815S817T819				11.2	61.5	R.SRSRTPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S815S817S823				10.1	45.0	R.SRSRTPPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	T819S822S823				13.8	50.6	R.SRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S815T819S823				7.6	49.6	R.SRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S802S804S806				15.2	14.4	R.SKSYSPGRR.R
		CHERP	CHERP	S815T819S822				9.1	37.7	R.SRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S817T819S823				9.3	36.3	R.SRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S815T819S822				7.7	17.0	R.SRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S813S815S817				9.3	10.7	R.SRSRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S815S817T819				10.1	27.4	R.SRSRTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S813S815S817				11.8	22.1	R.SRSRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S813S815S817				6.5	36.4	R.SRSRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S817T819S822				2.0	47.9	R.SRSPTPPSAGLGSNSAPPIDSR.L
		CHERP	CHERP	S815S817S822				2.6	61.0	R.SRSPTPPSAGLGSNSAPPIDSR.L
		CHL12	CHTF18	S871				65.8	102.3	R.VENSPQVDGSPPGLEQLGGIGEK.G
		CHMP family, member 7	CHMP7	S417				100.0	80.7	R.ISDAELEAELEK.L
		Chondrocyte protein with a poly proline region	MTFR1	S119				84.9	68.5	R.QISLPDLSQEEPQLK.T
		Chondroitin sulfate proteoglycan 6	SMC3	S1081				11.5	39.4	R.GSGSQSSVPSVDQFTGVGIR.V
		Chr2 synaptotagmin	ESYT2	S665				2.8	35.2	K.SHMSGPGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T656S660S663				5.0	33.5	R.KTSIKSHMSGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T656S657S660					59.6	R.KTSIKSHMSGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	S710				23.5	91.8	R.SSSLLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	S708				11.6	46.5	R.SSSLLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	S710S711				23.3	66.1	R.SSSLLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	S733				9.1	36.0	K.EPTPSIASDISLPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S730				37.7	118.8	K.EPTPSIASDISLPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S730S733				9.1	72.1	K.EPTPSIASDISLPATQELR.Q

Peak Area	iCV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Chr2 synaptotagmin	ESYT2	S727S730				7.7	62.1	K.EPT <b>P</b> S <b>I</b> A <b>S</b> *DISLPATQELR.Q
		Chr2 synaptotagmin	ESYT2	T725S730				9.9	43.1	K.EPT <b>P</b> S <b>I</b> A <b>S</b> *DISLPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S727S730S733				23.9	117.1	K.EPT <b>P</b> S <b>I</b> A <b>S</b> *DIS <b>S</b> LPATQELR.Q
		Chr2 synaptotagmin	ESYT2	T725S727S730				9.8	37.9	K.EPT <b>P</b> S <b>I</b> A <b>S</b> *DISLPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S648				27.7	29.7	K.R <b>P</b> S <b>S</b> *VSK.E
		Chr2 synaptotagmin	ESYT2	T656S660S665				5.1	58.6	R.K <b>T</b> *S <b>K</b> S <b>S</b> *HMSG <b>S</b> *PGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T656S660S663				4.6	28.9	R.K <b>T</b> *S <b>K</b> S <b>S</b> *HMS <b>S</b> *G <b>S</b> *PGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T656S657S660					27.8	R.K <b>T</b> *S <b>S</b> * <b>K</b> S <b>S</b> *HMS <b>S</b> *GSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	S711				12.6	60.8	R.SSS <b>S</b> *LLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	S709S711				11.8	76.8	R.S <b>S</b> *S <b>S</b> *LLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	S708S709				12.3	44.1	R.S <b>S</b> *S <b>S</b> LLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	S727S733				6.2	64.3	K.EPT <b>P</b> S <b>I</b> ASDI <b>S</b> *LPATQELR.Q
		Chr2 synaptotagmin	ESYT2	T725S727S733				6.6	65.0	K.EPT <b>P</b> S <b>I</b> ASDI <b>S</b> *LPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S709				-0.3	61.8	R.S <b>S</b> *S <b>S</b> LLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	S657S660S665				3.5	37.7	R.K <b>T</b> S <b>S</b> * <b>K</b> S <b>S</b> *HMSG <b>S</b> *PGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T725S733				12.3	35.9	K.EPT <b>P</b> S <b>I</b> ASDI <b>S</b> *LPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S657S660S663				3.5	46.4	R.K <b>T</b> S <b>S</b> * <b>K</b> S <b>S</b> *HMS <b>S</b> *GSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	S663S665				17.6	43.1	K.SHMS <b>S</b> *G <b>S</b> *PGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	S657S660S663				31.8	26.8	R.K <b>T</b> S <b>S</b> * <b>K</b> S <b>S</b> *HMS <b>S</b> *G <b>S</b> *PGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T725				2.8	19.4	K.EPT <b>P</b> S <b>I</b> ASDISLPATQELR.Q
		Chr2 synaptotagmin	ESYT2	T725S727				9.0	48.3	K.EPT <b>P</b> S <b>I</b> ASDISLPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S660S663S665				30.2	25.7	R.KTSIK <b>S</b> *HMS <b>S</b> *G <b>S</b> *PGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T725S730S733				23.2	76.1	K.EPT <b>P</b> S <b>I</b> A <b>S</b> *DI <b>S</b> *LPATQELR.Q
		Chr2 synaptotagmin	ESYT2	S663				3.8	11.9	K.SHMS <b>S</b> *GSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	T656S657				7.3	13.2	R.K <b>T</b> *S <b>S</b> * <b>K</b> SHMSGSPGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	S709S710				5.0	40.0	R.S <b>S</b> *S <b>S</b> *LLASPGHISVK.E
		Chr2 synaptotagmin	ESYT2	T656S657S665				-0.6	23.6	R.K <b>T</b> *S <b>S</b> * <b>K</b> SHMSG <b>S</b> *PGPGGSNTAPSTPVIGGSDKPGMEEK.A
		Chr2 synaptotagmin	ESYT2	S708S710				1.2	45.8	R.S <b>S</b> *S <b>S</b> *LLASPGHISVK.E
Chromatin accessibility complex, subunit 1				CHRA1	S124			20.4	41.8	R.EEDEENDNDNES <b>S</b> *DHDEADS.-
Chromatin assembly factor 1 subunit A				CHAF1A	S772			29.8	70.2	R.GLLSNHTGS <b>S</b> *PR.S
Chromatin assembly factor 1 subunit A				CHAF1A	S777			12.0	54.3	R.SP <b>S</b> *TTYLHTPTPSEDA <b>I</b> APSK.S
Chromatin assembly factor 1 subunit A				CHAF1A	S65			108.3	81.3	K.S <b>S</b> *PDLASDLTLENNCHVGS <b>I</b> DFRPK.L
Chromatin assembly factor 1 subunit A				CHAF1A	T770			22.0	44.8	R.GLLSN <b>H</b> T*GSPR.S
Chromatin assembly factor 1 subunit A				CHAF1A	S775			10.1	50.6	R.S <b>S</b> *PSTTYLHTPTPSEDA <b>I</b> APSK.S
Chromatin assembly factor 1 subunit A				CHAF1A	T778			7.2	45.3	R.SP <b>S</b> T*TYLHTPTPSEDA <b>I</b> APSK.S
Chromatin assembly factor 1 subunit A				CHAF1A	S206			56.6	32.9	R.S <b>S</b> *CPELTS <b>G</b> PR.M
Chromatin assembly factor 1 subunit B				CHAF1B	S429			12.1	67.6	R.TQDP <b>S</b> *PGTTP <b>P</b> QAR.Q
Chromatin assembly factor 1 subunit B				CHAF1B	S428T433			23.4	44.5	R.TQDP <b>S</b> *SPGT <b>T</b> *PPQAR.Q
Chromatin assembly factor 1 subunit B				CHAF1B	S538			42.1	33.6	K.TDTPPSSVPTSVISTP <b>T</b> EEIQSETPGDA <b>Q</b> G <b>S</b> *PPELK.R
Chromatin assembly factor 1 subunit B				CHAF1B	S410			6.6	25.3	R.G <b>S</b> S*PGRPV <b>E</b> GTPASR.T
Chromatin assembly factor 1 subunit B				CHAF1B	S428			35.2	54.0	R.TQDP <b>S</b> *SPGTTP <b>P</b> QAR.Q
Chromatin assembly factor 1 subunit B				CHAF1B	S429T433			17.7	10.9	R.TQDP <b>S</b> *PGT <b>T</b> *PPQAR.Q
Chromobox homolog 3				CBX3	S176			24.6	35.9	R.LTW <b>S</b> *CP <b>E</b> DEA <b>Q</b> .-
Chromobox homolog 3				CBX3	S93S95			21.8	58.9	K.R <b>K</b> S <b>S</b> *L <b>S</b> *D <b>S</b> ESDDSK.S
Chromobox homolog 3				CBX3	S95S97			13.6	38.9	K.SL <b>S</b> *D <b>S</b> *E <b>S</b> DDSK.S
Chromobox homolog 3				CBX3	S95			28.9	62.3	K.SL <b>S</b> *D <b>S</b> ESDDSK.S
Chromobox homolog 3				CBX3	S95S97S99			12.2	38.1	K.SL <b>S</b> *D <b>S</b> *E <b>S</b> *D <b>S</b> SK.S
Chromobox homolog 3				CBX3	S93			12.2	23.9	K.S <b>S</b> *L <b>S</b> DESDDSK.S
Chromobox homolog 3				CBX3	S93S95S97			10.9	24.1	K.S <b>S</b> *L <b>S</b> *D <b>S</b> *E <b>S</b> DDSK.S
Chromobox homolog 7				CBX7	Y28			100.0	21.4	R.KGKVEY <b>L</b> VK.W
Chromodomain helicase DNA binding				CHD1 protein 1	T250S252			109.3	31.4	K.EDEEM <b>K</b> T <b>D</b> S*DDLVECGEDVPOPEEEEF <b>T</b> IER.F
Chromodomain helicase DNA binding				CHD2 protein 2	S1364				32.7	R.LXEEHG <b>I</b> ELS*S <b>P</b> R.H
Chromodomain helicase DNA binding				CHD3 protein 3	S1646S1650			27.6	20.4	K.MET <b>E</b> ADAP <b>S</b> *PAP <b>S</b> *L <b>G</b> ER.L
Chromodomain helicase DNA binding				CHD4 protein 4	S512S528			38.4	20.7	K.WGQ <b>P</b> P <b>S</b> *PTPVPRPPDAD <b>P</b> NT <b>P</b> S*PKPLEGR <b>P</b> ER.Q
Chromodomain helicase DNA binding				CHD4 protein 4	S306S307S316			19.5	95.7	R.KR <b>S</b> S*S*EDD <b>L</b> D <b>V</b> E <b>S</b> *DFDASIN <b>S</b> Y <b>S</b> VG <b>S</b> T <b>S</b> R.S
Chromodomain helicase DNA binding				CHD4 protein 4	S305S306S307			49.4	119.1	R.KR <b>S</b> *S <b>S</b> *EDD <b>L</b> D <b>V</b> E <b>S</b> *DFDASIN <b>S</b> Y <b>S</b> VG <b>S</b> T <b>S</b> R.S
Chromodomain helicase DNA binding				CHD4 protein 4	S1360S1364S1			12.4	84.3	R.DWQ <b>D</b> D <b>S</b> *D <b>N</b> Q <b>S</b> *D <b>S</b> *V <b>A</b> S*E <b>E</b> GED <b>F</b> DER.S
Chromodomain helicase DNA binding				CHD4 protein 4	S1364Y1366S1			9.2	87.5	R.DWQ <b>D</b> D <b>S</b> D <b>N</b> Q <b>S</b> *D <b>S</b> *V <b>A</b> S*E <b>E</b> GED <b>F</b> DER.S
Chromodomain helicase DNA binding				CHD4 protein 4	S307S322			2.3	61.0	R.S <b>S</b> S*EDD <b>L</b> D <b>V</b> ESDFD <b>A</b> S*IN <b>S</b> Y <b>S</b> VG <b>S</b> T <b>S</b> R.S
Chromodomain helicase DNA binding				CHD4 protein 4	S307S316			6.3	20.5	R.S <b>S</b> S*EDD <b>L</b> D <b>V</b> E <b>S</b> *DFD <b>A</b> SIN <b>S</b> Y <b>S</b> VG <b>S</b> T <b>S</b> R.S
Chromodomain helicase DNA binding				CHD4 protein 4	S425			100.0	103.8	K.ED <b>N</b> S*EG <b>E</b> IL <b>E</b> VGGD <b>L</b> EEED <b>H</b> ME <b>F</b> CR.V
Chromodomain helicase DNA binding				CHD4 protein 4	S1560			13.9	38.7	K.MSQ <b>P</b> G <b>S</b> *P <b>S</b> PK.T



Peak Area		%CV		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM							
				CarT	RajiB	Ascor	MOWSE	Sequence			
Chromosome 14 open reading frame 173											
NF2											
S55											
											
22.8											
50.2											
R.EHNSMWASLS <sup>S</sup> SPDAEAVPDFSSIER.L											
Chromosome 14 open reading frame 173											
NF2											
S614											
											
14.7											
93.0											
K.DPTSLGLVLOAEADS <sup>T</sup> SEGLDAVHSR.G											
Chromosome 14 open reading frame 43											
ELMSAN1											
Y654S661											
											
39.3											
25.2											
R.SFELPPY <sup>T</sup> TPPILS <sup>S</sup> PVR.E											
Chromosome 14 open reading frame 43											
ELMSAN1											
T655S661											
											
30.6											
28.8											
R.SFELPPY <sup>T</sup> PPPILS <sup>S</sup> PVR.E											
Chromosome 14 open reading frame 43											
ELMSAN1											
T704T715											
											
26.9											
63.8											
R.TNSAEVT <sup>T</sup> PPVLSVMGEAT <sup>T</sup> PV <sup>S</sup> IEPR.I											
Chromosome 14 open reading frame 43											
ELMSAN1											
S700T704T715											
											
10.9											
36.2											
R.TNS <sup>S</sup> AEVT <sup>T</sup> PPVLSVMGEAT <sup>T</sup> PV <sup>S</sup> IEPR.I											
Chromosome 14 open reading frame 43											
ELMSAN1											
S461											
											
46.2											
26.1											
R.RAS <sup>S</sup> QEANLLTLAQK.A											
Chromosome 14 open reading frame 43											
ELMSAN1											
T704S709											
											
6.5											
23.4											
R.TNSAEVT <sup>T</sup> PPVLS <sup>S</sup> VMGEATPV <sup>S</sup> IEPR.I											
Chromosome 14 open reading frame 43											
ELMSAN1											
S148											
											
36.6											
15.6											
K.GS <sup>S</sup> PHPGVGVPYTYNHPEALKR.E											
Chromosome 14 open reading frame 46											
LIN52											
S28											
											
75.2											
42.1											
R.AS <sup>S</sup> PDLWPEQLPGVAEFAAFK.S											
Chromosome 14 open reading frame 92											
TOX4											
S178S182											
											
9.7											
36.2											
R.LSTTP <sup>S</sup> PTS <sup>S</sup> LHEDGVDFRR.Q											
Chromosome 14 open reading frame 92											
TOX4											
S178S181											
											
14.7											
45.7											
R.LSTTP <sup>S</sup> PTS <sup>S</sup> SLHEDGVDFRR.Q											
Chromosome 14 open reading frame 92											
TOX4											
T176S178S182											
											
9.3											
14.5											
R.LSTT <sup>T</sup> PS <sup>S</sup> PTS <sup>S</sup> LHEDGVDFRR.Q											
Chromosome 14 open reading frame 92											
TOX4											
T176S178T180											
											
23.2											
19.1											
R.LSTT <sup>T</sup> PS <sup>S</sup> PT <sup>T</sup> SSLHEDGVDFRR.Q											
Chromosome 15 open reading frame 42											
TICRR											
S1750											
											
122.0											
54.1											
R.TPILEDFELEGVCQLPDQS <sup>S</sup> PPR.N											
Chromosome 16 open reading frame 53											
PAGR1											
T138S143S148											
											
100.0											
12.6											
R.RPPT <sup>T</sup> PEAQS <sup>S</sup> EEERS <sup>S</sup> DEEPEAK.E											
Chromosome 17 open reading frame 49											
BAP18											
S96											
											
29.2											
38.7											
K.VYEDSGIPLAES <sup>S</sup> PK.K											
Chromosome 17 open reading frame 62											
C17orf62											
S178											
											
7.3											
34.5											
K.LITSFLELHCLSPTELSQSSD <sup>S</sup> EAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
S176											
											
16.5											
31.7											
K.LITSFLELHCLSPTELSQSS <sup>S</sup> DSEAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
S173S176											
											
9.8											
21.0											
K.LITSFLELHCLSPTELS <sup>S</sup> QSS <sup>S</sup> DSEAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
S175S176											
											
7.5											
30.4											
K.LITSFLELHCLSPTELSQ <sup>S</sup> S <sup>S</sup> DSEAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
S173S175S176											
											
19.7											
24.8											
K.LITSFLELHCLSPTELS <sup>S</sup> QSS <sup>S</sup> DSEAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
S168T170S176											
											
4.5											
11.5											
K.LITSFLELHCLS <sup>S</sup> PT <sup>T</sup> ELSQSS <sup>S</sup> DSEAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
T170S173S176											
											
9.4											
12.8											
K.LITSFLELHCLSP <sup>T</sup> EL <sup>S</sup> SQSS <sup>S</sup> DSEAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
S173S175S176											
											
19.4											
39.3											
K.LITSFLELHCLSPTELS <sup>S</sup> QSS <sup>S</sup> DS <sup>S</sup> EAGDPASQS.-											
Chromosome 17 open reading frame 62											
C17orf62											
T170S173S175											
											
9.6											
16.4											
K.LITSFLELHCLSP <sup>T</sup> EL <sup>S</sup> SQSS <sup>S</sup> DSEAGDPASQS.-											
Chromosome 18 open reading frame 9											
CEP76											
S82											
											
17.4											
18.2											
K.ELNFTVDSVEQELPS <sup>S</sup> SPKGPICFDR.Q											
Chromosome 19 open reading frame 13											
LSM14A											
S183											
											
-0.3											
33.4											
R.SS <sup>S</sup> PQLDPLR.K											
Chromosome 19 open reading frame 13											
LSM14A											
S192											
											
31.8											
87.4											
K.S <sup>S</sup> PTMEQAVQTASAHLPAPAAVGR.R											
Chromosome 19 open reading frame 13											
LSM14A											
S216											
											
36.6											
61.9											
R.S <sup>S</sup> PVSTRPLPSASQKA											
Chromosome 19 open reading frame 13											
LSM14A											
S183S192											
											
11.0											
33.3											
R.SS <sup>S</sup> PQLDPLRKS <sup>S</sup> PTMEQAVQTASAHLPAPAAVGR.R											
Chromosome 19 open reading frame 13											
LSM14A											
S182S192											
											
6.4											
25.6											
R.S <sup>S</sup> SPQLDPLRKS <sup>S</sup> PTMEQAVQTASAHLPAPAAVGR.R											
Chromosome 19 open reading frame 13											
LSM14A											
T194											
											
12.8											
57.2											
K.SPT <sup>T</sup> MIEQAVQTASAHLPAPAAVGR.R											
Chromosome 19 open reading frame 13											
LSM14A											
T201											
											
-1.6											
41.2											
K.SPTMEQAVQT <sup>T</sup> ASAHLPAPAAVGR.R											
Chromosome 19 open reading frame 13											
LSM14A											
S178											
											
26.9											
26.0											
K.TQLS <sup>S</sup> QGR.S											
Chromosome 19 open reading frame 13											
LSM14A											
S182S183											
											
30.9											
R.S <sup>S</sup> S <sup>S</sup> PQLDPLRKSPTMEQAVQTASAHLPAPAAVGR.R											
Chromosome 19 open reading frame 29											
CACTIN											
S57S59											
											
100.0											
12.4											
R.RS <sup>S</sup> DS <sup>S</sup> EEER.W											
Chromosome 19 open reading frame 43											
TRIR											
S31S33T35											
											
84.7											
R.WAES <sup>S</sup> SGSGTSPESGDEEVSGAGSSPVSGGVNLFANDGSFLELFK.											
Chromosome 19 open reading frame 43											
TRIR											
S31											
											
16.9											
R.WAES <sup>S</sup> SGSGTSPESGDEEVSGAGSSPVSGGVNLFANDGSFLELFK.											
Chromosome 19 open reading frame 43											
TRIR											
S31S33T35S36											
											
38.1											
R.WAES <sup>S</sup> SGSGTSPESGDEEVSGAGSSPVSGGVNLFANDGSFLELFK.											
Chromosome 19 open reading frame 43											
TRIR											
S31S33											
											
69.6											
R.WAES <sup>S</sup> SGSGTSPESGDEEVSGAGSSPVSGGVNLFANDGSFLELFK.											
Chromosome 19 open reading frame 43											
TRIR											
S39											
											
6.3											
71.2											
R.WAESGSGTSPES <sup>S</sup> GDEEVSGAGSSPVSGGVNLFANDGSFLELFK.											
Chromosome 19 open reading frame 47											
C19orf47											
S213											
											
34.2											
110.6											
R.LGATPETDEDLAWDS <sup>S</sup> DNDSSSVLQYAGVLK.K											
Chromosome 19 open reading frame 47											
C19orf47											
S217											
											
11.4											
R.LGATPETDEDLAWDSND <sup>S</sup> SSSVLQYAGVLK.K											
chromosome 19 open reading frame 7											
ZC3H4											
S1269S1275											
											
27.1											
84.1											
K.TGSGS <sup>S</sup> PFAGNS <sup>S</sup> PAR.E											
chromosome 19 open reading frame 7											
ZC3H4											
S1267S1275											
											
21.7											
74.4											
K.TGS <sup>S</sup> GSPFAGNS <sup>S</sup> PAR.E											
chromosome 19 open reading frame 7											
ZC3H4											
T1106S1114											
											
3.0											
18.7											
R.AAKPGPAEAPSP <sup>T</sup> ASPSGDAS <sup>S</sup> PPATAPYDPR.V											
chromosome 19 open reading frame 7											
ZC3H4											
S1104S1110											
											
19.2											
35.4											
R.AAKPGPAEAPSP <sup>T</sup> ASPS <sup>S</sup> GDASPPATAPYDPR.V											
chromosome 19 open reading frame 7											
ZC3H4											
S807S808											
											
12.4											
88.9											
R.ENEEGDTGNWY <sup>S</sup> S <sup>S</sup> DEDEGGSSVTSLK.T											
chromosome 19 open reading frame 7											
ZC3H4											
T802S808											
											
2.9											
27.7											
R.ENEEGDT <sup>T</sup> GNWYS <sup>S</sup> DEDEGGSSVTSLK.T											
chromosome 19 open reading frame 7											
ZC3H4											
S159											
											
30.1											
28.8											
R.EYS <sup>S</sup> PPYAPSHQYPPSHATPLPK.K											
chromosome 19 open reading frame 7											
ZC3H4											
S92S94											
											
100.0											
12.9											
K.HHS <sup>S</sup> DS <sup>S</sup> DEEK.S											
chromosome 19 open reading frame 7											
ZC3H4											
S1104S1114											
											
5.6											
29.7											
R.AAKPGPAEAPSP <sup>T</sup> ASPSGDAS <sup>S</sup> PPATAPYDPR.V											
chromosome 19 open reading frame 7											
ZC3H4											
Y806S807											
											
12.9											
88.1											
R.ENEEGDTGNWY <sup>S</sup> S <sup>S</sup> SDEDEGGSSVTSLK.T											
chromosome 19 open reading frame 7											
ZC3H4											
T1106S1110											
											
1.9											
30.7											
R.AAKPGPAEAPSP <sup>T</sup> ASPS <sup>S</sup> GDASPPATAPYDPR.V											
chromosome 19 open reading frame 7											
ZC3H4											
T802Y806											
											
9.2											
17.2											
R.ENEEGDT <sup>T</sup> GNWY <sup>S</sup> SDEDEGGSSVTSLK.T											
chromosome 19 open reading frame 7											
ZC3H4											
T802S807											
											
12.4											
61.9											
R.ENEEGDT <sup>T</sup> GNWYS <sup>S</sup> SDEDEGGSSVTSLK.T											
Chromosome 2 open reading frame 17											
RETREG2											
T279S281S283											
											
37.6											
29.1											
K.NAPPGDEPLAET <sup>T</sup> ES <sup>S</sup> ES <sup>S</sup> EALAGFSPVDWK.K											
Chromosome 2 open reading frame 17											
RETREG2											
S385											

Peak Area	Protein Name	Gene	Phosphosites	CarT		RajIB		Ascor	MOWSE	Sequence
				5 6 6 6	5 6 6 6	5 6 6 6	5 6 6 6			
<div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> </div>										
	Chromosome 20 open reading frame 172 DSN1 protein	S57						8.2	17.9	R.IHLGS <sup>S</sup> SPK.K
	Chromosome 20 open reading frame 172 DSN1 protein	S27528						12.5	36.3	K.THDHQL <sup>ES</sup> S <sup>S</sup> LS <sup>S</sup> PVEVFAK.T
	Chromosome 20 open reading frame 74 RALGAPA	S820S821						10.6	45.1	R.RS <sup>S</sup> S <sup>S</sup> PAELDLKDDLQOTGQK.C
	Chromosome 20 open reading frame 74 RALGAPA	S696						33.6	38.5	R.SFS <sup>S</sup> LSWR.S
	Chromosome 20 open reading frame 74 RALGAPA	S373S375						10.1	33.8	R.RL <sup>S</sup> N <sup>S</sup> SLCSIEEEHR.M
	Chromosome 22 open reading frame 19 THOCS protein	T328						100.0	33.0	R.RRPT <sup>S</sup> LGVQLDDK.R
	Chromosome 22 open reading frame 19 THOCS protein	S307S312						2.0	16.1	K.ALFKPPEDS <sup>S</sup> QDES <sup>S</sup> SDSAEEQTTKR.R
	Chromosome 22 open reading frame 19 THOCS protein	S312S314						25.5	45.6	K.ALFKPPEDSQDES <sup>S</sup> DS <sup>S</sup> DAEEEQTTK.R
	Chromosome 22 open reading frame 19 THOCS protein	S307S314						8.2	26.8	K.ALFKPPEDS <sup>S</sup> QDES <sup>S</sup> DAEEEQTTKR.R
	Chromosome 5 open reading frame 22 C5orf22	Y435						11.9	43.4	R.ALYGNLDLQVY <sup>S</sup> AAESPPS.-
	Chromosome 5 open reading frame 22 C5orf22	Y427						0.1	16.4	R.ALY <sup>S</sup> GNLDLQVYAAESPPS.-
	Chromosome 5 open reading frame 37 POC5	S53						20.3	58.6	R.ISTHDLHSQGNNS <sup>S</sup> EVR.E
	Chromosome 6 open reading frame 108 DNPH1	S169						32.7	56.7	R.YFEADPPGQVAAS <sup>S</sup> PDPTT.-
	Chromosome 6 open reading frame 108 DNPH1	S12						29.9	42.3	R.SES <sup>S</sup> WER.G
	Chromosome 6 open reading frame 203 C6orf203	S110S116						12.2	35.3	K.VDEEDSD <sup>ES</sup> S <sup>S</sup> HHDEM <sup>S</sup> SEQEELEDQPTVK.N
	Chromosome 6 open reading frame 203 C6orf203	S106S116						24.3	43.7	K.VDEEDS <sup>S</sup> DEESHDEM <sup>S</sup> SEQEELEDQPTVK.N
	Chromosome 6 open reading frame 206 RSPH9	T30						92.0	12.5	R.ASLT <sup>S</sup> SLMLVK.R
	Chromosome 6 open reading frame 209 LMBRD1	S528S531						6.6	15.3	K.SVIEGVDES <sup>S</sup> DIS <sup>S</sup> DDEPSVYSA.-
	Chromosome 6 open reading frame 93 LTV1	S352S355						13.6	34.8	K.EKWDCES <sup>S</sup> ICS <sup>S</sup> TYSLYNHPQLIK.Y
	Chromosome 6 open reading frame 93 LTV1	S352S355Y357						19.7	19.0	K.EKWDCES <sup>S</sup> ICS <sup>S</sup> TY <sup>S</sup> S <sup>S</sup> LYNHPQLIK.Y
	Chromosome 6 open reading frame 93 LTV1	S331						12.7	23.3	K.LNTLEPLEDQQLPMINELDES <sup>S</sup> EEEEMITVLEEAK.E
	Chromosome 6 open reading frame 93 LTV1	T314						13.9	18.7	K.LNT <sup>S</sup> LEPLEDQQLPMINELDESEEEEMITVLEEAK.E
	Chromosome 6 open reading frame 93 LTV1	S355T356Y357						0.3	12.4	K.EKWDCESICS <sup>S</sup> TY <sup>S</sup> S <sup>S</sup> LYNHPQLIK.Y
	Chromosome 7 open reading frame 47 PPP1R3S	S52						42.6	28.2	R.APVPEPGLDLSLSPRDS <sup>S</sup> QPR.H
	Chromosome 7 open reading frame 47 PPP1R3S	T84S87						100.0	22.4	R.FRLT <sup>S</sup> PPS <sup>S</sup> PVR.S
	Chromosome 7 open reading frame 50 C7orf50	S175						100.0	46.9	R.ELDEES <sup>S</sup> DPPLPGR.A
	Chromosome 9 open reading frame 142 PAXX	S148						32.3	51.9	R.LAAAEATAV <sup>S</sup> PR.K
	Chromosome 9 open reading frame 142 PAXX	S152						100.0	35.8	R.KS <sup>S</sup> PRPAGPQLFLPDQDQPR.G
	Chromosome 9 open reading frame 82 CAAP1 protein	S203						106.6	108.6	K.ILEGDNGMDS <sup>S</sup> DMEEEADGSK.M
	Chromosome 9 open reading frame 82 CAAP1 protein	S312						8.9	29.3	K.SVNEILGLAES <sup>S</sup> PNEPK.A
	Chromosome 9 open reading frame 82 CAAP1 protein	S311						111.6	38.6	K.SVNEILGLAES <sup>S</sup> SPNEPK.A
	Chromosome 9 open reading frame 86 RABL6	S597S598						54.3	80.9	R.LKNDSDLFLGLEEAGPKES <sup>S</sup> SEEGK.E
	Chromosome 9 open reading frame 86 RABL6	S382S384						100.0	84.7	K.AAQQDS <sup>S</sup> DS <sup>S</sup> DGEALGGNPMVAGFQDDVDLEDQPR.G
	Chromosome 9 open reading frame 86 RABL6	S411S421T425						8.1	42.6	R.GS <sup>S</sup> PPLPAGPVPS <sup>S</sup> QDIT <sup>S</sup> LSSEEEAEVAAPT.K
	Chromosome 9 open reading frame 86 RABL6	S553T556						100.0	84.9	R.DOPS <sup>S</sup> DVT <sup>S</sup> DEDEGPAEP PPPK.L
	Chromosome 9 open reading frame 86 RABL6	S411T425S427						0.2	35.3	R.GS <sup>S</sup> PPLPAGPVPSQDIT <sup>S</sup> LS <sup>S</sup> SEEEAEVAAPT.K
	Chromosome 9 open reading frame 86 RABL6	S411S421S428						14.3	33.1	R.GS <sup>S</sup> PPLPAGPVPS <sup>S</sup> QDITLS <sup>S</sup> SEEEAEVAAPT.K
	Chromosome 9 open reading frame 86 RABL6	S411S427S428						16.6	56.7	R.GS <sup>S</sup> PPLPAGPVPSQDITLS <sup>S</sup> S <sup>S</sup> SEEEAEVAAPT.K
	Chromosome 9 open reading frame 86 RABL6	S411T425S428						12.4	19.7	R.GS <sup>S</sup> PPLPAGPVPSQDIT <sup>S</sup> LS <sup>S</sup> SEEEAEVAAPT.K
	Chromosome associated kinesin KIF4A KIF4A	T1161						17.2	40.2	K.LEDPTTEVTRGLSFFNPVCAT <sup>S</sup> PNSK.I
	Chromosome associated kinesin KIF4A KIF4A	T799S801						30.0	24.6	R.RRT <sup>S</sup> FS <sup>S</sup> LTEVR.G
	Chromosome associated kinesin KIF4A KIF4A	S801						17.4	47.3	R.TFS <sup>S</sup> LTEVR.G
	Chromosome condensation 1 RCC1	S11						100.0	13.0	R.S <sup>S</sup> PPADAIPK.S
	Chromosome condensation protein NCAPG	S674						39.1	57.4	K.TLHCEGTEIN <sup>S</sup> DDEQESK.E
	Chromosome condensation protein NCAPG	T968S973						21.0	29.7	R.CQT <sup>S</sup> AEADS <sup>S</sup> ESDHEVPEPESEM.K
	Chromosome condensation protein NCAPG	S390						41.9	56.8	R.GDFS <sup>S</sup> YIGNLMTK.E
	NCAPG	S1015						100.0	69.0	K.LNLQAQLNEDLS <sup>S</sup> .-
	Chromosome condensation protein NCAPG	S1002						25.8	30.3	K.S <sup>S</sup> KLNLAQLNEDLS.-
	Chromosome condensation protein NCAPG	S973S975						9.2	34.7	R.CQTAEADS <sup>S</sup> ES <sup>S</sup> DHEVPEPESEM.K
	CIC CIC	S1373S1382						17.5	31.0	R.FAELPEFRPEEVLPS <sup>S</sup> PTLQSLATS <sup>S</sup> PR.A
	CIC CIC	S1373S1378						7.7	12.9	R.FAELPEFRPEEVLPS <sup>S</sup> PTLOS <sup>S</sup> LATSPR.A
	CIC CIC	T1375S1382						7.7	18.2	R.FAELPEFRPEEVLPSPT <sup>S</sup> LQSLATS <sup>S</sup> PR.A
	CIC CIC	S301						-0.4	31.7	R.SMS <sup>S</sup> ETGTAAAPGVSELLSVAQTLSSDSTK.A
	CIC CIC	S1373T1381						19.1	25.2	R.FAELPEFRPEEVLPS <sup>S</sup> PTLQSLAT <sup>S</sup> SPR.A
	Cingulin CGN	S338						100.0	40.9	R.KVS <sup>S</sup> LVLEK.M
	Cingulin CGN	S1182S1191						12.8	15.6	K.NEGLSSDEEFD <sup>S</sup> VYDPSSIAS <sup>S</sup> LLTESNLQTSSC.-
	Cisplatin resistance associated overexpressed protein	T419S431						10.0	29.2	K.NEVMGT <sup>S</sup> SEDIKSEGDTQS <sup>S</sup> N.-
	Cisplatin resistance associated overexpressed protein	S425S431						10.8	22.2	K.NEVMGTSEDIKS <sup>S</sup> EGDTQS <sup>S</sup> N.-
	Cisplatin resistance associated overexpressed protein	S425T429						2.3	11.4	K.NEVMGTSEDIKS <sup>S</sup> EGDT <sup>S</sup> QSN.-
	Citron CIT	S398						10.7	11.9	K.NSWVS <sup>S</sup> SPCQLSPGFSGEELPFVGFYSKY.A
	Claspin CLSPN	S225						41.7	83.1	K.DLFETGLEDENNS <sup>S</sup> PLEDEESLESIR.A
	Claspin CLSPN	T217						2.8	24.9	K.DLFET <sup>S</sup> GLEDENNSPLEDEESLESIR.A



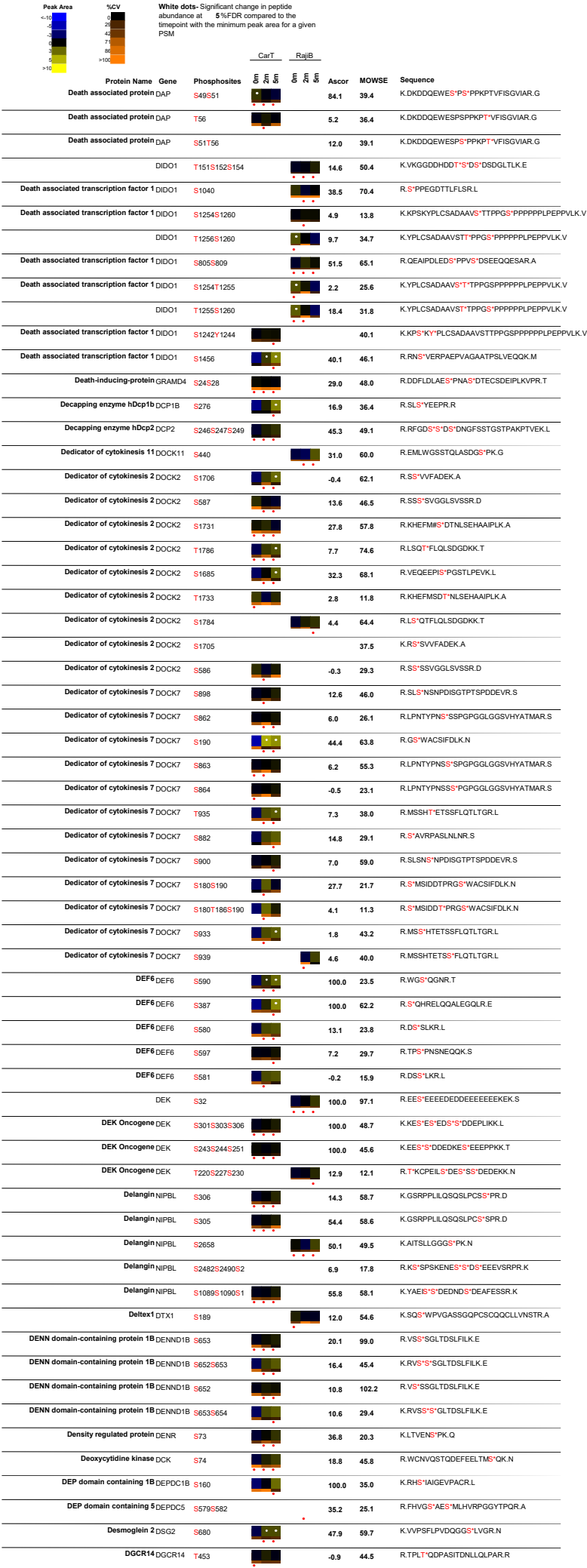


Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajIB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Coiled-coil domain containing 86	CDC86	S102Y109				2.7	21.5	R.QQDLHLE <sup>S</sup> *PQROPEY <sup>S</sup> *SPESPR.C
		Coiled-coil domain containing 86	CDC86	S102S110				14.9	31.9	R.QQDLHLE <sup>S</sup> *PQROPEY <sup>S</sup> *SPESPR.C
		Coiled-coil domain containing 86	CDC86	S217				8.9	48.8	R.KGS <sup>S</sup> *SQAPASK.K
		Coiled-coil domain containing 86	CDC86	T146					15.6	K.EELT <sup>S</sup> *PGAPQHQLPPVPGSPPEYPGQQAPGPEPSQPLELT <sup>S</sup> PR.A
		Coiled-coil domain containing 94	CDC94	S211S213				87.9	53.8	R.LLED <sup>S</sup> *D <sup>S</sup> *EDEAAPSPLOPALRPNPNTAILDEAPKPK.R
		Coiled-coil domain containing 94	CDC94	S305S306S316				6.7	17.7	K.EANPTPLTPGAS <sup>S</sup> *S <sup>S</sup> *LSQLGAYLD <sup>S</sup> *DDNSGN.-
			CDC94	S308Y313S316				15.7	36.6	K.EANPTPLTPGASSL <sup>S</sup> *QLGAY <sup>S</sup> *LD <sup>S</sup> *DDNSGN.-
		Coiled-coil domain containing 94	CDC94	Y313S316S322				6.5	15.6	K.EANPTPLTPGASSLSQLGAY <sup>S</sup> *LD <sup>S</sup> *DDNSG <sup>S</sup> *N.-
		Coiled-coil domain containing 94	CDC94	S308Y313S319				1.3	23.0	R.KEANPTPLTPGASSL <sup>S</sup> *QLGAY <sup>S</sup> *LDDSD <sup>S</sup> *NGSN.-
		Coiled-coil domain containing 94	CDC94	Y313S316				13.5	25.7	K.EANPTPLTPGASSLSQLGAY <sup>S</sup> *LD <sup>S</sup> *DDNSGN.-
			CDC94	Y313S316S319				12.5	34.2	K.EANPTPLTPGASSLSQLGAY <sup>S</sup> *LD <sup>S</sup> *DD <sup>S</sup> *NGSN.-
		Coiled-coil domain containing 94	CDC94	S211S213S220				57.9	14.1	R.LLED <sup>S</sup> *D <sup>S</sup> *EDEAAP <sup>S</sup> *PLQPALRPNPNTAILDEAPKPK.R
		Coiled-coil domain containing 94	CDC94	S319				-0.5	16.2	K.EANPTPLTPGASSLSQLGAYLSDSD <sup>S</sup> *NGSN.-
		Coiled-coil domain containing 94	CDC94	S308S316				7.8	27.2	K.EANPTPLTPGASSL <sup>S</sup> *QLGAYLD <sup>S</sup> *DDNSGN.-
		Coiled-coil domain containing 94	CDC94	Y313S319S322				0.8	27.2	R.KEANPTPLTPGASSLSQLGAY <sup>S</sup> *LDDSD <sup>S</sup> *NGS <sup>S</sup> *N.-
		Coiled-coil domain containing 94	CDC94	S308Y313S322				3.7	25.1	R.KEANPTPLTPGASSL <sup>S</sup> *QLGAY <sup>S</sup> *LDDSDSNG <sup>S</sup> *N.-
		Coiled-coil domain containing 94	CDC94	S308S316S319				1.3	18.1	R.KEANPTPLTPGASSL <sup>S</sup> *QLGAYLD <sup>S</sup> *DD <sup>S</sup> *NGSN.-
		Coiled-coil domain containing 97	CDC97	S257				100.0	49.9	R.LLQQQEEEEACLEEEEEED <sup>S</sup> *DEEDQR.S
		Coiled-coil domain containing 97	CDC97	S221				17.5	37.1	R.TPTHQPKPGSPGRPACPL <sup>S</sup> *NLLLSQYEER.E
		Coiled-coil domain containing 97	CDC97	S212				22.9	37.2	R.TPTHQPKPGS <sup>S</sup> *PGRPACPLNLLLSQYEER.E
		Coiled-coil domain containing 97	CDC97	T202T204				-2.9	30.1	R.T <sup>S</sup> *PT <sup>S</sup> *HQPMPKPGSPGRPACPLNLLLSQYEER.E
		Coiled-coil domain containing 97	CDC97	T204S212				8.4	37.3	R.TPT <sup>S</sup> *HQPMPKGS <sup>S</sup> *PGRPACPLNLLLSQYEER.E
		Coiled-coil domain containing 97	CDC97	S337				98.3	22.6	R.YFDEEEDAP <sup>S</sup> *PELDGD.-
		Coiled-coil domain containing 98	ABRAXAS	S386S387T390				100.0	36.1	K.MS <sup>S</sup> *S <sup>S</sup> *PET <sup>S</sup> *DEEIEK.M
		Coiled-coil domain-containing protein 149	CDC149	T337S341S354				1.6	11.5	R.T <sup>S</sup> *LEV <sup>S</sup> *GLWSLPLSYNVS <sup>S</sup> *VGFGRGK.D
		Coiled-coil-helix-coiled-coil-helix domain containing 3	CHCHD3	S50				13.9	111.3	R.YS <sup>S</sup> *GAYGASVSDEELK.R
		Coiled-coil-helix-coiled-coil-helix domain containing 3	CHCHD3	Y49				32.8	85.2	R.Y <sup>S</sup> *SGAYGASVSDEELK.R
		Collin COIL		T122				100.0	35.0	R.AFQLEEGET <sup>S</sup> *EPDCK.Y
		Cold shock domain protein A	YBX3	S201S203S204				54.1	45.5	R.NYAGEEEEEGS <sup>S</sup> *GS <sup>S</sup> *EGFDPPATDR.Q
		Cold shock domain protein A	YBX3	S203S204				8.7	26.6	R.NYAGEEEEEGS <sup>S</sup> *S <sup>S</sup> *EGFDPPATDR.Q
		Cold shock domain protein A	YBX3	S204				-0.2	24.8	R.NYAGEEEEEGS <sup>S</sup> *S <sup>S</sup> *EGFDPPATDR.Q
		Cold shock domain protein A	YBX3	S203					19.7	R.NYAGEEEEEGS <sup>S</sup> *SEGFDPPATDR.Q
		Cold shock domain protein A	YBX3	Y192S201S203				50.7	15.8	R.NY <sup>S</sup> *AGEEEEEGS <sup>S</sup> *GS <sup>S</sup> *SEGFDPPATDR.Q
		Collagen type IV alpha 3 binding protein	COL4A3B	S132S147				8.8	31.2	R.HGS <sup>S</sup> *MVSLSVSGASGYATS <sup>S</sup> *TSSFKK.G
		Collagen type IV alpha 3 binding protein	COL4A3B	S132T146				5.7	13.2	R.HGS <sup>S</sup> *MVSLSVSGASGYAT <sup>S</sup> *TSSFKK.G
		Conserved nuclear protein	NHN1 ZC3H18	S46				104.3	73.5	R.AS <sup>S</sup> *DLEDEESAAR.G
		Conserved nuclear protein	NHN1 ZC3H18	S534				17.8	51.6	K.LGVSV <sup>S</sup> *PSR.A
		Conserved nuclear protein	NHN1 ZC3H18	S78				63.6	78.6	K.S <sup>S</sup> *QQQDSEVNLSR.G
		Conserved nuclear protein	NHN1 ZC3H18	S532S534				15.5	31.7	K.LGVSV <sup>S</sup> *PSR.A
		Conserved nuclear protein	NHN1 ZC3H18	S487				40.8	37.2	R.S <sup>S</sup> *PQPPSR.Q
		Conserved nuclear protein	NHN1 ZC3H18	S868				100.0	46.1	R.LGS <sup>S</sup> *PKPER.Q
		Conserved nuclear protein	NHN1 ZC3H18	S78S83				71.2	41.6	K.S <sup>S</sup> *QQQDS <sup>S</sup> *EVNLSR.G
		Conserved nuclear protein	NHN1 ZC3H18	S118				6.5	12.4	R.DEAS <sup>S</sup> *VTR.E
		Conserved nuclear protein	NHN1 ZC3H18	S67S74				14.9	20.7	R.GPSQEEEDNH <sup>S</sup> *DEEDRAS <sup>S</sup> *EPK.S
		Conserved nuclear protein	NHN1 ZC3H18	S59S67S74					11.1	R.GPS <sup>S</sup> *QEEEDNH <sup>S</sup> *DEEDRAS <sup>S</sup> *EPKSQQQDSEVNLSR.G
		Conserved nuclear protein	NHN1 ZC3H18	S59S67S74S78					16.7	R.GPS <sup>S</sup> *QEEEDNH <sup>S</sup> *DEEDRAS <sup>S</sup> *EPKS <sup>S</sup> *QQQDSEVNLSR.G
		Conserved nuclear protein	NHN1 ZC3H18	S746				40.7	17.4	R.S <sup>S</sup> *PAPAQTR.K
		Conserved nuclear protein	NHN1 ZC3H18	S117				13.8	23.8	R.DEAS <sup>S</sup> *SVTR.E
		Conserved nuclear protein	NHN1 ZC3H18	S59S67S78				5.2	14.7	R.GPS <sup>S</sup> *QEEEDNH <sup>S</sup> *DEEDRASEPKS <sup>S</sup> *QQQDSEVNLSR.G
		Conserved nuclear protein	NHN1 ZC3H18	S532				-7.3	45.6	K.KKLGVS <sup>S</sup> *VSPSR.A
		Conserved nuclear protein	NHN1 ZC3H18	S67S74S78S83				8.5	11.9	R.GPSQEEEDNH <sup>S</sup> *DEEDRAS <sup>S</sup> *EPKS <sup>S</sup> *QQQDS <sup>S</sup> *EVNLSR.G
		Conserved nuclear protein	NHN1 ZC3H18	T851					15.3	K.RPNT <sup>S</sup> *SPDR.G
		Conserved oligomeric Golgi complex subunit 1 (Fragment)	COG1	S113S114T115				100.0	13.5	R.RS <sup>S</sup> *S <sup>S</sup> *T <sup>S</sup> *AWLPR.S
		Conserved oligomeric Golgi complex subunit 1 (Fragment)	COG1	S113S114				5.2	23.7	R.RS <sup>S</sup> *S <sup>S</sup> *T <sup>S</sup> *AWLPR.S
		Conserved oligomeric Golgi complex subunit 1 (Fragment)	COG1	S114T115				6.7	16.8	R.RS <sup>S</sup> *T <sup>S</sup> *T <sup>S</sup> *AWLPR.S
		Copper homeostasis protein cutC homolog	CUTC	S17				100.0	18.6	R.ARIPS <sup>S</sup> *GK.A
		Core binding factor, beta subunit	CBFB	S173				46.9	89.0	R.QQDP <sup>S</sup> *PGSNLGGGDDLK.L
		Coronin 7	CORO7-	S21				20.7	18.5	R.RES <sup>S</sup> *WISDIR.A
		Coronin 7	CORO7-	S462				39.8	82.2	R.S <sup>S</sup> *LQSLGPPSK.F
		CRDBP/GF2BP1		S181				100.0	79.9	R.QGS <sup>S</sup> *PVAAGAPAK.Q
		CRK	CRK	T42				6.5	97.1	R.DSS <sup>S</sup> *T <sup>S</sup> *SPGDYVLSVENS <sup>S</sup> .V
		CRK	CRK	S40				7.8	14.0	R.DS <sup>S</sup> *STS <sup>S</sup> *SPGDYVLSVENS <sup>S</sup> .V

Peak Area	%CV			CarT		RajiB		Ascor	MOWSE	Sequence
				5	6	5	6			
<10	0			5	6	5	6			
10-20	1			5	6	5	6			
20-30	2			5	6	5	6			
30-40	3			5	6	5	6			
40-50	4			5	6	5	6			
50-60	5			5	6	5	6			
60-70	6			5	6	5	6			
70-80	7			5	6	5	6			
80-90	8			5	6	5	6			
90-100	9			5	6	5	6			
>100	10			5	6	5	6			
White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM										
Protein Name	Gene	Phosphosites								
CRK CRK		S41						9.5	74.5	R.DS <sup>S</sup> *TSPGDYVLSVSENSR.V
CRKL CRKL		S107						2.0	33.0	R.YP <sup>S</sup> *PPMGVSAPNLPTAEDNLEYVR.T
CRKL CRKL		S112						10.6	49.2	R.YPSPPMGS <sup>S</sup> *VSAPNLPTAEDNLEYVR.T
CRKL CRKL		S195							13.8	R. ME <sup>S</sup> *EVGIGEDALLAVAGDPTTEDI DAUGGSGRAITDI RSTYMIDUEA
Cross immune reaction antigen PCIA1	DDA1	S95						50.6	54.7	R.TD <sup>S</sup> *PDMHEDT.-
CRSP2 MED14		S995						12.0	16.1	R.SVNEDDNPPSPIGGDMMD <sup>S</sup> *LISQLQPPQQQPFPK.Q
CRSP2 MED14		S998						37.2	17.8	R.SVNEDDNPPSPIGGDMMDLSI <sup>S</sup> *QLQPPQQQPFPK.Q
CRSP2 MED14		S986						2.6	20.3	R.SVNEDDNPP <sup>S</sup> *PIGGDMMDLSISQLQPPQQQPFPK.Q
CRSP2 MED14		S977							10.9	R.S <sup>S</sup> *VNEDDNPPSPIGGDMMDLSISQLQPPQQQPFPK.Q
CRSP2 MED14		S977S995						2.2	22.1	R.S <sup>S</sup> *VNEDDNPPSPIGGDMMD <sup>S</sup> *LISQLQPPQQQPFPK.Q
CTD phosphatase, subunit 1	CTDP1	S869S872						24.7	39.7	K.EVDDLGE <sup>S</sup> *DD <sup>S</sup> *DSEK.R
CTP synthetase 2	CTPS2	S568S571						13.4	27.2	K.LSSSDRY <sup>S</sup> *DAS <sup>S</sup> *DDSFSEPR.I
CTP synthetase 2	CTPS2	S562S563S576						3.3	11.1	K.LS <sup>S</sup> *SDRYSDASDDSF <sup>S</sup> *EPR.I
CTP synthetase 2	CTPS2	S563Y567S574						1.6	15.5	K.LS <sup>S</sup> *SDRY <sup>S</sup> *SDASDD <sup>S</sup> *FSEPR.I
CTP synthetase 2	CTPS2	Y567S568S574						0.3	11.6	K.LSSSDRY <sup>S</sup> *S <sup>S</sup> *DASDD <sup>S</sup> *FSEPR.I
CTP synthetase 2	CTPS2	S571S574S576						15.0	21.7	K.LSSSDRYSDA <sup>S</sup> *DD <sup>S</sup> *F <sup>S</sup> *EPR.I
CTP synthetase 2	CTPS2	S563S571						2.4	34.9	K.LS <sup>S</sup> *SDRYSDA <sup>S</sup> *DDSFSEPR.I
CTP synthetase 2	CTPS2	S563Y567S568						5.3	14.9	K.LS <sup>S</sup> *SDRY <sup>S</sup> *S <sup>S</sup> *DASDDSFSEPR.I
CTP synthetase 2	CTPS2	S563Y567						6.3	11.8	K.LS <sup>S</sup> *SDRY <sup>S</sup> *SDASDDSFSEPR.I
CTP synthetase 2	CTPS2	S563S564Y567						1.1	15.9	K.LS <sup>S</sup> *S <sup>S</sup> *DRY <sup>S</sup> *SDASDDSFSEPR.I
CTP synthetase 2	CTPS2	S564S571						2.5	17.6	K.LSS <sup>S</sup> *DRYSDA <sup>S</sup> *DDSFSEPR.I
CTP synthetase 2	CTPS2	S568S571S574						7.4	18.8	K.LSSSDRY <sup>S</sup> *DAS <sup>S</sup> *DD <sup>S</sup> *FSEPR.I
CUGBP Elav-like family member 1	CELF1 (Fragment)	S22						19.1	24.0	K.LDLPEMMVDHCSLNS <sup>S</sup> *PVS <sup>S</sup> *K
CUGBP Elav-like family member 1	CELF1 (Fragment)	S18						26.1	11.4	K.LDLPEMMVDHC <sup>S</sup> *LNSSPVSK.K
Cullin 4A	CUL4A	S10						29.8	70.3	R.KG <sup>S</sup> *FSALVGR.T
Cutaneous T cell lymphoma tumor antigen RBM26		S127						20.7	11.7	R.LNH <sup>S</sup> *PPQSSR.Y
Cutaneous T cell lymphoma tumor antigen RBM26		T614						2.3	11.0	R.EGSTQQLQ <sup>T</sup> *TSPKPLVQQIPLPVK.Q
CYBR	CYTIP	S65						-0.3	59.7	R.SS <sup>S</sup> *LSDFSWSQR.K
CYBR	CYTIP	S66						30.2	70.3	R.SS <sup>S</sup> *LSDFSWSQR.K
Cyclic GMP inhibited phosphodiesterase B	PDE3B	S295S296						32.9	69.6	R.RR <sup>S</sup> *S <sup>S</sup> *CVSLGETAASYYSCK.I
Cyclic GMP inhibited phosphodiesterase B	PDE3B	S981						-0.1	12.2	R.SS <sup>S</sup> *PQLAKL
Cyclic nucleotide gated channel beta 1	CNGB1	T1021						25.1	17.2	K.SVLV <sup>T</sup> *LK.A
Cyclin A1	CCNA1	T96T102						100.0	14.6	R.RT <sup>T</sup> *CGQGII <sup>T</sup> *R.I
Cyclin B2	CCNB2V	S92						32.3	59.7	K.GP <sup>S</sup> *PTPEDVSMKEENLQAFSDALLCK.I
Cyclin dependent kinase 2	CDK2	T160						10.2	42.2	R.TY <sup>T</sup> *HEVITLWYR.A
Cyclin dependent kinase 7	CDK7	S164						45.1	40.4	K.SFG <sup>S</sup> *PNR.A
CDKN3		S14S15						21.4	77.0	M.KPPSSIQTSEFD <sup>S</sup> *S <sup>S</sup> *DEEPIEDQTPHISWLSLR.V
Cyclin dependent kinase inhibitor 3	CDKN3	S10S14						19.0	46.8	M.KPPSSIQT <sup>S</sup> *EFD <sup>S</sup> *S <sup>S</sup> *DEEPIEDQTPHISWLSLR.V
Cyclin dependent kinase inhibitor 3	CDKN3	S5S6							60.3	M.KPP <sup>S</sup> *S <sup>S</sup> *IQTSEFDSSDEEPIEDQTPHISWLSLR.V
Cyclin G associated kinase GAK		S826S829						25.8	52.4	R.DE <sup>S</sup> *EV <sup>S</sup> *DEGGSPISSEGQEP.R.A
CCNH	T315							67.5	56.6	K.HEEEEE <sup>Y</sup> *DDDLVESL.-
Cyclin L1	CCNL1	S445						100.0	30.3	R.HHNHG <sup>S</sup> *PHLK.A
Cyclin L1	CCNL1	S352						27.8	67.6	K.AEEK <sup>S</sup> *PISINVK.T
Cyclin L1	CCNL1	S341							23.7	K.GLNPDGTALSTLGGFSPASKP <sup>S</sup> *SPR.E
Cyclin L1	CCNL1	S335S341						23.3	13.1	K.GLNPDGTALSTLGGF <sup>S</sup> *PASKP <sup>S</sup> *SPR.E
Cyclin L1	CCNL1	S335S338						14.0	14.0	K.GLNPDGTALSTLGGF <sup>S</sup> *PAS <sup>S</sup> *KPSSPR.E
Cyclin L1	CCNL1	S335S342						18.6	19.4	K.GLNPDGTALSTLGGF <sup>S</sup> *PASKP <sup>S</sup> *PR.E
Cyclin L1	CCNL1	S338S341						15.0	11.0	K.GLNPDGTALSTLGGFSPA <sup>S</sup> *KP <sup>S</sup> *SPR.E
Cyclin L2	CCNL2	S330						14.2	32.2	R.GLLPGGTQVLDTG <sup>S</sup> *GFSPAPK.L
Cyclin L2	CCNL2	S327						6.5	34.3	R.GLLPGGTQVLDTG <sup>S</sup> *GFSPAPK.L
Cyclin Y-like 1	CCNYL1	S274						25.1	85.8	R.SF <sup>S</sup> *ADNFIGQR.S
Cyclin Y-like 1	CCNYL1	S272						14.0	73.7	R.S <sup>S</sup> *FSADNFIGQR.S
Cyclin-dependent kinase 9 (Fragment)	CDK9	S56						12.2	44.9	R. I DADIGIAAASSGGGGGGGGGGGGGGAAGAABDGI SSTTTEED G
Cyclin-dependent kinase 9 (Fragment)	CDK9	S26							64.1	R. I DADIGIAAASSGGGGGGGGGGGGGGAAGAABDGI SSTTTEED G
Cyclin-dependent kinase 9 (Fragment)	CDK9	T54						12.2	68.7	R. I DADIGIAAASSGGGGGGGGGGGGGGAAGAABDGI SSTTTEED G
Cyldromatosis gene protein CYLD		S418S422						37.2	26.0	R.FH <sup>S</sup> *LPF <sup>S</sup> *LTLM
Cyldromatosis gene protein CYLD		S398						15.1	18.2	K.SLTEISTDFDR <sup>S</sup> *SPPLQPPVNSLTITNR.F
Cyldromatosis gene protein CYLD		S399						4.0	35.5	K.SLTEISTDFDR <sup>S</sup> *PPLQPPVNSLTITNR.F
Cyldromatosis gene protein CYLD		S392						-0.1	25.6	K.SLTEI <sup>S</sup> *TDFDRSSPPLQPPVNSLTITNR.F
Cysteine and glycine rich protein 1	CSRPI	S192						100.0	72.0	K.GFGFGQGAGALVH <sup>S</sup> *E.-
Cysteine string protein	DNAJC5	S12						1.4	84.6	R.SLST <sup>S</sup> *GESLYHVLGLDK.N
Cysteine string protein	DNAJC5	S10						25.6	139.0	R.SL <sup>S</sup> *TSGESLYHVLGLDK.N

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites					
		Cysteine string protein	DNAJC5	T11S12			8.9	77.1	R.SLST* <b>S</b> *GESLYHVLGLDK.N
		Cysteine string protein	DNAJC5	S10S15			14.2	90.6	R.SLS* <b>T</b> *SGES*LYHVLGLDK.N
		Cysteine string protein	DNAJC5	T11			-0.3	82.3	R.SLST* <b>S</b> *SGESLYHVLGLDK.N
		Cysteine string protein	DNAJC5	T11S15			21.6	114.2	R.SLST* <b>S</b> *GES*LYHVLGLDK.N
		Cysteine string protein	DNAJC5	S12S15			12.9	104.8	R.SLST* <b>S</b> *GE* <b>S</b> *LYHVLGLDK.N
		Cysteine string protein	DNAJC5	S10T11			7.9	64.8	R.SLS* <b>T</b> *SGESLYHVLGLDK.N
		Cysteine string protein	DNAJC5	S10S12			6.6	37.2	R.SLS* <b>T</b> * <b>S</b> *GESLYHVLGLDK.N
		Cysteine string protein	DNAJC5	S8S15			4.0	44.1	R.S* <b>L</b> STSGES*LYHVLGLDK.N
		Cytidine 5-prime triphosphate synthetase	CTPS1	S574S575			14.3	108.2	R.SGSS* <b>S</b> *PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S574S575			15.6	63.9	R.S* <b>G</b> SS* <b>S</b> *PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S573S574			18.0	47.8	R.DTYSDRS* <b>G</b> * <b>S</b> * <b>S</b> *PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S568S573S574			-0.4	25.5	R.DTYS* <b>D</b> RS <b>G</b> * <b>S</b> * <b>S</b> *PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S573S574			20.4	45.0	R.SG <b>S</b> * <b>S</b> *SPDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S568			16.9	21.9	R.DTYS* <b>D</b> R.S
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S574			6.0	24.8	R.S* <b>G</b> SS*SPDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S578			4.4	18.2	R.S* <b>G</b> SSSPD <b>S</b> *EITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	Y567S568S573			8.3	30.4	R.DT <b>Y</b> * <b>S</b> * <b>D</b> RS <b>G</b> * <b>S</b> * <b>S</b> *PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	Y567S568S571			13.2	46.7	R.DT <b>Y</b> * <b>S</b> * <b>D</b> R <b>S</b> * <b>G</b> SS*PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S573			9.1	87.0	R.S* <b>G</b> S*SPDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S573S574			9.4	63.6	R.S* <b>G</b> S* <b>S</b> *SPDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	Y567S571S574			6.7	11.6	R.DT <b>Y</b> * <b>S</b> DR <b>S</b> * <b>G</b> SS*PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	Y567S573S574			13.1	27.6	R.DT <b>Y</b> * <b>S</b> DRSG <b>S</b> * <b>S</b> *PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S573S575			5.3	115.3	R.SG <b>S</b> * <b>S</b> *PDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S573S574			21.7	35.1	R.DTYSDRS* <b>G</b> * <b>S</b> * <b>S</b> *PD <b>S</b> *EITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S562			100.0	28.6	K.GCRLS* <b>P</b> R.D
		CTPS1	S575			10.8	64.2	R.SGSS*PDSEITELK.F	
		Cytidine 5-prime triphosphate synthetase	CTPS1	S574			13.8	96.1	R.SGSS*SPDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S573			10.6	70.7	R.SG <b>S</b> *SPDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S573S574S575			11.6	21.7	R.DTYSDRSG <b>S</b> * <b>S</b> * <b>S</b> *PD <b>S</b> *EITELKFPSINH.D-
		CTPS1	S573S574S575			9.2	59.3	R.SG <b>S</b> * <b>S</b> * <b>S</b> *PDSEITELK.F	
		Cytidine 5-prime triphosphate synthetase	CTPS1	S568S571S573			2.0	29.4	R.DTYS* <b>D</b> R <b>S</b> * <b>G</b> S* <b>S</b> *SPDSEITELKFPSINH.D-
		Cytidine 5-prime triphosphate synthetase	CTPS1	S571S574S575			11.4	22.8	R.S* <b>G</b> SS* <b>S</b> *PD <b>S</b> *EITELKFPSINH.D-
		Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2 (Fragment)	S81			9.8	42.1	R.EAEALLQSMGLTPESPIVPPPM <b>S</b> *PSSK.S
		Cytoplasmic dynein 1 intermediate chain 2	DYNC1I2 (Fragment)	S83			5.3	20.2	R.EAEALLQSMGLTPESPIVPPPM <b>S</b> *SK.S
		Cytoplasmic linker associated protein 2	CLASP2	S603			9.3	84.3	R.SR <b>S</b> *DIDVNAAGAK.A
		Cytoplasmic linker associated protein 2	CLASP2	S758S762			15.6	25.4	R.IPRPSV <b>S</b> *QGCS* <b>R</b> E
		Cytoplasmic linker associated protein 2	CLASP2	S1224			26.5	43.5	K.ASLHSMPTH <b>S</b> *SPR.S
		Cytoplasmic linker associated protein 2	CLASP2	S808			56.2	90.8	R.VLNT <b>G</b> *DVEEAVADALKKPAR.R
		Cytoplasmic linker associated protein 2	CLASP2	S1164			54.8	66.7	R.GVTEAIQN <b>F</b> *FR.S
		Cytoplasmic linker associated protein 2	CLASP2	T806			11.1	54.8	R.VLNT*GSDVEEAVADALKKPAR.R
		Cytoplasmic linker associated protein 2	CLASP2	S1113S1118S11			5.7	100.4	R.S*PANW <b>S</b> * <b>S</b> *PLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLR.G
		Cytoplasmic linker associated protein 2	CLASP2	S1113S1118T11			9.7	100.4	R.S*PANW <b>S</b> *SPLT*SPTNTSQNTLSPSAFDYDTENMNSEDIYSSLR.G
		Cytoplasmic linker associated protein 2	CLASP2	S1113T1113S11			3.8	48.1	R.S*PANWSSPLTSPTNTSQNT <b>L</b> *SPSAFDYDTENMNSEDIYSSLR.G
		Cytoplasmic linker associated protein 2	CLASP2	S1241			16.1	55.5	R.DYNPNYNSDS <b>S</b> *PFNK.S
		Cytoplasmic linker associated protein 2	CLASP2	S1113T1125T11			2.9	94.3	R.S*PANWSSPLTSP*NTSQNTLSPSAFDYDTENMNSEDIYSSLR.G
		Cytoplasmic linker associated protein 2	CLASP2	S774			21.2	12.9	R.DT <b>S</b> *PVR.S
		Cytoplasmic linker associated protein 2	CLASP2	S756S758			6.8	17.5	R.IPRP <b>S</b> *V <b>S</b> *QGCSR.E
		Cytoplasmic linker associated protein 2	CLASP2	S1113S1128T11			2.6	52.2	R.S*PANWSSPLTSPTNT <b>S</b> *QNTLSPSAFDYDTENMNSEDIYSSLR.G
		Cytoplasmic linker associated protein 2	CLASP2	S1113S1119T11			5.4	89.2	R.S*PANW <b>S</b> *PLT*SPTNTSQNTLSPSAFDYDTENMNSEDIYSSLR.G
		Cytoplasmic linker associated protein 2	CLASP2	S1225			19.6		K.ASLHSMPTH <b>S</b> *PR.S
		Cytoskeleton-like bicaudal D protein homolog 2	BICD2 homolog 2	S582			100.0	32.3	R.S*PILLPK.G
		D4, zinc and double PHD fingers family 2	DPF2	S142			66.8	92.8	R.VDD <b>S</b> *LGEFPVTNS.RA
		D4, zinc and double PHD fingers family 2	DPF2	T176			27.3	48.2	R.ILEPDRFLDLDDEYED <b>T</b> *PK.R
		D4, zinc and double PHD fingers family 2	DPF2	S244T248			23.0	53.5	K.NRPGLSYHYAHSHLAE EEGEDKED <b>S</b> *QP <b>T</b> *PVSQR.S
		D4, zinc and double PHD fingers family 2	DPF2	S225Y226			36.0		K.NRPGLS*YHYAHSHLAE EEGEDKEDSQP <b>T</b> PV <b>S</b> Q <b>R</b> .S
		Damage specific DNA binding protein 2	DOB2	S24			6.0	41.2	R.S* <b>R</b> SPLELEPEAK.K
		Damage specific DNA binding protein 2	DOB2	S24S26			100.0	36.3	R.S* <b>R</b> S*PLELEPEAK.K
		Damage specific DNA binding protein 2	DOB2	S26			100.0	77.5	R.S*PLELEPEAK.K
		Daxx	DAXX	S737S739			82.8	32.2	K.TSVATQCDP <b>E</b> EIV <b>S</b> *D <b>S</b> -.D-
		Daxx	DAXX	S668S671			18.1	50.4	K.ICTLP <b>S</b> *PP <b>S</b> *PLASLAPVAD <b>S</b> STR.V
		Daxx	DAXX	S668S675			9.0	43.9	K.ICTLP <b>S</b> *PP <b>S</b> PLAS*LAPVAD <b>S</b> STR.V
		Daxx	DAXX	S495			46.9	42.5	K.DGD <b>K</b> S*PMSSLQISNEK.N

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Daxx	DAXX	S671				4.5	11.6	K.ICTLPSPSP*PLASLAPVADSTR.V
		Daxx	DAXX	S690S702				29.3	11.4	R.VDSPS*HGLVTSSLCPSP*PAR.L
		DBC1	CCAR2	S124				100.0	85.8	K.S*PAPPLLHVAALGQK.Q
		DBC1	CCAR2	S678S681				20.9	126.1	R.SVAS* <b>NQ</b> S*EMEFSSLQDMPK.E
		DBC1	CCAR2	S675S678				46.8	127.0	R.S*VAS* <b>NQ</b> S*EMEFSSLQDMPK.E
		DBC1	CCAR2	S675S678S681				88.7	172.4	R.S*VAS* <b>NQ</b> S*EMEFSSLQDMPK.E
		DBC1	CCAR2	S678				7.9	35.3	R.SVAS* <b>NQ</b> S*EMEFSSLQDMPK.E
		DBC1	CCAR2	S675S681				3.6	28.6	R.S*VAS <b>NQ</b> S*EMEFSSLQDMPK.E
		DDHD domain containing 1		DDHD1	S723S727			16.8	22.9	K.EPTSVSENEGISTIPS*PVTSP*PVLSSR.R
		DDX16	DHX16	S103S106				23.8	101.3	R.LLED <b>S</b> *EE <b>S</b> *SEETVSR.A
		DDX16	DHX16	S103S106S107				38.3	76.9	R.LLED <b>S</b> *EE <b>S</b> * <b>S</b> *EETVSR.A
		DDX18	DDX18	S86				29.8	19.0	K.VTK <b>S</b> *PQK.S
		DDX21	DDX21	S121				100.0	79.8	K.NEEP <b>S</b> *EEEIDAPKPK.K
		DDX21	DDX21	S164S171S173				2.2	14.8	K.LKNGFHPPEPDCNP <b>S</b> *EAASE <b>S</b> * <b>NS</b> *EIEQIPEQK.E
		DDX21	DDX21	S168S171S173				41.3	63.1	K.NGFHPPEPDCNPSEAA <b>S</b> *EE <b>S</b> * <b>NS</b> *EIEQIPEQK.E
		DDX21	DDX21	S89				55.6	48.9	K.KOKEEPSQND <b>I</b> <b>S</b> *PK.T
		DDX21	DDX21	S164S168S171				5.8	44.5	K.NGFHPPEPDCNP <b>S</b> *EAA <b>S</b> *EE <b>S</b> *NSEIEQIPEQK.E
		DDX23	DDX23	S14				32.2	50.2	R.DA <b>S</b> *PSKEER.K
		DDX23	DDX23	S107S109				14.6	26.9	K.R <b>S</b> <b>S</b> * <b>LS</b> *PGR.G
		DDX23	DDX23	S106S109				6.8	14.0	R.KR <b>S</b> * <b>SL</b> <b>S</b> *PGR.G
		DDX23	DDX23	S106S107					16.1	R.KR <b>S</b> * <b>S</b> * <b>LS</b> PGR.G
		DDX23	DDX23	T25				100.0	15.3	R.T*PDRE <b>R</b> .D
		DDX24	DDX24	T302				9.4	67.4	R.SPGKAEAESDALPDDT* <b>V</b> IESEALPSDIAAEA.R.A
		DDX24	DDX24	S295				16.7	22.0	R.SPGKAEAE <b>S</b> *DALPDDT <b>V</b> IESEALPSDIAAEA.R.A
		DDX24	DDX24	S82S94				27.2	23.7	K.AQAV <b>S</b> *EEEEEEGK <b>S</b> <b>S</b> *PK.K
		DDX24	DDX24	S82				100.0	103.2	K.AQAV <b>S</b> *EEEEEEGK.S
		DDX24	DDX24	S82S93				26.7	35.6	K.AQAV <b>S</b> *EEEEEEGK <b>S</b> <b>S</b> *SPK.K
		DDX3	DDX3X	S90				21.2	31.8	K.SSFFSDRG <b>S</b> *GSR.G
		DDX3	DDX3X	S594				100.0	48.6	R.F <b>S</b> *GGFGAR.D
		DDX3	DDX3X	S654				7.3	11.6	R.GFGGGYGGFYNSDGYGGNY <b>S</b> *QGVDDWWGN.-
		DDX39	DDX39A	S426				3.2	42.2	R.FEVNVAELPEEDISTYEQ <b>S</b> *R.-
		DDX3Y	DDX3Y	S588				16.5	19.4	K. <b>S</b> *NRFSGGFGAR.D
		DDX3Y	DDX3Y	S592				21.0	30.0	K.SNR <b>F</b> <b>S</b> *GGFGAR.D
		DDX41	DDX41	S66S68				52.3	45.4	K.GAAEEEQD <b>S</b> * <b>S</b> *EPRGDEDDIPLGPQSVNSLQDQHHLK.E
		DDX41	DDX41	S23				107.2	135.8	R. <b>S</b> *EAEDEDDYVPYVPLR.Q
		DDX41	DDX41	S21S23				33.8	35.2	R.TDEVPA <b>G</b> <b>S</b> * <b>RS</b> *EAEDEDDYVPYVPLR.Q
		DDX41	DDX41	S21				34.2	22.9	R.TDEVPA <b>G</b> <b>S</b> *R.S
		DDX42	DDX42	S104S111				16.0	72.0	R.QQF <b>H</b> <b>S</b> *KPVDS <b>S</b> *DDDPLEAFMAVEDQAAR.D
		DDX42	DDX42	S751S754				11.3	10.8	K.AGSSAAGASGWT <b>S</b> AGSLNSVPTNSAQ <b>Q</b> GH <b>S</b> *PD <b>S</b> *PVT <b>S</b> AAK. ^
		DDX42	DDX42	S109S111				26.5	71.3	R.QQF <b>H</b> SKPV <b>D</b> <b>S</b> * <b>DS</b> *DDDPLEAFMAVEDQAAR.D
		DDX42	DDX42	S104S109				7.0	44.9	R.QQF <b>H</b> <b>S</b> *KPVDS* <b>DS</b> DDDPLEAFMAVEDQAAR.D
		DDX42	DDX42	S754				12.0	67.4	K.AGSSAAGASGWT <b>S</b> AGSLNSVPTNSAQ <b>Q</b> GH <b>NS</b> PD <b>S</b> *PVT <b>S</b> AAK.G
		DDX42	DDX42	S185				28.4	57.3	R.YMAENPTAGVVQEEEDNLEY <b>D</b> *DGNPIA <b>P</b> T <b>K</b> .K
		DDX42	DDX42	S723					16.4	K.AG <b>S</b> *SAAGASGWT <b>S</b> AGSLNSVPTNSAQ <b>Q</b> GH <b>NS</b> PDSPV <b>T</b> <b>S</b> AAK.G
		DDX42	DDX42	S104				7.9	50.4	R.QQF <b>H</b> <b>S</b> *KPVDSDDDPLEAFMAVEDQAAR.D
		DDX42	DDX42	S751				8.6	24.7	K.AGSSAAGASGWT <b>S</b> AGSLNSVPTNSAQ <b>Q</b> GH <b>NS</b> *PDSPV <b>T</b> <b>S</b> AAK.G
		DDX42	DDX42	T742S754				6.4	21.5	K.AGSSAAGASGWT <b>S</b> AGSLNSV <b>P</b> T <b>NS</b> AQ <b>Q</b> GH <b>NS</b> PD <b>S</b> *PVT <b>S</b> AAK. ^
		DDX42	DDX42	S733S754				5.9	11.6	K.AGSSAAGASGWT <b>S</b> *AGSLNSVPTNSAQ <b>Q</b> GH <b>NS</b> PD <b>S</b> *PVT <b>S</b> AAK. ^
		DDX42	DDX42	T742S744				-0.4	16.6	K.AGSSAAGASGWT <b>S</b> AGSLNSV <b>P</b> T <b>NS</b> *AQ <b>Q</b> GH <b>NS</b> PDSPV <b>T</b> <b>S</b> AAK. ^
		DDX46	DDX46	S24S26				18.7	20.1	R. <b>S</b> * <b>RS</b> *PSDKR.S
		DDX46	DDX46	S804				145.3	89.5	K.AALGLQ <b>D</b> <b>S</b> *DDEAAVDIEQIESM <b>IF</b> NSK.K
		DDX46	DDX46	S295S296				10.6	48.4	K.GELMENDQDAMEY <b>S</b> * <b>S</b> *EEEEVLQ <b>T</b> ALT <b>G</b> Y <b>Q</b> T <b>K</b> .Q
		DDX46	DDX46	Y294S295				26.8	24.9	K.GELMENDQDAMEY <b>S</b> * <b>S</b> *EEEEVLQ <b>T</b> ALT <b>G</b> Y <b>Q</b> T <b>K</b> .Q
		DDX51	DDX51	S83				100.0	53.8	R.VNDAEP <b>G</b> <b>S</b> *PEAPQ <b>G</b> K.R
		DEAD (Asp-Glu-Ala-Asp) box polypeptide		DDX17	S599			14.7	22.9	R.RD <b>S</b> *AS <b>Y</b> R.D
		DEAD box polypeptide 55		DDX55	S544			144.0	87.8	R.EEG <b>S</b> *DIEDEDMELLND <b>T</b> R.L
		DEAD-box protein 54		DDX54	S75			20.8	43.5	K.LG <b>P</b> GRPL <b>T</b> FP <b>T</b> SECT <b>S</b> *D <b>V</b> EPD <b>T</b> R.E
		DEAD-box protein 54		DDX54	T74			42.1	35.0	R.K <b>L</b> G <b>P</b> GRPL <b>T</b> FP <b>T</b> SECT <b>S</b> *D <b>V</b> EPD <b>T</b> R.E
		DEAD-box protein 54		DDX54	S39S41			100.0	114.8	R. <b>G</b> <b>S</b> * <b>DS</b> *EDGEFEIAEQDAR.A
		DEAD-box protein 54		DDX54	S782			73.4	28.8	K.IDORD <b>S</b> *DEEGASDR.R
		DEAH box polypeptide 57		DHX57	S127			100.0	70.7	R.DLQEQDADAG <b>S</b> *ER.G
		Death associated protein		DAP	S51			58.6	84.7	K.DKDDQEWES <b>P</b> <b>S</b> *PPK <b>P</b> T <b>V</b> ISG <b>V</b> IA <b>R</b> .G



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Protein Name	Gene	Phosphosites							
Diacylglycerol kinase, eta	T26S27S31							39.0	MAAGAGGAWBBRAGCAAGAGAGAUTKAAASAGDPSERSDEE
Diacylglycerol kinase, zeta DGKZ	S52S53						133.6	58.9	R.RRRS*SQALQGCLLSCGVR.A
DiGeorge syndrome critical region gene 8 DGCR8	S35							75.3	R.
DiGeorge syndrome critical region gene 8 DGCR8	S27S1279						21.5	12.9	K.YGSDSDHP*DGET*SVQPMMTK.I
DiGeorge syndrome critical region gene 8 DGCR8	S377						6.8	27.7	R.EQSSDLTPSGDV*PVKPLSR.S
DiGeorge syndrome critical region gene 8 DGCR8	S373						14.0	14.6	R.EQSSDLTPS*GDVSPVKPLSR.S
Dihydropyrimidinase-related protein 2 DPYSL2	S27						24.1	45.6	K.NLGSGS*PKPR.Q
Dihydrouridine synthase 3-like DUS3L	T273S276						19.3	39.5	R.QENCGAQQVPAGPGT*TPPS*SPVR.T
Dihydrouridine synthase 3-like DUS3L	S272S276						17.7	41.9	R.QENCGAQQVPAGPGT*TPPS*SPVR.T
Dihydrouridine synthase 3-like DUS3L	T273S277						8.0	26.4	R.QENCGAQQVPAGPGT*TPPS*PVR.T
DIS3 DIS3	S730						20.9	49.4	K.SLAESLDQAE*PTFPYLNLTLLR.I
Disabled homolog 2-interacting protein DAB2IP	S35T37						100.0	16.1	R.S*RT*RPARE
Discs large associated protein 4 DLGAP4	S127						5.3	50.0	R.KLSS*IGIQVDCIQVPVK.E
Discs, large homolog 7 DLGAP5	S332						71.8	70.1	R.S*ANAFITPSYTWPLK.T
Discs, large homolog 7 DLGAP5	S806S812						44.0	61.9	K.SLTTECHLLDS*PGLNCS*NPFTQLER.R
Discs, large homolog 7 DLGAP5	S148S149						100.0	11.2	K.AIPS*S*VR.I
Disrupter of silencing 10 UTP3	S365S368						38.6	88.4	K.TSAAACAVTDL*DD*DFDEK.A
Disrupter of silencing 10 UTP3	T362S368						33.7	44.0	K.TSAAACAVT*DLSD*DFDEK.A
Disrupter of silencing 10 UTP3	T362S365						20.4	20.6	K.TSAAACAVT*DL*DDSDFDEK.A
DKFZP434C212 protein GAPVD1	S757T762						11.2	82.0	R.EVS*SRPST*PGLSVVSGISATSEDIPNK.I
DKFZP434C212 protein GAPVD1	S757S758						9.8	43.0	R.EVS*S*RPSTPGLSVVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein GAPVD1	T762S766						20.9	48.4	R.EVSSRP*ST*PGLS*VVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein GAPVD1	S761T762						5.5	63.7	R.EVSSRP*S*TPGLSVVSGISATSEDIPNK.I
DKFZP434C212 protein GAPVD1	S757S766						5.4	54.1	R.EVS*SRPSTPGLS*VVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein GAPVD1	S757S761						16.6	85.5	R.EVS*SRP*TPGLSVVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein GAPVD1	S758T762						9.8	32.4	R.EVS*RPST*PGLSVVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein GAPVD1	S761S766						5.2	39.4	R.EVSSRP*STPGLS*VVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein GAPVD1	S930						-0.3	38.4	R.SS*DIVSSVR.R
DKFZP434C212 protein GAPVD1	S929						17.0	36.0	R.S*SDIVSSVR.R
DKFZP434C212 protein GAPVD1	S757S769						1.9	30.6	R.EVS*SRPSTPGLSVV*SGISATSEDIPNK.I
DKFZP434C212 protein GAPVD1	S758S761						4.5	35.6	R.EVS*RP*TPGLSVVSGISATSEDIPNKIEDLR.S
DKFZP434C212 protein GAPVD1	S974						4.8	15.2	R.ELPPAAAGATSLVAAPH*SSSPSK.D
DKFZP434P1750 protein TBC1D10B S383							22.5	60.8	R.QQPPLGPS*LLSLPGLK.S
DKFZP434P1750 protein TBC1D10B S383S386							8.8	51.9	R.QQPPLGPS*LLS*LPGLK.S
DKFZP434P1750 protein TBC1D10B S382S386							17.7	53.3	R.QQPPLGPS*SLLS*LPGLK.S
DKFZP434P1750 protein TBC1D10B S382S383							5.9	45.4	R.QQPPLGPS*LLSLPGLK.S
DKFZP434P1750 protein TBC1D10B T422							-3.2	20.9	R.ASAGPAGPVVT*AEGLHPSLPSTGNSTPLGSSK.E
TBC1D10B S412							69.2	46.9	R.AS*AGPAGPVVTAEGLHPSLPSTGNSTPLGSSK.E
DKFZP434P1750 protein TBC1D10B S381							11.1	30.1	R.QQPPLGPS*SLLSLPGLK.S
DKFZP434P1750 protein TBC1D10B S412S432							17.7	13.3	R.RAS*AGPAGPVVTAEGLHPSL*PTGNSTPLGSSK.E
DKFZP434P1750 protein TBC1D10B S381S386							6.8	11.6	R.QQPPLGPS*SLLS*LPGLK.S
DKFZP564C186 protein NOC2L S672S673							59.4	101.1	K.DLFDLNS*SEEDTEGFSE.R
DKFZP564C186 protein NOC2L S225S26S30							16.5	39.9	R.LAELTVDEFLAS*GFD*ESE*ESENSQAQET.E
DKFZP564C186 protein NOC2L S672							13.9	87.6	K.DLFDLNS*SEEDTEGFSE.R
DKFZP564C186 protein NOC2L S49							35.4	16.5	R.S*PDKPGGSPSASR.R
DKFZP564C186 protein NOC2L S93S96S100S1							55.1		K.
DKFZP564C186 protein NOC2L S49S56							18.3	28.8	R.S*PDKPGG*PSASR.R
DKFZP564O123 protein CHMP2B S199							11.0	42.0	K.AT*DEEIER.Q
DKFZp761A052 protein OTUD5 S177							26.0	125.8	R.EEVGAGYNS*EDEYEAAAR.I
DKFZp761A052 protein OTUD5 S64							100.0	46.8	R.AS*PPPGPLPGPGALHR.W
DKFZp761A052 protein OTUD5 T507							67.4	29.9	R.AT*SPLVLYPALECR.A
DMAP1 DMAP1 T445							9.8	37.2	K.DTIDVVGAPLT*PNSR.K
Dmx like 1 DMXL1 T573							-0.5	25.8	R.ST*SMLISSGHNK.S
DNA damage inducible protein 2 DD12 T104							9.1	73.8	R.IDFSSIAVPGT*SSPR.Q
DNA damage inducible protein 2 DD12 S194							100.0	72.9	R.LFS*ADPFLEAQAK.I
DNA dependent protein kinase catalytic PRKDC subunit T2609S2612							22.1	68.5	R.STVLT*PMFVET*QAS*QGLTQTR.T
DNA dependent protein kinase catalytic PRKDC subunit S2612							7.4	43.6	R.STVLT*PMFVETQAS*QGLTQTR.T
DNA Ligase III LIG3 S210							1.0	74.0	K.LTTTGQVTS*PVKGASFVTS*TNPR.K
DNA Ligase III LIG3 S241							7.8	14.1	R.KFSGFSAKPNNSGEAPS*SPTPK.R
LIG3 T209							33.2	20.6	K.LTTTGQVT*SPVK.G
DNA methyltransferase 1 DNMT1 S714							100.0	86.5	K.EADDEEVD*DNIPEMP*PK.K
DNA methyltransferase 1 DNMT1 S394							21.2	28.5	K.LSIFDANE*GFESYEALPOHK.L

Peak Area	Protein Name	Gene	Phosphosites	CarT		RajIB		Ascor	MOWSE	Sequence
				5	6	5	6			
<div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>30</div> <div>40</div> <div>50</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> </div>										
	DNA mismatch repair protein PMS2	PMS2	S523					-11.2	48.5	K.DSGHGSTSVDSGEFSIPDTGSHCSSEYAAS <sup>S</sup> PGDR.G
	DNA mismatch repair protein PMS2	PMS2	S522					44.0	60.2	K.DSGHGSTSVDSGEFSIPDTGSHCSSEYAAS <sup>S</sup> SPGDR.G
	DNA mismatch repair protein PMS2	PMS2	S517					8.3	23.9	K.DSGHGSTSVDSGEFSIPDTGSHCS <sup>S</sup> EYAASSPGDR.G
	DNA polymerase delta interacting protein 3	POLDIP3	S127					-0.3	42.7	R.SS <sup>S</sup> PAAFINPPIGTIVTPALK.L
	DNA polymerase subunit B		S141					35.2	70.5	R.S <sup>S</sup> PHQLLSPPSFSFSPATSQK.Y
	DNA Polymerase, alpha	POLA1	S186					49.8	79.6	R.S <sup>S</sup> IGASPNPFVSHATATAVPSGK.I
	DNA primase large subunit	PRIM2	Y504					8.8	33.3	K.DASSALASLNSLEMDMEGLDY <sup>S</sup> FSEDS.-
	XRC4	S327S328						100.0	26.6	R.NS <sup>S</sup> S <sup>S</sup> PEDLFDEL-
	DNA replication licensing factor MCM4	MCM4	S131					58.4	86.5	K.GLOVDLQS <sup>S</sup> DGAAADIVASEQSLGQK.L
	DNA topoisomerase II alpha	TOP2A	S1469T1470S1					27.8	19.6	R.KPS <sup>S</sup> T <sup>S</sup> S <sup>S</sup> DDS <sup>S</sup> DSNFEK.I
	DNA topoisomerase II alpha	TOP2A	S1392					7.2	42.6	K.GSVPLSS <sup>S</sup> SPPATHFPDETEITNPVK.K
	DNA topoisomerase II alpha	TOP2A	S1377					23.4	62.9	K.SVV <sup>S</sup> S <sup>S</sup> DLEADDVK.G
	DNA topoisomerase II alpha	TOP2A	S1377S1391					6.5	40.4	K.SVV <sup>S</sup> S <sup>S</sup> DLEADDVKGSVPLS <sup>S</sup> SPPATHFPDETEITNPVK.K
	DNA topoisomerase II alpha	TOP2A	S1525					35.3	35.7	K.YLEES <sup>S</sup> DEDDLF.-
	DNA topoisomerase II alpha	TOP2A	S1332S1337T1					22.2	36.5	K.FTMDLDS <sup>S</sup> DEDF <sup>S</sup> DFDEKT <sup>S</sup> DDEDFVPSDAS <sup>S</sup> PPK.T
	DNA topoisomerase II alpha	TOP2A	S1332S1337T1					36.4	28.5	K.FTMDLDS <sup>S</sup> DEDF <sup>S</sup> DFDEKT <sup>S</sup> DDEDFVPS <sup>S</sup> DAS <sup>S</sup> PPK.T
	DNA topoisomerase II alpha	TOP2A	T1112					3.9	71.1	K.VPDEEENEESDNEKET <sup>S</sup> EKSDSVTDSGPTFNYYLLDMPLWYLTK.E
	DNA topoisomerase II alpha	TOP2A	S1115					4.3	71.0	K.VPDEEENEESDNEKETEK <sup>S</sup> DSVTDSGPTFNYYLLDMPLWYLTK.E
	DNA topoisomerase II alpha	TOP2A	T1124					-0.7	25.5	K.VPDEEENEESDNEKETKSDSVTDSGPT <sup>S</sup> FNYYLLDMPLWYLTK.E
	TOP2A	S1106						40.3	65.3	K.VPDEEENEES <sup>S</sup> DNEKETEK.S
	DNA topoisomerase II alpha	TOP2A	S1247					22.8	107.9	K.NENTEGS <sup>S</sup> PQEDGVELEGLK.Q
	DNA topoisomerase II alpha	TOP2A	S1391					32.8	33.3	K.GSVPLS <sup>S</sup> SPPATHFPDETEITNPVK.K
	DNA topoisomerase II alpha	TOP2A	S1377S1392					7.4	36.3	K.SVV <sup>S</sup> S <sup>S</sup> DLEADDVKGSVPLS <sup>S</sup> SPPATHFPDETEITNPVK.K
	DNA topoisomerase II alpha	TOP2A	S1121					7.5	51.9	K.VPDEEENEESDNEKETKSDSVTDS <sup>S</sup> GPTFNYYLLDMPLWYLTK.E
	DNA topoisomerase II alpha	TOP2A	S1393					5.3	24.7	K.GSVPLSS <sup>S</sup> PPATHFPDETEITNPVK.K
	DNA topoisomerase II alpha	TOP2A	S1332S1337					17.7	55.5	K.FTMDLDS <sup>S</sup> DEDF <sup>S</sup> DFDEKT
	DNA topoisomerase II alpha	TOP2A	S1332S1337T1					24.4	53.9	K.FTMDLDS <sup>S</sup> DEDF <sup>S</sup> DFDEKT <sup>S</sup> DDEDFVPSDASPPK.T
	DNA topoisomerase II alpha	TOP2A	S1332S1337T1					16.3	31.8	K.FTMDLDS <sup>S</sup> DEDF <sup>S</sup> DFDEKT <sup>S</sup> DDEDFVPS <sup>S</sup> DASPPK.T
	DNA topoisomerase II alpha	TOP2A	T1327S1332S1					18.2	13.7	K.FT <sup>S</sup> MDLDS <sup>S</sup> DEDF <sup>S</sup> DFDEKT <sup>S</sup> DDEDFVPS <sup>S</sup> DASPPK.T
	DNA topoisomerase II alpha	TOP2A	S1117					0.8	67.4	K.VPDEEENEESDNEKETKSDS <sup>S</sup> VTDSGPTFNYYLLDMPLWYLTK.E
	DNA topoisomerase II alpha	TOP2A	S1387S1392					3.1	10.8	K.SVVS <sup>S</sup> DLEADDVKGS <sup>S</sup> VPLS <sup>S</sup> SPPATHFPDETEITNPVK.K
	DNA topoisomerase II alpha	TOP2A	T1119					7.0	48.9	K.VPDEEENEESDNEKETKSDS <sup>S</sup> VTDSGPTFNYYLLDMPLWYLTK.E
	DNA-binding protein RFX7	RFX7	T1025S1028					26.8	33.3	R.HHDT <sup>S</sup> HFGRLT <sup>S</sup> PVS <sup>S</sup> PVQHGGATVNTNK.Q
	DNA-binding protein RFX7	RFX7	T1019T1025					5.3	10.8	R.HHDT <sup>S</sup> HFGRLT <sup>S</sup> PVSPVQHGGATVNTNK.Q
	DnaJ homology subfamily A member 5	DNAJC21	S283					100.0	26.5	K.EFGDGS <sup>S</sup> DENEMEHELKD
	DOCK10	DOCK10	S318S322					18.3	32.1	K.IPRPLS <sup>S</sup> LIGS <sup>S</sup> TLR.F
	DOCK10	DOCK10	S289S292					9.4	32.3	R.AS <sup>S</sup> LAS <sup>S</sup> LDSNPSTNEK.S
	DOCK8	DOCK8	S1177					20.1	54.9	R.TSGS <sup>S</sup> DEEQEGAGAINQNVALAIGNNFNLK.T
	DOCK8	DOCK8	S1175S1177					16.2	65.3	R.YRT <sup>S</sup> S <sup>S</sup> GS <sup>S</sup> DEEQEGAGAINQNVALAIGNNFNLK.T
	DOCK8	DOCK8	T1174S1175					14.0	50.9	R.YRT <sup>S</sup> S <sup>S</sup> GS <sup>S</sup> DEEQEGAGAINQNVALAIGNNFNLK.T
	DOCK8	DOCK8	T1174S1177					11.2	64.3	R.YRT <sup>S</sup> S <sup>S</sup> GS <sup>S</sup> DEEQEGAGAINQNVALAIGNNFNLK.T
	Docking protein 3	DOK3	S330					27.6	73.0	R.ATS <sup>S</sup> LPSLDTPGELR.E
	Docking protein 3	DOK3	S425					13.1	69.6	R.S <sup>S</sup> PTTSPYYHNGQQLSWPGPANDSTLEAQYR.R
	Docking protein 3	DOK3	S439					1.1	48.9	R.SPTTSPYYHNGQDLS <sup>S</sup> WPGPANDSTLEAQYR.R
	Docking protein 3	DOK3	T427T428					5.8	40.4	R.SPT <sup>S</sup> T <sup>S</sup> SPYYHNGQQLSWPGPANDSTLEAQYR.R
	Docking protein 3	DOK3	S429S439					1.6	18.7	R.SPTTSPYYHNGQDLS <sup>S</sup> WPGPANDSTLEAQYR.R
	Docking protein 3	DOK3	S429					1.8	14.2	R.SPTTSPYYHNGQQLSWPGPANDSTLEAQYR.R
	Docking protein 3	DOK3	S425Y432					7.2	69.2	R.S <sup>S</sup> PTTSPYYHNGQQLSWPGPANDSTLEAQYR.R
	Docking protein 4	DOK4	S35					16.9	25.9	R.KSS <sup>S</sup> SKGPQR.L
	Double strand break repair protein MRE11A	MRE11	S688S689					141.5	138.0	K.GVDFE <sup>S</sup> S <sup>S</sup> EDDDDDPFMNTSSLR.R
	Double strand break repair protein MRE11A	MRE11	S649					45.7	84.5	K.NYSEVIEVDE <sup>S</sup> DVEEDIFPTTSK.T
	Down regulated in metastasis	UTP20	S2601					64.7	21.0	K.AES <sup>S</sup> DGEKEEVKEELGRPATLLWLQKL
	Downregulator of transcription 1	DR1	S157					2.2	73.6	R.....
	Downregulator of transcription 1	DR1	S166S167					-0.6	32.2	R.....
	Downregulator of transcription 1	DR1	S157S159						35.2	R.....
	Downregulator of transcription 1	DR1	S159S161					2.1	28.7	R.....
	Drebrin E	DBN1	S341					4.0	90.8	R.SP <sup>S</sup> S <sup>S</sup> DSSTASTPVAEQIER.A
	Drebrin E	DBN1	S143					12.1	47.9	R.LS <sup>S</sup> SPVLHRL
	Drebrin E	DBN1	S339					21.2	96.2	R.S <sup>S</sup> PSDSSTASTPVAEQIER.A
	Drebrin E	DBN1	S274					8.4	20.0	K.S <sup>S</sup> ESEVEEAAAIAQRPNPRE
	Dual adapter for phosphotyrosine and 3-DAPP1 phosohotvrosine and 3-phosohoinositide		S276					7.6	13.2	R.SRS <sup>S</sup> FIK.-
	Dual-specificity protein phosphatase 22	DUSP22	S86					13.8	32.7	R.RWSS <sup>S</sup> FPALAPLYDNYTTET.-



Peak Area		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM																	
		-LCV		CarT		RajiB		Ascor		MOWSE		Sequence							
	Protein Name	Gene	Phosphosites																
	dUTP pyrophosphatase	DUT	S11					16.1	71.4			M.PCSEETPAIS*PSKR.A							
	Dynamin 2	DNM2	S736							32.5		K.EALNIIGDIS*TSTVSTPVPPVDDTWLQSASSHS*PTPQR.R							
	Dynamin 2	DNM2	T762					8.8	36.6			K.EALNIIGDISTVSTVSTPVPPVDDTWLQSASSHS*PTPQR.R							
	Dynamin 2	DNM2	S760					12.2	31.1			K.EALNIIGDISTVSTVSTPVPPVDDTWLQSASSHS*PTPQR.R							
	Dynamin 2	DNM2	S757					4.7	12.5			K.EALNIIGDISTVSTVSTPVPPVDDTWLQSAS*SHS*PTPQR.R							
	Dynamin 2	DNM2	S758							13.5		K.EALNIIGDISTVSTVSTPVPPVDDTWLQSAS*SHS*PTPQR.R							
	Dynamin related protein 1	DNM1L	S616					43.6	25.2			K.SKPIPIMPAS*PQK.G							
	Dynein light chain A	DYNCL1L1	S516					13.9	64.7			R.KPVTVSPTTPTS*PTEGEAS.-							
	Dynein light chain A	DYNCL1L1	T515					20.1	60.3			R.KPVTVSPTTPT*SPTEGEAS.-							
	Dynein light chain A	DYNCL1L1	S207					39.3	19.0			R.DFOEYVEPGEDFPAS*PQRR.N							
	Dynein light chain A	DYNCL1L1	T513T515					9.5	11.2			R.KPVTVSPTT*PT*SPTEGEAS.-							
	Dynein light chain A	DYNCL1L1	S510T515					8.5	14.8			R.KPVTVS*PTTP*SPTEGEAS.-							
	Dynein, axonemal, heavy polypeptide 8	DNAH8	S4103T4106					100.0	11.2			K.GVS*WNT*VR.Y							
	Dynein, cytoplasmic, heavy polypeptide 1	DYNCH1	T4369					6.5	44.1			R.TDST*SDGRPAWMR.T							
	Dynein, cytoplasmic, heavy polypeptide 1	DYNCH1	S4368					-0.4	32.7			R.TDS*TSGRPAWMR.T							
	Dynein, cytoplasmic, heavy polypeptide 2	DYNC2H1	T432					10.9	12.6			K.RPT*ISK.E							
	Dynein, cytoplasmic, light intermediate polypeptide 2	DYNCL1L2	S194					34.8	35.2			K.DFQDYMEPEGCGQS*PQRR.G							
	DYRK1B	DYRK1A	Y273					33.4	39.3			R.IYQV*IQSR.F							
	DYRK1B	DYRK1A	Y271					15.1	47.6			R.IY*QYQSR.F							
	Dyskerin	DKC1	S494					19.8	80.6			K.AGLESGAEPGGDS*DTTK.K							
	Dyskerin	DKC1	S451S455					30.9	36.9			R.KRES*ESES*DETPPAAPOLIK.K							
	DKC1	S513						100.0	42.9			K.EVELVS*E.-							
	Dyskerin	DKC1	S451S453S455					14.0	33.9			R.KRES*ES*ES*DETPPAAPOLIK.K							
	Dyskerin	DKC1	S451S455T458					8.8	28.9			R.KRES*ESES*DET*PPAAPOLIK.K							
	Dyskerin	DKC1	S21					126.1	49.7			K.S*LPEEDVAEQHAEFLIKPESK.V							
	Dyskerin	DKC1	S451S453T458					14.8	21.9			R.KRES*ES*ESDET*PPAAPOLIK.K							
	Dyskerin	DKC1	S451T458					1.2	15.7			R.KRES*ESESDET*PPAAPOLIK.K							
	Dyskerin	DKC1	S453S455					-0.1	26.4			R.KRESES*ES*DETPPAAPOLIK.K							
	Dyskerin	DKC1	S451S453S455					100.0	21.7			R.KRES*ES*ES*DET*PPAAPOLIK.K							
	Dyskerin	DKC1	S451S453					12.4	45.6			R.ES*ES*ESDETPPAAPOLIK.K							
	Dystrobrevin alpha	DTNA	S564					-0.3	14.8			R.SS*PSHTISRPIPIR.S							
	Dystrophin	DMD	S291					30.2	35.2			R.TSS*PKPR.F							
	Dystrophin	DMD	T289					10.0	13.4			R.T*SSPKPR.F							
	E1A binding protein p300	EP300	T1906T1909					11.0	57.6			K.AAGQVT*PP*PPQT AQPLPGPPPAAVEMAMQIQRA							
	E1A binding protein p300	EP300	T1909T1913					11.4	31.4			K.AAGQVT*PP*PPQT AQPLPGPPPAAVEMAMQIQRA							
	E1A binding protein p400	EP400	S23S37						50.3			R.AFGDS*EFGEDVAEQHAEFLIKPESK.V							
	E1A binding protein p400	EP400	S315T320					8.5	43.3			R.TPGVLLPGAGGAAGFGMT*SPPPPT*SPSR.T							
	E1A binding protein p400	EP400	T320					12.6	50.9			R.TPGVLLPGAGGAAGFGMT*SPPPPT*SPSR.T							
	E1A binding protein p400	EP400	T314S321					6.0	18.7			R.TPGVLLPGAGGAAGFGMT*SPPPPT*PSR.T							
	E1A binding protein p400	EP400	T314T320					25.3	38.1			R.TPGVLLPGAGGAAGFGMT*SPPPPT*SPSR.T							
	E1A binding protein p400	EP400	S904T908					23.0	14.4			R.KAS*ISLT*DDEVDDEETIEEEANEGVVDHETLSNLAKE							
	E2-230K	UBE2O	S87S89S96S99					100.0	13.0			R.LIHGEDS*DS*EGEEGRGS*GS*EAGGAGHEEGRA							
	E2-230K	UBE2O	S839					17.8	71.5			K.NMTVEQLLTGSPTS*PTVEPEKPTR.E							
	E2-230K	UBE2O	T838					19.3	47.5			K.NMTVEQLLTGSPT*PTVEPEKPTR.E							
	E2-230K	UBE2O	S836S839					11.5	54.9			K.NMTVEQLLTGS*PTS*PTVEPEKPTR.E							
	E2-230K	UBE2O	S115					100.0	23.2			R.AS*PLRR.G							
	E2-230K	UBE2O	S87S89					100.0	39.7			R.LIHGEDS*DS*EGEEGR.G							
	E2-230K	UBE2O	S836					15.4	55.0			K.NMTVEQLLTGS*PTSPTVEPEKPTR.E							
	E2-230K	UBE2O	T838S839					7.0	14.7			K.NMTVEQLLTGSPT*S*PTVEPEKPTR.E							
	E2-230K	UBE2O	T834T838					20.1	23.8			K.NMTVEQLLT*GSPT*PTVEPEKPTR.E							
	E2-230K	UBE2O	S836T838					1.9	25.4			K.NMTVEQLLTGS*PT*PTVEPEKPTR.E							
	E2-230K	UBE2O	S515					42.8	33.1			R.KKS*IPLSIK.N							
	E2-230K	UBE2O	T834					7.8	15.4			K.NMTVEQLLT*GSPTPTVEPEKPTR.E							
	E3 ubiquitin-protein ligase	RNF213	RNF213	S1307				51.3	77.2			K.EDQEAALLS*EPEEESER.H							
(E3-independent)	E2 ubiquitin-conjugating enzyme	UBE2O	S1166S1167					26.5				K.AEHEHEDEBAVAIEIEFGVNEBENGNSBABAASGVNENSGAAN							
(E3-independent)	E2 ubiquitin-conjugating enzyme	UBE2O	S1166S1167S11					16.6				K.AEHEHEDEBAVAIEIEFGVNEBENGNSBABAASGVNENSGAAN							
	E6 targeted protein 1	SIPA1L1	S258					-0.4	46.1			K.GSGFS*LDVIDGPISQR.E							
	E6 targeted protein 1	SIPA1L1	S206S211					1.8	58.4			R.EYGS*TS*SIDKQGTSGESFFDLK.G							
	E6 targeted protein 1	SIPA1L1	T209S210					5.0	58.4			R.EYGS*T*S*SIDKQGTSGESFFDLK.G							
	E6 targeted protein 1	SIPA1L1	Y206S208					13.6	12.6			R.EY*GS*TS*SIDKQGTSGESFFDLK.G							
	EBNA2 coactivator p100	SND1	S426					24.1	77.0			K.VNVTVDYIRPAS*PATETVPAFSER.T							
	Echinoderm microtubule associated protein like 3	EML3	S176					33.8	79.5			K.AIS*SANLLVR.S							



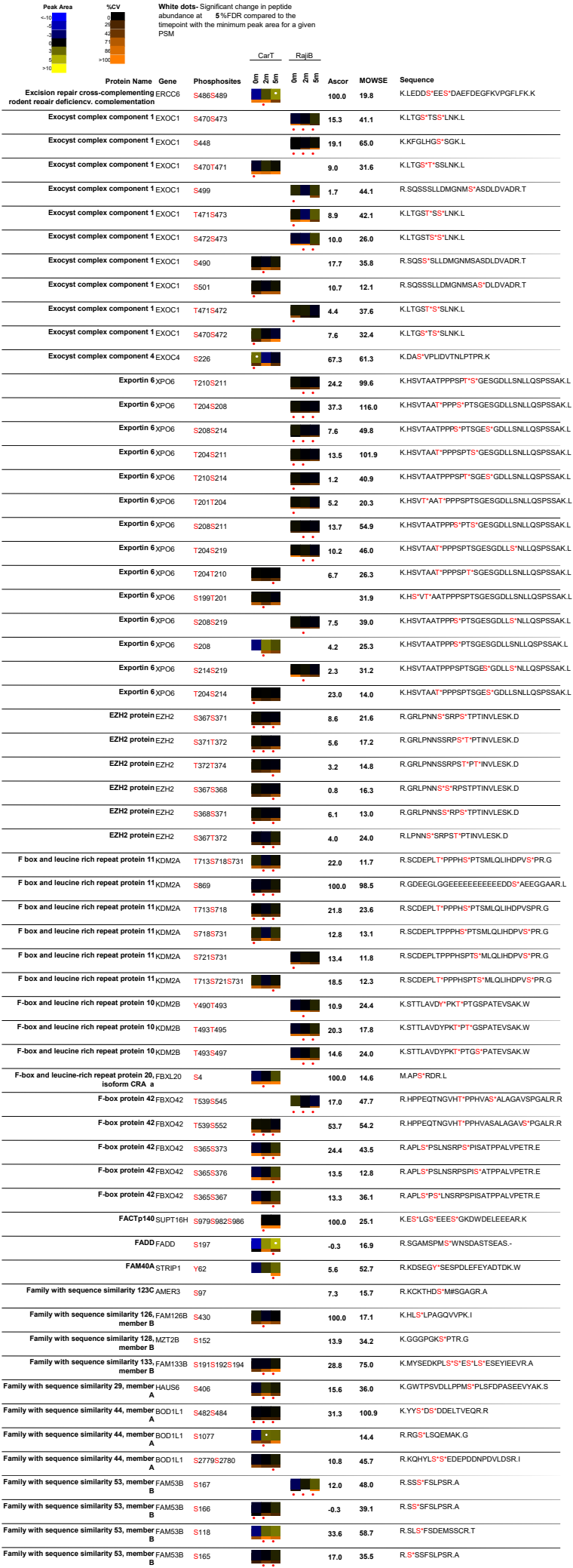


Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
<10	0	Protein Name	Gene	Phosphosites				Ascor	MOWSE	Sequence
10-20	1	EP515R	EP515L1	S255				6.0	12.6	R.STPSHGVSSSLNSTGSL\$*PK.H
20-30	2	EP515R	EP515L1	S246S255				7.8	44.5	R.STPSHGV\$S*SLNSTGSL\$*PK.H
30-40	3	EP515R	EP515L1	S575				6.0	29.7	R.SLEQYDQVLDGAHGAS*LTDLANLSEGVSLAER.G
40-50	4	EP515R	EP515L1	T577				8.9	60.1	R.SLEQYDQVLDGAHGASLT*LDLANLSEGVSLAER.G
50-60	5	EP515R	EP515L1	S804				6.9	47.7	K.STPVSQLGS\$*ADFEAPDPFQPLGADSGDPFQSK.K
60-70	6	EP515R	EP515L1	T797				-0.3	50.9	K.ST*PVSQLGSADFEAPDPFQPLGADSGDPFQSK.K
70-80	7	EP515R	EP515L1	S253				25.4	18.6	R.STPSHGVSSSLNSTGS\$*LSPK.H
80-90	8	EP515R	EP515L1	S247S255				5.9	21.3	R.STPSHGV\$S\$*LNSTGSL\$*PK.H
90-100	9	EP515R	EP515L1	S246S253				5.3	40.1	R.STPSHGV\$S\$*SLNSTGS\$*LSPK.H
>100	10	EP515R	EP515L1	S241S255				7.3	53.0	R.STPS\$*HGVSSSLNSTGSL\$*PK.H
		Epsin 1	EPN1	T444				53.6	61.0	K.T*PESFLGPNALVDLSLVRPGPTPPGAKA.A
		Epsin 1	EPN1	T390				52.7	78.9	R.TALPT\$*GSSAGELELLAGEVPAR.S
		Epsin 1	EPN1	S391				24.2	34.4	R.TALPT\$*GSSAGELELLAGEVPAR.S
		Epsin 1	EPN1	S447				5.5	44.0	K.TPES\$*FLGPNALVDLSLVRPGPTPPGAKA.A
		Epsin 1	EPN1	T444T468				31.5	14.9	K.T*PESFLGPNALVDLSLVRPGPT*PPGAKA.A
		Epsin 1	EPN1	S409				99.0	64.1	R.\$*PGAFDMGVR.G
		Epsin 1	EPN1	S393				10.7	28.7	R.TALPTSG\$*SAGELELLAGEVPAR.S
		Epsin 1	EPN1	S394				15.7	24.0	R.TALPTSG\$*AGELELLAGEVPAR.S
		Epsin 4	CLINT1	S299				-3.9	12.8	K.TIDLGAAAHYTGDKA\$*PDQNASTHTPQSVK.T
		Epsin 4	CLINT1	T294				6.5	19.3	K.TIDLGAAAHYT*GDKASPDQNASTHTPQSVK.T
		Epsin 4	CLINT1	S305				7.4	11.1	K.TIDLGAAAHYTGDKASPDQNA\$*THTPQSVK.T
		Epstein Barr virus induced gene 2	GPR183	S328S330				24.2	63.1	K.RQV\$*V\$*ISSAVK.S
		Epstein Barr virus induced gene 2	GPR183	S330S333				13.4	34.4	R.QV\$V\$*IS\$*AVK.S
		Epstein Barr virus induced gene 2	GPR183	S328S330S333				17.8	31.3	R.QV\$*V\$*IS\$*AVK.S
		Epstein Barr virus induced gene 2	GPR183	S337				27.8	22.1	K.\$*APEENSR.E
		Epstein Barr virus induced gene 2	GPR183	S328S333				9.9	61.5	K.RQV\$*V\$SIS\$*AVK.S
		Epstein Barr virus induced gene 2	GPR183	S333				8.2	53.6	R.QV\$V\$SIS\$*AVK.S
		Epstein Barr virus induced gene 2	GPR183	S328				35.4	83.4	R.QV\$*V\$ISSAVK.S
		Epstein Barr virus induced gene 2	GPR183	S343				9.5	17.2	K.SAPEEN\$*R.E
		Epstein Barr virus induced gene 2	GPR183	S332S333				5.4	35.1	R.QV\$V\$SIS\$*AVK.S
		Epstein Barr virus induced gene 2	GPR183	S332				16.1	52.4	R.QV\$V\$SIS\$*SAVK.S
		Epstein Barr virus induced gene 2	GPR183	S328S330S332				10.4	31.9	R.QV\$*V\$*IS\$*SAVK.S
		Epstein Barr virus induced gene 2	GPR183	S330S332S333				7.9	13.3	R.QV\$V\$*IS\$*S\$*AVK.S
		Erbin	ERBIN	S602S603				5.5	69.8	K.HIVNHDDVFESEEL\$*S\$*DEEMK.M
		Erbin	ERBIN	S598S602				12.5	57.7	K.HIVNHDDVFEE\$*EEL\$*S\$DEEMK.M
		ERBIN	ERBIN	T917S932				15.0	57.8	R.SK\$AT*LLYDQPLQVFTG\$S\$*SSDISGTK.A
		Erbin	ERBIN	S915S932				12.9	49.8	K.\$*ATLLYDQPLQVFTG\$S\$*SSDISGTK.A
		Erbin	ERBIN	S915				20.4	108.1	K.\$*ATLLYDQPLQVFTG\$SSSS\$SDISGTK.A
		Erbin	ERBIN	S915S933				14.1	54.8	K.\$*ATLLYDQPLQVFTG\$SS\$*SDISGTK.A
		Erbin	ERBIN	T917S933				13.6	49.2	K.\$AT*LLYDQPLQVFTG\$SS\$*SDISGTK.A
		Erbin	ERBIN	T917S930				12.2	39.5	R.SK\$AT*LLYDQPLQVFTG\$*SSSS\$SDISGTK.A
		Erbin	ERBIN	T917				12.2	41.4	R.SK\$AT*LLYDQPLQVFTG\$SSSS\$SDISGTK.A
		Erbin	ERBIN	S440				3.9	53.8	R.TEDVMFIS\$*DNESFNPSLWEEQR.K
		Erbin	ERBIN	S440S444				30.8	34.9	R.TEDVMFIS\$*DNES\$*FNPSLWEEQR.K
		ERCC5	BIVM-	S384				9.1	64.4	R.NAPAAVDEG\$S\$*PRT
		ERCC5	BIVM-	S562S563				31.2	30.6	K.FDSSL\$*S\$*DDETK.C
		ERCC5	BIVM-	S156S157				41.7	16.9	R.ENDLYVLPPLQEEKH\$S\$*EEDEKEWOER.M
		ERF	ERF	Y16				6.0	34.9	K.TPADTGFAFPDWAY*KPES\$PGSR.Q
		ERF	ERF	T3521				35.7	36.7	-MKT*PADTGFAFPDWAYKPES\$*PGSR.Q
		ERF	ERF	T3524				38.0	38.5	-MKT*PADTGFAFPDWAYKPES\$PQ\$*R.Q
		ERF	ERF	T3520				26.4	12.7	-MKT*PADTGFAFPDWAYKPES\$*SPGSR.Q
		ERF	ERF	S20				7.1	23.9	K.TPADTGFAFPDWAYKPES\$*SPGSR.Q
		ERK1	MAPK3	Y204				25.5	98.4	R.IADPEHDHTGFLTEY*VATR.W
		ERK1	MAPK3	T202Y204				38.3	92.7	R.IADPEHDHTGFLT*EY*VATR.W
		ERK1	MAPK3	T198Y204				11.9	33.6	R.IADPEHDHT*GFLTEY*VATR.W
		ERK2	MAPK1	Y187				27.8	96.3	R.VADPDHDHTGFLTEY*VATR.W
		ERK2	MAPK1	T185Y187				49.5	88.6	R.VADPDHDHTGFLT*EY*VATR.W
		ERK2	MAPK1	T181Y187				13.2	18.6	R.VADPDHDHT*GFLTEY*VATR.W
		Erythrocyte membrane protein band 4.1	EPB41	S684				20.7	40.8	K.HH\$S\$ISELKK.N
		Erythrocyte membrane protein band 4.1	EPB41	S709				18.0	21.8	K.RL\$*THSPFR.T
		Erythrocyte membrane protein band 4.1	EPB41	S84				9.8	31.9	R.LF\$S\$*FLK.R
		Erythrocyte membrane protein band 4.1	EPB41	S84S85				100.0	34.2	R.LF\$S\$*FLK.R

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		Phosphosites	CarT		RajIB		Ascor	MOWSE	Sequence
		5	6		5	6					
		Protein Name	Gene								
		Erythrocyte membrane protein band 4.1 EPB41	T710						6.5	20.3	K.RLST <sup>H</sup> SPFR.T
		Erythrocyte membrane protein band 4.1 EPB41	S510						8.9	14.6	K.FRYS <sup>G</sup> GR.T
		Erythrocyte membrane protein band 4.1 EPB41	Y509						14.1		K.FRY <sup>S</sup> SGR.T
		Erythrocyte membrane protein band 4.1 EPB41	S85						9.8	32.5	R.LFSS <sup>S</sup> FLK.R
		Erythrocyte membrane protein band 4.1-like EPB41L2 2	S87						16.9	46.8	K.QKS <sup>Y</sup> YTLVAK.D
		Erythrocyte membrane protein band 4.1-like EPB41L2 2	T600						5.8	60.1	R.SP <sup>T</sup> KAPHLQIEGK.K
		Erythrocyte membrane protein band 4.1-like EPB41L2 2	Y88						-0.2	34.1	K.SY <sup>T</sup> TLVAK.D
		Erythrocyte membrane protein band 4.1-like EPB41L2 2	S598						22.5	65.8	R.S <sup>P</sup> TKAPHLQIEGK.K
		Essential meiotic endonuclease 1 EME1	S85S87						17.6	90.2	R.LLS <sup>S</sup> ES <sup>S</sup> EDEEFIPLAQR.L
		Essential meiotic endonuclease 1 EME1	S84S85S87						100.0	56.8	R.LLS <sup>S</sup> S <sup>S</sup> ES <sup>S</sup> EDEEFIPLAQR.L
		Essential meiotic endonuclease 1 EME1	S84S87						12.1	20.2	R.LLS <sup>S</sup> SES <sup>S</sup> EDEEFIPLAQR.L
		Estrogen receptor binding protein DNTTIP2	S141S148						13.0	63.8	K.ESYTEIVS <sup>S</sup> EASHVS <sup>S</sup> GISR.I
		Estrogen receptor binding protein DNTTIP2	S141S145S148						11.8	41.2	K.ESYTEIVS <sup>S</sup> EAS <sup>S</sup> HVS <sup>S</sup> GISR.I
		Estrogen receptor binding protein DNTTIP2	S528S532S533						44.6	45.4	K.EEEEDEKS <sup>S</sup> EEDS <sup>S</sup> S <sup>S</sup> DHDENEDEF <sup>S</sup> DEEDFLNSTK.A
		Estrogen receptor binding protein DNTTIP2	S141S145						21.8	60.3	K.ESYTEIVS <sup>S</sup> EAS <sup>S</sup> HVSGISR.I
		Estrogen receptor binding protein DNTTIP2	Y135S145						12.9	42.4	K.ESY <sup>T</sup> TEIVSEAS <sup>S</sup> HVSGISR.I
		Estrogen receptor binding protein DNTTIP2	S141						20.7	56.0	K.ESYTEIVS <sup>S</sup> EASHVSGISR.I
		Estrogen receptor binding protein DNTTIP2	S141S151						3.4	17.3	K.ESYTEIVS <sup>S</sup> EASHVSGIS <sup>S</sup> R.I
		Estrogen receptor binding protein DNTTIP2	Y135S145S148						8.2	38.5	K.ESY <sup>T</sup> TEIVSEAS <sup>S</sup> HVS <sup>S</sup> GISR.I
		Estrogen receptor binding protein DNTTIP2	T136S145S148						13.0	29.7	K.ESYT <sup>T</sup> EIVSEAS <sup>S</sup> HVS <sup>S</sup> GISR.I
		Estrogen receptor binding protein DNTTIP2	S134Y135S151						-2.3	40.8	K.ES <sup>S</sup> Y <sup>T</sup> TEIVSEASHVSGIS <sup>S</sup> R.I
		Estrogen receptor binding protein DNTTIP2	T136S148						5.5	28.2	K.ESYT <sup>T</sup> EIVSEASHV <sup>S</sup> S <sup>S</sup> GISR.I
		ETS translocation variant 6 ETV6	Y233S251						12.1	15.4	R.AQGPRPHQENNHOES <sup>S</sup> Y <sup>T</sup> PLSVSPMENNHCASSES <sup>S</sup> HPKPSSPR. ^
		ETS translocation variant 6 ETV6	S203						100.0	40.7	R.S <sup>S</sup> PLDNMIR.R
		ETS translocation variant 6 ETV6	T18S22						36.4	68.3	R.ISYT <sup>T</sup> PPES <sup>S</sup> PVPSYASSTPLHVPVPRA
		ETS translocation variant 6 ETV6	S16S22						15.1	38.1	R.ISY <sup>T</sup> TPPES <sup>S</sup> PVPSYASSTPLHVPVPRA
		ETS translocation variant 6 ETV6	Y17S22S29						22.9	54.0	R.ISY <sup>T</sup> TPPES <sup>S</sup> PVPSYAS <sup>S</sup> STPLHVPVPRA
		ETS translocation variant 6 ETV6	Y17S22T31						22.5	41.3	R.ISY <sup>T</sup> TPPES <sup>S</sup> PVPSYASST <sup>S</sup> PLHVPVPRA
		ETS translocation variant 6 ETV6	T161						3.7	28.5	R.T <sup>T</sup> PRPSVDNVHNPPTIELLHR.S
		ETS translocation variant 6 ETV6	Y17S26						12.4	52.1	R.ISY <sup>T</sup> TPPESPVPS <sup>S</sup> YASSTPLHVPVPRA
		ETS translocation variant 6 ETV6	Y17T18						2.7	21.9	R.ISY <sup>T</sup> T <sup>T</sup> PPESPVPSYASSTPLHVPVPRA
		ETS translocation variant 6 ETV6	S16S26						23.4	49.1	R.ISY <sup>T</sup> TPPESPVPS <sup>S</sup> YASSTPLHVPVPRA
		ETS translocation variant 6 ETV6	S22S26						11.5	38.1	R.ISYT <sup>T</sup> PPES <sup>S</sup> PVPS <sup>S</sup> YASSTPLHVPVPRA
		ETS translocation variant 6 ETV6	Y17Y27S29						10.3	34.6	R.ISY <sup>T</sup> TPPESPVPSY <sup>S</sup> AS <sup>S</sup> STPLHVPVPRA
		ETS translocation variant 6 ETV6	Y17S22						26.9	44.2	R.ISY <sup>T</sup> TPPES <sup>S</sup> PVPSYASSTPLHVPVPRA
		ETS translocation variant 6 ETV6	S26Y27S29						30.2	32.7	R.ISYT <sup>T</sup> PPESPVPS <sup>S</sup> Y <sup>S</sup> AS <sup>S</sup> STPLHVPVPRA
		ETS translocation variant 6 ETV6	Y17S22S30						17.9	36.0	R.ISY <sup>T</sup> TPPES <sup>S</sup> PVPSYASS <sup>S</sup> TPLHVPVPRA
		ETS translocation variant 6 ETV6	S248S251						16.9	15.3	R.AQGPRPHQENNHOESY <sup>T</sup> PLSVSPMENNHCAPAS <sup>S</sup> SES <sup>S</sup> HPKPSSPR. ^
		ETS translocation variant 6 ETV6	S232Y233						13.8		R.AQGPRPHQENNHOES <sup>S</sup> Y <sup>T</sup> PLSVSPMENNHCAPASSESHPKPSSPR. ^
		ETS translocation variant 6 ETV6	S232S257						27.1	16.4	R.AQGPRPHQENNHOES <sup>S</sup> Y <sup>T</sup> PLSVSPMENNHCAPASSESHPKPS <sup>S</sup> PR. ^
		ETS translocation variant 6 ETV6	S213						100.0	27.2	R.RLS <sup>S</sup> PAER.A
		ETS translocation variant 6 ETV6	S165						3.3	19.1	R.TPRPS <sup>S</sup> VDNVHNPPTIELLHR.S
		ETS translocation variant 6 ETV6	T18S22S29						10.7	41.4	R.ISYT <sup>T</sup> PPES <sup>S</sup> PVPSYAS <sup>S</sup> STPLHVPVPRA
		ETS translocation variant 6 ETV6	S232S251						15.6	14.4	R.AQGPRPHQENNHOES <sup>S</sup> Y <sup>T</sup> PLSVSPMENNHCAPASSES <sup>S</sup> HPKPSSPR. ^
		ETS translocation variant 6 ETV6	Y233S256						11.0	10.8	R.AQGPRPHQENNHOES <sup>S</sup> Y <sup>T</sup> PLSVSPMENNHCAPASSESHPKPS <sup>S</sup> SPR. ^
		ETS translocation variant 6 ETV6	Y233S257						13.2	11.6	R.AQGPRPHQENNHOES <sup>S</sup> Y <sup>T</sup> PLSVSPMENNHCAPASSESHPKPS <sup>S</sup> PR. ^
		ETS translocation variant 6 ETV6	S182S184						3.2	11.9	R.S <sup>S</sup> RS <sup>S</sup> PITTNHRPSPDPEQRPLR.S
		ETS1 ETS1	Y283						9.8	34.0	R.VPSY <sup>T</sup> DSFSEDYPAALPNH <sup>S</sup> KPK.G
		ETS1 ETS1	T38						7.3	29.2	K.VOLELFPSPDMECADVLLT <sup>S</sup> PSSK.E
		ETS1 ETS1	S26T38						43.2	32.0	K.VOLELFPSPDMECADVLLT <sup>S</sup> PSSK.E
		ETS1 ETS1	S285						7.3	34.8	R.VPSYDS <sup>S</sup> FDSEDYPAALPNH <sup>S</sup> KPK.G
		ETS1 ETS1	S282S285						22.9	28.6	R.VPS <sup>S</sup> YDS <sup>S</sup> FDSEDYPAALPNH <sup>S</sup> KPK.G
		ETS1 ETS1	S282						7.4	15.2	R.VPS <sup>S</sup> YDSFSEDYPAALPNH <sup>S</sup> KPK.G
		ETS1 ETS1	S41						7.8	23.2	K.VOLELFPSPDMECADVLLTPS <sup>S</sup> K.E
		ETS1 ETS1	S40						3.5	20.0	K.VOLELFPSPDMECADVLLTPS <sup>S</sup> SK.E
		Eukaryotic translation elongation factor 1 EEF1B2 beta 2	Y79						79.6		K.Y <sup>T</sup> GPADEVDTTGS <sup>S</sup> GATDSKDDDDILFGSDDEESEEAK.R
		Eukaryotic translation elongation factor 1 EEF1B2 beta 2	S106						35.4	46.7	K.YGPADEVDTTGS <sup>S</sup> GATDSKDDDDILFGS <sup>S</sup> DDEESEEAK.R
		Eukaryotic translation elongation factor 1 EEF1B2 beta 2	S90S95						6.2	58.4	K.YGPADEVDTTGS <sup>S</sup> GATDS <sup>S</sup> KDDDDILFGSDDEESEEAK.R
		Eukaryotic translation elongation factor 1 EEF1B2 beta 2	T88S106						12.0	46.5	K.YGPADEVDTT <sup>S</sup> GSGATDSKDDDDILFGS <sup>S</sup> DDEESEEAK.R
		Eukaryotic translation elongation factor 1 EEF1B2 beta 2	S90						4.3	39.0	K.YGPADEVDTTGS <sup>S</sup> GATDSKDDDDILFGSDDEESEEAK.R
		Eukaryotic translation elongation factor 1 EEF1B2 beta 2	S90T93						16.8	69.3	K.YGPADEVDTTGS <sup>S</sup> GAT <sup>S</sup> DSKDDDDILFGSDDEESEEAK.R
		Eukaryotic translation elongation factor 1 EEF1B2 beta 2	S90S106						19.0	78.9	K.YGPADEVDTTGS <sup>S</sup> GATDSKDDDDILFGS <sup>S</sup> DDEESEEAK.R

Peak Area	ΔCV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM			CarT	RajiB	Ascort	MOWSE	Sequence
					5 6 6	5 6 6			
Eukaryotic translation elongation factor 1 EF1B2 beta 2	S95S106						18.6	69.1	K.YGPADVEDTTGSGATGS*KDDDDILFGS*DDEEESEEAK.R
Eukaryotic translation elongation factor 1 EF1B2 beta 2	S95						3.5	61.0	K.YGPADVEDTTGSGATGS*KDDDDILFGSDDEEESEEAK.R.L
Eukaryotic translation elongation factor 1 EF1B2 beta 2	T93						2.4	13.5	K.YGPADVEDTTGSGAT*DSKDDDDILFGSDDEEESEEAK.R.L
Eukaryotic translation elongation factor 1 EF1B2 beta 2	T87						-0.0	28.1	K.YGPADVEDT*TGSGATDSKDDDDILFGSDDEEESEEAK.R
Eukaryotic translation elongation factor 1 EF1G alpha	T46						100.0	40.0	R.T*PEFLR.K
Eukaryotic translation elongation factor 1, EF1D delta	S528						161.4	105.0	K.KPATPAEDDEDDDDILFGS*DNEEEK.E
Eukaryotic translation elongation factor 1, EF1D delta	T513S528						100.0	71.5	K.KPAT*PAEDDEDDDDILFGS*DNEEEKAAQLR.E
Eukaryotic translation elongation factor 1, EF1D delta	S499						19.1	37.0	R.ATAPQTQHS*PMR.Q
Eukaryotic translation elongation factor 1, EF1D delta	T495						5.3	26.8	R.ATAPQT*QHVSPMR.Q
Eukaryotic translation elongation factor 1, EF1D delta	T491						11.0	58.2	R.AT*APQTQHVSPMR.Q
Eukaryotic translation elongation factor 2 EF2	T57T59						100.0	21.3	R.FT*DT*RKDEQER.C
Eukaryotic translation initiation factor 2A EIF2A	S503						6.3	38.8	R.S*DKSPDLAPTPAPQSTPR.N
Eukaryotic translation initiation factor 2A EIF2A	S506						6.5	37.4	R.SDKS*PDLAPTPAPQSTPR.N
Eukaryotic translation initiation factor 3 EIF3K subunit k	S217						11.2	23.5	K.IDFDSVSSIMAS*S*Q.-
Eukaryotic translation initiation factor 3 EIF3K subunit k	S216						60.7	25.4	K.IDFDSVSSIMAS*S*SQ.-
Eukaryotic translation initiation factor 3, EIF3A subunit 10	S882						12.1	45.0	R.LGDS*SLSR.K
Eukaryotic translation initiation factor 3, EIF3A subunit 10	S881						2.3	12.6	R.LGDS*SLSR.K
Eukaryotic translation initiation factor 3, EIF3E subunit 6 48kDa	S399						27.8	27.2	K.LGHVVMGNNAV*S*PYQVQIEK.T
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	T68						38.5		R.T*DAEAEAAK*VDGEEDGDAECID*DAEEDB/DAGCAGPDA
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	T68S78						36.4		R.T*DAEAEAAK*VDGEEDGDAECID*DAEEDB/DAGCAGPDA
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	S152S164						13.8	43.9	R.ALENGDAEP*S*FSDPEDFVDVS*EEELLGOVLK.D
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	S152						78.9	103.5	R.ALENGDAEP*S*FSDPEDFVDVSEELLGOVLK.D
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	T68S78S1S83						30.9		R.T*DAEAEAAK*VDGEEDGDAECID*DAEEDB/DAGCAGPDA
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	S154S164						49.7	99.9	R.ALENGDAEP*S*FSDPEDFVDVS*EEELLGOVLK.D
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	S152S154						82.9	132.5	R.ALENGDAEP*S*FSDPEDFVDVSEELLGOVLK.D
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	S152S154S164						100.0	99.6	R.ALENGDAEP*S*FSDPEDFVDVS*EEELLGOVLK.D
Eukaryotic translation initiation factor 3, EIF3B subunit 9 eta, 116kDa	S83S85						13.6	16.8	R.T*DAEAEAAK*VDGEEDGDAECID*DAEEDB/DAGCAGPDA
Eukaryotic translation initiation factor 4B EIF4B	S445						58.9	75.3	K.S*LENETLNK.E
Eukaryotic translation initiation factor 4B EIF4B	S597						37.6	73.8	K.YAALS*VDGEGENEGEDYAE.-
Eukaryotic translation initiation factor 4B EIF4B	S409						28.8	29.8	R.S*EETQERE
Eukaryotic translation initiation factor 4B EIF4B	T97						5.8	75.6	K.SPPYT*AFGLNLPYDVTEESIK.E
Eukaryotic translation initiation factor 4B EIF4B	S93						30.1	135.8	K.S*PPYTAFLGNLPYDVTEESIK.E
Eukaryotic translation initiation factor 4B EIF4B	Y96						11.8	60.1	K.SPPY*TAFLGNLPYDVTEESIK.E
Eukaryotic translation initiation factor 4B EIF4B	S422						15.0	118.0	R.TGS*ESSQTGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S498S504						15.9	84.1	R.SQS*S*DEEQS*PTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	T420S425						20.8	70.9	R.T*GSESS*QTGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S406						100.0	26.8	R.HFS*WR.S
Eukaryotic translation initiation factor 4B EIF4B	S504						38.7	100.4	R.SQSDTEQQS*PTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	T500S504						4.6	13.6	R.SQSDT*EQQS*PTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	S497						14.0	121.1	R.SQS*SDTEQQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	T500						9.8	59.2	R.SQSDT*EQQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	S497T500						11.8	33.2	R.SQS*SDT*EQQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	S424S425						6.8	29.1	R.TGSES*S*QTGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S489						16.9	24.3	K.RSS*NPPAR.S
Eukaryotic translation initiation factor 4B EIF4B	S498						11.7	72.0	R.SQS*S*DEEQSPTSGGGK.V
Eukaryotic translation initiation factor 4B EIF4B	S422S425						5.9	35.7	R.TGS*ESS*QTGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S422S424						-0.4	11.1	R.TGS*S*ES*SQGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S424						-0.4	54.4	R.TGSES*S*SQGTSTTSSR.N
Eukaryotic translation initiation factor 4B EIF4B	S497S504						13.9	29.7	R.SQS*SDTEQQS*PTSGGGK.V
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	T70						14.0	61.7	K.T*PPRDLPTIPQVTSPPSSDEPPMEASQSHLR.N
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	T36S44						19.7	25.6	R.RVVLGDGVQLPPGDY*S*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	T36T45						14.4	22.3	R.RVVLGDGVQLPPGDY*S*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	T37S44						20.7	23.2	R.VVLGDGVQLPPGDY*S*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	T77						24.5	72.3	K.TPPRDLPT*IPQVTSPPSSDEPPMEASQSHLR.N
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	S35S44						10.5	32.6	R.VVLGDGVQLPPGDY*S*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	T36T41						16.1	13.8	R.VVLGDGVQLPPGDY*S*TPGGT*LFSTTPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	Y34S44						4.3	16.0	R.VVLGDGVQLPPGDY*S*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP1 binding protein 1	S35T45						9.4	26.7	R.RVVLGDGVQLPPGDY*S*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP2 binding protein 2	T37S44						17.8	34.2	R.TVAISDAQAQLPHDYCT*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP2 binding protein 2	T36T45						24.7	34.0	R.TVAISDAQAQLPHDYCT*TPGGTLFS*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP2 binding protein 2	T36T46						6.7	24.7	R.TVAISDAQAQLPHDYCT*TPGGTLFST*TPGGTR.I
Eukaryotic translation initiation factor 4E EIF4EBP2 binding protein 2	S25S44						13.0	25.5	R.TVAIS*DAQAQLPHDYCTTPGGTLFS*TPGGTR.I

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		Protein Name	Gene	Phosphosites					
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	T70			26.8	25.2	R.NSPMAQT*PPCHLPNIPGVTSPTGLIEDSK.V
		EIF4EBP2	S65T70			43.7	31.4	R.NS*PMAQT*PPCHLPNIPGVTSPTGLIEDSK.V	
		Eukaryotic translation initiation factor 4E binding protein 2	EIF4EBP2	T37T45			21.6	35.8	R.TVAISDAAQLPHDYCT*TPGGTLFS*TPGGTR.I
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	T36S44			6.2	22.3	R.TVAISDAAQLPHDYCT*TPGGTLFS*TPGGTR.I
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	S65			29.4	51.0	R.NS*PMAQT*PPCHLPNIPGVTSPTGLIEDSK.V
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	S25T45			11.4	26.0	R.TVAIS*DAQLPHDYCTTPGGTLFS*TPGGTR.I
		Eukaryotic translation initiation factor 4E binding protein 2	EIF4EBP2	T45			22.8	16.0	R.TVAISDAAQLPHDYCTTPGGTLFS*TPGGTR.I
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	S25T46			2.3	22.9	R.TVAIS*DAQLPHDYCTTPGGTLFS*TPGGTR.I
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	T36T50			4.9	14.2	R.TVAISDAAQLPHDYCT*TPGGTLFSTPGGT*TR.I
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	S65T82			19.4	17.7	R.RNS*PMAQT*PPCHLPNIPGV*TPGLIEDSK.V
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	Y34T45			5.0	21.2	R.TVAISDAAQLPHDY*CTPGGTLFS*TPGGTR.I
		Eukaryotic translation initiation factor 4E bindin protein 2	EIF4EBP2	Y34S44			3.5	17.4	R.TVAISDAAQLPHDY*CTPGGTLFS*TPGGTR.I
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S74			39.9	51.1	K.WHASLYPAS*GR.S
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S564			82.3	68.8	R.APS*PPLSQVQFQTRA
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S78			-0.3	34.3	R.SS*PVESLKK.E
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S951			30.2	61.6	R.SSS*PVGLAK.W
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S680S690			6.8	22.8	R.GNSS*SPAPAASITS*MLSPSFTPSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S679S690			8.4	19.4	R.GNS*SPAPAASITS*MLSPSFTPSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S301			100.0	37.6	R.DAVLPEQS*PGDFDNFFNLDK.V
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S69			8.2	42.7	K.YDSGDGVWDEPKWHAS*LYPASGR.S
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S680S693			9.1	28.2	R.GNSS*SPAPAASITSMLS*PSFTPSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S345			9.5	15.1	R.WFSNPS*R.S
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	Y71			-0.7	25.9	K.YDSGDGVWDEPKWHASLY*PASGR.S
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S681S693			6.3	16.7	R.GNSSS*PAPAASITSMLS*PSFTPSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S342			13.1		R.WFS*NPFR.S
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	Y382			4.1	14.0	R.LAGLEAQILSPQNSGNY*FAPILEDHAENKVDILEMLQK.A
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S374			23.5		R.LAGLEQAILS*PGQNSGNYFAPILEDHAENKVDILEMLQK.A
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S680S687			3.9	20.1	R.GNSS*SPAPAAS*ITSMSPSFTPSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S679S687			6.5	24.3	R.GNS*SPAPAAS*ITSMSPSFTPSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	T689			-10.9	22.1	R.GNSSSPAPAASIT*SMSPSFTPTSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S687S690			4.5	18.4	R.GNSSSPAPAAS*ITS*MLSPSFTPSVIR.K
		Eukaryotic translation initiation factor 4E nuclear import factor 1	EIF4ENIF1	S950			-0.6	27.6	R.SS*SPVGLAK.W
		Eukaryotic translation initiation factor 5EIF5	S389S390			107.4	76.1	K.EAEEES*SGEEDEEDENIEVYYSK.A	
		Eukaryotic translation initiation factor 5B EIF5B	S113			43.8	110.0	K.KQSFDDNDS*EELEDKDSK.S	
		Eukaryotic translation initiation factor 5B EIF5B	S107S113			94.5	70.2	K.KQS*FDDNDS*EELEDKDSK.S	
		Eukaryotic translation initiation factor 5B EIF5B	S588S589S591			20.2	60.8	K.EMS*S*DS*EYDS*DDORTK.E	
		Eukaryotic translation initiation factor 5B EIF5B	S214			147.1	111.7	K.NKPGNIES*GNEDDDASF.K	
		Eukaryotic translation initiation factor 5B EIF5B	S135S137			11.2	69.3	K.VEMY*S*GS*DDDDDFNLKPK.K	
		Eukaryotic translation initiation factor 5B EIF5B	S182S183S186			112.4	114.3	R.INS*S*GES*GDES*DEFLQSR.K	
		Eukaryotic translation initiation factor 5B EIF5B	S511			34.6	63.3	K.EETPPPVEPEEEDTEDAGLDOWEAMAS*DEETEK.V	
		Eukaryotic translation initiation factor 5B EIF5B	S164			115.1	74.4	K.WDGS*EEDDNSK.K	
		Eukaryotic translation initiation factor 5B EIF5B	S588S589S591			8.6	36.5	K.EMS*S*DS*EY*DSDDORTK.E	
		Eukaryotic translation initiation factor 5B EIF5B	S182S183S186			60.1	116.0	R.INS*S*GES*GDESDEFLQSR.K	
		Eukaryotic translation initiation factor 5B EIF5B	T498S511			43.0	43.4	K.EETPPPVEPEEEDT*EDAGLDOWEAMAS*DEETEK.V	
		Eukaryotic translation initiation factor 5B EIF5B	S107			4.8	58.6	K.QS*FDDNDS*EELEDKDSK.S	
		Eukaryotic translation initiation factor 5B EIF5B	S589S591Y593			14.9	13.1	K.EMS*S*DS*EY*DS*DDORTK.E	
		Eukaryotic translation initiation factor 5B EIF5B	Y134S135			5.7	37.4	K.VEMY*S*GSDDDDFNKLPK.K	
		Eukaryotic translation initiation factor 6EIF6	T245			16.9	30.2	K.LNEAQPSTIATSMRDSLIDSLT*.-	
		Eukaryotic translation initiation factor 6EIF6	S239			6.6	29.5	K.LNEAQPSTIATSMRDS*LIDSLT.-	
		Eukaryotic translation initiation factor 6EIF6	S243			13.0	13.3	K.LNEAQPSTIATSMRDSLIDS*LT.-	
		EVER1 TMC6	S62			9.5	29.5	R.EVTGS*SQQTILWRPEGTQSTATLRI	
		EVER1 TMC6	T60			21.6	21.0	R.EVT*GSSQQTILWRPEGTQSTATLRI	
		EVER1 TMC6	S63			6.5	43.0	R.EVTGS*QQTILWRPEGTQSTATLRI	
		EVER2 protein TMC8	S521			12.1	28.1	R.AS*SRPFR.A	
		EVER2 protein TMC8	S722			100.0	29.4	R.FRFP*S*GAEL*.-	
		EVER2 protein TMC8	S522			8.2	31.0	R.AS*RPFR.A	
		EV12B EV12B	S271			-1.0	21.5	K.RTSS*ILTPWKPSK.S	
		EV12B EV12B	T267S268			6.8	43.6	K.RT*S*ISLTPWKPSK.S	
		EV12B EV12B	S268S271			16.5	26.9	R.TS*IS*ILTPWKPSK.S	
		EV12B EV12B	T267			9.1	23.6	K.RT*SIISLTPWKPSK.S	
		EV12B EV12B	S294			16.9	119.8	K.LFES*SENIEDSNPK.T	
		EV12B EV12B	S268			-0.4	31.3	R.TS*ISLTPWKPSK.S	





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		Protein Name	Gene	Phosphosites						
		Family with sequence similarity 54, member	MTFR1L B	S103				100.0	36.1	R.NAS*VPNLR.G
		Family with sequence similarity 54, member	MTFR1L B	S238				30.2	67.2	K.ASS*FADMMGILK.D
		Family with sequence similarity 54, member	MTFR1L B	S41				22.1	55.4	R.ASS*FETLPNISDQLCR.D
		Family with sequence similarity 54, member	MTFR1L B	S237					60.6	K.ASS*SFADMMGILK.D
		Family with sequence similarity 65, member	RIPOR1 A	S22				6.4	42.5	R.SQS*FAGVLGSHER.G
		Family with sequence similarity 65, member	RIPOR1 A	S20				12.2	87.8	R.S*QSFAGVLGSHER.G
		Family with sequence similarity 76, member	FAM76B B	S193				52.0	61.1	K.ISNLS*PEEEQGLWK.Q
		Family with sequence similarity 82, member	RMDN2 A	S128S129				100.0	13.3	R.RRFS*S*R.K
		Family with sequence similarity 82, member	RMDN3 C	S46				8.3	39.8	R.SQS*LPNSLDYQTSDPGR.H
		Family with sequence similarity 83, member	FAM83G G	S127				51.9	57.8	R.S*IPQLDLGWPDTIAYR.G
		Family with sequence similarity 91, member	FAM91A1 A1	S829				25.6	75.4	R.SPS*LLIANLHLQ.-
		Family with sequence similarity 91, member	FAM91A1 A1	S828				13.8	53.5	R.SPS*LLIANLHLQ.-
		Family with sequence similarity 91, member	FAM91A1 A1	S671S674				100.0	21.2	R.KLS*DAS*DER.G
		Far upstream element binding protein	FUBP1	S630				-0.4	21.7	R.QQAAYYAQTS*PQGM#QHPHAPQGG.-
		Far upstream element binding protein	FUBP1	T629				30.1	72.4	R.QQAAYYAQIT*SPQGM#QHPHAPQGG.-
		Far upstream element binding protein	FUBP1	Y626				6.5	11.2	R.QQAAYY*AGTSPQGM#QHPHAPQGG.-
		FAS associated factor 1	FAF1	S320				84.4	64.7	K.S*PMMPENAEENGALLQFTAEFSS.R.Y
		FAS associated factor 1	FAF1	S278T283					66.4	R.ENKCEKNTFNVLMVENSQVNNEDATETGQVNPQVEVEMASALD.V
		Fas receptor	FAS	S212				21.4	60.5	K.ENQGSHE*PTLNPETVAINLSVDVLSK.Y
		Fas receptor	FAS	S209				5.6	44.9	K.ENQGS*HESPTLNPETVAINLSVDVLSK.Y
		Fas receptor	FAS	T214				-2.2	62.9	K.ENQGSHEST*LNPETVAINLSVDVLSK.Y
		Fatty acid synthase	FASN	S974				14.9	40.2	R.LFDHPES*PTPNPTEPLFQAQAEVYK.E
		Fatty acid synthase	FASN	T976				2.3	46.5	R.LFDHPESPT*PNPTEPLFQAQAEVYK.E
		FBP3	FUBP3	S258				24.3	36.7	R.QQVAFYGQTLGQAQAH*S*QEQ.-
		FBP3	FUBP3	S538				24.4	65.5	K.QSHAASAAPQAS*SPPDYTMAWAEYYR.Q
		FBP3	FUBP3	S539				13.8	60.7	K.QSHAASAAPQAS*PPDYTMAWAEYYR.Q
		FCH and double SH3 domains 2	FCHSD2	S596S609S613				9.2	12.9	R.EIQISPSPKPHAS*LPPLPLYDQPPSS*PYPS*PKDR.S
		FCH domain only 1	FCHO1	S523S529				59.1	66.9	R.APPLPDS*PQPLAS*SPGPWGLEALAGDLM#PAPADPTARE
		FCH domain only 1	FCHO1	S523S530				43.1	79.8	R.APPLPDS*PQPLASS*PGPWGLEALAGDLM#PAPADPTARE
		FCH domain only 1	FCHO1	S583S585S587				34.5	19.6	R.S*LS*PS*PLGSSAASTALERPS*FLSOTGHGVSR.G
		Ferm, RhoGEF and pleckstrin domain	FARP2 protein 2	S399Y407				19.8	55.8	R.TPAS*PSSANAFY*SLSPSTLVPSGLPEFK.D
		Ferm, RhoGEF and pleckstrin domain	FARP2 protein 2	S399S408				1.5	33.8	R.TPAS*PSSANAFY*S*LSPSTLVPSGLPEFK.D
		Ferm, RhoGEF and pleckstrin domain	FARP2 protein 2	S399S410				1.7	42.1	R.TPAS*PSSANAFYSL*S*PSTLVPSGLPEFK.D
		Ferritin heavy chain 1	FTH1	S179				17.9	44.7	K.HTLGD*S*DNES.-
		Fetal Alzheimer antigen	BPTF	S216				100.0	36.2	R.S*PILEEK.D
		Fetal Alzheimer antigen	BPTF	T938				38.7	22.6	R.KSLEGT*K.N
		FGD1 family member 3	FGD3	S128				34.5	41.2	K.VTPQEEADS*DVGEEDSENTPQK.A
		FGD1 family member 3	FGD3	T121				5.9	12.5	K.VT*PQEEADSDVGEEDSENTPQK.A
		FGD1 family, member 2	FGD2	S654				30.9	34.5	R.AASGWSPSPWPNQGLDLS*D.-
		FGFR1 oncogene partner	FGFR1OP	S156S160				35.9	30.6	K.EKGPTTGEGALDLS*VH*S*PPKS*PEGK.T
		FGFR1 oncogene partner	FGFR1OP	S152S160				18.8	14.7	K.GPTTGEGALDLS*DVHSPPKS*PEGK.T
		Fibrillarin	FBL	S124				29.7	67.2	K.RVS*ISEGDDKIEYR.A
		Filamin A, alpha	FLNA	S2144				51.1	41.8	R.RAPS*VANVGSHCDLCLK.I
		FIP1 like 1	FIP1L1	T494S500				44.8	42.8	R.ERDHSP*TPSVFNS*DEERY
		FIP1 like 1	FIP1L1	S492T494S500				23.9	37.2	R.ERDHSP*TP*PSVFNS*DEERY
		FIP1 like 1	FIP1L1	S492				53.8	87.0	R.DHS*PTPSVFNSDEERY
		FIP1 like 1	FIP1L1	S492S496				42.0	78.2	R.DHS*PTPS*VFNSDEERY
		FIP1 like 1	FIP1L1	T81S87S89				16.9	69.6	K.VTET*EDDS*S*DS*DDDEDVHVITGDIK.T
		FIP1 like 1	FIP1L1	S85S87S89				39.3	59.8	K.VTETEDDS*S*DS*DS*DDDEDVHVITGDIK.T
		FIP1 like 1	FIP1L1	S304				100.0	44.2	R.AES*PDLR.R
		FIP1 like 1	FIP1L1	T494				5.0	95.7	R.DHSP*TPSVFNSDEERY
		FIP1 like 1	FIP1L1	S492T494				34.3	84.9	R.DHS*PT*PSVFNSDEERY
		FIP1 like 1	FIP1L1	T494S496S500				10.3	24.6	R.DHSP*TPS*VFNS*DEERY
		FIP1 like 1	FIP1L1	T81S85S87				18.9	73.9	K.VTET*EDDS*S*DS*DS*DDDEDVHVITGDIK.T
		FIP1 like 1	FIP1L1	S496S500				25.1	54.0	R.DHSP*TPS*VFNS*DEERY
		FIP1 like 1	FIP1L1	T79T81S85S89				7.8	54.0	K.VT*ET*EDDS*DS*S*DDDEDVHVITGDIK.T
		FIP1 like 1	FIP1L1	T494S496				13.3	48.1	R.DHSP*TPS*VFNSDEERY
		FIP1 like 1	FIP1L1	T79T81S87S89				16.4	23.1	K.VT*ET*EDDS*S*DS*DDDEDVHVITGDIK.T
		FIP1 like 1	FIP1L1	T81S85S89				8.8	51.5	K.VTET*EDDS*DS*S*DDDEDVHVITGDIK.T
		FIP1 like 1	FIP1L1	S492S500				31.4	67.1	R.DHS*PTPSVFNS*DEERY
		FIP1 like 1	FIP1L1	S492T494S496				15.9	47.5	R.DHS*PT*PS*VFNSDEERY
		FIP1 like 1	FIP1L1	T79T81S85S87				12.7	39.6	K.VT*ET*EDDS*DS*DS*DDDEDVHVITGDIK.T




















































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	<10	>10								
FK506 binding protein 15, 133kDaFKBP15	S1164							19.8	87.9	R.SSLSGDEEDELFK.G
FK506 binding protein 15, 133kDaFKBP15	S1162S1164							9.6	92.1	R.SSLSGDEEDELFK.G
FK506 binding protein 15, 133kDaFKBP15	S1114							112.5	64.0	R.LSLTSDPEEGDPLALGPES*PGEPPQPK.K
FK506 binding protein 15, 133kDaFKBP15	S311							27.7	33.9	R.DSAAPS*PIPGADNLSADPVVSPPTSIPFK.S
FK506 binding protein 15, 133kDaFKBP15	S307S311							5.0	25.2	R.DS*AAPS*PIPGADNLSADPVVSPPTSIPFK.S
FK506 binding protein 15, 133kDaFKBP15	S295S297								12.9	R.DS*GS*DGHSVSSRDSAAPSPIPGADNLSADPVVSPPTSIPFK.S
FK506 binding protein 15, 133kDaFKBP15	S320							3.3	15.9	R.DSAAPSPIPGADNLS*ADPVVSPPTSIPFK.S
FK506 binding protein 15, 133kDaFKBP15	S320S326							17.5	18.3	R.DSAAPSPIPGADNLS*ADPVVS*PPTSIPFK.S
FK506 binding protein 15, 133kDaFKBP15	S939S940S941							10.4	22.1	K.MVTLQLLNQOEKEES*TS*EEEEEA
FK506 binding protein 15, 133kDaFKBP15	S956							22.8	64.5	R.RPS*EQQSASASSGQPAPLNR.E
FK506 binding protein 15, 133kDaFKBP15	S1162							-0.4	60.7	R.SSLSGDEEDELFK.G
FK506 binding protein 15, 133kDaFKBP15	S1161S1162							11.6	51.0	R.S*SSLSGDEEDELFK.G
FK506 binding protein 15, 133kDaFKBP15	S311S326							13.6	13.1	R.DSAAPS*PIPGADNLSADPVVS*PPTSIPFK.S
FK506 binding protein 4FKBP4	S453							29.8	75.3	K.SNTAGSQS*QVETEA-
FKHR FOXO1	S298S301							24.5	12.5	K.WPAS*PGS*HSNDDFDNWSTFRPR.T
FKHR FOXO1	S298S303							6.4	16.1	K.WPAS*PGSHS*NDDFDNWSTFRPR.T
FLI1 FLI1	S241							37.6	55.3	R.GAWGNMNSGLNK*S*PPLGGAQTISK.N
FLI1 FLI1	S236							18.6	42.8	R.GAWGNMNS*GLNKSPPLGGAQTISK.N
Flightless 1 FLII	S436							100.0	45.4	R.RKDS*AQDDQAK.Q
Flightless 1 FLII	S856							32.7	44.3	R.NAEAVLQS*PGLSGK.V
FLJ10378 LARP1B	T362							11.2	75.5	R.GLST*SLPDLDSEPVWIEVK.K
FLJ10378 LARP1B	S363							-0.2	82.5	R.GLST*SLPDLDSEPVWIEVK.K
FLJ10378 LARP1B	S340S343							100.0	27.4	R.LIGS*PLS*PK.K
FLJ12387 KLC2	S609							14.2	89.4	R.TLSS*SSMDLSR.R
FLJ12387 KLC2	S582							30.2	70.1	R.ASS*LNFLNK.S
FLJ12387 KLC2	S581							8.5	49.2	R.AS*LNFLNK.S
FLJ12387 KLC2	S610							12.1	84.7	R.TLSSS*SMDLR.R
FLJ12387 KLC2	S609S611							10.5	35.6	R.TLSS*SS*MDLSR.R
FLJ12387 KLC2	S609S610							2.4	38.4	R.TLSS*SS*MDLSR.R
PRPF38A	S193S194							68.7	95.0	R.VSALEEDMDVES*SE*EEEEEEDEKL
FLJ14936 PRPF38A	S92S94							100.0	22.1	R.S*KS*PGHHR.S
FLJ14936 PRPF38A	S22							100.0	36.2	R.VPS*PDHRR
FLJ14936 PRPF38A	S182S194							13.7	83.2	R.VS*ALEEDMDVES*SEEEEEDEKLER.V
FLJ14936 PRPF38A	S182S193							3.6	11.4	R.VS*ALEEDMDVES*SEEEEEDEKLER.V
FLJ14936 PRPF38A	S73S75							100.0	10.8	R.HRS*KS*PR.R
PRPF38A	S105S107S109							100.0	11.2	R.HRS*HS*KS*PER.S
FLJ14936 PRPF38A	S39							26.0	20.5	R.RS*PTLR.Y
FLJ20105 protein ERCC6L	S820							45.4	15.2	K.GFGS*VEELCTNSSLGMEK.S
FLJ20105 protein ERCC6L	S946							7.4	97.9	K.LEEEPSASS*PQYACDFNLFEDSADNR.Q
FLJ20105 protein ERCC6L	Y949							5.6	79.5	K.LEEEPSASSPQ*YACDFNLFEDSADNR.Q
FLJ20105 protein ERCC6L	S1028							24.1	62.0	R.NVS*DGEEEDDSFKDTSINPFNTSLFQFSSVK.Q
FLJ20105 protein ERCC6L	S1098							100.0	44.5	R.S*LINMVLHDHVEDMEER.L
FLJ20514 GEMIN8	T124S126							34.9	70.5	K.EEEMET*ES*DAVEECDLSNMEITEELR.Q
FLJ20514 GEMIN8	T124S135							11.2	62.3	K.EEEMET*ESDAVEECDLS*NMEITEELR.Q
FLJ20514 GEMIN8	S126S135							8.9	46.7	K.EEEMETES*DAVEECDLS*NMEITEELR.Q
FLJ21924 QSER1	S991S992							0.9	31.3	K.NLEHLSFS*TS*DEDDPGYSQDAYK.S
FLJ36874 protein PATL1	S36							13.8	47.0	R.STS*PIGSPPVRA
FLJ36874 protein PATL1	T35S36							2.7	25.1	R.STS*PIGSPPVRA
FLJ46354 protein MROH7-	Y1166								12.0	K.RAY*SR.K
FLN29 protein TRAFD1	S415							19.1	38.2	R.LDSQPOETS*PELPR.R
FLN29 protein TRAFD1	S327								66.4	R.ALPSLNTGSS*PR.G
FLN29 protein TRAFD1	S325							13.9	44.6	R.ALPSLNTGS*SSPR.G
FLN29 protein TRAFD1	T323							6.1	24.0	R.ALPSLNT*GSSSPR.G
FLN29 protein TRAFD1	T414							35.7	12.3	R.LDSQPOET*PELPR.R
FMRP interacting protein, 82-kD NUFIP2	S652							55.8	57.7	R.NDS*WGSFDLRA
FMRP interacting protein, 82-kD NUFIP2	S629							26.0	99.2	K.DYEIESQNPLAS*PTNTLLGSAGE
FMRP interacting protein, 82-kD NUFIP2	S572							23.9	47.5	K.RTS*PQVLGSILK.S
FMRP interacting protein, 82-kD NUFIP2	T571							37.7	38.6	K.RT*SPQVLGSILK.S
FBNP4	S497S506							100.0	32.8	K.IDENS*DKEMEVEES*PEKIK.V
FBNP4 FBNP4	Y111							36.4	113.5	K.ATGGLCLLGAY*ADSDDDNDVSEKL
FBNP4 FBNP4	S114							33.4	102.8	K.ATGGLCLLGAYADS*DDDDNDVSEKL
FBNP4 FBNP4	S462							19.9	35.4	R.ATS*PESTR.S

Peak Area	iCV		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
	<10	>10	0	>10	0	>10	0	>10		
Protein Name	Gene	Phosphosites								
FBNP4	FBNP4	S429						12.3	33.2	R.ALEEGDGSVSGS*SPR.S
FBNP4	FBNP4	S961S962S963						14.5	25.7	R.ELDEEDNS*SS*SEEDRESTAQKRI
FBNP4	FBNP4	T461						27.8	28.3	R.AT*SPESTSR.S
FBNP4	FBNP4	S430						7.0	32.7	R.ALEEGDGSVSGS*PR.S
Fodrin beta	SPTBN1	S2160S2161S2						4.3	22.6	R.TS*SS*KESS*PIPS*PTSDRK.A
Fodrin beta	SPTBN1	S2165S2169						18.0	38.1	K.ESS*PIPS*PTSDRK
Fodrin beta	SPTBN1	S2138						78.4	68.3	K.GEQVSONGLPAEQGS*PR.M
Fodrin beta	SPTBN1	S2341						9.1	69.3	R.AQTLPTSVVTTTSES*PGKRE
Fodrin beta	SPTBN1	S2358						100.0	32.7	K.RFS*LFGK.K
Fodrin beta	SPTBN1	Y17						5.5	60.5	R.TSSISGPLSPAY*TGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S10						16.7	72.6	R.TSSIS*GPLSPAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S8						13.4	89.4	R.TSS*ISGPLSPAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S14						7.4	88.3	R.TSSISGPLS*PAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S8Y17						8.0	88.0	R.TSS*ISGPLSPAY*TGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S7S8						6.2	150.4	R.TS*SS*ISGPLSPAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S7Y17						-0.3	60.1	R.TS*SSISGPLSPAY*TGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S2160S2164S2						2.5	19.5	R.TS*SKESS*PIPS*PTSDRK.A
Fodrin beta	SPTBN1	S8S14						9.9	75.1	R.TSS*ISGPLS*PAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S2319						23.0	19.8	K.DDEEMNTWQAISSAIS*SAISSDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2303T2320						13.6	26.3	K.DDEEMNTWQAISS*SAISSDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2307T2317						9.1	15.4	K.DDEEMNTWQAISSAIS*SDKHEVSAS*QSTPASSRA
Fodrin beta	SPTBN1	S2307S2319						5.4	14.3	K.DDEEMNTWQAISSAIS*SDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2319T2320						3.4	13.9	K.DDEEMNTWQAISSAIS*SDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2314S2319T2						13.2	11.3	K.DDEEMNTWQAISSAIS*SDKHEVS*ASTQS*TPASSRA
Fodrin beta	SPTBN1	T2317S2319T23						4.6	15.1	K.DDEEMNTWQAISSAIS*SDKHEVSAST*QS*TPASSRA
Fodrin beta	SPTBN1	S2161S2164S2						8.2	19.3	R.TSS*KESS*PIPS*PTSDRK.A
Fodrin beta	SPTBN1	S2338						10.8	27.5	R.AQTLPTSVVTTTSES*ESSPGKRE
Fodrin beta	SPTBN1	S8S10						10.4	115.4	R.TSS*IS*GPLSPAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S8T18						2.9	45.2	R.TSS*ISGPLSPAY*GQVPYNNQLEGR.F
Fodrin beta	SPTBN1	S2314T2320						5.0	15.2	K.DDEEMNTWQAISSAIS*SDKHEVS*ASTQS*TPASSRA
Fodrin beta	SPTBN1	S2303S2319						8.7	22.5	K.DDEEMNTWQAISS*SAISSDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2316S2319						7.5	22.0	K.DDEEMNTWQAISSAIS*SDKHEVSAS*TS*TPASSRA
Fodrin beta	SPTBN1	S2304S2307S2						-1.5	12.4	K.DDEEMNTWQAISS*AIS*SSDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2303S2319T2						10.7	21.1	K.DDEEMNTWQAISS*SAISSDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	T2317T2320						11.9	13.1	K.DDEEMNTWQAISSAIS*SDKHEVSAST*QSTPASSRA
Fodrin beta	SPTBN1	S2164S2165						31.0	19.9	K.ESS*PIPSPTSDRK.A
Fodrin beta	SPTBN1	T2159S2160S2						8.8	13.4	R.T*SS*KESSPIPS*PTSDRK.A
Fodrin beta	SPTBN1	S2316T2320						9.5	12.8	K.DDEEMNTWQAISSAIS*SDKHEVSAS*TS*TPASSRA
Fodrin beta	SPTBN1	S2303T2317						-1.1	13.2	K.DDEEMNTWQAISS*SAISSDKHEVSAST*QSTPASSRA
Fodrin beta	SPTBN1	S2303S2314						-0.1	11.3	K.DDEEMNTWQAISS*SAISSDKHEVS*ASTQS*TPASSRA
Fodrin beta	SPTBN1	S2304T2320						7.5	19.2	K.DDEEMNTWQAISS*AISSDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2160S2161S2						4.5	23.8	R.TS*SS*KESS*PIPS*PTSDRK.A
Fodrin beta	SPTBN1	S2102						49.2	46.2	R.RPPS*PEPSTK.V
Fodrin beta	SPTBN1	S2340						11.1	54.2	R.AQTLPTSVVTTTSES*SPGKRE
Fodrin beta	SPTBN1	S7						2.5	88.0	R.TS*SSISGPLSPAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	T2297						12.8		K.DDEEMNTWQAISSAIS*SDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	S2160S2161S2						9.1	11.7	R.TS*SS*KESSPIPS*PTSDRK.A
Fodrin beta	SPTBN1	T2328S2340						15.6	42.9	R.AQT*LPSTSVVTTTSES*SPGKRE
Fodrin beta	SPTBN1	T2320						6.8	36.8	K.DDEEMNTWQAISSAIS*SDKHEVSASTQS*TPASSRA
Fodrin beta	SPTBN1	Y17T18						3.5	12.4	R.TSSISGPLSPAY*TGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	T2328S2341						18.2	11.3	R.AQT*LPSTSVVTTTSES*PGKRE
Fodrin beta	SPTBN1	T2328						56.8	83.8	R.AQT*LPSTSVVTTTSESSPGKRE
Fodrin beta	SPTBN1	S7S14						0.7	106.7	R.TS*SSISGPLS*PAYTGQVPYNNQLEGR.F
Fodrin beta	SPTBN1	T2317						7.3	23.1	K.DDEEMNTWQAISSAIS*SDKHEVSAST*QSTPASSRA
Fodrin beta	SPTBN1	S2164S2169						16.7	15.7	K.ESS*PIPS*PTSDRK.A
Forkhead box J3	FOXJ3	S223						10.9	29.8	K.VTLYNTDQDGS*PR.S
Forkhead box K1	FO XK1	T436S441						32.4	36.4	R.SGGLQT*PECLS*RE
Forkhead box K1	FO XK1	S445						95.6	47.3	R.EGS*PIPHDPEFGSK.L
Forkhead box K1	FO XK1	S416S420S428						20.8	53.2	R.S*APAS*PTHPGMLS*PR.S
Forkhead box K1	FO XK1	S213S223						43.0	25.8	K.EEAPAS*PLRPLYPQIS*PLK.I
Forkhead box K1	FO XK1	S299						6.7	41.2	K.AASEQQADTSGGDS*PKDESKPFFSYAQLVQIAISSAQDR.Q
Forkhead box K1	FO XK1	S309						2.1	39.2	K.AASEQQADTSGGDS*PKDESKPFFS*YAQLVQIAISSAQDR.Q

Peak Area	%CV		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
<10	0	10	0	10	0	10	0	10		
10-20	20	30	20	30	20	30	20	30		
20-30	30	40	30	40	30	40	30	40		
30-40	40	50	40	50	40	50	40	50		
40-50	50	60	50	60	50	60	50	60		
50-60	60	70	60	70	60	70	60	70		
60-70	70	80	70	80	70	80	70	80		
70-80	80	90	80	90	80	90	80	90		
80-90	90	100	90	100	90	100	90	100		
>100										
Protein Name	Gene	Phosphosites								
Forkhead box K1 FOXK1	S416S420T422							14.0	27.9	R.S*APAS*PT*HPGLMSPR.S
Forkhead box K1 FOXK1	S416S420							47.3	45.0	R.S*APAS*PTHPGLMSPR.S
Forkhead box K1 FOXK1	Y219S223							39.4	18.4	K.EEAPASPLRPLY*PQIS*PLK.I
Forkhead box K1 FOXK1	S295S299							5.7	51.0	K.AASEQQADT*S*GGDS*PKDESKPPFSYAQLVQAISQAQR.Q
Forkhead box K1 FOXK1	T294S299							7.3	55.4	K.AASEQQADT*SGGDS*PKDESKPPFSYAQLVQAISQAQR.Q
Forkhead box K1 FOXK1	S309Y310							9.6	51.8	K.AASEQQADTSGGDS*PKDESKPPFS*Y*YAQLVQAISQAQR.Q
Forkhead box K1 FOXK1	S213							14.0	27.6	K.EEAPAS*PLRPLYQISPLK.I
Forkhead box K1 FOXK1	S441							11.1	18.0	R.SGGLQTPECLS*R.E
Forkhead box K1 FOXK1	S416T422							17.3	33.1	R.S*APASPT*HPGLMSPR.S
Forkhead box K1 FOXK1	S420T422S428							7.4	30.1	R.SAPAS*PT*HPGLMS*PR.S
Forkhead box K2 FOXK2	S398							100.0	49.9	R.EGS*PAPEPEPGAQPK.L
Forkhead box K2 FOXK2	S424S431							13.2	65.1	R.FAQS*APGSPLS*SQPVLITVQR.Q
Forkhead box K2 FOXK2	S428S431							9.1	38.2	R.FAQSAPGS*PLS*SQPVLITVQR.Q
Forkhead box K2 FOXK2	S428							20.9	45.3	R.FAQSAPGS*PLSSQPVLITVQR.Q
Forkhead box K2 FOXK2	S424S428							22.0	39.0	R.FAQS*APGS*PLSSQPVLITVQR.Q
Forkhead box P4 FOXP4	S443							-0.3	45.0	R.SS*DKFCSPISSELAQNHIFYK.N
Forkhead box protein O3A ZNF286B	S75I2							18.1	13.8	-MAEAPAS*PAPLS*PLEVLDPEFEPQSRPR.S
Formin binding protein 1 FNBP1	S497							19.2	61.8	R.RQ*S*GLYDSQNPPTVNNCAQDRES
Formin binding protein 1 FNBP1	T507							-1.4	17.0	R.RQSGLYDSQNPPTVNNCAQDRESPDGS*Y*YTEEQSQSEMK.V
Formin binding protein 1 FNBP1	S521							10.0	22.1	R.RQSGLYDSQNPPTVNNCAQDRESPDGS*Y*YTEEQSQSEMK.V
Formin binding protein 1 FNBP1	S497T507							12.9	20.7	R.RQ*S*GLYDSQNPPTVNNCAQDRESPDGSYTEEQSQSEMK.V
Formin binding protein 1 FNBP1	S497Y500								28.8	R.RQ*S*GLY*DSQNPPTVNNCAQDRESPDGSYTEEQSQSEMK.V
Formin binding protein 1 FNBP1	S296S299							19.0	40.6	R.TV*S*DNS*LSNSR.G
Formin binding protein 1 FNBP1	S296							25.3	63.3	R.TV*S*DNSLSNSR.G
Formin binding protein 1 FNBP1	T294							9.8	27.9	R.T*VSDNSLSNSR.G
Formin binding protein 1 FNBP1	S517S521							14.6	95.3	R.ES*PDGS*Y*YTEEQSQSEMK.V
Formin binding protein 1 FNBP1	T507S521							5.3	18.6	R.RQSGLYDSQNPPTVNNCAQDRESPDGS*Y*YTEEQSQSEMK.V
Formin binding protein 1 FNBP1	S497Y522							13.6	21.9	R.RQ*S*GLYDSQNPPTVNNCAQDRESPDGS*Y*YTEEQSQSEMK.V
Formin binding protein 1 FNBP1	S497S521							13.0	23.3	R.RQ*S*GLYDSQNPPTVNNCAQDRESPDGS*Y*YTEEQSQSEMK.V
Formin binding protein 1 FNBP1	S497S517S521							9.1	20.2	R.RQ*S*GLYDSQNPPTVNNCAQDRES*PDGS*Y*YTEEQSQSEMK.V
Formin binding protein 1 FNBP1	T507S517							5.4	42.2	R.QSGLYDSQNPPTVNNCAQDRES*PDGSYTEEQSQSEMK.V
Formin binding protein 1 FNBP1	T294S296							20.9	34.0	R.T*V*S*DNSLSNSR.G
Formin binding protein 1 FNBP1	T294S299							20.1	29.8	R.T*VSDNS*LSNSR.G
Formin binding protein 1 FNBP1	Y500							5.6	31.8	R.RQSGLY*DSQNPPTVNNCAQDR.E
FMNL1	S184							67.8	48.9	K.NKPLEQS*VEDLSK.G
Formin like FMNL1	S624							100.0	56.2	R.RD*S*ELGPGVKA
Formin like 2 FMNL3	T622							100.0	22.2	K.KPIKT*K.F
Formin like 3 FMNL3	S174							38.8	67.0	R.S*IEDLQPPSALSAPFTNSLAR.S
Formin like 3 FMNL3	S182							3.1	24.0	R.SIEDLQPP*S*ALSAPFTNSLAR.S
Formin-like protein 1 FMNL1	S681							48.8	85.8	R.RPPGPPPLQVTSOLS*L-
Formin-like protein 1 FMNL1	T677							2.2	27.8	R.RRPPGPPPLQVT*SOLS.L-
Forty-two-three domain containing 1 FYTTD1	S23							78.7	84.0	R.S*ENLKDIDMSLDDIK.L
FRAS1-related extracellular matrix protein 3 FREM3	Y1044							-0.3	19.6	K.DS*Y*QWVVGNSIEK.V
WAPL	S264S269							22.3	34.3	K.RPES*PSEIS*PIKGSVR.T
Friend of EBNA2 WAPL	S120							36.0	82.3	K.VEEESTGDPFGFDS*DDIESLPVSSK.N
Friend of EBNA2 WAPL	S502S504							54.6	79.8	K.IKYGFDDL*S*ES*EDDEDDCCQVER.K
Friend of EBNA2 WAPL	S111							6.5	19.8	K.VEEES*TGDPFGFDSDDIESLPVSSK.N
Friend of EBNA2 WAPL	S266S269							13.1	18.9	K.RPESP*S*EIS*PIKGSVR.T
Friend of EBNA2 WAPL	S264S266							3.0	47.8	K.RPES*PS*EISPIKGSVR.T
FtsJ homolog 3 FTSJ3	S335S336							40.2	155.7	K.ALDISL*S*SGEEDEGDEEDSTAGTTK.Q
FtsJ homolog 3 FTSJ3	T467S468S471							13.2	55.1	R.DDIYVSDVEDDGGDT*S*SLDS*DLDPPELAGVR.G
FtsJ homolog 3 FTSJ3	S458T467S468							24.4	94.1	R.DDIYV*S*DVEDDGGDT*S*SLDS*DLDPPELAGVR.G
FtsJ homolog 3 FTSJ3	Y456S458T467							11.6	85.1	R.DDIY*V*S*DVEDDGGDT*SLDS*DLDPPELAGVR.G
FtsJ homolog 3 FTSJ3	S458T467S471							2.2	64.3	R.DDIYV*S*DVEDDGGDT*SLDS*DLDPPELAGVR.G
FtsJ homolog 3 FTSJ3	S458T467S468							6.6	35.3	R.DDIYV*S*DVEDDGGDT*S*SLDS*DLDPPELAGVR.G
FtsJ homolog 3 FTSJ3	T436S448							9.1	64.0	R.GHQLLEVT*QGDMISAADTFLS*DLPR.D
FtsJ homolog 3 FTSJ3	S441S448							8.4	45.4	R.GHQLLEVTQGDM*S*AADTFLS*DLPR.D
FtsJ homolog 3 FTSJ3	S333S335S336							44.1	67.7	K.ALDIS*LS*S*SGEEDEGDEEDSTAGTTK.Q
FtsJ homolog 3 FTSJ3	Y456S458S468							4.4	74.7	R.DDIY*V*S*DVEDDGGDT*SLDS*DLDPPELAGVR.G
FtsJ homolog 3 FTSJ3	S333S335							25.1	52.9	K.ALDIS*LS*S*SGEEDEGDEEDSTAGTTK.Q
FtsJ homolog 3 FTSJ3	Y456S458T467							11.1	58.3	R.DDIY*V*S*DVEDDGGDT*S*SLDS*DLDPPELAGVR.G
FtsJ homolog 3 FTSJ3	S335S336S347							7.5	33.3	K.ALDISL*S*SGEEDEGDEEDS*TAGTTK.Q

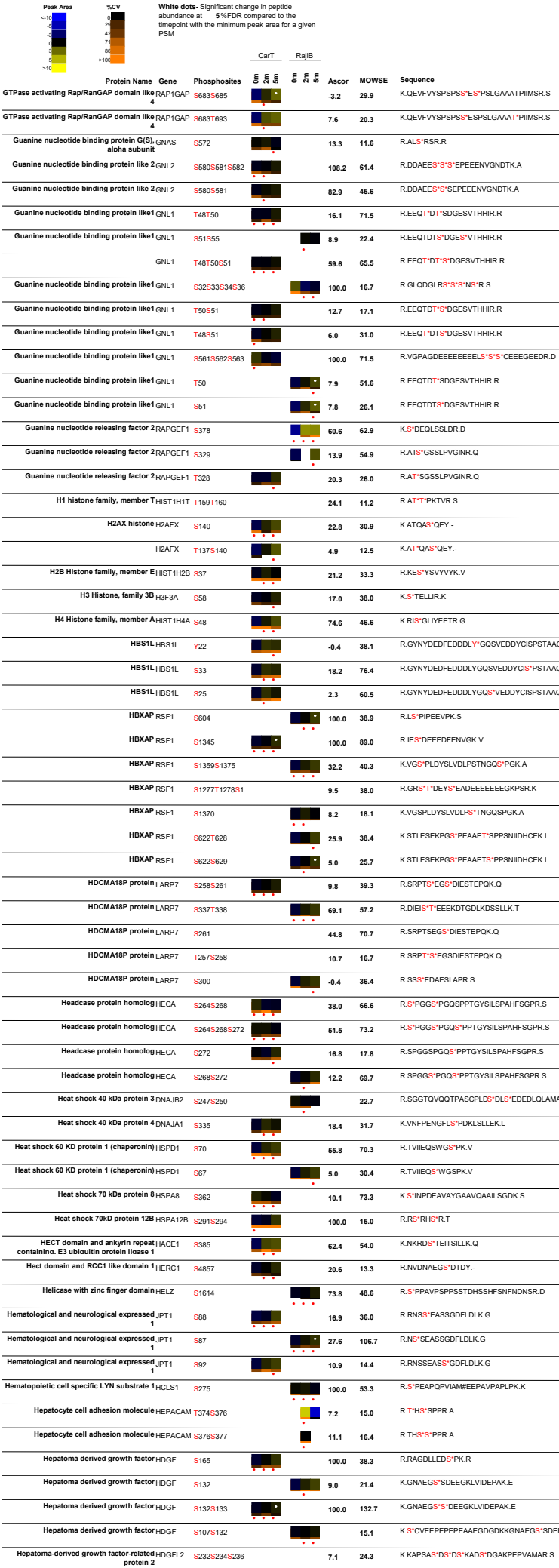
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
Protein Name	Gene	Phosphosites							
FUS FUS	S277						51.8	77.6	R.HD <sup>S</sup> EQDSDNNTIFVQGLGENVTIESVADYFK.Q
FUS interacting protein 1 SRSF10	T255S256						5.3	16.2	R.SWT <sup>S</sup> PK.S
FUS interacting protein 1 SRSF10	S133						28.6	27.8	R. <sup>S</sup> FDYNYRR.S
FUS interacting protein 1 SRSF10	S131S133						44.5	38.7	R. <sup>S</sup> RS <sup>S</sup> FDYNYR.R
FUS interacting protein 1 SRSF10	S156S158						24.4	18.1	R. <sup>S</sup> RS <sup>S</sup> HSDNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S158						30.0	66.3	R. <sup>S</sup> HSDNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S158S160						36.2	80.5	R. <sup>S</sup> HS <sup>S</sup> DNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S156S158S160						60.5	49.3	R. <sup>S</sup> RS <sup>S</sup> HS <sup>S</sup> DNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S171S173						100.0	12.2	R.NR <sup>S</sup> F <sup>S</sup> R.S
FUS interacting protein 1 SRSF10	S158S160						100.0	22.1	R. <sup>S</sup> HS <sup>S</sup> DNDRFK.H
FUS interacting protein 1 SRSF10	S253S256						16.7	19.9	R. <sup>S</sup> WT <sup>S</sup> PK.S
FUS interacting protein 1 SRSF10	S168						9.0	26.7	R.SHSDNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S156S158T171						14.5	32.4	R. <sup>S</sup> RS <sup>S</sup> HSDNDRPNC <sup>S</sup> WNT <sup>S</sup> QYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S160S168T171						9.4	24.4	R.SRSH <sup>S</sup> DNDRPNC <sup>S</sup> WNT <sup>S</sup> QYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S156S168						9.7	41.8	R. <sup>S</sup> RS <sup>S</sup> HSDNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S156T171						3.4	27.9	R. <sup>S</sup> RS <sup>S</sup> HSDNDRPNC <sup>S</sup> WNT <sup>S</sup> QYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S160						1.4	40.9	R.SH <sup>S</sup> DNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S156S158S160						100.0	17.6	R. <sup>S</sup> RS <sup>S</sup> HS <sup>S</sup> DNDRFK.H
FUS interacting protein 1 SRSF10	S251S253T255						2.7	11.1	R. <sup>S</sup> RS <sup>S</sup> WT <sup>S</sup> PK.S
FUS interacting protein 1 SRSF10	S156S158S168						19.2	29.2	R. <sup>S</sup> RS <sup>S</sup> HSDNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 CCNL2	S121S123						10.2	11.2	R. <sup>S</sup> RS <sup>S</sup> YER.T
FUS interacting protein 1 SRSF10	S256						22.5	16.5	R.SWT <sup>S</sup> PK.S
FUS interacting protein 1 SRSF10	S156S160S168						7.3	22.9	R. <sup>S</sup> RS <sup>S</sup> HS <sup>S</sup> DNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FUS interacting protein 1 SRSF10	Y136						1.9	19.4	R.SFDY <sup>N</sup> NYRR.S
FUS interacting protein 1 SRSF10	S156S168T171						-3.3	41.7	R. <sup>S</sup> RS <sup>S</sup> HSDNDRPNC <sup>S</sup> WNT <sup>S</sup> QYSSAYYTSR.K
FUS interacting protein 1 SRSF10	S160S168						-0.2	20.5	R.SH <sup>S</sup> DNDRPNC <sup>S</sup> WNTQYSSAYYTSR.K
FXR1 FXR1	S409						15.7	32.5	R.RGPNYTSGYGTNSELNPS <sup>S</sup> ETESER.K
FXR1 FXR1	S406S409						11.0	14.7	R.RGPNYTSGYGTNSELN <sup>S</sup> PS <sup>S</sup> ETESER.K
FXR2 FXR2	S601S603						18.7	56.4	R.TDGS <sup>S</sup> IS <sup>S</sup> GDRQPVTVADYISRA
FXR2 FXR2	S601						7.5	25.1	R.TDGS <sup>S</sup> ISGDRQPVTVADYISRA
FYB FYB1	T443						-1.2	39.7	K.SPVNEDNQDGV <sup>T</sup> HSDGAGNLDEEQDSEGETYEDIEASK.E
FYB FYB1	S432							76.2	K. <sup>S</sup> SPVNEDNQDGVTHSDGAGNLDEEQDSEGETYEDIEASK.E
FYB FYB1	S457						10.8	30.0	K.SPVNEDNQDGVTHSDGAGNLDEEQD <sup>S</sup> SEGETYEDIEASK.E
Fyn YES1	Y420						12.1	38.5	R.LIEDNE <sup>Y</sup> TAR.Q
G patch domain containing 2 GPATCH2	S115S117						100.0	54.0	K.DHS <sup>S</sup> DS <sup>S</sup> DDQMLVAK.R
G patch domain containing 8 GPATCH8	S1033						14.0	22.8	R. <sup>S</sup> QSPHYFR.S
G patch domain containing 8 GPATCH8	S1035						10.4	25.1	R.SQ <sup>S</sup> PHYFR.S
G protein coupled purinergic receptor P2Y8 P2RY8	S324						39.9	30.9	R.RES <sup>S</sup> LFSAR.T
G protein coupled purinergic receptor P2Y8 P2RY8	S324S327						100.0	44.6	R.RES <sup>S</sup> LFS <sup>S</sup> AR.T
G protein coupled purinergic receptor P2Y8 P2RY8	S335						45.6	16.1	R. <sup>S</sup> EAGAHPEGMEGATRPGLQR.Q
G protein coupled receptor kinase 6 GRK6	S484						13.9	50.4	K.DVLDIEQFS <sup>S</sup> TVK.G
G protein coupled receptor kinase 6 GRK6	S484T485						36.4	46.3	K.DVLDIEQFS <sup>S</sup> T <sup>S</sup> VKGVELEPTDQDFYQK.F
G protein dependent receptor kinase 2 GRK2	S670						71.9	50.3	R. <sup>S</sup> PVVELSK.V
G protein signalling modulator 3 GPSM3	S59						8.1	57.1	R.SASLL <sup>S</sup> LQTELLDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S54						10.1	51.7	R. <sup>S</sup> ASLLSLQTELLDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S54S59						12.3	68.9	R. <sup>S</sup> ASLL <sup>S</sup> LQTELLDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S54S56						24.8	31.5	R. <sup>S</sup> AS <sup>S</sup> LLSLOTELLDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S54T62						7.2	84.5	R. <sup>S</sup> ASLLSLQ <sup>T</sup> ELLDDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	T62						8.3	73.7	R.SASLLSLQ <sup>T</sup> ELLDDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S59T62						6.7	69.4	R.SASLL <sup>S</sup> LQ <sup>T</sup> ELLDDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S56S59						4.6	64.5	R.SA <sup>S</sup> LL <sup>S</sup> LQTELLDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S56T62						9.1	76.6	R.SA <sup>S</sup> LLSLQ <sup>T</sup> ELLDDLVAEAQSR.R
G protein signalling modulator 3 GPSM3	S56						-0.1	26.7	R.SA <sup>S</sup> LLSLQTELLDLVAEAQSR.R
G-protein signalling modulator 1 GPSM1	S469						23.9	84.4	R.APS <sup>S</sup> SDEECFFDLLTK.F
G-protein signalling modulator 1 GPSM1	S470						10.2	44.0	R.APS <sup>S</sup> SDEECFFDLLTK.F
Ga55 TACC1	S276						9.2	80.4	K.ASYHFSPEELDENTS <sup>S</sup> PLLGDAF.F
Gamma synergin SYNRG	S854S855						15.5	33.3	K.HVMSD <sup>S</sup> S <sup>S</sup> LDLPTVSGQHPPAADIEDLK.Y
Gamma synergin SYNRG	S852S854						19.0	21.1	K.HVMS <sup>S</sup> DS <sup>S</sup> SLDLPTVSGQHPPAADIEDLK.Y
Gamma synergin SYNRG	S752						12.4	13.6	R.QL <sup>S</sup> LEGSGLGEDLKDNTPSGK.S
Gamma synergin SYNRG	S935						12.1	56.3	K.ETSFGS <sup>S</sup> SENITMTLSK.V
Gamma synergin SYNRG	S852S855						14.7	41.6	K.HVMS <sup>S</sup> DS <sup>S</sup> SLDLPTVSGQHPPAADIEDLK.Y
Gamma synergin SYNRG	S1075						10.6	12.8	R.SL <sup>S</sup> LGDK.E

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence	
		Protein Name	Gene	Phosphosites							
		Gamma synergin	SYNRG	S812				46.8	86.9	K.S*LDLPSIGGSSVGK.E	
<hr/>											
		Gamma-tubulin complex component 3	TUBGCP3	S896				27.8	23.7	R.LRVLS*LGTR.G	
		Gasdermin domain containing 1	GSDMD	S252				11.9	76.0	R.STS*EGAWPQLPSGLSMMR.C	
		Gasdermin domain containing 1	GSDMD	T251				-0.3	75.6	R.ST*EGAWPQLPSGLSMMR.C	
		GATA binding protein 3	GATA3	S110S115				13.0	35.9	K.ALGSHHTAS*PWNLS*PFSK.T	
		GATA binding protein 3	GATA3	S10S115				11.2	18.2	K.ALGS*HHTASPWNLS*PFSK.T	
		GATA zinc finger domain containing 2B	GATAD2B	T120S135				5.0	47.1	R.GRLT*PSPDIVLSDNEAS*PR.S	
		GATA zinc finger domain containing 2B	GATAD2B	T120S122S129				67.5	38.9	R.GRLT*PS*PDIVLS*DNEASS*PR.S	
		GATA zinc finger domain containing 2B	GATAD2B	T120S122S135				50.0	12.0	R.GRLT*PS*PDIVLSDNEAS*PR.S	
		GATA zinc finger domain containing 2B	GATAD2B	T120S122S129				50.0	30.2	R.GRLT*PS*PDIVLS*DNEAS*SPR.S	
		GATA zinc finger domain containing 2B	GATAD2B	T120S122S134				37.1	10.7	R.GRLT*PS*PDIVLSDNEA*SPR.S	
		GCF	GCF2	T213S214S217				60.6	82.7	R.NEET*S*EES*QDEKQDTWEQQQMR.K	
		GCF	GCF2	S429S430				10.2	65.9	R.VLSGNCNHQEGT*S*DDELPSAEMIDFQK.S	
		GCF	GCF2	S419T428				6.1	12.2	R.VLS*GNCNHQEGT*SSDELPSAEMIDFQK.S	
		GCF	GCF2	T428S430				0.8	16.1	R.VLSGNCNHQEGT*S*DDELPSAEMIDFQK.S	
		GCF	GCF2	S16S17S19				27.0	26.0	R.AADS*S*DS*DGAEESPAEPGAPR.E	
		GEM interacting protein	GMIP	S437S440				11.3	15.5	R.SLDS*PTS*SPGAGTR.Q	
		GEM interacting protein	GMIP	S19				20.1	25.6	R.KRYS*DIFR.S	
		GEM interacting protein	GMIP	S437S441				12.6	65.2	R.SLDS*PTS*PGAGTR.Q	
		GEM interacting protein	GMIP	T439S441				12.6	46.4	R.SLDSPT*SS*PGAGTR.Q	
		GEM interacting protein	GMIP	Y18					31.0	R.KRY*SDIFR.S	
		Gemin 5	GEMIN5	S778				14.9	44.4	K.ENSGPVENGVS*DQEGEEQAR.E	
		General transcription factor 2 I	GTFF2I	S674				12.2	108.0	R.S*PGNSKVP EIVTVEGPNNNNPQTSAVR.T	
		General transcription factor 2 I	GTFF2I	S679				2.8	65.1	R.SPGNS*KVPEIVTVEGPNNNNPQTSAVR.T	
		General transcription factor 2 I	GTFF2I	S818					33.4	K.ES*TSSKSPPR.K	
		General transcription factor 2 I	GTFF2I	S830					17.4	42.0	K.INS*SPNVNTTASGVEDLNIIQVTIPDDNRL
		General transcription factor 2 I	GTFF2I	S677				8.7	80.2	R.SPGS*NSKVPEIVTVEGPNNNNPQTSAVR.T	
		General transcription factor 2 I	GTFF2I	S823				6.8	50.8	K.ESTSSKS*PPR.K	
		General transcription factor 2 I	GTFF2I	S831				22.8	67.7	R.KINS*PNVNTTASGVEDLNIIQVTIPDDNRL	
		General transcription factor IIA, 1, 19/37kDa	GTFA2I	S316S321				16.1	80.2	K.DGAEDGQVEEPLNS*EDDV*S*DEEGQELFDTENVVVCQYDK.I	
		General transcription factor IIC, GTF3C2 polypeptide 2, beta 110kDa	S892					27.8	56.0	R.AHFNAMFQPS*SPTR.R	
		General transcription factor IIC, GTF3C2 polypeptide 2, beta 110kDa	S893					21.2	55.9	R.AHFNAMFQPS*PTR.R	
		General transcription factor IIC, GTF3C2 polypeptide 2, beta 110kDa	S167					32.1	28.7	K.DLDRPESQS*PK.R	
		General transcription factor IIC, GTF3C2 polypeptide 2, beta 110kDa	S220					7.0	14.4	K.VSS*PTKPK.K	
		GFAT	GFPT1	S243					23.9	92.6	R.VDS*TTCLFPVEEKA
		GIGYF1	GIGYF1	S862					17.0	27.7	R.S*SPSLSDSYSHLSGRPIR.K
		Girdin	CCDC88A	S149T1509				8.1	51.4	R.SMS*MNDLVQSMVLAGQWTGST*ENLEVPDDISTGKR.R	
		Girdin	CCDC88A	S149T1506				15.2	38.7	R.SMS*MNDLVQSMVLAGQWT*GSTENLEVPDDISTGKR.R	
		Girdin	CCDC88A	S1489S1491				3.2	20.3	R.S*MS*MNDLVQSMVLAGQWTGSTENLEVPDDISTGKR.R	
		Girdin	CCDC88A	S1491S1508				4.6	42.6	R.SMS*MNDLVQSMVLAGQWTGS*TENLEVPDDISTGKR.R	
		GIT1	GIT1	S385S388				13.4	94.5	R.SQSOLDQDQHDY*S*VAS*DEDTDOEPLR.S	
		GIT1	GIT1	S362				30.2	93.9	K.SLSS*PTDNLELSLR.S	
		GIT1	GIT1	S361				11.4	83.3	K.SLS*SPTDNLELSLR.S	
		GIT1	GIT1	S414				5.8	63.0	R.SMDS*DLSDGAVTLQEYLELKK.A	
		GIT1	GIT1	Y383S385				14.7	26.4	R.SQSOLDQDQHDY*DS*VASDEDTDOEPLR.S	
		GIT1	GIT1	S410				37.7	81.5	R.S*MDSSDLSDGAVTLQEYLELKK.A	
		GIT1	GIT1	S592				7.4	13.4	R.HGS*GADSDYENTQSGDPLLGLEGK.R	
		GIT1	GIT1	S592S596				38.4	55.3	R.HGS*GAD*S*DYENTQSGDPLLGLEGK.R	
		GIT1	GIT1	Y383S388				27.5	92.3	R.SQSOLDQDQHDY*DSVAS*DEDTDOEPLR.S	
		GIT1	GIT1	S413				-0.3	76.0	R.SMDS*SDLSGAVTLQEYLELKK.A	
		GIT1	GIT1	S417				2.1	31.7	R.SMSSDL*S*DGAVTLQEYLELKK.A	
		GL004 protein	MEF	S157				35.1	34.6	R.SMS*ENAVR.Q	
		GL004 protein	MEF	S155				9.2	28.3	R.S*MS*ENAVR.Q	
		Glucocorticoid induced transcript 1	GLCC1	S76				7.4	32.9	R.GS*QHSPTRRPPVAAAAASGLSLPGPGAAR.G	
		Glucocorticoid induced transcript 1	GLCC1	T177				3.2	31.8	R.TTSLDTIT*GPYLTGQWPR.D	
		Glucocorticoid induced transcript 1	GLCC1	S258				59.9	45.0	K.DRQS*PLHGNHITISHTQATGSR.S	
		Glucocorticoid induced transcript 1	GLCC1	T175				3.0	45.9	R.TTSLDT*ITGPYLTGQWPR.D	
		Glucocorticoid induced transcript 1	GLCC1	S223				41.2	62.4	R.SA*S*WGSADQLK.E	
		Glucocorticoid induced transcript 1	GLCC1	S79				3.5	41.8	R.GSQHS*PTRPPVAAAAASGLSLPGPGAAR.G	
		Glucocorticoid induced transcript 1	GLCC1	S171				-0.4	61.2	R.TS*SLDTITGPYLTGQWPR.D	
		Glucocorticoid induced transcript 1	GLCC1	S172				-0.4	57.5	R.TS*LDTITGPYLTGQWPR.D	
		Glucocorticoid receptor DNA binding factor 1	ARHGAP3	S1150				46.9	53.5	R.KVS*IVSKPVLYR.T	

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				5	6	5	6	5	6			
Protein Name			Gene	Phosphosites								
Glucocorticoid receptor DNA binding factor ARHGAP3			1	S1179						32.3	54.4	R.TSFSVGS*QDDELGPRLK
Glucocorticoid receptor DNA binding factor ARHGAP3			1	S975						1.2	30.9	R.AGS*PLCNSLNQDSEEDIEPSYSLFR.E
Glucocorticoid receptor DNA binding factor ARHGAP3			1	S980S985						19.1	61.0	R.AGSPLCNS*NLQDS*EEDIEPSYSLFR.E
Glucocorticoid receptor DNA binding factor ARHGAP3			1	S1070						18.0	78.7	K.S*YSSSPVLPQDGFDPDSYAEPMADVKKPR.N
Glucocorticoid receptor DNA binding factor ARHGAP3			1	S970						60.6	86.6	K.NIEATHMYDNAEACSTTEEVFN*PR.A
Glucocorticoid receptor DNA binding factor ARHGAP3			1	S975S985						37.3	64.4	R.AGS*PLCNSLNQDS*EEDIEPSYSLFR.E
Glutamate-rich WD repeat-containing GRWD1 protein 1				S119S122						63.6	73.0	R.MHNLHGTKPPPS*EGS*DEEEEEEDEEDEER.K
Glutamate-rich WD repeat-containing GRWD1 protein 1				T114S122						10.8	64.2	R.MHNLHGTKPPPS*EGS*DEEEEEEDEEDEER.K
Glutamate-rich WD repeat-containing GRWD1 protein 1				T114S119						13.5	74.5	R.MHNLHGTKPPPS*EGS*DEEEEEEDEEDEER.K
CAD				S1859						100.0	49.9	R.AS*DPGLPAEPK.E
Glutamine dependent carbamoyl phosphate synthase				S1406						36.8	13.4	R.RLS*SFVTK.G
Glutamine-tRNA ligase (Fragment) QARS				T47						100.0	22.5	R.GLT*LAQGVK.W
Glutamine-fructose-6-phosphate transaminase 2				Y479S494						3.6	12.7	K.AY*TSQFSLVM*FGLMMHS*EDR.I
Glutamine-rich protein 1 GRICH1				T347						2.3	19.9	R.GDPQQQSITHIAIQEYNAVH*VSGSPT*ALAAVK.L
Glutamine-rich protein 1 GRICH1				S343						-0.5	15.2	R.GDPQQQSITHIAIQEYNAVH*V*GSPTALAAVK.L
Glutamyl-prolyl-tRNA synthetase EPRS				S885						16.1	45.6	K.EYIPGQPLPSQS*SDS*SPTR.N
Glutamyl-prolyl-tRNA synthetase EPRS				S883						8.9	36.8	K.EYIPGQPLPSQS*SDS*SPTR.N
Glutamyl-prolyl-tRNA synthetase EPRS				S882S885						13.6	31.4	K.EYIPGQPLPSQS*SDS*SPTR.N
Glutamyl-prolyl-tRNA synthetase EPRS				S882						14.7	33.4	K.EYIPGQPLPSQS*SDS*SPTR.N
Glutamyl-prolyl-tRNA synthetase EPRS				S883S886						9.9	11.6	K.EYIPGQPLPSQS*SDS*PTR.N
Glutamyl-prolyl-tRNA synthetase EPRS				S882S886						15.3	23.4	K.EYIPGQPLPSQS*SDS*PTR.N
Glutamyl-prolyl-tRNA synthetase EPRS				S886						7.0	11.9	K.EYIPGQPLPSQS*SDS*PTR.N
Glutamyl-prolyl-tRNA synthetase EPRS				S880S885						7.3	14.0	K.EYIPGQPLPS*QSSDS*SPTR.N
Glyceraldehyde 3 phosphate dehydrogenase				S210						8.9	26.3	R.GALQNIIPAS*TGAAK.A
Glyceraldehyde 3 phosphate dehydrogenase				T75						-4.2	20.9	K.LVINGNPIT*IFQERDPS*Y
Glyceraldehyde 3 phosphate dehydrogenase				T182						17.0	66.3	K.VIHDFGIVEGLMTT*VHAT*QTK.T
Glyceraldehyde 3 phosphate dehydrogenase				S83						-3.3	27.0	K.LVINGNPIT*FQERDPS*Y
Glycogen phosphorylase, brain type PYGB				S15						100.0	31.9	R.KQIS*YR.G
Glycogen synthase kinase 3 alpha GSK3A				S21						22.2	104.0	R.TSS*FAEPGGGGGGGGGGPGGSASPGGTGGGK.A
Glycogen synthase kinase 3 alpha GSK3A				S20						-0.4	94.4	R.TS*FAEPGGGGGGGGGGPGGSASPGGTGGGK.A
Glycogen synthase kinase 3 beta GSK3B				Y216						16.9	43.5	R.GEPNVSY*ICSR.Y
Glycogen synthase kinase 3 beta GSK3B				S9						8.7	53.4	R.TTS*FAESCKPVQSPASFGMK.V
Golgi autoantigen, golgin subfamily A, 4 GOLGA4				S41						11.7	93.5	R.TSS*FTEQLDEGTPNR.E
Golgi autoantigen, golgin subfamily A, 4 GOLGA4				S71						55.8	57.2	R.VPS*VESLFR.S
Golgi autoantigen, golgin subfamily A, 4 GOLGA4				S40						-0.5	49.8	R.TS*FTEQLDEGTPNR.E
Golgi autoantigen, golgin subfamily A, 4 GOLGA4				S118S122						22.4	46.4	R.LDLDSSTASFDPP*S*DMDS*EAEDLVGNSDLNK.E
Golgi reassembly stacking protein 2, 55Kda GORASP2				S449						6.6	15.6	R.VGSDTSPSEKPVSAAVDANAS*ESP.-
Golgi reassembly stacking protein 2, 55Kda GORASP2				S451						17.5	37.4	R.VGSDTSPSEKPVSAAVDANASES*P.-
Golgi specific brefeldin A resistance factor GBF1				S1298						61.7	79.3	R.ADAPDAGAS*QDSELPYHQNDVSLDR.G
Golgi specific brefeldin A resistance factor GBF1				T1337						19.9	98.2	R.SAT*DADVNVSGWLVLGKD.G
Golgi specific brefeldin A resistance factor GBF1				T1317						20.9		R.GYT*SDSEVYTHGRPGKI.Y
Golgi specific brefeldin A resistance factor GBF1				S1318						17.7	24.6	R.GYTS*DSEVYTHGRPGKI.Y
Golgi specific brefeldin A resistance factor GBF1				S1320						8.3	19.9	R.GYTS*SDS*EVYTHGRPGKI.Y
Golgi specific brefeldin A resistance factor GBF1				S1475						25.8	40.1	R.GGQS*DDDEDEGPVASYHTVSLQVSDLLMHLTHRA.A
Golgi specific brefeldin A resistance factor GBF1				S349S352						14.4	41.8	K.SQAS*VSES*IPVELECTSPADHSASVHMDMYVNP.R.G
Golgi specific brefeldin A resistance factor GBF1				S347S352						12.8	13.4	K.SQS*ASVSES*IPVELECTSPADHSASVHMDMYVNP.R.G
Golgin 84 GOLGA5				S116						134.5	111.8	K.S*EPDDELLFDPLNSSQK.E
GRAM domain containing 2 GRAMD2A				S248						100.0	12.2	R.KPPMS*EK.S
Grb2 GRB2				T159						15.4		R.DIEQVPQQT*YVQALFDPDFQEDGLGFR.R
GRB2 associated binding protein 3 GAB3				S173						8.5	22.5	R.S*ESELLFDPLYLVLSNCTGR.L
GRB2 associated binding protein 3 GAB3				S175						-0.3	12.3	R.SES*ELLFDPLYLVLSNCTGR.L
GRB2 associated binding protein 3 GAB3				Y183						2.1	15.9	R.SESELLFDPLYLVLSNCTGR.L
GRB2 associated binding protein 3 GAB3				T191						-3.2	13.7	R.SESELLFDPLYLVLSNCT*GR.L
Grb4 NCK2				Y110						100.0	64.1	R.IY*DLNIPAFVK.F
GRID GRAP2				Y222						100.0	26.0	R.Y*LQHH*HFQER.R
GRID GRAP2				T262						100.0	54.5	R.RHT*DPVQLQAGR.R
GRID GRAP2				S164						59.7	47.8	R.S*QGQPHLSGAVGEEIRPSMNR.K
GRID GRAP2				S187Y207						7.8	30.9	R.KLS*DHPTPLPQHQHQHQPPQPY*APAPQQLQPPQQR.Y
GRID GRAP2				S187						15.9	44.4	R.KLS*DHPTPLPQHQHQHQPPQPY*APAPQQLQPPQQR.Y
GRID GRAP2				S236						90.3	97.6	R.GGS*LDINDGHCQGLGLSEMNALMHR.R
GRID GRAP2				S159						100.0	27.7	R.GNS*LDLRR.S
GRID GRAP2				S181						19.9	26.7	R.SQGPHLSGAVGEEIRPS*MNR.K

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		GRID GRAP2		Y207				-0.3	18.5	R.KLSDHPPTLPQQHQHQPPQY* <b>Y</b> APAPQQLQQPPQQR.Y
		GRID GRAP2		T192Y207				2.9	14.0	R.KLSDHPPTLPQQHQHQPPQY* <b>Y</b> APAPQQLQQPPQQR.Y
		GRID GRAP2		S187T192					11.1	R.KLSDHPPTLPQQHQHQPPQYAPAPQQLQQPPQQR.Y
		GRINL1A downstream protein Gdown1	GCOM1	S179				15.0	110.2	R.VS* <b>Q</b> AEDTSSSF <del>N</del> LFI <del>R</del> .L
		GRINL1A downstream protein Gdown1	GCOM1	S178				30.1	54.6	R.VS* <b>Q</b> AEDTSSSF <del>N</del> LFI <del>R</del> .L
		GRINL1A downstream protein Gdown1	GCOM1	S364S365				100.0	32.1	R.DEDDD <b>W</b> S* <b>S</b> *DEF.-
		GRIP1 associated protein 1	GRIPAP1	S691				17.7	56.5	R.SLS* <b>S</b> PQAOPPRPAELSDEEVAELFQRL
		GRIP1 associated protein 1	GRIPAP1	S655				15.8	45.3	R.SGLEELVLSEMN <b>S</b> *PSR.T
		GRIP1 associated protein 1	GRIPAP1	S688S691				17.4	55.8	R.S* <b>L</b> SS* <b>S</b> PQAOPPRPAELSDEEVAELFQRL
		GRIP1 associated protein 1	GRIPAP1	S690S692				13.6	56.5	R.SL <b>S</b> * <b>SS</b> * <b>P</b> QAOPPRPAELSDEEVAELFQRL
		GRIP1 associated protein 1	GRIPAP1	S692				5.8	53.5	R.SLSSS* <b>P</b> QAOPPRPAELSDEEVAELFQRL
		GRIP1 associated protein 1	GRIPAP1	S690S691				16.9	59.1	R.SL <b>S</b> * <b>S</b> * <b>S</b> PQAOPPRPAELSDEEVAELFQRL
		GRIP1 associated protein 1	GRIPAP1	S688S692				8.8	68.7	R.S* <b>L</b> SSS* <b>P</b> QAOPPRPAELSDEEVAELFQRL
		GRIP1 associated protein 1	GRIPAP1	S690S691S692				-0.4	28.0	R.SL <b>S</b> * <b>S</b> * <b>S</b> * <b>P</b> QAOPPRPAELSDEEVAELFQRL
		GRK-interacting protein 2	GIT2	Y362S397				26.7	110.6	K.TINNGHSVESQNDQDPY* <b>D</b> SVAS* <b>D</b> EDTLETTASK.T
		GRK-interacting protein 2	GIT2	Y362S394				5.4	38.5	K.TINNGHSVESQNDQDPY* <b>D</b> S* <b>V</b> ASDEDTLETTASK.T
		GRK-interacting protein 2	GIT2	S418S421				7.4	41.7	K.SLD <b>S</b> * <b>DL</b> S* <b>D</b> GPVTVQEFMEVK.N
		GRK-interacting protein 2	GIT2	S415S418				12.3	34.5	K.S* <b>L</b> DS* <b>DL</b> SDGPVTVQEFMEVK.N
		GRK-interacting protein 2	GIT2	S415S421				5.8	41.2	K.S* <b>L</b> DSL <b>S</b> * <b>D</b> GPVTVQEFMEVK.N
		GRK-interacting protein 2	GIT2	S397				5.9	55.4	K.TINNGHSVESQNDQDPY <b>D</b> SVAS* <b>D</b> EDTLETTASK.T
		GIT2		S614				114.6	49.0	R.S* <b>M</b> VWPGDGLVPDTAEHPVAPSTLPSTEDVIRK
		Growth arrest specific 2 like 1	GAS2L1	S316				4.2	15.0	R.RG <b>S</b> * <b>R</b> PemptVSLR.S
		GTP binding protein 1	GTBPB1	S44S47				57.2	59.6	R.LHGGFD <b>S</b> * <b>DC</b> <b>S</b> * <b>E</b> DGEALNGEPLDLSKL
		GTP binding protein 1	GTBPB1	S25				6.5	42.2	R.SAMDSPVPASMFAPES <b>S</b> *PGAAR.A
		GTP binding protein 1	GTBPB1	S24				57.7	30.3	R.SAMDSPVPASMFAPES <b>S</b> *PGAAR.A
		GTP binding protein 4	GTBPB4	S468S470S472				17.5	114.1	R.TAAGEY <b>D</b> S* <b>V</b> S* <b>E</b> S* <b>E</b> DEEMLEIR.Q
		GTP binding protein 4	GTBPB4	Y466S470S472				5.1	81.2	R.TAAGEY* <b>D</b> SV <b>S</b> * <b>E</b> S* <b>E</b> DEEMLEIR.Q
		GTP binding protein 4	GTBPB4	Y466S468S472				6.1	113.8	R.TAAGEY* <b>D</b> S* <b>V</b> SE <b>S</b> * <b>E</b> DEEMLEIR.Q
		GTP binding protein 4	GTBPB4	Y466S468S470				5.3	84.5	R.TAAGEY* <b>D</b> S* <b>V</b> S* <b>E</b> SEDEEMLEIR.Q
		GTPase activating protein Ran 1	RANGAP1	S428S442				23.5	38.4	K.ILDPNTGEPAPVL <b>S</b> * <b>P</b> PPADVSTFLAF <b>P</b> S*PEK.L
		GTPase activating protein Ran 1	RANGAP1	S427S442				22.5	20.6	K.ILDPNTGEPAPVL <b>S</b> * <b>S</b> PPPADVSTFLAF <b>P</b> S*PEK.L
		GTPase activating protein Ran 1	RANGAP1	S428				-0.4	18.2	K.ILDPNTGEPAPVL <b>S</b> * <b>P</b> PPADVSTFLAF <b>P</b> S*PEK.L
		GTPase activating protein Ran 1	RANGAP1	S435S442				10.3	17.1	K.ILDPNTGEPAPVLSS <b>P</b> PPADV <b>V</b> S* <b>T</b> FLAF <b>P</b> S*PEK.L
		GTPase activating protein Ran 1	RANGAP1	T419S427				31.4		K.ILDPNT* <b>G</b> EPAPVL <b>S</b> * <b>S</b> PPPADVSTFLAF <b>P</b> S*PEK.L
		GTPase activating RapiRanGAP domain like 1	RALGAPA1	S860S861				33.1	12.4	R.RG <b>S</b> * <b>S</b> * <b>P</b> GSLEIPK.D
		GTPase activating RapiRanGAP domain like 1	RALGAPA1	S773				16.0	87.7	R.HF <b>S</b> * <b>Q</b> SEETGNEVFGALNEEQPLPR.S
		GTPase activating RapiRanGAP domain like 1	RALGAPA1	S797				15.0	69.8	R.SS <b>S</b> * <b>T</b> SDILEPTVER.A
		GTPase activating RapiRanGAP domain like 1	RALGAPA1	S831				23.9	46.0	K.LPPLNSDIG <b>S</b> * <b>S</b> ANVPLMDEFIERLL
		GTPase activating RapiRanGAP domain like 1	RALGAPA1	S775				3.5	42.2	R.HFSQ <b>S</b> * <b>E</b> ETGNEVFGALNEEQPLPR.S
		GTPase activating RapiRanGAP domain like 1	RALGAPA1	S1000T1002S1				12.3	31.6	R.S* <b>Q</b> T* <b>P</b> S* <b>P</b> STLNIDHMEQK.D
		GTPase activating RapiRanGAP domain like 1	RALGAPA1	T798				-0.4	26.2	R.SS <b>T</b> * <b>S</b> OLEPPTVER.A
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S609S613				14.2	51.2	K.SET <b>S</b> * <b>N</b> PS <b>S</b> * <b>P</b> EICPNK.E
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	T607S608S609				10.7	13.5	K.SET* <b>S</b> <b>S</b> * <b>N</b> SSPEICPNK.E
		RAP1GAP4		S45T49				34.7	24.4	K.QELANSSDATLPDRPL <b>S</b> * <b>P</b> PLT* <b>A</b> PPTMK.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S9				33.6	75.1	R.SV <b>S</b> * <b>F</b> GGFGWIDK.T
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S680S685				9.1	80.7	K.QEVFVY <b>S</b> * <b>P</b> SS <b>S</b> * <b>P</b> SLGAAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S678S685				14.5	35.2	K.QEVFVY <b>S</b> * <b>P</b> SPSS <b>S</b> * <b>P</b> SLGAAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	Y677S682				8.5	22.3	K.QEVFVY* <b>S</b> SP <b>S</b> * <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S680				5.6	76.0	K.QEVFVY <b>S</b> * <b>P</b> SS <b>S</b> * <b>P</b> SLGAAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S678S680				4.5	18.5	K.QEVFVY <b>S</b> * <b>P</b> S <b>S</b> * <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S34T49				4.0	39.2	K.QELAN <b>S</b> * <b>S</b> DATLPDRPL <b>P</b> PLT* <b>A</b> PPTMK.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S682				2.8	80.8	K.QEVFVY <b>S</b> SP <b>S</b> * <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S680S682				2.0	94.5	K.QEVFVY <b>S</b> * <b>P</b> S* <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S678S683T693				12.0	26.8	K.QEVFVY <b>S</b> * <b>P</b> SP <b>S</b> * <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S609S612S613				5.1	28.5	K.SET <b>S</b> * <b>N</b> P <b>S</b> * <b>S</b> * <b>P</b> EICPNK.E
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S678T693				23.4	54.7	K.QEVFVY <b>S</b> * <b>P</b> SPSS <b>S</b> * <b>P</b> SLGAAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S680S682T693				9.2	22.7	K.QEVFVY <b>S</b> * <b>P</b> S* <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S608S612S613				18.1	22.3	K.SET <b>S</b> * <b>S</b> NP <b>S</b> * <b>S</b> * <b>P</b> EICPNK.E
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S34S35				5.3	17.2	K.QELAN <b>S</b> * <b>S</b> DATLPDRPL <b>P</b> PLTAPPTMK.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S678S682				7.7	24.8	K.QEVFVY <b>S</b> * <b>P</b> SP <b>S</b> * <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S678S683				5.0	50.2	K.QEVFVY <b>S</b> * <b>P</b> SP <b>S</b> * <b>S</b> ESPSLGAATPIIMSR.S
		GTPase activating RapiRanGAP domain like 4	RAP1GAP4	S608S613				5.8	26.8	K.SET <b>S</b> * <b>S</b> NP <b>S</b> * <b>S</b> * <b>P</b> EICPNK.E





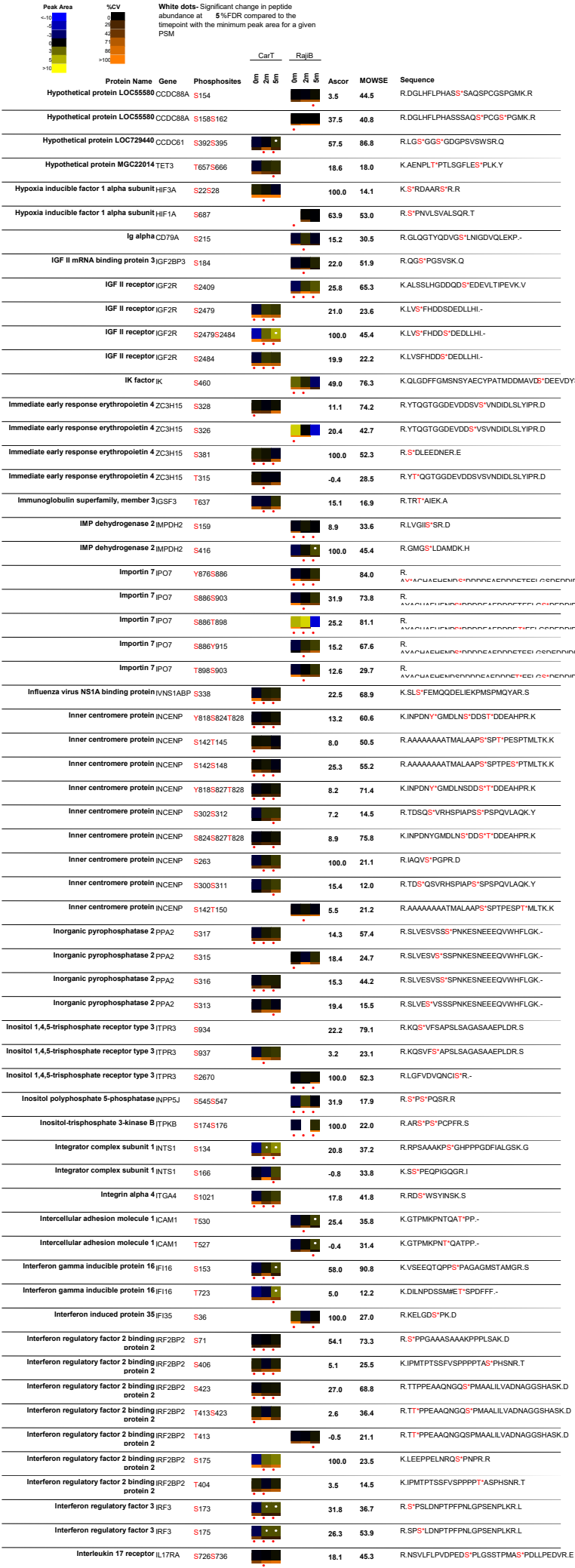
Peak Area	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM	Protein Name	Gene	Phosphosites	CarT	RajiB	Ascor	MOWSE	Sequence
<div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>40</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>40</div> <div>60</div> <div>70</div> <div>80</div> <div>90</div> <div>&gt;100</div> </div> </div>		Hepatoma-derived growth factor-related protein 2	HDGFL2	S454			42.5	50.4	R.S <sup>+</sup> EGFSMDR.K
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S137			9.8	80.4	R.GVMAVTAVTAA <sup>+</sup> DR.M
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S652			100.0	25.8	R.EGPDLD <sup>+</sup> RPGS <sup>+</sup> DR.Q
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S366S369S370			100.0	20.4	R.GEAERGS <sup>+</sup> GGSS <sup>+</sup> GDELREDD <sup>+</sup> EPVK.K
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S230S232S234			4.5	19.2	K.KAPS <sup>+</sup> AS <sup>+</sup> DS <sup>+</sup> DSKAS <sup>+</sup> DGAKPEPVAMAR.S
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S671			8.9	16.8	R.GDSEALDEES <sup>+</sup> .-
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S664			5.4	10.9	R.GDS <sup>+</sup> EALDEES.-
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S395S396S397			100.0	21.7	R.GRGPPS <sup>+</sup> S <sup>+</sup> S <sup>+</sup> DS <sup>+</sup> EPEAELEER.E
		Hepatoma-derived growth factor-related protein 2	HDGFL2	T132			18.8	14.0	R.GVM#AVTAVT <sup>+</sup> ATAASDR.M
		Hepatoma-derived growth factor-related protein 2	HDGFL2	T134			9.0	48.4	R.GVMAVTAVT <sup>+</sup> AASDR.M
		Hepatoma-derived growth factor-related protein 2	HDGFL2	S230S232S234			-2.6	24.2	K.KAPS <sup>+</sup> AS <sup>+</sup> DS <sup>+</sup> DS <sup>+</sup> KADSDGAKPEPVAMAR.S
		Heterochromatin protein 1 alpha	CBX5	S115S125S13S14			44.4	55.2	K.RTADS <sup>+</sup> S <sup>+</sup> S <sup>+</sup> S <sup>+</sup> EDEEEYVVEK.V
		Heterochromatin protein 1 alpha	CBX5	T8S115S13S14			6.7	14.4	R.T <sup>+</sup> ADS <sup>+</sup> S <sup>+</sup> S <sup>+</sup> S <sup>+</sup> EDEEEYVVEK.V
		Heterogeneous nuclear ribonucleoprotein A2	HNRNPA2	S259			40.6	129.0	R.GFGDGYNGYGGGPGGNFGGS <sup>+</sup> PGYGGGR.G
		Heterogeneous nuclear ribonucleoprotein A2	HNRNPA2	S341			15.8	119.1	R.NMGGPYGGNYGPGGS <sup>+</sup> GGSGGYGGR.S
		Heterogeneous nuclear ribonucleoprotein A2	HNRNPA2	Y331			13.3	37.0	R.NMGGPY <sup>+</sup> GGNYGPGSGSGSGGYGGR.S
		Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	S358			25.4	158.8	R.SSGS <sup>+</sup> PYGGGYGSGGGSGGYGSR.R
		Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	S356			-0.3	128.8	R.SS <sup>+</sup> GS <sup>+</sup> PGYGGYSGGGSGGYGSR.R
		Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	Y360			-0.5	13.6	R.SSGSPY <sup>+</sup> GGYSGGGSGGYGSR.R
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S253			68.8		K.MES <sup>+</sup> EGGADDSAEEGDLLLLDDDDNEDRGDQLELIKDDKE.E
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S253S260			100.0	81.6	K.MES <sup>+</sup> EGGADDS <sup>+</sup> AEEGDLDDDDNEDRGDQLELIKDDKE.E
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S260			98.8	107.2	K.MMESEGGADDS <sup>+</sup> AEEGDLDDDDNEDRGDQLELIK.D
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S299			58.5	71.3	K.EAEEGEDDRDS <sup>+</sup> ANGEDDS.-
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S306			3.2	15.9	K.DDEKEAEEGEDDRDSANGEDDS <sup>+</sup> .-
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S240S241			4.5	29.6	K.SEEEQSS <sup>+</sup> S <sup>+</sup> VKKDETNVK.M
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S233			56.4	65.6	K.NDKS <sup>+</sup> EEEQSSSVKK.D
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S238S240			13.2		K.SEEEQS <sup>+</sup> SS <sup>+</sup> SVKKDETNVK.M
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S238S241			7.0	38.0	K.SEEEQS <sup>+</sup> SS <sup>+</sup> VKKDETNVK.M
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S107			10.9	77.0	R.SAAEMYGS <sup>+</sup> SFDLDYDFQR.D
		Heterogeneous nuclear ribonucleoprotein C	HNRNPC	S238S239			18.1	19.5	K.SEEEQS <sup>+</sup> S <sup>+</sup> SVKKDETNVK.M
		Heterogeneous nuclear ribonucleoprotein D	HNRNPD	S80S83			12.8	45.6	K.NEEDEGH <sup>+</sup> SS <sup>+</sup> SPR.H
		Heterogeneous nuclear ribonucleoprotein D	HNRNPD	S83			23.9	89.0	K.NEEDEGHSS <sup>+</sup> PR.H
		Heterogeneous nuclear ribonucleoprotein D	HNRNPD	S82			19.8	58.6	K.NEEDEGHSS <sup>+</sup> SPR.H
		Heterogeneous nuclear ribonucleoprotein D	HNRNPD	S80			62.3	66.4	K.IDASKNEEDEGH <sup>+</sup> SS <sup>+</sup> NSSPR.H
		Heterogeneous nuclear ribonucleoprotein D	HNRNPD	S80S82			6.0	41.2	K.NEEDEGH <sup>+</sup> SS <sup>+</sup> SPR.H
		Heterogeneous nuclear ribonucleoprotein H1	HNRNPH1	S104			44.4	85.2	K.HTGPNSS <sup>+</sup> PDTANDGVR.L
		Heterogeneous nuclear ribonucleoprotein H1	HNRNPH1	T100			9.2	31.0	K.HT <sup>+</sup> GPNSPDTANDGVR.L
		Heterogeneous nuclear ribonucleoprotein H1	HNRNPH1	S310			42.3	48.8	K.ATENDIYNFFS <sup>+</sup> PLNPVR.V
		Heterogeneous nuclear ribonucleoprotein H1	HNRNPH1	T107			12.2	18.0	K.HTGPNSPDT <sup>+</sup> ANDGVR.L
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	S379			99.9	115.7	R.GS <sup>+</sup> YGDLGGPIIT <sup>+</sup> QVTIPK.D
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	Y380			-0.1	70.1	R.GS <sup>+</sup> YGDLGGPIIT <sup>+</sup> QVTIPK.D
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	T389			4.3	55.0	R.GSYGDLGGPIIT <sup>+</sup> QVTIPK.D
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	S216			26.0	64.4	K.IILDISES <sup>+</sup> PIK.G
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	T118			3.8	25.7	K.IIPTLEEGQLPSP <sup>+</sup> TATSQLPLESDAVECLNYQH <sup>+</sup> YK.G
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	T107				55.8	K.IIPT <sup>+</sup> LEEGQLPSPAT <sup>+</sup> SQLPLESDAVECLNYQH <sup>+</sup> YK.G
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	S116			28.4	62.6	K.IIPTLEEGQLPS <sup>+</sup> PTATSQLPLESDAVECLNYQH <sup>+</sup> YK.G
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	S284			32.7	37.5	R.RDYDDMS <sup>+</sup> PR.R
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	T120			5.0	16.3	K.IIPTLEEGQLPSPAT <sup>+</sup> SQLPLESDAVECLNYQH <sup>+</sup> YK.G
		Heterogeneous nuclear ribonucleoprotein K	HNRNPK	S214				21.6	K.IILDLS <sup>+</sup> ESPIKGR.A
		Heterogeneous nuclear ribonucleoprotein M	HNRNPM	S633			52.3	57.8	R.GNFGGS <sup>+</sup> FAGSFGAGGHAPGVAR.K
		Heterogeneous nuclear ribonucleoprotein U	HNRNPU	S59			54.1	55.4	R.LQAALDDEEAGRPAMEPGNS <sup>+</sup> LDLGGDSAGR.S
		Heterogeneous nuclear ribonucleoprotein U	HNRNPU	S271			7.7	41.5	K.S <sup>+</sup> PQPPVEEEDHFDDT <sup>+</sup> VCCLDTYNCDLHFK.I
		Heterogeneous nuclear ribonucleoprotein U	HNRNPU	T286			0.8	15.2	K.SPQPPVEEEDHFDDT <sup>+</sup> VCCLDTYNCDLHFK.I
		Heterogeneous nuclear ribonucleoprotein U-like 1	HNRNPUL	Y717			5.3	21.8	R.APQQQPPPPQPPPPQPPPPQPPPPPS <sup>+</sup> SPAR.N
		Heterogeneous nuclear ribonucleoprotein U-like 1	HNRNPUL	S716				26.1	R.APQQQPPPPQPPPPQPPPPQPPPPPS <sup>+</sup> YSPAR.N
		Heterogeneous nuclear ribonucleoprotein U-like 1	HNRNPUL	S718			5.8	19.5	R.APQQQPPPPQPPPPQPPPPQPPPPPS <sup>+</sup> PAR.N
		Heterogeneous nuclear ribonucleoprotein U-like 1	HNRNPUL	S194			11.9	21.3	R.S <sup>+</sup> PQPPAEDEEDFDDTLVAIDTYNCDLHFK.V
		Heterogeneous nuclear ribonucleoprotein U-like 2	HNRNPUL	S161T165			49.3	75.1	R.S <sup>+</sup> GDET <sup>+</sup> PGSEVPGDK.A
		Heterogeneous nuclear ribonucleoprotein U-like 2	HNRNPUL	S161T165S168			100.0	73.1	R.S <sup>+</sup> GDET <sup>+</sup> PGS <sup>+</sup> EVPGDK.A
		Heterogeneous nuclear ribonucleoprotein U-like 2	HNRNPUL	S193			10.4	27.7	K.SKPAGS <sup>+</sup> DGER.R
		Heterogeneous nuclear ribonucleoprotein U-like 2	HNRNPUL	S185			100.0	58.9	K.AAEEQQDDQDS <sup>+</sup> EK.S
		Heterogeneous nuclear ribonucleoprotein U-like 2	HNRNPUL	S228			39.8	52.7	R.SK <sup>+</sup> PLPPEEAK.D



Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Histone 1 H1C	HIST1H1C	T31				100.0	24.9	K.KAGG <b>T</b> *PR.K
		Histone 1 H1C	HIST1H1C	T146				100.0	48.1	K.KAAGGAT*PK.K
		Histone 1 H1E	HIST1H1E	T146				49.2	49.6	K.KATGAAT*PK.K
		Histone 1 H1E	HIST1H1E	S187				100.0	51.4	K.KAPK <b>S</b> *PAK.A
		Histone 1 H1E	HIST1H1E	T142				7.3	11.3	K.KAT*GAATPK.K
		Histone 1, H1a	HIST1H1A	S165S166				100.0	18.2	R.K <b>S</b> <b>S</b> *KNPK.K
		Histone 1, H1b	HIST1H1B	S18				47.5	47.0	M.SETAPAEATATPA <b>P</b> VE <b>S</b> *PAK.K
		Histone 1, H1b	HIST1H1B	S173				100.0	40.3	K.KVAK <b>S</b> *PK.K
		HIST1H1B	S189				26.0	31.0	K.ATK <b>S</b> *PAKPK.A	
		Histone 1, H1b	HIST1H1B	T138				100.0	19.0	K.AKKPAGAT*PK.K
		Histone acetyltransferase 1	HAT1	S361				10.9	21.1	R.LI <b>S</b> *PYK.K
		Histone deacetylase 1	HDAC1	S421S423				100.0	88.9	R.IACEEF <b>S</b> *D <b>S</b> *EEEEGGGR.K
		Histone deacetylase 1	HDAC1	S393				100.0	44.5	R.MLPHAPGVOMQAPEDIAPE <b>S</b> *GDEDEDPPK <b>R</b> .I
		HDAC2	S16S518				100.0	82.1	R.IACDEF <b>S</b> *D <b>S</b> *EDEGEGRR.N	
		Histone deacetylase 2	HDAC2	S488				100.0	30.3	R.MLPHAPGVOMQAPEDIAVHED <b>S</b> *GDEGDEDPK <b>R</b> .I
		Histone deacetylase 3	HDAC3	S424				49.9	30.1	R.GPEENYSRPEAPNEFYDDGHDNDK <b>S</b> *DVEI-
		Histone deacetylase 4	HDAC4	S632				35.8	110.8	R.AQ <b>S</b> *SPASATFPVSQEPPTK <b>R</b> .F
		Histone deacetylase 4	HDAC4	S467				12.1	45.6	R.TQ <b>S</b> *APLPQNAQALQHLVIQQHQGFLEK.H
		Histone deacetylase 7A	HDAC7	S486				56.6	83.2	R.AQ <b>S</b> *SPAAPASLSAPEPASQAR.V
		Histone deacetylase 7A	HDAC7	S487				-0.4	32.8	R.AQ <b>S</b> *PAAPASLSAPEPASQAR.V
		Histone H1x	H1FX	S31				29.3	73.1	K.AGGSAA <b>L</b> <b>S</b> *PSK.K
		Histone H1x	H1FX	S33				11.0	55.4	K.AGGSAA <b>L</b> <b>S</b> * <b>K</b> K.R
		Histone methyltransferase	DOT1L	DOT1L	S447			12.6	59.8	K.KNQTDALHAQTVSQTA <b>S</b> *SPQDAYR.S
		Histone methyltransferase	DOT1L	DOT1L	S448			7.2	61.9	K.KNQTDALHAQTVSQTA <b>S</b> *PQDAYR.S
		Histone1, H1D	HIST1H1D	T147				100.0	38.7	K.KVAGAA <b>T</b> *PK.K
		HIV 1 REV binding protein	AGFG1	T177S179				9.2	14.7	K.SLLGDSAPT <del>L</del> HLNK <b>G</b> <b>T</b> *P <b>S</b> *QSPVVGR.S
		HIV 1 REV binding protein	AGFG1	T177				28.8	43.5	K.G <b>T</b> *PSQSPVVGR.S
		HIV 1 REV binding protein	AGFG1	T177S181				16.0	21.1	K.SLLGDSAPT <del>L</del> HLNK <b>G</b> <b>T</b> *P <b>S</b> <b>Q</b> <b>S</b> *P <b>V</b> VGR.S
		HIV 1 REV binding protein	AGFG1	S162				78.9	54.1	K. <b>S</b> *LLGDSAPT <del>L</del> HLNK.G
		HIV 1 REV binding protein	AGFG1	T170S181				4.1	14.5	K.SLLGDSAP <b>T</b> <del>L</del> HLNK <b>G</b> <b>T</b> PS <b>Q</b> <b>S</b> *P <b>V</b> VGR.S
		HLA class I histocompatibility antigen, B-58	HLA-B	S359				12.1	69.6	K.GGSYSQAASSDSAQGS <b>DV</b> <b>S</b> *LTA-
		HLA class I histocompatibility antigen, B-58	HLA-B	S356				14.0	51.8	K.GGSYSQAASSDSAQGS <b>S</b> *DVSLTA-
		HLA class I histocompatibility antigen, B-58	HLA-B	S356S359				16.9	74.7	K.GGSYSQAASSDSAQGS <b>S</b> *DV <b>S</b> *LTA-
		HLA class I histocompatibility antigen, B-58	HLA-B	S352S356S359				11.0	38.4	K.GGSYSQAASSD <b>S</b> *AQGS <b>S</b> *DV <b>S</b> *LTA-
		HLA class I histocompatibility antigen, B-58	HLA-B	S350S352S359				10.2	16.6	K.GGSYSQAAS <b>S</b> *D <b>S</b> *AQGSDV <b>S</b> *LTA-
		HLA class I histocompatibility antigen, B-58	HLA-B	S350S352S356				-0.5	14.3	K.GGSYSQAAS <b>S</b> *D <b>S</b> *AQGS <b>S</b> *DVSLTA-
		HLA class I histocompatibility antigen, B-58	HLA-B	S350S356S359				14.4	35.9	K.GGSYSQAAS <b>S</b> *DSAQGS <b>S</b> *DV <b>S</b> *LTA-
		HLA-A	HLA-A	S359				28.2	114.2	R.KGGSY <b>T</b> QAASSDSAQGS <b>DV</b> <b>S</b> *LTACKV.-
		HLA-A	HLA-A	S352				33.2	107.3	R.KGGSY <b>T</b> QAASSD <b>S</b> *AQGSDVSLTACKV.-
		HLA-A	HLA-A	S350				10.9	68.8	R.KGGSY <b>T</b> QAAS <b>S</b> *DSAQGS <b>DV</b> SLTACKV.-
		HLA-A	HLA-A	S352S359				26.1	70.0	R.KGGSY <b>T</b> QAASSD <b>S</b> *AQGSDV <b>S</b> *LTACKV.-
		HLA-A	HLA-A	S352S356S359				20.0	70.8	R.KGGSY <b>T</b> QAASSD <b>S</b> *AQGS <b>S</b> *DV <b>S</b> *LTACKV.-
		HLA-A	HLA-A	Y344				17.7	54.7	R.KGG <b>S</b> *Y <b>T</b> QAASSDSAQGS <b>DV</b> SLTACKV.-
		HLA-A	HLA-A	S356				15.9	96.9	R.KGGSY <b>T</b> QAASSDSAQGS <b>S</b> *DVSLTACKV.-
		HLA-A	HLA-A	S356S359				19.4	50.0	R.KGGSY <b>T</b> QAASSDSAQGS <b>S</b> *DV <b>S</b> *LTACKV.-
		HLA-A	HLA-A	S350S359				8.3	33.8	R.KGGSY <b>T</b> QAAS <b>S</b> *DSAQGS <b>DV</b> <b>S</b> *LTACKV.-
		HLA-A	HLA-A	T345				9.0	27.2	R.KGGSY <b>T</b> *QAASSDSAQGS <b>DV</b> SLTACKV.-
		HLA-A	HLA-A	S352S356				8.9	39.6	R.KGGSY <b>T</b> QAASSD <b>S</b> *AQGS <b>S</b> *DVSLTACKV.-
		HLA-B associated transcript 2	PRRC2A	S342S350				100.0	41.3	K.LKF <b>S</b> *DEEDGRD <b>S</b> *DEEGAEGHR.D
		HLA-B associated transcript 2	PRRC2A	S456				22.5	81.7	R.KQ <b>S</b> *SSEISLAVER.A
		HLA-B associated transcript 2	PRRC2A	S1089S1092				52.2	83.2	R. <b>S</b> *EG <b>S</b> *EYEEIPK.R
		HLA-B associated transcript 2	PRRC2A	S1014				15.8	13.9	R.DY <b>S</b> *YER.V
		HLA-B associated transcript 2	PRRC2A	T825				-0.9	21.4	R.SET*PPVPPPPPYLASYPGFENGAPGPISR.F
		HLA-B associated transcript 2	PRRC2A	Y1013				18.1	21.2	R.DY <b>S</b> *YER.V
		HLA-B associated transcript 2	PRRC2A	S1168				100.0	11.1	R.GVP <b>S</b> *RR.G
		HLA-B associated transcript 2	PRRC2A	S1306S1310S1				11.9	18.4	K. <b>S</b> *PDL <b>S</b> *NQ <b>N</b> <b>S</b> *DQANEWE <b>T</b> *ASESSDFTSER.R
		HLA-B associated transcript 2	PRRC2A	S1306S1314S1				17.8	15.8	K. <b>S</b> *PDLNQ <b>N</b> <b>S</b> *DQANEWETAS <b>S</b> *SDFTSER.R
		HLA-B associated transcript 2	PRRC2A	S457				8.0	27.8	R.KQ <b>S</b> *SEISLAVER.A
		HLA-B associated transcript 2	PRRC2A	S1089				30.0	30.0	R. <b>S</b> *EGSEYEEIPK.R
		HLA-B associated transcript 3	BAT3	S973				75.8	114.5	R.ENA <b>S</b> *PAPGTTAEAMSR.G
		HLA-B associated transcript 3	BAT3	S964S973				36.3	44.8	R.A <b>S</b> *PEPQRENAS*PAPGTTAEAMSR.G
		HLA-B associated transcript 3	BAT3	S964				100.0	27.7	R.A <b>S</b> *PEPOR.E

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		HLA-B associated transcript 3	BAT3	S113				7.7	40.4	R.APQT <sup>H</sup> LP <sup>G</sup> SGASSGTGSASATHGGGS <sup>S</sup> PPGTR.G
		HLA-B associated transcript 3	BAT3	S964T978				5.9	19.9	R.AS <sup>S</sup> PEPQRENASAPAGT <sup>T</sup> TAE <sup>E</sup> AMSR.G
		HLA-B associated transcript 3	BAT3	T92				13.7		R.APQT <sup>H</sup> LP <sup>G</sup> SGASSGTGSASATHGGGSPPGTR.G
		HLA-B-associated transcript 1	DGX39B	S38				30.0	32.9	K.GS <sup>S</sup> YYSIHSSGFR.D
		HMG CoA reductase	HMGCR	S872				120.6	84.5	R.S <sup>S</sup> KINLQDLQGACTK.K
		HMG-BOX transcription factor	BBX	S478S479S481				19.4	35.3	K.KRQS <sup>S</sup> S <sup>S</sup> ES <sup>S</sup> DIESVIYTIEAVAK.G
		HMGN1	HMGN1	S86S89				45.2	78.0	K.TEES <sup>S</sup> PAS <sup>S</sup> DEAGEK.E
		HMGN1	HMGN1	S89				32.3	67.2	K.TEESPAS <sup>S</sup> DEAGEK.E
		HNRPLL	HNRNPLL	T46				100.0	12.0	R.REAT <sup>T</sup> PR.G
		Host cell factor C1	HCFC1	S666				50.0	72.9	K.S <sup>S</sup> PISVPGGSALISNLGK.V
		Host cell factor C1	HCFC1	S411				6.5	19.9	K.YDIPATAATA <sup>B</sup> PTPNPVPSPVANPPK.S
		Host cell factor C1	HCFC1	T413				-0.3	31.8	K.YDIPATAATATS <sup>P</sup> PNPVPSPVANPPK.S
		Host cell factor C1	HCFC1	S1205				113.9	56.1	R.S <sup>S</sup> PAFVQLAPLSSK.V
		HP1 beta	CBX1	S89				39.0	51.5	R.KADS <sup>S</sup> DSEDKGEEKPK.K
		HP1-BP74	HP1BP3	S441S442S446				84.1	40.7	K.KEPDSDRDEDEDEDS <sup>S</sup> EEDS <sup>S</sup> EDEEPPPK.R
		HPK1	MAP4K1	S376S377Y381				6.7	16.9	R.KQLSE <sup>S</sup> S <sup>S</sup> DDDY <sup>S</sup> DDVDIPTPAEDTPPLPPKPK.F
		HPK1	MAP4K1	S374S376S377				10.7	14.8	R.KQLS <sup>S</sup> ES <sup>S</sup> S <sup>S</sup> DDDYDDVDIPTPAEDTPPLPPKPK.F
		HPRP3P	PRPF3	S619				100.0	64.2	K.GDDDEES <sup>S</sup> DEEAVKK.T
		HPRP3P	PRPF3	T611				5.8	20.1	R.IKWDEQTSNT <sup>T</sup> KGDDDEESDEEAVK.K
		Hsc70 interacting protein	ST13	S79				16.4	86.4	K.KVEEDLKADEPS <sup>S</sup> E <sup>S</sup> DLEIDK.E
		Hsc70 interacting protein	ST13	S76				9.1	83.0	K.KVEEDLKADEPS <sup>S</sup> E <sup>S</sup> SDLEIDK.E
		Hsc70 interacting protein	ST13	S75S76S79				100.0	71.6	K.KVEEDLKADEPS <sup>S</sup> S <sup>S</sup> EE <sup>S</sup> DLEIDK.E
		Hsc70 interacting protein	ST13	S75S79				28.4	56.5	K.ADEPS <sup>S</sup> SEE <sup>S</sup> DLEIDK.E
		ST13		S75S76					39.6	K.ADEPS <sup>S</sup> S <sup>S</sup> EESDLEIDK.E
		ST13		S76S79				19.1	41.8	K.ADEPS <sup>S</sup> EE <sup>S</sup> DLEIDK.E
		Hsc70 interacting protein	ST13	S75				10.9	48.0	K.KVEEDLKADEPS <sup>S</sup> SEESDLEIDK.E
		HSN1	OTUD4	S480				15.3	54.8	K.RPEPSTLENITDDKYATVS <sup>S</sup> PSK.S
		HSN1	OTUD4	S95T958				103.0	105.1	K.EE <sup>S</sup> S <sup>S</sup> EDENEVSNILR.S
		HSN1	OTUD4	S827				33.4	19.1	K.GELDL <sup>S</sup> LENLDSK.D
		HSN1	OTUD4	S479				10.7	69.2	K.RPEPSTLENITDDKYATV <sup>S</sup> SPSK.S
		HSP90A	HSP90AA1	S263				144.9	97.3	K.ESEDKPEIEDVG <sup>S</sup> DEEEKK.D
		HSP90A	HSP90AA1	T725				76.3	74.7	K.LGLGIDEDOPTADDTSAVTEEMPLEGDDDT <sup>T</sup> SR.M
		HSP90AA1	S231					100.0	85.4	R.DKEY <sup>S</sup> DDEAEKEK.E
		HSP90A	HSP90AA1	S252					44.4	K.ES <sup>S</sup> EOKPEIEDVGSEEEKK.D
		HSP90B	HSP90AB1	S226				100.0	87.7	K.EIS <sup>S</sup> DDEAEKGEK.E
		HSP90B	HSP90AB1	S255				71.8	131.8	K.IEDV <sup>S</sup> SEEDDSGKDK.K
		HSP90B	HSP90AB1	S718				100.0	47.0	K.LGLGIDEDEVAEEFNAAVPDEIPPLEGDEDS <sup>S</sup> R.M
		HuG1 protein	LLGL1	S936				10.9	12.6	R.FS <sup>S</sup> LSAR.N
		Human immunodeficiency virus type1 HIVP2 enhancer-binding orotein2		S2130				100.0	15.0	R.RDLS <sup>S</sup> PR.R
		Huntingtin	HTT	S421S434				15.5	90.1	R.SG <sup>S</sup> VELIAGGGSSC <sup>S</sup> PVLSR.K
		Huntingtin	HTT	S432				9.1	52.0	R.SGSVELIAGGGSS <sup>S</sup> CSPVLSR.K
		Huntingtin	HTT	S419S434				12.8	70.4	R.S <sup>S</sup> GSVELIAGGGSSC <sup>S</sup> PVLSR.K
		Huntingtin	HTT	S421S432				1.4	23.9	R.SG <sup>S</sup> VELIAGGGSS <sup>S</sup> CSPVLSR.K
		Huntingtin interacting protein 1	SETD2	S121					20.5	R.LNDS <sup>S</sup> PTLK.K
		Huntingtin interacting protein 1	SETD2	T123				6.8	10.8	R.LNDSPT <sup>T</sup> LK.K
		Hydroxymethylglutaryl-CoA synthase, cytoplasmic	HMGCS1	T471					38.5	R.RPT <sup>T</sup> PNDDTLDEGVGLVHSNIATEHIPSPAKK.V
		HMGCS1		S495				49.7	24.6	R.RPTPNDDTLDEGVGLVHSNIATEHIP <sup>S</sup> PAKK.V
		Hyperpolarization activated cyclic nucleotide gated potassium channel	HCN3	T380				8.7	11.1	K.YKQVEQYMSFKLPADT <sup>T</sup> R.Q
		Hypothetical protein BC007540	C11orf84	S248S251				12.8	18.6	K.NLDPDPEPPS <sup>S</sup> PD <sup>S</sup> PTETFAAPAEVR.H
		Hypothetical protein BC008207	NAF1	S315				100.0	54.6	K.NDQEPPEALDF <sup>S</sup> DDEKEK.E
		Hypothetical protein DKFZp762E1312	HJURP	S473				68.0	40.8	R.GGPAS <sup>S</sup> PGGLOGLETR.R
		Hypothetical protein DKFZp762E1312	HJURP	T600				-9.4	20.0	K.SPQQMT <sup>T</sup> VLPGVSTDK.A
		Hypothetical protein FLJ10154	ARGLU1	S76				12.2	39.7	R.AS <sup>S</sup> SPDRIDIFGR.T
		Hypothetical protein FLJ10154	ARGLU1	S77				15.0	33.0	R.AS <sup>S</sup> PPDRIDIFGR.T
		Hypothetical protein FLJ10154	ARGLU1	S60				17.0	53.0	R.S <sup>T</sup> TNTAVSR.R
		Hypothetical protein FLJ10154	ARGLU1	S58S60				16.3	18.6	R.S <sup>S</sup> RS <sup>T</sup> TNTAVSR.R
		Hypothetical protein FLJ10154	ARGLU1	T61				-0.1	56.0	R.S <sup>T</sup> TNTAVSR.R
		Hypothetical protein FLJ20160	MFSD6	S644				5.3	59.4	R.IPVPS <sup>S</sup> PVIATIDLQQQTEDVMPL.I
		Hypothetical protein FLJ20309	NOB0D	S232				29.8	48.9	K.S <sup>S</sup> PQPQNTSLPMQGVAPTHTHIAQAR.Q
		RASAL3		S164S166				21.4	22.8	R.VGS <sup>S</sup> AS <sup>S</sup> EGSIHVAMGNFRDPRMPKGT
		Hypothetical protein FLJ21438	RASAL3	S166S167				2.6	78.4	R.VGSAS <sup>S</sup> S <sup>S</sup> EGSIHVAMGNFR.D
		Hypothetical protein FLJ21438	RASAL3	S164S167				12.5	80.0	R.VGS <sup>S</sup> ASS <sup>S</sup> EGSIHVAMGNFR.D

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites					
		Hypothetical protein FLJ21438	RASAL3	S228S231			12.8	75.4	R.DGPPSALGS* <b>RE</b> S*LATLSELDLGAER.D
		Hypothetical protein FLJ21438	RASAL3	S72			29.9	40.5	R.TQS*VPVVR
		Hypothetical protein FLJ21438	RASAL3	S164S166S167			6.7	44.2	R.VGS* <b>AS</b> *S*EGSIHVAMGNFR.D
		Hypothetical protein FLJ21438	RASAL3	S94			32.1	46.9	K.GS*LSMGPAAPRA
		Hypothetical protein FLJ21438	RASAL3	T70			12.2	35.7	R.T*QSPVVR.R
		Hypothetical protein FLJ21438	RASAL3	S247			-0.2	21.1	R.TRGS*WSPQPLKA
		Hypothetical protein FLJ21438	RASAL3	S166S167S170			5.5	22.4	R.VGSAS* <b>S</b> *EGS*IHVAMGNFR.D
		Hypothetical protein FLJ25476	ZNF362	S404			51.2	62.5	K.HTVVEHLVSHS*PQR.T
		Hypothetical protein FLJ25476	ZNF362	S401			7.1	60.8	K.HTVVEHLVS*HHSPQR.T
		Hypothetical protein KIAA0084 (HA2022) (Ffragment)		S32			100.0	14.4	R.RP <b>S</b> *PPR.R
		Hypothetical protein KIAA0826	FRYL	T745			-0.2	92.2	K.S*T*GQLNLST*SPINSSSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0826	FRYL	T752			5.8	43.7	K.S.TGQLNLST*SPINSSSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0826	FRYL	T745S751			8.2	76.4	K.S*T*GQLNL <b>S</b> *TSPINSSSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0826	FRYL	S753			19.1	51.5	K.S.TGQLNLST <b>S</b> *PINSSSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0826	FRYL	S744S757			11.9	14.8	K. <b>S</b> *TGQLNLSTSPIN <b>S</b> *SSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0826	FRYL	T745S757			4.0	55.0	K.S*T*GQLNLSTSPIN <b>S</b> *SSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0826	FRYL	S744			8.0	111.2	K. <b>S</b> *TGQLNLSTSPINSSSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0826	FRYL	T745S753			1.2	52.0	K.S*T*GQLNLST <b>S</b> *PINSSSYLGYN <b>S</b> NAR.S
		Hypothetical protein KIAA0889	SOGA1	S64			11.5	68.9	K.SVSSMSEF <b>S</b> *LLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S57S64			0.6	62.1	R.TK <b>S</b> V <b>S</b> *SMSEF <b>S</b> *LLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S55S60			-0.8	58.0	R.TK <b>S</b> *VSS <b>S</b> *EFESLLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S57S58			1.8	59.9	K.SV <b>S</b> * <b>S</b> *MSEFESLLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S55S57			6.9	72.6	K. <b>S</b> *V <b>S</b> *SMSEFESLLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S60S64			1.1	40.2	R.TK <b>S</b> VSS <b>M</b> <b>S</b> *EF <b>S</b> *LLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S57			15.8	27.6	K.SV <b>S</b> *SMSEFESLLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S55S58			6.8	60.0	K. <b>S</b> *V <b>S</b> *MSEFESLLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S60			1.2	70.5	K.SVSS <b>M</b> <b>S</b> *EFESLLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S58			9.8	19.6	K.SV <b>S</b> *MSEFESLLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S55S64			8.0	75.5	R.TK <b>S</b> *VSSMSEF <b>S</b> *LLDCSPYLAGGDAR.G
		Hypothetical protein KIAA0889	SOGA1	S55			16.1	115.2	K. <b>S</b> *VSSMSEFESLLDCSPYLAGGDAR.G
		Hypothetical protein LOC137886	UBXN2B	S17			10.9	16.0	K.R <b>S</b> <b>S</b> *GPR.A
		Hypothetical protein LOC137886	UBXN2B	S16			23.9	27.3	K.R <b>S</b> *SGPR.A
		Hypothetical protein LOC137886	UBXN2B	S235S242			5.6	54.9	K.LGSLTPEIVST <b>P</b> <b>S</b> *PEEEDK <b>S</b> *LINAVLIDSVPTTK.I
		Hypothetical protein LOC137886	UBXN2B	T232S242			2.6	52.0	K.LGSLTPEIVST* <b>P</b> SSPEEEDK <b>S</b> *LINAVLIDSVPTTK.I
		Hypothetical protein LOC137886	UBXN2B	T232S234			4.3	51.0	K.LGSLTPEIVST* <b>P</b> <b>S</b> *SPEEEDK <b>S</b> LINAVLIDSVPTTK.I
		Hypothetical protein LOC137886	UBXN2B	S16S17			100.0	21.7	K.R <b>S</b> * <b>S</b> *GPR.A
		Hypothetical protein LOC137886	UBXN2B	S234S235			2.9	31.3	K.LGSLTPEIVST <b>P</b> <b>S</b> *PEEEDK <b>S</b> LINAVLIDSVPTTK.I
		Hypothetical protein LOC137886	UBXN2B	S224S234			1.6	17.9	K.LG <b>S</b> *LTPEIVST <b>P</b> <b>S</b> *SPEEEDK <b>S</b> LINAVLIDSVPTTK.I
		Hypothetical protein LOC137886	UBXN2B	S234S242			11.4	23.4	K.LGSLTPEIVST <b>P</b> <b>S</b> *SPEEEDK <b>S</b> *LINAVLIDSVPTTK.I
		Hypothetical protein LOC137886	UBXN2B	S231S234			4.3	35.1	K.LGSLTPEIV <b>S</b> *T <b>P</b> <b>S</b> *SPEEEDK <b>S</b> LINAVLIDSVPTTK.I
		Hypothetical protein LOC162427	RETREG3	S258S260			171.7	58.0	R.AMDNH <b>S</b> *D <b>S</b> *EEELAAFCQLDDSTVAR.E
		Hypothetical protein LOC162427	RETREG3	T440			31.8	47.2	R.SPSSDLDT*DAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S435S436			8.4	90.0	R.SP <b>S</b> * <b>S</b> *DLDTDAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S433S436T440			3.9	67.6	R. <b>S</b> *P <b>S</b> <b>S</b> *DLDT*DAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S435S436T440			12.2	77.7	R.SP <b>S</b> * <b>S</b> *DLDT*DAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S390			12.1	70.9	R.DLPDFPSINMDPAGLDDDDT <b>S</b> *IGMP <b>S</b> LMYR.S
		Hypothetical protein LOC162427	RETREG3	T349			8.2	36.4	R.DLPDFPSINMDPAGLDDDDT <b>S</b> *SIGMP <b>S</b> LMYR.S
		Hypothetical protein LOC162427	RETREG3	S435T440			19.3	89.5	R.SP <b>S</b> *SDLDT*DAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S433S435			7.9	11.1	R. <b>S</b> *P <b>S</b> *SDLDTDAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S335			8.9	32.7	R.DLPDF <b>S</b> *INMDPAGLDDDDT <b>S</b> IGMP <b>S</b> LMYR.S
		Hypothetical protein LOC162427	RETREG3	S435			17.1	96.6	R.SP <b>S</b> *SDLDTDAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	T307T310S313			37.5	24.9	R.GQT*PLT*EG <b>S</b> *EDLDGH <b>S</b> *DPEESFAR.D
		Hypothetical protein LOC162427	RETREG3	S436T440			11.3	52.8	R.SP <b>S</b> <b>S</b> *DLDT*DAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S433S435T440			10.2	40.5	R. <b>S</b> *P <b>S</b> *SDLDT*DAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC162427	RETREG3	S436			-1.2	21.9	R.SP <b>S</b> <b>S</b> *DLDTDAEGDDFELLDQSELSQLDPASSR.S
		Hypothetical protein LOC348180	CTU2	S508			7.1	17.0	R.DCLIED <b>S</b> *DDEAG <b>S</b> .-
		Hypothetical protein LOC348262	MCRIP1	S21			28.1	87.1	R. <b>S</b> *PPSSSEIFT <b>P</b> AAHEENV <b>R</b> .F
		Hypothetical protein LOC348262	MCRIP1	S25			13.1	55.1	R.SP <b>P</b> <b>S</b> <b>S</b> *SEIFT <b>P</b> AAHEENV <b>R</b> .F
		Hypothetical protein LOC348262	MCRIP1	S24				14.2	R.SP <b>P</b> <b>S</b> <b>S</b> *SEIFT <b>P</b> AAHEENV <b>R</b> .F
		Hypothetical protein LOC55580	CCDC88A	S155S158			12.5	40.6	R.DGLHFLPHASS <b>S</b> *AQ <b>S</b> *PCGSPGMKR.T
		Hypothetical protein LOC55580	CCDC88A	S158			16.7	55.8	R.DGLHFLPHASS <b>SA</b> <b>S</b> *PCGSPGMKR
		Hypothetical protein LOC55580	CCDC88A	S153S162			14.7	10.8	R.DGLHFLPHAS <b>S</b> *SSAQSPCG <b>S</b> *PGMKR.T



Peak Area	iCV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
				5	6	5	6			
		Protein Name	Gene	Phosphosites						
		Interleukin enhancer binding factor 3	ILF3	S792				33.3	112.9	K.GYNHGQGSYSYSNS <sup>Y</sup> PGGGGGSDYNE <sup>S</sup> K.F
		Interleukin enhancer binding factor 3	ILF3	S787				9.1	21.9	K.GYNHGQGSYSYS <sup>N</sup> SYNSPGGGGGSDYNE <sup>S</sup> K.F
		Interleukin enhancer binding factor 3	ILF3	S476				51.5		R. <sup>R</sup> SGVRSACETEAKDAIADABAIAEATBAAEDBATAEQDRI
		Interleukin enhancer binding factor 3	ILF3	S482				76.2		K.GEDS <sup>A</sup> AEETEAKPAVAPAPVVEAVSTPSAAFPSDATAEQGPILT <sup>K</sup> .U
		Interleukin enhancer binding factor 3	ILF3	S382				28.4	73.6	K.RPMEEDGEES <sup>S</sup> PSK.K
		Interleukin enhancer binding factor 3	ILF3	S789				7.8	36.9	K.GYNHGQGSYSYSNS <sup>Y</sup> NSPGGGGGSDYNE <sup>S</sup> K.F
		Interleukin enhancer binding factor 3	ILF3	S476S477				35.4		R. <sup>R</sup> SGVRSACETEAKDAIADABAIAEATBAAEDBATAEQDRI
		Interleukin enhancer binding factor 3	ILF3	T469S476S477				23.9		K. <sup>K</sup> LDADIGI <sup>R</sup> TKAGEDR <sup>R</sup> SGVRSACETEAKDAIADABAIAEATBAAEDBATAEQDRI
		Interleukin enhancer binding factor 3	ILF3	S880				7.4	108.9	K.QGGYSQSNYS <sup>N</sup> PGSGQNYSGPPSSYQSGGGYGR.N
		Interleukin enhancer binding factor 3	ILF3	S868				10.2	66.9	K.QGGYSQSNYNSPGSGQNYSGPPSSYQSGGGYGR.N
		Interleukin enhancer binding factor 3	ILF3	S476S477S482				39.6		R. <sup>R</sup> SGVRSACETEAKDAIADABAIAEATBAAEDBATAEQDRI
		Interleukin enhancer binding factor 3	ILF3	Y858				61.6		K.QGGYSQSNY <sup>N</sup> NSPGSGQNYSGPPSSYQSGGGYGR.N
		Interleukin enhancer binding factor 3	ILF3	S854				9.0	31.0	K.QGGYS <sup>T</sup> QSNYNSPGSGQNYSGPPSSYQSGGGYGR.N
		Interleukin enhancer binding factor 3	ILF3	T469S476				15.3		K. <sup>K</sup> LDADIGI <sup>R</sup> TKAGEDR <sup>R</sup> SGVRSACETEAKDAIADABAIAEATBAAEDBATAEQDRI
		Interleukin enhancer binding factor 3	ILF3	Y790				-0.3	71.8	K.GYNHGQGSYSYSNS <sup>Y</sup> NSPGGGGGSDYNE <sup>S</sup> K.F
		Intersectin 1	ITSN1	S315				-0.3	29.0	R.SGS <sup>S</sup> GISVISSTVSDQR.L
		Intersectin 2	ITSN2	S883S888				14.2	54.0	R.TVS <sup>S</sup> PGSV <sup>S</sup> PIHGQGQVVENLK.A
		Intersectin 2	ITSN2	S886S888				12.6	33.2	R.TVSPGS <sup>V</sup> S <sup>S</sup> PIHGQGQVVENLK.A
		Intersectin 2	ITSN2	S883S886				10.1	57.1	R.TVS <sup>S</sup> PGS <sup>V</sup> SPIHGQGQVVENLK.A
		Intersectin 2	ITSN2	S888				0.4	41.6	R.TVSPGS <sup>V</sup> S <sup>S</sup> PIHGQGQVVENLK.A
		Intersectin 2	ITSN2	T881				10.1	26.4	R.TVSPGSVSPHGGQGQVVENLK.A
		Intersectin 2	ITSN2	S886				22.2	28.4	R.TVSPGS <sup>S</sup> VSPHGGQGQVVENLK.A
		Intersectin 2	ITSN2	S883				7.6	34.5	R.TVS <sup>S</sup> PGSVSPHGGQGQVVENLK.A
		Intersectin 2	ITSN2	T881S888				6.3	37.9	R.TVSPGSV <sup>S</sup> PIHGQGQVVENLK.A
		Intraflagellar transport protein IFT20	IFT20	S72S76				100.0	12.6	K.S <sup>S</sup> LAVS <sup>S</sup> PRL
		IQ motif and Sec7 domain 1	IQSEC1	S925				9.8	53.1	R.SALSS <sup>S</sup> LR.D
		IQ motif and Sec7 domain 1	IQSEC1	S512				76.7	84.8	R.NS <sup>S</sup> WDSPAFSNDVIR.K
		IQ motif and Sec7 domain 1	IQSEC1	S87					19.4	K.LQHS <sup>S</sup> TSILR.K
		IQ motif and SEC7 domain-containing	IQSEC1 protein 1	S802				-0.4	16.3	R.SALSS <sup>S</sup> SLRDLSEAGVHH.-
		IQ motif and SEC7 domain-containing	IQSEC1 protein 1	S926S940				27.5	74.8	R.RSS <sup>S</sup> AGSLESNVEGSIIS <sup>S</sup> SPHMR.R
		IQ motif and SEC7 domain-containing	IQSEC1 protein 1	S926S941				9.9	76.6	R.RSS <sup>S</sup> AGSLESNVEGSIIS <sup>S</sup> PHMR.R
		IQSEC1	S929S940					37.5	54.3	R.SSAGS <sup>S</sup> LESNVEGSIIS <sup>S</sup> SPHMR.R
		IQ motif and SEC7 domain-containing	IQSEC1 protein 1	S929S941				9.0	50.1	R.SSAGS <sup>S</sup> LESNVEGSIIS <sup>S</sup> PHMR.R
		IQ motif and SEC7 domain-containing	IQSEC1 protein 1	S929S932S941				8.1	12.4	R.RSSAGS <sup>S</sup> LES <sup>S</sup> NVEGSIIS <sup>S</sup> PHMR.R
		IQ motif and SEC7 domain-containing	IQSEC1 protein 1	S932S940				-2.2	46.7	R.SSAGSLES <sup>S</sup> NVEGSIIS <sup>S</sup> SPHMR.R
		IQGAP2	IQGAP2	S16				39.3	53.9	R.YGS <sup>S</sup> IVDDER.L
		IQGAP2	IQGAP2	Y14				20.1	34.0	R.Y <sup>S</sup> GSIVDDER.L
		MPST	S15					7.3	37.8	R.AR <sup>S</sup> PSVAAMASPQLCR.A
		Isoform 2 of Armadillo repeat-containing	ARMC10 protein 10	S45				29.0	80.4	K.S <sup>S</sup> AEDLDGSGYDDVLNAEQQLK.L
		Isoform 2 of Chromatin complexes subunit	BAP18 BAP18	S35				-0.2	26.1	K.LGELTMQLHPVADS <sup>S</sup> SPAGAIK.A
		Isoform 2 of EF-hand calcium-binding	CRACR2A domain-containing protein 4B	S473				120.5	60.6	R.IIS <sup>S</sup> VEEDPLQLLDGGFEQLSK.C
		Isoform 2 of Eomesodermin homolog	EOMES	T177S187				4.5	25.2	R.DNYDSMY <sup>T</sup> ASENDRLTPS <sup>S</sup> PTDSFPR.S
		Isoform 2 of Golgi-specific brefeldin A-	GBF1 resistance quanine nucleotide exchange	S1487				11.2	16.4	R.GGGSDDDEDEGVPA <sup>S</sup> YHTVSLQLLDLMHTLR.A
		Isoform 2 of Golgi-specific brefeldin A-	GBF1 resistance quanine nucleotide exchange	S1476				26.2	55.3	R.GGGS <sup>S</sup> DDDEDEGVPA <sup>S</sup> YHTVSLQLLDLMHTLR.A
		Isoform 2 of HBS1-like protein	HBS1L	S483				24.5	50.5	R.S <sup>S</sup> PGIDSNIOLSVLIK.N
		Isoform 2 of Hematopoietic lineage cell-	HCLS1 specific protein	T166S167				100.0	13.5	R.RRN <sup>T</sup> S <sup>S</sup> PRE
		Isoform 2 of Protein SOGA1	SOGA1	S141S142				46.7	64.6	R.LLGLLELAL <sup>S</sup> S <sup>S</sup> DAESAAGGPAGVR.T
		Isoform 2 of Rho guanine nucleotide	ARHGEF1 exchange factor 18	S153				8.7	32.5	R.S <sup>S</sup> RSVPVSFYEIR.S
		Isoform 2 of Rho guanine nucleotide	ARHGEF1 S94					97.3	75.0	R.RL <sup>S</sup> LDASVDEEPLPR.T
		Isoform 2 of Rho guanine nucleotide	ARHGEF1 S159					13.3	38.3	R.SVPVS <sup>S</sup> FYEIR.S
		Isoform 2 of Rho guanine nucleotide	ARHGEF1 S263					100.0	17.8	R.RL <sup>S</sup> CLR.S
		Isoform 2 of Rho guanine nucleotide	ARHGEF1 S71					36.8	63.9	R.DSLFSSLAGS <sup>S</sup> QDLSR.R
		ARHGEF1	S155					-0.3	28.6	R.SRS <sup>S</sup> VPVSFYEIR.S
		Isoform 2 of Uncharacterized protein	C15orf39 C15orf39	S496S497				100.8	76.2	K.EGARPP <sup>S</sup> S <sup>S</sup> PPMPVIDNVFSLAPYR.D
		Isoform 3 of Proline-rich protein 12	PRR12	S651				73.0	34.4	R.TEDEFLLQHLLOAPS <sup>S</sup> PPR.T
		Isoform 3 of UV excision repair protein	RAD23A RAD23 homolog A	Y197					71.6	R.AVEY <sup>L</sup> LTGIPGSPPEPHGSGVQESQVSEQPATEAGENPLEFLR.D
		Isoform 3 of UV excision repair protein	RAD23A RAD23 homolog A	S219				3.0	26.2	R.AVEYLLTGIPGSPPEPHGSGVQESQV <sup>S</sup> EQPATEAGENPLEFLR.D
		Isoform 3 of UV excision repair protein	RAD23A RAD23 homolog A	S205				2.2	39.8	R.AVEYLLTGIPG <sup>S</sup> PEPEHSGVQESQVSEQPATEAGENPLEFLR.D
		Isoform 4 of Interleukin enhancer-binding	ILF3 factor 3	S476				49.6		R. <sup>R</sup> SGVRSACETEAKDAIADABAIAEATBAAEDBATAEQDRI
		Isoform 4 of Interleukin enhancer-binding	ILF3 factor 3	S482				60.3	70.0	K.GEDS <sup>A</sup> AEETEAKPAVAPAPVVEAVSTPSAAFPSDATAENVK.Q
		Isoform 4 of Interleukin enhancer-binding	ILF3 factor 3	T486				0.3	37.4	K.GEDSAEET <sup>T</sup> EAKPAVAPAPVVEAVSTPSAAFPSDATAENVK.Q
		Isoform 4 of Interleukin enhancer-binding	ILF3 factor 3	T469S476S477					21.4	K. <sup>K</sup> LDADIGI <sup>R</sup> TKAGEDR <sup>R</sup> SGVRSACETEAKDAIADABAIAEATBAAEDBATAEQDRI



Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		0	2	4	6	8	10			
<10	0									
10	2									
20	4									
30	6									
40	8									
50	10									
60	12									
70	14									
80	16									
90	18									
>10	>10									
Protein Name		Gene	Phosphosites							
Isoform 4 of Interleukin enhancer-binding factor 3		T469S476							18.2	K. LIRNDAGI DTGAEGDPS*EVEDERAEETEAVDAIAADADACAVETE
Isoform 4 of Protein YIF1B YIF1B		T285S287						100.0	11.3	R.ITRS*GR.C
Isoform 5 of Mitochondrial fission factor MFF		S146						100.0	24.0	R.NDS*LPVLR.G
ITK ITK		Y512						26.0	48.1	R.FVLDDQY*TSSTGTGKFPVK.W
IWS1 homolog IWS1		S302S304S313						8.9	29.6	R.VSDS*ES*EGPQKGPAS*DS*ETEDASR.H
IWS1 homolog IWS1		S287S289						100.0	46.8	R.NQAS*DS*ENEELPKPR.V
IWS1 homolog IWS1		S398S400						100.0	58.0	K.AAVLS*DS*EDEEK.A
IWS1 homolog IWS1		S415S420S422						100.0	53.9	R.VVS*DADD*DS*DAVS*DK.S
IWS1 homolog IWS1		S300S302S304						17.4	38.3	R.VS*DS*ES*EGPQKGPASDS*ET*EDASR.H
IWS1		S438S440						29.4	89.1	K.TIAS*DS*EEAGKELSDK.K
IWS1 homolog IWS1		S274S276S287						12.5	13.1	R.IS*DS*ESEDPPRNOAS*DS*ENEELPKPR.V
IWS1 homolog IWS1		T67S69S80S82						56.4	43.6	K.GHHVT*DS*ENDEPLNLNAS*DS*ESELHR.Q
IWS1 homolog IWS1		T67S69S80S82						100.0	22.6	K.GHHVT*DS*ENDEPLNLNAS*DS*ES*EELHR.Q
IWS1 homolog IWS1		S511S513						100.0	89.5	K.EAEDS*DS*DDNIKR.G
IWS1 homolog IWS1		S248S250						28.3	53.4	R.IS*DS*ESEDPPR.H
IWS1 homolog IWS1		S248S250S261						19.2	13.3	R.IS*DS*ESEDPPRHOAS*DS*ENEELPKPR.I
IWS1 homolog IWS1		S93S95						5.7	13.3	R.QKDS*DS*ESEER.A
IWS1 homolog IWS1		S300S304S313						12.6	17.8	R.VS*DSES*EGPQKGPAS*DS*ETEDASR.H
IWS1 homolog IWS1		S415S420S422						52.3	75.8	R.VVS*DADD*DS*DAVSDK.S
IWS1 homolog IWS1		S300S302S304						5.8	11.5	R.VS*DS*ES*EGPQKGPAS*DS*ETEDASR.H
IWS1 homolog IWS1		S196S198						100.0	26.2	R.HQAS*DS*ENEPPKPR.M
IWS1 homolog IWS1		S261S263						100.0	49.8	R.HQAS*DS*ENEELPKPR.I
IWS1 homolog IWS1		S80S82						13.8	38.7	K.GHHVTDSENEPLNLNAS*DS*ESELHR.Q
IWS1 homolog IWS1		S69S80S82						19.1	34.5	K.GHHVTD*SENEPLNLNAS*DS*ESELHR.Q
IWS1 homolog IWS1		T67S80S84						3.8	14.5	K.GHHVT*DSENEPLNLNAS*DSES*EELHR.Q
IWS1 homolog IWS1		S377						100.0	91.7	K.MDS*DEDEKEGEEK.V
IWS1 homolog IWS1		S313S315						25.1	33.1	K.GPAS*DS*ETEDASR.H
IWS1 homolog IWS1		S400						24.1	32.2	K.AAVLSDS*EDEEK.A
IWS1 homolog IWS1		T67S69S80S84						14.4	15.0	K.GHHVT*DS*ENDEPLNLNAS*DSES*EELHR.Q
IWS1 homolog IWS1		S300S302S313						18.5	22.8	R.VS*DS*ESEGPKGPAS*DS*ETEDASR.H
IWS1 homolog IWS1		S276S278S287						3.9	13.0	R.ISDS*ES*EDPPRNOAS*DS*ENEELPKPR.V
Janus kinase 3 JAK3		S17S20						18.2	79.2	R.SCS*LLS*TEAGALHVLLPAR.G
Janus kinase and microtubule interacting protein 1		S382						30.2	40.0	R.HTS*LNDLSLTR.D
JAW1 LRMP		S73						13.2	71.0	R.S*ASPTIEAQGTSPAHDNIAFDQDSTSK.D
JAW1 LRMP		S75						18.4	87.1	R.SAS*PTIEAQGTSPAHDNIAFDQDSTSK.D
JAW1 LRMP		S75T83						27.7	47.8	R.SAS*PTIEAQGT*SPAHDNIAFDQDSTSK.D
JAW1 LRMP		S36						5.1	29.0	R.HTS*STDGTTSSDPGLEILNMA SCOLD.R.N
JAW1 LRMP		S403						10.4	27.6	R.TRKPS*LSEK.K
JAW1 LRMP		S388S391						52.2	67.7	K.TKDS*EP*GEETVER.T
JAW1 LRMP		S75S84						28.9	49.6	R.SAS*PTIEAQGT*SPAHDNIAFDQDSTSK.D
JAW1 LRMP		T319						26.4	29.0	R.RVT*IASLPR.N
JAW1 LRMP		S322						48.6	55.2	R.VTIAS*LPR.N
JAW1 LRMP		T41						12.4	56.4	R.HTSSDGT*ITSSDPGLEILNMA SCOLD.R.N
JAW1 LRMP		T77						5.0	23.7	R.SASPT*IEAQGTSPAHDNIAFDQDSTSK.D
JAW1 LRMP		S73T83						5.4	35.6	R.S*ASPTIEAQGT*SPAHDNIAFDQDSTSK.D
Joubertin AHI1		S267							23.2	K.KES*SVR.S
Jumonji domain containing 1B KDM3B		S727S743						8.3	21.8	R.SSS*PTSSLTQPIEMPTLSS*SPTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S727S742						5.9	22.9	R.SSS*PTSSLTQPIEMPTLS*SSPTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S730S743						7.1	16.5	R.SSSPT*SLTQPIEMPTLSS*SPTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S731S744						9.8	19.3	R.SSSPTSS*LTQPIEMPTLSS*PTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S727S744						7.6	14.7	R.SSS*PTSSLTQPIEMPTLSS*PTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S725S726							14.9	R.S*SPSSLTQPIEMPTLSSSPTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S730S744						7.5	18.5	R.SSSPT*SLTQPIEMPTLSS*PTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S725S744						7.6	10.9	R.S*SSPTSSLTQPIEMPTLSS*PTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S727T746						5.1	13.7	R.SSS*PTSSLTQPIEMPTLSSPT*EERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		S730S742						8.2	22.4	R.SSSPT*SLTQPIEMPTLS*SSPTEERPTVGPQQDNPLLK.T
Jumonji domain containing 1B KDM3B		T733S742						6.3	11.2	R.SSSPTSSLT*QPIEMPTLS*SSPTEERPTVGPQQDNPLLK.T
Jumonji domain containing 2B KDM4B		S632S633						44.2	14.7	K.QEAS*DEEASFFSGEEDVSDPDALRPLLSLQWK.N
JUN-D JUND		S251S259						22.8	10.8	K.DEPQTVPDVPS*FGESPPLS*PIDMDTQER.I
KAISO ZBTB33		T208							11.6	K.ET*LPNNNTVAQVQSNPGPVAISDVAPSASNNSPLLTNITPTQK.L
Kanamaptin SLCA41AP S466								26.0	152.3	K.NWEDEDFYD*DDDTFLDR.T
Kanamaptin SLCA41AP S258								118.6	115.5	K.MLGEDS*DEEEMDTSER.K

Peak Area		%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence	
			Protein Name	Gene						Phosphosites
			Kanadaplin	SLC4A1AP	Y464			10.9	96.5	K.NWEDEDFYDSDDTFLDR.T
			CEP170		S356S359			70.4	52.7	K.SIKSVDVPVYLK.R
			KARP 1 binding protein	CEP170	S1165			13.1	20.1	R.SDSEATISR.S
			KARP 1 binding protein	CEP170	S359			11.8	36.2	K.SIKSVDVPVYLKRL
			KARP 1 binding protein	PLIN5	S1160			13.9	13.6	R.LGSL.SAR.S
			KARP 1 binding protein	CEP170	S356			4.2	12.7	K.SIKSDVPVYLKRL
			KARP 1 binding protein	CEP170	S838			9.5	15.0	R.QGSFTIEKPSNPIELIPHINK.Q
			KARP 1 binding protein	CEP170	S1167			-0.8	26.4	R.SDSSEATISR.S
			Karyopherin alpha3	KPNA3	S60			51.5	75.1	R.NVPQEESESDSDVDADFK.A
			Karyopherin alpha3	KPNA3	S56			9.4	43.6	R.NVPQEESESDSDVDADFK.A
			Karyopherin beta 3	PO5	S670			2.5	26.7	K.TASIKPEVALLDTQDMENMSDDDGWEFVNLGDQGSFGK.T
			Kelch domain containing 4	KLHDC4	S413S418			76.0	117.2	R.SSEDEDSLEEAGSPAPGPCPR.S
			Kelch domain containing 4	KLHDC4	S413			11.6	45.7	R.SSEDEDSLEEAGSPAPGPCPR.S
			Kelch domain containing 4	KLHDC4	S418			-0.5	58.8	R.SEDEDSLEEAGSPAPGPCPR.S
			Keratin 13	KRT13	T319			12.3	11.4	K.TEITELR.R
			KH type splicing regulatory protein	KHSRP	S181			25.4	41.1	K.VQISPDGGGLPER.S
			KIAA0056	NCAPD3	S1382			18.4	36.1	R.SLGLVPFTLNSGSPEK.T
			KIAA0056	NCAPD3	S1384			16.1	45.5	R.SLGLVPFTLNSGSP.EK.T
			KIAA0082	CMTR1	T48S49S55			6.0	58.7	K.ASTTSLSGSDSETEGK.Q
			KIAA0082	CMTR1	S51S53S55			7.1	63.1	K.ASTTSLSGSSETEGK.Q
			KIAA0082	CMTR1	T47T48S55			9.1	47.8	K.ASTTSLSGSDSETEGK.Q
			KIAA0146	SPIDR	S132			100.0	64.3	R.DELOFIDWEIDSDRA
			KIAA0153 protein	TLL12	S16			9.1	99.9	R.SSPGQTPEEGAQALAEFAALHGPALR.A
			KIAA0153 protein	TLL12	S15			10.5	66.5	R.SSPGQTPEEGAQALAEFAALHGPALR.A
			KIAA0157	ABRAXAS	S368S372Y377			9.6	46.4	R.AAGDSEDSDDSDYENLIDPTESNSEYSHSK.D
			KIAA0157	ABRAXAS	S368S372S375			15.2	55.5	R.AAGDSEDSDDSDYENLIDPTESNSEYSHSK.D
			KIAA0157	ABRAXAS	S368S375Y377			4.6	46.6	R.AAGDSEDSDDSDYENLIDPTESNSEYSHSK.D
			KIAA0179	RRP1B	S732S735			28.4	38.5	K.TPTSSPASPLVAK.K
			KIAA0179	RRP1B	T728S732			14.5	28.4	R.VAFDPEQKPLHGVLTPTSSPASSPLVAK.K
			KIAA0179	RRP1B	S731S732S736			14.1	20.4	R.VAFDPEQKPLHGVLTPTSSPASSPLVAK.K
			KIAA0179	RRP1B	T728T730			7.1	18.3	R.VAFDPEQKPLHGVLTPTSSPASSPLVAK.K
			KIAA0179	RRP1B	T728S731S736			14.6	16.3	R.VAFDPEQKPLHGVLTPTSSPASSPLVAK.K
			KIAA0179	RRP1B	S731S735			35.5	36.6	K.TPTSSPASPLVAK.K
			KIAA0179	RRP1B	T728S732S736			10.4	21.2	R.VAFDPEQKPLHGVLTPTSSPASSPLVAK.K
			KIAA0179	RRP1B	T728T730S736			11.9	23.7	R.VAFDPEQKPLHGVLTPTSSPASSPLVAK.K
			KIAA0179	RRP1B	T728S732S735			11.4	35.3	R.VAFDPEQKPLHGVLTPTSSPASPLVAK.K
			KIAA0179	RRP1B	T728S731			18.2	29.6	R.VAFDPEQKPLHGVLTPTSSPASSPLVAK.K
			KIAA0182	GSE1	S10			44.9	59.5	K.SPSLGLMLSTATR.T
			KIAA0217 protein	LARP4B	S516T518			14.5	24.7	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	S511S512			5.7	15.4	K.FTSSSTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	T514T518S526			7.8	37.7	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	T510S511S516			5.9	14.2	K.FTSSSTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	S498			34.4	37.4	R.KNSFGYR.K
			KIAA0217 protein	LARP4B	T510S511			8.7	18.2	K.FTSSSTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	S601			11.4	30.0	R.SPSPAHLPODPK.V
			KIAA0217 protein	LARP4B	Y501			13.8	25.6	R.KNSFGYR.K
			KIAA0217 protein	LARP4B	T518S532			2.9	17.6	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	S511T518S526			12.4	25.7	K.FTSSSTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	S516S524S526			6.0	16.5	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	S516T518S524			19.3	38.4	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	T518S524			4.7	16.9	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	T514T518S524			8.5	16.9	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0217 protein	LARP4B	S568			-0.5	14.4	R.TLSADASVNTLPVWSR.E
			KIAA0217 protein	LARP4B	S516S524			7.0	12.4	K.FTSSQTQSPTPPKPPSPFELGLSSFFPLPGAAGNLK.T
			KIAA0284 protein	CEP170B	S221			100.0	13.1	K.FSLRQR.R
			KIAA0409 protein	RRP8	S104S106			100.0	20.7	K.QGPPCSDEEEVER.K
			KIAA0409 protein	RRP8	S62S64			17.3	55.4	R.ALEAASLQHPSPSLCISDSDEEEER.K
			KIAA0409 protein	RRP8	S58S62			8.3	11.6	R.ALEAASLQHPSPSLCISDSDEEEER.K
			KIAA0409 protein	RRP8	S58S64			4.6	20.8	R.ALEAASLQHPSPSLCISDSDEEEER.K
			KIAA0433 protein	PP1P5K2	S38			100.0	59.1	R.HFFHHADEDEEDDSPPER.Q
			KIAA0433 protein	PP1P5K2	S492S493			-0.4	22.1	K.TSSSEEDSRR.E
			KIAA0433 protein	PP1P5K2	S1151			-0.2	26.2	R.SSPIMR.K

Peak Area	iCV		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence	
	<10	>10	(0	>10	5	6	5	6			
KIAA0460	RPRD2	S899S902							41.9	R.GNEPGS <sup>DRS</sup> *PSPSKNDSFFTPDSNHNLSQSTTGHLSLPQK.Q	
KIAA0460	RPRD2	S348							71.6	112.6	R.DVEDMEL <sup>S</sup> *DVEDDGS.K
KIAA0460	RPRD2	S459							15.2	20.5	K.NTGVS <sup>PASRPS</sup> PGTPTS <sup>S</sup> *PSNLTSGLK.T
KIAA0460	RPRD2	S902S904							12.3	24.2	R.GNEPGSDRS <sup>S</sup> *PS <sup>S</sup> *PSKNDSFFTPDSNHNLSQSTTGHLSLPQK.Q
KIAA0460	RPRD2	S902S906							17.4	36.7	R.GNEPGSDRS <sup>S</sup> *PSP <sup>S</sup> *KNDSFFTPDSNHNLSQSTTGHLSLPQK.Q
KIAA0460	RPRD2	T458							4.0	26.2	K.NTGVS <sup>PASRPS</sup> PGTPT <sup>S</sup> *SPSNLTSGLK.T
KIAA0460	RPRD2	S330T332							53.2	20.0	K.S <sup>S</sup> *AT <sup>S</sup> *PEPVTNDR.D
KIAA0460	RPRD2	S902S910							15.7	14.6	R.GNEPGSDRS <sup>S</sup> *PSPSKNDS <sup>S</sup> *FFTPDSNHNLSQSTTGHLSLPQK.Q
KIAA0467	SZT2	S920S926							23.0	57.6	R.AEGIEGETLTAS <sup>S</sup> *POAPGS <sup>S</sup> *PEDSEGVPLISLR.V
KIAA0515 protein	PRRC2B	S388							100.0	36.1	K.LKFS <sup>S</sup> *DDEEEEVVK.D
KIAA0515 protein	PRRC2B	T225							23.9	91.5	R.HIISATSLST <sup>S</sup> *SPTELGSR.N
KIAA0515 protein	PRRC2B	S226							17.2	36.0	R.HIISATSLSTS <sup>S</sup> *PTELGSR.N
KIAA0515 protein	PRRC2B	S224							0.5	38.1	R.HIISATSLS <sup>S</sup> *TSPTELGSR.N
KIAA0528	C2CD5	S260							80.2	40.7	K.LSSPA <sup>AF</sup> L <sup>PACN</sup> S <sup>S</sup> *PSK.E
KIAA0528	C2CD5	S817							12.2	42.7	R.AS <sup>S</sup> *TNEELLQFPLELCDSLSPHPFPAK.A
KIAA0556	KIAA0556	S753S758							5.8	10.8	K.TP <sup>S</sup> *S <sup>S</sup> *WLQPS <sup>S</sup> *PTGK.D
KIAA0592	WASHC2C	S539							75.8	173.2	K.GLFS <sup>S</sup> *DEEDSEDLFSSQSASNLK.G
KIAA0592	WASHC2C	S544							5.1	33.2	K.GLFS <sup>S</sup> *DEEDS <sup>S</sup> *EDLFSSQSASNLK.G
KIAA0592	WASHC2A	S695S702							11.3	32.2	R.VSLLFEDDVS <sup>S</sup> *GGS <sup>LFGS</sup> *PPTS <sup>V</sup> PPATK.K
KIAA0592	WASHC2A	S284S288							11.1	16.4	R.S <sup>S</sup> *RPT <sup>S</sup> *FADELAAR.I
KIAA0592	WASHC2A	S352							23.9	62.8	K.LTDEDF <sup>S</sup> *PFGSGGLFSGGK.G
KIAA0592	WASHC2A	S284T287							8.6	12.1	R.S <sup>S</sup> *RPT <sup>S</sup> *FADELAAR.I
KIAA0592	WASHC2A	S686S695							2.7	16.9	R.VS <sup>S</sup> *LLFEDDVS <sup>S</sup> *GGS <sup>LFGS</sup> *PPTS <sup>V</sup> PPATK.K
KIAA0592	WASHC2A	S695S698S702							13.7	12.0	R.VSLLFEDDVS <sup>S</sup> *GGS <sup>S</sup> *LFGS <sup>S</sup> *PPTS <sup>V</sup> PPATK.K
KIAA0592	WASHC2A	S698S702							2.4	34.5	R.VSLLFEDDVS <sup>S</sup> *GGS <sup>S</sup> *LFGS <sup>S</sup> *PPTS <sup>V</sup> PPATK.K
KIAA0652 gene product	ATG13	S324							86.0	45.5	R.AS <sup>S</sup> *PHDVLETIFVR.K
KIAA0683	TELO2	T632							5.6	48.8	R.T <sup>S</sup> *PQPGSPSPNTPCLPEAAVSQPGSAVASDWR.V
KIAA0683	TELO2	S637							5.0	57.4	R.TPQPGS <sup>S</sup> *PSNTPCLPEAAVSQPGSAVASDWR.V
KIAA0683	TELO2	S639							2.3	55.1	R.TPQPGSP <sup>S</sup> *NTPCLPEAAVSQPGSAVASDWR.V
KIAA0685	PPP6R2	S766							13.8	28.6	K.AFS <sup>S</sup> *PASPCA <sup>WN</sup> CVTR.K
KIAA0692	ANKLE2	S662							19.4	19.1	R.NN <sup>S</sup> *PPTVGAFGHTR.C
KIAA0701 protein	UHRF1BP	S889S891							7.6	37.4	K.SPVS <sup>S</sup> *VS <sup>S</sup> *PVVPDYLP <sup>TENG</sup> D <sup>FLSS</sup> K.R
KIAA0701 protein	UHRF1BP	S887S889							23.8	46.0	K.SPVS <sup>S</sup> *ES <sup>S</sup> *VSPVVPDYLP <sup>TENG</sup> D <sup>FLSS</sup> K.R
KIAA0701 protein	UHRF1BP	S935							7.6	27.7	R.SM <sup>S</sup> *VDLSH <sup>PLK</sup> D <sup>PLLF</sup> K.S
KIAA0748	TESPA1	S454							61.4	77.6	K.S <sup>S</sup> *LDLSITQOK.W
KIAA0776	UFL1	S458							69.6	98.6	R.KDD <sup>S</sup> *DDESQSSHTGK.K
KIAA0776	UFL1	S790							12.1	23.7	R.KSS <sup>S</sup> *VTEE.-
KIAA0912 protein	CEP152	S717							4.0	16.5	R.THLQLRS <sup>S</sup> *ELDK.L
KIAA0912 protein	CEP152	S1405							100.0	47.9	R.NV <sup>S</sup> *PEFVPC <sup>EGEG</sup> GLHK.K
KIAA0999 protein	SIK3	S568							60.3	51.0	R.RFS <sup>S</sup> *DGAASIQAFK.A
KIAA0999 protein	SIK3	T163							37.8	89.6	K.T <sup>S</sup> *WCGSP <sup>PPYA</sup> AP <sup>ELFEG</sup> K.E
KIAA0999 protein	SIK3	S167							-0.5	47.9	K.TWCGS <sup>S</sup> *PPYA <sup>AP</sup> ELFEGK.E
KIAA1002 protein	R3HDM2	S10							10.2	66.6	K.AS <sup>S</sup> *FSGISILTR.G
KIAA1002 protein	R3HDM2	S9							12.2	74.3	K.AS <sup>S</sup> *SFGISILTR.G
KIAA1115 protein	PPP6R1	S540S541							12.7	56.0	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *DDEDRLK.E
KIAA1115 protein	PPP6R1	S539S540							11.0	38.0	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *SDDEDRLK.E
KIAA1115 protein	PPP6R1	S541							11.3	41.8	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *DDEDRLK.E
KIAA1115 protein	PPP6R1	S539S540S541							15.0	30.3	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *SDDEDRLK.E
KIAA1115 protein	PPP6R1	T735							11.0	22.1	R.GGATPLSYSPGQPPG <sup>PSWT</sup> ATFD <sup>PVPT</sup> DAPT <sup>S</sup> *SPR.V
KIAA1115 protein	PPP6R1	S712T735							18.0	30.5	R.GGATPLSYSP <sup>S</sup> *PGQPPG <sup>PSWT</sup> ATFD <sup>PVPT</sup> DAPT <sup>S</sup> *SPR.V
KIAA1115 protein	PPP6R1	S540							13.9	48.2	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *DDEDRLK.E
KIAA1115 protein	PPP6R1	S677T678S680							6.2	68.3	R.SGS <sup>S</sup> *T <sup>S</sup> *D <sup>S</sup> *EDEEEEEEEEEEGIGCAAR.G
KIAA1115 protein	PPP6R1	T534S539S541							3.6	12.5	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *SDDEDRLK.E
KIAA1115 protein	PPP6R1	S674S677T678							4.3	85.8	R.S <sup>S</sup> *GG <sup>S</sup> *T <sup>S</sup> *DSEEEEEEEEEEGIGCAAR.G
KIAA1115 protein	PPP6R1	T534							16.7		K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *DDEDRLK.E
KIAA1115 protein	PPP6R1	T534S540S541							8.3	22.7	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *DDEDRLK.E
KIAA1115 protein	PPP6R1	T731							4.2	22.3	R.GGATPLSYSPGQPPG <sup>PSWT</sup> ATFD <sup>PVPT</sup> DAPT <sup>S</sup> *SPR.V
KIAA1115 protein	PPP6R1	S736							8.0	38.9	R.GGATPLSYSPGQPPG <sup>PSWT</sup> ATFD <sup>PVPT</sup> DAPT <sup>S</sup> *SPR.V
KIAA1115 protein	PPP6R1	S539S541							7.9	16.9	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *SDDEDRLK.E
KIAA1115 protein	PPP6R1	T706							22.5		R.GGAT <sup>S</sup> PLSYSPGQPPG <sup>PSWT</sup> ATFD <sup>PVPT</sup> DAPT <sup>S</sup> *SPR.V
KIAA1115 protein	PPP6R1	T723T735							23.8	15.9	R.GGATPLSYSPGQPPG <sup>PSWT</sup> ATFD <sup>PVPT</sup> DAPT <sup>S</sup> *SPR.V
KIAA1115 protein	PPP6R1	T534S539							0.1	15.4	K.NM <sup>S</sup> *DLVNT <sup>HHLHS</sup> <sup>S</sup> *SDDEDRLK.E

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence	
		Protein Name	Gene	Phosphosites					
		KIAA1115 protein PPP6R1		T534S539S540			5.9	16.2	K.NMVDLVNT <sup>H</sup> HLHS <sup>S</sup> SDDEDDLK.E
		KIAA1115 protein PPP6R1		S887			16.7	18.0	K.SPEPLGLPQSQAALTPPPINGSAPEGPA <sup>S</sup> PGSQ.-
		KIAA1115 protein PPP6R1		S645S648			75.2	101.4	R.IQOFDDDEEEDEEEAQS <sup>S</sup> GES <sup>S</sup> DGEDGAWQGSQALR.G
		KIAA1115 protein PPP6R1		S712			12.2	31.1	R.GGATPLSYPS <sup>S</sup> PGQPPPGPSWTATFDVPVPTDAPTSPLRV
		KIAA1115 protein PPP6R1		S712S736			6.5	22.1	R.GGATPLSYPS <sup>S</sup> PGQPPPGPSWTATFDVPVPTDAPTS <sup>S</sup> PR.V
		KIAA1115 protein PPP6R1		S539			-0.3	22.0	K.NMVDLVNTHHLHS <sup>S</sup> SDDEDDLK.E
		KIAA1143 protein KIAA1143		S50			100.0	22.6	R.IQPQPPDEDGDHS <sup>S</sup> DKEDEQPQVVLLK.K
		KIAA1211 protein KIAA1211		T968S975			5.0	25.6	K.MPLAQKPALAPKPT <sup>S</sup> SQTPPAS <sup>S</sup> PLSK.L
		KIAA1211 protein KIAA1211		T968S969			3.1	21.1	K.MPLAQKPALAPKPT <sup>S</sup> SQTPPASPLSK.L
		KIAA1211 protein KIAA1211		T971S975			9.4	20.5	K.MPLAQKPALAPKPTSQT <sup>S</sup> PPAS <sup>S</sup> PLSK.L
		KIAA1267 KANSL1		S268			31.8	100.3	K.S <sup>S</sup> PLSSILFSALDSSTR.I
		KIAA1267 KANSL1		S271			-2.8	38.3	K.SPLS <sup>S</sup> SILFSALDSSTR.I
		KIAA1271 protein MAVS		S222			67.6	24.7	R.GPV <sup>S</sup> PSVSFQPLAR.S
		KIAA1370 FAM214A		T32			49.3	10.8	R.TPECSVKGR.T
		KIAA1429 VIRMA		S1579			9.8	23.9	R.SFLSEPS <sup>S</sup> PGR.T
		KIAA1429 VIRMA		S1578			42.4	16.6	R.SFLSEPS <sup>S</sup> SPGR.T
		KIAA1429 VIRMA		T184			25.5	14.4	R.TPPGPPPPDDDEDDPVPLPVSGDK.E
		KIAA1432 RIC1		T913S916			7.0	43.1	K.AIGSGESET <sup>S</sup> PPS <sup>S</sup> TPTAQEPSSGGFEFFR.N
		KIAA1462 protein JCAD		S948S949S951			4.9	19.5	K.EVS <sup>S</sup> VS <sup>S</sup> RMWRVLSFR.N
		KIAA1467 FAM234B		S167T26S33			16.9	41.5	K.S <sup>S</sup> PDLGEYDPLT <sup>S</sup> QADSDES <sup>S</sup> EDDLVLNLQK.N
		KIAA1467 FAM234B		S167T26S30			8.4	16.3	K.S <sup>S</sup> PDLGEYDPLT <sup>S</sup> QADS <sup>S</sup> DESEDDLVLNLQK.N
		KIAA1467 FAM234B		T26S30			7.6	13.6	K.SPDLGEYDPLT <sup>S</sup> QADS <sup>S</sup> DESEDDLVLNLQK.N
		KIAA1467 FAM234B		S30S33			23.1	68.3	K.SPDLGEYDPLTQADS <sup>S</sup> DES <sup>S</sup> EDDLVLNLQK.N
		KIAA1468 RELCH		S45S51S54			33.6		R.LVADGVDRDQSHACH <sup>S</sup> EPNDNMLGSSAGS <sup>S</sup> DEACANMLGR
		KIAA1542 Protein PHRF1		S973			51.5	61.3	R.TVTCVTVEPEAPP <sup>S</sup> PDVLQAATHR.V
		KIAA1542 Protein PHRF1		S1032S1034			37.7	38.0	R.S <sup>S</sup> AS <sup>S</sup> PSVGEERPR.R
		KIAA1542 Protein PHRF1		S1114S1116			100.0	15.8	R.RS <sup>S</sup> AS <sup>S</sup> RPRL.G
		KIAA1542 Protein PHRF1		S1032S1036			11.8	37.6	R.S <sup>S</sup> ASP <sup>S</sup> VGEERPR.R
		KIAA1542 Protein PHRF1		S1359S1371			29.4	13.3	K.AEAPS <sup>S</sup> SPDVAPAGKES <sup>S</sup> PSASGR.V
		KIAA1542 Protein PHRF1		S1034S1036			6.7	39.2	R.SAS <sup>S</sup> PS <sup>S</sup> VGEERPR.R
		KIAA1542 Protein PHRF1		S101			20.4	29.2	K.LEAAGSFNS <sup>S</sup> DDDAESCPICLNAFR.D
		KIAA1542 Protein PHRF1		S98			4.3	19.6	K.LEAAGS <sup>S</sup> FNSDDDAESCPICLNAFR.D
		KIAA1602 NCKAP5L		S571S577			10.6	16.5	R.GP <sup>S</sup> PEPPPS <sup>S</sup> PLQVPTYQLTLEVPQAEVLRS
		KIAA1604 protein CWC22		S91S93			25.1	13.8	R.SRK <sup>S</sup> PS <sup>S</sup> PGR.R
		KIAA1604 protein CWC22		S831			5.2	14.5	R.RNSF <sup>S</sup> ENEK.H
		KIAA1604 protein CWC22		S829			13.4	23.0	R.RN <sup>S</sup> FSENEK.H
		KIAA1704 protein GPALPP1		S105			100.0	47.3	K.QQDS <sup>S</sup> PPRIIGPALPPGFIK.S
		GPALPP1		T138S140S141			100.0	30.1	R.DDPGQOET <sup>S</sup> DS <sup>S</sup> SEDEIIGPMPAK.G
		KIAA1706 protein EEPD1		S173			100.0	50.6	R.S <sup>S</sup> VEDLVR.M
		KIAA1706 protein EEPD1		S25S31			100.0	63.8	R.KFS <sup>S</sup> AACNF <sup>S</sup> NILVQER.L
		KIAA1826 protein MSANTD4		S152			78.4	37.9	R.DPQS <sup>S</sup> PEFEIEEEEMLSSVIPDSR.R
		KIAA1836 protein CC2D1B		T824			100.0	10.8	R.NPT <sup>S</sup> GGKLEVK.V
		KIAA1949 PPP1R1B		S224			67.0	50.0	R.LS <sup>S</sup> PGESAYQKL
		KIDINS220 KIDINS220		S1411			-0.4	42.2	R.SS <sup>S</sup> PHSTYYMQSSSGGSIHSNLEQEK.G
		Kinase suppressor of ras 1 KSR1		T133T136			50.0	44.9	R.ALHSFIT <sup>S</sup> PPT <sup>S</sup> TPQLR.R
		Kinase suppressor of ras 1 KSR1		T133T137			11.6	31.9	R.ALHSFIT <sup>S</sup> PPTT <sup>S</sup> PQLR.R
		Kindlin 2 FERMT2		T188T190T192			24.8		K.TLPTNTVDAUGSPLSTPAWIGSALSGSRLALSGRTDPL
		Kinectin KTN1		S75			14.4	20.0	K.EIQGNLHES <sup>S</sup> DSESVPR.D
		Kinesin 2 KLC1		S521			18.7	53.9	R.S <sup>S</sup> RESLNVDVK.Y
		Kinesin 2 KLC1		S521S524			100.0	37.5	R.S <sup>S</sup> RES <sup>S</sup> LNVDVK.Y
		Kinesin 2 KLC1		S524			1.3	31.8	R.SRES <sup>S</sup> LNVDVK.Y
		Kinesin family member 13B KIF13B		S1778			12.1	17.3	R.RS <sup>S</sup> TGLRL
		Kinesin family member 1B KIF1B		S1612			15.2	52.3	R.AS <sup>S</sup> SPCFEPEQFQIVPAVETPYLAR.A
		Kinesin family member 1B KIF1B		S1613			16.9	24.8	R.ASS <sup>S</sup> PCPEFEQFQIVPAVETPYLAR.A
		Kinesin family member 1C KIF1C		S1033			100.0	34.3	R.RN <sup>S</sup> LDGGGR.S
		Kinesin family member 1C KIF1C		S674S676			37.5	65.6	R.LYADS <sup>S</sup> DS <sup>S</sup> GDDSDKR.S
		Kinesin family member 21B KIF21B		S1167			31.4	12.3	K.S <sup>S</sup> LASLVEIK.E
		Kinesin family member 23 KIF23		S684			5.1	73.4	R.SVS <sup>S</sup> PSPVLLFQPDQNAPPRI.L
		Kinesin family member 23 KIF23		S686			-0.3	44.6	R.SVS <sup>S</sup> PS <sup>S</sup> PVLLFQPDQNAPPRI.L
		Kinesin family member 23 KIF23		S684S686			-0.4	31.4	R.SVS <sup>S</sup> PS <sup>S</sup> PVLLFQPDQNAPPRI.L
		Kinesin family member 23 KIF23		S682S684			6.2	47.2	R.S <sup>S</sup> VS <sup>S</sup> PSPVLLFQPDQNAPPRI.L
		Kinesin family member 3A KIF3A		T692			3.3	16.1	R.SAKPET <sup>S</sup> VIDSLQ.-

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<10	0			5	5	5	9.1	15.1	R.HSAQIAKIPRPQGH <del>PAAS</del> *PTHPSAIR.G
10-20	1			5	5	5	24.1	13.0	K.EIDLESIFS <del>LN</del> POLVPDEEIEPSPET* <del>PPPP</del> PASSAK.V
20-30	2			5	5	5	8.3	21.9	K.EIDLESIFS <del>LN</del> POLVPDEEIEPSP*PETPPPPPASSAK.V
30-40	3			5	5	5	9.8	59.4	R.AS* <del>SL</del> NVLNVGGK.A
40-50	4			5	5	5	25.6	75.4	R.AS* <del>LN</del> NVLNVGGK.A
50-60	5			5	5	5	29.8	73.4	R.ALSAS* <del>HT</del> DLAH.-
60-70	6			5	5	5	44.2	130.8	R.AAS* <del>LN</del> YLNQPSAAPLQVSR.G
70-80	7			5	5	5	7.0	18.5	R.GLSAST* <del>MD</del> LSSSS.-
80-90	8			5	5	5	16.1	38.2	R.GLSAS* <del>TMD</del> LSSSS.-
90-100	9			5	5	5	110.9	154.1	R.AFVEDS* <del>EDED</del> GAGEGSSLLQK.R
>100	10			5	5	5	48.5	14.7	R.QLPALDGS <del>LM</del> GPES*PPAQEEEA <del>PV</del> S*PHKKPA <del>PQ</del> KR.R
				5	5	5	17.7	61.2	R.TAS* <del>S</del> S* <del>DS</del> *EEDPEALEK.Q
				5	5	5	70.9	119.5	R.S* <del>PG</del> NVNTIV <del>VP</del> LLEDGR.G
				5	5	5	1.7	52.6	R.QSKS* <del>DS</del> *DDDDLP <del>N</del> VLDSVNETGSTALSIA <del>R</del> .A
				5	5	5	12.2	74.0	R.QS* <del>KSD</del> S*DDDDLP <del>N</del> VLDSVNETGSTALSIA <del>R</del> .A
				5	5	5	11.0	74.5	R.QS* <del>KSD</del> SDDDDLP <del>N</del> V <del>T</del> LDSVNETGSTALSIA <del>R</del> .A
				5	5	5	7.3	11.4	R.SESPD <del>S</del> * <del>RK</del> .R
				5	5	5	100.0	48.7	R.GLL <del>T</del> *PPAS* <del>PLE</del> LEAKPK.R
				5	5	5	25.1	22.9	R.EAGELP <del>T</del> * <del>SPL</del> HLLS* <del>PG</del> T <del>PR</del> .S
				5	5	5	5.6	21.4	R.EAGELP <del>T</del> S* <del>PL</del> HLLS* <del>PG</del> T <del>PR</del> .S
				5	5	5	100.0	43.4	K.DQLI <del>Y</del> * <del>NLL</del> K.E
				5	5	5	15.6	27.6	K.VSKDDR <del>S</del> * <del>DVES</del> * <del>S</del> S* <del>S</del> * <del>SEED</del> VTTCTK <del>S</del> .S
				5	5	5	43.5	44.8	K.VS* <del>KDDR</del> S <del>DVES</del> * <del>S</del> S* <del>S</del> * <del>SEED</del> VTTCTK <del>S</del> .S
				5	5	5	100.0	20.2	R.S* <del>PGR</del> PPK.S
				5	5	5	100.0	18.6	R.S* <del>RS</del> * <del>PGR</del> PPK.S
				5	5	5	11.1	76.7	R.SAS* <del>ASH</del> QADIK.E
				5	5	5	23.5	46.2	R.S* <del>AS</del> ASHQADIK.E
				5	5	5	6.5	16.4	R.KGGS* <del>T</del> *SSSPSR <del>R</del> .R
				5	5	5	22.4	22.4	R.LKLS* <del>PSP</del> SR.V
				5	5	5	20.6	39.2	R.LKLS* <del>PS</del> * <del>PSS</del> R.V
				5	5	5	15.2	24.0	R.AGGPT <del>T</del> * <del>PLS</del> * <del>P</del> TR.L
				5	5	5	114.9	29.0	K.TTIPEEEEEEAAGVVVEELFHQ <del>GT</del> *PRA
				5	5	5	9.0	18.4	R.AGGP <del>T</del> * <del>TPLS</del> * <del>P</del> TR.L
				5	5	5	10.4	73.5	R.DSHS* <del>S</del> *EED <del>EA</del> SQTDL <del>SQT</del> ISK <del>T</del> .T
				5	5	5	9.0	64.4	K.VNFSEEGE <del>T</del> *EEDQDDSSH <del>S</del> VTTVKA
				5	5	5	24.0	45.4	R.LQQQHSEQ <del>PLQPS</del> * <del>P</del> VMTR.R
				5	5	5	64.6	66.5	R.GL <del>RDS</del> * <del>HS</del> * <del>S</del> *EED <del>EA</del> SQTDL <del>SQT</del> ISK <del>K</del> .K
				5	5	5	8.9	41.2	R.DS* <del>HS</del> * <del>S</del> *EED <del>EA</del> SQTDL <del>SQT</del> ISK <del>K</del> .K
				5	5	5	9.4	26.5	R.RGLRDS* <del>HS</del> * <del>SEED</del> EA <del>S</del> SQTDL <del>SQT</del> ISK <del>K</del> .K
				5	5	5	24.1	17.3	R.DS* <del>HS</del> * <del>SEED</del> EA <del>S</del> SQTDL <del>SQT</del> ISK <del>K</del> .K
				5	5	5	25.6	49.9	R.SLPTTV <del>PES</del> * <del>PN</del> YR.N
				5	5	5	30.0	54.0	R.S* <del>LP</del> TTVPES <del>PN</del> YR.N
				5	5	5	18.3	38.2	R.S* <del>LP</del> TTVPES* <del>PN</del> YR.N
				5	5	5	3.4	64.3	R.TAS* <del>ISS</del> SPS*EGTPTVGSYGCTPQSLPK <del>F</del> .F
				5	5	5	105.7	139.4	R.ESPR <del>LQ</del> LPGAEGPAIS* <del>DGEE</del> GGGEPGAGGGAAGA <del>AG</del> AGR.R
				5	5	5	79.2		R.ES* <del>PR</del> LQ <del>LPGA</del> EGPAIS <del>DGEE</del> GGGEPGAGGGAAGA <del>AG</del> AGR.R
				5	5	5	15.3	83.4	R.HSS* <del>NP</del> PLESHV <del>GW</del> MDSR.E
				5	5	5	100.0	47.5	R.ES* <del>PR</del> LQ <del>LPGA</del> EGPAIS* <del>DGEE</del> GGGEPGAGGGAAGA <del>AG</del> AGR.R
				5	5	5	37.8	137.9	K.NTFTAWS* <del>DEES</del> * <del>D</del> YIDDR.D
				5	5	5	23.9	104.4	K.GLSAS* <del>LP</del> DLSENWIEVK.K
				5	5	5	23.4	52.2	K.ETES* <del>APG</del> S* <del>P</del> R.A
				5	5	5	26.5	40.7	R.AV <del>T</del> * <del>PV</del> PTK.T
				5	5	5	23.6	49.7	R.SLPT <del>T</del> * <del>VP</del> ESPNYR.N
				5	5	5	11.4	29.2	K.I <del>LIV</del> <del>T</del> * <del>Q</del> TPHYMR.R
				5	5	5	8.0	56.2	R.TAS* <del>ISS</del> SPSEG <del>T</del> *PTVGSYGCTPQSLPK <del>F</del> .F
				5	5	5	3.5	38.8	R.TASISS <del>S</del> * <del>PS</del> *EG <del>T</del> *PTVGSYGCTPQSLPK <del>F</del> .F
				5	5	5	2.3	19.3	R.TASISS <del>S</del> * <del>PSEG</del> TPVGSYGCTPQSLPK <del>F</del> .F
				5	5	5	10.8	13.0	K.N <del>T</del> * <del>FT</del> *AWSDEESDYEIDDR <del>D</del> VN <del>K</del> .I
				5	5	5	18.9	76.8	K.NTFTAWS* <del>DEESDY</del> *EIDDR.D
				5	5	5	-0.2	16.3	R.SLPT <del>T</del> * <del>VP</del> ESPNYR.N
				5	5	5	25.3	54.3	K.NTFTAWS* <del>DEESDY</del> EIDDR.D
				5	5	5	19.3	27.3	K.ETESAPG <del>S</del> * <del>P</del> R.A

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		Protein Name	Gene	Phosphosites						
		LARP	LARP1	S979				18.8	19.3	R.CP <b>S</b> *QSSSRPAAMISOPPTPTGQPV.R.E
		LARP	LARP1	T779				9.1	73.3	R.TASISSSPSEG <b>T</b> *PTVGSYGCTPQSLPK.F
		LARP	LARP1	S143				30.7	42.4	K.NALPPVLTTVNGQ <b>S</b> *PPEHSAPAK.V
		LARP	LARP1	S746				69.6	61.3	R.H <b>S</b> *SNPPLESHVGVWMDSR.E
		LARP	LARP1	S772S773S776				6.0	17.3	R.TAS <b>S</b> * <b>S</b> * <b>S</b> * <b>P</b> S*EGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	S469				37.2	66.9	K.GL <b>S</b> *ASLPDLDSENWIEVK.K
		LARP	LARP1	S776				-0.2	48.0	R.TASISS <b>S</b> *EGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	S554Y556				10.3	43.7	R.KNTFTAWSDEE <b>S</b> * <b>D</b> *Y*EIDDR.D
		LARP	LARP1	S770				5.8	49.3	R.TA <b>S</b> *ISSSPSEGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	S770S772S773				8.7	33.3	R.TA <b>S</b> * <b>I</b> <b>S</b> * <b>S</b> *SPSEGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	S772T779				9.4	44.9	R.TAS <b>S</b> *SSPSEG <b>T</b> *PTVGSYGCTPQSLPK.F
		LARP	LARP1	S770S774				1.6	25.1	R.TA <b>S</b> *ISS <b>S</b> *PSEGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	T693S697				5.1	14.2	R.SLP <b>T</b> *VPES*PNYR.N
		LARP	LARP1	S772S776				4.4	21.3	R.TAS <b>S</b> *SS <b>S</b> *EGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	S774S776T781				4.6	24.3	R.TASISS <b>S</b> * <b>P</b> S*EGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	T438S444				19.3	45.8	K.ET*ESAPG <b>S</b> *PR.A
		LARP	LARP1	S770S773				3.8	48.7	R.TA <b>S</b> * <b>I</b> <b>S</b> * <b>S</b> *PSEGTPTVGSYGCTPQSLPK.F
		LARP	LARP1	S770S772				0.5	43.1	R.TA <b>S</b> * <b>I</b> <b>S</b> * <b>S</b> *PSEGTPTVGSYGCTPQSLPK.F
		LASS2	CERS2	S341T346S348				100.0	59.0	K.LVEDER <b>S</b> *DREET* <b>E</b> <b>S</b> * <b>S</b> *EGEEAAAGGGA.K.S
		LASS2	CERS2	S341				100.0	51.6	K.LVEDER <b>S</b> *DR.E
		LASS2	CERS2	T346S348S349				100.0	112.3	R.EET* <b>E</b> <b>S</b> * <b>S</b> *EGEEAAAGGGA.K.S
		LATS1	LATS1	S278				25.6	53.2	K.RY <b>S</b> *GNMEYVISR.I
		LATS1	LATS1	S1111				15.1	31.0	R.FFDONGYPYNYKPIEYINQQSGEQ <b>S</b> *DEDDQNTGSEIK.N
		LBA	LBA	S2064				15.2	112.3	R.SQALGNQNSEIILLGDDDTL <b>S</b> *SVDEK.D
		LBA	LBA	S1787				11.1	80.6	K.LPSVPTVD <b>S</b> * <b>V</b> QDPVSNMISER.L
		LBA	LBA	S1767				17.2	83.4	K.SAVSPSTFNTSIPTNAVSVSSVDSQAQSDMGGE <b>S</b> *PGSR.S
		LBA	LBA	S1785				8.0	45.5	K.LPSVPTVD <b>S</b> * <b>V</b> QDPVSNMISER.L
		LBA	LBA	S1733				38.4		K. <b>S</b> *AVSPSTFNTSIPTNAVSVSSVDSQAQSDMGGE <b>S</b> *PGSR.S
		LBH limb bud and heart development homolog	LBH	S63				89.5	31.5	R.LP <b>S</b> *IVVEPTGEVESGELR.W
		Lck	LCK	Y192				32.1	58.9	R.NLDNGGF <b>Y</b> *ISPR.I
		Lck	LCK	S42				45.6		R. <b>L</b> CK <b>S</b> *NPPASPLQDNLVIALHSYEPHDGDLGFEK.G
		Lck	LCK	T50				74.5		R.DPLVT <b>Y</b> EGSNPPASPLQDNLVIALHSYEPHDGDLGFEK.G
		Lck	LCK	S59				48.9	53.0	R.DPLVT <b>Y</b> EGSNPPAS*PLQDNLVIALHSYEPHDGDLGFEK.G
		Lck	LCK	Y505				27.9	28.7	R.SVLEDFFTATEGQ <b>Y</b> *QPQP.-
		Lck	LCK	T501				13.4	19.1	R.SVLEDFFTAT*EGQYQPQP.-
		Lck	LCK	S42T50				41.4		R. <b>L</b> CK <b>S</b> *NPPASPLQDNLVIALHSYEPHDGDLGFEK.G
		Lck-interacting transmembrane adapter 1	LIME1	S86				31.1	51.7	R.AAPGPAQQQGAACQHG <b>S</b> *PAPTLAGGVQGHHR.T
		LEM domain containing 2	LEM2	S496				9.1	42.3	R.WTK <b>S</b> *SFSDSER.-
		Leucine rich repeat containing 47	LRRC47	S518				12.6	76.9	K.EEG <b>S</b> *LSDTEADAVSQQLPDPTTNPSAGK.D
		Leucine rich repeat containing 47	LRRC47	S520				18.8	71.3	K.EEGSL <b>S</b> *DTEADAVSQQLPDPTTNPSAGK.D
		Leucine rich repeat containing 47	LRRC47	S518S520				5.6	14.2	K.EEG <b>S</b> * <b>L</b> <b>S</b> *DTEADAVSQQLPDPTTNPSAGK.D
		Leucine rich repeat containing 47	LRRC47	T522				18.4	73.8	K.EEGSL <b>S</b> <b>T</b> *EADAVSQQLPDPTTNPSAGK.D
		Leucine rich repeat in FLII interacting protein 1	LRRFIP1	S115				9.8	57.6	R.NMPQLSAATLASLG <b>T</b> * <b>S</b> R.R
		Leucine rich repeat in FLII interacting protein 1	LRRFIP1	T114				29.3	51.3	R.NMPQLSAATLASLG <b>T</b> * <b>S</b> R.R
		Leucine rich repeat in FLII interacting protein 1	LRRFIP1	S116				6.8	69.8	R.NMPQLSAATLASLG <b>T</b> * <b>S</b> *R.R
		Leucine rich repeat in FLII interacting protein 1	LRRFIP1	S110				6.2	60.4	R.NMPQLSAATLAS*LG <b>T</b> SSR.R
		Leucine rich repeats and calponin homology domain containing protein 1	LRCH1	S532S536				37.0	72.5	R.ENS*PA <b>S</b> *PTTNSTAPFLKPR.S
		Leucine rich repeats and calponin homology domain containing protein 1	LRCH1	T538T539				17.2	26.4	R.ENSPAVSP <b>T</b> *TNSTAPFLKPR.S
		Leucine zipper protein 1	LUZP1	S659				57.5	46.2	R.EKPD <b>S</b> *DDDLIASLVTAK.L
		Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	S124				8.5	53.8	R.RGSG <b>D</b> * <b>S</b> *ISIDTEASIR.E
		Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	S120				68.1	81.4	R.RG <b>S</b> *GD <b>S</b> ISIDTEASIR.E
		Leucine-rich repeat flightless-interacting protein 1	LRRFIP1	S126				6.5	55.0	R.RGSG <b>D</b> * <b>S</b> * <b>I</b> <b>S</b> IDTEASIR.E
		Leucine-rich repeats and IQ motif containing 2	CEP97	S770				21.9	83.2	K.ESSNNEQDN <b>S</b> *LLEQYLTSVQQLQEDADER.T
		Leucine-rich repeats and IQ motif containing 2	CEP97	T811S813				2.4	44.5	K.LHIACFPVQLD <b>T</b> <b>L</b> <b>S</b> *DGASVDESHGISPPQGEISQTOENSK.L
		Leucine-rich repeats and IQ motif containing 2	CEP97	S813S817				0.1	28.5	K.LHIACFPVQLD <b>T</b> <b>L</b> <b>S</b> *DGAS*VDESHGISPPQGEISQTOENSK.L
		Leucine-rich repeats and IQ motif containing 2	CEP97	S782				15.2	58.5	K.E <b>S</b> *SNNEQDNLLEQYLTSVQQLQEDADER.T
		Leucine-rich repeats and IQ motif containing 2	CEP97	S783				-0.4	36.6	K.E <b>S</b> *SNNEQDNLLEQYLTSVQQLQEDADER.T
		Leucine-rich repeats and IQ motif containing 2	CEP97	S783S770				4.1	83.8	K.E <b>S</b> *SNNEQDN <b>L</b> *LLEQYLTSVQQLQEDADER.T
		Leupaxin	L PXN	S19				7.4	49.2	R.STLQD <b>S</b> *DEYSNPAPLPDQHSR.K
		Leupaxin	L PXN	S81				58.0	33.3	K.E <b>S</b> *PPPSK.T
		LIG1 DNA ligase 1	LIG1	T195				32.3	63.0	K.AE <b>T</b> *PTESVSEPEVATK.Q
		LIG1 DNA ligase 1	LIG1	S911T918				15.2	67.9	R.KQSQIQNQQGED <b>S</b> *GSDPED <b>T</b> *Y.-

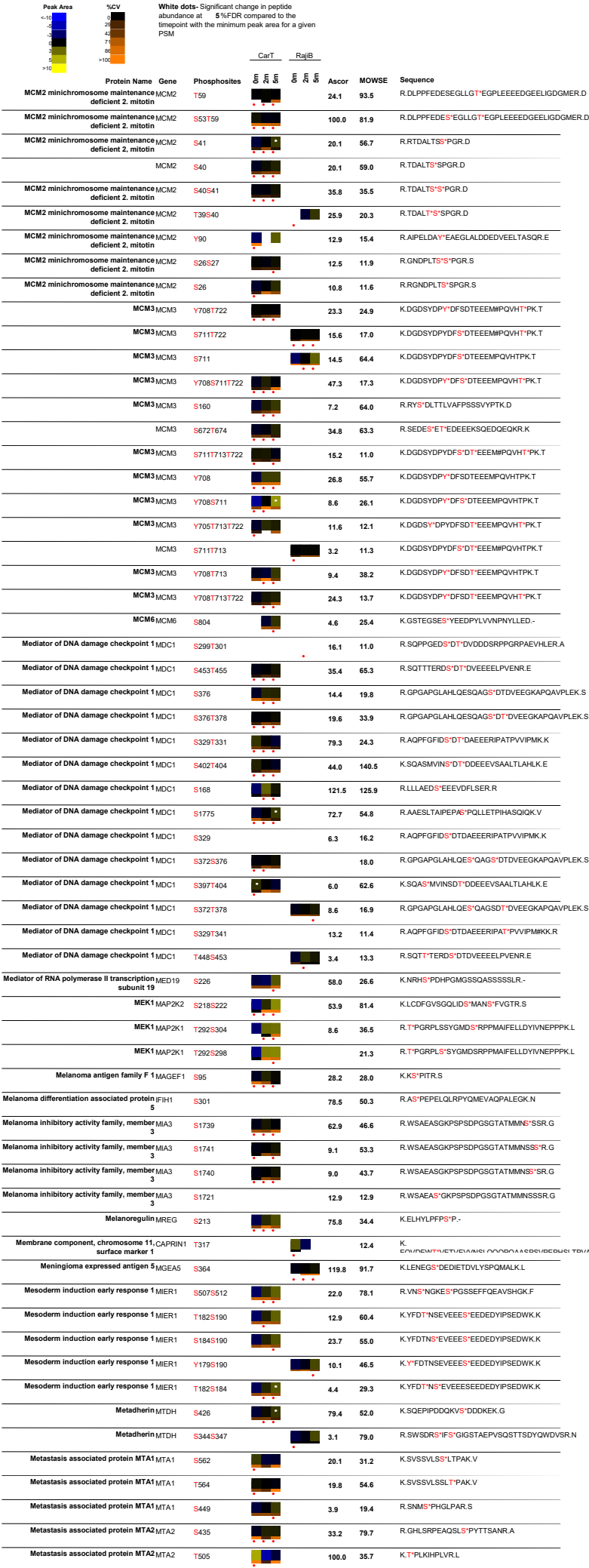
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites				
		LIG1 DNA ligase I	LIG1	T918Y919			7.6	18.3
		LIG1 DNA ligase I	LIG1	T195S201			10.6	70.4
		LIG1	LIG1	S911S913			33.9	37.5
		LIG1	LIG1	S51			49.9	
		LIG1 DNA ligase I	LIG1	S66S76			100.0	105.0
		LIG1 DNA ligase I	LIG1	S141			134.4	95.6
		LIG1 DNA ligase I	LIG1	S91S109			13.1	32.8
		LIG1 DNA ligase I	LIG1	S91T108			6.1	30.2
		LIG1 DNA ligase I	LIG1	S91T197			14.4	37.3
		LIG1 DNA ligase I	LIG1	S91			2.3	35.8
		LIG1 DNA ligase I	LIG1	S91S113			16.2	26.0
		LIG1 DNA ligase I	LIG1	S76			84.2	99.6
		LIG1 DNA ligase I	LIG1	S91S98			3.9	41.8
		LIG1 DNA ligase I	LIG1	S88S91			0.1	20.0
		LIG1 DNA ligase I	LIG1	S49			22.4	30.6
		LIG1 DNA ligase I	LIG1	T97			-5.7	38.9
		LIG1 DNA ligase I	LIG1	S47			17.4	
		LIG1 DNA ligase I	LIG1	S911Y919			6.8	23.5
		LIG1 DNA ligase I	LIG1	S88S109			2.2	18.1
		LIG1 DNA ligase I	LIG1	S91S104			11.4	22.3
		Lim and SH3 protein 1	LASP1	S146			41.3	50.8
		LIM domain containing 2	LIMD2	S29			39.8	43.6
		LIM domain only 7	LMO7	S1159			12.0	64.2
		LIM domain only 7	LMO7	S342			60.7	85.1
		LIM domain only 7	LMO7	S863			21.8	63.9
		LIM domain only 7	LMO7	S531			35.4	51.0
		LIM domain only 7	LMO7	S1157			6.2	13.2
		LIMD1	LIMD1	S316			14.5	73.9
		LIMD1	LIMD1	S424			12.2	144.3
		LIMD1	LIMD1	S421			-0.3	82.2
		Limkain b1	MARF1	S1093			22.5	62.3
		Limkain b1	MARF1	S1091			12.2	71.1
		Limkain beta 2	CDC92	S211			18.6	14.3
		Lin 9 homolog	LIN9	S325S337			87.5	49.7
		Lin 9 homolog	LIN9	T320S325S337			52.0	34.7
		Lin 9 homolog	LIN9	Y319S325S337			39.3	32.1
		Linker for activation of T cells	LAT	S224			67.0	71.5
		Linker for activation of T cells	LAT	S84			66.8	40.6
		Lipase hormone sensitive	LIPE	S950			10.5	27.9
		Liprin beta 2	PPFIBP2	S387			29.8	33.1
		Liprin beta 2	PPFIBP2	S512			19.9	108.8
		Liprin beta 2	PPFIBP2	S414			32.7	21.6
		Liver-specific bHLH-Zip transcription factor	LSR	S530			43.4	41.5
		Liver-specific bHLH-Zip transcription factor	LSR	S643S646			100.0	15.7
		Liver-specific bHLH-Zip transcription factor	LSR	T336			11.4	23.4
		Liver-specific bHLH-Zip transcription factor	LSR	S643			100.0	13.1
		LKB1 interacting protein 1	STK11IP	T614			4.7	35.8
		LKB1 interacting protein 1	STK11IP	S610			8.6	42.4
		LKB1 interacting protein 1	STK11IP	S616			21.3	52.5
		LKB1 interacting protein 1	STK11IP	S415S431			18.2	25.9
		LNK SH2B3	S121				-0.4	15.4
		LNK SH2B3	S120				8.5	14.5
		LOC115294 protein	PCMTD1	S302			100.4	56.7
		LOC159090	FAM122B	S58			100.0	66.7
		LOC159090	SPACIA2	S115S119			36.8	44.6
		LOC159090	SPACIA2	S50			8.9	32.7
		LOC159090	SPACIA2	S33			15.5	24.4
		LOC159090	SPACIA2	S25			6.6	24.7
		LOC388974	RGPD2	S520S525			14.9	17.0
		LOC388974	RGPD2	S990			28.4	35.4
		LOC389677 protein	RBM12B	S638			24.9	47.7
		LOC389677 protein	RBM12B	S710S718			100.0	22.6

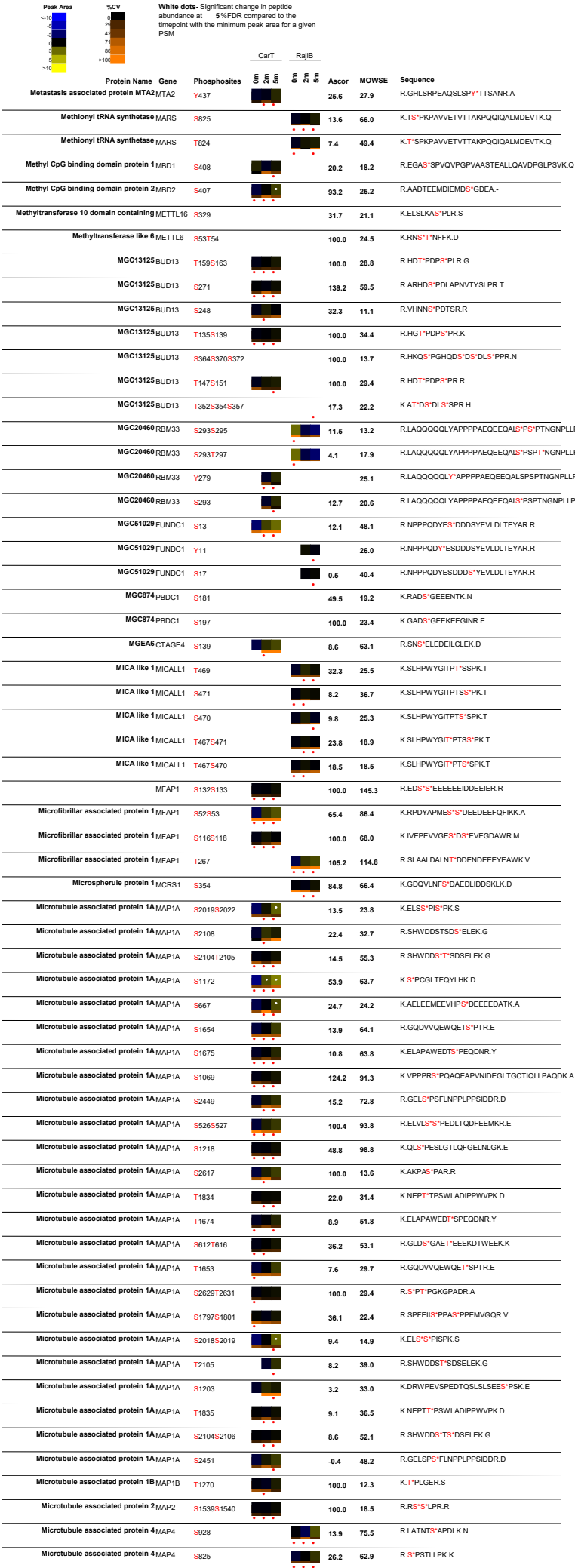
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence
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10	2							
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40	8							
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60	12							
70	14							
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Protein Name	Gene	Phosphosites						Sequence
LOC389677 protein RBM12B		S278S280				50.8	28.8	R.S <sup>RS</sup> PLGFYVHLK.N
LOC389677 protein RBM12B		S250S254				100.0	29.1	R.S <sup>S</sup> EEHS <sup>S</sup> PPR.G
LOC389677 protein RBM12B	T640					16.9	50.6	R.SPT <sup>T</sup> EDFR.Q
LOC389677 protein RBM12B	S98T100					16.0	42.7	R.GRP <sup>GS</sup> GT <sup>T</sup> SGVDSLNFIESVK.E
LOC389677 protein RBM12B	T100S101					6.4	31.7	R.GRP <sup>GS</sup> GT <sup>T</sup> SGVDSLNFIESVK.E
LOC389677 protein RBM12B	T100					1.8	54.0	R.GRP <sup>GS</sup> GT <sup>T</sup> SGVDSLNFIESVK.E
LRRFIP2 LRRFIP2	S328					29.9	65.1	R.RG <sup>S</sup> GDTSSLIDPDTLSLELR.D
LRRFIP2 LRRFIP2	S333					4.2	20.2	R.RGSGDT <sup>S</sup> S <sup>S</sup> LIDPDTLSLELR.D
LUC7 like LUC7L	S363					100.0	39.8	R.S <sup>S</sup> EEKEAGEI.-
LUC7 like 2 LUC7L2	T17						39.0	R.AMLDQLMG <sup>T</sup> SR.D
LUC7 like 2 FMC1	S383S384					14.2	24.1	R.SEDRR <sup>S</sup> S <sup>S</sup> EER.E
LUC7 like 2 FMC1	S378S383					6.7	18.3	R.S <sup>S</sup> EDRR <sup>S</sup> S <sup>S</sup> EER.E
LUC7 like 2 LUC7L2	S18					6.5	48.3	R.AMLDQLMG <sup>T</sup> S <sup>S</sup> R.D
LUC7 like 2 FMC1	S281S283S285					100.0	10.9	R.S <sup>S</sup> RS <sup>S</sup> MS <sup>S</sup> R.E
Lymphocyte antigen 9 LY9	S648					9.1	24.7	R.KPQVVP <sup>PP</sup> QQNDLIPES <sup>S</sup> PTYENFT.-
Lymphocyte antigen 9 LY9	T650					13.9	18.9	R.KPQVVP <sup>PP</sup> QQNDLIPESPT <sup>T</sup> YENFT.-
Lymphocyte cytosolic protein 1 LCP1	S5					17.7	102.5	R.GS <sup>V</sup> VSDEEMM <sup>S</sup> ELR.E
Lymphocyte cytosolic protein 1 LCP1	S7					-0.1	84.6	R.GS <sup>V</sup> S <sup>S</sup> DEEMM <sup>S</sup> ELR.E
Lymphocyte cytosolic protein 1 LCP1	S257					100.0	75.0	R.EGES <sup>S</sup> LEDLMK.L
Lymphocyte cytosolic protein 1 LCP1	Y28					35.4	71.8	K.VDTGNG <sup>Y</sup> ISFNELNDFK.A
Lymphocyte cytosolic protein 1 LCP1	S406					100.0	45.0	R.NWMN <sup>S</sup> LGVNPR.V
Lymphocyte specific protein LSP1	S139					5.4	36.3	K.EDSDEVHLEEL <sup>S</sup> LSK.E
Lymphocyte specific protein LSP1	S130					99.2	87.5	K.ED <sup>S</sup> S <sup>S</sup> DEVHLEELSLSK.E
Lymphocyte specific protein LSP1	S111S130					7.5	33.2	R.S <sup>S</sup> PEGEQEDR <sup>PL</sup> GHAYEKED <sup>S</sup> DEVHLEELSLSK.E
Lymphocyte specific protein LSP1	S252					60.5	102.9	R.QA <sup>S</sup> S <sup>S</sup> IELPSMAVASTK.S
Lymphocyte specific protein LSP1	S189					9.2	94.0	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQSS <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T184					32.4	74.8	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S177					21.0	77.5	R.TP <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S177S189					26.8	47.7	R.TP <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSS <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S188S189					40.0	68.0	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQ <sup>S</sup> S <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S188T196					14.8	41.8	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQ <sup>S</sup> S <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T175S177					30.0	53.2	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S177S189S193					14.1	21.0	R.TP <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSS <sup>S</sup> PPLS <sup>S</sup> P <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T244					33.1	59.1	K.IDQWLEQYTQAIETAGRI <sup>T</sup> PK.L
Lymphocyte specific protein LSP1	T175T184					9.9	36.7	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T175S177S189					23.1	52.2	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSS <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S177T184S189					15.1	45.9	R.TP <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSS <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T175S177S189					22.3	16.4	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSS <sup>S</sup> PPLS <sup>S</sup> P <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T175S177S188					19.1	14.2	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S204					38.1	32.7	R.TES <sup>S</sup> LNR.S
Lymphocyte specific protein LSP1	S188					62.3	88.9	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQ <sup>S</sup> S <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T184S189					24.1	40.6	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQSS <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T175S177T184					13.2	17.4	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S177T184					16.7	51.4	R.TP <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S188S193					11.2	41.0	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQ <sup>S</sup> S <sup>S</sup> PPLS <sup>S</sup> P <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S111					53.7	24.0	R.S <sup>S</sup> PEGEQEDR <sup>PL</sup> GHAYEKE
Lymphocyte specific protein LSP1	S24					5.7	56.3	R.EELLGPTAQW <sup>S</sup> VEDEEEAVHEQQQHER.D
Lymphocyte specific protein LSP1	T20					4.3	16.3	R.EELLGPT <sup>T</sup> AQW <sup>S</sup> VEDEEEAVHEQQQHER.D
Lymphocyte specific protein LSP1	T175S177T184					6.6	14.6	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S141					22.5	113.1	K.EDSDEVHLEELSL <sup>S</sup> K.E
Lymphocyte specific protein LSP1	S177T184S188					18.5	11.2	R.TP <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQ <sup>S</sup> S <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	S177S188S189					15.6	21.7	R.TP <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQ <sup>S</sup> S <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T184S188					8.0	56.4	R.TPSP <sup>PL</sup> VLEG <sup>T</sup> IEQ <sup>S</sup> S <sup>S</sup> PPLSP <sup>TT</sup> TK.L
Lymphocyte specific protein LSP1	T175S177T184					5.5	11.5	R.T <sup>T</sup> P <sup>S</sup> S <sup>S</sup> PLVLEG <sup>T</sup> IEQSSP <sup>PL</sup> SP <sup>TT</sup> TK.L
Lymphoid enhancer binding factor 1 LEF1	S132					2.6	21.4	K.GPSYSSYSGYIMPMNNDPYMSNGSL <sup>S</sup> PP <sup>IP</sup> R.T
LYN	S13					25.3	80.3	K.DSL <sup>S</sup> S <sup>S</sup> DDGVDLK.T
LYN LYN	Y501					7.4	56.2	K.AEERPTFDYLSVLD <sup>DF</sup> Y <sup>T</sup> ATEGQYQQQP.-
LYN LYN	T502					6.5	54.7	K.AEERPTFDYLSVLD <sup>DF</sup> Y <sup>T</sup> ATEGQYQQQP.-
LYN LYN	S11					13.3	62.9	K.DS <sup>S</sup> LSDDGVDLK.T
LysM, peptidoglycan-binding, domain containina 2	S33					-0.2	77.1	R.SG <sup>S</sup> S <sup>S</sup> ESEEAE <sup>S</sup> LSLRL.T
Lysosomal trafficking regulator LYST	S2105					61.9	80.4	R.S <sup>S</sup> LPAPFTSSLLTQSQKL

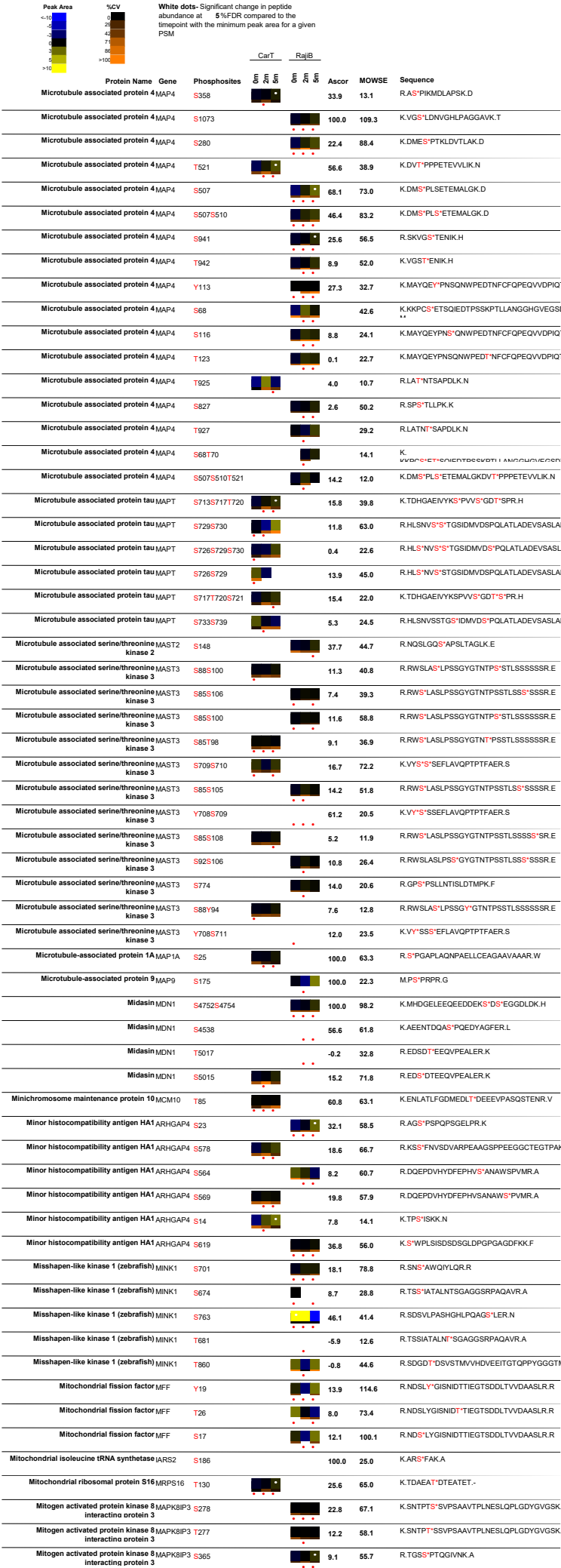


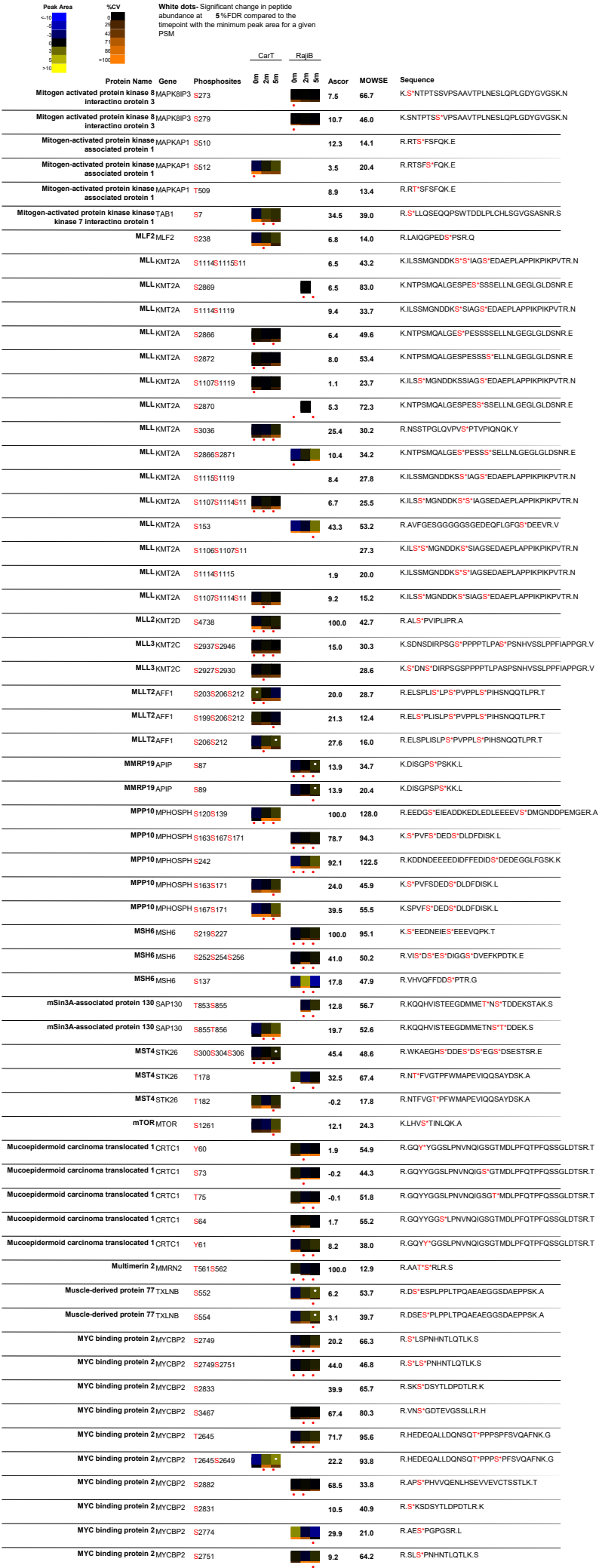
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
<10	0									
10	2									
20	4									
30	6									
40	8									
50	10									
60	12									
70	14									
80	16									
90	18									
100	20									
>100	22									
		M phase phosphoprotein 9	MPHOSPH S854					61.2	19.7	K.NE\$ <sup>S</sup> SPIRFDILLDDLDTPVPVSTLQR.T
		M phase phosphoprotein, mpp8	MPHOSPH S51					100.0	112.8	R.GAEAFGDS <sup>S</sup> EEDGEDVFVEK.I
		M phase phosphoprotein, mpp8	MPHOSPH S188S189					21.0	46.3	K.SKPOLES <sup>S</sup> *LES <sup>L</sup> LVFDLR.T
		M phase phosphoprotein, mpp8	MPHOSPH S188S192					12.8	33.9	K.SKPOLES <sup>S</sup> *SLES <sup>L</sup> LVFDLR.T
		M phase phosphoprotein, mpp8	MPHOSPH S136S138					10.0	60.3	R.LSLNNDIFEANS <sup>S</sup> *DS <sup>L</sup> DQQSETK.E
		M phase phosphoprotein, mpp8	MPHOSPH S189S192					7.3	60.9	K.SKPOLES <sup>S</sup> *LES <sup>L</sup> LVFDLR.T
		M phase phosphoprotein, mpp8	MPHOSPH S392					100.0	11.2	R.RLS <sup>S</sup> *GEER.G
		M phase phosphoprotein, mpp8	MPHOSPH S188S189S192					3.5	28.8	K.SKPOLES <sup>S</sup> *LES <sup>L</sup> LVFDLR.T
		Macrophin 1	MACF1 S2956					100.0	36.1	K.AFLAELEQNS <sup>S</sup> *PK.I
		Macrophin 1	MACF1 S5829					7.2	21.5	K.LKRPTPTFHSS <sup>S</sup> *R.T
		Macrophin 1	MACF1 S5828					29.8	26.0	K.LKRPTPTFHSS <sup>S</sup> *SR.T
		ZCRRB1	S155					42.5	76.0	K.APEPEEEEEVEES <sup>S</sup> *EDEGEDPALDSLQAIAFQQAQ.I
		MADP 1 protein	ZCRRB1 S210S216					12.4	26.2	K.STYFS <sup>S</sup> *DEEELS <sup>S</sup> *D.-
		MADP 1 protein	ZCRRB1 Y208S216					7.7	18.7	K.STY <sup>S</sup> *FSDEEELS <sup>S</sup> *D.-
		Maestro heat-like repeat-containing protein family member 6 (Fragment)	MROH6 T506					100.0	11.4	R.HT <sup>S</sup> *GLNPR.L
		Major vault protein	MVP S873					28.2	75.9	R.VASGSPSGEGIS <sup>S</sup> *PQSAQAQAPAGDINHVPVLR.-
		Major vault protein	MVP S876					12.0	29.5	R.VASGSPSGEGISPS <sup>S</sup> *AQAPQAPGDINHVPVLR.-
		Major vault protein	MVP S864					3.5	24.9	R.VAS <sup>S</sup> *GPSPGEGISPSQAQAQAPAGDINHVPVLR.-
		Major vault protein	MVP S867					5.6	29.6	R.VASGS <sup>S</sup> *PGEGISPQSAQAQAPAGDINHVPVLR.-
		Male specific lethal 3 like 1	MSL3 S400T405					6.4	16.1	R.SSS <sup>S</sup> *PIPLT <sup>S</sup> *PSKEGSAVFAGEGR.R
		Male-specific lethal 2-like 1	MSL2 S447					9.5	41.6	K.EKIPSHHFMPGS <sup>S</sup> *PTK.T
		Male-specific lethal-1 homolog	MSL1 S99					121.5	51.5	K.HS <sup>S</sup> *PIKEPCGSLSETVCK.R
		MAN antigen 1	LEMID3 S259S261					6.6	69.8	R.ENYS <sup>S</sup> *DS <sup>S</sup> *EEEEDDDDVASSR.Q
		MAN antigen 1	LEMID3 Y258S259					6.5	102.2	R.ENY <sup>S</sup> *S <sup>S</sup> *DSEEDDDDDVASSR.Q
		MAN antigen 1	LEMID3 S144					9.1	45.6	K.VLLGFSSDES <sup>S</sup> *DVEASPR.D
		MAN antigen 1	LEMID3 Y258S261					77.7	115.6	R.ENY <sup>S</sup> *SDS <sup>S</sup> *EEEEDDDDVASSR.Q
		MAP kinase activating death domain protein	MADD S1239					21.2	148.5	R.GTLS <sup>S</sup> *DSEIETNSATSTIFGKA
		MAP kinase activating death domain protein	MADD S1241					-0.2	73.9	R.GTLD\$S <sup>S</sup> *EIETNSATSTIFGKA
		MAP kinase activating death domain protein	MADD T1237					9.2	59.6	R.GT <sup>S</sup> *LSDSEIETNSATSTIFGKA
		MAP2K2	MAP2K2 T396					25.6	31.7	R.LNQPGTPT <sup>S</sup> *R.T
		MAP2K2	MAP2K2 T394						32.8	R.LNQPGT <sup>S</sup> *PTR.T
		MAP3K2	MAP3K2 S163					77.8	93.2	R.DRS <sup>S</sup> *SPPGGYIPDELHQVAR.N
		MAP3K2	MAP3K2 S239					10.3	35.8	R.AQS <sup>S</sup> *YPDNHQEFSDYDNPFEK.F
		MAP3K2	MAP3K2 S153					67.4	45.0	K.RLS <sup>S</sup> *IGPTSR.D
		MAP3K2	MAP3K2 S164					5.8	73.6	R.DRSS <sup>S</sup> *PPPGYIPDELHQVAR.N
		MAP3K4	MAP3K4 S66S84					17.1	16.9	K.SPES <sup>S</sup> *DLEDFSDETNTENLYGTS <sup>S</sup> *PPSTPR.Q
		MAP3K4	MAP3K4 S66T77S84					11.3	13.6	K.SPES <sup>S</sup> *DLEDFSDETNT <sup>S</sup> *ENLYGTS <sup>S</sup> *PPSTPR.Q
		MAP3K4	MAP3K4 S66T83					12.8	26.7	K.SPES <sup>S</sup> *DLEDFSDETNTENLYGT <sup>S</sup> *SPPSTPR.Q
		MAP3K4	MAP3K4 S499					2.0	14.4	R.LES <sup>S</sup> *EDDSLGWGAPDWSTEAGFSR.H
		MAP3K4	MAP3K4 S503					2.0	24.6	R.LESEDS <sup>S</sup> *LGWGAPDWSTEAGFSR.H
		MAP3K7	MAP3K7 S439					39.3	68.8	R.S <sup>S</sup> *IQDLTVGTGTEPGQVSSR.S
		MAP3K7	MAP3K7 S417					-0.9	53.4	K.TAS <sup>S</sup> *FGNILDVPEIMSGNGQPR.R
		MAP4K4	MAP4K4 S981					79.5	20.4	R.KGS <sup>S</sup> *VNVNPTNTRPQSDTPEIR.K
		MAP4K4	MAP4K4 S787					-0.2	42.4	R.SS <sup>S</sup> *SKSEGPSQR.L
		MAP4K4	MAP4K4 T705S708					5.7	15.1	R.TT <sup>S</sup> *SR\$ <sup>S</sup> *PVL\$R.R
		MAP4K4	MAP4K4 S934					-0.1	71.4	K.SS <sup>S</sup> *SSFTPFIDPRL
		MAP4K4	MINK1 T187					12.7	75.3	R.NT <sup>S</sup> *FIGTGYWMAPEVIACDENPDATYDYLR.S
		MAP4K4	MAP4K4 S933					22.8	29.8	K.HKS <sup>S</sup> *SSSFTPFIDPRL
		MAP4K4	MAP4K4 S936T938					4.4	16.9	K.HKSSS <sup>S</sup> *FT <sup>S</sup> *PFIDPRL
		MAP4K4	MAP4K4 S933S934					9.3	22.0	K.HKS <sup>S</sup> *S <sup>S</sup> *SSFTPFIDPRL
		MAP4K4	MAP4K4 S933S936					14.2	63.6	K.HKS <sup>S</sup> *SS <sup>S</sup> *FTPFIDPRL
		MAP4K4	MAP4K4 T319S324					3.1	26.7	K.DET <sup>S</sup> *EYEYS <sup>S</sup> *GSEEEEEVPQELEGPSSIVNVPGESTLR.R
		MAP4K4	MAP4K4 S324S326					9.6	28.8	K.DETEYEYS <sup>S</sup> *GS <sup>S</sup> *EEEEEEVPQELEGPSSIVNVPGESTLR.R
		MAP4K4	MAP4K4 Y323S324					6.8	44.6	K.DETEYEY <sup>S</sup> *S <sup>S</sup> *GSEEEEEVPQELEGPSSIVNVPGESTLR.R
		MAP4K4	MAP4K4 T705S706					8.6	11.0	R.TT <sup>S</sup> *SR\$PVL\$R.R
		MAP4K4	MAP4K4 S935S936					6.4	14.5	K.HKSS <sup>S</sup> *S <sup>S</sup> *FTPFIDPRL
		MAP4K4	MAP4K4 S934S935					4.3	11.8	K.HKSS <sup>S</sup> *S <sup>S</sup> *FTPFIDPRL
		MAP4K4	MAP4K4 T319S326					7.6	14.2	K.DET <sup>S</sup> *EYEYSGS <sup>S</sup> *EEEEEEVPQELEGPSSIVNVPGESTLR.R
		MAP4K4	MAP4K4 Y323S326					12.4	31.2	K.DETEYEY <sup>S</sup> *SGS <sup>S</sup> *EEEEEEVPQELEGPSSIVNVPGESTLR.R
		MAP4K4	MAP4K4 S788					11.7	28.1	R.SS\$ <sup>S</sup> *KSEGPSQR.L
		MAP4K4	MAP4K4 T704T705					8.5	14.8	R.T <sup>S</sup> *T <sup>S</sup> *SR\$PVL\$R.R
		MAP7 domain containing 1	MAP7D1 S644S648T554					5.1	22.4	K.ESAAPAS <sup>S</sup> *PAPS <sup>S</sup> *PAPSPT <sup>S</sup> *PAPPQK.E

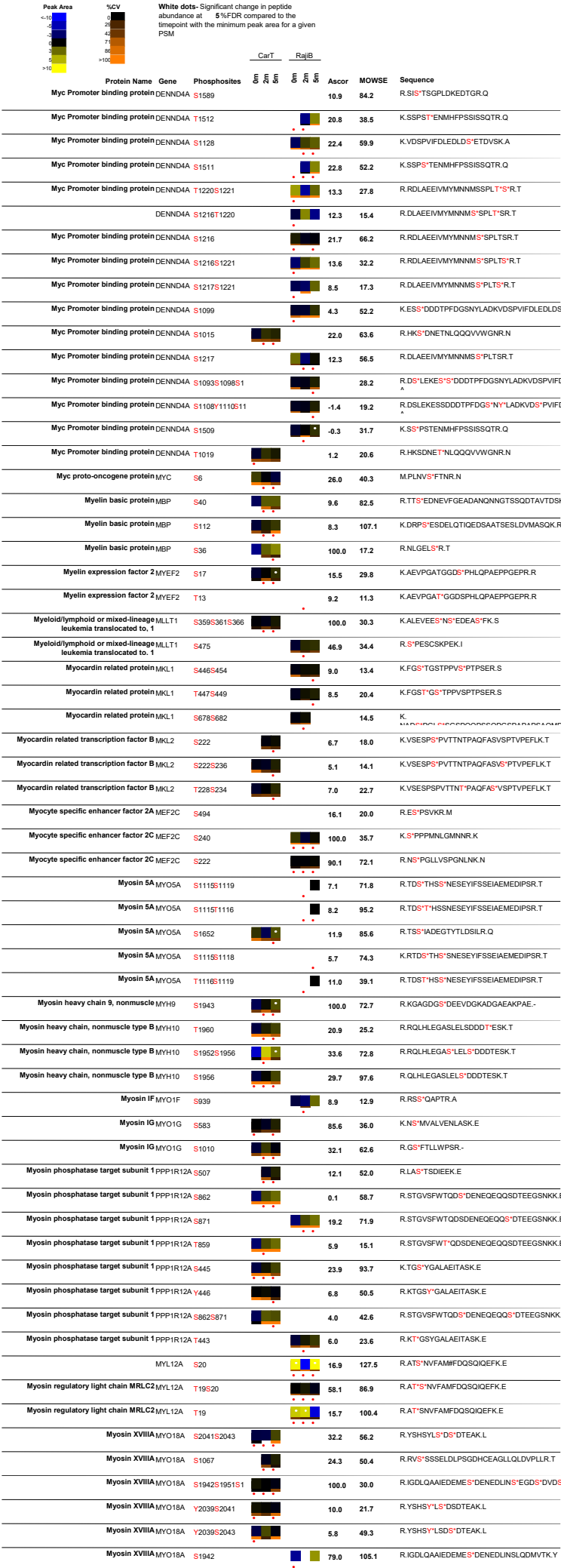






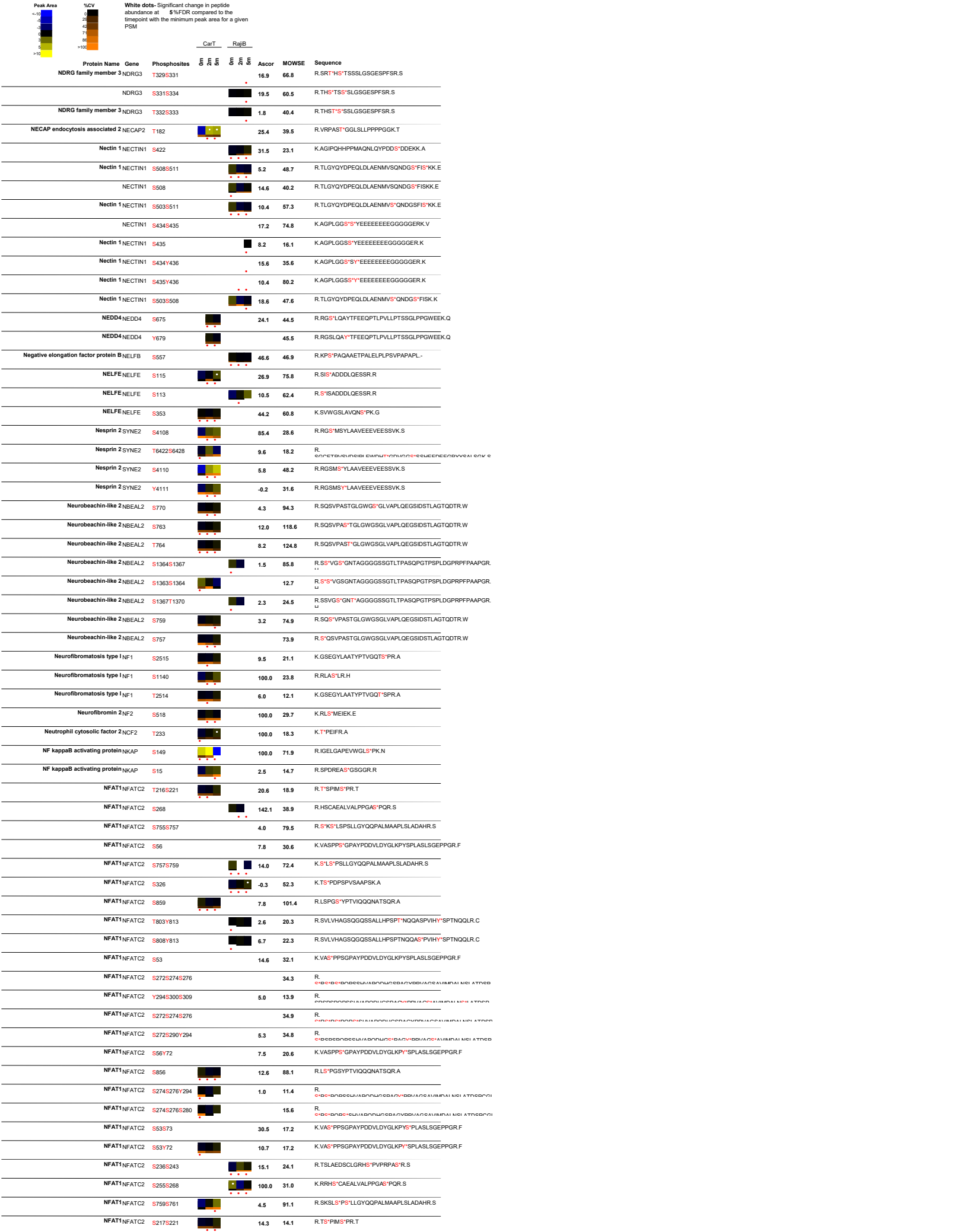


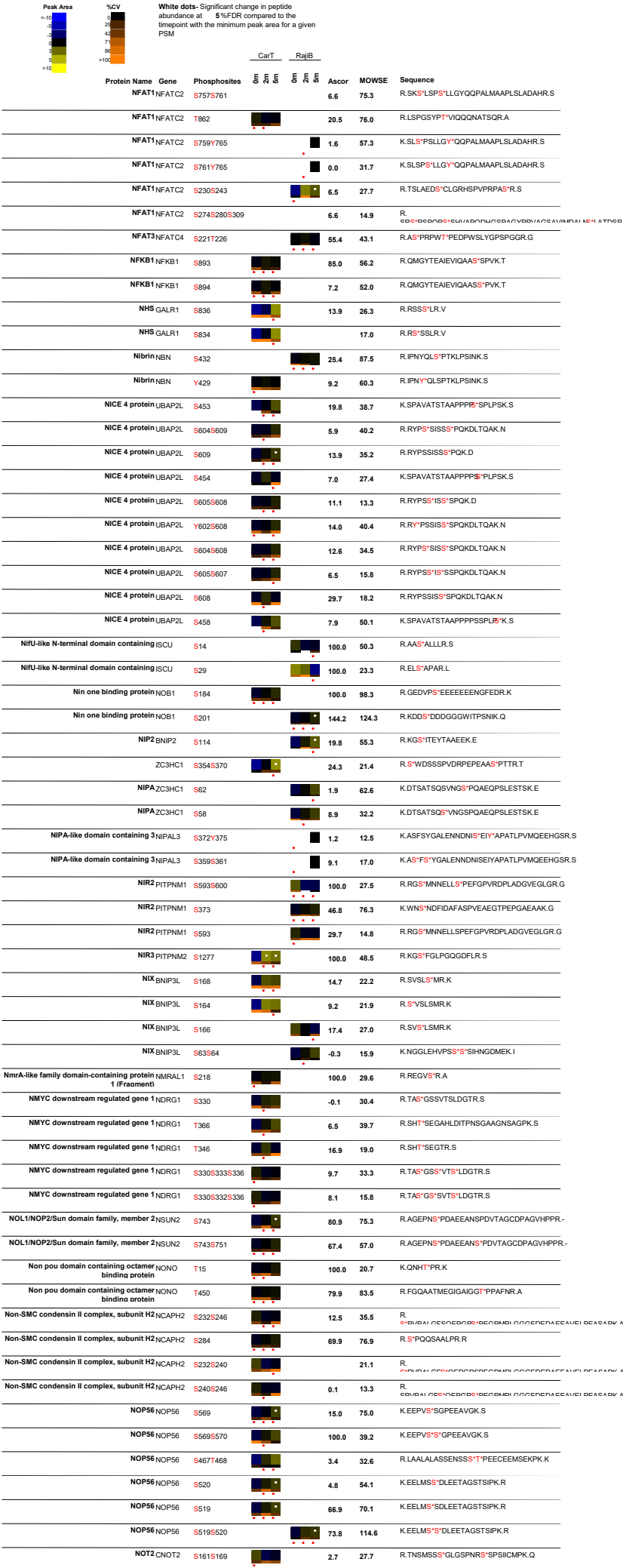




Peak Area	iCV	White dots: Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Myosin XVIIIa	MYO18A	S1069				35.1	43.0	R.RVSSS*SELDLPSGDHCEAGLLQLDVPILR.T
		Myosin XVIIIa	MYO18A	S1068				6.5	18.5	R.RVSS*SSELDLPSGDHCEAGLLQLDVPILR.T
		Myosin XVIIIa	MYO18A	S2007				27.6	44.3	K.SSS*PTSYWK.S
		Myosin XVIIIa	MYO18A	S140				24.1	15.2	K.RFS*FSQR.S
		Myosin XVIIIa	MYO18A	Y2039S2041S2				-0.2	31.0	R.YSHSY*LS*DS*DTEAK.L
		Myosin XVIIIa	MYO18A	S2041S2043T2				9.0	21.7	R.YSHSYLS*DS*DT*EAK.L
		Myosin XVIIIa	MYO18A	S2038S2043				8.3	14.1	R.YSHS*YLSDS*DTEAK.L
		Myosin XVIIIb	MYO18B	T2549				100.0	19.6	R.REPGT*GR.K
		Myotubularin	MTM1	S588S591				2.7	11.8	K.LSDPPTS*PSS*PSQMMPHVQTHF.-
		Myotubularin	MTM1	S590S591				6.5	23.8	K.LSDPPTS*PSS*PSQMMPHVQTHF.-
		Myotubularin	MTM1	T587S591				8.0	19.9	K.LSDPPT*SPSS*PSQMMPHVQTHF.-
		Myotubularin	MTM1	S591S593				4.6	30.6	K.LSDPPTSPSS*PSS*QMMPHVQTHF.-
		Myotubularin related protein 1	MTMR1	S652				13.8	14.8	R.GS*SPSHSATSVHTSV.-
		Myotubularin related protein 3	MTMR3	S647				43.2	107.0	R.S*LESLSLGAGEDPLSADSLGKPTR.V
		MYST histone acetyltransferase 2	KAT7	T118S124				30.9		K.NT*ADHDS*PPRPTGNAPSESIDISSPNVSHDESIK.D
		MYST histone acetyltransferase 2	KAT7	S99S100S102				39.7	93.1	R.S*S*GS*ETEQVDFSDR.E
		MYST histone acetyltransferase 2	KAT7	S124T128				13.6	25.2	K.NTADHDS*PPRT*PTGNAPSESIDISSPNVSHDESIK.D
		MYST histone acetyltransferase 2	KAT7	S56				9.8	51.7	R.LSQSSQDS*SPVR.N
		MYST histone acetyltransferase 2	KAT7	S100S102T104				9.8	14.3	R.SS*GS*ET*EQVDFSDR.E
		MYST histone acetyltransferase 2	KAT7	S57				7.6	58.2	R.LSQSSQDS*PVR.N
		N-acetylglucosamine kinase	NAGK	S76				10.9	82.5	R.SLGLSL*GGDQEDAGR.I
		N-myristoyl transferase 1	NMT1	S47				59.6	82.9	R.GGLS*PANDTGAK.K
		NACHT and WD repeat domain-containing protein 2	NWD2	T69S698				100.0	11.7	K.ENT*RPSS*NPLR.V
		NACSIN EHP1	EHBP1	S335				21.0	14.6	K.EVQTPQYLNPFDEPEAFVTIKDS*PPQSTK.R
		NACSIN EHP1	EHBP1	T16S171				20.2	20.9	K.AT*DEDMQS*LASLMSMK.Q
		NACSIN EHP1	EHBP1	S171S174				8.5	16.4	K.ATDEDMQS*LAS*LMSMK.Q
		NACSIN EHP1	EHBP1	T16S174				8.4	41.7	K.AT*DEDMQSLAS*LMSMK.Q
		NAD synthetase 1	NADSYN1	S280Y281				18.1	12.3	R.S*Y*RAEISSR.N
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S159S160S164				6.3	111.8	R.KVTSPPSSSSSSS*S*S*DS*SD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S162				6.0	58.1	R.KVTSPPSSSSSSSSSDS*ESD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S159S162S164				10.6	116.7	R.KVTSPPSSSSSSSS*S*SDS*ES*SD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S158S159S160				7.6	74.7	K.VTSPSSSSSSS*S*S*SDS*ESD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S160S162				1.3	66.0	R.KVTSPPSSSSSSSSSS*DS*ESD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S160S162S164				11.2	102.1	R.KVTSPPSSSSSSSSSS*DS*ES*SD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S159S160				16.2	69.4	R.KVTSPPSSSSSSSS*S*S*SDS*ESD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S159S160S162				62.0		R.KVTSPPSSSSSSSS*S*S*SDS*ESD*EADVSEVTPR.V
		NADH ubiquinone oxidoreductase flavoprotein 3	NDUFV3	S158S159S162				5.4	62.5	K.VTSPSSSSSSS*S*S*SDS*ESD*EADVSEVTPR.V
		NAG NBAS	S473					13.9	91.2	R.AGEEDEGEEDS*DS*DYEISAK.A
		NAG NBAS	S473S475					28.8	29.7	R.AGEEDEGEEDS*DS*DYEISAK.A
		NaGLT1	MFS4B	S474				10.2	22.7	R.SS*L*EPTAEVYNGYPSNALVFESSPFNTGSA*HK.H
		NaGLT1	MFS4B	T476				-0.8	26.2	R.SSLT*EPTAEVYNGYPSNALVFESSPFNTGSA*HK.H
		Nardilysin	NRDC	S94				17.8	40.8	R.RGS*LSNAGDPEIK.S
		Nascent polypeptide associated complex, NACA alpha polypeptide	S166					11.5	129.6	K.VGGEAVSNIGENTQTPTVQEESE*EEEEVD*ETGVEVK.D
		Nascent polypeptide associated complex, NACA alpha polypeptide	T161					44.9	83.9	K.VGGEAVSNIGENTQTPT*VQEESEEEEEVD*ETGVEVK.D
		Nascent polypeptide associated complex, NACA alpha polypeptide	T159					5.1	44.0	K.VGGEAVSNIGENTQT*PTVQEESEEEEEVD*ETGVEVK.D
		Nascent polypeptide associated complex, NACA alpha polypeptide	S151					76.4		K.VGGEAVS*INIGENTQTPTVQEESEEEEEVD*ETGVEVK.D
		Nascent polypeptide associated complex, NACA alpha polypeptide	T157S166					13.3	74.5	K.VGGEAVSNIGENT*QTPTVQEESE*EEEEVD*ETGVEVK.D
		NATH	NAA15	S855				22.0	11.3	K.ITVNGDS*S*AAEAEELANEI.-
		NATH	NAA15	S855S856				45.1	26.3	K.ITVNGDS*S*AAEAEELANEI.-
		TRA2B	S225Y226					17.5	17.8	R.SRS*Y*SPR.R
		Natural killer tumor recognition sequence	RBM26	S699S701				17.4	23.1	R.S*RS*YSR.D
		Natural killer tumor recognition sequence	NKTR	S613				9.1	44.0	R.ATMAQENNVVQPVVAENIPVILSDS*PPPSR.W
		Natural killer tumor recognition sequence	RBM26	S701Y702				9.6	13.5	R.SRS*Y*SR.D
		Natural killer tumor recognition sequence	NKTR	S611				15.6	21.8	R.ATMAQENNVVQPVVAENIPVILS*DSPPSR.W
		NCK1	NCK1	Y105				190.9	66.4	R.LY*DLNPAYVK.F
		NDRG family member 2	NDRG2	S332				12.3	65.0	R.TAS*LTSAASVQGNR.S
		NDRG family member 3	NDRG3	S331				19.9	73.1	R.THST*SSSLGSGESPFPSR.S
		NDRG family member 3	NDRG3	T332				-0.3	26.6	R.THST*SSSLGSGESPFPSR.S
		NDRG family member 3	NDRG3	S335				18.0	44.0	R.THSTSSS*LGSGESPFPSR.S
		NDRG family member 3	NDRG3	T329S333				2.6	66.1	R.SRT*HST*SSSLGSGESPFPSR.S
		NDRG family member 3	NDRG3	T329T332				16.7	86.8	R.SRT*HST*SSSLGSGESPFPSR.S
		NDRG3	S331T332					3.3	54.6	R.SRTHS*TT*SSSLGSGESPFPSR.S







Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		NOT2	CNOT2	S165S169				4.0	26.3	R.TNSMSSSGLGS* <b>P</b> NRS*SPSIICMPK.Q
		NOT2	CNOT2	S165				27.8	78.2	R.TNSMSSSGLGS* <b>P</b> NRS
		NOT2	CNOT2	S101S120				2.8	12.8	R.SLS*QGTQLPSHVPTTGTPTMS*LHTPPSPSR.G
		NOT2	CNOT2	S160S161				6.8	12.6	R.TNSMSS* <b>S</b> *GLGSPNRSSPSIICMPK.Q
		NOT4	CNOT4	T328				18.4	60.5	R.SPFEHAVT* <b>E</b> SQSLFSDNFR.H
		NOT4	CNOT4	S321				3.6	73.7	R. <b>S</b> *PFEHAVTESQSLFSDNFR.H
		Notch2	NOTCH2	S1841				5.5	36.0	R.GGS* <b>S</b> DLSDEDEDAEDSSANIITDLVYOGASLQAQDTR.T
		NPAT	NPAT	S775S779				8.8	29.7	K.VIIISDPFVSSDTELTSAVSSINGENLPTILS* <b>P</b> TKS*PTK.N
		NPAT	NPAT	S774S779				13.9	31.9	K.VIIISDPFVSSDTELTSAVSSINGENLPTILS* <b>S</b> PTKS*PTK.N
		NPAT	NPAT	S774T781				10.1	17.5	K.VIIISDPFVSSDTELTSAVSSINGENLPTILS* <b>S</b> PTKSP* <b>T</b> K.N
		NPAT	NPAT	S762T770				5.1	16.4	K.VIIISDPFVSSDTELTSAVSS*INGENLPT* <b>I</b> LSSPTKSPTK.N
		NSFL1C	NSFL1C	S140				80.8	23.6	K. <b>S</b> *PGETSKPRPFAGGGYRL
		NSFL1C	NSFL1C	S114				100.0	100.6	K. <b>S</b> *PNELVDDLK.G
		NTBA	SLAMF6	S277				12.1	64.6	R.NLEYVSV* <b>P</b> TNNTVYASVTHSNR.E
		NTBA	SLAMF6	S275				40.8		R.NLEYV <b>S</b> *VSPNTNTVYASVTHSNR.E
		Nuclear autoantigenic sperm protein	NASP	T479S482				52.2	52.8	K.EGET* <b>E</b> GS*EEDDKENDKTEEMPNDVLENK.S
		Nuclear autoantigenic sperm protein	NASP	S728				100.0	45.9	R.KPEE <b>S</b> *PR.K
		Nuclear autoantigenic sperm protein	NASP	S505				100.0	81.1	K. <b>S</b> *LQNEEEEEIGNLEAWDMLDLAK.I
		NASP		S141				34.5	57.5	K.TEDESIVENNDNIDETGS*EEDDKENDK.T
		Nuclear autoantigenic sperm protein	NASP	S127				12.8	41.4	K.TEDES*LVENNDNIDETEGSEEDDKENDK.T
		NASP		T138S141				9.5	42.5	K.TEDESIVENNDNIDET* <b>E</b> GS*EEDDKENDK.T
		Nuclear autoantigenic sperm protein	NASP	T123S127				49.5		K. <b>T</b> *EDES*LVENNDNIDETEGSEEDDKENDKTEEMPNDVLENK.S
		Nuclear autoantigenic sperm protein	NASP	S127T138				11.1	42.1	K.TEDES*LVENNDNIDET*EGSEEDDKENDKTEEMPNDVLENK.S
		NASP		T138				6.8	56.4	K.TEDESIVENNDNIDET*EGSEEDDKENDK.T
		NASP		S127S141				10.0	47.2	K.TEDES*LVENNDNIDETGS*EEDDKENDK.T
		Nuclear autoantigenic sperm protein	NASP	T123				16.7		K. <b>T</b> *EDESIVENNDNIDETEGSEEDDKENDKTEEMPNDVLENK.S
		Nuclear envelope pore membrane protein	POM121	S127				-0.2	96.6	R. <b>S</b> *SMSSLTGAYASGIPSSSR.N
		Nuclear envelope pore membrane protein	POM121	S130				16.1	75.2	R.SSSMS*SLTGAYASGIPSSSR.N
		Nuclear envelope pore membrane protein	POM121	S127S131				4.3	41.5	R. <b>S</b> *SMSS*LTGAYASGIPSSSR.N
		Nuclear envelope pore membrane protein	POM121	S131				0.3	58.7	R.SSSMSS*LTGAYASGIPSSSR.N
		Nuclear factor IIA	NFIA	S300				49.3	66.6	R. <b>S</b> *PGSGSQSSGWHEVPGMPSPPTLKK.S
		Nuclear factor IIA	NFIA	S258				23.9	47.6	R.VSQTPIAAGTGNFSLDLESSYYSMS*PGAMR.R
		Nuclear factor of activated T-cells, NFATC1 cytosolic, calcineurin-dependent 1		S233				54.3	66.3	R.GLGACTLLGS*PR.H
		Nuclear factor related to kappa B binding	NFRKB protein	S372S376				52.1	40.7	K.SEAEDLAEPLSSTEGVAPLS*QAPS*PLAIPAIK.E
		Nuclear factor related to kappa B binding	NFRKB protein	S376				27.2	51.1	K.SEAEDLAEPLSSTEGVAPLSQAPS*PLAIPAIK.E
		Nuclear factor related to kappa B binding	NFRKB protein	T365S376				8.3	16.5	K.SEAEDLAEPLS <b>T</b> *EGVAPLSQAPS*PLAIPAIK.E
		Nuclear FMRP interacting protein 1	NJFIP1	S338S342S351				13.3	31.5	K.LEGPPEANADPLGVLIN <b>S</b> *DSES*DKEEKQHS*VIPK.E
		Nuclear FMRP interacting protein 1	NJFIP1	S338S340S342				28.7	24.6	K.LEGPPEANADPLGVLIN <b>S</b> *D <b>S</b> *DKEEKQHSVIPK.E
		Nuclear mitotic apparatus protein 1	NUMA1	S1757				42.5	64.1	R.TQPDGTSVPGEPA <b>S</b> *PISQR.L
		Nuclear mitotic apparatus protein 1	NUMA1	T2055				41.9	89.9	R.QSMAFSIL <b>T</b> *PK.K
		Nuclear mitotic apparatus protein 1	NUMA1	S1862				82.2	78.1	R.LGS*PDYGNALLSLPGYRPTTR.S
		Nuclear mitotic apparatus protein 1	NUMA1	S1721S1724				30.5	51.4	K.SREPAQAKPQLD <b>S</b> *ID <b>S</b> *LDLSCEEGTPLSITSK.L
		Nuclear mitotic apparatus protein 1	NUMA1	S1225				9.3	54.9	R.K <b>N</b> <b>S</b> *LISLEEVSILNR.Q
		Nuclear mitotic apparatus protein 1	NUMA1	S1760				-9.8	21.2	R.TQPDGTSVPGEPA <b>S</b> *QR.L
		Nuclear mitotic apparatus protein 1	NUMA1	S1721S1724S1				21.4	36.0	K.SREPAQAKPQLD <b>S</b> *ID <b>S</b> *LDL <b>S</b> *CEEGTPLSITSK.L
		Nuclear mitotic apparatus protein 1	NUMA1	S200S203T211				16.8	41.1	K.VASSSSGNFNLSGS* <b>P</b> AS*PMGDIQT*PQFQMR.R
		Nuclear mitotic apparatus protein 1	NUMA1	S1228				6.9	41.4	R.K <b>N</b> <b>S</b> *LISLEEVSILNR.Q
		Nuclear mitotic apparatus protein 1	NUMA1	S1769T1776				26.1	54.4	K.V <b>E</b> <b>S</b> *LESLY <b>F</b> *PIPAR.S
		Nuclear mitotic apparatus protein 1	NUMA1	S1792S1800				5.1	11.2	R.SQAPLESSLD <b>S</b> *LGDVFLD <b>S</b> *GRK.T
		Nuclear mitotic apparatus protein 1	NUMA1	S1788S1789				0.0	11.2	R.SQAPLES* <b>S</b> *LDLGDVFLDSGRK.T
		Nuclear protein UKP68	ZC3H14	S515				100.0	43.9	R.DLVQDPK <b>P</b> AS*PK.F
		Nuclear protein UKP68	ZC3H14	S274				9.0	57.0	R.LCEPEVLN <b>S</b> LEET <b>S</b> *PFFR.N
		Nuclear protein UKP68	ZC3H14	S527S533				33.0	32.3	K.FIVTLDGVP <b>S</b> *PPGYMS*DQEDMCFEGMKPVNQTAASNK.G
		Nuclear protein UKP68	ZC3H14	Y531S533				10.1	11.4	K.FIVTLDGVPSPPGY* <b>M</b> S*DQEDMCFEGMKPVNQTAASNK.G
		Nuclear protein UKP68	ZC3H14	T521S527				21.1		K.FIVT*LDGV <b>S</b> *PPGYMSDQEDMCFEGMKPVNQTAASNK.G
		Nuclear receptor coactivator 5	NCOA5	S126				16.9	29.9	R.EGS*YDR.Y
		Nuclear receptor coactivator 5	NCOA5	S29S34				100.0	15.5	R.DRS*PIRG <b>S</b> *PR.R
		Nuclear receptor coactivator 5	NCOA5	S29				100.0	14.9	R.DRS*PIR.G
		Nuclear receptor coactivator 5	NCOA5	S378T379				-0.4	38.8	R. <b>S</b> <b>S</b> *T*DSLPGPISR.Q
		Nuclear receptor coactivator 6 interacting	TGS1 protein	S89				41.9	95.1	K.GIGLDESLD <b>S</b> *EAELMR.S
		Nuclear receptor coactivator 6 interacting	TGS1 protein	S85S89				100.0	90.8	K.GIGLDES* <b>E</b> LD <b>S</b> *EAELMR.S
		Nuclear receptor coactivator 7	NCOA7	S376				12.1	13.1	K.KLD <b>S</b> *SRE

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajIB	Ascor	MOWSE	Sequence
Protein Name	Gene	Phosphosites							
Nuclear receptor corepressor 1	NCOR1	S2120					100.0	36.8	R.VS*PENLVDK.S
Nuclear receptor corepressor 1	NCOR1	S2337					69.6	21.1	K.S*PIPGQGYLGRPSSVSSVHSEGDYHR.Q
Nuclear receptor corepressor 1	NCOR1	S2151					50.4	60.5	R.SHVSSEPYEPIS*PPQVPVWEK.Q
Nuclear receptor corepressor 1	NCOR1	S992T996					11.8	30.3	R.SSTS*PCGT*SKSPNREWEVLQAPHQVITNLPEGVR.L
Nuclear receptor corepressor 1	NCOR1	S999					104.6	59.7	K.S*PNREWEVLQAPHQVITNLPEGVR.L
Nuclear receptor corepressor 1	NCOR1	S2436S2438					11.5	18.7	R.EPAPLLSAQYETLS*DS*DD.-
Nuclear receptor corepressor 1	NCOR1	S2184					48.4	98.7	R.S*PGSISYLPFFTK.L
Nuclear receptor corepressor 1	NCOR1	S992S999					-0.3	26.3	R.SSTS*PCGTSKS*PNREWEVLQAPHQVITNLPEGVR.L
Nuclear receptor corepressor 1	NCOR1	S1977S1981					14.5	34.2	R.YETPSDAIEVIS*PASS*PAPPQEK.L
Nuclear receptor corepressor 1	NCOR1	S2395T2399					20.6	68.9	R.MLS*TPPT*PIACAPSAVNQAAPHQQNR.I
Nuclear receptor corepressor 2	NCOR2	S149S152					102.2	53.9	K.LEPV*S*PPS*PHTDPELELVPR.L
Nuclear receptor corepressor 2	NCOR2	S2056S2064					20.9	16.9	R.SLGYHGSSYS*PEGVEPV*S*PVSSPSLTHDK.G
Nuclear receptor corepressor 2	NCOR2	S2056S2064S2					12.3	20.6	R.SLGYHGSSYS*PEGVEPV*S*PVSSPSLTHDK.G
Nuclear receptor corepressor 2	NCOR2	S2268					33.2	54.0	K.S*PGNTSQPPAFFS.K.L
Nuclear receptor corepressor 2	NCOR2	S2056S2067					10.7	28.4	R.SLGYHGSSYS*PEGVEPV*S*PVSSPSLTHDK.G
Nuclear receptor corepressor 2	NCOR2	S2054S2064S2					10.6	11.0	R.SLGYHGSS*YSPEGVEPV*S*PVSSPSLTHDK.G
Nuclear receptor corepressor 2	NCOR2	Y2055S2064S2					14.0	14.1	R.SLGYHGSS*YSPEGVEPV*S*PVSSPSLTHDK.G
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S181					35.4	80.3	R.LKATVTPS*PVK.G
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	T179S181					32.2	27.3	R.LKATVTPS*PVK.G
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S19					83.0	114.9	K.VVDYSQFQES*DDADEYGR.D
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	Y13					15.9	76.8	K.VVDY*SQFQESDDADEYGR.D
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	T202S204					100.0	26.2	K.EKT*PS*PK.E
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	T222					27.6	23.9	K.TST*SPPEK.S
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S75S79					28.0	55.5	K.DDSHS*AEDS*EDEKDKV.K
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S58					42.5	96.6	K.NSQEDS*EDSEDKDV.K.T
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S54S58S61					19.2	46.1	R.SGKNS*QEDS*EDS*EDKDKV.T
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S73S75S79					100.0	40.4	K.DDS*HS*AEDS*EDEKDKHNR.Q
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S58S61					70.3	78.7	K.NSQEDS*EDS*EDKDKV.T
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S214					100.0	59.7	K.EEDEEPES*PPEKK.T
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	T177T179					10.3	11.8	K.AT*VT*PSPVKG.G
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S234S240					46.1	41.6	K.SGDEGS*EDEAP*S*GED.-
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	T179					13.9	76.1	R.LKATVTPSPVKG.G
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S229S234S240					100.0	47.2	K.S*GDEGS*EDEAP*S*GED.-
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S130S132S144					75.7	97.3	K.DS*GS*DEDFLM#EDDDS*DYGSSK.K
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S130S132					91.1	100.2	K.DS*GS*DEDFLMEDDDSDSYGSSK.K
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S223					10.8	42.2	K.TSTS*PPPEK.S
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S54S58					7.6	28.4	K.NS*QEDS*EDSEDKDV.K.T
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S14					14.3	89.9	R.KVVDYS*QFQESDDADEYGR.D
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	Y13S14					6.9	22.2	R.KVVDY*S*QFQESDDADEYGR.D
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S204					14.7	27.4	K.EKTPS*PK.E
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S54S61					7.5	28.8	K.NS*QEDSEDS*EDKDKV.K.T
NUCKS1	S113S130S132						39.6		R. R.LKATVTPS*PVK.G
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	S50S4S58					8.7	15.2	R.S*GKNS*QEDS*EDSEDKDV.K.T
Nuclear ubiquitous casein kinase and cyclin dependent kinase substrate	NUCKS1	T177S181					23.0	17.1	R.LKATVTPS*PVKG.G
Nucleolar phosphoprotein p130	NOLC1	S84S85S86S88					55.3		K.KKAS*S*S*DS*EDS*S*EEEEVQGPPAK.K
Nucleolar phosphoprotein p130	NOLC1	S699					78.2	69.9	R.GGSISVQVNSIKFDS*E.-
Nucleolar phosphoprotein p130	NOLC1	S539					100.0	40.4	K.GKGS*PRPOAPK.A
Nucleolar phosphoprotein p130	NOLC1	S624					25.6	43.5	R.ASS*PFR.R
Nucleolar phosphoprotein p130	NOLC1	S644					100.0	23.1	R.VADNS*FDAK.R
Nucleolar phosphoprotein p130	NOLC1	T608T611					100.0	42.7	K.LQT*PNT*FPK.R
NOLC1	S564						100.0	22.0	K.NS*EEEEKKK.A
Nucleolar phosphoprotein p130	NOLC1	S694					10.4	20.5	R.GGSISVQVNS*IKFDSE.-
Nucleolar protein 1	NOP2	S177T181					108.6	77.4	R.EAAAGIQWS*EET*EDEEEKEVTPESGPPK.V
Nucleolar protein 1	NOP2	S728					6.9	64.0	K.GTDQTQPAVLS*PSK.T
Nucleolar protein 1	NOP2	S782					14.7	24.8	K.GPOPTVS*PIR.S
Nucleolar protein 8	NOL8	S296S298T302					100.0	39.3	K.KRNS*IS*DDDT*DS*EDEL.R.M
Nucleolar protein 8	NOL8	T888S890					100.0	41.4	R.FLET*DS*EEQEVEINEKK.T
Nucleolar protein 8	NOL8	S1082S1083S1					79.6	123.4	R.LQDS*S*S*EEEDVTEETDHR.N
Nucleolar protein 8	NOL8	S298T302S304					48.2	66.2	R.NSIS*DDDT*DS*EDEL.R.M
Nucleolar protein 8	NOL8	S837S838S843					40.8	51.5	K.LFDS*S*DDDES*DS*EDDSNRFK.I
NOL8	Y376S378						6.0	13.3	R.EY*DS*GDTDEIAMKK.N
Nucleolar protein NOP5	NOP58	S502S514					29.1	53.1	K.EEPLS*EEEPCTSTAIAS*PEKK.K

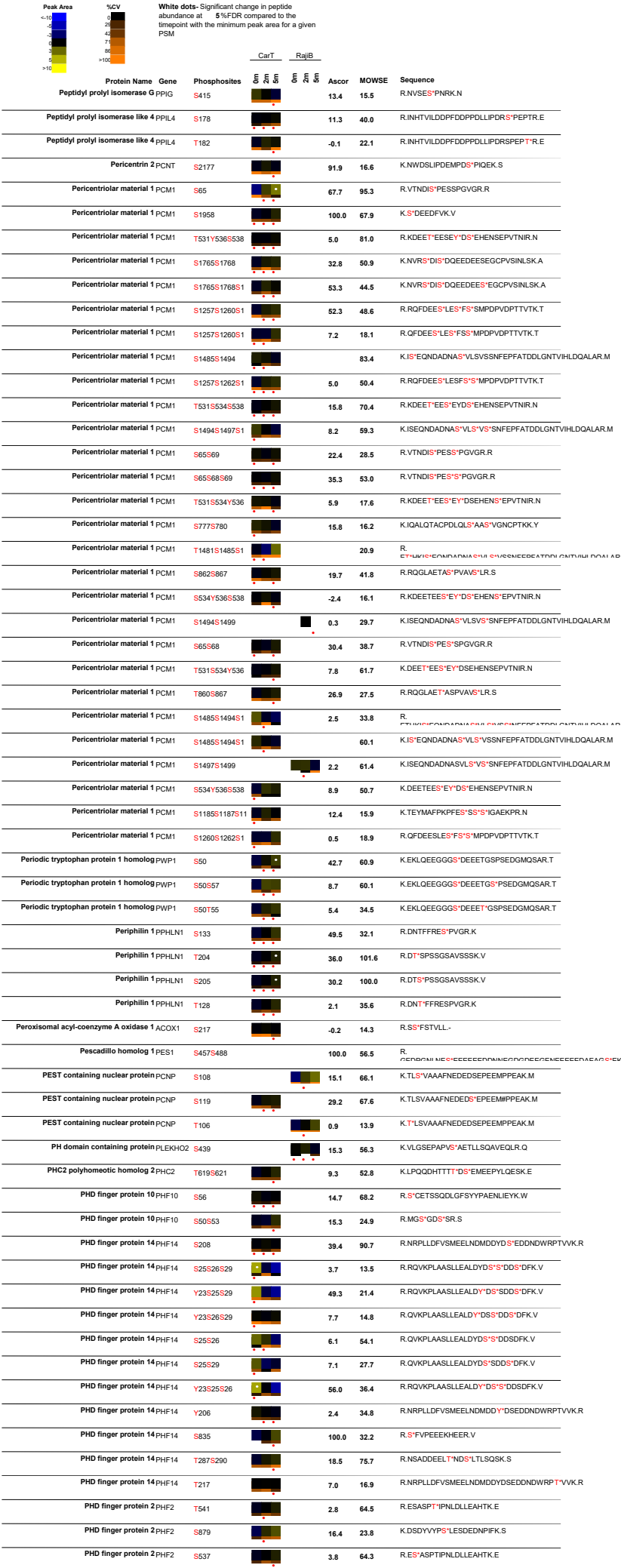
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites					
<10	0	NOP58		S502			101.3	101.5	K.EEPLS*EEEPCTSTAISPEKK
10-20	1	Nucleolar protein with MIF4G domain 1							
20-30	2	NCL		S317S320S321			40.0	36.3	R.FAEDEEK*S*ENS*S*EDGDITDK.S
30-40	3	NCL		S145S153			100.0	101.1	K.KEDS*DEEEDDS*EDEDDEDEDEDEIEPAA#KA
40-50	4	Nucleolin	NCL	S184S206			70.9	77.0	K.AAAAA*PAS*EDEDDEDEDDEDDDDDEEDS*EEEA#METTPAK.G
50-60	5	Nucleolin	NCL	S153			26.3	146.8	K.KEDSDEEEDDS*EDEDDEDEDEDEIEPAA#KA
60-70	6	Nucleolin	NCL	S145			53.4	135.0	K.KEDS*DEEEDDDSEDEDDEDEDEDEIEPAA#KA
70-80	7	Nucleolin	NCL	S41S42			17.0	33.2	K.EVEEDSEDEEMSEDEEDDS*S*GEEV#PQKK.G
80-90	8	Nucleolin	NCL	S34S41			27.0	35.3	K.EVEEDSEDEEM*S*EDEEDDS*S*GEEV#PQKK.G
90-100	9	NCL		S28S34S41S42			100.0	38.4	K.EVEEDS*EDEEM#S*EDEEDDS*S*GEEV#PQKK.G
>100	>10	Nucleolin	NCL	S28S34S41			19.0	41.3	K.EVEEDS*EDEEM*S*EDEEDDS*S*GEEV#PQKK.G
		Nucleolin	NCL	S67			25.8	44.5	K.VVV*S*PTKK.V
		Nucleolin	NCL	T69			22.5	41.3	K.VVV#PT*KK.V
		Nucleolin	NCL	Y495			-0.2	39.5	K.TLVLSNLS*Y*SATEETLQEVFEK.A
		Nucleolin	NCL	S184			4.3	42.6	K.AAAAA*PAS*EDEDDEDEDDEDDDDDEEDSEEA#METTPAK.G
		Nucleolin	NCL	S28S41			8.2	20.0	K.EVEEDS*EDEEMSEDEEDDS*S*GEEV#PQKK.G
		Nucleolin	NCL	S206			18.7	45.9	K.AAAAA#ASEDEDDEDEDDEDDDDDEEDS*EEEA#METTPAK.G
		Nucleolin	NCL	S28S34S42			-2.0	16.8	K.EVEEDS*EDEEM*S*EDEEDDS*S*GEEV#PQKK.G
		Nucleolin	NCL	S34S41S42			5.6	11.0	K.EVEEDSEDEEM*S*EDEEDDS*S*GEEV#PQK.K
		Nucleolin	NCL	S34S42			7.5	18.8	K.EVEEDSEDEEM#S*EDEEDDS*S*GEEV#PQKK.G
		Nucleolin	NCL	S491				22.3	K.TLVLS*NLSYSATEETLQEVFEK.A
		NCL		S28S41S42			13.1	31.1	K.EVEEDS*EDEEMSEDEEDDS*S*S*GEEV#PQK.K
		Nucleolin	NCL	S28S34			4.6	16.2	K.EVEEDS*EDEEM*S*EDEEDDS#GEEV#PQKK.G
		Nucleophosmin 1	NPM1	S243			23.9	36.5	K.GPS*S*VEDIK.A
		Nucleophosmin 1	NPM1	S125			118.9	75.9	K.CGSGPVHISGQHLVAVEADAES*EDEEEEDVK.L
		Nucleophosmin 1	NPM1	S70			14.6	69.3	K.DELHIVEAEAM#N#YEGS*PIK.V
		Nucleophosmin 1	NPM1	S218			15.5	20.6	K.DSKPS*S*TPR.S
		Nucleophosmin 1	NPM1	S214			8.1	12.9	K.DS*KPSSTPR.S
		Nucleophosmin 1	NPM1	S254			100.0	28.3	K.MQAS*IEK.G
		NPM1		Y67			3.6	32.3	K.DELHIVEAEAM#N*Y*EGSPIKVTLATUK.M
		Nucleophosmin 1	NPM1	S106				51.3	K.CG*S*GPVHISGQHLVAVEADAES#EDEEEEDVK.L
		Nucleophosmin 1	NPM1	S137			27.7	41.7	K.LLS*ISGKR.S
		Nucleophosmin 1	NPM1	S217			7.6	11.1	K.DSKPS*S*TPR.S
		Nucleoporin 160kDa	NUP160	Y1151			12.7	35.1	R.LIRPEYAWIVQPVSGAV*YDRPGASPK.R
		Nucleoporin 160kDa	NUP160	S1157			37.3	28.9	R.LIRPEYAWIVQPVSGAVYDRPGAS*PK.R
		Nucleoporin 205kDa	NUP205	S1165			20.0	83.8	R.S*VSGLFHFDATK.V
		Nucleoporin 205kDa	NUP205	S1167			-0.4	105.3	R.SV*S*GFLHFDATK.V
		Nucleoporin 50kDa	NUP50	T219			10.9	38.1	R.NSESESNKVAET*QSPSLFGSTK.L
		Nucleoporin 50kDa	NUP50	S221			26.0	100.4	K.VAAETGS*PSLFGSTK.L
		Nucleosome assembly protein 1 like 1	NAP1L1	S10			100.3	68.3	K.EQS*ELDQDLDDVEVEEEE#TEETK.L
		Nucleosome assembly protein 1 like 1	NAP1L1	T62			14.0	62.0	R.LDGLVET*PTGYIESLPR.V
		Nucleosome assembly protein 1 like 1	NAP1L1	S143			1.8	30.9	R.FEINAIY#PTEECEWKPDEEIS*EELK.E
		Nucleosome assembly protein 1 like 4	NAP1L4	S125			38.9	71.4	R.EFITGDVEPTDAESEWHS*ENEEEEK.L
		Nucleosome assembly protein 1 like 4	NAP1L4	S304			21.1	114.9	K.ASGDGS*LD#EDSEFTLASDFEIGH#FFR.E
		Nucleosome assembly protein 1 like 4	NAP1L4	S304S309			5.5	60.4	K.ASGDGS*LD#EDS*EFTLASDFEIGH#FFR.E
		Nucleosome assembly protein 1 like 4	NAP1L4	S299S309			4.7	44.7	K.AS*GDG#SL#EDS*EFTLASDFEIGH#FFR.E
		Nucleosome assembly protein 1 like 4	NAP1L4	S299			15.0	65.2	K.AS*GDG#SL#EDSEFTLASDFEIGH#FFR.E
		Nucleosome assembly protein 1 like 4	NAP1L4	S121			30.7		R.EFITGDVEPTDAES*EWHSENEEEK.L
		Numb homolog	NUMB	S228S229			22.6		K.IVVGS*S*VAPGNTAPSPSSPTSPTSDATTSLEMN#PHAIPR.R
		NUP107	NUP107	S86			31.7	38.0	R.QPDISOLGTGGK*S*PRL
		NUP133	NUP133	S45S50			43.2	49.1	K.GLPLGSAVS*S*PVLFS*PVGR.R
		NUP133	NUP133	S44S50			53.6	15.7	K.GLPLGSAVS*S*PVLFS*PVGR.R
		NUP133	NUP133	S57			31.9	19.0	R.RS*S*LSSR.G
		NUP153	NUP153	S192			41.4	51.4	R.AS*DKDITVSK.N
		NUP153	NUP153	T102			9.1	37.4	R.IT*PEPAVSNTEEPSTTSTASNYPDVLT#PSL#R.S
		NUP153	NUP153	S333			76.7	101.0	R.IPSIVS*S*PLNSPLDR.S
		NUP153	NUP153	S334S338			11.9	18.1	K.RIP#IVSS*PLNS*PLDR.S
		NUP210	NUP210	S1852			3.2	51.4	R.ASPGHS*PHYFAASSPTSPNALPPAR.K
		NUP210	NUP210	S1848			6.2	75.8	R.AS*PGHSPHYFAASSPTSPNALPPAR.K
		NUP210	NUP210	S1874			14.9	48.8	R.KAS*PPSGLWSPAYASH.-
		NUP210	NUP210	S1877			4.6	43.9	R.KASPPS*GLWSPAYASH.-
		NUP210	NUP210	Y1855			0.7	58.9	R.ASPGHS#PHY*FAASSPTSPNALPPAR.K
		NUP210	NUP210	S1859			13.9	16.0	R.ASPGHS#PHYFAAS*SPTSPNALPPAR.K

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		Protein Name	Gene	Phosphosites						
		NUP214	NUP214	S433T436				14.6	43.5	K.SPGS* <b>TPT</b> *TPTSSQAPQKL
		NUP214	NUP214	S1023				15.7	81.0	R.TPS*IQPSLLPHAAPFAK.S
		NUP214	NUP214	S433T437				11.8	47.0	K.SPGS* <b>TPTT</b> *PTSSQAPQKL
		NUP214	NUP214	S1081				2.8	33.0	K.HGAP*S*PSHPISAPQAAAAALR.R
		NUP98	NUP98	S35				39.9	43.2	K.NQ*S*PTEAEKPASSSLPSSPPQLLTR.N
		NUP98	NUP98	S871				64.3	45.6	K.YGLQDS*DEEEEHPK.S.T
		NUP98	NUP98	S606				32.1	78.7	R.DSENLAS*PSEYPENGER.F
		NUP98	NUP98	S595				67.0	83.3	K.NLNNSNLS*PVNR.D
		NUP98	NUP98	S591				61.4	70.2	K.NLNNS*NLFSPVNR.D
		NUP98	NUP98	S608				10.9	27.8	R.DSENLASPS*EYPENGER.F
		OdinANKS1A		S620				100.0	28.7	K.AELKLS*R.S
		OdinANKS1A		S663				35.1	70.5	K.SPS*FASEWDEIEK.I
		OdinANKS1A		S647				9.9	26.0	R.SES*LSNCSIGK.K
		OIP106	TRAK1	S919				30.0	101.3	R.S*FPTMVGSSMQMK.A
		Opa interacting protein 5	OIP5	S48				-0.2	70.3	K.GS*PLGPAGLGAEEPAAGPQLPSWLQPER.C
		Opioid growth factor receptor	OGFR	S315				52.0	64.6	R.KVEEEGS*PGDPDHEASTQGR.T
		Opioid growth factor receptor	OGFR	S378				55.8	41.9	R.SQGDEAGGHGEDRPEPLS*PK.E
		OSBP related protein 10	OSBPL10	S199				26.0	45.4	R.SLTLLPHGTPNS*ASPCSOR.H
		OSBP related protein 10	OSBPL10	S201				6.7	55.7	R.SLTLLPHGTPNSAS*PCSOR.H
		OSBP related protein 11	OSBPL11	S189				75.4	76.6	R.RPS*QNAISFFNVGHSK.L
		OSBP related protein 11	OSBPL11	S181				12.9	73.1	R.SFSLASSNS*PISQR.R
		OSBP related protein 11	OSBPL11	S179				5.2	16.3	R.SFSLASS*S*NSPISQR.R
		OSBP related protein 9	OSBPL9	S334				17.6	33.5	R.LIDSSGSASVLTH*S*SGNSLKR
		OSBP related protein 9	OSBPL9	S329				6.4	24.3	R.LIDSSGSA*S*VLTHSSGNSLKR
		OSBP related protein 9	OSBPL9	S335				9.1	20.6	R.LIDSSGSASVLTHS*S*SGNSLKR
		Osmosis responsive factor	TTC33	S197				15.6	52.2	K.SEAPAEVTHF*S*PK.S
		Osteoclast stimulating factor 1	OSTF1	S213				53.5	94.1	R.TLSNAEDYLDDED*S*D.-
		Osteoclast stimulating factor 1	OSTF1	S202S213				26.9	84.2	R.TLS*NAEDYLDDED*S*D.-
		Osteoclast stimulating factor 1	OSTF1	Y207				21.7	17.6	R.TLSNAEDY*LDDEDSD.-
		Osteoclast stimulating factor 1	OSTF1	S202Y207				9.9	34.3	R.TLS*NAEDY*LDDEDSD.-
		Osteoclast stimulating factor 1	OSTF1	Y207S213				3.5	38.2	R.TLSNAEDY*LDDED*S*D.-
		Osteoclast stimulating factor 1	OSTF1	T200S202				6.9	43.8	R.T*LS*NAEDYLDDEDSD.-
		Osteoclast stimulating factor 1	OSTF1	T200S213				6.1	14.1	R.T*LSNAEDYLDDED*S*D.-
		Osteopetrosis associated transmembrane protein 1	OSTM1	T324				21.2	21.9	K.SST*SFANIQENSN.-
		Osteopetrosis associated transmembrane protein 1	OSTM1	S325				-0.3	23.5	K.SSTS*FANIQENSN.-
		OTUBAIN 1	OTUB1	S18				13.8	87.1	K.OEPLGS*EGVNCLAYDEAIIAQQDR.I
		OTUBAIN 1	OTUB1	S16				16.2	82.7	K.OEPLGS*DSEGVNCLAYDEAIIAQQDR.I
		Oxidative stress responsive 1	OXSRI1	S339				92.5	98.5	K.TEDGGWEW*S*DDEFDEESEEGK.A
		Oxidative stress responsive 1	OXSRI1	S325				20.1	29.8	R.RVPGSS*GRL
		Oxysterol binding protein	OSBP	S379				10.9	88.4	R.TGS*NISGASSDISLDEQYK.H
		Oxysterol binding protein	OSBP	T377S382S385				17.2	76.2	R.T*GSNIS*GAS*SDISLDEQYKHQLEETKK.E
		Oxysterol binding protein	OSBP	S190S193				60.8	98.5	K.MLAES*DE*S*GDEESVSQTKTELQNTLR.T
		Oxysterol binding protein	OSBP	S351				91.6	82.3	K.GDM*S*DEDDENEFFDAPEIT*MPENLGHK.R
		Oxysterol binding protein	OSBP	S379S382S385				21.1	124.5	R.TGS*NIS*GAS*SDISLDEQYK.H
		Oxysterol binding protein	OSBP	T367				13.6	25.7	K.GDM*DEDDENEFFDAPEIT*MPENLGHK.R
		Oxysterol binding protein	OSBP	S382S386				11.9	47.8	R.TGSNIS*GAS*SDISLDEQYKHQLEETKK.E
		Oxysterol binding protein	OSBP	T377S382				9.5	51.1	R.T*GSNIS*GASSDISLDEQYK.H
		Oxysterol binding protein	OSBP	T377S379S389				16.0	20.0	R.T*GS*NISGASSDI*S*LDQYKHQLEETKK.E
		Oxysterol binding protein	OSBP	S379S382				3.4	51.8	R.TGS*NIS*GASSDISLDEQYK.H
		Oxysterol binding protein like 8	OSBPL8	S328S331S342				19.2	35.2	K.DQDMY*S*DKS*DKENDQEHDES*ONEVMGK.S
		Oxysterol binding protein like 8	OSBPL8	S807S808S810				39.3	25.0	K.GYSSPEPDIQDS*S*GS*EAQSVKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S799S807S810				13.4	30.3	K.GYSS*PEPDIQDS*SGS*EAQSVKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S798S799S810				10.8	35.8	K.GY*S*S*PEPDIQDSSGS*EAQSVKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S799S810S814				15.3	20.6	K.GYSS*PEPDIQDSSGS*EAQ*S*VKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S799S808S810				9.4	27.6	K.GYSS*PEPDIQDS*S*GS*EAQSVKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S327S328S342				13.3	27.2	K.DQDMY*S*DKSDKENDQEHDES*ONEVMGK.S
		Oxysterol binding protein like 8	OSBPL8	S798S799S807				8.9	24.7	K.GY*S*S*PEPDIQDS*SGSEAQSVKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S798S799S807				25.8	20.9	K.GY*S*S*PEPDIQDS*S*GS*EAQSVKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S807S810S814				16.2	24.0	K.GYSSPEPDIQDS*SGS*EAQ*S*VKPSTR.R
		Oxysterol binding protein like 8	OSBPL8	S327S328S331				4.9	18.1	K.DQDMY*S*DKS*DKENDQEHDES*ONEVMGK.S
		Oxysterol binding protein like 8	OSBPL8	S799S807S808				2.5	27.5	K.GYSS*PEPDIQDS*S*GSEAQSVKPSTR.R
		Oxysterol binding protein-like 3	OSBPL3	S304				7.2	54.5	R.LHSS*NPNLSTLDFGEEK.N

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		Protein Name	Gene	Phosphosites						
		Oxysterol binding protein-like 3	OSBPL3	S303				56.7	42.9	R.LH\$*SNPNLSTLDFGEEK.N
		Oxysterol binding protein-like 3	OSBPL3	S251				12.1	71.0	R.TY\$*APAINAQGGSFESPKK.E
		P160 MYBBP1A	S1163					5.2	40.0	K.EIP\$ATQ\$*PI\$ISK.K
		P160 MYBBP1A	S1267					25.1	43.0	K.NQKPSQVNGAPG\$*PTEPAGQK.Q
		P160 MYBBP1A	S111					59.4	23.2	R.DPAQPM\$*PGEATQSGARPADR.Y
		P160 MYBBP1A	S731S732S734					17.7	11.0	K.SEEGEDNR\$*\$E\$*E\$E\$*EGEE\$*EEEEER.D
		P160 MYBBP1A	T1161					8.1	28.1	K.EIP\$AT*Q\$PI\$ISK.K
		p21 activated kinase 3	PAK3	T421				-0.3	68.5	R.ST*MVGTPYWMapeVvTR.K
		p21 activated kinase 4	PAK4	S474				48.7	76.9	K.S*LVGTPYWMapeLISR.L
		p21 activated kinase 4	PAK4	T478				5.3	19.9	K.SLVGT*PYWMapeLISR.L
		p21 activated kinase 4	PAK4	S181				28.9	39.2	R.DKRPL\$*GPDVGTQPAGLASGAK.L
		p21 activated kinase 4	PAK4	Y480				2.7	40.0	K.SLVGTPY*WMapeLISR.L
		p53 induced gene 8	EI24	S56				100.0	39.5	R.AQ\$*IER.K
		p53 induced gene 8	EI24	S320				-0.2	23.3	K.TVYLQSALSS\$*AEKFPSPHP\$PAK.L
		p53 induced gene 8	EI24	S316				-0.0	14.6	K.TVYLQSAL\$*S\$TSAEKFPSPHP\$PAK.L
		PA2G4	PA2G4	T386				39.9	56.1	K.TAENATSGE*T\$EENEAGD.-
Paf1, RNA polymerase II associated factor, PAF1 homolog		S456S460S466						100.0	43.8	R.DKEIFG\$*DAD\$*EDDAD\$*DDED.R
		PAG	PAG1	S296				9.1	30.9	R.F\$S*LSYK.S
		PAG	PAG1	S295				9.8	23.5	K.RF\$*LSYK.S
		PAG	PAG1	S295S296				5.4	19.8	K.RF\$*LSYK.S
		PAG	PAG1	S351				35.4	92.8	R.S*P\$SCNDLYATVK.D
		PAG	PAG1	S229				23.9	55.3	K.AEFAEY\$*VDR.N
		PAG	PAG1	S288S295S298				4.7	16.0	K.EGGEAEESATD\$*ETNKRFS\$*SL\$*YK.S
		PAG	PAG1	S351S354				25.4	19.7	K.SGQSLTPESTYTSIQGDPQR\$*P\$*SCNDLYATVK.D
		PAG	PAG1	S170				19.7	65.8	K.D\$S*\$QENMV\$EDCLYETVK.E
		PAG	PAG1	S301				26.8	78.0	K.S*REEDPTLT\$E\$EISAMYS\$V\$NKGQLV\$N\$K.S
		PAG	PAG1	S288				18.4	59.1	K.EGGEAEESATD\$*ETNKR.F
		PAG	PAG1	T286				-0.3	38.3	K.EGGEAEESATD*T\$T\$ETNKR.F
		PAG	PAG1	S295S298				12.6	21.4	K.RF\$*SL\$*YK.S
		PAG	PAG1	S354				33.6	81.4	R.SP\$S*\$CNDLYATVK.D
		PAG	PAG1	S351S353				6.0	15.2	K.SGQSLTPESTYTSIQGDPQR\$*P\$*SCNDLYATVK.D
		PAG	PAG1	S169				67.8	53.4	K.D\$*\$QENMV\$EDCLYETVK.E
		PAG	PAG1	S353				11.7	82.3	R.SP\$*\$CNDLYATVK.D
		PAG	PAG1	Y417				38.2	69.2	K.ENDY*\$E\$ISD\$QQGR.D
		PAG	PAG1	S171				-0.2	99.6	K.D\$S*\$QENMV\$EDCLYETVK.E
		PAG	PAG1	S150				51.7	38.0	R.S*VDGQGLGMEG\$PYEV\$K.D
		PAG	PAG1	S298				7.8	24.1	R.F\$SSL\$*YK.S
		PAG	PAG1	S353S354				-5.9	13.0	K.SGQSLTPESTYTSIQGDPQR\$*P\$*SCNDLYATVK.D
		PAK2	PAK2	S197				81.1	41.1	R.S*VIDPVPAPVGD\$SHVDGA\$K.S
		PAK2	PAK2	S141				25.3	56.3	K.YL\$*FTPPEK.D
		PAK2	PAK2	S141S152				18.6	36.2	K.YL\$*FTPPEKDGFP\$*GTPALNAK.G
		PAK2	PAK2	S141T154				4.9	22.2	K.YL\$*FTPPEKDGFP\$GTP*PALNAK.G
		PAK2	PAK2	T143S152				14.9	21.3	K.YL\$FT*PPEKDGFP\$*GTPALNAK.G
		PAK2	PAK2	T143				50.1		K.YL\$FT*PPEKDGFP\$GTPALNAK.G
		PAK2	PAK2	S141T143				6.2	18.2	K.YL\$*FT*PPEKDGFP\$GTPALNAK.G
		PAK2	PAK2	Y139				13.9	35.1	K.Y*LSFTPPEK.D
		PAK2	PAK2	S55				28.4	45.3	K.IIS*IFSGTEK.G
		Palladin	PALLD	S892S894S897				100.0	21.9	R.S*RS*RD\$*G\$DENEPIQER.F
		Palladin	PALLD	S669				37.6	35.7	R.IA\$*DEEIQTK.D
		Palladin	PALLD	S763S766				14.3	11.9	K.QFIAAQNLGPASGHGT\$PASSP\$SSSLP\$*PMS*\$PTPR.Q
		Pannexin 1	PANX1	S182				3.5	28.6	R.DGAC\$VPGVTENLQ\$S*LWEV\$ESHFK.Y
		Pantothenate kinase 4	PANK4	S393				18.4	93.1	K.GAEQDNPNQY\$WGENYAG\$SSGLMSA\$*PEL\$GPAQR.A
		Pantothenate kinase 4	PANK4	S404				16.7	58.1	R.S*GT\$D\$LLEMDR.L
		Pantothenate kinase 4	PANK4	Y383				12.4	22.4	K.GAEQDNPNQY\$WGENY*AG\$SSGLMSA\$PEL\$GPAQR.A
		Pantothenate kinase 4	PANK4	T406				-0.8	36.3	R.SGT*\$D\$LLEMDR.L
		PARD3	PARD3	S174				12.1	25.8	R.W\$*TTAGFLK.Q
		PARN	PARN	S619				42.4	59.6	K.EL\$*PAGSISK.N
		PARN	PARN	S626				16.4	36.3	K.N\$*PATLFEV\$PDTW.-
		PARN	PARN	S570T589				8.4	112.3	R.NL\$*\$PSQEEAGLEDGV\$GEISD*T\$ELEQTD\$SCAEPL\$SEGR.K
		PARN	PARN	S570S583				7.8	72.4	R.NL\$*\$PSQEEAGLEDGV\$*GEISDTELEQTD\$SCAEPL\$SEGR.K
		PARN	PARN	S570S587				8.3	41.3	R.NL\$*\$PSQEEAGLEDGV\$GEIS*DTELEQTD\$SCAEPL\$SEGR.K
		Parvin beta	PARVB	T9				14.8	22.6	R.SPT*PRPR.R

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	Protein Name	Gene	Phosphosites						
	Parvin beta	PARVB	S7				-4.7	18.2	R.S*PTRPR.R
	PAS kinase	PASK	S119				-0.4	24.5	R.GLSSGW*S*PLLPAPVCNPNKA
	Patatin like phospholipase domain containing 2	PNPLA2	S404				55.8	58.3	R.VQS*LPSVPLSCAAAY.E
	Patatin like phospholipase domain containing 2	PNPLA2	S428				100.0	37.6	R.NNLS*LGDALAK.W
	Patatin like phospholipase domain containing 2	PNPLA2	S407				15.8	43.7	R.VQSLPS*VPLSCAAAY.E
	Paxillin	PXN	S336				8.0	61.7	K.TGSSS*PPGGPPKPGSQLDSMLGSLQSDLNK.L
	Paxillin	PXN	S346				6.8	45.0	K.TGSSSPPGGPPKPGS*QLDSMLGSLQSDLNK.L
	Paxillin	PXN	T332				6.7	12.4	K.T*GSSSPPGGPPKPGSQLDSMLGSLQSDLNK.L
	PC2 CBX4	S432S434					50.4		R.S*IS*TP TCLGGSPAERPADLPAAALPOPEVILLDSLDLDEPIDL.R
	PC2 CBX4	S432S434T435					34.7		R.S*IS*T*TP TCLGGSPAERPADLPAAALPOPEVILLDSLDLDEPIDL.R
	PC2 CBX4	S434T435					-0.8	12.7	R.SIS*T*TP TCLGGSPAERPADLPAAALPOPEVILLDSLDLDEPIDL.R
	PC2 CBX4	T437S442					0.3	26.4	R.SISTP*T*CLGGS*PAERPADLPAAALPOPEVILLDSLDLDEPIDL.R
	PC4 and SFRS1 interacting protein 1	PSIP1	T272S273S275				16.8	95.9	K.TGVTST*S*DS*EEEGDDQEGEK.K
	PC4 and SFRS1 interacting protein 1	PSIP1	S177				10.9	50.3	K.QVETEEAGVTTATASNVLK*S*PK.R
	PC4 and SFRS1 interacting protein 1	PSIP1	S106				16.9	96.5	K.QSNASS*DVEEEK.E
	PC4 and SFRS1 interacting protein 1	PSIP1	S273S275				22.9	105.8	K.TGVTST*S*DS*EEEGDDQEGEK.K
	PC4 and SFRS1 interacting protein 1	PSIP1	T272S275				17.3	75.4	K.TGVTST*SDS*EEEGDDQEGEK.K
	PSIP1	T272S273					9.9	125.6	K.TGVTST*S*DS*EEEGDDQEGEK.K
	PC4 and SFRS1 interacting protein 1	PSIP1	T270S275				6.7	26.3	K.TGVT*STSDS*EEEGDDQEGEK.K
	PC4 and SFRS1 interacting protein 1	PSIP1	T270S271				13.9	13.6	K.TGVT*S*TSDEEGDDQEGEK.K
	PC4 and SFRS1 interacting protein 1	PSIP1	S118S129				7.0	17.0	K.ETSVS*KEDTDHEEKAS*VEDVTKA
	PC4 and SFRS1 interacting protein 1	PSIP1	S271S275				3.5	31.9	K.TGVT*S*TSDS*EEEGDDQEGEK.R.K
	PC4 and SFRS1 interacting protein 1	PSIP1	S271T272				7.5	42.0	K.TGVT*S*T*SDSEEGDDQEGEK.K
	PC4 and SFRS1 interacting protein 1	PSIP1	S271T272S273				7.7	52.6	K.TGVT*S*T*S*DSEEGDDQEGEK.K
	PC4 and SFRS1 interacting protein 1	PSIP1	S271T272S275				9.8	44.7	K.TGVT*S*T*SDS*EEEGDDQEGEK.K
	PCTAIRE protein kinase 1	CDK16	S119				100.0	43.7	K.RLS*LPADIR.I
	PCTAIRE protein kinase 1	CDK16	S153				32.3	44.9	R.RV*S*LSEIGFGK.L
	PCTAIRE protein kinase 2	CDK17	S9				19.8	30.6	R.RLS*LTLR.G
	PCTAIRE protein kinase 2	CDK17	S180				40.2	58.8	R.RAS*LSEIGFGK.M
	PCTAIRE protein kinase 2	CDK17	S182				10.9	33.4	R.RASLS*EIGFGK.M
	PCTAIRE protein kinases 3	CDK18	S132				38.2	61.1	R.RAS*LSDIGFGK.L
	PCTAIRE protein kinases 3	CDK18	S98				100.0	48.1	K.RLS*LPMDIR.L
	PCTAIRE protein kinases 3	CDK18	S14				19.8	37.7	R.RF*S*LSVPR.T
	PDAP1	S60S63					45.3	83.5	K.KSLDS*DES*EDEEDDYQQK.R
	PDGF alpha associated protein 1	PDAP1	S63				0.7	32.9	K.SLDSDES*EDEEDDYQQK.R
	PDGF alpha associated protein 1	PDAP1	S60				23.6	44.0	K.SLDS*DESEDEEDDYQQK.R
	PDGF alpha associated protein 1	PDAP1	S57S60				8.3	20.6	K.KS*LDS*DESEDEEDDYQQK.K
	PDGF alpha associated protein 1	PDAP1	S57S63				6.8	40.3	K.KS*LDSDES*EDEEDDYQQK.R
	PDZ and LIM domain 5	PDLIM5	S360				24.0	33.0	K.S*PSWQRPNQGVPTGR.I
	PDZ binding kinase	PBK	S23S32				25.1	30.8	K.SVLC*S*TP TINIPAS*PFMQK.L
	PDZ binding kinase	PBK	T26S32				13.9	13.8	K.SVLCSTP*TP TINIPAS*PFMQK.L
	PDZ binding kinase	PBK	T24S32				17.9	19.3	K.SVLCST*TP TINIPAS*PFMQK.L
	PEPP2 PLEKHA5	S885					65.4	27.2	R.S*AVEQLCLAESTRPR.M
	PEPP2 PLEKHA5	T857					5.0	64.3	R.AKSPT*PESSTIASYVTLR.K
	PLEKHA5	S410					28.9	76.3	R.TNS*MQQLEQWIK.I
	PEPP2 PLEKHA5	S382					100.0	60.1	K.IVVV*S*LADLR.G
	PEPP2 PLEKHA5	S355					9.6	23.8	K.LNSLPSEY*S*GSACPAQTVHYRPINLSSSENK.I
	PEPP2 PLEKHA5	S855					10.1	55.5	K.S*PTPESSTIASYVTLR.K
	PEPP2 PLEKHA5	S933					15.5	35.5	K.GLVIGASDQ*S*PLQSPNLR.D
	PEPP2 PLEKHA5	T408					9.2	67.4	R.T*NSMQQLEQWIK.I
	PEPP2 PLEKHA5	S372					4.7	18.5	K.LNSLPSEYSGSACPAQTVHYRPINLS*SENK.I
	PEPP2 PLEKHA5	Y366						14.3	K.LNSLPSEYSGSACPAQTVHY*RPINLSSSENK.I
	PEPP2 PLEKHA5	S861					0.8	15.2	R.AKSPTPESS*TIASVYTLR.K
	PEPP2 PLEKHA5	S809					6.4	48.8	K.S*EPELTTVAEVDSENGEEK.S
	Peptidyl prolyl isomerase	G PPIG	S356T358				100.0	53.6	R.S*ET*PPHWR.Q
	Peptidyl prolyl isomerase	G PPIG	S413S415				100.0	30.5	R.NV*S*ES*PNRK.N
	PPIG	S290					100.0	26.9	R.KS*PPKADEK.E
	Peptidyl prolyl isomerase	G PPIG	S687				27.6	29.8	K.ADRDQ*S*PFSK.I
	Peptidyl prolyl isomerase	G PPIG	S744S745T748				100.0	18.8	K.FDHES*S*PGT*DEDKS*G.-
	Peptidyl prolyl isomerase	G PPIG	S587				30.0	21.7	R.S*KEYHR.Y
	Peptidyl prolyl isomerase	G PPIG	S254S256S257				69.1	44.6	K.S*AS*S*ES*EAENLEAQPOSTVPRPEIPPIPENR.F
	Peptidyl prolyl isomerase	G PPIG	S546				37.5	25.2	R.S*RECDITK.G





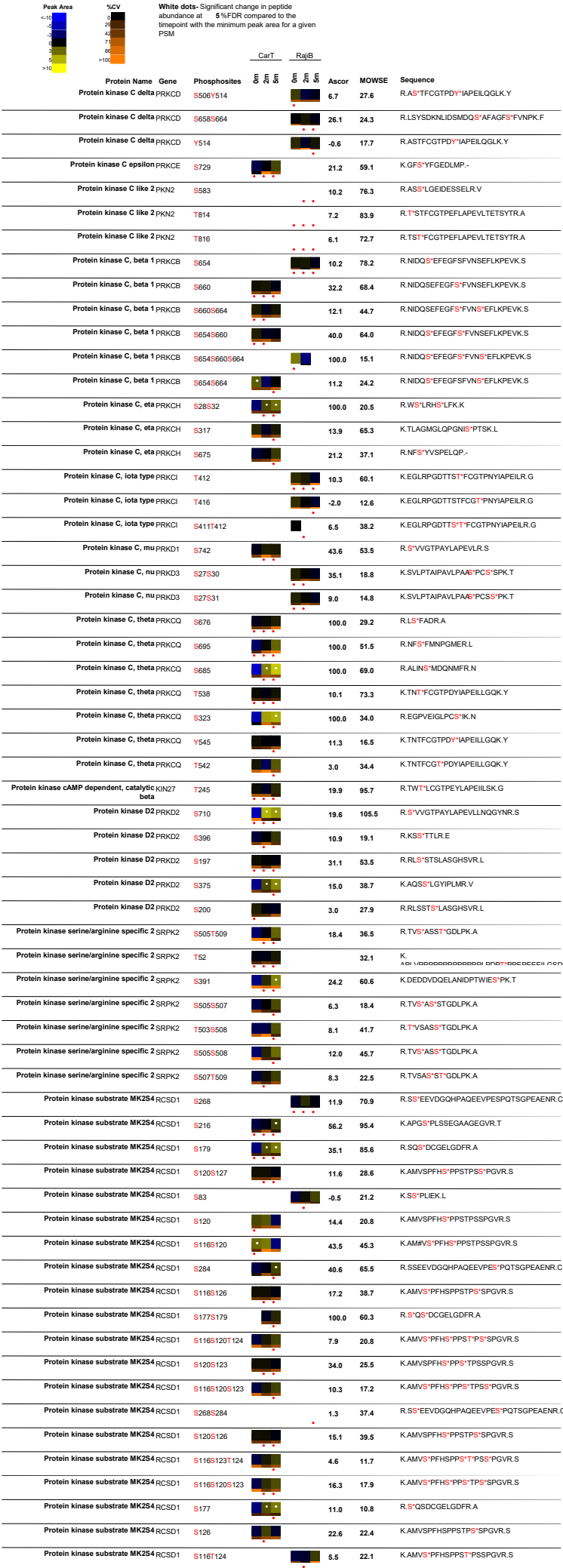
Peak Area		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajIB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		PHD finger protein 2 PHF2		S882				12.9	52.6	K.DSDYVYPSLE <sup>S</sup> DEDNP <sup>F</sup> K.S
		PHD finger protein 2 PHF2		S539				5.6	75.1	R.ESAS <sup>P</sup> TPINL <sup>L</sup> DLLEAHT <sup>K</sup> .E
		PHD finger protein 3 PHF3		S682				10.9	80.9	K.SF <sup>S</sup> LDEPPL <sup>F</sup> IPDN <sup>I</sup> ATIR.R
		PHD finger protein 3 PHF3		S680				17.0	65.4	K. <sup>S</sup> FSLDEPPL <sup>F</sup> IPDN <sup>I</sup> ATIR.R
		PHD finger protein 3 PHF3		S680S682				11.2	34.0	R.SK <sup>S</sup> <sup>S</sup> FS <sup>L</sup> LDEPPL <sup>F</sup> IPDN <sup>I</sup> ATIR.R
		PHD finger protein 3 PHF3		S678S680				4.8	21.6	R.RS <sup>S</sup> <sup>S</sup> K <sup>S</sup> FS <sup>L</sup> LDEPPL <sup>F</sup> IPDN <sup>I</sup> ATIR.R
		PHD finger protein 6 PHF6		S145S154				27.6	36.0	K.TAHNSEADLEES <sup>S</sup> FNEHELEPS <sup>S</sup> SPK.S
		PHD finger protein 6 PHF6		S154				61.4	48.0	K.TAHNSEADLEESFNEHELEPS <sup>S</sup> SPK.S
		PHD finger protein 6 PHF6		S146S155				33.8	30.9	K.TAHNSEADLEES <sup>S</sup> FNEHELEPS <sup>S</sup> SPK.S
		PHD finger protein 6 PHF6		S155				51.0	41.3	K.TAHNSEADLEESFNEHELEPS <sup>S</sup> SPK.S
		PHD finger protein 6 PHF6		S145S155				16.9	23.4	K.TAHNSEADLEES <sup>S</sup> FNEHELEPS <sup>S</sup> PK.S
		PHD finger protein 6 PHF6		S199S203				22.2	20.2	R. <sup>S</sup> PHRS <sup>S</sup> SPSDTRPK.C
		PHD finger protein 6 PHF6		S138S154				39.6	14.7	K.TAHNS <sup>S</sup> EADLEESFNEHELEPS <sup>S</sup> SPK.S
		PHD finger protein 6 PHF6		S199S204				11.4	17.9	R. <sup>S</sup> PHRS <sup>S</sup> PSDTRPK.C
		Phosducin like PDCL		S296				39.4	28.8	R.NSATCHSED <sup>S</sup> DLEID.-
		Phosducin like PDCL		Y16Y17S19S25				11.8	20.3	K.LQYY <sup>Y</sup> <sup>Y</sup> <sup>S</sup> <sup>S</sup> SEDED <sup>S</sup> DHEDKDR.G
		Phosducin like PDCL		S293S296				21.8	37.0	R.NSATCHS <sup>S</sup> ED <sup>S</sup> DLEID.-
		Phosducin like PDCL		T290S296				17.2	12.8	R.NSAT <sup>T</sup> CHSED <sup>S</sup> DLEID.-
		Phosducin like PDCL		Y16Y17S18S19				11.1	19.6	K.LQYY <sup>Y</sup> <sup>Y</sup> <sup>S</sup> <sup>S</sup> SEDEDS <sup>D</sup> HEDKDR.G
		Phosducin like PDCL		Y17S18S19S25				5.5	40.9	K.LQYY <sup>Y</sup> <sup>Y</sup> <sup>S</sup> <sup>S</sup> SEDED <sup>S</sup> DHEDKDR.G
		Phosphatidylinositol 3 kinase, class 2 PIK3C2A alpha		S338				33.6	46.6	R.SQS <sup>S</sup> LNIR.T
		Phosphatase and actin regulator PHACTR2		S70					22.8	R.VHS <sup>S</sup> GSVDGLK.A
		Phosphatase and actin regulator 4 PHACTR4		S127				-0.3	54.3	R.SS <sup>S</sup> SPVQVEEPEVR.L
		Phosphatase and actin regulator 4 PHACTR4		S638				31.2	48.3	R.KLS <sup>S</sup> QRPTVAELLAR.K
		Phosphatase and actin regulator 4 PHACTR4		S474				61.5	59.2	R. <sup>S</sup> LPTIEMLK.V
		Phosphatase and actin regulator 4 PHACTR4		S354T368				22.2	14.3	R.SPS <sup>S</sup> PPLP <sup>T</sup> HIPPEPR <sup>T</sup> PPFAKT
		Phosphatase and actin regulator 4 PHACTR4		T436T442				32.4	37.4	R.IQQALT <sup>T</sup> SPLPMT <sup>T</sup> PILEGSHR.A
		Phosphatase and actin regulator 4 PHACTR4		S128					10.2	R.SS <sup>S</sup> SPVQVEEPEVR.L
		Phosphatase and actin regulator 4 PHACTR4		T436S437				10.3	18.4	R.IQQALT <sup>T</sup> <sup>S</sup> PLPMT <sup>T</sup> PILEGSHR.A
		Phosphate cytidylyltransferase 1 choline PCYT1A alpha isoform		S343S347				5.0	14.0	K.TS <sup>S</sup> PPCS <sup>S</sup> PANLSRH
		Phosphate cytidylyltransferase 1 choline PCYT1A alpha isoform		S315					100.0	R.MLQAI <sup>S</sup> PK.Q
		Phosphate cytidylyltransferase 1 choline PCYT1A alpha isoform		S362				31.9	41.4	K.AAAVD <sup>S</sup> EDEED.-
		Phosphate cytidylyltransferase 1 choline PCYT1A alpha isoform		S329S331				22.7	15.9	R.ERS <sup>S</sup> PS <sup>S</sup> PSFR.W
		Phosphate cytidylyltransferase 1 choline PCYT1A alpha isoform		S319S321				10.0	12.4	K.QS <sup>S</sup> PS <sup>S</sup> SSPTR.E
		Phosphate cytidylyltransferase 1 choline, PCYT1B beta		S335				10.6	66.3	R.SPS <sup>S</sup> PTFSWLPLK.T
		Phosphatidylinositol 3-phosphate 3 MTMR12 phosphatase adaptor subunit		S716				20.0	62.4	R.HSS <sup>S</sup> KPVLPTSGWKA
		Phosphatidylinositol 3-kinase, regulatory 4 PIK3R4		S903				-1.5	37.9	R.SESSAGICVPLS <sup>T</sup> TSSQVPEVTTVQNK.K
		Phosphatidylinositol 4-kinase catalytic beta P44KB polypeptide		S440				92.3	56.6	R. <sup>S</sup> VENLPEGGTHEQRA
		Phosphatidylinositol 4-kinase catalytic beta P44KB polypeptide		S523				37.4	19.6	R.RLS <sup>S</sup> EQLAHTPTAFK.R
		Phosphatidylinositol 4-kinase type II P44K2A		S462				11.7	69.5	R.SSS <sup>S</sup> ESYTSQFSQR.K
		Phosphatidylinositol 4-kinase type II P44K2A		S475S1				12.9	34.0	R.VAAAAAGSGPS <sup>S</sup> PPGS <sup>S</sup> PGHORE
		Phosphatidylinositol 4-kinase alpha P44KA		S172				100.0	24.6	R. <sup>S</sup> FNDFR.S
		Phosphatidylinositol transfer protein, beta PITPNB		S262				100.0	14.6	R.KRGS <sup>S</sup> VR.G
		Phosphatidylinositol transfer protein, PITPNC1 cytosolic		S270				5.1	26.6	R. <sup>S</sup> APSSAPSTPLSTDAPEFLSVPK.D
		Phosphatidylinositol transfer protein, PITPNC1 cytosolic 1		S274				8.0	49.2	R.SAPS <sup>S</sup> APSTPLSTDAPEFLSVPK.D
		Phosphatidylinositol-3-PiKFYVE phosphatase/phosphatidylinositol 5-kinase		T22S23				4.2	44.0	R.SPT <sup>T</sup> <sup>S</sup> PSHLTHFKPLTPDQDEPPFK.S
		Phosphatidylinositol-3-PiKFYVE phosphatase/phosphatidylinositol 5-kinase		S307				18.9	56.6	R.SAS <sup>S</sup> ITNLSLDR.S
		Phosphatidylinositol-3-PiKFYVE ohosphate/ohosphatidinositol 5-kinase		S20S25				6.4	45.1	R. <sup>S</sup> PTPS <sup>S</sup> HLTHFKPLTPDQDEPPFK.S
		Phosphatidylinositol-4-phosphate 5-kinase PiPAK2B type II beta		T322S326				50.5	63.0	R.AEDECENDGVGNLLCSYG <sup>T</sup> PPDS <sup>S</sup> PGNLLSFPR.F
		Phosphatidylinositol-4-phosphate 5-kinase PiPAK2B type II beta		Y320				6.6	49.9	R.AEDECENDGVGNLLCS <sup>Y</sup> GTPPDS <sup>S</sup> PGNLLSFPR.F
		Phosphatidylinositol-4-phosphate 5-kinase PiPAK2B type II beta		S319S326				22.3	28.8	R.AEDECENDGVGNLLCS <sup>Y</sup> GTPPDS <sup>S</sup> PGNLLSFPR.F
		Phosphatidylinositol-4-phosphate 5-kinase PiPAK2B type II beta		Y320S326				20.2	17.1	R.AEDECENDGVGNLLCS <sup>Y</sup> GTPPDS <sup>S</sup> PGNLLSFPR.F
		Phosphatidylinositol-4-phosphate 5-kinase PiPAK2B type II beta		T322				2.2	53.0	R.AEDECENDGVGNLLCSYG <sup>T</sup> PPDSPGNLLSFPR.F
		Phosphatidylserine synthase 1 PTDSS1		S417				28.6	61.1	K.TY <sup>S</sup> ECEDDGTYSPEISWHHR.K
		Phosphatidylserine synthase 1 PTDSS1		Y416				-0.5	22.5	K.TY <sup>S</sup> ECEDDGTYSPEISWHHR.K
		Phosphatidylserine synthase 1 PTDSS1		T423				-1.7	10.9	K.TYSECEDGT <sup>T</sup> YSPEISWHHR.K
		Phosphodiesterase 7A PDE7A		Y61				19.7	34.5	R.RGSHPY <sup>T</sup> IDFR.I
		Phosphofructokinase 1 PFKM		S775				100.0	19.0	R.KRS <sup>S</sup> GEAAV.-
		PFKP		S386				89.8	73.8	R. <sup>S</sup> FAGNLNTYKR.L
		Phosphofurin acidic cluster sorting protein PACS1 1		S779				29.0	29.0	K.VGLVEDSPSTAGDGDSPVSLTV <sup>RS</sup> TSPSSSGLSR.D
		Phosphofurin acidic cluster sorting protein PACS1 1		S379				19.3	78.8	R.EVEEDLDLYDSLEMYPNS <sup>S</sup> DGPEMEETESILSTPKPK.L
		Phosphofurin acidic cluster sorting protein PACS1 1		S379S381				42.7	84.6	R.EVEEDLDLYDSLEMYPNS <sup>S</sup> <sup>D</sup> S <sup>S</sup> GPEMEETESILSTPKPK.L

Peak Area		%CV		White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
Phosphofurin acidic cluster sorting protein	1	Protein Name	Gene	Phosphosites								
				S529S531						11.0	45.2	R.TNNS <sup>S</sup> DS <sup>S</sup> ERSPDLGHSTQIPR.K
Phosphofurin acidic cluster sorting protein	1			Y370S372							50.0	R.EVEEDLD <sup>EY</sup> DS <sup>S</sup> LEMVNPDSGSGPEMEETESILSTPKK.L
Phosphofurin acidic cluster sorting protein	1			S410						6.8	12.6	K.LKPFEGMSQS <sup>S</sup> SQTEIGSLNSK.G
Phosphofurin acidic cluster sorting protein	1			S781						9.0	35.5	K.VGLVEDSPSTAGDGDDSPVSLTVPS <sup>TS</sup> PPSSSGLSR.D
Phosphofurin acidic cluster sorting protein	1			S529S534						3.1	45.2	R.TNNS <sup>S</sup> DSERS <sup>S</sup> PDLGHSTQIPR.K
Phosphoglucutase 1	PGM1			S117						6.1	68.0	K.AIGGILT <sup>AS</sup> HNPGGPNGDGFQIK.F
Phosphoglucutase 1	PGM1			T115							76.2	K.AIGGILT <sup>T</sup> ASHNPGGPNGDGFQIK.F
Phosphoglucutase 2 like 1	PGM2L1			T173						10.9	61.8	K.AVAGVMIT <sup>T</sup> ASHNR.K
Phosphoglucutase 2 like 1	PGM2L1			S175						6.7	39.0	K.AVAGVMIT <sup>AS</sup> HNR.K
Phosphoglucutase 3	PGM3			T62						9.1	118.8	K.STIGVMVT <sup>T</sup> ASHNPEEDNGVK.L
Phosphoglucutase 3	PGM3			S64						13.0	119.7	K.STIGVMVT <sup>AS</sup> HNPEEDNGVK.L
Phosphoglycerate kinase 1	PGK1			S203						100.0	71.2	K.ALES <sup>S</sup> PERPFLAILGGA.V
Phosphoglycerate mutase 1	PGAM1			S14						100.0	67.3	R.HGES <sup>S</sup> AWNLENR.F
Phosphoglycerate mutase 1	PGAM1			S23						45.2	57.0	R.FS <sup>S</sup> GWYDADLSPAGHEEAK.R
Phosphoglycerate mutase 1	PGAM1			Y119						-0.2	47.8	R.SY <sup>S</sup> DVPPPPMEPDHPFYSNISK.D
Phosphoinositide 3 kinase adaptor protein	PIK3AP1			S759						19.6	25.0	R.SR <sup>S</sup> PGPPQVDGTPMTSLERPPR.V
Phosphoinositide 3 kinase adaptor protein	PIK3AP1			S757						16.5	20.7	R.S <sup>S</sup> RSPGPPQVDGTPMTSLERPPR.V
AGAP2				S312						13.9	23.2	R.RTS <sup>S</sup> LFANR.R
Phosphoinositide 3 kinase enhancer	AGAP2			Y272S278						6.3	14.8	K.SLPSSPSHSAASTPVAGQASNGGHTSDY <sup>S</sup> SSLP <sup>S</sup> SPNVGHR.E
Phosphoinositide 3 kinase enhancer	AGAP2			S245S248							18.5	K.S <sup>S</sup> LPS <sup>S</sup> SPSHSAASTPVAGQASNGGHTSDYSSSLP <sup>S</sup> SPNVGHR.E
Phosphoinositide 3 kinase enhancer	AGAP2			T311						8.2	39.1	K.RRT <sup>S</sup> SLFANR.R
Phosphoinositide 3 kinase enhancer	AGAP2			T269S279						8.2	11.7	K.SLPSSPSHSAASTPVAGQASNGGHT <sup>T</sup> SDYSSLP <sup>S</sup> SPNVGHR.E
Phosphoinositide 3 kinase enhancer	AGAP2			S274S279						7.1	15.2	K.SLPSSPSHSAASTPVAGQASNGGHTSDY <sup>S</sup> S <sup>S</sup> SLP <sup>S</sup> SPNVGHR.E
Phospholipase C like 1	PLCL1			S762S764						100.0	20.8	K.RS <sup>S</sup> LS <sup>S</sup> VR.M
Phospholipase C, beta 3	PLCB3			S537						100.0	13.9	K.S <sup>S</sup> LGDEGLNR.G
Phospholipase C, gamma 1	PLCG1			Y783						158.2	71.6	R.NPGFY <sup>S</sup> VEANPMPTFK.C
Phospholipase C, gamma 1	PLCG1			Y775Y783						59.8	41.9	K.IGTAEPDY <sup>GALY</sup> EGRNPGFY <sup>S</sup> VEANPMPTFK.C
PLCG1				S1248						9.8	21.0	R.AREGS <sup>S</sup> FESR.Y
Phospholipase C, gamma 1	PLCG1			Y771Y775Y783						48.0	15.4	K.IGTAEPDY <sup>T</sup> GALY <sup>S</sup> EGRNPGFY <sup>S</sup> VEANPMPTFK.C
Phosphoribosylformylglycinamide synthase	PFAS			S569						93.9	35.3	R.S <sup>S</sup> PNRDLTHVSAR.E
Phosphorybosylaminimidazole PAICS carboxylase				S27						112.3	58.9	K.TKEVYELLD <sup>S</sup> PGK.V
Phosphorylase B kinase, beta	PHKB			S700S701						4.3	46.0	K.RQ <sup>S</sup> S <sup>S</sup> TPSAPELQQQPDVNISEWK.D
Phosphorylase kinase liver alpha 2 subunit	PHKA2			T1041S1044						3.4	24.2	R.SS <sup>T</sup> PSS <sup>S</sup> PTGTSSSDSGHHIGWGER.Q
Phosphorylase kinase liver alpha 2 subunit	PHKA2			T1041S1043						6.0	11.4	R.SS <sup>T</sup> P <sup>S</sup> SPTGTSSSDSGHHIGWGER.Q
Phosphorylated CTD interacting factor 1	PCIF1			S144						12.1	27.0	K.IEIPVTPTGQSVPS <sup>S</sup> PSIPGTPTLK.M
Phosphorylated CTD interacting factor 1	PCIF1			T137S144						5.5	10.8	K.IEIPVTPT <sup>T</sup> GQSVPS <sup>S</sup> PSIPGTPTLK.M
Phosphorylated CTD interacting factor 1	PCIF1			S144T150						13.1	12.1	K.IEIPVTPTGQSVPS <sup>S</sup> PSIPG <sup>T</sup> PTLK.M
Phosphorylated CTD interacting factor 1	PCIF1			S140S144						6.2	21.5	K.IEIPVTPTGQ <sup>S</sup> VPSS <sup>S</sup> PSIPGTPTLK.M
Phosphorylated CTD interacting factor 1	PCIF1			T137S143						6.5	19.6	K.IEIPVTPT <sup>T</sup> GQSVPS <sup>S</sup> SPSIPGTPTLK.M
Phosphorylated CTD interacting factor 1	PCIF1			S143T150						9.5	11.6	K.IEIPVTPTGQSVPS <sup>S</sup> SPSIPG <sup>T</sup> PTLK.M
Phosphorylated CTD interacting factor 1	PCIF1			S143S146						8.4	11.0	K.IEIPVTPTGQSVPS <sup>S</sup> SPS <sup>S</sup> IPGTPTLK.M
PI3 kinase related kinase	SMG1			T3569S3570						26.2	22.7	K.NLAT <sup>S</sup> S <sup>S</sup> ADTPSTVPGTGK.S
Pinin PNN				S347						100.0	55.5	K.EIAVH <sup>S</sup> DAEK.E
Pinin PNN				S99						122.4	67.1	R.QE <sup>S</sup> DPEDDDVKPALQSSVWATSK.E
Pinin PNN				S442						18.6	81.4	K.SLS <sup>S</sup> PGKENVSALDMEK.E
Pinin PNN				S718S720						27.7	36.1	R.SIS <sup>S</sup> ES <sup>S</sup> SR.S
Pinin PNN				S684						15.8	19.6	R.DTS <sup>S</sup> GLER.S
Pinin PNN				S720S721						8.0	16.9	R.SISES <sup>S</sup> S <sup>S</sup> R.S
Pinin PNN				S380						34.9	80.4	R.ESEKQOD <sup>S</sup> QPEEVMVLEMVENVK.H
Pinin PNN				S718S721						16.4	28.0	R.SIS <sup>S</sup> ES <sup>S</sup> R.S
Pinin PNN				S440S442						30.5	10.8	K.S <sup>S</sup> LS <sup>S</sup> PGKENVSALDMEK.E
Pinin PNN				S449						-18.5	30.9	K.SLSPGKENVS <sup>S</sup> ALDMEK.E
Pinin PNN				S716S718						7.6	16.3	R.S <sup>S</sup> IS <sup>S</sup> ESSR.S
PKD1like KIAA0319L	S998S1003S10									6.4	28.8	K.GLLLS <sup>S</sup> SLMH <sup>S</sup> ES <sup>S</sup> ELDSDAIFTWPOR.E
PKD1like KIAA0319L	S998S1003S10									8.8	16.2	K.GLLLS <sup>S</sup> SLMH <sup>S</sup> SELD <sup>S</sup> DDAIFTWPOR.E
PKR protein activator	PRKRA			S18						39.3	75.2	R.EDS <sup>S</sup> GTFSLGK.M
Plasma membrane Ca(2+) ATPase type 4	ATP2B4			S326						47.3	41.5	K.TODGVALEIQPLN <sup>S</sup> QEGIDNEEK.D
Plasma membrane Ca(2+) ATPase type 4	ATP2B4			T1145						100.0	65.0	R.T <sup>S</sup> PLLDEEEENPDK.A
Plasma membrane Ca(2+) ATPase, type 1	ATP2B1			S1140						9.6	59.6	R.SS <sup>S</sup> HNFMTHPEFR.I
Plasma protease C1 inhibitor	SERPINC1			T47						13.3		K.VAT <sup>T</sup> TVISK.M
Platelet-activating factor receptor	PTAFR			S339						50.2	22.3	R.ATTDTVTVEVVPFNQIPGN <sup>S</sup> LKN.-
PLC, gamma 2	PLCG2			S677						32.1	50.6	R.EGS <sup>S</sup> DSYAITFRA

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		Raj1β		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Pleckstrin PLEK		S199T204					41.0	K.S <sup>+</sup> AVDGT <sup>+</sup> AENFLNDPDAFYFFPDS <sup>+</sup> GFFCEENS <sup>+</sup> DDDVILK.E
		Pleckstrin PLEK		S222S231				5.3	32.6	K.SAVDGTAE <sup>+</sup> NFLNDPDAFYFFPDS <sup>+</sup> GFFCEENS <sup>+</sup> DDDVILK.E
		Pleckstrin PLEK		S239S231				4.8	27.0	K.SAVDGTAE <sup>+</sup> NFLNDPDAFYFFPDS <sup>+</sup> GFFCEEN <sup>+</sup> S <sup>+</sup> DDDVILK.E
		Pleckstrin PLEK		S222S230				4.8	11.1	K.SAVDGTAE <sup>+</sup> NFLNDPDAFYFFPDS <sup>+</sup> GFFCEENS <sup>+</sup> DDDVILK.E
		Pleckstrin and Sec7 domain containing 4 PSD4		S118				11.5	46.4	R.QDAPPW <sup>+</sup> GSGVEL <sup>+</sup> THLGS <sup>+</sup> PSAQR.E
		Pleckstrin and Sec7 domain containing 4 PSD4		T114				17.8	21.5	R.QDAPPW <sup>+</sup> GSGVEL <sup>+</sup> T <sup>+</sup> HLGSPSAQR.E
		Pleckstrin and Sec7 domain containing 4 PSD4		S461S464S465					41.7 10.7	R.GPGPRP <sup>+</sup> S <sup>+</sup> PAS <sup>+</sup> S <sup>+</sup> QEGS <sup>+</sup> PQLQHSSGILPK.W
		Pleckstrin homology domain containing, PLEKHF2 familv F (with FYVE domain) member 2		S239S248				36.6	100.6	K.SPLNDMS <sup>+</sup> DDDDDDSS <sup>+</sup> D.-
		Pleckstrin homology domain containing, PLEKHF2 familv F (with FYVE domain) member 2		S239S247S248				81.6	107.8	K.SPLNDMS <sup>+</sup> DDDDDDSS <sup>+</sup> S <sup>+</sup> D.-
		Pleckstrin homology domain containing, PLEKHF2 familv F (with FYVE domain) member 2		S226				23.9	38.2	R.SD <sup>+</sup> S <sup>+</sup> YSQLK.S
		Pleckstrin homology domain containing, PLEKHF2 familv F (with FYVE domain) member 2		S239S247				46.6	50.7	K.SPLNDMS <sup>+</sup> DDDDDDSS <sup>+</sup> SD.-
		Pleckstrin homology domain containing, PLEKHM2 familv M (with RUN domain) member 2		S544				3.0	29.2	R.TGS <sup>+</sup> PGDAPERPLCDFSEGLSAPMDFYR.F
		Pleckstrin homology domain containing, PLEKHM2 familv M (with RUN domain) member 2		T542				10.1	55.4	R.T <sup>+</sup> GSPGDAPERPLCDFSEGLSAPMDFYR.F
		Pleckstrin homology domain interacting PHIP protein		S1783				60.5	87.4	R.TAFYNEDDS <sup>+</sup> EEEEQR.Q
		Pleckstrin homology domain interacting PHIP protein		S911				100.0	45.6	K.DGPIS <sup>+</sup> PK.K
		Pleckstrin homology domain interacting PHIP protein		S674				8.9	55.8	R.GS <sup>+</sup> ISSTSEVHSPPNVGLR.R
		PHIP		S1315					16.9 12.6	R.AQ <sup>+</sup> S <sup>+</sup> YDIAWKK.Q
		Pleckstrin homology domain-containing PLEKHA2 familv A member 2		S134				15.1	20.7	R.SQ <sup>+</sup> S <sup>+</sup> YIPTSGCR.A
		Pleckstrin homology domain-containing PLEKHA2 familv A member 2		S351				100.0	20.9	R.S <sup>+</sup> EPQHPK.E
		Pleckstrin homology domain-containing PLEKHA2 familv A member 2		S299				24.3	24.3	K.AP <sup>+</sup> S <sup>+</sup> VASSWQPWTPVQAQEK.L
		Pleckstrin homology domain-containing PLEKHA2 familv A member 2		S132				12.3	18.4	R.S <sup>+</sup> QS <sup>+</sup> YIPTSGCR.A
		Plectin 1 PLEC		T4623				27.6	78.6	K.GYSPYSVSGSGS <sup>+</sup> T <sup>+</sup> AGSR.T
		Plectin 1 PLEC		S4626				19.1	64.7	K.GYSPYSVSGSGSTAGS <sup>+</sup> R.T
		Plectin 1 PLEC		S4386				11.7	79.4	R.SS <sup>+</sup> S <sup>+</sup> VGSSSSYPISPAVSR.T
		Plectin 1 PLEC		S4620S4622				3.7	20.6	K.GYSPYSVSGS <sup>+</sup> GS <sup>+</sup> TAGSR.T
		Plectin 1 PLEC		S21				16.9	97.8	R.TS <sup>+</sup> S <sup>+</sup> EDNLYLAVLR.A
		Plectin 1 PLEC		S4385				-0.2	82.2	R.SS <sup>+</sup> S <sup>+</sup> VGSSSSYPISPAVSR.T
		Plectin 1 PLEC		S20				10.8	90.3	R.TS <sup>+</sup> S <sup>+</sup> EDNLYLAVLR.A
		Plectin 1 PLEC		S4620				9.1	33.6	K.GYSPYSVSGS <sup>+</sup> GSTAGSR.T
		Plectin 1 PLEC		S4622				7.8	22.1	K.GYSPYSVSGGS <sup>+</sup> TAGSR.T
		Plectin 1 PLEC		S4622T4623				1.5	53.5	K.GYSPYSVSGGS <sup>+</sup> T <sup>+</sup> AGSR.T
		Plectin 1 PLEC		S4618				10.9	29.1	K.GYSPYSVS <sup>+</sup> S <sup>+</sup> GSGSTAGSR.T
		Plectin 1 PLEC		S4618T4623				0.6	43.7	K.GYSPYSVS <sup>+</sup> S <sup>+</sup> GSGS <sup>+</sup> TAGSR.T
		PLEKHA7 PLEKHA7		T992				8.3	107.4	R.SYVSEPELAT <sup>+</sup> LSGDMAQPSLGLVGPESR.Y
		PLEKHA7 PLEKHA7		S994				4.2	88.5	R.SYVSEPELAT <sup>+</sup> S <sup>+</sup> GDMAQPSLGLVGPESR.Y
		PLEKHA7 PLEKHA7		S986				7.1	98.5	R.SYVS <sup>+</sup> S <sup>+</sup> EPELATLSGDMAQPSLGLVGPESR.Y
		PML PML		S518S527				100.0	51.1	K.AVS <sup>+</sup> PPHLDGPPS <sup>+</sup> PR.S
		PML PML		S530				82.5	76.0	R.S <sup>+</sup> PVIGSEVFLPNSNHVASGAGEAGRE
		PML PML		S530				108.4	76.0	R.S <sup>+</sup> PVIGSEVFLPNSNHVASGAGEAER.V
		PML PML		S505				-0.3	39.0	R.SS <sup>+</sup> PEQRP <sup>+</sup> PTSKA
		PML PML		S518S527S530				18.4	20.5	K.AVS <sup>+</sup> PPHLDGPPS <sup>+</sup> PR <sup>+</sup> S <sup>+</sup> PVIGSEVFLPNSNHVASGAGEAER.V
		PML PML		S518S527S530				12.5	25.2	K.AVS <sup>+</sup> PPHLDGPPS <sup>+</sup> PR <sup>+</sup> S <sup>+</sup> PVIGSEVFLPNSNHVASGAGEAGRE
		PML PML		S504				12.4	33.6	R.S <sup>+</sup> SPEQRP <sup>+</sup> PTSKA
		Poly A polymerase alpha PAPOLA		S24				23.9	58.0	K.HYGIT <sup>+</sup> S <sup>+</sup> PISLAAPK.E
		Poly adenyate binding protein 2 PABPN1		S150				74.7	36.4	K.QMNM <sup>+</sup> S <sup>+</sup> PPGNAGPVIMSIEEK.M
		Poly(rC) binding protein 1 PCBP1		S189				29.8	57.9	R.VMTIPYQMPAS <sup>+</sup> SPVICAGGQDR.C
		Poly(rC) binding protein 1 PCBP1		S262				53.2	42.0	R.QQSHFAMMHGGTG <sup>+</sup> FAGIDS <sup>+</sup> SSPEVK.G
		Poly(rC) binding protein 1 PCBP1		S190				4.6	68.5	R.VMTIPYQMPAS <sup>+</sup> PVICAGGQDR.C
		Poly(rC) binding protein 1 PCBP1		Y183				21.2	72.0	R.VMTIPY <sup>+</sup> QMPASSPVICAGGQDR.C
		Poly(rC) binding protein 1 PCBP1		S264				9.1	26.4	R.QQSHFAMMHGGTG <sup>+</sup> FAGIDS <sup>+</sup> S <sup>+</sup> PEVK.G
		Poly(rC) binding protein 2 PCBP2		S189				34.0	40.1	K.GVTIPYRPKPSS <sup>+</sup> PVIFAGGQDR.Y
		Poly(rC) binding protein 2 PCBP2		Y182				13.1	28.3	K.GVTIPY <sup>+</sup> RPKPSSSPVIFAGGQDR.Y
		Poly(rC) binding protein 2 PCBP2		S187				12.2	21.1	K.GVTIPYRPKP <sup>+</sup> S <sup>+</sup> SSPVIFAGGQDR.Y
		Poly(rC) binding protein 2 PCBP2		S270				-1.4	16.0	K.LHQLAMQQSHFPMTHGNTGFSGIES <sup>+</sup> SSPEVK.G
		Poly(rC) binding protein 2 PCBP2		S272				3.6	21.2	K.LHQLAMQQSHFPMTHGNTGFSGIESS <sup>+</sup> PEVK.G
		Poly(rC) binding protein 2 PCBP2		S188				16.9	39.3	K.GVTIPYRPKPSS <sup>+</sup> SPVIFAGGQDR.Y
		Polycomb protein SUZ12 SUZ12		S546				89.9	131.8	K.ASMSEFLES <sup>+</sup> EDGEVEQQR.T
		Polycomb protein SUZ12 SUZ12		S539				12.2	78.6	K.AS <sup>+</sup> MSEFLESEDGEVEQQR.T
		Polycomb protein SUZ12 SUZ12		S583				15.5	20.4	R.LYFHSDTCLPLRPOEMEVS <sup>+</sup> EDEKDPFWLR.E
		Polyhomeotic like 3 PHC3		S773				32.7	22.1	K.HADN <sup>+</sup> S <sup>+</sup> SDTEMEDIAEETLEEMDSSELLK.C
		Polyhomeotic like 3 PHC3		S774				7.8	71.4	K.HADNS <sup>+</sup> DTMEDIAEETLEEMDSSELLK.C
		Polymyositis/scleroderma autoantigen 1 EXOSC9		S306				25.6	61.8	K.APIDT <sup>+</sup> S <sup>+</sup> DVEEKA

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		Protein Name	Gene	Phosphosites					
Polymyositis/scleroderma autoantigen 1	EXOSC9	S392S394					11.5	30.5	K.MDTGVEVSDIGSDQADAPILS'DS'E'EEEEILEFPDKNPK.K
Polymyositis/scleroderma autoantigen 1	EXOSC9	S384S392					16.9	14.5	K.MDTGVEVSDIGS'QDAPILS'DS'E'EEEEILEFPDKNPK.K
Polynucleotide kinase 3 prime phosphatase	PNKP	T118T122					31.4	34.7	R.TPESQPD'T'PGT'PLVSQDEKR.D
Polypyrimidine tract binding protein 1	PTBP1	S141					23.9	54.5	K.TDSS'PNQAR.A
Polypyrimidine tract binding protein 1	PTBP1	S140					16.9	55.8	K.TDS'SPNQAR.A
POM121 membrane glycoprotein-like	POM121C	S805S1S83						15.7	R.RHDS'S'GS'GHS'AFEPLVASGVPA5FVKPGSLK.R
POM121 membrane glycoprotein-like	POM121C	S127					-0.5	92.6	R.SS'SMSSLTGAYTS'GIPSSSR.N
POM121 membrane glycoprotein-like	POM121C	S81S83S86					4.5	24.2	R.RHDS'S'GS'GHS'AFEPLVASGVPA5FVKPGSLK.R
POM121 membrane glycoprotein-like	POM121C	S128S130					13.5	85.7	R.SS'S'MS'SLTGAYTS'GIPSSSR.N
POM121 membrane glycoprotein-like	POM121C	S127S130					5.9	108.9	R.SS'S'MS'SLTGAYTS'GIPSSSR.N
POM121 membrane glycoprotein-like	POM121C	S127S131					10.3	93.0	R.SS'S'MS'SLTGAYTS'GIPSSSR.N
POM121 membrane glycoprotein-like	POM121C	S128S131					11.8	116.6	R.SS'S'MS'SLTGAYTS'GIPSSSR.N
POM121 membrane glycoprotein-like	POM121C	S130					7.6	54.9	R.SSSMS'SLTGAYTS'GIPSSSR.N
POM121 membrane glycoprotein-like	POM121C	S128					9.6	57.8	R.SS'S'MSSLTGAYTS'GIPSSSR.N
POP1	POP1	S729					28.4	20.5	R.VQAYEEPS'AS'SP'NGK.E
Positive cofactor 2 glutamine	MED15	S505S511					9.3	52.7	R.TPQNFS'VPS'PGPLNT'PNVPSSVMS'PAGSSQAEQQYLDK.L
Positive cofactor 2 glutamine	MED15	S505S517					7.7	27.6	R.TPQNFS'VPS'PGPLNTP'VNPSS'VMS'PAGSSQAEQQYLDK.L
Potassium channel tetramerisation domain	KCTD15 containing 15	S35					24.0	62.8	R.S'PV5PLAAQGIPLPAQLTK.S
Potassium channel tetramerisation domain	KCTD15 containing 15	S38					0.3	14.3	R.SPV5'PLAAQGIPLPAQLTK.S
Potassium channel tetramerisation domain	KCTD15 containing 15	S35S38					43.6	12.8	R.S'PV5'PLAAQGIPLPAQLTK.S
Potassium channel, calcium activated, KCNN3 intermediate/small conductance subfamily		S128					57.2	16.8	R.QG'S'QLNLNDHLHGSSSTATSGPGGGR.H
Potassium channel, voltage gated, KQT like subfamily, member 4	KCNQ5	S484					17.3	18.0	K.SW5'FNDR.T
Potassium channel, voltage gated, KQT like subfamily, member 4	KCNQ5	S482					12.2	17.5	K.S'W5FNDR.T
Potassium voltage gated channel, shaker KCNAB1 related subfamily, beta member 1		S153					7.6	16.0	R.RSS'LVITTK.I
Potassium voltage gated channel, shaker KCNAB1 related subfamily, beta member 1		S152					39.1	11.6	R.RS'SLVITTK.I
Potassium voltage-gated channel, KQT-like KCNQ5 subfamily, member 5		S831					2.7	62.8	K.SLS'VQNLIR.S
Potassium voltage-gated channel, KQT-like KCNQ5 subfamily, member 5		S829					9.3	51.0	K.S'LSVQNLIR.S
Pre mRNA cleavage complex II protein	PCF11 Pcf11	S705					100.0	52.9	R.S'PFNDRFPLK.R
Pre mRNA cleavage complex II protein	PCF11 Pcf11	S489S494					29.1	16.6	K.SRS'PIIHS'PK.R
Pre mRNA splicing factor	PRP17 CDC40	S46					15.9	100.2	K.SPSS'KPSLAVAVDS'APVAVK.E
Pre mRNA splicing factor	PRP17 CDC40	S43					8.4	50.2	K.S'PSKPSLAVAVDS'APVAVK.E
Pre mRNA splicing factor	PRP17 CDC40	S45					11.5	68.8	K.SP5'SKPSLAVAVDS'APVAVK.E
Pre mRNA splicing factor	PRP17 CDC40	S49					8.0	35.0	K.SPSSKPS'LAVAVDS'APVAVK.E
Pre-B-cell leukemia transcription factor	PBXIP1 interacting protein 1	S146S147S148					100.0	13.5	R.EEGRCS'S'S'DDD'T'DVDMEGLRR.R
PREDICTED: lateral signaling target protein 2 homolog isoform X5 [Homo sapiens]		S921					-0.9	16.0	K.SS'ARAAPR.S
PREDICTED: paired box protein Pax-2 isoform X5 [Homo sapiens]		S337						19.1	K.RS'YPR.LN
Prefoldin 4	PFND4	S125					16.4	36.0	K.FGS'NINLEADES.-
PRO1770	PELO	S374S380S381					100.0	44.0	R.FPVPELS'DQEGDS'S'S'EED.-
Probable ATP-dependent RNA helicase	DDX27 DDX27	S23S25					26.3	69.5	M.LADLGLIGTGEDDEVPVEPS'DS'GDEEEGPVLGR.R
Processing of precursor 5, ribonuclease	POP5 P/IRP subunit	S154					108.1	112.0	R.SCLLEEEES'GEEAAEAM.-
Profilin 1	PFN1	T93					-0.3	72.7	K.ST'GGAPT'FWTVTK.T
Progesterone receptor membrane	PGRMC1 component 1	S181					19.8	74.7	K.EGEEPTVYS'DEEEPKDESAR.K
Progesterone receptor membrane	PGRMC1 component 1	Y180					5.8	42.5	K.EGEEPTV'Y'SDEEEPKDESAR.K
Progesterone receptor membrane	PGRMC1 component 1	T178						22.2	K.EGEEPT'VYSDEEEPK.D
Progesterone receptor membrane	PGRMC2 component 2	S208					15.7	43.0	R.LLKPGEEPS'EYTDDEEDTKDHNKQD.-
Progesterone receptor membrane	PGRMC2 component 2	Y210					12.2	55.5	R.LLKPGEEPSE'Y'TDEEDTKDHNKQD.-
Programmed cell death 4	PDCD4	S94					8.2	44.5	R.SGLTVPT'S'PK.G
Programmed cell death 4	PDCD4	T93					32.3	44.2	R.SGLTVPT'S'PK.G
Programmed cell death 4	PDCD4	S457					100.0	23.6	R.FVS'EGDGGRL
Programmed cell death 5	PDCD5	S119					63.8	53.0	R.KVMD5'DEDDDY.-
Programmed cell death 5	PDCD5	Y125					21.6	67.3	R.RKVMSDEDDDY'Y.-
Programmed cell death 8	AIFM1	S286					10.5	42.4	R.S'LSAIDR.A
Programmed cell death 8	AIFM1	S288					15.1	32.6	R.SLS'AIDR.A
Proline glutamic acid leucine-rich protein 1	PELP1	S481					35.4	70.2	R.GS'PDGSLQTGKPSAPK.K
Proline-rich transmembrane protein 3	PRRT3	S924S928					15.9	35.3	R.HGLS'SVDS'LPLDELPSTVQLLPAPTAPDSTAAR.Q
Proline-rich transmembrane protein 3	PRRT3	S798S808					21.1	18.6	R.NGVGPAP'S'LELDRPPS'PINLSR.S
Proline-rich transmembrane protein 3	PRRT3	S925S928					5.1	38.9	R.HGLS'S'VDS'LPLDELPSTVQLLPAPTAPDSTAAR.Q
Proline-rich transmembrane protein 3	PRRT3	S924S925					7.7	25.6	R.HGLS'S'VDSLPLDELPSTVQLLPAPTAPDSTAAR.Q
Proline-rich transmembrane protein 3	PRRT3	S798S800S808					38.3	13.8	R.NGVGPAP'S'LELDRPPS'PINLSR.S
Proline-rich transmembrane protein 3	PRRT3	S815					100.0	37.7	R.S'IDAALFR.E
Proline/serine-rich coiled-coil 1	PSRC1	S65S70					100.0	17.6	R.LS'LGPLS'PEKLEILDEANRL
Proteasome 26S subunit	ATPase 4	PSMC4	S19S21T25					28.1	K.AQDEIPALS'VS'RPQT'GLSFLGPEPEDLEDLYSR.Y

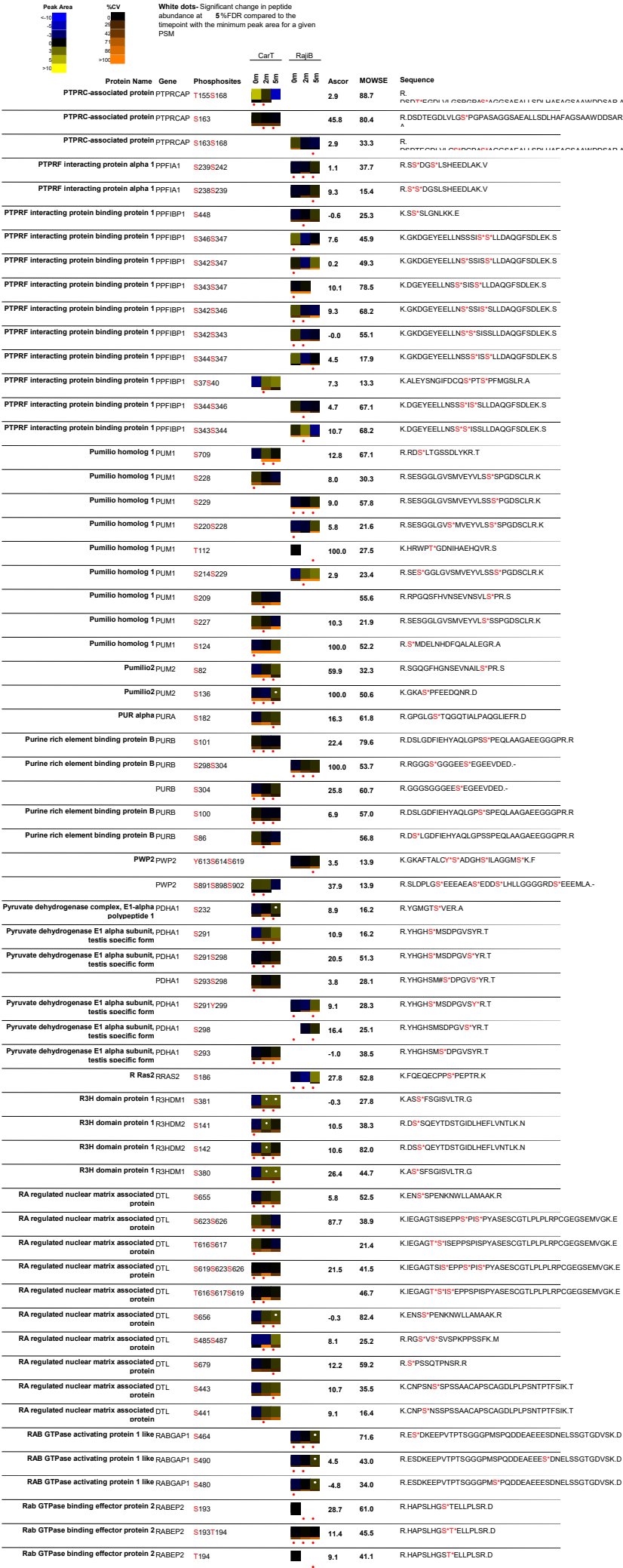
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
<10	0								
10	1								
20	2								
30	3								
40	4								
50	5								
60	6								
70	7								
80	8								
90	9								
>100	>10								
Protein Name	Gene	Phosphosites							
Proteasome 26S subunit ATPase 4	PSMC4	S19T25S28					29.6	37.2	K.AQDEIPAL <b>S</b> *VSRPQT* <b>GLS</b> *FLGPEPEDLEDLYSR.Y
Proteasome 26S subunit ATPase 4	PSMC4	S21T25S28					13.6	52.8	K.AQDEIPAL <b>S</b> *V <b>S</b> *RPQT* <b>GLS</b> *FLGPEPEDLEDLYSR.Y
Proteasome 26S subunit ATPase 4	PSMC4	S19S21					10.0	25.9	K.AQDEIPAL <b>S</b> *V <b>S</b> *RPQTGLSFLGPEPEDLEDLYSR.Y
Proteasome 26S subunit ATPase 4	PSMC4	S19S28					4.7	15.7	K.AQDEIPAL <b>S</b> *VSRPQT <b>GLS</b> *FLGPEPEDLEDLYSR.Y
Proteasome 26S subunit, non ATPase, 2	PSMD2	S16					92.8	68.3	R.DKAPVQ <b>PGQS</b> *PAAAPGGTDEKPSGK.E
Proteasome subunit alpha type 2	PSMA2	S7					10.8	77.3	R.GY <b>S</b> *FSLTTFSPSGKL
	PSMA3	S250					100.0	10.8	K.EE <b>DES</b> *DDDNM.-
Protein ABHD11 (Fragment)	ABHD11	S106					44.9	14.6	K.TAM <b>L</b> LALQR <b>S</b> *AQWKA
Protein arginine N methyltransferase 3	PRMT3	S25S27					100.0	86.9	R.GAVENEED <b>PELS</b> * <b>DS</b> *GDEAAWEDEDADLPHGK.Q
Protein disulfide isomerase P5	PDIAB	S428					100.0	80.0	R.DGELPVEDD <b>ILS</b> *DVELDOLGKDEL.-
Protein FAM117B	FAM117B	S220					24.4	88.9	R.T <b>S</b> <b>S</b> *LDTLAAPYLAGHWPR.D
Protein FAM117B	FAM117B	S219					-0.4	51.2	R.T <b>S</b> <b>S</b> *LDTLAAPYLAGHWPR.D
Protein FAM117B	FAM117B	T149S152T158					25.1	62.2	R.GSPRP <b>P</b> PPPP <b>LLGT</b> *V <b>S</b> * <b>PSSSPT</b> *HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	T149S151T158					25.3	52.8	R.GSPRP <b>P</b> PPPP <b>LLGT</b> *V <b>S</b> * <b>SPSSPT</b> *HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136T149S156					11.9	17.6	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> *V <b>SSPS</b> <b>S</b> *PTHLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136T149S154					27.1	40.3	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> *V <b>SSPS</b> <b>S</b> *SSPTHLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136T149T158					29.2	26.0	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> *V <b>SSPS</b> <b>SPT</b> *HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136S154T158					34.5	54.9	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> V <b>SSP</b> <b>S</b> * <b>SSPT</b> *HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136S151S156					27.4	40.6	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> V <b>S</b> * <b>SPSS</b> <b>S</b> *PTHLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S151S154					2.6	17.7	R.GSPRP <b>P</b> PPPP <b>LLGT</b> V <b>S</b> * <b>SPS</b> * <b>SSPT</b> HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136S151S154					10.5	22.1	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> V <b>S</b> * <b>SPS</b> * <b>SSPT</b> HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136T149S151					36.9		R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> *V <b>S</b> * <b>SPSSSPT</b> HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	T223					7.4	44.0	R.T <b>SSLDT</b> *LAAPYLAGHWPR.D
Protein FAM117B	FAM117B	S136S155T158					17.2	20.6	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> V <b>SSPS</b> <b>SPT</b> *HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136S154S156					18.1	18.9	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> V <b>SSPS</b> <b>S</b> * <b>SP</b> *THLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S10					39.3	129.0	R.NG <b>S</b> *PTPAGSLGGAVATAGGPGSRL
Protein FAM117B	FAM117B	S151S152T158					14.4	27.5	R.GSPRP <b>P</b> PPPP <b>LLGT</b> V <b>S</b> * <b>S</b> * <b>PSSSPT</b> *HLWTGEVSAAPPPAR.V
Protein FAM117B	FAM117B	S136T158T162					27.6	39.9	R.G <b>S</b> * <b>PRP</b> PPPP <b>LLGT</b> V <b>SSPSSSPT</b> *HLWT*GEVSAAPPPAR.V
Protein FAM189A1	FAM189A1	S18S20					100.0	22.2	R. <b>S</b> * <b>L</b> <b>S</b> *RLR.E
Protein HSPC148	CWC15	T110S121					45.3	78.3	R.LDQIPAA <b>N</b> LADDP <b>L</b> T*DEEDEFEE <b>S</b> *DDDDTAALLAEK.I
Protein inhibitor of activated STAT, 1	PIAS1	S510					4.5	46.6	R.T <b>P</b> <b>S</b> *LPADVTSY <b>INT</b> SLIQDYR.H
Protein inhibitor of activated STAT, 1	PIAS1	T508					12.2	86.3	R.T*PSLPADVTSY <b>INT</b> SLIQDYR.H
Protein inhibitor of activated STAT, 1	PIAS1	S503					18.8	66.7	K.GILSLPHQ <b>AS</b> *PVSR.T
Protein inhibitor of activated STAT, 1	PIAS1	S517					-2.9	51.1	R.TPSLPADV <b>T</b> <b>S</b> *Y <b>INT</b> SLIQDYR.H
Protein kinase B, beta	AKT2	S447T449					14.8	15.5	R.YFDD <b>E</b> FT <b>AGS</b> * <b>T</b> *ITPPDRYDSLGLLELDQR.T
Protein kinase C alpha	PRKCA	S226					48.5	75.7	R.STLNPQW <b>NE</b> <b>S</b> *FTK.L
Protein kinase C alpha	PRKCB	T497					19.5	92.0	R.T*FCGTPDYIA <b>PE</b> IAYQPYGK.S
Protein kinase C alpha	PRKCB	T501					1.8	39.4	R.TFCG <b>T</b> *PDYIA <b>PE</b> IAYQPYGK.S
Protein kinase C and casein kinase	PACSLN2 substrate in neurons 2	T321T325					12.3		K. <b>T</b> * <b>PD</b> YIA <b>PE</b> IAYQPYGK.S
Protein kinase C binding protein 1	ZMYND8	S445					22.4	45.0	R.R <b>S</b> * <b>L</b> SDMPR.S
Protein kinase C binding protein 1	ZMYND8	S426					35.4	60.2	K.LNFD <b>MTAS</b> *PK.I
Protein kinase C binding protein 1	ZMYND8	S510					20.7	65.8	K.TGQAGSL <b>SGS</b> *PKPFSPQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S508					14.9	58.1	K.TGQAGSL <b>S</b> *GSPKPFSPQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S506S515					9.2	24.4	K.TGQAG <b>S</b> *L <b>SG</b> SPK <b>PF</b> <b>S</b> *PQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S506S510					8.4	50.7	K.TGQAG <b>S</b> *L <b>SG</b> <b>S</b> *PKPFSPQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S510S515					18.1	35.6	K.TGQAGSL <b>SGS</b> *PK <b>PF</b> <b>S</b> *PQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S506					4.2	31.0	K.TGQAG <b>S</b> *L <b>SG</b> SPK <b>PF</b> SPQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S506S508					18.7	52.7	K.TGQAG <b>S</b> *L <b>S</b> *GSPKPFSPQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S515					20.4	30.8	K.TGQAGSL <b>SG</b> SPK <b>PF</b> <b>S</b> *PQLSAPITTK.T
Protein kinase C binding protein 1	ZMYND8	S508S515					13.6	24.8	K.TGQAGSL <b>S</b> *GSPK <b>PF</b> <b>S</b> *PQLSAPITTK.T
Protein kinase C delta	PRKCD	S506					9.2	60.4	R.A <b>S</b> *TFCGTPDYIA <b>PE</b> ILQGLK.Y
Protein kinase C delta	PRKCD	T507					11.2	94.2	R.A <b>S</b> <b>T</b> *FCGTPDYIA <b>PE</b> ILQGLK.Y
	PRKCD	S654					15.5	60.8	R.LSYS <b>D</b> KNLID <b>S</b> *MDQSAFAGFSFVNPK.F
Protein kinase C delta	PRKCD	Y646					5.3	73.8	R.L <b>S</b> <b>Y</b> *SDKNLID <b>S</b> MDQSAFAGFSFVNPK.F
Protein kinase C delta	PRKCD	Y646S664					54.2	82.2	R.L <b>S</b> <b>Y</b> *SDKNLID <b>S</b> MDQSAFAGFS*FVNPK.F
Protein kinase C delta	PRKCD	S645S664					33.4	79.9	R.L <b>S</b> <b>S</b> *YSDKNLID <b>S</b> MDQSAFAGFS*FVNPK.F
Protein kinase C delta	PRKCD	S645					23.9	44.7	R.L <b>S</b> <b>S</b> *YSDK.N
Protein kinase C delta	PRKCD	T511					0.1	21.6	R.A <b>S</b> TFCG <b>T</b> *PDYIA <b>PE</b> ILQGLK.Y
Protein kinase C delta	PRKCD	S647					5.8	44.8	R.L <b>S</b> <b>Y</b> <b>S</b> *DKNLID <b>S</b> MDQSAFAGFSFVNPK.F
Protein kinase C delta	PRKCD	S664					62.3	85.1	K.NLID <b>S</b> MDQSAFAGFS*FVNPK.F
Protein kinase C delta	PRKCD	S506T507					8.0	48.3	R.A <b>S</b> <b>T</b> *FCGTPDYIA <b>PE</b> ILQGLK.Y
Protein kinase C delta	PRKCD	S654S664					25.7	69.6	K.ARLSYS <b>D</b> KNLID <b>S</b> *MDQSAFAGFS*FVNPK.F



Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
Protein kinase substrate MK2S4	RCS01	Protein Name	Gene	Phosphosites	S116S127			14.2	30.1	K.AMV\$*PFHSPSTP\$S*PGVR.S
Protein kinase, cAMP dependent, regulatory tvee II. aloha	PRKAR2A	S99						40.7	55.9	R.RV\$*VCAETYNPDEEEEDTPR.V
	PRKAR2A	S78S80						85.8	51.4	R.VADAKG\$*E\$*EDEDLEVVPVSR.F
	PRKAR1A	S83						100.0	20.2	R.EDEIS*PPPPNPVK.G
Protein kinase, cAMP dependent, regulatorv. tvee II. beta	PRKAR2B	S83S85						100.0	50.4	K.GVNFAEPPMQ\$*D\$*EDGEEEEAAPADAGAFNAPVINR.F
Protein kinase, cAMP dependent, regulatorv. tvee II. beta	PRKAR2B	S114						49.8	73.6	R.RA\$*VCAEAYNPDEEEDDAESR.I
Protein kinase, lysine deficient 1 WNK1	WNK1	S2011						26.0	21.3	K.KEKPELSEPSHLNGP\$*SDPEAAFLSR.D
Protein kinase, lysine deficient 1 WNK1	WNK1	S2027S2029S2						49.9	24.4	R.DVDDG\$*G\$*PH\$*PHQLSK.S
Protein kinase, lysine deficient 1 WNK1	WNK1	S1978						100.0	50.3	K.EGPV\$*PPFMDLEQAVLPAVIPK.K
Protein kinase, lysine deficient 1 WNK1	WNK1	S2011S2012						6.8	34.4	K.EKPELSEPSHLNGP\$*S*DPEAAFLSR.D
Protein kinase, lysine deficient 4 WNK1	WNK1	S331						100.0	21.8	K.RA\$*FAK.S
Protein phosphatase 1 regulatory subunit 10	PPP1R10	S587						2.2	41.8	K.GPOGPGGGGINVQELT\$*IMGSPNSHPSEELLK.Q
Protein phosphatase 1 regulatory subunit 10	PPP1R10	S591						4.4	37.1	K.GPOGPGGGGINVQELT\$IMG\$*PN\$HPSEELLK.Q
Protein phosphatase 1 regulatory subunit 7	PPP1R7	S27						18.2	33.4	R.VESEE\$*GDEEGKH\$SGIVADLSEQSLK.D
Protein phosphatase 1 regulatory subunit 7	PPP1R7	S24S36						9.8	66.4	R.VES\$*EESGDEEGKH\$*SGIVADLSEQSLK.D
Protein phosphatase 1 regulatory subunit 7	PPP1R7	S27S36						6.0	55.2	R.VESEE\$*GDEEGKH\$*SGIVADLSEQSLK.D
Protein phosphatase 1 regulatory subunit 7	PPP1R7	S24S27						100.0	70.2	R.VES\$*EES\$*GDEEGKK.H
Protein phosphatase 1 regulatory subunit 7	PPP1R7	S27S37						-0.2	20.8	R.VESEE\$*GDEEGKH\$*SGIVADLSEQSLK.D
Protein phosphatase 1, regulatory subunit 11	PPP1R11	S73S7477S77						125.5	68.4	R.AFGES\$*T\$*E\$*DEEEEGCGTHCVR.G
Protein phosphatase 1, regulatory subunit 9B	PPP1R9B	S192						32.0	67.1	R.FNG\$*TEALDKLDADAVPTVSQLSAVFEKA
Protein phosphatase 1, regulatory subunit 9B	PPP1R9B	T193S205						17.1	28.3	R.FNG\$T*EALDKLDADAV\$*PTVSQLSAVFEKA
Protein phosphatase 1, regulatory subunit 9B	PPP1R9B	S205						3.7	23.3	R.FNG\$TEALDKLDADAV\$*PTVSQLSAVFEKA
Protein phosphatase 4, regulatory subunit 2	PPP4R2	S226						12.1	46.0	K.NHSDSSTSESEVSV\$*PLK.N
Protein phosphatase 4, regulatory subunit 2	PPP4R2	S223						11.2	16.9	K.NHSDSSTSESEV\$*SV\$PLK.N
Protein phosphatase inhibitor 2	PPP1R2	S121						55.5	151.5	R.IOEQE\$*SGEEDSDLSPEER.E
Protein phosphatase inhibitor 2	PPP1R2	S121S122						73.3	155.0	R.IOEQE\$*S*GEEDSDLSPEER.E
Protein phosphatase inhibitor 2	PPP1R2	Y75						2.3	54.0	K.IDEPSTPY*H\$MMGGDEEDACSDTEATEAMAPDILAR.K
	PPP1R2	S87						22.0	99.3	K.IDEPSTPYH\$MMGGDEEDAC\$*DTEATEAMAPDILAR.K
Protein phosphatase inhibitor 2	PPP1R2	S72						15.8	17.6	K.IDEP\$*TPYH\$MMGGDEEDACSDTEATEAMAPDILAR.K
	PPP1R2	T89						18.7	79.6	K.IDEPSTPYH\$MM#GGDEEDACSDT*EATEAMAPDILAR.K
Protein phosphatase inhibitor 2	PPP1R2	S77						-2.2	31.9	K.IDEPSTPYH\$*MMGGDEEDACSDTEATEAMAPDILAR.K
Protein phosphatase methyltransferase 1	PPME1	S42						80.2	99.6	R.DF\$*PVPWSQYFESMEDVEVENETGKDTFR.V
Protein phosphatase methyltransferase 1	PPME1	S47						2.3	16.2	R.DFSPVPW\$*QYFESMEDVEVENETGKDTFR.V
Protein phosphatase methyltransferase 1	PPME1	S52						11.1	30.6	R.DFSPVPWSQYF\$*MEDVEVENETGK.D
Protein phosphatase methyltransferase 1	PPME1	Y49						2.3	14.0	R.DFSPVPWSQY*FESMEDVEVENETGK.D
Protein RUFY3 (Fragment)	RUFY3	S50S55						24.9		R.EFCAARBDG\$*BAGAE*EDP\$E*IADECI*LYD\$V\$V\$CA\$E\$V\$D\$D\$D\$
Protein SET	SET	S7						100.0	36.7	K.RQ\$*PLPPQK.K
Protein strawberry notch homolog 1	SBNO1	S754S755						52.6	84.3	K.NM\$*S*GDDDDFN\$FLDES\$NEDDEND\$FWLIR.K
Protein strawberry notch homolog 1	SBNO1	S754S768						4.8	22.7	K.NM\$*SGDDDDFN\$FLDE\$*NEDDEND\$FWLIR.K
Protein transport protein SEC61 beta subunit	SEC61B	S17						7.4	41.9	M.PGPTPSGTNVGSSGR\$*PSK.A
Protein tyrosine phosphatase nonreceptor 7	PTPN7	S83						100.0	13.4	R.RG\$*NVALMLDVR.S
Protein tyrosine phosphatase nonreceptor 7	PTPN7	S398						52.7	20.9	R.GGMIQTAEQYQFLH\$HTLALYAGQLPEERS*P.-
Protein tyrosine phosphatase nonreceptor type 12	PTPN12	S435						100.0	22.9	R.NL\$*FEK.K
Protein tyrosine phosphatase receptor type C	PTPRC	S992						100.0	66.9	R.VPLKHELEMS*K.E
Protein tyrosine phosphatase receptor type C	PTPRC	S1297						16.8	23.5	K.EQAEGSEPTSGTEGPEH\$VNGPAS*PALNQG\$.-
Protein tyrosine phosphatase receptor type C	PTPRC	S973						95.6	55.3	R.N\$*NWPYDYNR.V
Protein tyrosine phosphatase receptor type C	PTPRC	S1291						7.4	11.4	K.EQAEGSEPTSGTEGPEH\$*VNGPASPALNQG\$.-
Protein tyrosine phosphatase receptor type C	PTPRC	S992S995S999						26.9		K.HELEMS*KE\$*EHD\$*DE\$*S*DDO\$*DSEEPSK.Y
Protein tyrosine phosphatase receptor type C	PTPRC	S999S1002S10						16.2	26.3	K.ESEHD\$*DE\$*S*DDO\$*DSEEPSK.Y
Protein tyrosine phosphatase, non receptor type 2	PTPN2	S304						39.1	54.2	K.EDLSPAFDH\$*PNK.I
PRP38 pre-mRNA processing factor 38 PRPF38B domain containing B	PRPF38B	S266S268						100.0	16.0	R.R\$*L\$*PR.R
PRP38 pre-mRNA processing factor 38 PRPF38B domain containing B	PRPF38B	S268						39.7	31.1	R.RSL\$*PR.R
	PRPF38B	S527S529						73.3	60.9	R.\$*Q\$*IEQESQEK.Q
PRP38 pre-mRNA processing factor 38 PRPF38B domain containing B	PRPF38B	S266						17.8	28.5	R.R\$*L\$PR.R
PRP38 pre-mRNA processing factor 38 PRPF38B domain containing B	PRPF38B	S318S320						100.0	21.9	R.\$*R\$*IDR.G
PRP38 pre-mRNA processing factor 38 PRPF38B domain containing B	PRPF38B	S529						19.9	47.9	R.\$Q\$*IEQESQEK.Q
PRP38 pre-mRNA processing factor 38 PRPF38B domain containing B	PRPF38B	S527						9.2	49.8	R.\$*Q\$IEQESQEK.Q
PRP4 pre-mRNA processing factor 4 PRPF4B homolog B	PRPF4B	S431S437						21.0	21.1	K.DA\$*PINRW\$*PTR.R
PRP4 pre-mRNA processing factor 4 PRPF4B homolog B	PRPF4B	Y849						52.3	76.6	K.LCDFGSASHVADNDITPY*LVLSR.F
PRP4 pre-mRNA processing factor 4 PRPF4B homolog B	PRPF4B	T847						9.3	68.5	K.LCDFGSASHVADNDIT*PYLVLSR.F
PRP4 pre-mRNA processing factor 4 PRPF4B homolog B	PRPF4B	S518S519S520						100.0	51.5	K.VEQE\$*S\$*DDNLED\$FVDEE\$EALIEQR.R
PRP4 pre-mRNA processing factor 4 PRPF4B homolog B	PRPF4B	S257						11.1	11.4	K.AR\$*PTDDKVK.I



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	Protein Name	Gene	Phosphosites						
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S354S356				100.0	38.0	R.S*LS*PKPR.D
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S277				91.7	54.5	R.KKS*PIINESR.S
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S294				100.0	35.0	R.S*PVDLR.G
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S292S294				100.0	26.1	K.S*RS*PVDLR.G
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		T576S578S580				100.0	27.1	R.T*RS*PS*PDILER.V
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S239S241				29.0	24.7	K.S*KS*PTLR.R
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S427S431S437				18.5	14.4	R.S*KDAS*PINRWS*PTR.R
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S636				5.4	24.8	K.LLAPDMFTES*DDMFAAYFDSAR.L
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S205S23S32				47.4	19.7	R.EQPEMEDANS*EKS*INEENGEVS*EDQSQNK.H
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S427S431T439				14.6	13.9	R.S*KDAS*PINRWSPT*RR
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S427S431				100.0	27.7	R.S*KDAS*PINR.W
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S131Y140				6.4	13.1	K.VQS*GMGLILQGY*ESGSEEEGEIHEK.A
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S131S144				5.3	14.2	K.VQS*GMGLILQGYESGS*EEEGEIEHK.A
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		Y140S142				4.8	27.0	K.VQSGMGLILQGY*SG*GSEEEGEIHEK.A
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		T259				16.6	12.3	R.SPT*DDKVK.I
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S431				100.0	18.9	K.DAS*PINR.W
	PRPF4B		S87S93				100.0	38.6	K.EIDAS*DKEGMS*PAKR.T
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S578S580				31.8	28.3	R.TRS*PS*PDILER.V
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S20S23				34.5	21.5	R.EQPEMEDANS*EKS*INEENGEVSEDQSQNK.H
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		Y140S144				4.5	21.8	K.VQSGMGLILQGY*ESGS*EEEGEIEHK.A
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		T634				45.0	44.5	K.LLAPDMFT*ESDDMFAAYFDSAR.L
	PRP4 pre-mRNA processing factor 4 PRPF4B homolog B		S142S144				9.4	11.3	K.VQSGMGLILQGYES*GS*EEEGEIEHK.A
	PRPF40A	T190S191S193					35.1	83.3	K.DSGNWDT*S*GS*ELS*EGELEK.R
	PRP40 pre-mRNA processing factor 40 PRPF40A homolog A		S141S143S146				100.0	26.0	R.HKS*DS*PES*DAEREK.D
	PRP40 pre-mRNA processing factor 40 PRPF40A homolog A		S143S146				5.7	13.9	R.HKSDS*PES*DAERE
	PRPF31 PRPF31		T455				17.6	67.0	R.SSGTASSVAF*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		T448T455				12.2	92.9	R.SSGT*ASSVAF*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		T448				-0.5	24.8	R.SSGT*ASSVAFPLQGLEIVNPQAAEK.V
	PRPF31 PRPF31		S450T455				14.6	77.7	R.SSGTAS*SVAF*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		S445T448				4.9	37.4	R.S*SGT*ASSVAFPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		S450				7.3	77.6	R.SSGTAS*SVAFPLQGLEIVNPQAAEK.V
	PRPF31 PRPF31		S445T455				3.6	40.1	R.S*SGTASSVAF*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		S451T455				11.9	51.1	R.SSGTASS*VAF*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		S450S451				11.5	65.9	R.SSGTAS*S*VAFPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		S446T455				-0.7	27.6	R.SS*GTASSVAF*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		T448S450				3.1	45.7	R.SSGT*AS*SVAFPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		T448S451T455				-2.3	12.0	R.SSGT*ASS*VAF*PLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		S445S446T448				-6.1	12.7	R.S*S*GT*ASSVAFPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		T448S450S451				5.0	20.6	R.SSGT*AS*S*VAFPLQGLEIVNPQAAEK.K
	PRPF31 PRPF31		S445S446				3.4	55.4	R.S*S*GTASSVAFPLQGLEIVNPQAAEK.K
	PRPP synthetase associated protein 2 PRPSAP2		S227				16.4	61.6	R.LGIAVIHGEAQDAESDLVDGRH*SPMIVR.S
	PRPP synthetase associated protein 2 PRPSAP2		S219				4.6	15.7	R.LGIAVIHGEAQDAES*DLVDGRHSPPMIVR.S
	PSD3 PSD3		S337				23.9	23.8	K.ES*SKVPR.H
	PSD3 PSD3		S338				8.9	22.7	K.ES*KVPR.H
	Pseudoautosomal gene XE7 AKAP17A		T639S640				-0.2	13.1	R.ST*S*PDHTR.S
	Pseudouridine synthase 1 PUS1		T426				47.1	72.7	K.VPSPLEGSEGDDGT*D.-
	Pseudouridine synthase 1 PUS1		S420T426				22.7	46.7	K.VPSPLEGS*EGDDGT*D.-
	PSPC1 PSPC1		S409				100.0	58.0	R.GAINMGDAFS*PAPAGNQPPPMGMNMNVR.A
	PTK2B protein tyrosine kinase 2 beta PTK2B		S375				100.0	58.6	K.RNS*LPQIPMLNLEAR.R
	PTK2B protein tyrosine kinase 2 beta PTK2B		S839T842				10.2	54.5	K.SLDPMV*YMNDS*PLT*PEKEVGYLEFGPPQKPRRL
	PTK2B protein tyrosine kinase 2 beta PTK2B		Y834T842				20.1	60.8	K.SLDPMV*Y*MNDSPLT*PEKEVGYLEFGPPQKPRRL
	PTK2B protein tyrosine kinase 2 beta PTK2B		S746T765				18.7	18.7	K.LQFQVPEGLCAS*SPTLTSPMEYPSPVNSLHT*PPLHR.H
	PTK2B protein tyrosine kinase 2 beta PTK2B		S778				100.0	18.8	K.RHS*MR.E
	PTK2B protein tyrosine kinase 2 beta PTK2B		S746S762				10.0	12.1	K.LQFQVPEGLCAS*SPTLTSPMEYPSPVNSLHTPPLHR.H
	PTK2B protein tyrosine kinase 2 beta PTK2B		S746				13.6	42.2	K.LQFQVPEGLCAS*SPTLTSPMEYPSPVNSLHTPPLHR.H
	PTPRC-associated protein PTPRCAP		S99				22.5	91.0	R.AELGS*TDNDLER.Q
	PTPRC-associated protein PTPRCAP		S153					57.8	R.AEEADPS*ETERN.VLGGSDRBAAGGSAEALLSPN.UAAGASAMWD
	PTPRC-associated protein PTPRCAP		S153T155					58.7	R.AEEADPS*ETERN.VLGGSDRBAAGGSAEALLSPN.UAAGASAMWD
	PTPRC-associated protein PTPRCAP		S163S172				6.1	39.9	R.DNTPEQNLGGSDRBAAGGSAEALLSPN.UAAGASAMWDSPAD.A
	PTPRC-associated protein PTPRCAP		T155				-0.3	90.4	R.DSDT*EGDLVLGSPGASAGGSAEALLSDLHAFAGSAAWDSAR.A
	PTPRC-associated protein PTPRCAP		S153T155S163					42.7	R.AEEADPS*ETERN.VLGGSDRBAAGGSAEALLSPN.UAAGASAMWD
	PTPRC-associated protein PTPRCAP		T155S172				1.4	28.8	R.DNTPEQNLGGSDRBAAGGSAEALLSPN.UAAGASAMWDSPAD.A



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	<10	>10			5	6	5	6			
Rab GTPase binding effector protein 2			RABEP2	S200					12.8	59.4	R.HAPSLHGS <sup>T</sup> TELLPLS <sup>R</sup> .D
Rab GTPase binding effector protein 2			RABEP2	T194S200					11.4	60.6	R.HAPSLHGS <sup>T</sup> TELLPLS <sup>R</sup> .D
Rab GTPase binding effector protein 2			RABEP2	S193S200					12.3	15.7	R.HAPSLHGS <sup>T</sup> TELLPLS <sup>R</sup> .D
Rab-coupling protein			RAB11FIP	S315					73.8	50.0	R.S <sup>T</sup> NVQINGNHVYLEQPEAK.G
Rab-coupling protein			RAB11FIP	S202					19.1	49.4	K.NKDSGSDTASAIIPSTTPSVDS <sup>S</sup> DDSEVVK.D
RAB11FIP			T154						64.0	76.3	R.NNMT <sup>T</sup> ASMFDLSMKD.K
Rab-coupling protein			RAB11FIP	S356					9.5	119.0	K.HLFS <sup>T</sup> STENLAAGSWK.E
Rab-coupling protein			RAB11FIP	T358					25.4	62.7	K.HLFSST <sup>T</sup> ENLAAGSWK.E
Rab-coupling protein			RAB11FIP	S357					20.1	102.1	K.HLFS <sup>T</sup> STENLAAGSWK.E
Rab-coupling protein			RAB11FIP	S156					27.6	79.7	R.NNMTAS <sup>T</sup> MFDLSMK.D
Rab-coupling protein			RAB11FIP	S296					26.9	76.3	K.SPIMADLNLSLPSIPEVAS <sup>T</sup> DDER.I
Rab-coupling protein			RAB11FIP	S234					6.7	38.6	K.TPLSQS <sup>T</sup> MSVLPTSKPEK.V
Rab-coupling protein			RAB11FIP	S287					12.9	69.5	K.SPIMADLNLS <sup>T</sup> LPSIPEVASDDER.I
Rab-coupling protein			RAB11FIP	S290					5.3	43.1	K.SPIMADLNLSLPS <sup>T</sup> IPEVASDDER.I
Rab-coupling protein			RAB11FIP	S280					12.2	15.4	R.TAS <sup>T</sup> TDLK.Q
Rab-coupling protein			RAB11FIP	S190S202					13.3	21.9	K.NKDSGSDTAS <sup>T</sup> AIPSTTPSVDS <sup>S</sup> DDSEVVK.D
Rab-coupling protein			RAB11FIP	S435					9.8	26.7	R.RSS <sup>T</sup> LLSLMTGK.K
Rab-coupling protein			RAB11FIP	S435S438					13.4	38.7	R.RSS <sup>T</sup> LLS <sup>T</sup> LMTGK.K
RAB11 interacting protein			RAB11FIP	S174					41.9	34.6	R.NNLS <sup>T</sup> ASMFDLSMK.D
RAB11 interacting protein			RAB11FIP	S176					7.8	46.0	R.NNLSAS <sup>T</sup> MFDLSMK.D
RAB14			Y99						-0.4	17.8	R.STY <sup>T</sup> NHLSWLTDAR.N
RAB3A interacting protein			RAB3IP	T289					15.2	44.7	R.NKST <sup>T</sup> SSAMSGHQDLSVIQPIVK.D
RAB3A interacting protein			RAB3IP	S288					15.3	14.0	R.NKS <sup>T</sup> TSSAMSGHQDLSVIQPIVK.D
RAB7			RAB7A	S72					75.4	63.7	R.FQS <sup>T</sup> LGVAFYR.G
Rabaptin 5			RABEP1	T486					22.0	47.9	K.AMTPEQEET <sup>T</sup> ASLLSSVTQGMESAYVSPSGYR.L
Rabaptin 5			RABEP1	S374S377					41.0	25.7	R.GS <sup>T</sup> VHS <sup>T</sup> LDAGLLPSGDPFSK.S
Rabaptin 5			RABEP1	S407S410					22.6	54.5	RAQS <sup>T</sup> TD <sup>S</sup> LGTSGLQSK.A
Rabaptin 5			RABEP1	T480					2.7	19.4	K.AMT <sup>T</sup> PEQEETASLLSSVTQGMESAYVSPSGYR.L
Rabaptin 5			RABEP1	S437T454S456					1.4	27.4	K.SAGNLDES <sup>T</sup> DFGPLVGADSVSENFDT <sup>T</sup> AS <sup>T</sup> LS <sup>T</sup> LQMPSGFMLTK. <sub>n</sub>
Rabaptin 5			RABEP1	S488					6.0	24.0	K.AMTPEQEETAS <sup>T</sup> LSSVTQGMESAYVSPSGYR.L
Rabaptin 5			RABEP1	S430S437S447					5.7	20.6	K.S <sup>T</sup> AGNLDES <sup>T</sup> DFGPLVGADS <sup>T</sup> VSENFDT <sup>T</sup> ASLGSLOMPSGFMLTK. <sub>n</sub>
Rabconnectin-3			DMXL2	S1857					49.2	78.9	R.NLAS <sup>T</sup> PEGTLATLGK.T
Rabconnectin-3 beta			WDR7	S1153					-0.4	52.3	R.SS <sup>T</sup> QIPEGFGLTSGGSNYSLAR.H
Rabconnectin-3 beta			WDR7	S1154					7.2	32.4	R.SS <sup>T</sup> QIPEGFGLTSGGSNYSLAR.H
Rabphilin 3A			RPH3A	S259					100.0	17.0	R.S <sup>T</sup> PAGLRRA
RAD18			RAD18	S99S103					15.8	45.3	R.NHLLQFALES <sup>T</sup> PAKS <sup>T</sup> PASSSSK.N
RAD18			RAD18	S99					100.0	64.6	R.NHLLQFALES <sup>T</sup> PAK.S
RAD18			RAD18	S471					39.7	55.9	R.DLLEEEAWEASHKNLDQTE <sup>S</sup> PR.Q
RAD21			RAD21	S153					100.0	62.2	R.EEVGNIS <sup>T</sup> LGENDFGDFGMDDR.E
RAD21			RAD21	Y105					21.4		R.EAAY <sup>T</sup> NAITLPEEFHDFDQPLPLDDIDVAQQFSLNQS.R.V
RAD23A			RAD23A	Y197					72.7		R.AVEY <sup>T</sup> LLTGIPGS <sup>T</sup> PEPEHGSVOESQVSEQPATEAAGENPLEFLR.D
RAD23A			RAD23A	S295					46.1		R. <sub>n</sub> QFGGRLNRPDPLANRPLGFGVAFERADNVAQMDPKY
RAD23A			RAD23A	S128					-2.8	17.8	R.EDKSPSEES <sup>T</sup> APTTSPESVSGVSPSSGSSGR.E
RAD23A			RAD23A	S123					11.8	34.2	R.EDKS <sup>T</sup> PSEESAPTTSPESVSGVSPSSGSSGR.E
RAD23A			RAD23A	S205					7.4	28.6	R.AVEYLLTGIPGS <sup>T</sup> PEPEHGSVOESQVSEQPATEAAGENPLEFLR.D
RAD23A			RAD23A	Y313					2.7	14.6	R. <sub>n</sub> QFGGRLNRPDPLANRPLGFGVAFERADNVAQMDPKY
RAD23B			RAD23B	S180					11.3	59.0	K.QEKPAEKPAETPVAT <sup>S</sup> PTATDSTSGDSSR.S
RAD23B			RAD23B	T155					22.0		K.QEKPAEKPAET <sup>T</sup> PVATSPTATDSTSGDSSR.S
RAD23B			RAD23B	T159					15.6	25.2	K.QEKPAEKPAETPVAT <sup>T</sup> SPTATDSTSGDSSR.S
RAD51 interacting protein			RAD51AP1	S21S27					7.1	16.7	R.HKKPVNYSQFDHS <sup>S</sup> DDDFVS <sup>T</sup> ATVPLNK.K
RAD51 interacting protein			RAD51AP1	S14S19					9.5	13.9	R.HKKPVNYS <sup>T</sup> QFDHS <sup>T</sup> DSDDDFVSATVPLNK.K.S
RAD51AP1			S19S21						27.2	28.7	K.KPVNYSQFDHS <sup>T</sup> DS <sup>T</sup> DDDFVSATVPLNK.K.S
RAD51 interacting protein			RAD51AP1	Y13S19					4.6	13.8	R.HKKPVNYS <sup>T</sup> QFDHS <sup>T</sup> DSDDDFVSATVPLNK.K.S
RAD51 interacting protein			RAD51AP1	Y13S21					3.0	27.8	R.HKKPVNYS <sup>T</sup> QFDHSD <sup>S</sup> DDDFVSATVPLNK.K.S
RAD51 interacting protein			RAD51AP1	S19S27					6.7	16.4	R.HKKPVNYSQFDHS <sup>T</sup> DSDDDFVS <sup>T</sup> ATVPLNK.K
RAD54-like 2			RAD54L2	S1061S1064					66.2	116.5	K.APDPQGLARPVS <sup>T</sup> PD <sup>S</sup> PEISELQQADYVAAR.E
RAD54-like 2			RAD54L2	S1089					12.2	45.5	R.QSSP <sup>T</sup> TNAALPGPAQLMDSSAVPGTALGTEPR.L
RAD9			RAD9A	S37S387					19.6	56.0	R.S <sup>T</sup> POGPPVLAEDS <sup>S</sup> EGEG.-
RAD9			RAD9A	S277					25.0	90.1	K.DSLLDGHFVLATLSOTDSHSQDLGS <sup>T</sup> PER.H
RAD9			RAD9A	S272					67.8		K.DSLLDGHFVLATLSOTDSHS <sup>T</sup> QDLGSPER.H
RAD9			RAD9A	S387					66.8	48.6	R.SPOGPPVLAEDS <sup>S</sup> EGEG.-
RAD9			RAD9A	S266					4.3	15.7	K.DSLLDGHFVLATLS <sup>T</sup> DTDSHSQDLGSPER.H

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		Protein Name	Gene	Phosphosites						
		Radial spokehead like 2	RSPH3	S530				15.0	22.6	R.RS\$*QER.K
		Raf kinase inhibitor protein	PEBP1	S52				22.4	75.4	K.NRPT\$*ISWDGLDSGKL
		Raf kinase inhibitor protein	PEBP1	T51				2.8	18.4	K.NRPT\$*ISWDGLDSGKL
		RAF1	RAF1	S259				9.6	71.2	R.STS*TPNVHVM\$*TTLPVDSR.M
		RAF1	RAF1	S29				6.5	104.1	K.DAVFDGSSCIS*PTIVQQFGYQR.R
		RAF1	RAF1	S25				5.3	58.1	K.DAVFDGS*SCISPTIVQQFGYQR.R
		RAF1	ARAF	S621				16.6	35.6	R.SAS*EPSLHR.T
		RAF1	RAF1	T258				8.2	76.0	R.ST*STPNVHVM\$*TTLPVDSR.M
		RAF1	RAF1	S296				6.8	91.1	R.SHSESASPSALS\$*SPNNLSPTGWSQPK.T
		RAF1	RAF1	S295				17.4	62.8	R.SHSESASPSALS\$*SPNNLSPTGWSQPK.T
		RAF1	RAF1	S26				10.3	38.3	K.DAVFDGS*CSPTIVQQFGYQR.R
		RAF1	RAF1	T260				7.4	25.8	R.STST*PNVHVM\$*TTLPVDSR.M
		RAF1	RAF1	S295S301				18.6	21.8	R.SHSESASPSALS\$*SPNNLS*PTGWSQPK.T
		RAF1	ARAF	S619				7.2	45.3	R.S*ASEPSLHR.T
		Raft linking protein	RFTN1	S199				80.7	59.6	R.GDHAS*LENEKPGTGDVCSAPAGR.N
		Raft linking protein	RFTN1	S220				76.1	35.5	R.NQ\$*PEPSSGPR.G
		Ral guanine nucleotide dissociation stimulator-like 3	RGL3	S361S366				100.0	11.7	K.RS\$*WGAV\$*R.E
		RalA binding protein 1	RALBP1	S92S93				70.9	122.0	R.TEGYAAFOED\$*SGDEAESPSK.M
		RalA binding protein 1	RALBP1	S30				17.7	57.3	R.TPSS*EEISPTKFGPLYR.T
		RalA binding protein 1	RALBP1	S29S34				17.3	59.5	R.TPS*SEEIS*PTKFGPLYR.T
		RalA binding protein 1	RALBP1	S29				13.4	31.1	R.TPS*SEEISPTKFGPLYR.T
		RalA binding protein 1	RALBP1	S29S30				6.1	43.7	R.TPS*\$*EEISPTKFGPLYR.T
		RalA binding protein 1	RALBP1	S30S34				13.4	56.9	R.TPSS*EEIS*PTKFGPLYR.T
		RalA binding protein 1	RALBP1	Y85S92				13.1	29.4	R.TEGY*AAFOED\$*SGDEAESPSK.M
		RalA binding protein 1	RALBP1	T27S29				6.6	33.3	R.T*PS*SEEISPTKFGPLYR.T
		RALBP1	REPS1	S656				30.0	18.5	R.LK\$*EDELRPVEDEHTQK.T
		RALBP1	REPS1	S220				6.1	43.3	R.RQ\$*SSYDDPWKI
		RALBP1	REPS1	S110S114S118S				42.3	22.6	R.TSADAQEPAS*PVV\$*PQQS*PPTS*PHTWRK
		RALBP1	REPS1	T429				51.2	26.3	R.TGSDHTNPT\$*PLLVKPSDLLEENK.I
		RALBP1	REPS1	S340				28.4	50.0	K.LIDLEDSADVGDPQGEVGYSG\$*PAEAPPSKS
		RALBP1	REPS1	S508				-0.3	35.5	R.S\$*SLDMNR.T
		RALBP1	REPS1	S378				19.7	54.6	R.SS\$*SQTLTQFDSNIAPADPTAIVHPVIPR.M
		RALBP1	REPS1	S378T383				13.1	15.6	R.SS\$*SQTLT*QFDSNIAPADPTAIVHPVIPR.M
		RALBP1	REPS1	S484S505				8.9	28.9	R.SH\$*GTSPDNTAPPPPPRPQPSHSR.S
		RALBP1	REPS1	S484T491				13.2	25.2	R.SH\$*GTSPDNT*APPPPPRPQPSHSR.S
		RALBP1	REPS1	S376				-1.7	54.6	R.S\$*SSQTLTQFDSNIAPADPTAIVHPVIPR.M
		RALBP1	REPS1	S378S379				7.6	63.0	R.SS\$*\$*SQTLTQFDSNIAPADPTAIVHPVIPR.M
		RALBP1	REPS1	T358				6.1	62.2	K.SPSMPSLNQT*WPELNQ\$SEQWETFSER.S
		RALBP1	REPS1	S349				7.2	13.4	K.S*PSMPSLNQTWPELNQ\$SEQWETFSER.S
		RALBP1	REPS1	T486S487				27.6	23.2	R.SHSGT*\$*PDNTAPPPPPRPQPSHSR.S
		RALBP1	REPS1	S484T486				5.1	15.7	R.SH\$*GT*SPDNTAPPPPPRPQPSHSR.S
		RALBP1	REPS1	S484S487S505				8.3	11.8	R.SH\$*GT\$*PDNTAPPPPPRPQPSHSR.S
		RALBP1	REPS1	S484T486S505				13.2	10.9	R.SH\$*GT*SPDNTAPPPPPRPQPSHSR.S
		RALBP1	REPS1	S110S118S122				12.5	15.8	R.TSADAQEPAS*PVV\$*PQQS*PPTS*PHTWRK
		RALBP1	REPS1	S110S114S118T				26.2	22.0	R.TSADAQEPAS*PVV\$*PQQS*PPT*SPHTWRK
		RALBP1	REPS1	S378S387				2.0	23.4	R.SS\$*SQTLTQFDS*NIAPADPTAIVHPVIPR.M
		RALBP1	REPS1	S354				21.6	57.7	K.SPSMPS*LNQTWPELNQ\$SEQWETFSER.S
		RALBP1	REPS1	S387				8.4	27.9	R.SSSSQTLTQFDS*NIAPADPTAIVHPVIPR.M
		RALBP1	REPS1	S487S505				10.7	13.0	R.SHSGT\$*PDNTAPPPPPRPQPSHSR.S
		RALBP1	REPS1	S68				-5.2	48.5	R.HAASYSSDS*ENQGSYSGVIPPMPGR.G
		RALBP1	REPS1	S110S118T121				15.4	15.2	R.TSADAQEPAS*PVV\$*PQQS*PPT*SPHTWRK
		RALBP1	REPS1	Y223				5.9	18.4	R.RQSSY*DDPWKI
		RALBP1	REPS1	S66				9.5	25.4	R.HAASY\$*DSENGSYSGVIPPMPGR.G
		RALBP1	REPS1	S430				7.2	29.9	R.TGSDHTNPTS*PLLVKPSDLLEENK.I
		RALBP1	REPS1	S114S118T121				15.6	12.8	R.TSADAQEPASPVV\$*PQQS*PPT*SPHTWRK
		RALBP1	REPS1	S509				9.1	19.9	R.SS\$*LDMNR.T
		RAM2	CDC47L	S21				100.0	95.2	K.EVADIFNAPS*DDEEFVGFR.D
		RAM2	CDC47L	T77T81				19.4	57.1	R.IFIEDT*DSET*EDFAGFTQSDUNGK.T
		RAM2	CDC47L	S195T196S197				10.1	31.7	R.EDS*TS*ES*EDDSRDE\$QESSDALLKR.T
		RAM2	CDC47L	S79T81				9.4	52.4	R.IFIEDTD6*ET*EDFAGFTQSDUNGK.T
		RAM2	CDC47L	T77S79				31.4	50.5	R.IFIEDT*DS*ETEDFAGFTQSDUNGK.T
		Ran binding protein 1	RANBP1	T13S14				11.2	20.9	K.DTHEDHDT*\$*STENTDESNDHPQFEPVSLPEQEI.K

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<10 10 20 40 60 70 80 90 >100	( 0 20 40 60 70 80 90 >100	Protein Name	Gene	Phosphosites			8.4	12.1	K.DTHEDHDTSTENT <sup>*</sup> DESNHDPQFEPIVSLPEQEI.K
		Ran binding protein 1	RANBP1	T18					
		Ran binding protein 1	RANBP1	T18S21			-1.7	10.8	K.DTHEDHDTSTENT <sup>*</sup> DESNHDPQFEPIVSLPEQEI.K
		Ran binding protein 1	RANBP1	S14115			5.6	21.8	K.DTHEDHDTST <sup>*</sup> TENTDESNHDPQFEPIVSLPEQEI.K
		Ran binding protein 1	RANBP1	T15S21			7.1	14.3	K.DTHEDHDTST <sup>*</sup> TENTDES <sup>*</sup> NHDPQFEPIVSLPEQEI.K
		Ran binding protein 2	RANBP2	T1156			4.0	20.1	K.NHET <sup>*</sup> DGGSAGHDODDDGHPFEPVPLPKIEVK.T
		Ran binding protein 2	RANBP2	S2900			64.1	38.3	K.VGEDEDGS <sup>*</sup> DEEVVHNEDIHFEPIVSLPEVEVK.S
		Ran binding protein 2	RANBP2	S1509			13.8	24.9	R.KQS <sup>*</sup> LPATSIPTPASFK.F
		Ran binding protein 2	RANBP2	S788			16.1	21.3	K.YSLSS <sup>*</sup> PSK.S
		Ran binding protein 2	RANBP2	S1400			-0.2	47.2	K.TS <sup>*</sup> PENVQDR.F
		Ran binding protein 3	RANBP3	S539			24.2	49.8	K. K.MADGEDTAAD <sup>*</sup> NEEDNS <sup>*</sup> MDPDLAAGDGTAAAGDPEGNGATTG
		Ran binding protein 3	RANBP3	S548			9.6	40.8	K. K.MADGEDTAAD <sup>*</sup> NEEDNS <sup>*</sup> MDPDLAAGDGTAAAGDPEGNGATTG
		Ran binding protein 3	RANBP3	S211			18.2	15.5	K.ALSQTVPSSTNGVSLPADCTGAVPA <sup>*</sup> S <sup>*</sup> PDTAAWR.S
		Ran binding protein 3	RANBP3	S101S108			4.5	22.1	R.SAGGSS <sup>*</sup> PEGGEDS <sup>*</sup> DREDGNYCPPVKR.E
		Ran binding protein 3	RANBP3	S333			62.7	51.6	R.VLSS <sup>*</sup> PPKLENVSSDANR.E
		Ran binding protein 3	RANBP3	S96S101S108			3.7	13.3	R.S <sup>*</sup> AGGSS <sup>*</sup> PEGGEDS <sup>*</sup> DREDGNYCPPVKR
		Ran binding protein 3	RANBP3	S533S539			15.5	12.9	K. K.MADGEDTAAD <sup>*</sup> NEEDNS <sup>*</sup> MDPDLAAGDGTAAAGDPEGNGATTG
		Ran binding protein 3	RANBP3	S100S108			16.2	12.0	R.SAGGS <sup>*</sup> SPEGGEDS <sup>*</sup> DREDGNYCPPVKR.E
		Ran binding protein 3	RANBP3	S100S101S108			13.8	12.1	R.SAGGS <sup>*</sup> S <sup>*</sup> PEGGEDS <sup>*</sup> DREDGNYCPPVKR
		Ran binding protein 3	RANBP3	S533				35.5	K. K.MADGEDTAAD <sup>*</sup> NEEDNS <sup>*</sup> MDPDLAAGDGTAAAGDPEGNGATTG
		Ran binding protein 3	RANBP3	S96S100S108			10.2	11.1	R.S <sup>*</sup> AGGS <sup>*</sup> SPEGGEDS <sup>*</sup> DREDGNYCPPVKR
		RAN binding protein 3-like	RANBP3L	T142			100.0	14.2	R.KT <sup>*</sup> FGHK.A
		RAN binding protein 9	RANBP9	S470S485			-0.7	15.3	K.S <sup>*</sup> QDSYPVSPRPFS <sup>*</sup> SPSM <sup>*</sup> PSHGMNIHNLASGK.G
		RANBP9	S477S482S487			19.0	11.3	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSM <sup>*</sup> S <sup>*</sup> PSHGMNIHNLASGK.G	
		RANBP9	S477S482S485			23.4	21.2	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G	
		RAN binding protein 9	RANBP9	S477S487			26.2	26.5	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSM <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S483S487			27.8	37.2	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSM <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S487S489			15.1	11.9	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSM <sup>*</sup> S <sup>*</sup> HGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S482S483S485			12.6	18.0	K.SQDSYPVSPRPFS <sup>*</sup> S <sup>*</sup> S <sup>*</sup> PS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S482			15.6	15.4	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSMSPSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S482S483			16.8	18.6	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> S <sup>*</sup> PSMSPSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S474S487			9.8	16.9	K.SQDSY <sup>*</sup> VPSPRPFS <sup>*</sup> SPSM <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S485			22.1	25.6	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S485S487			19.2	18.5	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S474S485			11.1	23.2	K.SQDSY <sup>*</sup> VPSPRPFS <sup>*</sup> SPS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S482S485			-1.1	13.2	K.SQDSYPVSPRPFS <sup>*</sup> S <sup>*</sup> S <sup>*</sup> PS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S483S485			4.1	11.9	K.SQDSYPVSPRPFS <sup>*</sup> S <sup>*</sup> PS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S483			18.5	12.0	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSMSPSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S482S483			3.1	10.9	K.SQDSYPVSPRPFS <sup>*</sup> S <sup>*</sup> S <sup>*</sup> PSMSPSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S470S473Y474				22.2	K.S <sup>*</sup> QDS <sup>*</sup> Y <sup>*</sup> VPSPRPFS <sup>*</sup> SPSM <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S485S487			6.0	11.6	K.SQDSYPVSPRPFS <sup>*</sup> SPS <sup>*</sup> MS <sup>*</sup> PSHGMNIHNLASGK.G
		RAN binding protein 9	RANBP9	S477S483S489			13.4	23.7	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSMSPS <sup>*</sup> HGMNIHNLASGK.G
		RANBP9	S477S482S489			9.9	15.1	K.SQDSYPV <sup>*</sup> S <sup>*</sup> PRPFS <sup>*</sup> SPSM <sup>*</sup> SPS <sup>*</sup> HGMNIHNLASGK.G	
		RAN, member RAS oncogene family	RAN	S135			100.0	27.4	K.S <sup>*</sup> IVFHR.K
		Rap guanine nucleotide exchange factor 6	RAPGEF6	S1590			8.4	19.9	K.LGVDVTADS <sup>*</sup> EADENEQVSA.-
		Rap guanine nucleotide exchange factor 6	RAPGEF6	S1094			9.8	22.4	R.RSS <sup>*</sup> LLNAK.K
		Rap guanine nucleotide exchange factor 6	RAPGEF6	S1494			16.9	27.9	K.GLUVYCVTS <sup>*</sup> PK.K
		RAP1 GTPase activating protein 1	RAP1GAP	S484			13.9	35.1	K.AAGISLNVGKS <sup>*</sup> PTR.K
		Rap1 interacting factor 1	RIF1	S1579			6.9	39.9	K.SNES <sup>*</sup> VDIQDQEEK.V
		Rap1 interacting factor 1	RIF1	S2196			12.1	47.2	R.SQEDEISS <sup>*</sup> PVNK.V
		Rap1 interacting factor 1	RIF1	S2144			60.1	76.6	K.VEEPSOCLASGTASIELIEDNNA <sup>*</sup> S <sup>*</sup> POK.L
		Rap1 interacting factor 1	RIF1	S2195			47.7	19.7	R.SQEDEISS <sup>*</sup> SPVNK.V
		Rap1 interacting factor 1	RIF1	S1454			100.0	60.5	K.S <sup>*</sup> PLHIKDDVLPK.Q
		APBB1IP	S526			-0.4	59.6	R.SS <sup>*</sup> DTSGSPATPLK.A	
		RAP80 UIMC1	S677			100.0	23.1	R.DLNESS <sup>*</sup> PVK.S	
		RAP80 UIMC1	S463			18.8	17.6	R.EVS <sup>*</sup> PGSR.D	
		Raptor RPTOR	S722			15.0	35.5	R.SVSS <sup>*</sup> YGNIR.A	
		Raptor RPTOR	S877			62.5	108.0	K.GVHIHQAGGS <sup>*</sup> PPASSTSSSSLTNDVAK.Q	
		Raptor RPTOR	T857S863			15.6	56.6	R.VLDTSSLT <sup>*</sup> QSAPAS <sup>*</sup> PTNK.G	
		Raptor RPTOR	S859S863			24.3	72.4	R.VLDTSSLTQS <sup>*</sup> APAS <sup>*</sup> PTNK.G	
		Raptor RPTOR	S863			19.3	71.8	R.VLDTSSLTQSAPAS <sup>*</sup> PTNK.G	
		Raptor RPTOR	S721			10.6	12.3	R.SVS <sup>*</sup> SYGNIR.A	
		Ras association (RalGDS/AF-6) domain	RASSF4 family 4	S91			15.1	34.3	R.RPS <sup>*</sup> CPLKEPSQNGNITAQGPSIQPVHKA

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM												
<10	0													
10	2													
20	4													
40	6													
60	7													
80	8													
>100	>10													
				CarT	RajiB									
Protein Name				Gene	Phosphosites			Ascor	MOWSE	Sequence				
RAS family, member RAB11B				RAB11A	S42			17.0	64.5	K.S*TIGVEFATR.S				
RAS guanyl nucleotide releasing protein 1				RASGRP1	T710S715			19.6	18.6	K.TAQDTLVLPSPF*T*SPCP.S*PVLVR.K				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S616S625S627			16.7	21.2	R.AQS*VSLEGSA.P.S*P.MHSH*HHR.A				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S616S625			25.4	65.3	R.AQS*VSLEGSA.P.S*PSP.MHSH*HHR.A				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S616			43.4	92.5	R.AQS*VSLEGSA.PSPSP.MHSH*HHR.A				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S178			45.4	45.8	R.RH.S*SLIDIDSVPTYK.W				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S638			26.0	32.1	R.A.F.S*FSLPRPGR.R				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S618S627			5.4	34.1	R.AQSV.S*LEGSA.PSP.S*P.MHSH*HHR.A				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S618			5.3	60.9	R.AQSV.S*LEGSA.PSPSP.MHSH*HHR.A				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S178S179			39.0	14.6	R.RH.S*S*SLIDIDSVPTYK.W				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S616S627			8.0	45.4	R.AQS*VSLEGSA.PSP.S*P.MHSH*HHR.A				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S622S625			16.0	33.2	R.AQSVSLEG.S*AP.S*PSP.MHSH*HHR.A				
RAS guanyl nucleotide releasing protein 2				RASGRP2	S622S627			13.9	20.1	R.AQSVSLEG.S*APSP.S*P.MHSH*HHR.A				
RAS guanyl releasing protein 3				RASGRP3	S559T580			10.8	10.8	R.APSLSG.HGS*LPGSPSLPAAQDEVFEFFPGV*AGHR.D				
Ras-GTPase activating protein binding G3BP2 protein 2					T227			18.6	68.3	K.STT*PPPAEPVSLPQEPKPR.V				
Ras-GTPase activating protein binding G3BP2 orolein 2					S141S149			64.3	122.5	R.YEDEVFGD.S*EPELDEE.S*EDEVEEEQEER.Q				
Ras-GTPase activating protein binding G3BP2 orolein 2					S149			23.5	34.9	R.YEDEVFGDSEPELDEE.S*EDEVEEEQEER.Q				
Ras-GTPase activating protein binding G3BP2 orolein 2					S141			13.8	32.8	R.YEDEVFGD.S*EPELDEESEDEVEEEQEER.Q				
Ras-GTPase activating protein binding G3BP2 protein 2					S225			8.4	23.9	K.S*TPPPAEPVSLPQEPKPR.V				
Ras-GTPase-activating protein SH3- G3BP1 domain-binding orolein					S232			22.2	130.8	K.S.S*S*PAPADIAQTQEDLR.T				
Ras-GTPase-activating protein SH3- G3BP1 domain-binding orolein					S149			62.9	84.4	R.YQDEVFGVFTEPQEE.S*EEEVEEPEER.Q				
Ras-GTPase-activating protein SH3- G3BP1 domain-binding protein					S231			-0.3	117.9	K.S.S*SPAPADIAQTQEDLR.T				
Ras-GTPase-activating protein SH3- G3BP1 domain-binding protein					S230			5.5	12.7	K.S*SPAPADIAQTQEDLR.T				
RB1 inducible coiled coil 1				RB1CC1	T238			-0.2	94.1	R.ST*ELVLS.PDMPR.T				
RBM15B				RBM15B	S552			12.1	37.3	R.TFLEGDWTS*PSK.S				
RBM15B				RBM15B	S231S232S233			12.6	12.3	R.RSS.S*S*S*AAASTPPPGPAPADPLGYLPLHGGYQYK.Q				
RBM15B				RBM15B	S265S267			100.0	18.8	R.S*LS*PVAAPPLREPR.A				
RBMX				RBMX	S208			39.3	26.3	R.DVYLS*PR.D				
RCAS1				EBAG9	S36			84.9	120.9	R.KLS*GDQITLPTTVDYSSVPK.Q				
RCAS1				EBAG9	T41			8.7	39.3	R.KLSGDQIT*LPTTVDYSSVPK.Q				
RE repeats encoding gene				RE	T144			-5.5	11.4	R.SPT*PALCDPPACSLPVASQPPQHLSEAGR.G				
RE repeats encoding gene				RE	S600			-0.4	23.1	R.TS*PNEDIR.S				
RE repeats encoding gene				RE	S1106S1113S111			27.1	18.5	K.EEALDDAEEPS*PPPPRS*PS*PEPTVVDTPSHASQSAR.F				
Receptor expressed in lymphoid tissues				RELL1 like 1	S109			9.5	47.2	K.IELND.S*VNENSDTVGQIVHYMK.N				
Receptor expressed in lymphoid tissues				RELL1 like 1	S109T116			4.4	20.3	K.IELND.S*VNENSDT*VGQIVHYMK.N				
Receptor expressed in lymphoid tissues				RELL1 like 1	S109S114			15.4	34.2	K.IELND.S*VNEN.S*DTVGGQIVHYMK.N				
Receptor expressed in lymphoid tissues				RELL1 like 1	S114T116			5.4	17.1	K.IELND.SVNEN.S*DT*VGQIVHYMK.N				
Receptor TNFRSF-interacting serine- threonine kinase 1				RIPK1	S320			117.6	101.9	R.MQS*LQLDCVAVPSSR.S				
RecQ protein like 3				BLM	S147			1.7	43.4	K.KLEFSSSPD.S*LSTINDWDDDFDTSK.S				
Regulating synaptic membrane exocytosis				RIMS3	S299S298			19.7	18.5	R.RL.S*QSS*LESATSPSCS.-				
Regulating synaptic membrane exocytosis				RIMS4	S6			10.9	15.1	M.ERSQS*R.L				
Regulator of G protein signaling				14RG	S14	S218			100.0	38.5	K.S*LPLGVEELQQLPPVEGPGGRPLRK.S			
Regulator of G protein signaling				14RG	S14	S40S45			1.5	48.0	R.GS*S*LSIH*S*LPSGPPSPFTEEQPVASWALSFER.L			
Regulator of G protein signaling				14RG	S14	S40S48			3.7	41.2	R.GS*S*LSIHS.LP.S*GPSPFPTEEQPVASWALSFER.L			
Regulator of G protein signaling				14RG	S14	S48S51S52			1.6	31.7	R.GSSLSIHS.LP.S*GPS*S*PFPTEEQPVASWALSFER.L			
Regulator of G protein signaling				14RG	S14	S39S40S42			11.1	49.5	R.GS*S*LS*IHSLPSGPSPFPTEEQPVASWALSFER.L			
Regulator of G protein signaling				14RG	S14	S39S40S46			4.0	29.7	R.GS*S*LSIHSLP.S*GPSPFPTEEQPVASWALSFER.L			
Regulator of G protein signaling				14RG	S14	S39S42S48			7.1	40.5	R.GS*S*LS*IHSLP.S*GPSPFPTEEQPVASWALSFER.L			
Regulator of G protein signaling				3RG	S3	S943			33.7	21.7	R.TH.S*EGSLQEP.R.G			
Regulator of G protein signaling				3RG	S3	S943S946			45.4	28.1	R.TH.S*EGS*LLQEPR.G			
Regulator of G protein signaling				3RG	S3	S916			3.1	27.4	K.R.S*SMIETGQGAEGGLSLR.V			
Regulator of nonsense transcripts				1UP	F1	S1107			37.7	124.5	K.SQIDVALS*QDSTYQGER.A			
Regulator of nonsense transcripts				1UP	F1	S1127			28.2	72.4	R.AYOHGGVTGLS*QY.-			
Regulator of nonsense transcripts				1UP	F1	S1107S1110			20.4	98.5	K.SQIDVALS*QDS*TYQGER.A			
Regulator of nonsense transcripts				1UP	F1	Y1129			12.1	71.6	R.AYOHGGVTGLSQY*.-			
Regulatory factor X				1RFX	1	S117			20.7	55.9	R.ASETVS*EASPGSTASQTGVPTQVQQVQGTQQR.L			
Regulatory factor X				1RFX	1	S120			4.6	36.8	R.ASETVSEAS*PGSTASQTGVPTQVQQVQGTQQR.L			
Regulatory factor X 3 influences HLA class II expression				REFX3	S664			54.3	85.6	R.VAQATGETPIAMGEFGDLNAV.S*PGNLDK.D				
Regulatory factor X domain containing 2				REFX7	S1178			35.4	76.4	R.NL.S*GSTLYPVSNIPR.S				
Renal cell carcinoma, papillary				1PRCC	S157S159			45.9	43.8	K.IAAPELHKGD.S*DS*EEDEPTK.K				
Renal cell carcinoma, papillary				1PRCC	S287			43.5	77.0	K.QITQEDDS*DEEVAPENFFSLPEK.A				
Replication factor C				1RFC1	S108T110			-0.1	47.8	R.QDPVTVYIS*ET*DEEDDFMCKK.A				

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM									
<10	0			CarT	RajiB						
10-20	1-2			5 6 6 6	5 6 6 6	Ascor	MOWSE	Sequence			
20-30	3-4	Protein Name	Gene	Phosphosites		10.2	37.5	K.NKPLS*PIKLTPTS*VLDFYGT*GSVQR.S			
30-40	5-6	Replication factor C1 RFC1		S156S164T171							
40-50	7-8	Replication factor C1 RFC1		S281S283		15.6	23.5	R.S*YS*PR.S			
50-60	9-10	Replication factor C1 RFC1		S368		28.9	52.1	K.ESVS*PEDSEK.K			
60-70	>10	Replication factor C1 RFC1		S69S71		43.7	84.3	R.IIVDS*DS*ESEETLQVK.N			
		Replication factor C1 RFC1		Y67S71		19.1	85.2	R.IIV*DSDS*ESEETLQVK.N			
		Replication factor C1 RFC1		S156T163		14.5	32.3	K.NKPLS*PIKLTP*SVLDYFGTGSVQR.S			
		Replication factor C1 RFC1		S156T161		26.8	65.7	K.NKPLS*PIKLTP*PTSVLDFYFGTGSVQR.S			
		Replication factor C1 RFC1		S156T161T171		14.3	40.4	K.NKPLS*PIKLTP*SVLDYFGT*GSVQR.S			
		Replication factor C1 RFC1		S281Y282		14.0	17.3	R.S*Y*SPR.S			
		Replication factor C1 RFC1		Y282S283		10.6	26.2	R.S*Y*SPR.S			
		Replication factor C1 RFC1		T161T171		18.2	40.7	K.LT*PTSVLDYFGT*GSVQR.S			
		Replication factor C1 RFC1		T163T171		9.0	44.1	K.LTPT*SVLDYFGT*GSVQR.S			
		Replication factor C1 RFC1		S156S164S173		6.3	51.9	K.NKPLS*PIKLTPTS*VLDFYFGTS*VQR.S			
		Replication factor C1 RFC1		T163S164T171		5.3	41.8	K.NKPLSPIKLTPT*S*VLDFYGT*GSVQR.S			
		REST corepressor RCOR1		S457		24.1	16.1	K.S*PDNSIK.M			
		REST corepressor RCOR1		S257		100.0	46.8	R.EREES*EDELEEANGNNPIDIEVDQNK.E			
		REST corepressor 3 RCOR3		S156S171		24.5	31.1	R.HNQGDS*DDVEETHPMGDND*S*DYDPKK.E			
		Reticulon 2 RTN2		S94		10.6	12.1	R.SVS*EPR.D			
		RTN4		S182		10.3	41.3	K.RRGSS*GSVDETLFALPAASEPVIR.S			
		RTN4		S184		12.2	48.5	K.RRGSSGS*VDETLFALPAASEPVIR.S			
		Reticulon 4 RTN4		T188		10.5	17.3	R.RGSSGSVDET*LFALPAASEPVIR.S			
		Reticulon 4 RTN4		S181S182		16.4	48.9	R.RGS*S*GSVDETLFALPAASEPVIR.S			
		RTN4		S181		9.1	43.8	K.RRGSS*GSVDETLFALPAASEPVIR.S			
		Reticulon 4 RTN4		S184T188		5.5	12.5	R.RGSSGS*VDET*LFALPAASEPVIR.S			
		Reticulon 4 RTN4		S181S184		10.6	41.2	R.RGS*GS*VDETLFALPAASEPVIR.S			
		RTN4		S182S184		3.1	21.9	R.GS*S*GS*VDETLFALPAASEPVIR.S			
		Reticulon 4 RTN4		S181T188		21.8	13.6	K.RRGSS*GSVDETL*LFALPAASEPVIR.S			
		Retinoblastoma 1 RB1		S249		82.7	50.4	K.TAVIPINGS*PR.T			
		Retinoblastoma 1 RB1		T823T826		21.5	34.6	K.ISEGLP*PT*TKMT*PR.S			
		Retinoblastoma 1 RB1		T373		124.8	44.3	R.KSNLDEEVNIPPH*TPVR.LT			
		Retinoblastoma 1 RB1		T821T826		18.9	20.0	K.ISEGLP*PT*TKMT*PR.S			
		Retinoblastoma 1 RB1		T353		17.2	24.3	K.TLQTDSDISFET*QRTPR.K			
		Retinoblastoma 1 RB1		S788		18.0	51.7	R.S*PYKFPSS*PLR.I			
		Retinoblastoma 1 RB1		S788S794		26.8	36.3	R.S*PYKFP*S*PLR.I			
		Retinoblastoma 1 RB1		S788S795		10.0	25.2	R.S*PYKFPSS*PLR.I			
		Retinoblastoma 1 RB1		Y790S794		24.3	39.9	R.SPY*KFPS*PLR.I			
		RB1		T9			58.4	R.KT*ATAAAAAEPPAPPPPPPEEDPEQDS*GPEDLPLVR.L			
		Retinoblastoma 1 RB1		S807S811		55.8	55.3	R.IPGGNIYS*PLKS*PYK.I			
		RB1		S37		80.2	47.6	R.KTAATAAAAAEPPAPPPPPPEEDPEQDS*GPEDLPLVR.L			
		Retinoblastoma 1 RB1		Y606S612		7.3	17.9	K.DREGPTDHLESACPLN*PLQNNHTAADM*Y*LS*PVRS*PK.K			
		Retinoblastoma 1 RB1		S608S612		20.9	31.7	K.DREGPTDHLESACPLN*PLQNNHTAADM*Y*LS*PVRS*PK.K			
		Retinoblastoma 1 RB1		T601		8.2	38.4	K.DREGPTDHLESACPLN*PLQNNHT*AADMY*LS*PVRS			
		Retinoblastoma 1 RB1		S788S794S807		37.8	23.9	R.S*PYKFP*S*PLRIPGGNIYS*PLK.S			
		Retinoblastoma 1 RB1		S838		33.2	34.1	R.I.LVSIGES*FGTSEK.F			
		Retinoblastoma 1 RB1		S855		100.0	58.7	K.INQMVCN*S*DR.V			
		Retinoblastoma 1 RB1		S807S811T821		13.1	29.3	R.IPGGNIYS*PLKS*PYKISEGLPT*PTK.M			
		Retinoblastoma 1 RB1		S807		44.9	65.7	R.IPGGNIYS*PLK.S			
		Retinoblastoma 1 RB1		T583S588			16.1	K.DREGPT*DHLES*ACPLN*PLQNNHTAADM*Y*LS*PVRS*PK.K			
		Retinoblastoma 1 RB1		S794		71.6	30.4	R.SPYKFP*S*PLR.I			
		Retinoblastoma 1 RB1		S811Y813		5.9	13.4	R.IPGGNIYS*PLKS*PYK.I			
		Retinoblastoma 1 RB1		T601S612		5.9	14.9	R.EGPTDHLESACPLN*PLQNNHT*AADMY*LS*PVRS*PK.K			
		Retinoblastoma 1 RB1		S807Y813		8.9	12.7	R.IPGGNIYS*PLKSPY*K.I			
		Retinoblastoma 1 RB1		S608		3.8	12.2	R.EGPTDHLESACPLN*PLQNNHTAADM*Y*LS*PVRS			
		Retinoblastoma 1 RB1		S624		6.5	19.6	R.VNS*танаetQATSAFQTQKPLK.S			
		Retinoblastoma 1 RB1		S350		28.3	15.3	K.TLQTDSDIS*S*FETQRTPR.K			
		Retinoblastoma 1 RB1		Y790		9.2	47.2	R.SPY*KFPSS*PLR.I			
		Retinoblastoma 1 RB1		Y606S608S612		1.1	16.0	R.EGPTDHLESACPLN*PLQNNHTAADM*Y*LS*PVRS*PK.K			
		Retinoblastoma 1 RB1		T841		13.8	21.1	R.I.LVSIGES*FGT*SEK.F			
		Retinoblastoma 1 RB1		Y790S795		5.8	32.3	R.SPY*KFPSS*PLR.I			
		Retinoblastoma 1 RB1		Y606S608		21.5	10.7	K.DREGPTDHLESACPLN*PLQNNHTAADM*Y*LS*PVRS*PK.K			
		Retinoblastoma 1 RB1		S788S795S807		9.6	11.6	R.S*PYKFPSS*PLRIPGGNIYS*PLK.S			
		Retinoblastoma associated factor 600 UBR4		S2718		40.2	30.8	R.HVTLPS*SPR.S			

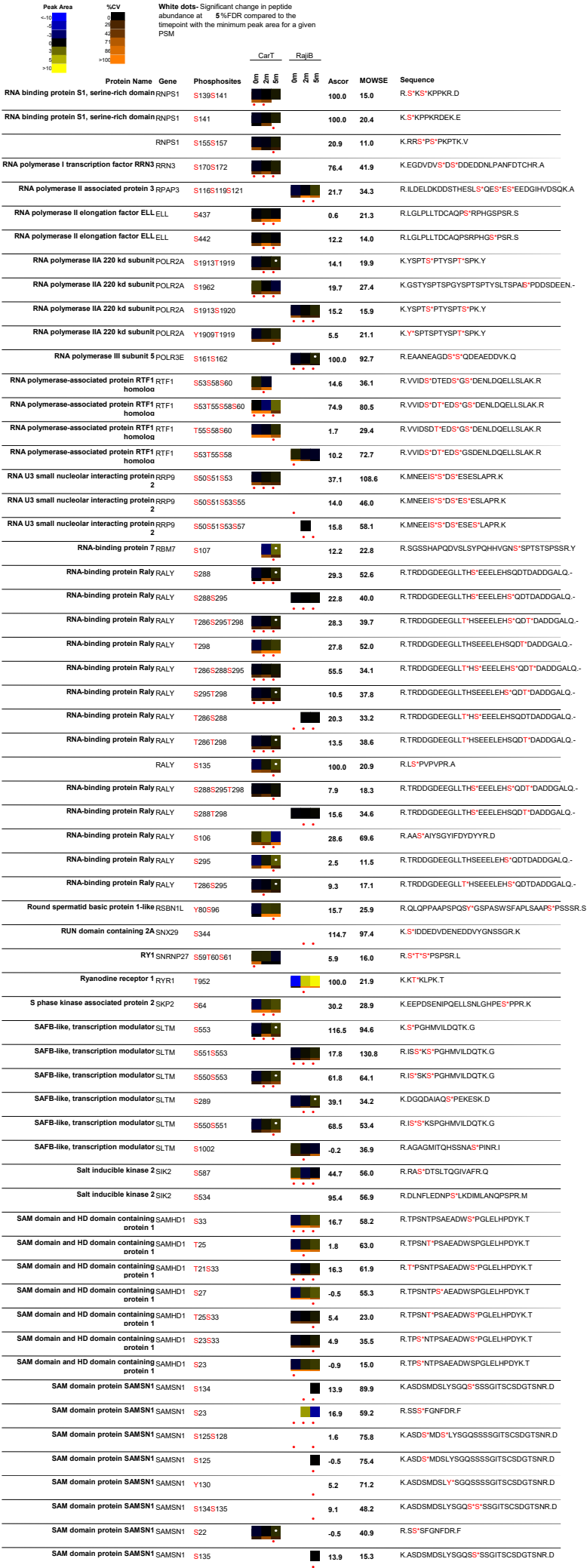
Peak Area	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM	Protein Name	Gene	Phosphosites	CarT	RajIB	Ascor	MOWSE	Sequence
<div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>40</div> <div>60</div> <div>70</div> <div>80</div> <div>&gt;100</div> </div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>40</div> <div>60</div> <div>70</div> <div>80</div> <div>&gt;100</div> </div> </div>		Retinoblastoma associated factor 600	UBR4	S2719			8.2	26.3	R.HVTLPS*PR.S
		Retinoblastoma binding protein 2	KDMA5A	S1111			109.0	101.6	K.DLDLEPLS*OLEEGLEETR.D
		Retinoblastoma binding protein 5	RBBP5	S350			100.0	66.8	R.ES*EFDIEDEK.S
		Retinoblastoma binding protein 5	RBBP5	S525			29.3	28.2	K.VQAELS*QPLTAGGAISELL.-
		Retinoblastoma binding protein 6	RBBP6	S1277			11.8	33.1	K.VTGTEGSSSTLVDTSTSGGS*PVRK.S
		Retinoblastoma binding protein 6	RBBP6	S1179			65.5	71.4	K.LEVTEVYKPS*PK.R
		Retinoblastoma binding protein 6	RBBP6	S1328			100.0	79.5	K.WKDDFES*EEEDVK.S
		Retinoblastoma binding protein 6	RBBP6	S873			46.9	34.3	R.NS*PFTR.G
		Retinoblastoma binding protein 6	RBBP6	S770S772			100.0	33.4	R.S*RS*PQAFR.G
		Retinoblastoma binding protein 6	RBBP6	S861			100.0	21.3	R.ENFS*PER.F
		Retinoblastoma like 1	RBL1	S988T997			16.2	14.9	R.ISQQHSIYIS*PHKNGSGLT*PR.S
		Retinoblastoma like 1	RBL1	S749S762			25.7	36.6	K.VKS*PVSLTAHSLIGA*PK.Q
		Retinoblastoma like 2	RBL2	T1065S1068			11.7	31.8	R.IQLSQNHVPYISPHKNET*MLS*PR.E
		Retinoblastoma like 2	RBL2	S1059S1068			9.8	21.2	R.IQLSQNHVPYIS*PHKNETMLS*PR.E
		Retinoblastoma like 2	RBL2	S1059T1065			13.9	32.9	R.IQLSQNHVPYIS*PHKNET*MLSPR.E
		RFFL ring finger and FYVE-like domain containing 1	hCG_2039	S240			19.2	75.9	R.RAS*LSLDLTLEDIEGLTVR.Q
		RFFL ring finger and FYVE-like domain containing 1	hCG_2039	S242			6.1	137.1	R.ASLS*DLTDLEDIEGLTVR.Q
		RFFL ring finger and FYVE-like domain containing 1	RFFL	S226S229S232			18.2	42.3	R.VPAEDETQS*IDS*EDS*FVPGR.R
		RFFL ring finger and FYVE-like domain containing 1	hCG_2039	T245			-0.2	15.2	R.ASLSDLT*DLEDIEGLTVR.Q
		RGD, leucine-rich repeat, tropomodulin and CARMIL2 proline-rich containin protein	S1362				100.0	23.2	R.AVS*VHEDQLQAPAEPLR.L
		Rho family-interacting cell polarization RIPOR1 regulator 1	RIPOR1	S20			19.6	19.8	R.THS*MMSLSVRPQR.R
		RHO GDP dissociation inhibitor beta	ARHGDIIB	S145			9.0	30.6	K.ATFMVGS*YGRPEEYEFLTPVEEAPK.G
		Rho GTPase activating protein 11A	ARHGAP1	S285			60.5	42.7	R.RQS*VGDFVSGALNK.F
		Rho GTPase activating protein 12	ARHGAP1	T231S240			19.1	33.5	R.ATT*PPNQGRPD*S*PVYANLQELK.I
		Rho GTPase activating protein 15	ARHGAP1	S43			61.5	58.7	K.S*MILTQVGK.V
		Rho GTPase activating protein 15	ARHGAP1	S212			12.0	51.1	R.SSS*TELLSHYDSIK.E
		Rho GTPase activating protein 15	ARHGAP1	S64			100.0	21.5	R.NHS*QHILK.D
		Rho GTPase activating protein 15	ARHGAP1	T213			12.6	39.8	R.SSST*ELLSHYDSIK.E
		Rho GTPase activating protein 17	ARHGAP1	S598			18.6	61.1	R.SPS*PPTQHTGQPPGQPSAPSQLSAPLR.R
		Rho GTPase activating protein 17	ARHGAP1	S517			32.7		R.NNS*QIASGQNQPQAAAGSHQLSMGQPHNAAGPSPHTLR.R
		Rho GTPase activating protein 17	ARHGAP1	S596S598			40.0	46.0	R.S*PS*PPTQHTGQPPGQPSAPSQLSAPLR.R
		Rho GTPase activating protein 17	ARHGAP1	S596T601			11.6	33.7	R.S*PSPPT*QHTGQPPGQPSAPSQLSAPLR.R
		Rho GTPase activating protein 17	ARHGAP1	S547			15.6	31.0	R.NNSQIASGQNQPQAAAGSHQLSMGQPHNAAGP*S*PHTLR.R
		Rho GTPase activating protein 17	ARHGAP1	S598T601			16.7	44.4	R.SPS*PPT*QHTGQPPGQPSAPSQLSAPLR.R
		Rho GTPase activating protein 17	ARHGAP1	S598T604			3.4	39.2	R.SPS*PPTQHT*GQPPGQPSAPSQLSAPLR.R
		Rho GTPase activating protein 17	ARHGAP1	T604			24.1	35.2	R.SPSPPTQHT*GQPPGQPSAPSQLSAPLR.R
		Rho GTPase activating protein 17	ARHGAP1	S596T604			-1.9	16.7	R.S*PSPPTQHT*GQPPGQPSAPSQLSAPLR.R
		Rho GTPase activating protein 25	ARHGAP2	S487			13.8	28.8	R.TMS*QDLR.Q
		Rho GTPase activating protein 30	ARHGAP3	S630			26.0	83.0	K.GS*GSLEGEAAGCGR.Q
		Rho GTPase activating protein 30	ARHGAP3	S630S632			100.0	71.4	K.GS*GS*LEGEAAGCGR.Q
		Rho GTPase activating protein 30	ARHGAP3	S875			17.0	76.9	R.S*YAFETQANPGK.G
		Rho GTPase activating protein 30	ARHGAP3	S632			-0.1	86.0	K.GSGS*LEGEAAGCGR.Q
		Rho GTPase activating protein 30	ARHGAP3	Y876			-0.3	79.5	R.SY*AFETQANPGK.G
		Rho GTPase activating protein 30	ARHGAP3	S785			13.9	68.6	R.NGSLS*FDAAVALAR.D
		Rho GTPase activating protein 30	ARHGAP3	S291			100.0	33.6	R.S*IFNLGR.S
		Rho GTPase activating protein 9	ARHGAP9	S456			54.2	65.9	R.LSGSGPAELS*AGEDEESELSVKPLRL.L
		Rho guanine nucleotide exchange factor 1	ARHGEF1	S384S388			27.4	35.9	R.SES*LRVS*DR.R
		Rho guanine nucleotide exchange factor 1	ARHGEF1	S25			102.6		R.DAAS*GGRSDDI*VDSIGAFEDENIG*ETUSEEAGQDQI*EAV
		Rho guanine nucleotide exchange factor 1	ARHGEF1	S410			-0.4	62.3	R.SRS*DVMDPSSATAVLGPAP.R
		Rho guanine nucleotide exchange factor 1	ARHGEF1	S29			-0.5	26.5	R.DAAS*GGRSDDI*VDSIGAFEDENIG*ETUSEEAGQDQI*EAV
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S174			32.1	82.2	R.ILSQS*TDSLNMNR.N
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S172			13.4	98.4	R.ILS*QSTDSLNMNR.N
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S122			25.6	52.2	R.ERPSS*AIYPSDSFR.Q
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S151			12.6	155.4	K.SVS*TTNIAGHFNDESPLGLR.R
		ARHGEF2	S151S163				33.2	56.4	K.SVS*TTNIAGHFNDES*PLGLR.R
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S885			66.7	125.0	R.S*LPAGDALYLSFNPPQPSR.G
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S955S959			100.0	22.4	R.LS*PPHS*PR.D
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S174S177			16.9	50.7	R.ILSQS*TD*LNMR.N
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S163			17.6	21.9	K.SVSTTNIAGHFNDES*PLGLR.R
		Rho guanine nucleotide exchange factor 2	ARHGEF2	Y893			25.4	66.2	R.SLPAGDALY*LSFNPPQPSR.G
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S174T175			13.0	48.2	R.ILSQS*T*DSLNMNR.N
		Rho guanine nucleotide exchange factor 2	ARHGEF2	S695			6.8	30.7	R.EPALPLEPDSGGNTS*PGVTANGEAR.T



Peak Area		%CV		White dots: Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a given PSM				Ascor	MOWSE	Sequence
				CarT	RajiB					
Rho guanine nucleotide exchange factor 2	ARHGEF2	S690						4.8	25.3	R.EPALPLEPDS*GGNTSPGVTANGEAR.T
Rho guanine nucleotide exchange factor 2	ARHGEF2	S151T153						9.4	15.9	K.SVS*TT*NIAGHFNDESPGLGR.I
Rho guanine nucleotide exchange factor 2	ARHGEF2	T678						100.0	48.5	K.DLLVGPGEVLLT*PR.E
Rho guanine nucleotide exchange factor 2	ARHGEF2	S172T175						4.1	11.3	R.ILS*QST*DSLNM.R
Rho guanine nucleotide exchange factor 2	ARHGEF2	S931						100.0	48.0	R.QELGS*PEER.L
Rho guanine nucleotide exchange factor 2	ARHGEF2	S151T152						5.9	18.3	K.SVS*TT*NIAGHFNDESPGLGR.I
Rho guanine nucleotide exchange factor 2	ARHGEF2	S122S127						18.9	11.2	R.ERPSS*AIYPS*DSFRQSLGSR.R
Rho guanine nucleotide exchange factor 2	ARHGEF2	T152						8.0	88.2	K.SVST*TTNIAGHFNDESPGLGR.R
Rho guanine nucleotide exchange factor 2	ARHGEF2	T153S163						14.3	43.8	K.SVSTT*NIAGHFNDE*S*PLGLR.R
Rho guanine nucleotide exchange factor 2	ARHGEF2	S121						41.9	18.6	R.ERPSS*AIYPSDSFR.Q
Rho guanine nucleotide exchange factor 2	ARHGEF2	S172S177						10.0	21.2	R.ILS*QSTD*S*LNMR.N
Rho guanine nucleotide exchange factor 38	ARHGEF3	S553						100.0	17.6	R.KLS*FEKK.K
Rho guanine nucleotide exchange factor 6	ARHGEF6	S640						49.2	25.6	R.KPS*EEEVIR.K
Rho guanine nucleotide exchange factor 6	ARHGEF7	S488						45.8	46.7	R.MS*GFYQGI
Rho guanine nucleotide exchange factor 6	ARHGEF6	T133						45.7	105.0	R.SSSLSAANTSQT*NPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 6	ARHGEF6	S684						100.0	85.0	R.KDS*IPQVLLPEEEK.L
Rho guanine nucleotide exchange factor 6	ARHGEF7	S649						11.0	54.4	K.S*TALEEDAQILK.V
Rho guanine nucleotide exchange factor 6	ARHGEF6	S123						5.3	76.4	R.SS*LSAANTSQTNPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 6	ARHGEF6	S124						7.9	47.1	R.SSS*LSAANTSQTNPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 6	ARHGEF6	S124S126						8.4	87.9	R.SSS*LS*AAANTSQTNPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 6	ARHGEF6	S124T133						4.2	72.0	R.SSS*LSAANTSQT*NPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 6	ARHGEF7	T650						-0.4	34.9	K.ST*AALEEDAQILK.V
Rho guanine nucleotide exchange factor 6	ARHGEF6	S126						14.9	205.3	R.SSSLS*AAANTSQTNPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 6	ARHGEF6	S124T130						7.7	84.1	R.SSS*LSAANT*SQTNPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 6	ARHGEF6	S126T133						1.0	71.8	R.SSSLS*AAANTSQT*NPOGAVSSTVSGLQR.Q
Rho guanine nucleotide exchange factor 7	HIVEP3	S739S740S742						100.0	13.0	R.RS*S*LS*RL
Rho guanine nucleotide exchange factor 7	HIVEP3	S739S740						28.6	15.5	R.RS*S*LSR.L
Rho guanine nucleotide exchange factor 7	HIVEP3	S739						14.9	24.9	R.RS*S*LSR.L
Rho guanine nucleotide exchange factor 7	HIVEP3	S739S742						10.3	13.3	R.RS*S*LS*RL
Rho specific guanine nucleotide exchange factor	ARHGEF1 factor	S994S1002						18.6	26.1	K.AGGTALLPGPPAPS*PLPATPLS*AK.E
Rho specific guanine nucleotide exchange factor	ARHGEF1 factor	S943S945							21.8	R.S*LS*PILGRHSPAPPPDGPAPSPPPADSPSEGSFLK.A
Rho specific guanine nucleotide exchange factor	ARHGEF1 factor	S943S945S953							15.3	R.S*LS*PILGRHS*PAPPPDGPAPSPPPADSPSEGSFLK.A
Rho specific guanine nucleotide exchange factor	ARHGEF1 factor	S1002						6.9	43.9	K.AGGTALLPGPPAPSPPLPATPS*AK.E
Rho specific guanine nucleotide exchange factor	ARHGEF1 factor	T999S1002						28.3	26.7	K.AGGTALLPGPPAPSPPLPA*PLS*AK.E
Rho specific guanine nucleotide exchange factor	ARHGEF1 factor	S945						16.9	21.6	R.SLS*PILGR.H
Rho specific guanine nucleotide exchange factor	ARHGEF1 factor	T999						31.1	21.9	K.AGGTALLPGPPAPSPPLPA*PLSAK.E
RhoGAP1	ARHGAP1	S51						12.6	51.0	K.SSS*PELVTHLK.W
Ribonuclease P, 29 KD	POP4	S38T39						100.0	30.9	R.RS*TT*PR.S
Ribonucleotide reductase M2 subunit	RRM2	S20						137.3	71.7	R.VPLAPITDPQQQLS*PLK.G
Ribosomal L1 domain containing 1	RSL1D1	S361						25.8	80.4	K.ATNES*EDEIQLVPIGK.K
Ribosomal L1 domain containing 1	RSL1D1	T358						6.1	31.3	K.AT*NESEDEIQLVPIGK.K
Ribosomal phosphoprotein large P2	RPPLP2	S102S105						100.0	68.8	K.DEKKEES*EES*DDMGFGFLD.-
Ribosomal phosphoprotein large P2	RPPLP2	S17						7.6	43.9	R.YVASYLLAALGGNS*PSAK.D
Ribosomal phosphoprotein large P2	RPPLP2	S16						13.9	70.5	R.YVASYLLAALGGNS*SPSAK.D
Ribosomal protein L14	RPL14	S139						100.0	47.3	K.AALLKAS*PK.K
Ribosomal protein L17	RPL17-	S142						14.9	45.1	R.INPYMS*S*PCHEMILTEK.E
Ribosomal protein L17	RPL17-	S141						8.5	40.2	R.INPYMS*SPCHEMILTEK.E
Ribosomal protein L23a	RPL23A	T42						8.0	18.4	K.IRT*SPFTR.R
Ribosomal protein L23a	RPL23A	S43						8.9	22.0	K.IRT*SPFTR.R
Ribosomal protein L31	RPL31	S98						15.5	55.1	R.NEEDS*PNKLYTLVTYVPVTTFK.N
Ribosomal protein L31	RPL31	Y103						5.5	33.7	R.NEEDSPNKLY*TLVTYVPVTTFK.N
Ribosomal protein S17	RP517	S115						-0.3	71.7	K.LLDFGSL*S*NLQVTQPTVGMNF.K.T
Ribosomal protein S17	RP517	S113						9.1	68.1	K.LLDFGS*LSNLQVTQPTVGMNF.K.T
Ribosomal protein S2	RP52	S264						17.2	50.7	K.S*PYQEFTDHLVK.T
Ribosomal protein S3	RP53	T221						13.9	41.8	K.DEILPT*PISEQK.G
Ribosomal protein S3	RP53	T220						25.4	31.3	K.DEILPT*PISEQK.G
Ribosomal protein S3a	RP53A	S263						102.5	36.0	R.ADGYEPPVQES*V.-
Ribosomal protein S3a	RP53A	S237						12.1	28.8	K.LMELHGEGS*S*GKA
Ribosomal protein S3a	RP53A	S238						9.8	44.4	K.LMELHGEGS*S*GKA
RPS6	S236S240							17.7	43.2	R.RLS*S*LRAS*TSK.S
Ribosomal protein S6	RP56	S235S236						100.0	25.2	R.RRLS*S*LR.A
Ribosomal protein S6	RP56	S235						8.9	23.6	R.RRLS*SLR.A

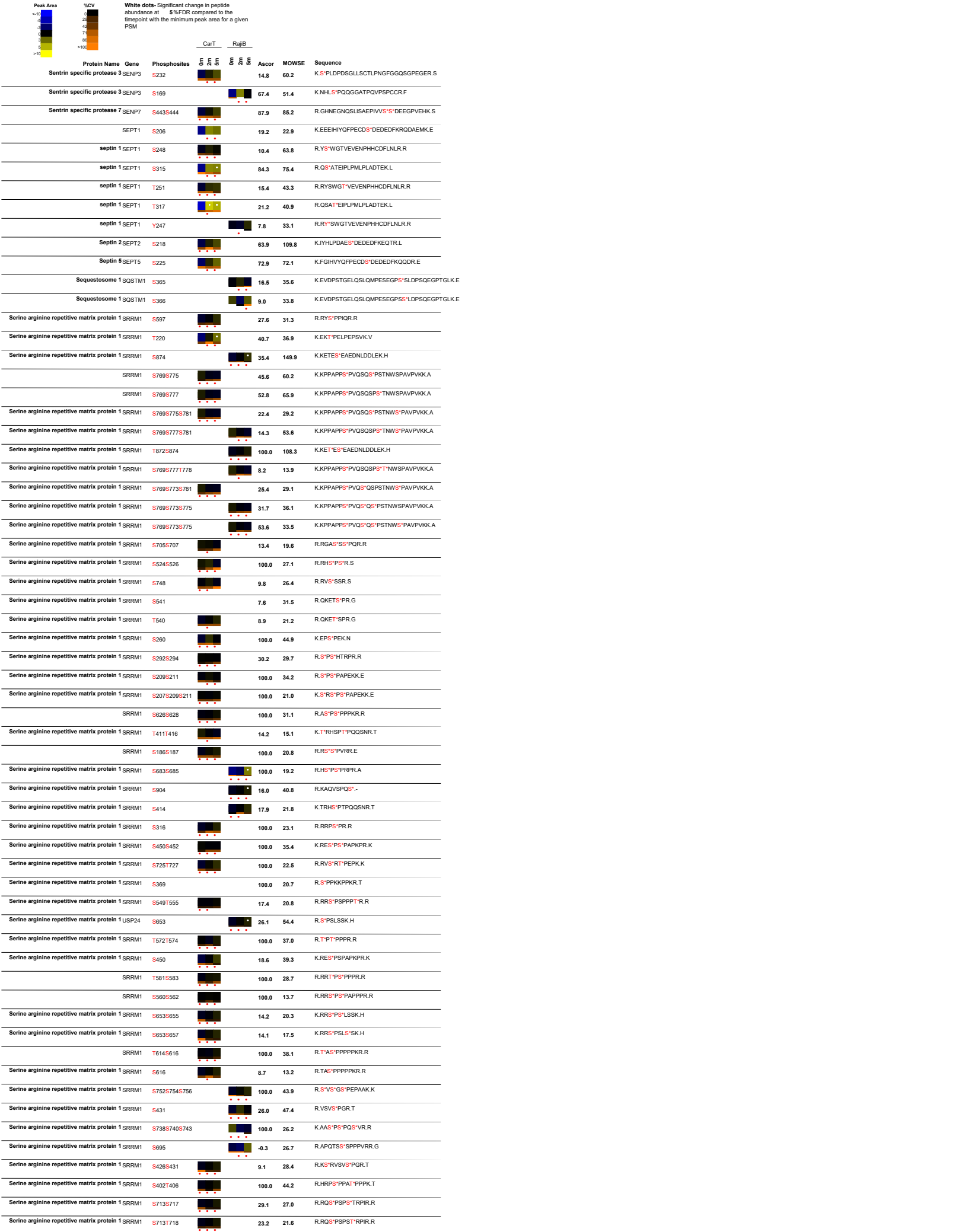
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Ribosomal protein S6	RPS6	S236S240T241				0.7	12.3	R.RLSS*LRAS* <b>T</b> *SK.S
		Ribosomal protein S6	RPS6	S236T241				11.0	41.1	R.LLS*LRAS <b>T</b> *SK.S
		Ribosomal protein S6	RPS6	S235S236S240				1.1	12.6	R.RL <b>S</b> *S*LRAS* <b>T</b> *SK.S
		Ribosomal protein S6	RPS6	S236				9.8	26.7	R.RRLSS*LR.A
		Ribosomal protein S6 kinase alpha 3	RPS6KA1	Y226				8.8	66.2	K.AY* <b>S</b> FCGTVEYMAPEVVNR.Q
		Ribosomal protein S6 kinase alpha 3	RPS6KA1	T231				-0.2	26.0	K.AYSFCGT <b>V</b> EYMAPEVVNR.Q
		Ribosomal protein S6 kinase alpha 3	RPS6KA3	S369				43.9	25.6	K.D <b>S</b> *PGIPPSANAHQLFR.G
		Ribosomal protein S6 kinase alpha 3	RPS6KA1	S227				5.8	31.8	K.AY <b>S</b> *FCGTVEYMAPEVVNR.Q
		Ribosomal protein S6 kinase alpha 5	RPS6KA5	Y375S3376				19.9	34.4	K.LFQGY <b>S</b> *FVAPSLFK.R
		Ribosomal protein S6 kinase alpha 5	RPS6KA5	Y375S3381				12.6	55.7	K.LFQGY* <b>S</b> VFAP <b>S</b> *LLFK.R
		Ribosomal protein S6 kinase, 70kDa, RPS6KB1 polypeptide 1		T444S447				75.3	79.5	R.T*PV <b>S</b> *PVKFS*PGDFWGR.G
		Ribosomal protein S6 kinase, 70kDa, RPS6KB1 polypeptide 1		S447S452				30.3	11.0	R.TPV <b>S</b> *PVKFS*PGDFWGR.G
		Ribosomal protein, large, P0	RPLP0	S307				28.1	49.7	K.EE <b>EE</b> <b>S</b> *DEDMGFLD.-
		Ribosomal protein, large, P0	RPLP0	S304				16.1	41.8	K.E <b>ES</b> *EESDEDMGFLD.-
		Ribosomal protein, large, P0	RPLP0	S304S307				100.0	53.2	K.E <b>ES</b> * <b>ES</b> *DEDM#GFGLD.-
		RPLP1		S101				24.6	74.8	K.K <b>EE</b> <b>S</b> *EESDDMGFLD.-
		RPLP1		S101S104				100.0	69.2	K.K <b>EE</b> <b>S</b> * <b>ES</b> *DDMGFLD.-
		RPLP1		S104				22.8	27.1	K.EE <b>EE</b> <b>S</b> *DDMGFLD.-
		Ribosomal RNA processing 12 homolog	RRP12	S1080				40.6	91.3	K.GDSIEILAD <b>S</b> *EDEEDNEEEER.S
		Ribosomal RNA processing 12 homolog	RRP12	S1072				5.2	23.9	K.GD <b>S</b> *IEILADSEDEEDNEEEER.S
		Rictor	RICTOR	S1385Y1386				21.8	72.1	K.AL <b>S</b> * <b>Y</b> ASLDKEDLLSPINQNTLQR.S
		Rictor	RICTOR	S1385S1388				16.2	43.5	K.AL <b>S</b> * <b>Y</b> AS*LDKEDLLSPINQNTLQR.S
		Rictor	RICTOR	S1282				13.1	56.1	K. <b>S</b> *NSVSLVPPGSSHTLPR.R
		RIMS1	RIMS1	S989T991				21.6	17.0	R.RSR <b>S</b> * <b>P</b> T*RL.H
		Ring Finger Protein 1	RING1	S163T166T167				94.3		R.LVGGGVPAG <b>S</b> *DEYEDCPHIALSSLN.R.E
		Ring Finger Protein 1	RING1	T238T243				24.2		R.GGT* <b>L</b> GGT* <b>L</b> GPPSPGAPSPPEPGGEIELVFRPHLLVEK.G
		Ring Finger Protein 1	RING1	S170S187S188				12.9	40.1	R.LVGGGVPAG <b>S</b> *DEYEDCPHIALSSLN.R.E
		Ring Finger Protein 1	RING1	S248S254				69.3	12.1	R.GGT <b>L</b> GGGT <b>L</b> GPP <b>S</b> *PPGAP <b>S</b> *PPEPGGEIELVFRPHLLVEK.G
		Ring Finger Protein 1	RING1	S163T166T167				16.8		R.LVGGGVPAG <b>S</b> *DEYEDCPHIALSSLN.R.E
		Ring finger protein 126	RNF126	S301				12.2	42.0	K.SLTGQNTATNPGLTGVFS <b>SSSSSSSS</b> * <b>S</b> SPSENATSNS.-
		Ring finger protein 126	RNF126	S297				3.7	22.9	K.SLTGQNTATNPGLTGVFS <b>SSSSSS</b> * <b>S</b> SPSENATSNS.-
		Ring finger protein 126	RNF126	S303				8.0	19.9	K.SLTGQNTATNPGLTGVFS <b>SSSSSSSSSS</b> * <b>S</b> SPSENATSNS.-
		Ring finger protein 126	RNF126	S298				5.9	23.8	K.SLTGQNTATNPGLTGVFS <b>SSSSSSS</b> * <b>S</b> SPSENATSNS.-
		Ring finger protein 146	RNF146	T288S290S293				6.0	64.0	R.VPAPDTSIE <b>T</b> * <b>E</b> S* <b>D</b> AS*SDSEDVSAVVAQHS <b>L</b> TQQLL
		Ring finger protein 169	RNF169	S403				100.0	49.4	R.VLS*PLI <b>K</b> .S
		Ring finger protein 2	RNF2	T197T199				10.9		R.T* <b>K</b> T*SDSGLELDNNNAAMIDPVMGASEIELVFRPHPTLM <b>E</b> K.
		RING finger protein 20	RNF20	S138				7.8	17.6	K.ALVVPEPEPDS <b>S</b> *NQER.K
		RING finger protein 29	TRIM55	S292				37.7	40.8	K.KISEA <b>S</b> *K.A
		Ring finger protein 4	RNF4	S94S95				36.1	50.3	R.RLPQDHADSCV <b>S</b> * <b>S</b> DDEELSR.D
		RIO kinase 1	RIOK1	S22				7.0	71.6	R.VVPGQFDAD <b>S</b> *DSENRLD
		RIO kinase 1	RIOK1	S21				22.0	42.0	R.VVPGQFDAD <b>S</b> *DSENRLD
		RIO kinase 2	RIOK2	S380S382S385				22.3	58.5	R.SSGDPEQIKED <b>S</b> * <b>L</b> <b>S</b> * <b>E</b> ES*ADAR.S
		RIO kinase 2	RIOK2	S337				10.2	43.8	K.EGSEF <b>S</b> *DGEVAEK.A
		RIO kinase 2	RIOK2	S442				52.5	50.8	R.VQGGVPAG <b>S</b> *DEYEDCPHIALSSLN.R.E
		RIO kinase 2	RIOK2	S332S335S337				100.0	80.6	K.EG <b>S</b> * <b>E</b> F <b>S</b> * <b>F</b> <b>S</b> *DGEVAEK.A
		RIO kinase 2	RIOK2	S390				71.4	99.8	R. <b>S</b> *FEMTEFNQALEEK.G
		RIO kinase 2	RIOK2	S370S382S385				13.8	24.2	R.S <b>S</b> *GDPEQIKED <b>S</b> * <b>L</b> <b>S</b> * <b>E</b> ES*ADAR.S
		RIO kinase 2	RIOK2	S335				13.4	52.7	K.EGSEF <b>S</b> *FSDGEVAEK.A
		RIO kinase 2	RIOK2	S380S382				13.2	24.0	R.SSGDPEQIKED <b>S</b> * <b>L</b> <b>S</b> * <b>E</b> ESADAR.S
		RIO kinase 2	RIOK2	Y445				16.4	15.1	R.VQGGVPAG <b>S</b> *DEY*EDCPHIALSSLN.R.E
		RIP2	RIPK2	S393				24.5	65.9	K.LHHCPGN <b>H</b> S*WDSTIGSQRA
		RIP2	RIPK2	S527				29.8	56.0	K.QMGLQPYPEILV <b>S</b> *R.S
		RIP2	RIPK2	S363				56.8	28.2	R. <b>S</b> *LPAPQDN <b>D</b> LSR.K
		RIP2	RIPK2	S176				35.4	20.8	R.MMS <b>L</b> <b>S</b> *QSR.S
		RIP2	RIPK2	S531				1.4	56.9	R.S <b>P</b> <b>S</b> *LNLQNK.S
		RIP2	RIPK2	S396				13.7	61.8	K.LHHCPGN <b>H</b> WD <b>S</b> *TIGSQRA
		RNA binding motif protein 10	RBM10	S89				42.3	42.2	R.HRH <b>S</b> *PTGPPGFPR.D
		RNA binding motif protein 10	RBM10	S736S738				36.7	88.9	R.GLVAAY <b>S</b> GE <b>S</b> * <b>D</b> <b>S</b> *EEEQER.G
		RNA binding motif protein 10	RBM10	S733S736S738				35.1	89.3	R.GLVAAY <b>S</b> *GE <b>S</b> * <b>D</b> <b>S</b> *EEEQER.G
		RNA binding motif protein 10	RBM5	S661				100.0	13.0	R. <b>S</b> *LNK <b>K</b> .E
		RNA binding motif protein 10	RBM10	S733S738				22.1	30.5	R.GLVAAY <b>S</b> *GE <b>S</b> <b>S</b> *EEEQER.G
		RNA binding motif protein 10	RBM10	Y732S736S738				17.6	62.0	R.GLVAAY <b>S</b> *GE <b>S</b> * <b>D</b> <b>S</b> *EEEQER.G

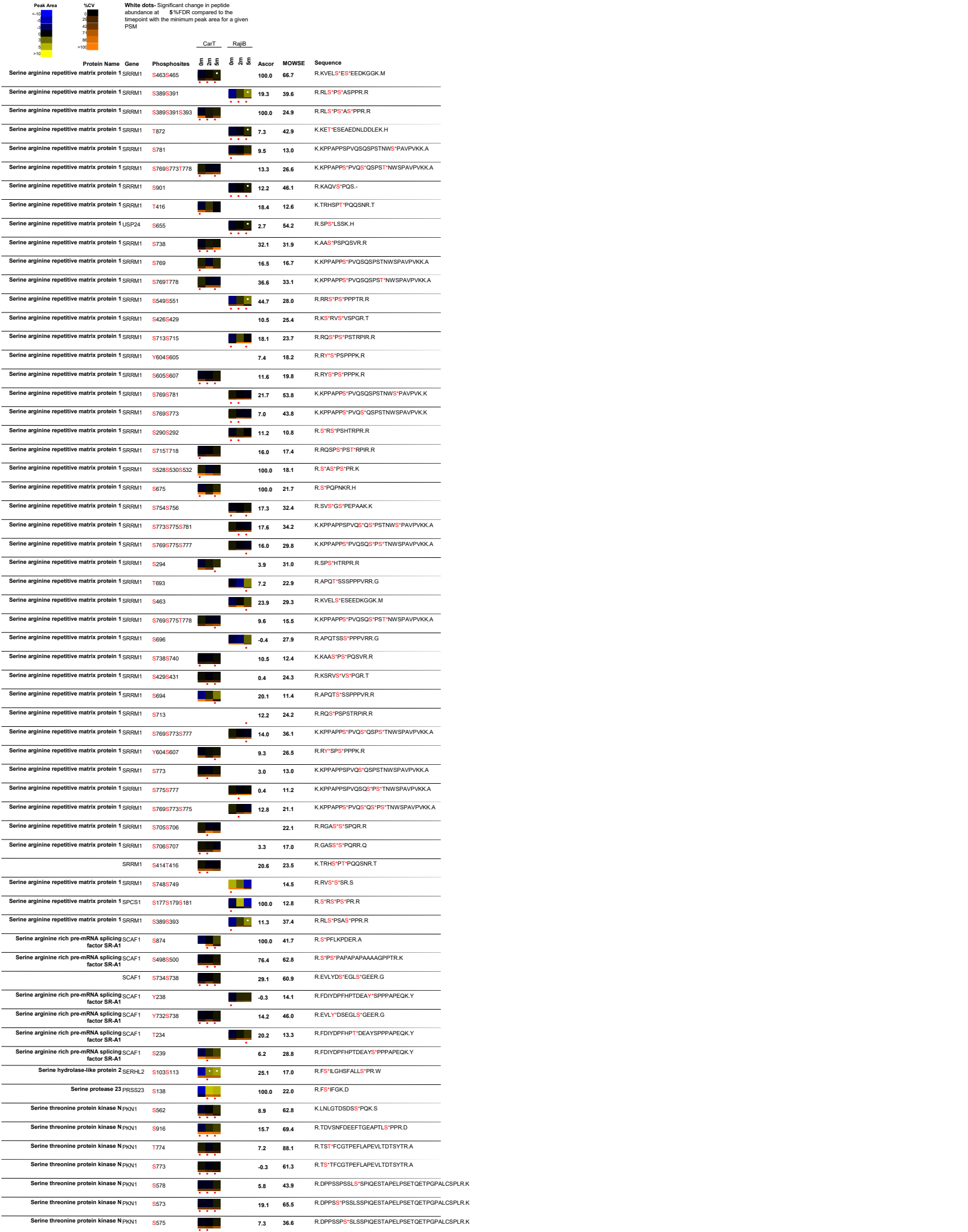
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajIB		Ascor	MOWSE	Sequence
		0	2	4	6	8	10			
Protein Name	Gene	Phosphosites								
RNA binding motif protein 10	RBM10	T91						10.9	19.0	R.HRHSP <sup>T</sup> GGPGFPR.D
RNA binding motif protein 10	RBM10	Y732S <sup>T</sup> 33S <sup>T</sup> 738						5.6	26.7	R.GLVAAY <sup>S</sup> SGESD <sup>S</sup> EEEQER.G
RNA binding motif protein 12	RBM12	S411						12.2	20.1	R.S <sup>S</sup> KSPSGQKR.S
RNA binding motif protein 12	RBM12	S413						39.8	32.1	R.SK <sup>S</sup> PSGQKR.S
RNA binding motif protein 13	MAK16	S199S <sup>T</sup> 200						1.9	80.6	K.ALEQQEAE <sup>SD</sup> S <sup>S</sup> DTEEKDDDDDEEDVGKR.E
RNA binding motif protein 13	MAK16	S197S <sup>T</sup> 199						22.9	57.0	K.ALEQQEAE <sup>S</sup> DS <sup>S</sup> SDTEEKDDDDDEEDVGKR.E
RNA binding motif protein 13	MAK16	S197S <sup>T</sup> 199S <sup>T</sup> 200						20.1	55.9	K.ALEQQEAE <sup>S</sup> DS <sup>S</sup> S <sup>T</sup> DEEKDDDDDEEDVGKR.E
RNA binding motif protein 13	MAK16	S229S <sup>T</sup> 232						100.0	82.9	R.EFVEDGEVDS <sup>S</sup> DIS <sup>S</sup> DFEDMDK.L
RNA binding motif protein 13	MAK16	S197S <sup>T</sup> 199S <sup>T</sup> 200						100.0	58.1	K.ALEQQEAE <sup>S</sup> DS <sup>S</sup> S <sup>T</sup> EEKDDDDDEEDVGKR.E
RNA binding motif protein 13	MAK16	S197S <sup>T</sup> 200						8.3	53.5	K.ALEQQEAE <sup>S</sup> DS <sup>S</sup> S <sup>T</sup> DEEKDDDDDEEDVGKR.E
RNA binding motif protein 13	MAK16	S199T <sup>T</sup> 202						7.8	19.8	K.ALEQQEAE <sup>SD</sup> S <sup>S</sup> DT <sup>T</sup> EEKDDDDDEEDVGKR.E
RNA binding motif protein 13	MAK16	S199S <sup>T</sup> 200T <sup>T</sup> 202						-0.2	19.7	K.ALEQQEAE <sup>SD</sup> S <sup>S</sup> DT <sup>T</sup> EEKDDDDDEEDVGKR.E
RNA binding motif protein 14	RBM14	S520						28.6	93.7	R.TQS <sup>S</sup> SASLAASYAAQHPQAAASYR.G
RNA binding motif protein 14	RBM14	T572						19.1	92.0	R.GQPGNAYDGAGQPSAAYLSMSQGAVANAN <sup>S</sup> PPPYER.T
RNA binding motif protein 14	RBM14	S555						5.3	18.5	R.GQPGNAYDGAGQPS <sup>S</sup> AAYLSMSQGAVANANSTPPPYER.T
RNA binding motif protein 14	RBM14	S291							78.9	R. R.NH A C H E S E N C A A A G S I R E V V G A N D S A S I R E V V G A A A A G S I R E V
RNA binding motif protein 14	RBM14	S582						32.3	28.0	R.TRLS <sup>S</sup> PPR.A
RNA binding motif protein 14	RBM14	S520S <sup>T</sup> 521						10.6	90.7	R.TQS <sup>S</sup> S <sup>S</sup> ASLAASYAAQHPQAAASYR.G
RNA binding motif protein 14	RBM14	T206						100.0	30.4	R.OPT <sup>T</sup> PPFFGR.D
RNA binding motif protein 14	RBM14	S571						33.7	62.4	R.GQPGNAYDGAGQPSAAYLSMSQGAVANAN <sup>S</sup> TPPPYER.T
RNA binding motif protein 14	RBM14	S618						17.0	21.9	R.RLS <sup>S</sup> ESQLSFR.R
RNA binding motif protein 14	RBM14	Y548							39.5	R.GQPGNAY <sup>T</sup> DGAGQPSAAYLSMSQGAVANANSTPPPYER.T
RNA binding motif protein 14	RBM14	T579						14.9	20.9	R.TRLSPPR.A
RNA binding motif protein 15	RBM15	T568						56.6	29.9	R.DRT <sup>T</sup> PPLLYR.D
RNA binding motif protein 15	RBM15	T265Y <sup>T</sup> 266						16.2	61.5	R.SRSLDKD <sup>T</sup> Y <sup>T</sup> PPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	S257Y <sup>T</sup> 266						5.1	59.4	R.S <sup>S</sup> RSPLDKD <sup>T</sup> Y <sup>T</sup> PPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	S259T <sup>T</sup> 265						4.9	59.9	R.SRS <sup>S</sup> PLDKD <sup>T</sup> YPPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	S292						10.6	60.5	R.S <sup>S</sup> LSPGGAALGYR.D
RNA binding motif protein 15	RBM15	S51						100.0	13.3	K.ERS <sup>S</sup> PVK.A
RNA binding motif protein 15	RBM15	S708						100.0	16.4	R.RGS <sup>S</sup> LEK.S
RNA binding motif protein 15	RBM15	S259Y <sup>T</sup> 266						6.8	45.7	R.SRS <sup>S</sup> PLDKD <sup>T</sup> YPPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	S294						16.7	69.7	R.SLS <sup>S</sup> PGGAALGYR.D
RNA binding motif protein 15	RBM15	S670S <sup>T</sup> 674						39.0	18.1	R.HCAP <sup>S</sup> PDRS <sup>S</sup> PELSSSR.D
RNA binding motif protein 15	RBM15	S257S <sup>T</sup> 259						2.8	36.7	R.S <sup>S</sup> RS <sup>S</sup> PLDKDTYPPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	S259						3.9	60.7	R.S <sup>S</sup> PLDKDTYPPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	T265						2.0	18.9	R.SPLDKD <sup>T</sup> YPPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	S700						100.0	17.3	R.LLLERPS <sup>S</sup> PIRDR.R
RNA binding motif protein 15	RBM15	S622						100.0	19.0	R.DGWS <sup>S</sup> LDR.D
RNA binding motif protein 15	RBM15	S257T <sup>T</sup> 265						7.0	42.4	R.S <sup>S</sup> RSPLDKD <sup>T</sup> YPPSASVVGASVGGHR.H
RNA binding motif protein 15	RBM15	S656						12.2	31.0	R.S <sup>S</sup> PESDRPR.K
RNA binding motif protein 19	RBM19	S949T <sup>T</sup> 957						9.9	29.1	R.SVVLDEILEQEGS <sup>S</sup> DSDSEEQ <sup>T</sup> LQL.-
RNA binding motif protein 19	RBM19	S953T <sup>T</sup> 957						13.4	19.2	R.SVVLDEILEQEGSDSDS <sup>S</sup> EEQ <sup>T</sup> LQL.-
RNA binding motif protein 19	RBM19	S949S <sup>T</sup> 951						6.2	20.1	R.SVVLDEILEQEGS <sup>S</sup> DS <sup>S</sup> DSEEQ <sup>T</sup> LQL.-
RNA binding motif protein 19	RBM19	S949S <sup>T</sup> 953T <sup>T</sup> 957						19.5	17.3	R.SVVLDEILEQEGS <sup>S</sup> DS <sup>S</sup> DS <sup>S</sup> EEQ <sup>T</sup> LQL.-
RNA binding motif protein 25	RBM25	S677						55.2	101.9	K.LGASN <sup>S</sup> PGQPNSVK.R
RNA binding motif protein 25	RBM25	S703						100.0	60.8	K.FEDES <sup>S</sup> DDVPR.K
RNA binding motif protein 33	RBM33	S41						206.3	153.6	R.AADEWD <sup>S</sup> SELEDDLGEDLLSGK.K
RNA binding motif protein 33	RBM33	S205						119.4	79.0	K.EES <sup>S</sup> DEEEEDDEESGR.L
RNA binding motif protein 34	RBM34	S9						100.0	57.4	R.S <sup>S</sup> VQEGENPDQVGR.G
RNA binding motif protein 5	RBM5	S624						39.4	130.0	R.GLVAAYSGD <sup>S</sup> DNEEELVER.L
RNA binding motif protein 6	RBM6	S362						20.3	73.6	R.EGETQGVAFEHESPADFONS <sup>S</sup> PVQDDOK.S
RNA binding motif protein 6	RBM6	Y908						17.6	66.7	K.VVNPLIGLLGEY <sup>T</sup> GGSDYEEEEEEQTPPPQPR.T
RNA binding motif protein 6	RBM6	Y914						5.5	48.4	K.VVNPLIGLLGEYGGSDY <sup>T</sup> EEEEEEQTPPPQPR.T
RNA binding motif protein 6	RBM6	S360						7.3	22.5	R.EGETQGVAFEHESPADFONS <sup>S</sup> GSPVQDDOK.S
RNA binding motif protein 6	RBM6	Y923						-0.0	19.4	K.VVNPLIGLLGEYGGSDYEEEEEEQTPPPQPR.T
RNA binding motif protein 6	RBM6	S912						7.0	41.6	K.VVNPLIGLLGEYGGDS <sup>S</sup> DYEEEEEEQTPPPQPR.T
RNA binding motif protein 7	RBM7	S136						16.9	14.9	R.SFS <sup>S</sup> SPENFOR.Q
RNA binding motif protein 8A	RBM8A	S42						41.9	30.3	R.GFGS <sup>S</sup> EEGSR.A
RNA binding motif protein 8A	RBM8A	S166S <sup>T</sup> 168						100.0	15.6	R.S <sup>S</sup> RS <sup>S</sup> PDRR.R
RNA binding protein 4	RBM4	S309						100.0	16.6	R.DRS <sup>S</sup> PLRR.S
RNA binding protein 4	RBM4	S86						10.9	38.8	K.LHVGNIS <sup>S</sup> PTCTNKE
RNA binding protein S1, serine-rich domain	RNPS1	S27						22.6	28.3	R.APS <sup>S</sup> PTKR.K



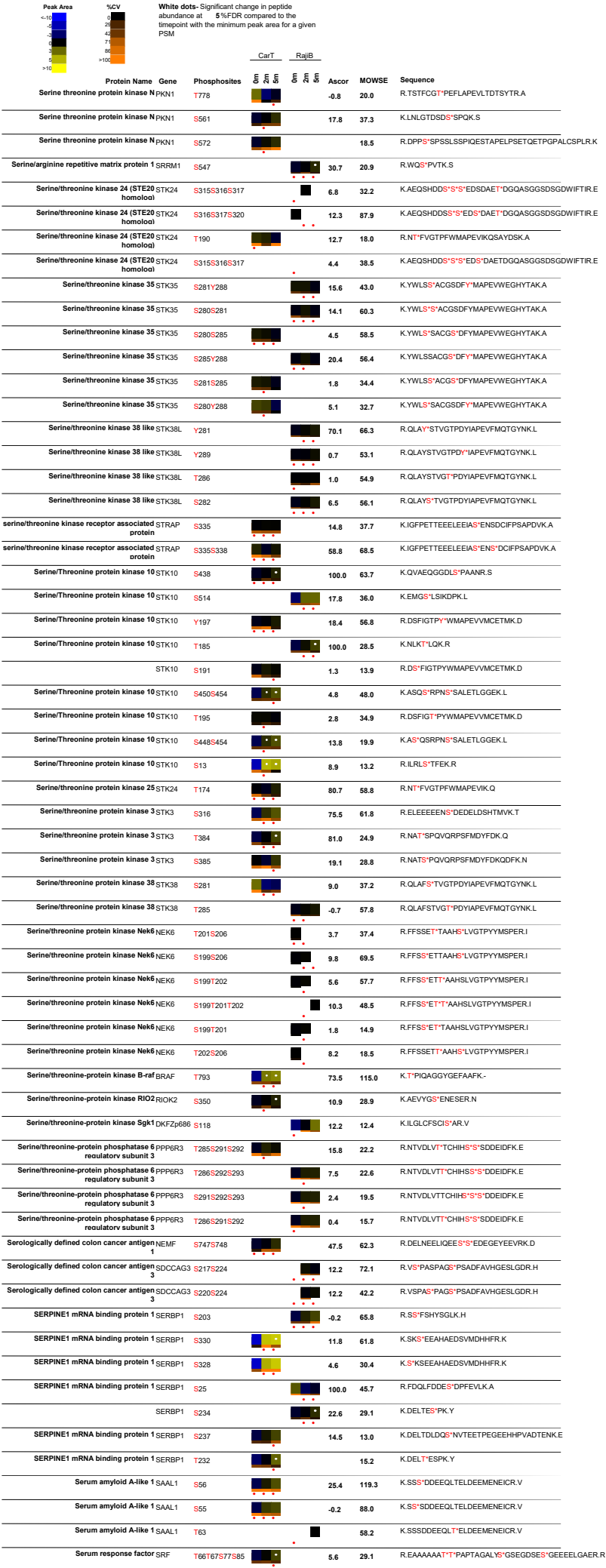
Peak Area	%CV		White dots- Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
	(0-20)	(20-40)	(40-60)	(60-80)	(80-100)	(100-120)	(120-140)			
SAM domain protein SAMSN1	SAMS	N1	S123	S125				3.3	44.9	K.AS*DS*MDSLYSGQSSSGITSCSDGTSNR.D
SAM domain protein SAMSN1	SAMS	N1	S134	S136				6.3	66.8	K.ASDSMDSLYSGQSS*SS*SGITSCSDGTSNR.D
SAM domain protein SAMSN1	SAMS	N1	S131					10.0	44.6	K.ASDSMDSLYS*GQSSSGITSCSDGTSNR.D
Sam68	KHDRBS1	S58						30.2		R.AS*PATQPPPLPPSATGPDATVGGPAPTPLPPSATASVK.M
Sam68	KHDRBS1	S20						9.1	36.5	R.SGS*MDPSGAHPSVR.Q
Sam68	KHDRBS1	T61						5.9	24.5	R.ASPAT*QPPPLPPSATGPDATVGGPAPTPLPPSATASVK.M
Sam68	KHDRBS1	S18						10.1	15.7	R.S*GSMDPGAHPSVR.Q
SAP30-like SAP30L	S93	S99						22.0	72.0	R.KTS*DDGGDS*PEHDTDIPEDVLFQLQVNTLR.R
SAP30-like SAP30L	S93	T104						7.1	31.5	R.KTS*DDGGDSPEDT*TDIPEVDLFQLQVNTLR.R
SAP30-like SAP30L	T92	T104						2.4	39.1	R.KT*SDGGDSPEDT*TDIPEVDLFQLQVNTLR.R
SAP30-like SAP30L	T92	S99						4.8	22.6	R.KT*SDGGDS*PEHDTDIPEDVLFQLQVNTLR.R
SAPK substrate protein 1	UBXN1	S200						9.2	13.0	K.YGGSVGSQPPVAEPGPVPSS*PSQEPPTKR.E
Sarcoma antigen NY-SAR-91	MEAF6	S118	T120	S122				12.8		K.REPGS*GT*ES*DTSPDFHNQENEPSQEDPEDLDGSVGQVKPQK.A
Sarcoma antigen NY-SAR-91	MEAF6	S118	T120	T124				3.3	20.7	K.REPGS*GT*ESDT*SPDFHNQENEPSQEDPEDLDGSVGQVKPQK.A
Sarcoma antigen NY-SAR-91	MEAF6	S118	S122					2.2	18.4	K.REPGS*GTES*DTSPDFHNQENEPSQEDPEDLDGSVGQVKPQK.A
Sarcoma antigen NY-SAR-91	MEAF6	S118	S125					-1.0	13.4	R.EPGS*GTESDTS*PDFHNQENEPSQEDPEDLDGSVGQVKPQK.A
Sarcoma antigen NY-SAR-91	MEAF6	S122	T124	S125				13.6	25.9	K.REPGSGTES*DT*S*PDFHNQENEPSQEDPEDLDGSVGQVKPQK.A
Sarcoma antigen NY-SAR-91	MEAF6	S118	T120	S125				0.0	27.9	K.REPGS*GT*ESDTS*PDFHNQENEPSQEDPEDLDGSVGQVKPQK.A
SART1	SART1	S448						112.6	30.1	R.RVS*EVEEEKVPQPLPSDDTR.V
SART1	SART1	S474	S486					100.0	72.2	R.VENMDS*DEEEGAPPPGS*PQVLEDEAELELQK.Q
SART1	SART1	S596	S607	T608				11.8	25.0	R.SANGGS*ESDGEENIGW*S*T*VNLDEEK.Q
SART1	SART1	S596	S598	S607				17.2	33.3	R.SANGGS*ES*DGEENIGW*S*TVNLDEEK.Q
SART1	SART1	S591	S596	S598				26.3	37.7	R.S*ANGGS*ES*DGEENIGW*ST*VNLDEEK.Q
SART1	SART1	S598	S607	T608				8.8	12.6	R.SANGGSE*S*DGEENIGW*S*T*VNLDEEK.Q
Scaffold Attachment Factor B	SAFB	S604						44.5	32.5	R.SVV*S*FDK.V
Scaffold Attachment Factor B	SAFB2	T307							97.7	R.TDCEPVGLEPAVEQSSAASELAESSELAEP*EAPSPPEAR.D
Scaffold Attachment Factor B	SAFB2	S344						18.0	101.6	R.TDCEPVGLEPAVEQSSAASELAESSELAEP*EAPSPPEAR.D
Scaffold Attachment Factor B	SAFB	S197						10.4	69.4	K.ETINNLDTS*SS*DFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S195						29.0	79.0	K.ETINNLDTS*SSDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S195	S196					10.6	46.4	K.ETINNLDTS*S*SDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	T194	S195	S197				13.2	42.5	K.ETINNLDT*S*SS*DFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S195	S196	S197				9.5	36.1	K.ETINNLDTS*S*S*DFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S373	S384					14.1	58.1	K.ESS*TSEGADQKMS*SPEDSDTKR.L
Scaffold Attachment Factor B	SAFB2	T340						6.8	35.3	R.TDCEPVGLEPAVEQSSAASELAESSELAEP*EAPSPPEAR.D
Scaffold Attachment Factor B	SAFB	S196						8.0	69.1	K.ETINNLDTS*SDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	T374	S383					0.4	40.4	K.ESS*TSEGADQKMS*SPEDSDTKR.L
Scaffold Attachment Factor B	SAFB	T194						16.9		K.ELPEQLQEHAIKETINNLD*SSSDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S373	S383					13.7	47.9	K.ESS*TSEGADQKMS*SPEDSDTKR.L
Scaffold Attachment Factor B	SAFB	T194	S195					7.5	49.1	K.ETINNLDT*S*SSDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	T374	S384					10.8	52.8	K.ESS*TSEGADQKMS*PEDSDTKR.L
Scaffold Attachment Factor B	SAFB	S375	S383					4.5	25.5	K.ESSTS*EGADQKMS*SPEDSDTKR.L
Scaffold Attachment Factor B	SAFB	T194	S195	S196				-1.1	27.8	K.ETINNLDT*S*S*SDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S373	S375					0.7	31.4	K.ESS*TS*EGADQKMSPEDSDTKR.L
Scaffold Attachment Factor B	SAFB	S195	T200					11.3	23.0	K.ETINNLDTS*SSDFT*ILQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S375	S384					7.1	21.1	K.ESSTS*EGADQKMS*PEDSDTKR.L
Scaffold Attachment Factor B	SAFB2	T245						31.6	25.4	K.SEPVKESSELEQPFAQDT*SSVGPDQR.L
Scaffold Attachment Factor B	SAFB2	S321	S344					10.2	16.7	R.TDCEPVGLEPAVEQS*SAASELAESSELAEP*EAPSPPEAR.D
Scaffold Attachment Factor B	SAFB	S195	S197					4.8	43.4	K.ETINNLDTS*S*SDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	S197	T200					7.5	46.8	K.ETINNLDTS*SDFT*ILQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	T188						32.8		K.ET*INNLDTS*SDFTLQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	T200						1.2	12.4	K.ETINNLDTS*SDFT*ILQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	T194	S195	T200				3.7	33.4	K.ETINNLDT*S*SSDFT*ILQIEEIPSPLEPENK.I
Scaffold Attachment Factor B	SAFB	T188	S195	S197				8.7	11.1	K.ET*INNLDTS*SS*DFTLQIEEIPSPLEPENK.I
Scaffold attachment factor B2	SAFB2	S109						59.8	45.9	K.MEEEGTEDNGLEDSS*R.D
Scaffold attachment factor B2	SAFB2	S832						100.0	15.9	K.RLS*EGR.Q
SCC112 protein	PD5A	S1265						100.0	73.9	R.AAVGQES*PGGLEAGNAKA
Scribble	SCRIB	S688	T689					96.4	90.1	R.AEEEEAS*TEEDKEGAVVSAPSVK.G
Scribble	SCRIB	S1220						57.3	52.2	R.NS*LESISSIDR.E
Scribble	SCRIB	S1559	S1566					13.2	32.7	R.LAEAPSPAPTPSPPTVEDLGPQTS*TSQGRLS*PDFAEELR.S
Scribble	SCRIB	T1558	S1566					6.0	31.9	R.LAEAPSPAPTPSPPTVEDLGPQ*TS*TSQGRLS*PDFAEELR.S
Scribble	SCRIB	T1342	S1348					30.4	37.3	R.AFAAVPTSHPPEDAPAQPP*TPGPAAS*PEQLSFR.E
Scribble	SCRIB	T1560	S1566					17.9	32.0	R.LAEAPSPAPTPSPPTVEDLGPQTS*TSQGRLS*PDFAEELR.S

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence	
		Protein Name	Gene	Phosphosites						
		Scribble	SCRIB	T1549S1566				7.2	11.4	R.LAEAPSPAPT <b>PS</b> *PVEDLGPQTSTSPGR <b>LS</b> *PDFAEELR.S
		Scribble	SCRIB	S1547S1566				8.0	21.0	R.LAEAPSPAPT <b>PS</b> *PTPVEDLGPQTSTSPGR <b>LS</b> *PDFAEELR.S
		SCY1 like 1	SCYL1	S651				7.2	87.5	R.WDDEDWGS*LEQEAESVLAQDDWSTGGQVSR.A
		SCY1-like 2	SCYL2	T679				10.9	28.4	K.RASLT*LEEK.Q
		SCY1-like 2	SCYL2	S677				20.1	35.3	K.RA <b>S</b> *LTLEEK.Q
		SDAD1	SDAD1	S525				84.9	73.3	K.YIELD <b>S</b> *DEEPR.G
		SDS3	SUDS3	S234S236				47.5	37.3	K.RPAS* <b>PS</b> *SPEHLPATPAESPAQR.F
		SDS3	SUDS3	S236S237				8.2	30.6	K.RPAS <b>PS</b> * <b>S</b> *SPEHLPATPAESPAQR.F
		SDS3	SUDS3	S45T49T55				19.0	24.7	R.GRES*DED <b>T</b> *EDASE <b>T</b> *DLAKHDEEDYVEMK.E
		SDS3	SUDS3	S45T49S53				24.3	31.4	R.GRES*DED <b>T</b> *EDAS*ETDLAK.H
		SEC16 homolog A	SEC16A	S587S595T600				13.3	35.4	R.GS*V <b>SQ</b> PS <b>T</b> <b>PS</b> *PPK <b>T</b> *GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S587T593				5.8	36.5	R.GS*V <b>SQ</b> PS <b>T</b> *PSPPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S587T593S595				9.1	20.6	R.GS*V <b>SQ</b> PS <b>T</b> <b>PS</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S342				100.0	18.3	R.GD <b>S</b> *PENR.T
		SEC16 homolog A	SEC16A	S589S592				8.5	74.3	R.GSV <b>S</b> *Q <b>PS</b> *TPSPPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	T197S201				36.1		R. R.NIDGPNVAT <b>T</b> *DA <b>A</b> *D <b>S</b> I <b>S</b> D <b>S</b> D <b>S</b> I R.NIDGPNVAT <b>T</b> *DA <b>A</b> *D <b>S</b> I <b>S</b> D <b>S</b> D <b>S</b> I
		SEC16 homolog A	SEC16A	S592T593S595				18.7	44.0	R.GSV <b>SQ</b> PS <b>T</b> <b>PS</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S589S592T593				13.4	36.0	R.GSV <b>S</b> *Q <b>PS</b> <b>T</b> <b>PS</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S592T593				19.7	55.2	R.GSV <b>SQ</b> PS <b>T</b> *PSPPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S589T593S595				16.0	43.6	R.GSV <b>S</b> *Q <b>PS</b> <b>T</b> <b>PS</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S589S592S595				14.0	77.2	R.GSV <b>S</b> *Q <b>PS</b> *TP <b>S</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S587S592S595				12.2	41.6	R.GS*V <b>SQ</b> PS*TP <b>S</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S587S592T600				10.7	29.3	R.GS*V <b>SQ</b> PS*TPSPPK <b>T</b> *GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S2022				68.3	61.2	R. <b>S</b> *PDGIVPQEA <b>P</b> VGNLS <b>EL</b> SEENFDGK.F
		SEC16 homolog A	SEC16A	S587S592T593				13.9	35.8	R.GS*V <b>SQ</b> PS <b>T</b> <b>PS</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S587T593T600				10.3	44.2	R.GS*V <b>SQ</b> PS <b>T</b> *PSPPK <b>T</b> *GIFQTSANSSFE <b>PV</b> K.S
		SEC16 homolog A	SEC16A	S587S589T593				11.3	33.4	R.GS*V <b>S</b> *Q <b>PS</b> <b>T</b> <b>PS</b> *PPK <b>T</b> GIFQTSANSSFE <b>PV</b> K.S
		SEC22B	SEC22B	S137				46.9	104.7	R.NLGS*INTELQDVQR.I
		SEC31 like 1	SEC31A	T1161				30.5	64.9	R.EQT*LSPTTISGLHN <b>IA</b> R.S
		SEC31 like 1	SEC31A	S527				17.1	54.9	K.DSDQVAG <b>S</b> *DGEESPAEEQLLGEHIK.E
		SEC31 like 1	SEC31A	S1163				10.7	57.6	R.EQT <b>LS</b> *PTTISGLHN <b>IA</b> R.S
		SEC31 like 1	SEC31A	S527S532				21.5	13.9	K.DSDQVAG <b>S</b> *DGEES*PAEEQLLGEHIK.E
		SEC63	SEC63	S593S597				100.0	39.7	K.DDG <b>S</b> *DRD <b>S</b> *DREQDEK.Q
		Second step splicing factor 1	PPAN-	S359				79.1	121.0	R.VGG <b>S</b> *DEEASGIPSR.T
		Second step splicing factor 1	PPAN-	S238S240				4.8	78.9	R.LQDISELLATGAG <b>LS</b> *EAE <b>P</b> DGDH <b>IN</b> TEL <b>PO</b> AVAGR.G
		Second step splicing factor 1	PPAN-	S228T233				15.0	96.9	R.LQD <b>IS</b> *ELLAT*GAGLSEAE <b>P</b> DGDH <b>IN</b> TEL <b>PO</b> AVAGR.G
		Second step splicing factor 1	PPAN-	S238				17.2	64.0	R.LQDISELLATGAG <b>LS</b> *EAE <b>P</b> DGDH <b>IN</b> TEL <b>PO</b> AVAGR.G
		Second step splicing factor 1	PPAN-	T233				5.4	69.1	R.LQDISELLAT*GAGLSEAE <b>P</b> DGDH <b>IN</b> TEL <b>PO</b> AVAGR.G
		Second step splicing factor 1	PPAN-	T233S240				20.2	69.8	R.LQDISELLAT*GAG <b>LS</b> <b>S</b> *EAE <b>P</b> DGDH <b>IN</b> TEL <b>PO</b> AVAGR.G
		Second step splicing factor 1	PPAN-	T233S238				26.1	49.8	R.LQDISELLAT*GAG <b>LS</b> *EAE <b>P</b> DGDH <b>IN</b> TEL <b>PO</b> AVAGR.G
		Secreted frizzled related protein 2	SFRP2	S287S289				100.0	16.9	K.RIS* <b>RS</b> *IR.K
		Secreted frizzled related protein 2	SFRP2	S289				29.8	23.4	K.RIS <b>S</b> *IR.K
		Secretory carrier membrane protein 2	SCAMP2	S320				-0.2	59.5	R.AAS <b>S</b> *AAQGA <b>FQGN</b> .-
		Secretory carrier membrane protein 2	SCAMP2	S319					53.6	R.AA <b>S</b> *SAAQGA <b>FQGN</b> .-
		Secretory carrier membrane protein 3	SCAMP3	S32				111.4	36.7	R.DG <b>GN</b> PFA <b>EP</b> SEL <b>DN</b> PFQ <b>DP</b> AV <b>IQ</b> HR <b>S</b> *R.Q
		Secretory carrier membrane protein 3	SCAMP3	S76				25.8	36.3	R.K <b>LS</b> *PTEPK.N
		Selectin P ligand	SELPLG	S358				7.2	70.9	R.NY <b>S</b> *PT <b>EM</b> VCIS <b>LL</b> PDGGEGPSATANG <b>LS</b> K.A
		Selectin P ligand	SELPLG	Y357				5.7	33.4	R.NY* <b>S</b> PT <b>EM</b> VCIS <b>LL</b> PDGGEGPSATANG <b>LS</b> K.A
		Selectin P ligand	SELPLG	T360				9.1	31.2	R.NY <b>S</b> PT* <b>EM</b> VCIS <b>LL</b> PDGGEGPSATANG <b>LS</b> K.A
		Senataxin	SETX	S1017S1019				100.0	82.5	R.GQ <b>VIII</b> <b>S</b> *D <b>S</b> *DDDDDER.I
		Senescence downregulated leol1 like	LEO1	T188S197				100.0	31.5	K.MQ <b>NT</b> *DDEER <b>PQLS</b> *D <b>DER</b> .Q
		Senescence downregulated leol1 like	LEO1	S212S220S229				100.0	35.1	K.A <b>NS</b> *DDE <b>RP</b> VAS*DND <b>DEK</b> Q <b>NS</b> *D <b>DEE</b> Q <b>PQLS</b> *D <b>E</b> E <b>K</b> .M
		Senescence downregulated leol1 like	LEO1	S294S296S300				47.4	77.9	K.NA <b>IAS</b> *D <b>S</b> *EAD <b>S</b> *DTE <b>VP</b> K.D
		Senescence downregulated leol1 like	LEO1	S658				12.3	44.8	K.YV <b>IS</b> *DEEEEDD.-
		Senescence downregulated leol1 like	LEO1	S171S179				100.0	90.0	R.AQ <b>GS</b> *DED <b>KLQNS</b> *D <b>DEE</b> K.M
		Senescence downregulated leol1 like	LEO1	S151S154S162				100.0	31.8	R.ED <b>KS</b> *D <b>QS</b> *D <b>DE</b> K <b>IONS</b> *D <b>DEE</b> R.A
		Senescence downregulated leol1 like	LEO1	S171S179T188				100.0	21.7	R.AQ <b>GS</b> *DED <b>KLQNS</b> *D <b>DEE</b> K <b>MON</b> *DDEER <b>PQLS</b> *D <b>DER</b> .Q
		Senescence downregulated leol1 like	LEO1	S271S273S277				100.0	15.1	K. <b>S</b> *E <b>S</b> *ARG <b>S</b> *D <b>S</b> *EDEV <b>LR</b> .M
		Senescence downregulated leol1 like	LEO1	S162				100.0	40.2	K.IQ <b>NS</b> *DDEE <b>R</b> .A
		Senescence downregulated leol1 like	LEO1	S205				100.0	40.4	R.QQ <b>LS</b> *EE <b>E</b> E <b>K</b> .A
		Senescence downregulated leol1 like	LEO1	S66S72S75S77				100.0	13.9	K.EL <b>F</b> GD <b>S</b> *E <b>DE</b> GA <b>S</b> *H <b>HS</b> *G <b>S</b> *DN <b>HS</b> *E <b>R</b> .S
		Senescence downregulated leol1 like	LEO1	S84S88S91				100.0	17.5	R. <b>S</b> *D <b>NR</b> <b>S</b> *EAS*E <b>R</b> .S









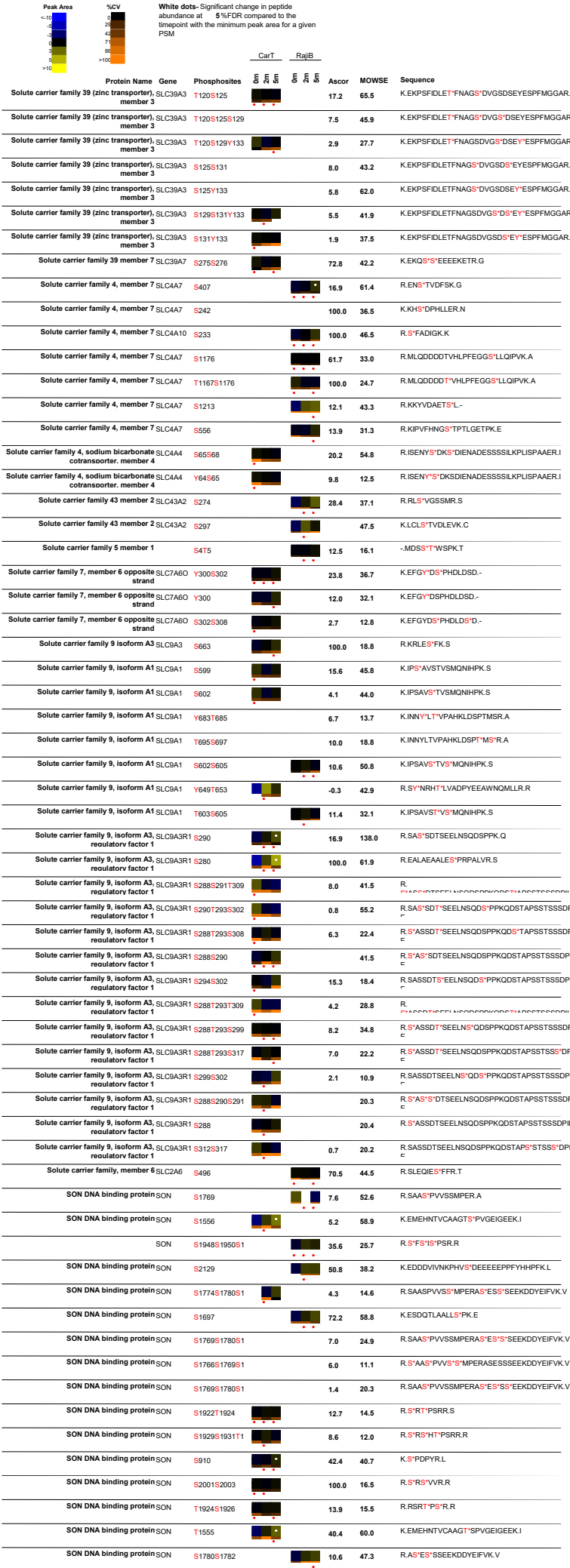
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
<10	(0	Serum response factor binding protein 1	SRFBP1	S264				16.8	41.9	K.EYFDS*TEER.F
10-20	1-2	SET binding factor 1	SBF1	T1747				-0.3	72.3	R.ST*STLYSQFOTAESEN.R.S
20-30	3-4	SET binding factor 1	SBF1	S1141				7.0	74.3	R.LGLGLTSS*LSR.A
30-40	5-6	SET binding factor 1	SBF1	S1140				10.8	54.8	R.LGLGLTSS*SLSR.A
40-50	7-8	SET binding factor 1	SBF1	S1139				9.5	29.3	R.LGLGLT*SSLSR.A
50-60	9-10	SET domain containing 1A	SETD1A	S468S470				34.2	52.6	R.S*GS*PAPETTNE.SVPFAQHS.LDSR.I
60-70	11-12	SET domain-containing protein 5	SETD5	T70S74				33.3	18.4	R.GLPYADHNYGAPPPPT*PPAS*PPVQTIIPR.S
70-80	13-14	SET protein	SET	T23				6.0	50.5	K.ELNSNHGADET*SEKEQQEAIEHIDEVONEIR.L
80-90	15-16	Sex comb on midleg like 2	SCML2	S499S511				43.5	50.9	R.S*PQQTVPYVVPLS*PK.L
90-100	17-18	Sex comb on midleg like 2	SCML2	S511				17.6	11.8	K.RSPQQTVPYVVPLS*PK.L
>10	>10	Sex comb on midleg like 2	SCML2	S499				43.6	94.9	R.S*PQQTVPYVVPLSPK.L
		Sex comb on midleg like 2	SCML2	T503S511				36.2	16.3	R.SPQQT*VPYVVPLS*PK.L
		SFRS protein kinase 1	SRPK1	S51				76.1	95.7	R.GSAPHSES.DLPEQE.EEILGS*DDDEQEDPNDYCK.G
		SFRS15	SCAF4	T138				65.0		K.IEIQPLDMAAGT*SNAAPVAENVNTNNEGSPPPPVK.V
		SFRS15	SCAF4	S139				3.6	41.1	K.IEIQPLDMAAGT*SNAAPVAENVNTNNEGSPPPPVK.V
		SFRS15	SCAF4	S154				19.5	29.0	K.IEIQPLDMAAGTSNAAPVAENVNTNNEG*SPPPPVK.V
		SGEF	ARHGEF2	S222				62.9	22.8	R.LPS*QENELLENPSV.LSTNSPAALK.V
		SGT	SGTA	S305				10.9	71.2	R.SRTPS*ASNDDQQE.-
		SGT	SGTA	S77T81				40.9	33.8	R.S*PART*PPSEEDSAEAER.L
		SGT	SGTA	T303				13.9	46.7	R.SRT*PSASNDDQQE.-
		SGT	SGTA	T81S84				0.9	16.4	R.SPART*PPS*EEDSAEAER.L
		SGT1 protein	ECD	S503S505S518				66.4	32.9	K.I.LGPRPNE*S*DS*DDLDDED.FECLDS*DDDLDFETHEPGEAEASK.G
		SGTB	SGTB	S297				13.9	27.2	R.SFS*SSAEHS.-
		SH2 B homolog	SH2B1	S88S96				19.4	42.0	R.ASGSLS*PPLAPLS*PGAESISPHDLSLESCR.V
		SH2 domain binding protein 1	CTR9	T925				67.7	89.8	K.KGGEFDEFVNDT*DDDLPISK.K
		SH2 domain binding protein 1	CTR9	S101S51016S1				100.0	15.0	K.AIIS*S*S*DS*S*S*DEDKLKI
		SH2D3C	SH2D3C	S343S346				17.4	14.7	R.YLEASYGLQGGS.KPAS*PV*S*PSGPK.G
		SH3 domain binding protein 1	BARGIN	S550				42.4	50.4	R.S*PPETAAPVEDMAR.R
		SH3 domain binding protein 1	BARGIN	S262				15.6	61.3	R.ENHGGADHS*PSMTATHFPR.V
		SH3 domain kinase binding protein 1	SH3KBP1	S511				11.6	23.0	R.RPPSQSLTSSLS.SPDIFDPS*PEEDKEEHISLAHR.G
		SH3 domain kinase binding protein 1	SH3KBP1	S509S511				40.7	43.4	R.RPPSQSLTSSLS.SPDIFD*PS*PEEDKEEHISLAHR.G
		SH3 domain kinase binding protein 1	SH3KBP1	S493				9.4	45.6	R.RPPS*QSLTSSLS.SPOIFDPSPEEDKEEHISLAHR.G
		SH3 domain kinase binding protein 1	SH3KBP1	S79				40.7	90.4	K.APEKPLHEVP*S*GNSLLSSETILR.T
		SH3 domain kinase binding protein 1	SH3KBP1	S230				100.0	97.6	R.S*IEVENDFLPVEK.T
		SH3 domain kinase binding protein 1	SH3KBP1	T179				7.9	93.7	R.ETT*GSESDGGDS.SSTK.S
		SH3 domain kinase binding protein 1	SH3KBP1	S183				14.7	113.6	R.ETTGS*S*GGDS.SSTK.S
		SH3 domain kinase binding protein 1	SH3KBP1	S503S511				25.0	36.1	R.RPPSQSLTSSLS*POIFDPS*PEEDKEEHISLAHR.G
		SH3 domain kinase binding protein 1	SH3KBP1	T178				7.4	84.9	R.ET*TGSESDGGDS.SSTK.S
		SH3 domain kinase binding protein 1	SH3KBP1	S493S495				31.4		R.RPPS*QS*LTSSLS.SPDIFDPSPEEDKEEHISLAHR.G
		SH3 domain kinase binding protein 1	SH3KBP1	S495				0.0	43.9	R.RPPSQS*LTSSLS.SPOIFDPSPEEDKEEHISLAHR.G
		SH3 domain kinase binding protein 1	SH3KBP1	T49T503				-0.3	14.9	R.RPPSQSLT*SSLS*S*POIFDPSPEEDKEEHISLAHR.G
		SH3 domain kinase binding protein 1	SH3KBP1	S181				10.9	107.6	R.ETTGS*ESDGGDS.SSTK.S
		SH3 multiple domains 2	SH3RF1	S73S739				15.1	33.2	R.V*S*PPAS*PTLEVELGSAELPLQGA.VGPELPGGGHGR.A
		SH3 protein expressed in lymphocytes	SASH3	S27				21.2	59.8	R.SS*S*FKDFAK.S
		SH3 protein expressed in lymphocytes	SASH3	S26S27				6.7	48.1	R.SS*S*FKDFAK.S
		SH3 protein expressed in lymphocytes	SASH3	S108				14.4	88.3	K.ALSEEMADTLEEGS*ASPTSPDYS.LDSPGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S120				23.9	63.2	K.ALSEEMADTLEEGSASPTSPDYS.LD*PGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	T103				9.2	83.3	K.ALSEEMADT*LEEGSASPTSPDYS.LDSPGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S97				4.3	13.4	K.ALS*EEMADTLEEGSASPTSPDYS.LDSPGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S108S113				15.9	30.6	K.ALSEEMADTLEEGS*ASPT*S*PDYS.LDSPGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	T112S120				20.8	38.4	K.ALSEEMADTLEEGSASPT*SPDYS.LD*PGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S113S120				16.6	48.5	K.ALSEEMADTLEEGSASPT*S*PDYS.LD*PGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S108S120				18.9	46.3	K.ALSEEMADTLEEGS*ASPTSPDYS.LD*PGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	T318S320				14.5	74.3	K.LLTA.AE.LLDYD*TS*EEAEEGAESSQEPVAHTVSEPK.V
		SH3 protein expressed in lymphocytes	SASH3	T308T318				12.0	70.7	K.LLT*AAE.LLDYD*TGSEAEEGAESSQEPVAHTVSEPK.V
		SH3 protein expressed in lymphocytes	SASH3	Y316S320				24.6	72.6	K.LLTA.AE.LLDY*DTGS*EEAEEGAESSQEPVAHTVSEPK.V
		SH3 protein expressed in lymphocytes	SASH3	S7				26.7	32.3	R.RKP*S*NASEKPTOK.K
		SH3 protein expressed in lymphocytes	SASH3	S38S42				16.9	28.6	K.SKP*S*PVVS*EKE
		SH3 protein expressed in lymphocytes	SASH3	S37S42				11.5	13.9	K.SKP*S*SPVVS*EKE
		SH3 protein expressed in lymphocytes	SASH3	Y316T318				25.3	79.7	K.LLTA.AE.LLDY*DT*GSEAEEGAESSQEPVAHTVSEPK.V
		SH3 protein expressed in lymphocytes	SASH3	S26				-0.6	58.4	R.SS*SFKDFAK.S
		SH3 protein expressed in lymphocytes	SASH3	S110S120				21.1	56.5	K.ALSEEMADTLEEGSAS*PTSPDYS.LD*PGPEK.M

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		SH3 protein expressed in lymphocytes	SASH3	S110T112				12.4	20.0	K.ALSEEMADTLEE <del>GS</del> A <del>S</del> *PT*SPDYSLDSPGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S108T112				6.7	42.9	K.ALSEEMADTLEE <del>GS</del> *ASPT*SPDYSLDSPGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	T308Y316				36.9		K.LLT*AAELLLOY*DTGSEEAEEGAESSQEPVAHTVSEPK.V
		SH3 protein expressed in lymphocytes	SASH3	T103S120				13.7	73.8	K.ALSEEMADT*LEE <del>GS</del> ASPTSPDYSLD <del>S</del> *PGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S97S113S120				6.7	16.6	K.ALS*EEMADTLEE <del>GS</del> ASPT <del>S</del> *PDYSLD <del>S</del> *PGPEK.M
		SH3 protein expressed in lymphocytes	SASH3	S97S120				15.8	66.0	K.ALS*EEMADTLEE <del>GS</del> ASPTSPDYSLD <del>S</del> *PGPEK.M
		SH3-domain GRB2-like 1	SH3GL1	S288				8.9	37.7	K.IAASS <del>S</del> *FR.S
		SH3-domain GRB2-like 1	SH3GL1	S287				8.2	34.2	K.IAASS <del>S</del> *SFR.S
		SH3-domain GRB2-like 1	SH3GL1	S286					22.7	K.IAAS <del>S</del> *SSFR.S
		SH3KBP1 binding protein 1	SHKBP1	S631S636				1.7	19.4	R.ISLTS* <del>L</del> H <del>SA</del> S* <del>S</del> NTLS <del>SG</del> HR.G
		SH3KBP1 binding protein 1	SHKBP1	S636S637				0.6	16.9	R.ISLTSLH <del>SA</del> S* <del>S</del> NTLS <del>SG</del> HR.G
		SHARP	SPEN	S2120S2124				13.7	24.4	R.ESGVVA <del>V</del> <del>S</del> *PE <del>K</del> <del>S</del> *ESPQEDGLSSQLK.S
		SHARP	SPEN	S312				4.9	61.2	R.SVQ <del>S</del> *AAVPAPTSQLLSLEK.D
		SHARP	SPEN	S309				22.2	40.4	R. <del>S</del> *VQSAAPAPTSQLLSLEK.D
		SHARP	SPEN	S725S727				100.0	17.5	R. <del>S</del> *Q <del>S</del> *PVHLR.R
		Shaw related voltage gated potassium channel	KCNK4	S577T578				19.2	33.2	R.R <del>S</del> *T*TRDR.N
		SHD1	SAC3D1	S356				16.2	51.9	R.TLEEVMAEEEDGTRD <del>RG</del> <del>S</del> *PA.-
		SHIP1	INPP5D	S970				39.2	32.7	R.GESPTTPPGQPPI <del>S</del> *PK.K
		SHIP1	INPP5D	T962S970				47.7	15.1	R.GESPTT*PPGQPPI <del>S</del> *PK.K
		SHIP1	INPP5D	Y864				100.0	37.5	R.EKL <del>Y</del> *DFVK.T
		SHIP1	INPP5D	S959T962				44.7	20.4	R.GE <del>S</del> *PPT*PPGQPPI <del>S</del> PK.K
		SHIP1	INPP5D	Y1021				11.1	12.2	K.NAGDTLPQEDLPLTKPEMFEN <del>FLY</del> *GSLSSFPKPAPR.K
		SHIP1	INPP5D	S959S970				12.5	17.9	R.GE <del>S</del> *PTTPPGQPPI <del>S</del> *PK.K
		Sialophorin	SPN	S336				27.5	33.1	K.GSGFPDGE <del>G</del> <del>S</del> *SR.R
		Sialophorin	SPN	S291				99.3	49.0	R.TGALVL <del>S</del> *R.G
		Sialophorin	SPN	S351S355				100.0	45.8	K. <del>S</del> *RQ <del>G</del> <del>S</del> *LAMELK.S
		Sialophorin	SPN	S355				100.0	64.8	R.QG <del>S</del> *LAMELK.S
		Sialophorin	SPN	T341				32.3	54.6	R.RP <del>T</del> *LTTFGR.R
		Sialophorin	SPN	S368				25.4	58.3	K.SGSGP <del>S</del> *LK.G
		Sialophorin	SPN	S351				35.9	52.1	K. <del>S</del> *RQ <del>GS</del> LAMEELK.S
		Sialophorin	SPN	S365				20.6	28.8	K.SG <del>S</del> *GP <del>SL</del> K.G
		SID1 transmembrane family, member 2	SIDT2	S422S424S425				33.1	44.9	R.VD <del>S</del> *M <del>S</del> <del>S</del> *VVEEDYDTLTDDSDKN <del>IV</del> .T
		SIGLEC2	CD22	S725				19.0	34.0	R.TQSQQGLQEN <del>S</del> *SGQSFFVR.N
		SIGLEC2	CD22	S717				8.9	35.1	R.TQ <del>S</del> *QQGLQENSSGQSFFVR.N
		Signal induced proliferation associated protein 1	SIPA1	S839				7.7	32.7	R.TEFLHSQN <del>SL</del> <del>S</del> *PR.S
		Signal induced proliferation associated protein 1	SIPA1	S834				35.2	22.2	R.TEFLH <del>S</del> *QN <del>SL</del> SPR.S
		Signal recognition particle receptor	SRPRA	S296S297S298				44.1	87.6	R.GTGGGQLQDL <del>CS</del> <del>S</del> <del>S</del> <del>S</del> *DDEGAAGNSTKPSATK.G
		Signal sequence receptor alpha	SSR1	S246				14.3	31.0	K.VEMGT <del>S</del> *SQNDVDM <del>SW</del> IPQETLNQINKA
		Signal sequence receptor alpha	SSR1	S247				14.3	30.0	K.VEMGT <del>S</del> *QNDVDM <del>SW</del> IPQETLNQINKA
		Signal sequence receptor alpha	SSR1	T245				28.1	19.9	K.VEMGT*SQNDVDM <del>SW</del> IPQETLNQINKA
		Signal sequence receptor alpha	SSR1	S268				31.5	16.9	K.VEM#GTSQNDVDM <del>SW</del> IPQETLNQINKA <del>S</del> *PR.R
		Signal sequence receptor alpha	SSR1	S247S268				19.0	20.7	K.VEMGT <del>S</del> *QNDVDM <del>SW</del> IPQETLNQINKA <del>S</del> *PR.R
		Signaling lymphocytic activation molecule	SLAMF1	Y281				42.9	31.8	K.SLT <del>Y</del> *AQVKPGPLQK.K
		Similar to BMP2 inducible kinase	AAK1	S36				21.6	104.0	K. <del>S</del> *MEELTVIQCTSQELPAQTGLLSQTGDVPLPAGRL.E
		Similar to BMP2 inducible kinase	AAK1	T46				2.3	54.9	K.SM#EELTVIQCT*SQELPAQTGLLSQTGDVPLPAGRL.E
		Similar to KIAA0592 protein	WASHC2A	S250S265				20.8	22.3	R.HTTQMS*DEEEDDDGDLFAD <del>S</del> *EKEEEDIEENTRPK.R
		Similar to KIAA0592 protein	WASHC2A	S539				75.8	142.8	K.GLFS*DEEDSEDLFSSQSASK.L
		Similar to KIAA0592 protein	WASHC2A	S619S620				47.0	85.3	K.ASALLF <del>S</del> *S*DEEDQWNIPASQTHLASDSR.S
		Similar to KIAA0592 protein	WASHC2A	S619				35.8	61.5	K.ASALLF <del>S</del> *SDEEDQWNIPASQTHLASDSR.S
		Similar to KIAA0592 protein	WASHC2A	S230S238				100.0	32.3	K.EEEE <del>S</del> *DEDFAH <del>S</del> *DNEQNR.H
		Similar to KIAA0592 protein	WASHC2A	S620				5.8	32.2	K.ASALLF <del>S</del> *DEEDQWNIPASQTHLASDSR.S
		Similar to RIKEN cDNA 4933437K13	SNX29	S86S92				27.1	66.2	R.YSVEA <del>S</del> *SPGHG <del>S</del> *PLSSLPSASVPESMTISELR.Q
		Similar to RIKEN cDNA 4933437K13	SNX29	S86S87				12.5	52.2	R.YSVEA <del>S</del> *SPGHGSPLSSLPSASVPESMTISELR.Q
		Similar to RIKEN cDNA 4933437K13	SNX29	S92S96				0.1	34.9	R.YSVEASSPGHG <del>S</del> *PLS <del>S</del> *LLPSASVPESMTISELR.Q
		Similar to RIKEN cDNA 4933437K13	SNX29	S86				9.8	25.5	R.YSVEA <del>S</del> *SPGHGSPLSSLPSASVPESMTISELR.Q
		Similar to RIKEN cDNA 4933437K13	SNX29	S92S100				3.4	20.5	R.YSVEASSPGHG <del>S</del> *PLSSLP <del>S</del> *ASVPESMTISELR.Q
		Similar to RIKEN cDNA 4933437K13	SNX29	S92				2.2	17.1	R.YSVEASSPGHG <del>S</del> *PLSSLPSASVPESMTISELR.Q
		Similar to S-100 protein, alpha chain	SNTN	S39				12.3	20.2	K.RI <del>S</del> *YSK.Q
		Similar to TSG118.1	KNOP1	S42				20.5	12.9	R.YSVLNNDYFAD <del>V</del> <del>S</del> *PLR.A
		Sin3 associated polypeptide 30KD	SAP30	S131				25.9	78.0	R.KG <del>S</del> *DDGGDSPVQDIDTPEVDLYQLQVNTLR.R
		Sin3 associated polypeptide 30KD	SAP30	S138				10.6	28.1	R.KGSDDDGGD <del>S</del> *PVQDIDTPEVDLYQLQVNTLR.R
		Sin3 associated polypeptide 30KD	SAP30	S131S138				101.4	89.3	R.KG <del>S</del> *DDGGD <del>S</del> *PVQDIDTPEVDLYQLQVNTLR.R

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence	
<10	(0	Protein Name	Gene	Phosphosites					
10	20	Sin3 associated polypeptide 30KD	SAF30	S131T145			-0.1	37.6	R.KG\$ <sup>S</sup> DDGGDSPVDIDIT <sup>T</sup> PEVDLYQLQVLTNR.R
20	40		SAF30	S138T145			20.0	39.6	R.KGSDDGGDS <sup>S</sup> PVQDIDIT <sup>T</sup> PEVDLYQLQVLTNR.R
30	60	SIN3A	SIN3A	T284			13.6	57.2	R.SPPVQPH <sup>T</sup> PVTISLGTAPSLQNNQPVFNHAINYNK.I
40	80	SIN3A	SIN3A	S277			1.5	53.9	R.\$ <sup>S</sup> PPVQPH <sup>T</sup> PVTISLGTAPSLQNNQPVFNHAINYNK.I
50	>100	SIN3A	SIN3A	S277T284			3.4	59.1	R.\$ <sup>S</sup> PPVQPH <sup>T</sup> PVTISLGTAPSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	S832			157.7	120.2	R.GDLS <sup>D</sup> VVEEEEEEMDVEATGAVK.K
		SIN3A	SIN3A	T287			1.0	39.2	R.SPPVQPH <sup>T</sup> PVT <sup>T</sup> ISLGTAPSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	S277S289			6.3	39.6	R.\$ <sup>S</sup> PPVQPH <sup>T</sup> PVT <sup>T</sup> IS <sup>S</sup> LGTAAPSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	T287S289			17.4	43.3	R.SPPVQPH <sup>T</sup> PVT <sup>T</sup> IS <sup>S</sup> LGTAAPSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	S277T287			7.3	54.7	R.\$ <sup>S</sup> PPVQPH <sup>T</sup> PVT <sup>T</sup> ISLGTAPSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	S289T292			-0.5	12.9	R.SPPVQPH <sup>T</sup> PVTIS <sup>S</sup> LG <sup>T</sup> APSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	T284T287			7.0	46.4	R.SPPVQPH <sup>T</sup> PVT <sup>T</sup> ISLGTAPSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	T292S295			14.8	37.8	R.SPPVQPH <sup>T</sup> PVTISLGT <sup>T</sup> AP\$ <sup>S</sup> LQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	T287T292			2.0	26.4	R.SPPVQPH <sup>T</sup> PVT <sup>T</sup> ISLGT <sup>T</sup> APSLQNNQPVFNHAINYNK.I
		SIN3A	SIN3A	Y272			6.0	20.4	K.VSKPSQLAHTPASQQTPLP\$ <sup>Y</sup> ASPR.S
		SIN3A	SIN3A	T292			4.5	41.5	R.SPPVQPH <sup>T</sup> PVTISLGT <sup>T</sup> APSLQNNQPVFNHAINYNK.I
		Single Ig IL 1R related molecule	SIGIRR	S383			-0.3	20.0	R.S\$ <sup>S</sup> EVDVSLGSR.N
		Single stranded DNA binding protein 2	SSBP2	S354			7.6	37.4	R.DGEMGGNFLNPFQSESY\$ <sup>S</sup> PSMTMSV.-
		Single stranded DNA binding protein 2	SSBP2	S350			-0.3	26.1	R.DGEMGGNFLNPFQ\$ <sup>S</sup> ESYSPSMTMSV.-
		Single stranded DNA binding protein 2	SSBP2	Y353			5.3	13.1	R.DGEM#GGNFLNPFQSES\$ <sup>Y</sup> SPSMTMSV.-
		Single stranded DNA binding protein 2	SSBP2	S360			27.6	37.6	R.DGEMGGNFLNPFQSESYSPSMTMS\$ <sup>V</sup> .-
		Single stranded DNA binding protein 2	SSBP2	S352			12.8	34.3	R.DGEMGGNFLNPFQSE\$ <sup>S</sup> YSPSMTMSV.-
		Single stranded DNA binding protein 2	SSBP2	S356			12.1	16.4	R.DGEMGGNFLNPFQSESYSP\$ <sup>S</sup> MTMSV.-
		Single stranded DNA binding protein 3	SSBP3	S387			18.6	46.8	R.DGELGGNFLHSFQNDNYS\$ <sup>S</sup> PSMTMS\$ <sup>V</sup> .-
		Single stranded DNA binding protein 3	SSBP3	S381			14.0	56.1	R.DGELGGNFLHSFQNDNYS\$ <sup>S</sup> PSMTMSV.-
		Single stranded DNA binding protein 3	SSBP3	S381S387			12.9	49.5	R.DGELGGNFLHSFQNDNYS\$ <sup>S</sup> PSMTMS\$ <sup>V</sup> .-
		Single stranded DNA binding protein 3	SSBP3	S374S387			3.7	15.0	R.DGELGGNFLHS\$ <sup>F</sup> QNDNYS\$ <sup>S</sup> PSMTMS\$ <sup>V</sup> .-
		Single stranded DNA binding protein 3	SSBP3	Y380S387			19.5	49.7	R.DGELGGNFLHSFQNDNYS\$ <sup>S</sup> PSMTMS\$ <sup>V</sup> .-
		Single stranded DNA binding protein 3	SSBP3	Y380			10.3	16.1	R.DGELGGNFLHSFQNDNYS\$ <sup>S</sup> SPSMTMSV.-
		Single stranded DNA binding protein 3	SSBP3	S383S387			7.4	37.7	R.DGELGGNFLHSFQNDNYS\$ <sup>S</sup> MTMS\$ <sup>V</sup> .-
		Single stranded DNA binding protein 3	SSBP3	S383			7.3	19.8	R.DGELGGNFLHSFQNDNYS\$ <sup>S</sup> MTMSV.-
		Single stranded DNA binding protein 3	SSBP3	T360			7.7	72.5	K.NSPNNISGISNPGT <sup>T</sup> PR.D
		Single stranded DNA binding protein 3	SSBP3	S347T360			43.3	58.5	K.N\$ <sup>S</sup> PNNISGISNPGT <sup>T</sup> PR.D
		Sirtuin 1	SIRT1	S47			100.0	75.3	R.\$ <sup>S</sup> PGEPGGAAPER.E
		Sirtuin 2	SIRT2	T365			8.0	58.6	R.EHASIDAQSGAGVNP\$ <sup>T</sup> SASPK.K
		SIT	SIT1	S182			25.1	33.2	R.ARAS\$ <sup>F</sup> PDQAYANSQPAAS.-
		SIT	SIT1	Y188			15.4	58.7	R.A\$ <sup>F</sup> PDQAY\$ <sup>Y</sup> ANSQPAAS.-
		SIT	SIT1	S191			3.5	38.2	R.A\$ <sup>F</sup> PDQAYAN\$ <sup>S</sup> QPAAS.-
		SIT	SIT1	S83			22.3	73.3	R.\$ <sup>G</sup> ES\$ <sup>V</sup> VEEVPLYGNLHYLOTGR.L
		SIT	SIT1	S80S83			84.0	63.3	R.\$ <sup>S</sup> GES\$ <sup>V</sup> VEEVPLYGNLHYLOTGR.L
		SIT	SIT1	S80Y90			19.6	24.2	R.\$ <sup>S</sup> GESVEEVPLY\$ <sup>Y</sup> GNLHYLOTGR.L
		SIT	SIT1	S80			7.5	41.6	R.\$ <sup>S</sup> GESVEEVPLYGNLHYLOTGR.L
		SIT	SIT1	S102			122.6	81.7	R.L\$ <sup>S</sup> QDPEPDQDPTLGGPAR.A
		SKI2W	SKI2L	S256			33.8	64.9	R.A\$ <sup>S</sup> LEDLVLK.E
		SKI2W	SKI2L	S270T271			13.3	47.3	K.EASTAV\$ <sup>T</sup> PEAPEPPSQEQWAI\$ <sup>P</sup> VDATSPVGFYR.L
		Skip	SNW1	S224S232			36.1	28.1	R.GPP\$ <sup>S</sup> PPAPVMH\$ <sup>S</sup> PSRK.M
		SLAIN motif family, member 2	SLAIN2	S349S353			100.0	18.8	R.N\$ <sup>S</sup> PRPS\$ <sup>S</sup> PK.Q
		Slit 3	SLIT3	S685			100.0	28.1	R.N\$ <sup>S</sup> GNPR.C
		SLIT-ROBO Rho GTPase activating protein	SRGAP2 2	S1013			4.9	64.9	R.SA\$ <sup>S</sup> TAGDIACAFPVK.S
		Smad nuclear-interacting protein 1	SNIP1	S35			100.0	32.4	R.L\$ <sup>S</sup> PEVAPPAHR.R
		SNIP1	SNIP1	S394			9.2	79.7	K.DDEDEEEEEVS\$ <sup>S</sup> DS.-
		Smad nuclear-interacting protein 1	SNIP1	S74S76			100.0	14.0	R.GV\$ <sup>S</sup> RS\$ <sup>S</sup> PPK.K
		SMAD4 interacting transcription factor	DCP1A	S315S319			33.6	70.4	K.HAPTYTIPL\$ <sup>S</sup> PVLS\$ <sup>S</sup> PTLPAEAPTAQVPPSLR.N
		SMAD4 interacting transcription factor	DCP1A	S319T321			3.2	28.4	K.HAPTYTIPLSPVLS\$ <sup>S</sup> PTLPAEAPTAQVPPSLR.N
		SMAD4 interacting transcription factor	DCP1A	S144			10.0	27.7	R.DKQSP\$ <sup>S</sup> QANGCSDHRPIDLEMLSR.A
		SMAD4 interacting transcription factor	DCP1A	T309Y310				40.5	K.HAPT\$ <sup>Y</sup> TIPLSPVLSPTLPAEAPTAQVPPSLR.N
		SMAD4 interacting transcription factor	DCP1A	S62			8.6	34.1	R.SA\$ <sup>S</sup> PYHGFTVNR.L
		SMAD4 interacting transcription factor	DCP1A	S176				40.5	R.NQMGDS\$ <sup>S</sup> NISSPGLQPSTQLSNLGTETLEEMPSGSQDK.S
		SMAD4 interacting transcription factor	DCP1A	S180				108.9	R.NQMGDSNIS\$ <sup>S</sup> PGLQPSTQLSNLGTETLEEMPSGSQDK.S
		SMAD4 interacting transcription factor	DCP1A	Y310T311			5.3	29.6	K.HAPT\$ <sup>Y</sup> TIPLSPVLSPTLPAEAPTAQVPPSLR.N
		SMAD4 interacting transcription factor	DCP1A	S353			72.1	32.1	R.\$ <sup>S</sup> PLLNQPVPELHASLIANGSPFR.A
		SMAD4 interacting transcription factor	DCP1A	S315T321			4.8	16.2	K.HAPTYTIPL\$ <sup>S</sup> PVLSPTLPAEAPTAQVPPSLR.N

Peak Area	iCV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		Small integral membrane protein 13	SMIM13	S50S60				17.6	44.2	R.ELVGD <sup>T</sup> GS <sup>S</sup> *QEGDHEPSGS <sup>S</sup> *ET <sup>E</sup> EEDTSSSPHR.I
		Small integral membrane protein 13	SMIM13	S60T62				-0.4	16.2	R.ELVGD <sup>T</sup> GSQEGDHEPSGS <sup>S</sup> *ET <sup>E</sup> EEDTSSSPHR.I
		Small integral membrane protein 13	SMIM13	T48T62				12.0	27.9	R.ELVGD <sup>T</sup> *GSQEGDHEPSGSET <sup>E</sup> EEDTSSSPHR.I
		Small integral membrane protein 13	SMIM13	T48S60				20.3	53.9	R.ELVGD <sup>T</sup> *GSQEGDHEPSGS <sup>S</sup> *ET <sup>E</sup> EEDTSSSPHR.I
		Small integral membrane protein 13	SMIM13	T48S50				1.0	27.7	R.ELVGD <sup>T</sup> *GS <sup>S</sup> *QEGDHEPSGSEET <sup>E</sup> EEDTSSSPHR.I
		Small integral membrane protein 13	SMIM13	T48S58				8.1	24.1	R.ELVGD <sup>T</sup> *GSQEGDHEP <sup>S</sup> *GSEET <sup>E</sup> EEDTSSSPHR.I
		Small integral membrane protein 13	SMIM13	S58S60				5.8	25.4	R.ELVGD <sup>T</sup> GSQEGDHEP <sup>S</sup> *GS <sup>S</sup> *ET <sup>E</sup> EEDTSSSPHR.I
		Small nuclear ribonucleoprotein 70 kD	SNRNP70	S226				35.9	31.2	R.YDERP <sup>G</sup> PS <sup>S</sup> *PLPHR.D
		Small nuclear ribonucleoprotein 70 kD	SNRNP70	S268				100.0	17.3	R.S <sup>S</sup> *RDKEER.R
		Small nuclear ribonucleoprotein 70 kD	SNRNP70	S410				100.0	101.8	R.GGGGGQDNGLEGLGND <sup>S</sup> *R.D
		Small nuclear ribonucleoprotein 70 kD	SNRNP70	S320				100.0	18.9	R.GGGGDMAEP <sup>S</sup> *EAGDAPDDGPPGLGPDGPDGPPEEK.G
		SMAP	SMAP	S17				16.8	110.5	R.SA <sup>S</sup> *PDDDLGSSNWEAADLGNEER.K
		SMAP	SMAP	S147				100.0	36.1	K.EE <sup>S</sup> *AEELQAAEH <sup>P</sup> DEVEDPK.N
		SMAP	SMAP	S17S24				1.8	24.9	R.SA <sup>S</sup> *PDDDLG <sup>S</sup> *SNWEAADLGNEER.K
		SMAP	SMAP	S17S25				8.9	52.3	R.SA <sup>S</sup> *PDDDLGSS <sup>S</sup> *NWEAADLGNEER.K
		SMAP	SMAP	S15S17				6.5	16.8	R.S <sup>S</sup> *AS <sup>S</sup> *PDDDLGSSNWEAADLGNEER.K
		SMAP	SMAP	S24				6.2	76.6	R.SASPDDDLG <sup>S</sup> *SNWEAADLGNEER.K
		SMAP	SMAP	S25				3.2	52.8	R.SASPDDDLGSS <sup>S</sup> *NWEAADLGNEER.K
		SMARCA2	SMARCA2	S1512S1516S1				41.2	53.1	K.EEE <sup>S</sup> *EDES <sup>S</sup> *NEEEEEDEEEES <sup>S</sup> *ESEAK.S
		SMARCA2	SMARCA2	S1568S1572				100.0	53.6	K.AKPVV <sup>S</sup> *DFDS <sup>S</sup> *DEEQDER.E
		SMARCA2	SMARCA2	S1572				49.2	54.9	K.AKPVV <sup>S</sup> DFDS <sup>S</sup> *DEEQDER.E
		SMARCA4	SMARCA4	S1627S1631				100.0	74.8	R.AKPVV <sup>S</sup> *DDDS <sup>S</sup> *EEEEQEEDR.S
		SMARCA4	SMARCA4	S1570S1575S1				33.2	74.3	K.EDDS <sup>S</sup> *EGEE <sup>S</sup> *EEEEEGEEGS <sup>S</sup> *EESR.S
		SMARCA4	SMARCA4	S1627S1631S1				100.0	28.6	R.AKPVV <sup>S</sup> *DDDS <sup>S</sup> *EEEEQEDRS <sup>S</sup> *GS <sup>S</sup> *EED.-
		SMARCA4	SMARCA4	T609S610				12.7	32.6	K.AENAEQGT <sup>P</sup> PAIGPDGEPLDET <sup>S</sup> *SQMSDL <sup>P</sup> VK.V
		SMARCA4	SMARCA4	S655S657S660				68.8	38.4	R.S <sup>S</sup> *DS <sup>S</sup> *EE <sup>S</sup> *GS <sup>S</sup> *EEEEEEEEEPQAAQ <sup>P</sup> PTLPVEEK.K
		SMARCA4	SMARCA4	S610S613				10.8	53.3	K.KAENAEQGT <sup>P</sup> PAIGPDGEPLDETS <sup>S</sup> *QMS <sup>S</sup> *DL <sup>P</sup> VK.V
		SMARCA4	SMARCA4	S1382				19.8	37.7	K.EVDYSD <sup>S</sup> *LTEK.Q
		SMARCA4	SMARCA4	S1380				13.9	25.1	K.EVDY <sup>S</sup> *DSLTEK.Q
		SMARCA4	SMARCA4	S1422				8.2	35.6	R.DSDAGSS <sup>S</sup> *TPTTSTR.S
		SMARCA4	SMARCA4	T609S613				8.4	16.4	K.AENAEQGT <sup>P</sup> PAIGPDGEPLDET <sup>S</sup> *SQMS <sup>S</sup> *DL <sup>P</sup> VK.V
		SMARCA5	SMARCA5	T113T115				35.0	52.3	K.QTELF <sup>A</sup> HFIQPAAGK <sup>T</sup> *PT <sup>S</sup> *PLK.M
		SMARCA5	SMARCA5	T113S116				9.0	36.0	K.QTELF <sup>A</sup> HFIQPAAGK <sup>T</sup> *PTS <sup>S</sup> *PLK.M
		SMARCA5	SMARCA5	S116				12.1	28.7	K.TPTS <sup>S</sup> *PLK.M
		SMARCA5	SMARCA5	T115S116				8.0	23.4	K.QTELF <sup>A</sup> HFIQPAAGK <sup>T</sup> *PT <sup>S</sup> *PLK.M
		SMARCAD1	SMARCAD	S211S214				12.5	54.8	R.KLS <sup>S</sup> *SSS <sup>S</sup> *EPYEEDEFNDQSIKK.T
		SMARCAD1	SMARCAD	S211S212S214				15.2	64.6	R.KLS <sup>S</sup> *S <sup>S</sup> *SS <sup>S</sup> *EPYEEDEFNDQSIKK.T
		SMARCAD1	SMARCAD	S96				10.3	48.7	R.GIQYIDL <sup>S</sup> *DSEDV <sup>S</sup> SPNCNTVQEK.T
		SMARCAD	SMARCAD	S124S127				46.7	105.8	K.TFNKDTVIV <sup>S</sup> *EP <sup>S</sup> *EDEESQGLPTMAR.R
		SMARCAD1	SMARCAD	S95S96				41.9	53.4	R.GIQYIDL <sup>S</sup> *S <sup>S</sup> *DSEDV <sup>S</sup> SPNCNTVQEK.T
		SMARCAD1	SMARCAD	S152				58.1	64.2	R.RND <sup>S</sup> ISELEDLS <sup>S</sup> *ELEDLKDAK.L
		SMARCAD1	SMARCAD	S146S152				100.0	80.4	R.RND <sup>S</sup> IS <sup>S</sup> *ELEDLS <sup>S</sup> *ELEDLKDAK.L
		SMARCAD1	SMARCAD	S124S127S132				40.8	62.4	K.DTVIIV <sup>S</sup> *EP <sup>S</sup> *EDES <sup>S</sup> *QGLPTMAR.R
		SMARCAD1	SMARCAD	S211S212S213				14.8	65.2	R.KLS <sup>S</sup> *S <sup>S</sup> *S <sup>S</sup> *SEPYEEDEFNDQSIKK.T
		SMARCAD1	SMARCAD	T119S124				29.5	43.5	K.DTVIIV <sup>S</sup> *EPSEDEESQGLPTMAR.R
		SMARCAD1	SMARCAD	T54S57				29.2	32.0	R.ANT <sup>S</sup> *PDS <sup>S</sup> *DITEK.T
		SMARCAD1	SMARCAD	S211S212				12.8	29.4	R.KLS <sup>S</sup> *S <sup>S</sup> *SEPYEEDEFNDQSIKK.T
		SMARCAD1	SMARCAD	T54S57T60S66				24.5	25.6	R.ANT <sup>S</sup> *PDS <sup>S</sup> *DIT <sup>S</sup> *EKTEDS <sup>S</sup> *VPETPONER.K
		SMARCAD1	SMARCAD	S79				16.1	38.1	R.KAS <sup>S</sup> *ISYFK.N
		SMARCAD1	SMARCAD	S127				32.8	54.4	K.DTVIIVSEPS <sup>S</sup> *EDEESQGLPTMAR.R
		SMARCAD1	SMARCAD	S95S98S103				12.4	18.4	R.GIQYIDL <sup>S</sup> *SD <sup>S</sup> *EDVVS <sup>S</sup> *PNCNTVQEK.T
		SMARCAD1	SMARCAD	S95S98				19.2	25.3	R.GIQYIDL <sup>S</sup> *SD <sup>S</sup> *EDVVS <sup>S</sup> PNCSNTVQEK.T
		SMARCC1	SMARCC1	T404				1.0	18.3	K.DSENT <sup>P</sup> VKGGT <sup>S</sup> *VADLDEQDEETV <sup>T</sup> AGGK.E
		SMARCC1	SMARCC1	S310				100.0	18.4	K.NEEPVR <sup>S</sup> *PERR.D
		SMARCC1	SMARCC1	S328S330				132.3	59.5	R.KH <sup>S</sup> *PS <sup>S</sup> *PPPTPTESR.K
		SMARCC1	SMARCC1	T398				32.3	37.0	K.DSENT <sup>T</sup> *PVK.G
		SMARCC1	SMARCC1	S328S330T335				66.3	29.3	R.KH <sup>S</sup> *PS <sup>S</sup> *PPPT <sup>T</sup> *PTESR.K
		SMARCC1	SMARCC1	S573				100.0	19.8	R.S <sup>S</sup> *PQVPAQQMLN <sup>F</sup> PEK.N
		SMARCC2	SMARCC2	S347				71.0	51.3	K.DMDEPS <sup>S</sup> *PVPNV <sup>E</sup> EVTL <sup>P</sup> K.T
		SMARCC2	SMARCC2	S302S304				22.8	30.3	R.KRS <sup>S</sup> *PS <sup>S</sup> *PSPTPEAK.K
		SMARCC2	SMARCC2	S302T308				8.7	12.6	R.KRS <sup>S</sup> *PSPPT <sup>T</sup> *PEAK.K
		SMC4 structural maintenance of chromosomes 4	SMC4	S22S28				40.3	35.7	R.RREEGPPPP <sup>S</sup> *PDGASS <sup>S</sup> *DAEPEPPSGR.T

Peak Area		%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajIB		Ascor	MOWSE	Sequence
			Protein Name	Gene	Phosphosites						
			SMC4 structural maintenance of SMC4 chromosomes 4	S28					10.3	19.7	R.RREEGPPPPSPDGAS*SDAEPEPPSGR.T
			SMC4 structural maintenance of SMC4 chromosomes 4	S22S27					33.0	38.9	R.EEGPPPPS*PDGAS*SDAEPEPPSGR.T
			SMC4 structural maintenance of SMC4 chromosomes 4	S27S28					4.8	33.6	R.EEGPPPPSPDGAS*SDAEPEPPSGR.T
			SMC4 structural maintenance of SMC4 chromosomes 4	S41					13.6	121.3	R.TES*PATAETASELDNR.S
			SMC4 structural maintenance of SMC4 chromosomes 4	T44					19.1	64.2	R.TESPAT*AAETASELDNR.S
			SMC4 structural maintenance of SMC4 chromosomes 4	S27					20.6	24.4	R.RREEGPPPPSPDGAS*SDAEPEPPSGR.T
			SMCR7L MIEF1	S94					33.4	52.6	R.S*LQTLPTDSSTFDTDTCPPRPKPVARK
			SMCR7L MIEF1	T97					-0.4	60.5	R.SLQT*LPTDSSTFDTDTCPPRPKPVARK
			SMEK homolog 1, suppressor of mek1 PPP4R3A	S771S777					16.9	15.5	K.TNLTQSSTNTLPGSPGS*PGSPGS*PGSPGVPK.N
			SMEK homolog 1, suppressor of mek1 PPP4R3A	S774S780					16.3	10.8	K.TNLTQSSTNTLPGSPGSPGS*PGSPGS*PGSPGVPK.N
			SMEK homolog 1, suppressor of mek1 PPP4R3A	S117S126					18.3	19.7	K.DPSVDITQDLVDES*EERFDDMS*SPGLELPSECLSR.L
			SMEK homolog 2, suppressor of mek1 PPP4R3B	S117					82.1	78.1	K.DPSVEVTQDLDES*EER.F
			Smith Magenis syndrome chromosome SMCR8 region candidate 8 protein	S417					13.9	36.5	K.VLISVGS*YK.S
			SNAP190 SNAPC4	S1398S1400					46.1	41.7	R.VGS*ES*EDEDLLSELELADR.D
			SNAP190 SNAPC4	S1398S1400S1					100.0	121.9	R.VGS*ES*EDEDLLS*ELELADR.D
			SLK	S189					9.8	67.3	R.RDS*FIGTPYWMapevVMCETSK.D
			SNF1 sucrose nonfermenting like kinase SLK	Y195					22.4	61.3	R.DSFIGTPY*WMAPEVVMCETSK.D
			SNF1 sucrose nonfermenting like kinase SLK	S779					4.0	37.2	K.DSGS*ISLQETR.R
			Sno SBN01	S688S692					10.1	28.9	K.LYSLLGIDLTAPS*NNSS*PR.D
			Sno SBN01	S793					42.4	135.6	K.S*IDPDSIQSALLASGLGSK.R
			Sno SBN01	S798					2.8	14.5	K.SIDPD*S*IQSALLASGLGSK.R
			SNX17 SNX17	S437S440					35.0	33.8	K.LSSKLS*AVS*LR.G
			SNX5 SNX5	S22					4.5	46.1	R.SVS*VDLNVDPQLDIPDALSER.D
			SODD BAG4	Y255S259						26.2	R.Y*PWPS*SAPSAPPGLNLYMTESTSPWPSSGSPGSPPPVPQPK. n
			Soluble lamin-associated protein of 75 kDa FAM169A	S575S576					13.0	60.3	K.AVDS*S*SEEIEVVPVDRR.N
			Soluble scavenger receptor cysteine-rich domain-containing protein SSC5D	S174					100.0	26.3	K.KS*PRPK.Q
			Solute carrier family 16 (monocarboxylic acid transporters), member 1	S461S467					9.4	53.0	K.KE*S*KEEETS*IDVAGKPNEVT.K.A
			Solute carrier family 16 (monocarboxylic acid transporters), member 1	S461					68.5	65.6	K.KE*S*KEEETSIDVAGKPNEVT.K.A
			Solute carrier family 16 (monocarboxylic acid transporters), member 1	S467					5.9	20.1	K.EEETS*IDVAGKPNEVT.K.A
			Solute carrier family 16 (monocarboxylic acid transporters), member 1	S461T466					44.5	34.8	K.KE*S*KEET*SIDVAGKPNEVT.K.A
			Solute carrier family 16 (monocarboxylic acid transporters), member 1	T466					69.7	41.0	K.EEET*SIDVAGKPNEVT.K.A
			Solute carrier family 16 (monocarboxylic acid transporters), member 1	S461T466S467					35.9	14.4	K.KE*S*KEET*SIDVAGKPNEVT.K.A
			Solute carrier family 16 (monocarboxylic acid transporters), member 1	S213					23.6	38.8	K.SKAS*LEK.A
			Solute carrier family 20 member 1 SLC20A1	Y421					14.3	64.9	R.NNSYTS*Y*TAICGMPLDSFRL.A
			Solute carrier family 20 member 1 SLC20A1	T419					9.1	80.5	R.NNSYT*SYTMAICGMPLDSFRL.A
			Solute carrier family 20 member 1 SLC20A1	Y418					-0.3	17.5	R.NNSY*TSYTMAICGMPLDSFRL.A
			Solute carrier family 20 member 1 SLC20A1	T422					0.8	76.4	R.NNSYTSYT*MAICGMPLDSFRL.A
			Solute carrier family 20 member 1 SLC20A1	S417					5.2	22.7	R.NNS*YTSYTMAICGMPLDSFRL.A
			Solute carrier family 20, member 2 SLC20A2	S385						68.5	R.NNS*YTCYTAICGLPV/HATFRA
			Solute carrier family 20, member 2 SLC20A2	Y389					5.5	10.7	R.NNSYTCY*TAICGLPV/HATFRA
			Solute carrier family 20, member 2 SLC20A2	S324					28.8	11.0	K.S*PISNGTFGFGHTR.S
			Solute carrier family 25, member 46 SLC25A46	T35					12.2	61.8	R.SFS*TGSDLGHWVTPPDIPGSR.N
			Solute carrier family 25, member 46 SLC25A46	S34T35					10.9	60.9	R.SFS*TGSDLGHWVTPPDIPGSR.N
			Solute carrier family 25, member 46 SLC25A46	S34S37					9.4	54.3	R.SFS*TG*DLGHWVTPPDIPGSR.N
			Solute carrier family 25, member 46 SLC25A46	S37					14.7	63.0	R.SFSTGS*DLGHWVTPPDIPGSR.N
			Solute carrier family 25, member 46 SLC25A46	S34					12.2	59.3	R.SFS*TGSDLGHWVTPPDIPGSR.N
			Solute carrier family 26 (Sulfate transporter), member 2	S16					70.4	49.6	R.DS*AEGNDSPYSGIHLELQR.E
			Solute carrier family 35 member C2 SLC35C2	S335					21.2	86.4	K.GLGS*SPDELLLR.S
			Solute carrier family 35, member F2 SLC35F2	S371					17.8	38.0	K.LEENLQETHS*AVL.-
			Solute carrier family 38 member 1 SLC38A1	S52					9.2	16.0	R.S*LTNSHLEK.K
			Solute carrier family 38 member 1 SLC38A1	S52T54					9.6	31.1	R.S*LT*NSHLEK.K
			Solute carrier family 38 member 1 SLC38A1	T54S56					10.6	40.9	R.SLT*NS*HLEK.K
			Solute carrier family 38 member 1 SLC38A1	S52S56					17.5	39.2	R.S*LTNS*HLEK.K
			Solute carrier family 38 member 1 SLC38A1	T17S28					2.1	41.9	K.SGLELTELQNM*TPEDDNISND*NDFTVEVNGQINSK.F
			Solute carrier family 38 member 1 SLC38A1	T54					-0.2	60.4	R.SLT*NSHLEK.K
			Solute carrier family 38 member 1 SLC38A1	S6T11						30.5	K.S*GLELT*ELQNM*TPEDDNISND*NDFTVEVNGQINSK.F
			Solute carrier family 38 member 1 SLC38A1	S25S28					12.2	60.6	K.SGLELTELQNM*TPEDDNISND*NDFTVEVNGQINSK.F
			Solute carrier family 39 (zinc transporter), SLC39A3 member 3	T120S129					7.6	70.4	K.EKPSFIDLET*FNAGSDVGS*DSEYSPFMGGAR.G
			Solute carrier family 39 (zinc transporter), SLC39A3 member 3	S125S129					28.6	103.0	K.EKPSFIDLET*FNAGS*DVGSDSEYSPFMGGAR.G
			Solute carrier family 39 (zinc transporter), SLC39A3 member 3	S125S129S131					18.4	98.3	K.EKPSFIDLET*FNAGS*DVGSDS*EYESPFMGGAR.G
			Solute carrier family 39 (zinc transporter), SLC39A3 member 3	S125S129Y133					9.1	72.6	K.EKPSFIDLET*FNAGS*DVGSDSEY*ESPFMGGAR.G
			Solute carrier family 39 (zinc transporter), SLC39A3 member 3	T120S129S131					1.2	22.0	K.EKPSFIDLET*FNAGSDVGS*DSEYSPFMGGAR.G



Peak Area		%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajIB	Ascor	MOWSE	Sequence
<10		0							
10		20							
20		40							
40		60							
60		80							
80		100							
>100									
	Protein Name	Gene	Phosphosites						
	SON DNA binding protein	SON	S1782S1783				-0.3	40.7	R.ASESS* <b>S</b> *SEEKDDYEIVK.V
	SON DNA binding protein	SON	S1774S1782S1				4.4	19.1	R.SASPVS <b>S</b> *MPERASE <b>S</b> * <b>S</b> *SEEKDDYEIVK.V
	SON DNA binding protein	SON	S1769S1782S1				3.3	24.9	R.SAAS*PVVSSMPERASE <b>S</b> * <b>S</b> * <b>S</b> *EEKDDYEIVK.V
	SON DNA binding protein	SON	S1769S1773S1				-4.0	19.1	R.SAAS*PVV <b>S</b> * <b>S</b> *MPERAS <b>S</b> *ESSEEKDDYEIVK.V
	SON DNA binding protein	SON	S2020T2022				100.0	16.0	R <b>S</b> *RT*PLRR.R
	SON DNA binding protein	SON	S1766S1769S1				5.7	12.4	R <b>S</b> *AAS*PVV <b>S</b> *MPERASESS <b>S</b> *EEKDDYEIVK.V
	SON DNA binding protein	SON	S1766S1769S1				6.4	19.7	R <b>S</b> *AAS*PVV <b>S</b> * <b>S</b> MPERASESS <b>S</b> *EEKDDYEIVK.V
	SON DNA binding protein	SON	S1769S1773S1				6.7	21.9	R.SAAS*PVV <b>S</b> * <b>S</b> *MPERASESS <b>S</b> *EEKDDYEIVK.V
	SON DNA binding protein	SON	S1769S1773S1				1.7	23.5	R.SAAS*PVV <b>S</b> * <b>S</b> MPERAS <b>S</b> * <b>S</b> *SEEKDDYEIVK.V
	Sortilin	SORT1	S825				27.8	41.3	K.SGYHDS <b>S</b> *DEDLLE.-
	Sorting nexin 1	SNX1	S32S39				34.4	93.0	R.LPPPPGLEPESEGAAGGS*EPEAGD <b>S</b> *DTEGEDIFTGAAVVSK.H
	Sorting nexin 1	SNX1	S39T41				3.1	31.7	R.LPPPPGLEPESEGAAGGSEPEAGD <b>S</b> *DT*EGEDIFTGAAVVSK.H
	Sorting nexin 1	SNX1	S25S32S39				91.2		R.LPPPPGLEPES*EGAAGGS*EPEAGD <b>S</b> *DTEGEDIFTGAAVVSK. L
	Sorting nexin 1	SNX1	S25S39T41				6.4	52.1	R.LPPPPGLEPES*EGAAGGSEPEAGD <b>S</b> *DT*EGEDIFTGAAVVSK. ..
	Sorting nexin 1	SNX1	S32S39T41				29.5	47.0	R.LPPPPGLEPESEGAAGGS*EPEAGD <b>S</b> *DT*EGEDIFTGAAVVSK. ..
	Sorting nexin 1	SNX1	S25S32				81.8		R.LPPPPGLEPES*EGAAGGS*EPEAGDSDTTEGEDIFTGAAVVSK.H
	Sorting nexin 1	SNX1	S32T41				5.2	56.5	R.LPPPPGLEPESEGAAGGS*EPEAGDSDT*EGEDIFTGAAVVSK.H
	Sorting nexin 11	SNX11	S191S192					14.7	R. D <b>S</b> *H <b>S</b> *DGGDEECVPLVLMVADIAKCEVDSI EEDT DSI SEDV PCKE
	Sorting nexin 15	SNX15	S179S180					20.3	R.RGLEEEVVPVDP <b>PPS</b> * <b>S</b> *PQAEALDLLFNCESTEEASGSPAR.G
	Sorting nexin 15	SNX15	S179S201				6.5	14.4	R.RGLEEEVVPVDP <b>PPS</b> *SPAQEALDLLFNCESTEEASG <b>S</b> *PAR.G
	Sorting nexin 2	SNX2	S185				55.8	32.6	R.RF <b>S</b> *DFLGLHSK.L
	Sorting nexin 2	SNX2	S119				33.7	58.4	K.SM <b>S</b> *APVIFDR.S
	Sorting nexin 3	SNX3	Y71				8.9	39.7	R.RY* <b>S</b> DFEWLR.S
	Sorting nexin 3	SNX3	S72				27.6	46.7	R.RY <b>S</b> *DFEWLR.S
	Source of immunodominant MHC associated peptides	STT3B	S498S499				77.9	32.0	R.ENPPVED <b>S</b> * <b>S</b> *DEDKRNQGNLYDK.A
	SP100	SP100	S407S409S410				101.6	43.9	R.VIGQDHDF <b>S</b> * <b>S</b> * <b>S</b> *EEEAPAEASSGALR.S
	SP100	SP100	S157				100.0	45.8	K.GFENVHDKLPLQ <b>S</b> *EEEEER.E
	SP100	SP100	S451S452				25.5	41.9	R.RF <b>S</b> * <b>S</b> *SDFSLNGEELQETCSSSLR.R
	SP100	SP100	S18				72.0	47.0	R.LNECIS*PVANEMNHLPAHSHDLQR.M
	SP100	SP100	S327S328S331				27.4	41.7	R.THHNQASDIVIS* <b>S</b> *ED <b>S</b> *EG <b>S</b> *T*DVDEPLEVISAPR.S
	SP110 nuclear body protein	SP110	S256				103.8	37.5	R.DN <b>S</b> *PEPNDEEPQEVSTSPDKK.G
	SP110 nuclear body protein	SP110	S244				39.1	39.1	R.DKEDPQEMPH <b>S</b> *PLGSMPEIR.D
	SPAK	STK39	S385				161.4	104.7	K.TEDGGWEW <b>S</b> *DDEMDEK.S
	SPAK	STK39	S370				17.8	36.5	R.RVPG <b>S</b> *SGHLHK.T
	Spatacsin	SPG11	T1956S1969S1				3.9	53.9	R.VHST*SSLD <b>S</b> QKFVTV <b>PS</b> * <b>S</b> *NEVVTNLEVLTSK.C
	Spatacsin	SPG11	S1955T1966S1				9.6	51.5	R.VH <b>S</b> *TSSLD <b>S</b> QKFVTV <b>PS</b> * <b>S</b> *NEVVTNLEVLTSK.C
	Spatacsin	SPG11	S1955S1958S1				9.6	96.7	R.VH <b>S</b> *TSS*LD <b>S</b> *QKFVTVPSSNEVVTNLEVLTSK.C
	Spatacsin	SPG11	T1956S1958S1				3.6	35.3	R.VHST*SS*LD <b>S</b> *QKFVTVPSSNEVVTNLEVLTSK.C
	Spatacsin	SPG11	T1956S1957S1				0.4	24.5	R.VHST* <b>S</b> *SLD <b>S</b> *QKFVTVPSSNEVVTNLEVLTSK.C
	Spatacsin	SPG11	S1969S1970T1				-0.2	23.6	R.VHSTSSLD <b>S</b> QKFVTV <b>PS</b> * <b>S</b> *NEVVTNLEVLTSK.C
	Spatacsin	SPG11	S1955S1958S1				6.4	64.4	R.VH <b>S</b> *TSS*LD <b>S</b> QKFVTV <b>PS</b> * <b>S</b> *NEVVTNLEVLTSK.C
	Spatacsin	SPG11	S1955T1956T19				0.1	14.7	R.VH <b>S</b> *T*SSLD <b>S</b> QKFVTV <b>PS</b> SNEVVTNLEVLTSK.C
	SPECC1-like	SPECC1L	S384				33.8	22.4	R.KG <b>S</b> *SGNA <b>S</b> EVSVACLT <b>R</b> .I
	SPECC1-like	SPECC1L	S389				9.1	58.9	R.KGSSGNA <b>S</b> *EVSVACLT <b>R</b> .I
	SPECC1-like	SPECC1L	S973S981				6.9	24.7	R.DISAQEGASPASLMAMGT <b>S</b> *PQLSS <b>S</b> *PTASVTP <b>T</b> R.S
	SPECC1-like	SPECC1L	S887				20.7	22.0	R.H <b>S</b> *ISGP <b>I</b> STSKPLTASDK.R
	Spectrin, alpha, non-erythrocytic 1 (alpha-SPTAN1 fodrin)	S1031					10.9	32.9	K.KLDPAQ <b>S</b> *R.E
	Spectrin, alpha, non-erythrocytic 1 (alpha-SPTAN1 fodrin)	S1190					45.2	33.8	K.TA <b>S</b> *PWK.S
	Spectrin, alpha, non-erythrocytic 1 (alpha-SPTAN1 fodrin)	S1217					100.0	53.3	R <b>S</b> *LQQLAER.S
	Spectrin, alpha, non-erythrocytic 1 (alpha-SPTAN1 fodrin)	S1029						18.1	K.KLDPAQ <b>S</b> *ASR.E
	Spectrin, beta, non erythrocytic 5	SPTBN5	S766S767				100.0	36.4	R.R <b>S</b> * <b>S</b> *LER.A
	Sperm associated antigen 9	SPAG9	S716S719				17.2	87.2	R.SA <b>S</b> *QSS*LDKLDQELK.E
	Sperm associated antigen 9	SPAG9	S203T217				100.0	49.7	K.ERPIS*LGIFPLPAGDGL <b>T</b> *PDAQK.G
	Sperm associated antigen 9	SPAG9	T217				82.2	30.2	K.ERPISLGIFPLPAGDGL <b>T</b> *PDAQK.G
	Sperm associated antigen 9	SPAG9	S718S719				6.1	22.1	R.SAQ <b>S</b> * <b>S</b> *LDKLDQELK.E
	Sperm associated antigen 9	SPAG9	S718				20.1	51.8	R.SAQ <b>S</b> *SLDKLDQELK.E
	Sperm associated antigen 9	SPAG9	S716S718				3.2	22.6	R.SA <b>S</b> *Q <b>S</b> *SLDKLDQELK.E
	Sperm associated antigen 9	SPAG9	S536S537				19.4	11.6	K.R <b>S</b> * <b>S</b> *IWQFFSR.L
	Sperm associated antigen 9	SPAG9	S203				100.5	53.1	K.ERPIS*LGIFPLPAGDGL <b>T</b> PDAQK.G
	Sperm associated antigen 9	SPAG9	S537S543				15.0	13.0	K.R <b>S</b> * <b>S</b> *IWQFF <b>S</b> *R.L
	Sperm specific antigen 2	S2FA2	S739				28.9	82.2	R.S <b>S</b> *LPT <b>T</b> LLSPVR.V
	Sperm specific antigen 2	S2FA2	S737				12.2	69.2	R <b>S</b> *QSLPT <b>T</b> LLSPVR.V



Peak Area	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM	Protein Name	Gene	Phosphosites	CarT	RajiB	Ascor	MOWSE	Sequence
		Sperm specific antigen 2	SFA2	S1055			8.4	18.9	R.S*ADNLSCPSPLNVMEPVTELMQEQSYLK.S
		Spermatid perinuclear RNA binding protein	STRBP	S465S466			4.6	36.0	K.VLQAMGYPTGFDADIECMS* <b>S</b> *DEKSDNESK.N
		Spermatid perinuclear RNA binding protein	STRBP	T455S470			11.8	11.1	K.VLQAMGYPT*GFDADIECMSDEK <b>S</b> *DNESK.N
		Spermatid perinuclear RNA binding protein	STRBP	Y453T455			4.8	26.3	K.VLQAMG <b>Y</b> *PT*GFDADIECMSDEKSDNESK.N
		Spermatogenesis associated 5 like 1	SPATASL1	S93S95			100.0	11.4	R.RS* <b>L</b> S*LNRL.L
		Sphingosine kinase 2	SPHK2	T402S414			41.7	29.0	R.AKSELT*LTDPAPPM <b>H</b> *PLHR.S
		Sphingosine kinase 2	SPHK2	S399S414			48.4	12.2	R.AK <b>S</b> *ELTLTPDPAPPM <b>H</b> *PLHR.S
		Sphingosine-1-phosphate phosphatase 1	SGPP1	S112			35.4	80.2	R.NS*LTGEEGQLAR.V
		Spliceosome associated protein 145	SF3B2	S307S309			12.8	50.7	R.SSLGQ <b>S</b> * <b>A</b> S*ETEDTVSVSK.K
		Spliceosome associated protein 145	SF3B2	T780			5.9	75.2	K.IEEAMDG <b>S</b> ET*PQLFTVLPEKR.T
		Spliceosome associated protein 145	SF3B2	S360			13.1	74.7	R.G <b>S</b> *DSPAADVEIEYVTEEP EIEPNFIFFK.R
		Spliceosome associated protein 145	SF3B2	S431S435S436			100.0	50.8	K.GFEEHHK <b>S</b> * <b>D</b> DD <b>S</b> * <b>S</b> *DDEQEKKEAPK.L
		Spliceosome associated protein 145	SF3B2	S360S362			2.7	31.3	R.SRG <b>S</b> * <b>D</b> S*PAADVEIEYVTEEP EIEPNFIFFK.R
		Spliceosome associated protein 145	SF3B2	S357S362			5.5	26.1	R. <b>S</b> *RG <b>S</b> D <b>S</b> *PAADVEIEYVTEEP EIEPNFIFFK.R
		Spliceosome associated protein 145	SF3B2	T706S714S718			15.8		R. T*GMDI EDG <b>S</b> DEE <b>S</b> * <b>H</b> EEEEEE <b>S</b> * <b>S</b> DEEDTVSVSK.E
		Spliceosome associated protein 145	SF3B2	T706S714S718			17.9		R. T*GMDI EDG <b>S</b> DEE <b>S</b> * <b>H</b> EEEEEE <b>S</b> * <b>S</b> DEEDTVSVSK.E
		Spliceosome associated protein 145	SF3B2	S302S309			8.5	18.4	R. <b>S</b> *SLGQ <b>S</b> A <b>S</b> *ETEDTVSVSK.E
		Spliceosome associated protein 145	SF3B2	S309			10.9	47.1	R.SSLGQ <b>S</b> A <b>S</b> *ETEDTVSVSK.K
		Spliceosome associated protein 145	SF3B2	S778			64.0	96.9	K.IEEAMDG <b>S</b> *ETPQLFTVLPEKR.T
		Spliceosome associated protein 145	SF3B2	S362			-0.1	11.3	R.GSD <b>S</b> *PAADVEIEYVTEEP EIEPNFIFFK.R
		Splicing factor 1	SF1	S80S82			32.3	15.7	R.TGDLGIPPNPEDR <b>S</b> * <b>P</b> S*PEPIYNSEGK.R
			SF3A1	S329			7.8	49.5	K.FGESEEVEMIEVE <b>S</b> * <b>D</b> EEDDKQEK.A
		Splicing factor 3 subunit 1	SF3A1	S344				25.5	K. T*GMDI EDG <b>S</b> DEE <b>S</b> * <b>H</b> EEEEEE <b>S</b> * <b>S</b> DEEDTVSVSK.E
		Splicing factor 3 subunit 1	SF3A1	S359			57.0	68.0	K.AEPPSQLDQDOTQVQMD <b>E</b> G <b>S</b> * <b>D</b> EEEGQK.V
		Splicing factor 3A, subunit 3	SF3A3	S365S367S369			102.2	76.2	R.EEEEEQ <b>S</b> * <b>E</b> S* <b>E</b> S*EDEENIYNPK.N
		Splicing factor 3B subunit 1	SF3B1	S308T313			20.8	52.4	R.DTPGHG <b>S</b> *GWAET*PR.T
		Splicing factor 3B subunit 1	SF3B1	T244T248			19.1	53.3	K.G <b>S</b> ET*PGAT*PGSK.I
		Splicing factor 3B subunit 1	SF3B1	T235			100.0	20.3	R.WDET*PGRA
		Splicing factor 3B subunit 1	SF3B1	T434T436			27.5	106.6	R.KLTAT* <b>P</b> T*PLGGMGTGFHMQTEDR.T
		Splicing factor 3B subunit 1	SF3B1	T303T313			20.5	23.2	R.DT*PGHGS <b>G</b> WAET*PR.T
		Splicing factor 3B subunit 1	SF3B1	S129T142			12.6	16.4	R.TMIIS*PERLPFADGGK <b>T</b> *PDPK.M
		Splicing factor 3B subunit 1	SF3B1	T211			12.7	23.6	R.WDQTADQTPGAT*PK.K
		Splicing factor 3B subunit 1	SF3B1	T267T273			17.3	16.2	K.IWDP <b>T</b> * <b>P</b> S*HTPAGAATPGRGDT*PGHATPGHGATSSAR.K
		Splicing factor 3B subunit 1	SF3B1	T257S259				12.0	K.IWDP <b>T</b> * <b>P</b> S*HTPAGAATPGRGDT*PGHATPGHGATSSAR.K
		Splicing factor 3B subunit 1	SF3B1	T223S229			9.3	16.3	K.KLSSWDQ <b>A</b> ET*PGHT <b>P</b> S*LR.W
		Splicing factor 3B subunit 1	SF3B1	T303S308			7.8	10.8	R.DT*PGHGS*GWAETPR.T
		Splicing factor 3B subunit 1	SF3B1	T223T227			10.6	17.3	K.LSSWDQ <b>A</b> ET*PGHT*PSLR.W
		Splicing factor 4	SUGP1	S485			31.5	99.4	K.AVQHQHQHG <b>Y</b> D <b>S</b> *DEEVDSELGTWEHQLR.R
		Splicing factor 4	SUGP1	S491			5.8	45.7	K.AVQHQHQHG <b>Y</b> D <b>S</b> DEE <b>V</b> D <b>S</b> *ELGTWEHQLR.R
		Splicing factor arginine/serine rich 5	SRSF5	S248S250S253			100.0	34.7	R. <b>S</b> * <b>K</b> S* <b>P</b> AS*VDR.Q
		Splicing factor arginine/serine rich 5	SRSF5	S250S253			100.0	21.8	K. <b>S</b> * <b>P</b> AS*VDR.Q
		Splicing factor arginine/serine rich 5	SRSF5	S248S250			18.5	36.4	R. <b>S</b> * <b>K</b> S* <b>P</b> ASVDR.Q
		Splicing factor arginine/serine rich 5	SRSF5	S116				20.9	R.LIVEN <b>L</b> S*SR.C
		Splicing factor HCC1	RBM39	S136			212.6	64.8	K.DK <b>S</b> *PVREPIDNLTP <del>EE</del> R.D
		Splicing factor HCC1	RBM39	Y95			42.3	19.9	R. <b>Y</b> * <b>R</b> S* <b>P</b> YSGPK.F
		Splicing factor HCC1	RBM39	S127S129			100.0	17.6	R. <b>S</b> * <b>K</b> S* <b>P</b> FRK.D
		Splicing factor HCC1	RBM39	S125S127S129			100.0	11.9	R. <b>S</b> * <b>R</b> S* <b>K</b> S* <b>P</b> FR.K
		Splicing factor HCC1	RBM39	S97			-10.2	29.8	R.YR <b>S</b> * <b>P</b> YSGPK.F
		Splicing factor YT521-B	YTHDC1	S424			7.7	54.5	R.LSSESHHGG <b>S</b> *PIHWVLPAGMSAK.M
		Splicing factor YT521-B	YTHDC1	S308			100.0	40.9	R.G <b>S</b> *PIVFDR.S
		Splicing factor YT521-B	YTHDC1	S146T148			24.6	21.1	R.AK <b>S</b> * <b>P</b> T*PDGSR.I
		Splicing factor YT521-B	YTHDC1	S119			2.8	16.2	R.L <b>S</b> S* <b>S</b> ASR.E
		Splicing factor YT521-B	YTHDC1	S419			-0.4	33.4	R.LSSE <b>S</b> *HHGGSPIHWVLPAGMSAK.M
		Splicing factor YT521-B	YTHDC1	S417			3.0	35.2	R.L <b>S</b> S*ESHGGSPIHWVLPAGMSAK.M
		Splicing factor, 45 kd	RBM17	S222			10.1	119.7	R. <b>S</b> *PTGPSNSFLANMGGTVAHK.I
		Splicing factor, 45 kd	RBM17	S155			76.7	77.7	R.RPDPD <b>S</b> *DEDEDYER.E
			RBM17	S229			4.3	68.3	R.SPTGPS <b>N</b> S*FLANM#GGTVAHK.I
		Splicing factor, 45 kd	RBM17	S227			0.5	74.4	R.SPT*GPS <b>N</b> S*FLANMGGTVAHK.I
			RBM17	T224			-0.0	16.3	R.SP <b>T</b> *GPSNSFLANMGGTVAHK.I
		Splicing factor, arginine/serine rich 1	SRSF1	Y237S238			6.1	15.6	R. <b>Y</b> * <b>S</b> *PRHSR.S
		Splicing factor, arginine/serine rich 1	SRSF1	S199			14.0	42.8	R. <b>S</b> * <b>P</b> SYGR.S
		Splicing factor, arginine/serine rich 1	TRA2B	Y226S227			15.0	15.9	R.S <b>Y</b> * <b>S</b> *PRR.S

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites					
		Splicing factor, arginine/serine rich 1	TRA2B	<a href="#">S225</a> <a href="#">Y226</a> <a href="#">S227</a>			9.7	16.7	R.SRS*Y*Y*SPR.R
		Splicing factor, arginine/serine rich 1	SRSF1	<a href="#">S199</a> <a href="#">S201</a>			14.5	14.1	R.VKVDGPR*PS*YGR.S
		Splicing factor, arginine/serine rich 1	SRSF1	<a href="#">S231</a> <a href="#">S234</a>			100.0	18.0	R.RS*RGSP*RY
		Splicing factor, arginine/serine rich 1	SRSF1	<a href="#">Y237</a> <a href="#">S242</a>			10.8	12.5	R.Y*SPRHS*R.S
		Splicing factor, arginine/serine rich 1	TRA2B	<a href="#">S223</a> <a href="#">S225</a> <a href="#">Y226</a>			8.3	13.4	R.S*RS*Y*SPR.R
		Splicing factor, arginine/serine rich 1	SRSF1	<a href="#">S201</a> <a href="#">Y202</a>			5.5	14.8	R.VKVDGPRSP*Y*YGR.S
		Splicing factor, arginine/serine rich 1	TRA2B	<a href="#">S223</a> <a href="#">S225</a> <a href="#">S227</a>			9.0	17.7	R.S*RS*Y*SPR.R
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">S483</a>			100.0	30.4	K.VNGDDHHIEDMDMS*D.-
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">S207</a>			27.7	71.5	K.LNHVAAGLV*PSLK.S
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">S323</a> <a href="#">T325</a>			100.0	17.9	R.S*KT*PPK.S
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">S449</a>			29.8	36.8	K.KPIETGS*PK.T
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">T260</a> <a href="#">S262</a>			13.1	25.0	R.RRT*PS*SSR.H
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">Y432</a>			9.1	34.2	R.DYDEEEQGY*DSEKEK.K
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">S434</a>			9.7	31.6	R.DYDEEEQGYDS*EKEK.K
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">T260</a> <a href="#">S263</a>			4.0	11.2	R.RRT*PS*SSR.H
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">T447</a>			-19.1	40.0	K.KPIET*GSPK.T
		Splicing factor, arginine/serine rich 11	SRSF11	<a href="#">S263</a> <a href="#">S264</a>			6.3	15.0	R.RRTPSS*SR.H
		Splicing factor, arginine/serine rich 2	RTBDN	<a href="#">S119</a> <a href="#">S121</a>			100.0	19.0	R.RS*RS*PR.R
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S145</a>			19.1	21.7	R.SRY*RS
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S191</a>			45.2	47.3	R.S*PPPVSK.R
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S189</a> <a href="#">S191</a>			61.7	31.0	R.S*RS*PPPVSK.R
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S187</a> <a href="#">S189</a> <a href="#">S191</a>			70.4	21.7	R.S*RS*RS*PPPVSK.R
		SRSF2	<a href="#">S26</a>				15.0	35.2	R.TS*PDTLR.R
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S206</a> <a href="#">S208</a>			45.0	28.6	R.S*KS*PPKSPEEEAGVSS.-
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S206</a> <a href="#">S208</a> <a href="#">S220</a>			14.3	38.8	R.S*KS*PPKSPEEEAGVS*.-
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S206</a> <a href="#">S208</a> <a href="#">S212</a>			41.8	12.1	R.S*KS*PPK*PEEEAGVSS.-
		Splicing factor, arginine/serine rich 2	SRSF2	<a href="#">S206</a> <a href="#">S212</a> <a href="#">S220</a>			4.7	22.1	R.S*KSPPK*PEEEAGVS*.-
		Splicing factor, arginine/serine-rich 2, SCAF11 interactino protein	<a href="#">S796</a> <a href="#">S802</a>				18.3	32.2	R.FHS*PSTTW*PNKDTPQEK.K
		Splicing factor, arginine/serine-rich 2, SCAF11 interactino protein	<a href="#">S796</a> <a href="#">S798</a>				33.6	44.6	R.FHS*PS*TTWSPNKDTPQEK.K
		Splicing factor, arginine/serine-rich 2, SCAF11 interactino protein	<a href="#">S338</a>				11.0	46.4	R.S*PIDNSGCDAPGNSNPPLSVPPSAESEK.Q
		Splicing factor, arginine/serine-rich 2, SCAF11 interacting protein	<a href="#">S901</a>					44.5	R.VKDS*SPGEK.S
		Splicing factor, arginine/serine-rich 2, SCAF11 interactino protein	<a href="#">S816</a> <a href="#">S818</a>				100.0	13.8	K.KRPQS*PS*PR.R
		Splicing factor, arginine/serine-rich 2, SCAF11 interactino protein	<a href="#">S878</a> <a href="#">S880</a> <a href="#">S882</a>				100.0	12.4	R.RS*ES*LS*PR.R
		Splicing factor, arginine/serine-rich 2, SCAF11 interacting protein	<a href="#">S796</a> <a href="#">T800</a>				18.9	33.2	R.FHS*PSTT*WSPNKDTPQEK.K
		Splicing factor, arginine/serine-rich 2, SCAF11 interacting protein	<a href="#">S341</a>				7.9	27.4	R.SPIS*DNSGCDAPGNSNPPLSVPPSAESEK.Q
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S364</a> <a href="#">S366</a>			24.4	20.1	R.SREE*RS*RS.R
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S316</a>			10.2	32.1	K.RGS*VSR.G
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S330</a>			16.0	21.2	K.SLRQS*RS
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S318</a>			9.1	26.8	K.RGS*V*RG
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S267</a> <a href="#">S269</a>			100.0	36.4	R.S*KS*KDQAEK.I
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S410</a> <a href="#">S412</a>			100.0	16.9	R.S*VS*KER.E
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S456</a>			12.8	20.0	K.SKPNLPS*ESR.S
		Splicing factor, arginine/serine-rich 4	SRSF4	<a href="#">S458</a>			5.9	30.9	K.SKPNLPS*RS
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S303</a>			33.6	63.0	R.SNS*PLVPVPSKA
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S218</a> <a href="#">S220</a> <a href="#">S222</a>			100.0	17.5	R.S*IS*KS*RS
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S314</a> <a href="#">S316</a>			100.0	29.5	R.S*VS*PPPKR.A
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S265</a>			49.2	47.4	R.S*KDEYEK.S
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S263</a> <a href="#">S265</a>			39.9	18.3	R.S*RS*KDEYEK.S
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S257</a> <a href="#">S259</a> <a href="#">S261</a>			18.5	28.4	K.SDRGS*HS*HS*RS
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S301</a> <a href="#">S303</a>			50.0	18.8	R.S*NS*PLVPVPSKA
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S45</a>			36.9	49.3	K.NGYGFVEFED*RD
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S265</a> <a href="#">Y269</a>			-2.4	20.2	R.S*KDEY*EKSR.S
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S295</a> <a href="#">S297</a> <a href="#">S299</a>			22.5	10.9	R.S*RS*QS*RS*NS*PLVPVPSKA
		Splicing factor, arginine/serine-rich 6	SRSF6	<a href="#">S265</a> <a href="#">S272</a>			14.1	26.4	R.S*KDEYEK*RS
		Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	<a href="#">S165</a> <a href="#">S167</a>			100.0	19.4	R.S*IS*LRR.S
		Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	<a href="#">S163</a> <a href="#">S165</a> <a href="#">S167</a>			100.0	13.3	R.S*RS*IS*LRR
		Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	<a href="#">Y189</a> <a href="#">S192</a>			12.0	22.9	R.Y*FQS*PSR.S
		Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	<a href="#">S223</a> <a href="#">S225</a> <a href="#">S227</a>			100.0	24.1	R.S*PS*GS*PRR.S
		Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	<a href="#">S215</a> <a href="#">S217</a>			100.0	27.0	R.S*PS*PKR.S
		SRSF7	<a href="#">S231</a> <a href="#">S233</a>				100.0	16.2	R.RS*AS*PER.M
		Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	<a href="#">S181</a> <a href="#">S183</a>			34.8	31.7	R.S*GS*IKGSR.Y
		Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	<a href="#">S179</a> <a href="#">S181</a> <a href="#">S183</a>			34.7	16.6	R.S*RS*GS*IKGSR.Y

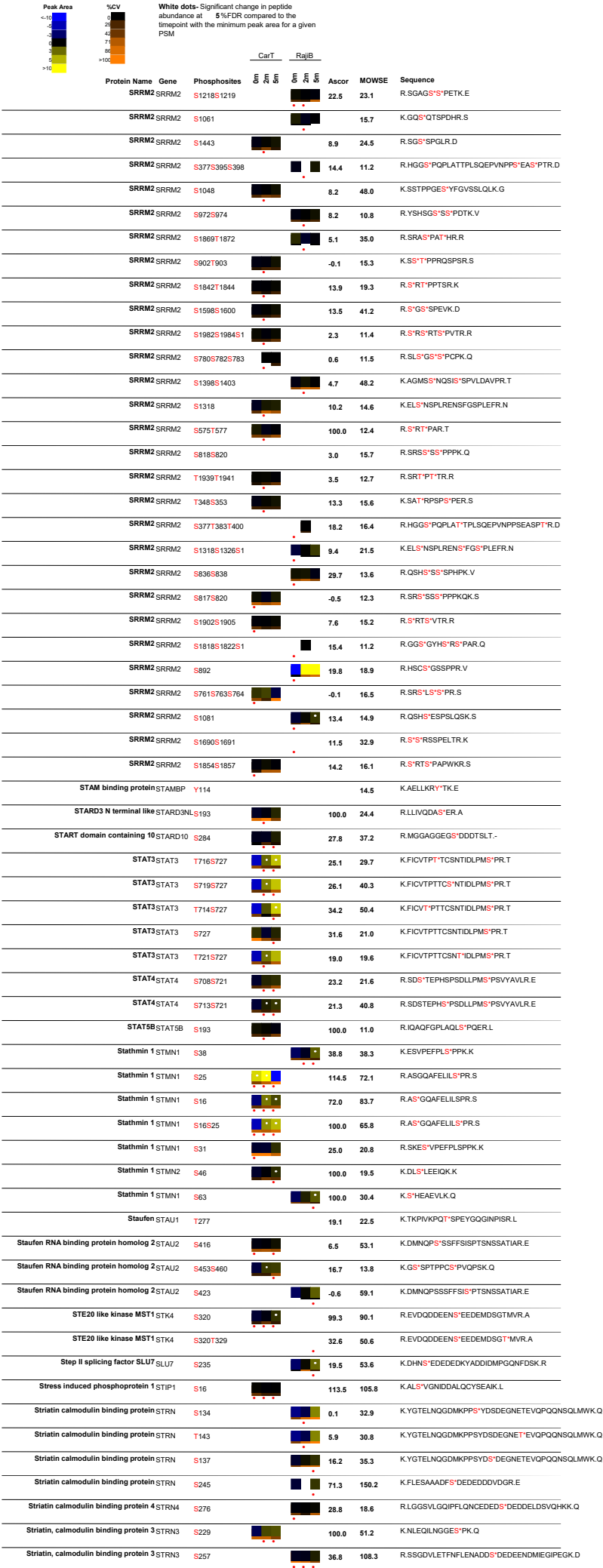
Peak Area		%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S173	S175					100.0	18.4	R.S* <b>AS</b> *LRR.S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S202	S204					100.0	19.7	R.S* <b>IS</b> *RPR.S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	Y189	S192S196					10.8	14.2	R.Y*FQ <b>S</b> *PS <b>R</b> *R.S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	Y189	S194					11.0	32.4	R.Y*FQ <b>S</b> *PS <b>R</b> .S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S192	S194					42.3	32.4	R.YFQ <b>S</b> *PS <b>R</b> .S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S155	S157S159					100.0	11.1	R.S* <b>RS</b> * <b>AS</b> *PR.R
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	Y189	S192S194					6.8	11.8	R.Y*FQ <b>S</b> *PS <b>R</b> *SR.S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S213	S215S217					100.0	12.9	K.S* <b>RS</b> *PS*PKR.S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S181	S183S187					100.0	19.9	R.S* <b>GS</b> * <b>KG</b> S*R.Y
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S165						11.0	19.4	R.S*ISLR.R.S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S192	S194S196					10.8	22.4	R.YFQ <b>S</b> *PS* <b>RS</b> *R.S
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	S171	S173S175					100.0	12.5	R.R <b>S</b> * <b>RS</b> * <b>AS</b> *LRR
Splicing factor, arginine/serine-rich 7,35kDa	SRSF7	Y189	S194S196					8.9	11.3	R.Y*FQ <b>S</b> *PS* <b>RS</b> *R.S
Splicing factor, arginine/serine-rich 8SF	SWAP	S604						8.1	12.7	R.VKLDD <b>S</b> *DDDEESKEQESSSAAINTPAVPPCVVEEK.K
Splicing factor, arginine/serine-rich 8SF	SWAP	S283						12.1	76.8	K.SGV <b>S</b> *DNEDDDDEEDGNYLHPSLFASK.K
Splicing factor, arginine/serine-rich 8SF	SWAP	S282						24.9	72.3	K.SGV <b>S</b> *SDNEDDDDEEDGNYLHPSLFASK.K
Splicing factor, arginine/serine-rich 8SF	SWAP	S815						100.0	40.3	R.A <b>HS</b> *PER.R
SPT2, Suppressor of Ty, domain containing	SPTY2D1	Y597						52.0	51.0	R.EYEEDDDDDDEY*DSEMEDFIEDEGEPEQEEISK.H
SPT2, Suppressor of Ty, domain containing	SPTY2D1	S599						13.0	69.3	R.EYEEDDDDDDEYD <b>S</b> *EMEDFIEDEGEPEQEEISK.H
	SPT6	S735	S757S78					100.0	26.0	K.GFINDDDDEGEDEGS*D <b>S</b> *G <b>S</b> *EDDVGHKK.R
	SPT6	S1703	S1712					11.4	29.3	R.LTPRP <b>S</b> *PMIESTPM <b>S</b> *IAGDATPLLDEMDR.-
	SPT6	T1532	S1535					20.9	65.7	R.TRT*PAS*INATPANINLADLTRA
	SPT6	S1703	T1718					20.1	48.8	R.LTPRP <b>S</b> *PMIESTPM <b>S</b> IAGDAT*PLLDEMDR.-
	SPT6	S1701	T1718					15.0	36.8	R.LTPRP <b>S</b> *PSMIESTPM <b>S</b> IAGDAT*PLLDEMDR.-
	SPT6	S1701	S1712					6.5	32.4	R.LTPRP <b>S</b> *PSMIESTPM <b>S</b> *IAGDATPLLDEMDR.-
	SPT6	S1535						6.1	25.0	R.TPAS*INATPANINLADLTRA
	SPT6	T1532	S1535T15					11.6	38.5	R.TRT*PAS*INAT*PANINLADLTRA
	SPT6	T1530	S1535T15					13.1	13.8	R.T*RTPAS*INAT*PANINLADLTRA
	SPT6	T1530	S1535					12.6	46.4	R.T*RTPAS*INATPANINLADLTRA
Src like adapter protein 2	SLA2	S129						16.9	31.6	R.RGS*YLSVL.R.L
	SRP20	SRSF3	S148					100.0	33.2	R.NHK <b>P</b> <b>S</b> *R.S
	SRP20	SRSF3	S128	S130				100.0	14.4	R.S* <b>LS</b> *RDR.R
	SRP20	TXLNG	S115					100.0	21.7	R.RR <b>S</b> *PR.R
	SRP20	SRSF3	S126	S128S130				100.0	12.8	R.S* <b>RS</b> * <b>LS</b> *RDR.R
	SRP20	SRSF3	S138	S140				100.0	16.6	R.ER <b>S</b> * <b>LS</b> *RER.N
	SRP20	KMT2E	S120	S122S124				100.0	16.6	K.S* <b>F</b> <b>S</b> * <b>RS</b> *R.T
	SRp30c	SRSF9	S211					21.8	63.1	R.G <b>S</b> *PHYFSFPRPY.-
	SRp30c	SRSF9	S204	S208S211				10.5	22.0	R.GRD <b>S</b> *PYQ <b>S</b> *RG <b>S</b> *PHYFSFPRPY.-
	SRp30c	SRSF9	S211	S216				25.3	35.7	R.G <b>S</b> *PHY <b>F</b> <b>S</b> *PFRPY.-
	SRp30c	SRSF9	S204					37.8	43.9	R.GRD <b>S</b> *PYQSR.G
	SRp30c	SRSF9	S189	Y190				10.3	17.2	R.ST <b>S</b> *Y*GYSR.S
	SRp30c	SRSF9	S187	T188				24.7	21.9	R.S* <b>T</b> *SYGYSR.S
	SRp30c	SRSF9	Y214					7.7	46.3	R.GSPHY*FSPFRPY.-
	SRp30c	SRSF9	T188					-0.1	31.4	R.ST*SYGYSR.S
	SRp30c	SRSF9	S189	Y192				15.4	23.9	R.ST <b>S</b> *YGY*SR.S
	SRp30c	SRSF9	S204	Y206S211				8.0	12.6	R.GRD <b>S</b> *PY*QSRG <b>S</b> *PHYFSFPRPY.-
	SRp30c	SRSF9	S216	Y221				26.6	22.6	R.GSPHY <b>F</b> <b>S</b> *PFRPY.-
	SRp30c	SRSF9	S211	Y214				23.7	33.0	R.G <b>S</b> *PHY*FSPFRPY.-
	SRp30c	SRSF9	S189					16.9	35.1	R.ST <b>S</b> *YGYSR.S
	SRp30c	SRSF9	Y192					11.5	12.0	R.STSYGY*SR.S
	SRp30c	SRSF9	Y214	S216				-2.6	28.9	R.GSPHY* <b>F</b> <b>S</b> *PFRPY.-
	SRp46	SRSF8	S100					100.0	21.2	R.RDLPR <b>S</b> *R.Q
	SRP72	SRP72	S620					22.5	63.2	K.TV <b>S</b> *SPPTSPRPGSAATVSASTSNIIPPR.H
	SRP72	SRP72	S621	T624				16.6	92.1	K.TV <b>S</b> *PPT*SPRPGSAATVSASTSNIIPPR.H
	SRP72	SRP72	S621	S625				13.7	92.5	K.TV <b>S</b> *PPT <b>S</b> *PRPGSAATVSASTSNIIPPR.H
	SRP72	SRP72	S621					8.0	69.6	K.TV <b>S</b> *PPTSPRPGSAATVSASTSNIIPPR.H
	SRP72	SRP72	S620	S625				13.8	77.6	K.TV <b>S</b> *SPPT <b>S</b> *PRPGSAATVSASTSNIIPPR.H
	SRP72	SRP72	S621	S630				11.2	89.5	K.TV <b>S</b> *PPTSPRPG <b>S</b> *AATVSASTSNIIPPR.H
	SRP72	SRP72	S620	S630				1.9	28.4	K.TV <b>S</b> *SPPTSPRPG <b>S</b> *AATVSASTSNIIPPR.H
	SRP72	SRP72	T618	S620				8.1	49.6	K.T*V <b>S</b> *SPPTSPRPGSAATVSASTSNIIPPR.H
	SRP72	SRP72	S621	S635				4.5	48.5	K.TV <b>S</b> *PPTSPRPGSAATV <b>S</b> *ASTSNIIPPR.H
	SRP72	SRP72	S630	T633				8.0	31.4	K.TVSSPPTSPRPG <b>S</b> *AAT*VSASTSNIIPPR.H

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajIB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
<10	(0	SRP72	SRP72	S621T633				-1.7	24.5	K.TVSSPTSPRPGSAATVSASTSNIIPR.H
10-20	20	SRP72	SRP72	S625S630				7.9	36.6	K.TVSSPTSPRPGSAAATVSASTSNIIPR.H
20-40	40	SRP72	SRP72	T624				4.5	12.1	K.TVSSPTSPRPGSAATVSASTSNIIPR.H
40-60	60	SRP72	SRP72	S620S621				-0.3	30.6	K.TVSSPTSPRPGSAATVSASTSNIIPR.H
60-80	80	SRP72	SRP72	T624S625				1.6	13.7	K.TVSSPTSPRPGSAATVSASTSNIIPR.H
80-100	100	SRRM2	SRRM2	S1876S1878T1				35.3	11.3	R.SRSRTPLISR.R
>100	>100	SRRM2	SRRM2	S2100S2102				23.8	13.8	R.NHSGSRTTPVALNSSR.M
		SRRM2	SRRM2	S771				8.2	36.4	K.SRLSLR.R
		SRRM2	SRRM2	S1727S1729S1				100.0	36.0	R.SPSVSSPEPAEK.S
		SRRM2	SRRM2	S1320				29.8	42.5	K.ELSNSPLR.E
		SRRM2	SRRM2	T1003				75.8	40.6	K.AQTTPGPSLSGSK.S
		SRRM2	SRRM2	T1003S1014				29.4	31.6	K.VKAQTTPGPSLSGSKSPCQEK.S
		SRRM2	SRRM2	T2104				66.3	53.5	R.TPPVALNSSR.M
		SRRM2	SRRM2	T856S864				10.3	30.1	R.QGSITSPQANEQSVPQRR.S
		SRRM2	SRRM2	T856T866				11.6	29.2	R.QGSITSPQANEQSVTPQRR.S
		SRRM2	SRRM2	S857S864				26.8	51.6	R.QGSITSPQANEQSVPQRR.S
		SRRM2	SRRM2	T1856S1857				10.2	21.4	R.SRTSPAPWK.R
		SRRM2	SRRM2	S1857				-0.2	41.9	R.TSPAPWK.R
		SRRM2	SRRM2	S1318S1320				100.0	34.0	K.ELSNSPLR.E
		SRRM2	SRRM2	S1382S1387				24.6	53.3	R.SSGHSSELSPDAVEKA
		SRRM2	SRRM2	S2044S2046				100.0	30.3	R.SRSPLAIR.R
		SRRM2	SRRM2	S322				9.2	27.1	R.GEGDAPFSEPGTTSTQRPSPETATK.Q
		SRRM2	SRRM2	S2032T2034				100.0	22.0	R.SRTPLLLR.K
		SRRM2	SRRM2	S1541S1542S1				8.6	61.4	R.SGSSQELDVKPSAPQER.S
		SRRM2	SRRM2	S1539S1542S1				12.4	51.7	R.SGSSQELDVKPSAPQER.S
		SRRM2	SRRM2	S1102				-0.2	52.2	R.SSPVTELASR.S
		SRRM2	SRRM2	S2398				-0.2	55.2	R.TSPPLLD.RA
		SRRM2	SRRM2	S322S323				4.5	16.8	R.GEGDAPFSEPGTTSTQRPSPETATK.Q
		SRRM2	SRRM2	S2692S2694				12.3	43.3	R.SLSYSPVER.R
		SRRM2	SRRM2	S876				10.8	37.3	R.SCFESSDPPELK.S
		SRRM2	SRRM2	T2289				55.4	70.2	R.TPTAPAVNLGAR.T
		SRRM2	SRRM2	S1099S1101S11				17.8	32.2	R.SRSSPVTELASR.S
		SRRM2	SRRM2	S1102S1103				12.2	61.0	R.SSPVTELASR.S
		SRRM2	SRRM2	S2272				171.2	119.7	R.TPAAAAAMNLASPR.T
		SRRM2	SRRM2	S2690S2692S2				20.9	33.1	R.SLSYSPVER.R
		SRRM2	SRRM2	S875S876				58.5	36.2	R.SCFESSDPPELK.S
		SRRM2	SRRM2	S2132				105.4	56.3	R.SPGMLEPLGSSR.T
		SRRM2	SRRM2	S2118S2121				10.3	23.5	R.MSCFSRPSMSPPTLDR.C
		SRRM2	SRRM2	S2118S2123				9.3	25.4	R.MSCFSRPSMSPPTLDR.C
		SRRM2	SRRM2	S377T384S395				23.4	22.2	R.HGGSPPQLATTPLSQEPVNPSPASPTR.D
		SRRM2	SRRM2	S377S398				27.2	44.4	R.HGGSPPQLATTPLSQEPVNPSEASPTR.D
		SRRM2	SRRM2	S351S353S357				32.9	42.2	K.SATRPSPSPERSSTGPEPPAPTLLAER.H
		SRRM2	SRRM2	S2449				18.0	28.5	R.MGQAPSQLLPAAQDQPRSPVPSAFSDQSR.C
		SRRM2	SRRM2	S1404				9.1	82.5	K.AGMSNQSSISPVLDVAPR.T
		SRRM2	SRRM2	S1403				45.8	70.7	K.AGMSNQSSISPVLDVAPR.T
		SRRM2	SRRM2	S1329				37.7	66.0	R.ENSFSGPLEFR.N
		SRRM2	SRRM2	S1398S1401				13.8	62.7	K.AGMSNQSSISPVLDVAPR.T
		SRRM2	SRRM2	S1401S1404				23.0	103.6	K.AGMSNQSSISPVLDVAPR.T
		SRRM2	SRRM2	S1318S1329				8.5	53.5	K.ELSNPLRENSFGSPLEFR.N
		SRRM2	SRRM2	T1043				11.9	99.0	K.SSTPPGESYFGVSSLQK.G
		SRRM2	SRRM2	S1042				-0.2	90.1	K.SSTPPGESYFGVSSLQK.G
		SRRM2	SRRM2	S484S486				16.6	15.0	R.SRSPTAK.R
		SRRM2	SRRM2	S818S819				5.0	19.6	R.SRSSSPPPK.Q
		SRRM2	SRRM2	S713S715T717				100.0	13.0	R.SHSRTPQR.R
		SRRM2	SRRM2	S1219				23.9	36.7	R.SGAGSPETK.E
		SRRM2	SRRM2	S562S564S566				47.7	20.8	R.SHSRSPATR.G
		SRRM2	SRRM2	T1231				34.7	72.1	K.EQNSALPTSSQDEELMEVVEK.S
		SRRM2	SRRM2	S1819Y1820				6.4	46.7	R.GGSGYHSR.S
		SRRM2	SRRM2	S1232				5.2	55.7	K.EQNSALPTSSQDEELMEVVEK.S
		SRRM2	SRRM2	S1318S1320S1				46.6	53.8	K.ELSNPLRENSFGSPLEFR.N
		SRRM2	SRRM2	S1318S1320S1				18.2	46.7	K.ELSNPLRENSFGSPLEFR.N
		SRRM2	SRRM2	S1014				100.0	25.3	K.SPCQEK.S

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
<10	0	SRRM2	SRRM2	T627S629				100.0	12.1	R.LT*RS*PVR.R
10-20	1	SRRM2	SRRM2	S1937T1939				9.8	18.6	R.S*RT*PTTR.R
20-30	2	SRRM2	SRRM2	S2426				39.3	31.5	R.APS*PSSR.M
30-40	3	SRRM2	SRRM2	S836S839				24.9	15.1	R.QSHS*SSS*PHPK.V
40-50	4	SRRM2	SRRM2	S1064				9.8	27.5	K.GQSQTS*PDHR.S
50-60	5	SRRM2	SRRM2	S295S297				34.5	20.3	R.S*PS*PASGRR.G
60-70	6	SRRM2	SRRM2	S1866S1869				31.0	37.4	R.S*RAS*PATHR.R
70-80	7	SRRM2	SRRM2	T1986				12.8	22.4	R.SRT*SPVTR.R
80-90	8	SRRM2	SRRM2	S970S973				5.9	13.5	R.YSHS*GSS*SPDTK.V
90-100	9	SRRM2	SRRM2	S902S908				8.7	24.9	K.SS*TPPRQS*PSR.S
>100	10	SRRM2	SRRM2	S1842S1848				13.1	15.5	R.S*RTPTTS*R.K
		SRRM2	SRRM2	S1682T1684				16.4	18.3	K.TKS*RT*PPR.R
		SRRM2	SRRM2	S2727S2729				19.9	27.9	R.GDS*RS*PSHKR.R
		SRRM2	SRRM2	S1913S1916				55.0	32.0	R.S*RAS*PVSRR.R
		SRRM2	SRRM2	T1892S1893				20.5	26.4	R.SRT*SPVSR.R
		SRRM2	SRRM2	S1112				100.0	21.4	R.S*PIRQDR.G
		SRRM2	SRRM2	S1984S1987				16.6	19.5	R.S*RTS*PVTR.R
		SRRM2	SRRM2	S1600S1601				20.0	55.9	R.SGS*SPVEVK.D
		SRRM2	SRRM2	S454S456				19.9	36.6	R.EIS*SP*PTSK.N
		SRRM2	SRRM2	S1987				9.8	22.8	R.SRT*SPVTR.R
		SRRM2	SRRM2	S454S455				13.0	29.2	R.EIS*SP*PTSK.N
		SRRM2	SRRM2	S2702S2706				100.0	26.0	R.RRP*SPQPS*PR.D
		SRRM2	SRRM2	S351S353				30.2	21.0	K.SATRP*PS*PER.S
		SRRM2	SRRM2	S1975				-0.1	30.4	R.TS*PITR.R
		SRRM2	SRRM2	S454S455S456				24.0	34.5	R.EIS*SP*PTSK.N
		SRRM2	SRRM2	T1531				100.0	29.6	R.T*PLGOR.S
		SRRM2	SRRM2	S1598S1600S1				100.0	27.5	R.S*GS*SPVEVK.D
		SRRM2	SRRM2	S1577S1579S1				62.5	24.1	R.S*RS*GS*SP*PEVDSK.S
		SRRM2	SRRM2	S1923S1925T1				31.1	13.8	R.S*RS*RT*PPVTR.R
		SRRM2	SRRM2	S1132				35.2	55.2	K.SGMS*PEQSR.F
		SRRM2	SRRM2	S1925T1927				24.3	19.0	R.S*RT*PPVTR.R
		SRRM2	SRRM2	S2407T2409				22.2	41.6	R.S*RT*PPSAPSQSR.M
		SRRM2	SRRM2	S2407S2412				20.9	39.1	R.S*RTPPS*APSQSR.M
		SRRM2	SRRM2	S1444				19.1	52.0	R.SGS*SPGLR.D
		SRRM2	SRRM2	S759S761S763				100.0	17.4	R.S*RS*LS*SPR.S
		SRRM2	SRRM2	S1616S1618S1				100.0	23.6	R.AQS*GS*DS*SP*PEPK.A
		SRRM2	SRRM2	S1083				24.1	58.9	R.QSHSE*PSLSQK.S
		SRRM2	SRRM2	S435S436S437				103.8	33.0	R.HAS*SS*PES*PKPAPAPGSHR.E
		SRRM2	SRRM2	S435S436S437				100.0	18.6	R.HAS*SS*PES*PKPAPAPGS*HR.E
		SRRM2	SRRM2	S1443S1444				27.9	43.3	R.SGS*SPGLR.D
		SRRM2	SRRM2	S1694				-0.1	34.4	R.SS*PELTR.K
		SRRM2	SRRM2	S2581				19.8	41.7	K.RVPS*PTPAPK.E
		SRRM2	SRRM2	S1064S1069T1				8.5	11.5	K.GQSQTS*PDHRS*DT*SS*PEVR.Q
		SRRM2	SRRM2	S1691S1693				7.4	20.6	R.SS*RS*SPELTR.K
		SRRM2	SRRM2	S1497S1499S1				13.7	24.6	R.S*RS*PS*PELNNK.C
		SRRM2	SRRM2	S778S783				10.1	38.3	R.S*LSGSS*PCPK.Q
		SRRM2	SRRM2	S1064T1071S1				2.9	10.8	K.GQSQTS*PDHRS*DT*SS*PEVR.Q
		SRRM2	SRRM2	S778S780S783				20.9	40.0	R.S*LS*GSS*PCPK.Q
		SRRM2	SRRM2	T289S297				3.4	13.6	K.THTT*ALAGRSP*PASGR.R
		SRRM2	SRRM2	S2018S2020T2				100.0	15.5	R.S*RS*RT*PPAIR.R
		SRRM2	SRRM2	S2020T2022				100.0	19.0	R.S*RT*PPAIR.R
		SRRM2	SRRM2	T1453S1458S1				10.8	21.8	R.DSGGT*PSRH*LSGS*SPGMK.D
		SRRM2	SRRM2	S2688				40.2	33.7	R.KPIDSLRDS*R.S
		SRRM2	SRRM2	S2684				5.1	27.6	R.KPID*SLRDSR.S
		SRRM2	SRRM2	S508S510				100.0	18.0	R.S*RS*PQWR.R
		SRRM2	SRRM2	S950S952S954				33.6	18.7	R.S*RS*VS*PCSNVESR.L
		SRRM2	SRRM2	S536				16.3	22.5	R.S*PQRPQWSR.S
		SRRM2	SRRM2	S534S536				42.1	18.4	R.S*RS*PQRPQWSR.S
		SRRM2	SRRM2	S952S954				46.7	48.6	R.S*VS*PCSNVESR.L
		SRRM2	SRRM2	S1854T1856				24.3	16.0	R.S*RT*SPAPVKR.S
		SRRM2	SRRM2	T2397				10.2	37.1	R.T*SPILLDR.A
		SRRM2	SRRM2	T315S322				27.8	18.1	R.GEGDAPFSEPGT*TTSTORP*SPETATK.Q

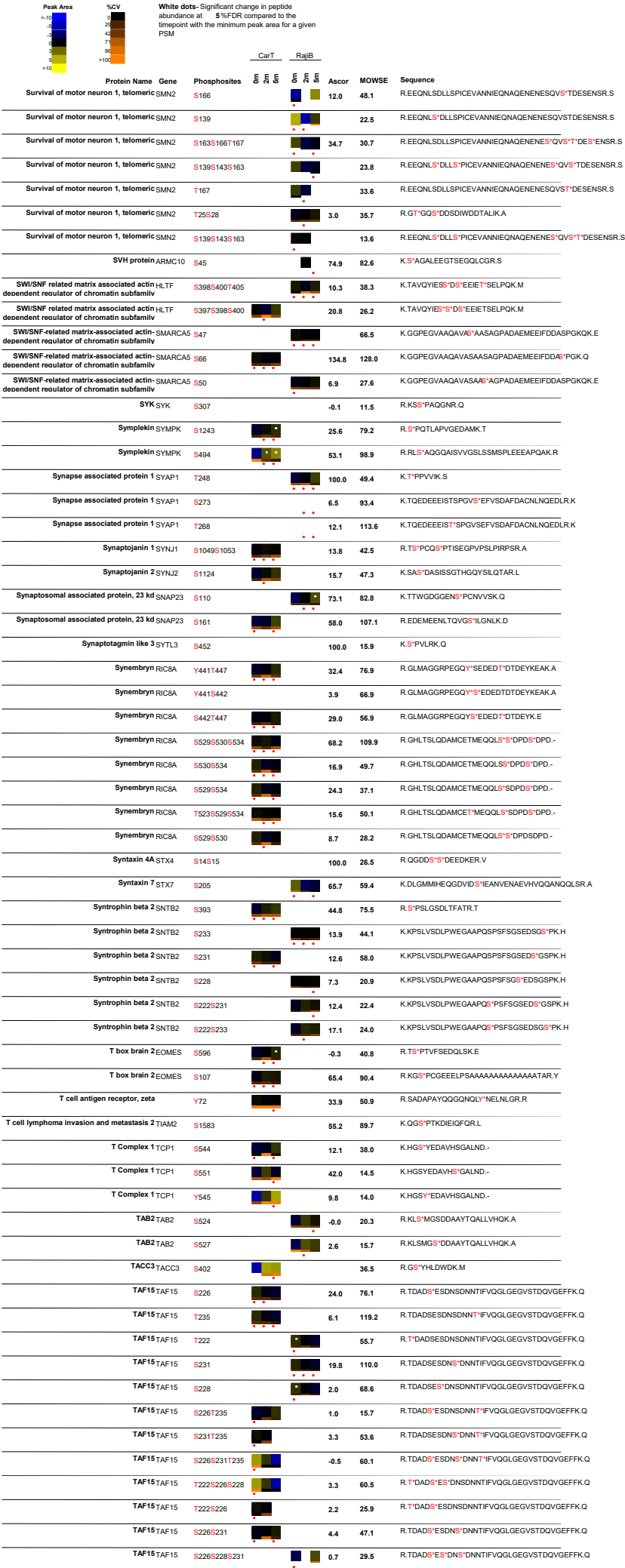
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB	Ascor	MOWSE	Sequence	
<10	0			5	5	5		10.2	27.7	R.S <sup>+</sup> RS <sup>+</sup> S <sup>+</sup> SPVTELASR.S
10	2			5	5	5		87.4	21.9	K.DKFS <sup>+</sup> PFVQDRPESSLVFK.D
20	4			5	5	5		6.8	11.1	R.SRS <sup>+</sup> S <sup>+</sup> SSPPPK.Q
40	6			5	5	5		11.5	57.7	R.TPAALAALS <sup>+</sup> LTGS <sup>+</sup> GPPTAANYPSSSR.T
60	8			5	5	5		100.0	15.7	R.S <sup>+</sup> RS <sup>+</sup> PQRR.G
70	10			5	5	5		21.5	34.8	R.S <sup>+</sup> RASPAT <sup>+</sup> HR.R
80	12			5	5	5		100.0	17.7	R.GRS <sup>+</sup> PS <sup>+</sup> PKPR.G
90	14			5	5	5		22.2	21.9	R.DKS <sup>+</sup> HS <sup>+</sup> HT <sup>+</sup> PSRR.M
>100	16			5	5	5		34.3	19.3	R.S <sup>+</sup> RT <sup>+</sup> S <sup>+</sup> PVTR.R
				5	5	5		17.3	40.3	R.SRT <sup>+</sup> PPS <sup>+</sup> APSQSR.M
				5	5	5		57.6	19.2	R.S <sup>+</sup> RT <sup>+</sup> S <sup>+</sup> PITR.R
				5	5	5		12.8	18.9	R.SRT <sup>+</sup> S <sup>+</sup> PITR.R
				5	5	5		17.7	26.0	R.SRS <sup>+</sup> PS <sup>+</sup> S <sup>+</sup> PELNKK.C
				5	5	5		100.0	12.6	R.S <sup>+</sup> RS <sup>+</sup> PS <sup>+</sup> S <sup>+</sup> PELNKK.C
				5	5	5		15.3	24.0	R.S <sup>+</sup> SRS <sup>+</sup> S <sup>+</sup> PELTR.K
				5	5	5		9.9	41.3	K.SRLS <sup>+</sup> LR.R
				5	5	5		49.0	35.8	R.NHS <sup>+</sup> GS <sup>+</sup> RT <sup>+</sup> PPVALNSSR.M
				5	5	5		100.0	22.7	R.S <sup>+</sup> LT <sup>+</sup> RS <sup>+</sup> PPAIR.R
				5	5	5		10.0	45.9	R.S <sup>+</sup> S <sup>+</sup> SPVTELASR.S
				5	5	5		20.3	24.0	R.HGGS <sup>+</sup> POPLAT <sup>+</sup> TPLSQEPVNPPEAS <sup>+</sup> PTR.D
				5	5	5		21.1	29.5	K.SATRP <sup>+</sup> PS <sup>+</sup> PERSS <sup>+</sup> TGPEPPAPTLLAER.H
				5	5	5		-0.3	52.1	K.SSTPPGESY <sup>+</sup> FGVSSLQLK.G
				5	5	5		10.2	66.9	R.TPAALAALSLT <sup>+</sup> GS <sup>+</sup> GPPTAANYPSSSR.T
				5	5	5		8.1	16.8	R.SRS <sup>+</sup> S <sup>+</sup> SSPPPK.Q
				5	5	5		5.1	18.5	K.TKSRT <sup>+</sup> PPR.R
				5	5	5		12.9	18.8	R.SRT <sup>+</sup> PPTS <sup>+</sup> R.K
				5	5	5		23.1	29.2	R.SRTPTT <sup>+</sup> S <sup>+</sup> R.K
				5	5	5		18.2	22.3	R.SRT <sup>+</sup> S <sup>+</sup> PVTR.R
				5	5	5		6.5	19.1	R.S <sup>+</sup> RS <sup>+</sup> RT <sup>+</sup> SPVTR.R
				5	5	5		16.0	15.5	R.S <sup>+</sup> RT <sup>+</sup> SPTR.R
				5	5	5		4.1	12.5	R.HAS <sup>+</sup> S <sup>+</sup> S <sup>+</sup> PESPKPAPAGSHR.E
				5	5	5		4.3	26.9	R.SS <sup>+</sup> RS <sup>+</sup> S <sup>+</sup> PELTR.K
				5	5	5		7.8	14.4	K.THT <sup>+</sup> T <sup>+</sup> ALAGRSPSPASGR.R
				5	5	5		8.8	16.4	R.NHSGS <sup>+</sup> RT <sup>+</sup> PPVALNSSR.M
				5	5	5		9.3	14.0	R.SGS <sup>+</sup> QELDVKPS <sup>+</sup> ASPQER.S
				5	5	5		8.3	13.1	R.SRS <sup>+</sup> GS <sup>+</sup> S <sup>+</sup> QELDVKPSA <sup>+</sup> POER.S
				5	5	5		19.7	18.5	K.SATRP <sup>+</sup> PS <sup>+</sup> PERSS <sup>+</sup> TGPEPPAPTLLAER.H
				5	5	5		9.3	61.6	K.ELSNS <sup>+</sup> PLRENSFGS <sup>+</sup> PLEFR.N
				5	5	5		0.1	29.3	R.TPAALAALSLTGS <sup>+</sup> GT <sup>+</sup> PPTAANYPSSSR.T
				5	5	5		15.2	16.2	R.QSHS <sup>+</sup> S <sup>+</sup> SPHPK.V
				5	5	5		14.6	24.5	R.S <sup>+</sup> RT <sup>+</sup> SPVSR.R
				5	5	5		47.1	23.3	R.S <sup>+</sup> AT <sup>+</sup> PPATR.N
				5	5	5		16.2	32.7	R.EISS <sup>+</sup> S <sup>+</sup> PTSK.N
				5	5	5		7.7	22.1	R.S <sup>+</sup> RT <sup>+</sup> PITR.R
				5	5	5		5.1	15.7	R.S <sup>+</sup> RSRT <sup>+</sup> S <sup>+</sup> PITR.R
				5	5	5		100.0	15.7	R.RET <sup>+</sup> PS <sup>+</sup> PRPMR.H
				5	5	5		38.3	73.0	R.S <sup>+</sup> LS <sup>+</sup> GSSPCPK.Q
				5	5	5		100.0	34.7	R.S <sup>+</sup> GS <sup>+</sup> S <sup>+</sup> PGLR.D
				5	5	5		13.5	13.8	R.DGSGT <sup>+</sup> PSRH <sup>+</sup> LS <sup>+</sup> GSSPGMK.D
				5	5	5		45.0	13.6	R.S <sup>+</sup> RT <sup>+</sup> PLISR.R
				5	5	5		14.7	11.5	R.SGSS <sup>+</sup> QELDVKPS <sup>+</sup> ASPQER.S
				5	5	5		14.3	28.7	R.GEGDAPFSEPGTTSTQRPSS <sup>+</sup> PETATK.Q
				5	5	5		7.7	17.0	R.GDSRS <sup>+</sup> PS <sup>+</sup> hKR.R
				5	5	5		4.4	18.2	R.GEGDAPFSEPGTTST <sup>+</sup> QRPSS <sup>+</sup> SPETATK.Q
				5	5	5		5.0	32.1	R.SRS <sup>+</sup> S <sup>+</sup> S <sup>+</sup> PVTELASR.S
				5	5	5		13.9	12.8	R.HGGS <sup>+</sup> POPLATTPLS <sup>+</sup> QEPVNPPEASPT <sup>+</sup> R.D
				5	5	5		24.2	14.9	R.HGGS <sup>+</sup> POPLATTPLS <sup>+</sup> QEPVNPPEAS <sup>+</sup> PTR.D
				5	5	5		10.8	22.8	K.AGMSNQSS <sup>+</sup> SPVLDAVPRT <sup>+</sup> PSR.E
				5	5	5		12.1	48.2	K.ELSNS <sup>+</sup> PLRENS <sup>+</sup> FGSPLEFR.N
				5	5	5		9.5	61.9	R.TPAALAALSLTGS <sup>+</sup> GT <sup>+</sup> PPTAANYPSSSR.T
				5	5	5		11.2	34.3	K.ELSNS <sup>+</sup> PLRENS <sup>+</sup> FGS <sup>+</sup> PLEFR.N
				5	5	5		12.8	12.2	R.QSHS <sup>+</sup> S <sup>+</sup> S <sup>+</sup> PHPK.V

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
<10	(0	SRRM2	SRRM2	S248S250T251				6.8	11.1	R.S* <b>RS</b> *T*TPAPK.S
10	2	SRRM2	SRRM2	S1984				8.8	17.3	R.S*RTSPVTR.R
20	4	SRRM2	SRRM2	S2749S2751				25.6	14.8	R.HRSS* <b>RS</b> *P.-
30	6	SRRM2	SRRM2	S1069T1071S1				10.5	12.9	K.GSQSTSPDHR <b>S</b> *DT <b>S</b> *S*PEVR.Q
40	8	SRRM2	SRRM2	T315				0.7	16.9	R.GEGDAPFSEPGT* <b>T</b> STQRPSSPETATK.Q
50	10	SRRM2	SRRM2	S1403S1404				2.1	52.3	K.AGMSSNQ <b>SIS</b> *S*PVLDAVPR.T
60	12	SRRM2	SRRM2	S1320S1326				13.8	64.2	K.ELSN <b>S</b> *PLRE <b>S</b> *FGSPLEFR.N
70	14	SRRM2	SRRM2	S1233				1.0	67.8	K.EQNSALPT <b>S</b> *QDEELMEVVEK.S
80	16	SRRM2	SRRM2	Y1820S1822				1.2	36.7	R.GGSGY* <b>H</b> S*R.S
>100	18	SRRM2	SRRM2	Y1820				-0.3	15.7	R.GGSGY*HSR.S
		SRRM2		S790T792				100.0	14.0	K.QK <b>S</b> *QT*PPRR.S
		SRRM2	SRRM2	S1672S1675				25.6	25.8	R.RG <b>S</b> *RS <b>S</b> *PEPK.T
		SRRM2		S1818S1822				16.1	38.9	R.RGGS*GY <b>S</b> *R.S
		SRRM2	SRRM2	S472S474S478				15.7	13.5	R.DK <b>S</b> * <b>H</b> S*HTPS*RR.M
		SRRM2	SRRM2	S972S973				8.0	16.7	R.YSHGS* <b>S</b> *SPDTK.V
		SRRM2	SRRM2	T1892				-0.4	14.4	R.SRT*SPVSR.R
		SRRM2	SRRM2	T1927				25.5	24.8	R.T*PPVTR.R
		SRRM2	SRRM2	S759S761S763				-0.1	12.1	R.S* <b>RS</b> * <b>L</b> S*SPR.S
		SRRM2	SRRM2	S780S783				14.1	41.4	R.SL <b>S</b> *G <b>S</b> *PCPK.Q
		SRRM2	SRRM2	S1451S1458S1				10.2	16.6	R.DG <b>S</b> *GTPSR <b>H</b> S* <b>L</b> S*GSSPGMK.D
		SRRM2	SRRM2	S543				18.5	18.4	R.SPQRPGW <b>S</b> *R.S
		SRRM2	SRRM2	T1856				5.4	13.7	R.SRT*SPAPWKR.S
		SRRM2	SRRM2	T2034				100.0	37.5	R.T*PLLPR.K
		SRRM2	SRRM2	S317S322				0.8	18.6	R.GEGDAPFSEPGT <b>S</b> *TQR <b>P</b> S*SPETATK.Q
		SRRM2	SRRM2	S2123				14.0	26.2	R.MSCFSRP <b>S</b> M <b>S</b> *PTPLDR.C
		SRRM2	SRRM2	S377T384T400				21.5	15.6	R.HGGS*PQPLATT*PLSQEPVNP <b>P</b> SEAS <b>P</b> T*R.D
		SRRM2	SRRM2	S819S820				4.6	22.4	R.SRS <b>S</b> * <b>S</b> *PPPK.Q
		SRRM2	SRRM2	S486T489				3.2	14.4	R.SR <b>S</b> *PAT*AKR.G
		SRRM2	SRRM2	S970S974				6.8	12.7	R.YSH <b>S</b> *G <b>S</b> <b>S</b> *PDTK.V
		SRRM2	SRRM2	S1497S1499				15.4	33.5	R.S* <b>RS</b> *PSSPELN <b>K</b> .C
		SRRM2	SRRM2	S2100T2104				7.7	21.5	R.N <b>H</b> S*GSRT*PPVALN <b>S</b> SR.M
		SRRM2	SRRM2	S1103				12.6	55.9	R.S <b>S</b> *PVT <b>E</b> LA <b>S</b> R.S
		SRRM2	SRRM2	S875				10.8	34.6	R.SCF <b>E</b> S*SPD <b>P</b> ELK.S
		SRRM2	SRRM2	S1124				7.8	13.7	R.GE <b>F</b> SA <b>S</b> *P <b>M</b> LK.S
		SRRM2	SRRM2	S1401S1403				15.5	58.8	K.AGMSSNQ <b>S</b> * <b>IS</b> *SPVLDAVPR.T
		SRRM2	SRRM2	T1063				22.4	31.7	K.GSQ <b>T</b> *SPDHR.S
		SRRM2	SRRM2	S1916				10.4	28.7	R.SRA <b>S</b> *P <b>V</b> SR.R
		SRRM2	SRRM2	S1690S1691S1				13.5	16.4	R.S* <b>S</b> *RS <b>S</b> *PE <b>L</b> TR.K
		SRRM2	SRRM2	S1397				-0.0	17.1	K.AG <b>M</b> S*SNQ <b>SIS</b> SPVLDAVPR.T
		SRRM2	SRRM2	S2310				13.6	61.9	R.TPAALA <b>L</b> <b>S</b> *LTGSGTPPTA <b>AN</b> YP <b>S</b> SSR.T
		SRRM2	SRRM2	T1844T1847				7.1	14.3	R.SRT*P <b>P</b> T*SR.K
		SRRM2	SRRM2	S895				6.0	15.8	R.HSCSG <b>S</b> *P <b>P</b> R.V
		SRRM2	SRRM2	S1923S1925T1				13.8	13.3	R.S* <b>RS</b> *RT <b>PP</b> VT <b>R</b> .R
		SRRM2	SRRM2	T1974				8.2	12.6	R.SRT*SP <b>I</b> TR.R
		SRRM2	SRRM2	S1541S1552				4.4	29.2	R.SG <b>S</b> *SQELDV <b>K</b> PS <b>A</b> *PQER.S
		SRRM2	SRRM2	S377T384S398				23.4	19.5	R.HGGS*PQPLATT*PLSQEPVNP <b>P</b> SEAS*PTR.D
		SRRM2	SRRM2	S377S395				11.7	19.2	R.HGGS*PQPLATTPLSQEPVNP <b>P</b> S*EASPTR.D
		SRRM2	SRRM2	S1691S1693S1				7.5	13.5	R.S <b>S</b> * <b>RS</b> * <b>S</b> *PE <b>L</b> TR.K
		SRRM2	SRRM2	S1537S1539S1				25.7	11.1	R.S* <b>RS</b> *G <b>S</b> *SQELDV <b>K</b> PS*ASPQER.S
		SRRM2	SRRM2	S1541S1542S1				7.7	44.8	R.SG <b>S</b> * <b>S</b> *QELDV <b>K</b> PS*ASPQER.S
		SRRM2	SRRM2	S2115S2118				3.7	10.7	R.M <b>S</b> *CF <b>S</b> *R <b>P</b> S <b>M</b> SP <b>T</b> PLDR.C
		SRRM2	SRRM2	T2312S2314				9.9	36.7	R.TPAALA <b>L</b> <b>S</b> L <b>T</b> *G <b>S</b> *GTPPTA <b>AN</b> YP <b>S</b> SSR.T
		SRRM2	SRRM2	S596T598				8.8	10.8	R.S*RT*P <b>T</b> R.R
		SRRM2	SRRM2	S295S300				8.6	12.8	R.S*PSPAS*GRR.G
		SRRM2	SRRM2	T903S908				18.1	21.7	K.S <b>S</b> T*P <b>P</b> RQ <b>S</b> *P <b>S</b> R.S
		SRRM2	SRRM2	S1674S1675				5.0	11.1	R.RGSR <b>S</b> * <b>S</b> *PEPK.T
		SRRM2	SRRM2	S1890S1893				9.1	20.5	R.S*RT <b>S</b> *P <b>V</b> SR.R
		SRRM2	SRRM2	S1984T1986				10.8	17.0	R.S*RT*SPVTR.R
		SRRM2	SRRM2	S857T866				13.1	45.0	R.QGS <b>I</b> T*PQANEQ <b>S</b> VT*PQRR.S
		SRRM2	SRRM2	S1539S1541S1				7.6	13.3	R.SR <b>S</b> *G <b>S</b> * <b>S</b> *QELDV <b>K</b> PS*ASPQER.S
		SRRM2	SRRM2	S1404T1413				14.0	35.4	K.AGMSSNQ <b>SIS</b> *PVLDAV <b>P</b> RT*PSR.E
		SRRM2	SRRM2	S815S817				3.6	12.2	R.S* <b>RS</b> *SSSP <b>P</b> PK.Q

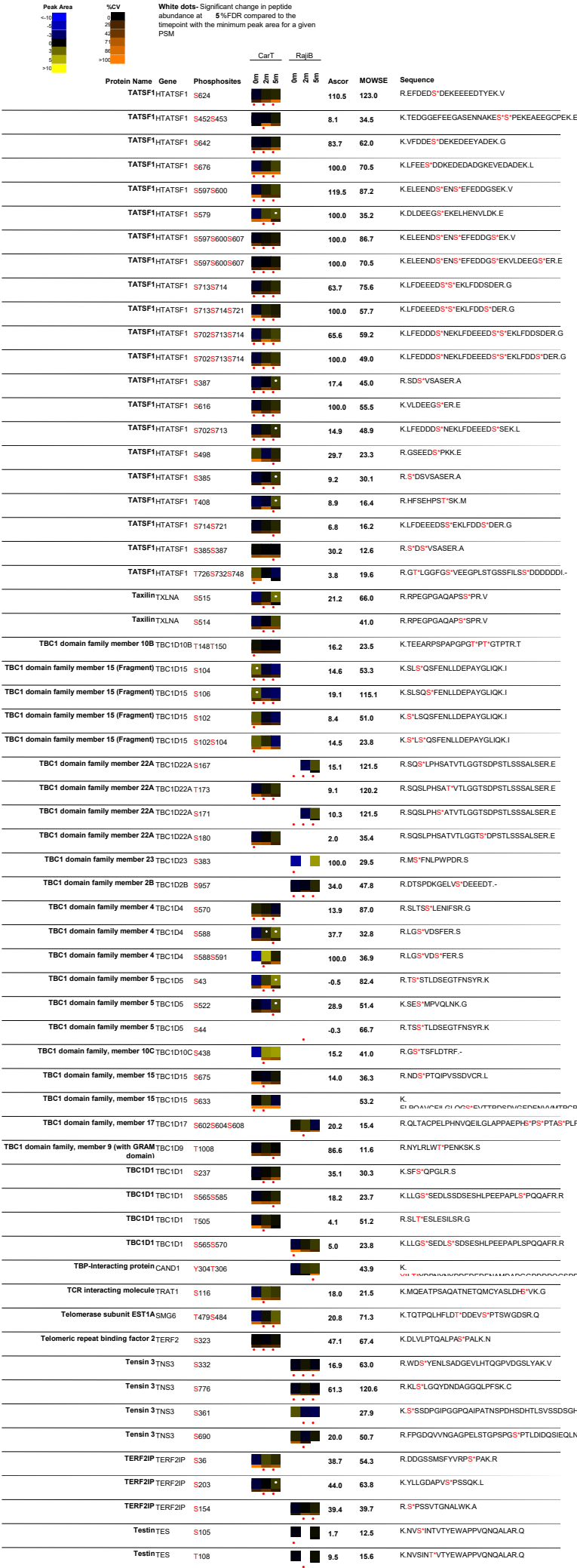




Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence
		Phosphosites						
<10	0							
10	1							
20	2							
30	3							
40	4							
50	5							
60	6							
70	7							
80	8							
90	9							
>100	>10							
Protein Name	Gene	Phosphosites						
Stromal antigen 2	STAG2	S1058S1061S1			10.7	69.4		R.NSLLAGDDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	S1061S1064			7.1	26.5		R.NSLLAGDDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	S1047S1061S1			11.9	26.3		R.NSLLAGGDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	T1056S1061S1			12.6	80.1		R.NSLLAGGDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	S1058			16.1	34.7		R.NSLLAGGDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	S1058S1061			13.1	57.5		R.NSLLAGGDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	T1056S1058S1			13.5	37.4		R.NSLLAGGDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	T1056S1058S1			11.7	32.7		R.NSLLAGGDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	T1056S1058			13.5	109.4		R.NSLLAGGDDDTMSVISGISSR.G
Stromal antigen 2	STAG2	S1047S1064			10.9	28.0		R.NSLLAGGDDDTMSVISGISSR.G
Stromal interaction molecule 1	STIM1	S618			7.3	62.4		R.SHSSPSPPDPTSPVVGDSRA
Stromal interaction molecule 1	STIM1	S521			18.7	65.4		R.DLTHSDSESLHMSDR.Q
Stromal interaction molecule 1	STIM1	S575			82.3	28.4		R.LIEGVHPGSLVEKLPSPALAK.K
Stromal interaction molecule 1	STIM1	S519			17.2	54.7		R.DLTHSDSESLHMSDR.Q
Stromal interaction molecule 1	STIM1	S521S523			6.5	26.7		R.DLTHSDSESLHMSDR.Q
Stromal interaction molecule 1	STIM1	S621			5.8	24.8		R.SHSPSSPPDPTSPVVGDSRA
Stromal interaction molecule 1	STIM1	S519S521S524			5.3	30.5		R.DLTHSDSESLHMSDR.Q
Stromal interaction molecule 1	STIM1	S257			100.0	71.8		R.AEQSLHDLQER.L
Stromal interaction molecule 1	STIM1	S519S521			0.6	17.1		R.DLTHSDSESLHMSDR.Q
Stromal interaction molecule 1	STIM1	S512			4.4	11.9		R.LTEPQHGLGSQR.D
Stromal interaction molecule 1	STIM1	T504			5.1	30.7		R.LTEPQHGLGSQR.D
Stromal interaction molecule 1	STIM1	S519S521S523			14.4	16.8		R.DLTHSDSESLHMSDR.Q
Stromal interaction molecule 1	STIM1	S519S523S524			2.3	15.4		R.DLTHSDSESLLHMSDR.Q
Stromal interaction molecule 1	STIM1	S620			5.8	43.3		R.SHSPSSPPDPTSPVVGDSRA
Stromal interaction molecule 2	STIM2	S767			35.2	67.0		K.SCSSMQLSSGIPVKPR.H
Stromal membrane associated protein 1	SMAP1	S152			15.3	97.2		K.NAIAITNISSDAPLQPLVSPSLQAAVDK.N
Stromal membrane associated protein 1	SMAP1	S151				11.4		K.NAIAITNISSDAPLQPLVSPSLQAAVDK.N
Stromal membrane-associated protein 1- SMAP2 like		S240			43.7	69.5		R.KVVGSIMPTAGSAGSVPENLNFPEPGSK.S
Stromal membrane-associated protein 1- SMAP2 like		S219			12.2	41.7		K.DLDLLASVSPSSSGSR.K
SSRP1	S667S668S671				16.7	68.3		K.SKEFVSDESISGENKS
Structure specific recognition protein 1	SSRP1	S667S668S671			29.3	24.1		K.EFVSDESISGENKSK.K
Structure specific recognition protein 1	SSRP1	S444			62.9	82.2		K.EGMNPSYDEYADSDAQHDAYLER.M
Structure specific recognition protein 1	SSRP1	S437S444			25.4	47.1		K.EGMNPSYDEYADSDAQHDAYLER.M
Structure specific recognition protein 1	SSRP1	Y441			3.5	61.3		K.EGMNPSYDEYADSDAQHDAYLER.M
Structure specific recognition protein 1	SSRP1	S667S668S671			7.9	33.3		K.EFVSDESISGENKS
SUDD RICK3	S125S127S128				3.2	40.7		R.KVHPYEDSDSEDEVDWQDTR.D
SUDD RICK3	Y122S127S128				6.3	15.3		R.KVHPYEDSDSEDEVDWQDTR.D
SUMO 1 specific protease 1	SENPE	S335S336			64.7	66.8		R.KTSLSDLNPIILSSDDDDNDRT
SUMO1 activating enzyme subunit 2	UBA2	S565				70.5		K.SITNGSDGGAQPSSTAQEGDDVLVSDSEEDSSNNAVDSEER.
Supervillin	SVIL	S1000			100.0	20.6		R.RGSRLER.A
SUPTSH	SUPTSH	S32S36			37.8	57.3		R.SAAGSEKEEPEDEEEEEEEYDEEEEEEDDORPPKPKR.H
SUPTSH	S666				76.7	57.8		R.DVTNFTVGGFAPMSR.I
Surfeit 2	SURF2	S155S156S163			14.1	45.0		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S155S163S166			8.6	27.1		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S163S166			14.6	58.5		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S155S156			10.6	37.6		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	T154S155			8.8	24.7		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S155S166			6.3	22.5		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	T154S155S156			5.9	35.7		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	T154S155S156			-0.8	21.7		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S155S156S166			1.5	13.2		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S166T168			2.9	13.4		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	T190T195			23.9	62.5		R.KDLGSTEDGGTDFLTKEDEK.A
Surfeit 2	SURF2	S156S166			7.2	20.3		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S156S163			5.7	14.1		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	S155S156S163			5.8	32.8		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Surfeit 2	SURF2	T154S155S163			6.0	38.1		R.EAFWEPTSDEGGAASSDSTMIDLYPELFT.R.K
Survival of motor neuron 1, telomeric	SMN2	T25			7.4	36.5		R.RGTGGSDSDIWDOTALI.K.A
Survival of motor neuron 1, telomeric	SMN2	T25S31			28.5	53.4		R.RGTGGSDSDIWDOTALI.K.A
Survival of motor neuron 1, telomeric	SMN2	S28			19.8	150.8		R.GTGGSDSDIWDOTALI.K.A
Survival of motor neuron 1, telomeric	SMN2	T25S28S31			38.7	19.8		R.RGTGGSDSDIWDOTALI.K.A
Survival of motor neuron 1, telomeric	SMN2	S28S31			47.3	166.2		R.GTGGSDSDIWDOTALI.K.A



Peak Area	%CV	White dots: Significant change in peptide abundance at 5 %FDR compared to the timepoint with the minimum peak area for a given PSM				CarT	RajiB	Ascor	MOWSE	Sequence		
		Protein Name	Gene	Phosphosites		0m	2m	0m	2m	0m		
		TAF15	TAF15	S226S228T235						1.5	13.5	R.TDADS*E*S*DNSDNN*IFVQGLGEGVTDQVGEFFK.Q
		TAF15	TAF15	S226S228						0.7	24.7	R.TDADS*E*S*DNSDNNIFVQGLGEGVTDQVGEFFK.Q
TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa		TAF3	TAF3	S236S243						53.0	11.6	K.IPPMLSPVHVQDS*TDLAPPS*PEPMLAPVAK.S
TAF3 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 140kDa		TAF3	TAF3	T237S243						24.8	27.2	K.IPPMLSPVHVQDS*TLAPPS*PEPMLAPVAK.S
TAF6 like RNA polymerase II TAF6L		TAF6L	TAF6L	S495S501						7.6	19.3	R.KMPQLTASAMS*PHGDES*PR.G
TAF9 RNA polymerase II TAF9		TAF9	TAF9	T154S158						17.9	61.7	R.LSVGSVT*SRPS*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S152T154						14.8	52.6	R.LSVGS*VT*SRPSTPTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S152T159						7.0	75.1	R.LSVGS*VTSRPS*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S155T159						10.1	74.7	R.LSVGSVTS*RPST*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	T154S155						-5.2	31.3	R.LSVGSVT*S*RPSTPTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	T154T159						12.8	77.6	R.LSVGSVT*SRPS*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S152T161						13.1	50.7	R.LSVGS*VTSRPS*TLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S152T159T164						11.9	36.7	R.LSVGS*VTSRPS*PTLGT*PTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S152S158T164						8.7	50.7	R.LSVGS*VTSRPS*PTLGT*PTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S152S158T161						7.7	31.3	R.LSVGS*VTSRPS*PT*TLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S158T159T161						4.7	18.0	R.LSVGSVTSRPS*PT*TLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S149S152T154						7.5	58.5	R.LS*VGS*VT*SRPSTPTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	T154T161						3.5	70.8	R.LSVGSVT*SRPSTPTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S152S158						4.0	54.8	R.LSVGS*VTSRPS*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S149T161						5.7	45.6	R.LS*VGSVTSRPS*TLGTPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S149T154S155						6.3	44.3	R.LS*VGSVT*S*RPSTPTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S155T161						18.8	47.2	R.LSVGSVTS*RPSTPTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S149S158						6.3	33.7	R.LS*VGSVTSRPS*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S158T159						10.3	54.8	R.LSVGSVTSRPS*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S158T159T164						10.4	32.8	R.LSVGSVTSRPS*PTLGT*PTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S149S158T159						5.7	45.9	R.LS*VGSVTSRPS*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S155S158T159						9.0	23.2	R.LSVGSVTS*RPST*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	T154S155S158						9.5	31.2	R.LSVGSVT*S*RPST*PTLTGPTPQTMSVSTK.V
TAF9 RNA polymerase II TAF9		TAF9	TAF9	S155S158						13.6	52.6	R.LSVGSVTS*RPSTPTLTGPTPQTMSVSTK.V
TAF9L TAF9B		TAF9B	TAF9B	S152S153						9.6	33.5	R.LSVGAVS*S*KPTTPTIATPQTIVSPNK.V
TAF9L TAF9B		TAF9B	TAF9B	S152T156						9.6	51.3	R.LSVGAVS*SKPT*TTIATPQTIVSPNK.V
Talin TLN1		TLN1	TLN1	S425						9.1	55.4	K.SKDHFGLEGDEESTMLEDSVS*PK.K
TANC TANC1		TANC1	TANC1	S63S66						29.7	67.3	K.GVSM*S*LPS*SPLLPR.Q
TANC TANC1		TANC1	TANC1	S63S67						16.4	52.0	K.GVSM*S*LPS*P*LLPR.Q
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	S1620S1621						151.0	76.3	R.VPS*S*DEEVVEEPQSR.R
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	S494S498						20.1	81.2	R.LDS*PPPS*PITEASEAAEAAEAGNLAVSSR.E
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	S1554						17.1	75.2	R.SPS*QDFSFIEDTEILDSAMYR.S
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	S672						79.7	39.7	R.AS*PEPPGP*ESSSR.W
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	S1024						31.2	36.7	R.GS*GGLFSPSTAHPDQALGQR.D
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	T501						-0.1	17.2	R.LDSPPPSPIT*EASEAAEAAEAGNLAVSSR.E
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	T501S504						5.5	18.8	R.LDSPPPSPIT*EAS*EAAEAAEAGNLAVSSR.E
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	S872						43.4	11.6	R.DS*LGTYSSR.D
Tankyrase 1 binding protein 182KD TNKS1BP1		TNKS1BP1	TNKS1BP1	S1552						-2.7	44.9	R.S*PSQDFSFIEDTEILDSAMYR.S
TAO kinase 1 TAOK1		TAOK1	TAOK1	S965						100.0	25.6	R.NS*PQALR.R
TAO kinase 1 TAOK1		TAOK1	TAOK1	S9						100.0	30.9	R.AGS*LKDPEIAELFFK.E
TAPP1 PLEKHA1		PLEKHA1	PLEKHA1	S332						35.1	74.9	R.SNS*LVSTFTMEK.R
TAPP1 PLEKHA1		PLEKHA1	PLEKHA1	S330						12.2	66.8	R.S*NSLVSTFTMEK.R
TAR (HIV) RNA binding protein 2 TARBP2		TARBP2	TARBP2	S156						-0.2	48.6	R.SPMELOPPVSPQ*S*ECNPVGALQELVQK.G
TAR (HIV) RNA binding protein 2 TARBP2		TARBP2	TARBP2	S142S156						6.4	36.9	R.S*PPMELOPPVSPQ*S*ECNPVGALQELVQK.G
TAR (HIV) RNA binding protein 2 TARBP2		TARBP2	TARBP2	S152S156						2.6	38.5	R.SPMELOPPV*S*PQQS*ECNPVGALQELVQK.G
TAR (HIV) RNA binding protein 2 TARBP2		TARBP2	TARBP2	S142S152						6.5	38.9	R.S*PPMELOPPV*S*PQQSECNPVGALQELVQK.G
TAR (HIV) RNA binding protein 2 TARBP2		TARBP2	TARBP2	S152						6.0	59.4	R.SPMELOPPV*S*PQQSECNPVGALQELVQK.G
Tara like protein TRIOBP		TRIOBP	TRIOBP	T248						100.0	13.6	R.ART*PAR.T
Target of EGR1 TOE1		TOE1	TOE1	S5						46.0	79.8	MAADS*DDGAVSAPASDGGVSK.S
Target of myb1 like 2 TOM1L2		TOM1L2	TOM1L2	S378						77.6	52.3	R.KQS*SEGIPVAQPSVMDIEIWL.R
TASK 5 KCNK15		KCNK15	KCNK15	S5						100.0	13.5	M.RRP*S*VR.A
Taste receptor type 2 member 7 TAS2R7		TAS2R7	TAS2R7	S305						100.0	10.9	K.VM#S*ILK.G
TATA element modulatory factor 1 TMF1		TMF1	TMF1	S344						51.5	69.0	R.SVSEINS*DDELSGK.G
TatD DNase domain containing 2 TATDN2		TATDN2	TATDN2	S328S329S331						57.4	35.7	R.EVMEHP*S*S*GS*DW*S*DVEEISTVR.F
TATS F1 HTATS F1		HTATS F1	HTATS F1	S453						-0.2	17.4	K.ESS*PEKEAEGGPEKESEEGCPK.R
TATS F1 HTATS F1		HTATS F1	HTATS F1	S702						100.0	52.8	K.LFEDDS*S*NEK.L
TATS F1 HTATS F1		HTATS F1	HTATS F1	S721						100.0	62.5	K.LFDDS*DER.G



Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the timepoint with the minimum peak area for a given PSM		CarT	RajiB		Ascor	MOWSE	Sequence
<10	0		Protein Name	Gene	Phosphosites				
10	1		Testis specific histone H2B	HIST1H2B	S89T90			11.1	K.RS*T*ISSR.E
20	2		Testis specific histone H2B	HIST1H2B	S89S92		7.6	17.5	K.RS*TISSR.E
30	3		Testis specific protein kinase 2	TESK2	S456		56.5	48.5	R.S*LPGSPEFLHQEACPFVGR.E
40	4		Tetratricopeptide repeat protein 16	TTC16	T76S767		6.9	17.0	K.TT*RS*PR.Q
50	5		TFIIIF beta	GTFF2	S248		52.9	22.8	R.HYQGEES*D.-
60	6		Thioredoxin domain containing 13	TMX4	S251S259		100.0	29.4	R.AEQLQDAEEEKDDSS*NEEENKDS*LVDEEEK.E
70	7		Thioredoxin domain containing protein 1	TMX1	S247		57.3	143.7	K.VEEEQEADEEDVS*EEEAESK.E
80	8		Thioredoxin interacting protein	TXNIP	S314S315S318		-0.1	24.8	R.TS*S*EMS*WVLDNIPDTPAAPCYMDVIPEDHRL
90	9		Thioredoxin interacting protein	TXNIP	T348S358		-0.2	17.4	R.LESP*TPLLDDMDGS*QDSPIFYAPEFK.F
>100	>10		Thioredoxin interacting protein	TXNIP	S361		-0.1	26.4	R.LESP*TPLLDDMDGQDS*PIFYAPEFK.F
			THRAP2	MED13L	S806S826		26.4	61.7	R.AGSSSLTQVTDLAPS*LHOLDNIFONSDDDELGAVS*PALR.S
			THRAP2	MED13L	S796T798		11.3	31.3	R.AGSSS*LT*QVTDLAPSLHOLDNIFONSDDDELGAVSPALR.S
			THRAP2	MED13L	T801S806		5.6	41.1	R.AGSSSLTQV*TDLAP*S*LHOLDNIFONSDDDELGAVSPALR.S
			THRAP2	MED13L	S817S826		19.5	53.3	R.AGSSSLTQVTDLAPSLHOLDNIFONS*DDDELGAVS*PALR.S
			THRAP2	MED13L	S817		7.6	24.2	R.AGSSSLTQVTDLAPSLHOLDNIFONS*DDDELGAVSPALR.S
			THRAP2	MED13L	S806		1.1	39.6	R.AGSSSLTQVTDLAP*S*LHOLDNIFONSDDDELGAVSPALR.S
			THRAP2	MED13L	S794			26.1	R.AGS*S*SLTQVTDLAPSLHOLDNIFONSDDDELGAVSPALR.S
			THRAP2	MED13L	S794S795			40.3	R.AGS*S*SLTQVTDLAPSLHOLDNIFONSDDDELGAVSPALR.S
			Thyroid hormone receptor interactor 11	TRIP11	T1846S1854		7.6	21.8	K.SVPNT*PLRPNQQS*VVNSFSSELFVK.F
			Thyroid hormone receptor interactor 11	TRIP11	S1842T1846		46.5	37.2	K.S*VPNT*PLRPNQQSVVNSFSSELFVK.F
			Thyroid hormone receptor interactor 11	TRIP11	S1891		46.8	32.3	K.LSVHDMKPLDS*PGRR.K
			THUMP1	S86S88		100.0	54.2		K.DQQPS*GS*EGEDDDAEAAKKE
			Thymidine kinase soluble	TK1	S231		100.0	15.3	K.LFAPQQLQCS*PAN.-
			Thymopoietin	TMPO	Y183		5.6	36.9	R.QNGSNSDR*Y*SDNEEDSKIELK.L
			Thymopoietin	TMPO	S177S180		25.9	42.3	R.QNGS*ND*S*DRYSDNEEDSKIELK.L
			Thymopoietin	TMPO	S177Y183		15.0	34.7	R.QNGS*NDSDRY*SDNEEDSKIELK.L
			Thymopoietin	TMPO	S159		-0.3	70.7	R.SS*TLPTISSSAENTR.Q
			Thymopoietin	TMPO	S158S159T160		30.7	37.9	R.EQGTESR*S*ST*PLPTISSSAENTR.Q
			Thymopoietin	TMPO	S66		5.8	22.2	K.GPPDFS*S*DEEREPT*PVLGSGAAAAGR.S
			Thymopoietin	TMPO	S310		12.2	48.9	K.SSSSSSQPEHSAMLVSTAAS*PSLIK.E
			Thymopoietin	TMPO	S66S67		42.6	92.3	K.GPPDFS*S*DEEREPT*PVLGSGAAAAGR.S
			Thymopoietin	TMPO	S306		112.4	69.8	K.HAS*PILPITEFSIDIPR.R
			Thymopoietin	TMPO	S156		26.0	28.7	K.LREQGTES*R.S
			Thymopoietin	TMPO	T160		10.2	70.6	R.SS*TLPTISSSAENTR.Q
			Thymopoietin	TMPO	S159T160		-0.2	52.8	R.SS*TLPTISSSAENTR.Q
			Thymopoietin	TMPO	S66T74		10.4	22.3	K.GPPDFS*S*DEEREPT*PVLGSGAAAAGR.S
			Thymopoietin	TMPO	S444		-0.4	62.5	R.DSGS*FVAFQNPFGSELMSSFAK.T
			Thymopoietin	TMPO	T154S156S158		24.9	38.3	R.EQGT*ES*RS*STPLPTISSSAENTR.Q
			Thymopoietin	TMPO	S184		16.4	35.7	R.QNGSNSDRY*S*DNEDSKIELK.L
			Thymopoietin	TMPO	S156S158S159		6.5	14.7	K.LREQGTES*RS*STPLPTISSSAENTR.Q
			Thymopoietin	TMPO	S312		10.7	22.6	K.SSSSSSQPEHSAMLVSTAAPS*LIK.E
			Thymopoietin	TMPO	S177S184		13.3	17.2	R.QNGS*NDSDRY*SDNEEDSKIELK.L
			Thymopoietin	TMPO	S180Y183		5.1	12.3	R.QNGSNS*DRY*SDNEEDSKIELK.L
			Thymopoietin	TMPO	S67T74		6.9	30.6	K.GPPDFS*S*DEEREPT*PVLGSGAAAAGR.S
			Thymopoietin	TMPO	T154S156T160		4.3	35.9	R.EQGT*ES*RSS*TLPTISSSAENTR.Q
			Thyroid hormone receptor interactor 12	TRIP12	S1317S1322		22.1	64.3	R.VREDDSD*DDGS*DEEIDSLAQFLNSGNVR.H
			Thyroid hormone receptor interactor 12	TRIP12	S1322S1329		23.9	47.5	R.VREDDSDDDGS*DEEIDES*LAAQFLNSGNVR.H
			Thyroid hormone receptor interactor 12	TRIP12	S1317S1329		10.6	45.7	R.VREDDSD*DDGSDEEIDES*LAAQFLNSGNVR.H
			Thyroid hormone receptor interactor 3	ZNHIT3	S80		46.3	60.0	K.TVKPVENKDDSDIADFLNS*DEEDR.V
			Thyroid hormone receptor interactor 8	JMJD1C	S966		9.2	21.4	R.S*PTHLTVSSTNTLR.S
			TIF2	NCOA2	S493		34.0	11.1	R.MS*PGVAGSPR.I
			Tight junction protein 2	TJP2	S1159		32.3	78.6	R.GSYGS*DAEEEEYR.Q
			Tight junction protein 2	TJP2	S398S400		8.1	61.7	R.DSQQTINIPSLNDS*DS*EIEDISEIESNR.S
			Tight junction protein 2	TJP2	S394S398		28.0	78.4	R.DSQQTINIP*S*LNDS*DSIEIDISEIESNR.S
			Tight junction protein 2	TJP2	S920Y932T933		13.3	82.3	R.LIS*DFEDTDGEGGAY*TDNELDEPAEPLVSSITR.S
			Tight junction protein 2	TJP2	S920T925Y932		42.0	73.3	R.LIS*DFEDT*DGEAGAY*TDNELDEPAEPLVSSITR.S
			Tight junction protein 2	TJP2	S244		56.7	29.7	R.S*IDQDYERA
			Tight junction protein 2	TJP2	S394S400		10.6	50.9	R.DSQQTINIP*S*LNDS*DS*EIEDISEIESNR.S
			Tight junction protein 2	TJP2	S170S174		30.2	19.6	R.SRS*WEDS*PER.G
			Tight junction protein 2	TJP2	S1156		5.0	48.6	R.GS*YGSDAEEEEYR.Q
			Tight junction protein 2	TJP2	T925Y932T933		0.1	41.1	R.LISDFEDT*DGEAGAY*TDNELDEPAEPLVSSITR.S
			Tight junction protein 2	TJP2	S920T925T933		6.2	76.1	R.LIS*DFEDT*DGEAGAY*TDNELDEPAEPLVSSITR.S

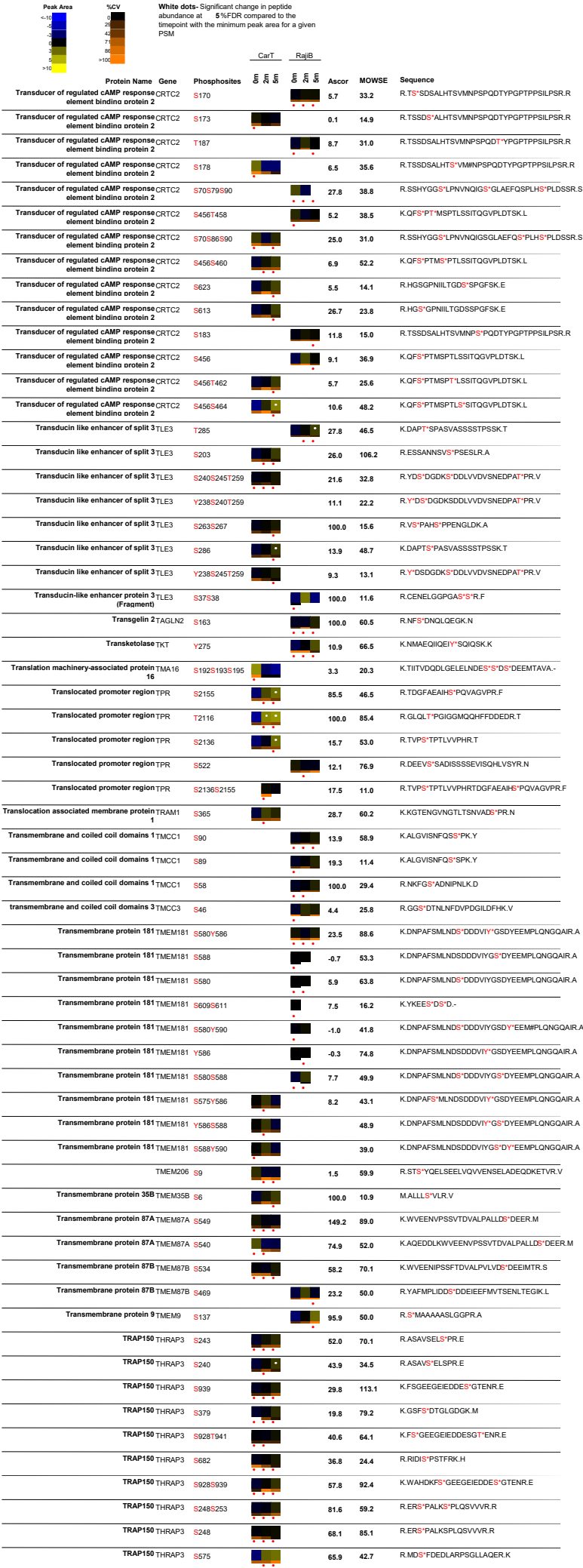
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
<10	(0	Protein Name	Gene	Phosphosites						
10	2	Tight junction protein 2	TJP2	S400				11.5	25.1	R.DSQGTLLINPSLNDSDS*EIEDIESIESNR.S
20	4	Tight junction protein 2	TJP2	T925Y932				6.5	44.7	R.LISDFEDT*DGEAGAY*TNDELDEPAEEPLVSSITR.S
30	6	Tight junction protein 2	TJP2	S394				2.4	54.6	R.DSQGTLLINPS*LNDSDSEIEDIESIESNR.S
40	8	Tight junction protein 3	TJP3	S183				34.4	58.5	R.S*PGGGSEANGLALVSGFK.R
50	10	Tight junction protein 3	TJP3	S371S375				12.2	11.3	R.RES*SVD*S.R.T
60	12	Tight junction protein 4, peripheral	TJAP1	S535				8.0	61.1	R.KDS*LTQAQEQGNLLN.-
70	14	TIM1	TIMELESS	S1173				100.0	86.7	R.QLLDS*DEEQEEDEGR.N
80	16	Titin	TTN	Y15335S15339				17.6	13.6	K.IRIY*AM#NS*EGLGEPALVPGTPKAEDR.M
90	18	TLOC1	SEC62	T375				98.5	101.5	K.EELEQQT*DGDCDEEEENDGETPK.S
100	20	TLOC1	SEC62	S117				100.0	33.5	K.AES*GKEEDKK.S
110	22	TNFAIP3 interacting protein 1	TNIP1	T431S434				32.7	73.9	K.ALEEALSIQT*PPS*SPPTAFGSPEGAGALLR.K
120	24	TNFAIP3 interacting protein 1	TNIP1	S434S435				6.6	43.1	K.ALEEALSIQTPPS*S*PPTAFGSPEGAGALLR.K
130	26	TNFAIP3 interacting protein 1	TNIP1	S428S434				14.5	55.3	K.ALEEALS*IQTPPS*SPPTAFGSPEGAGALLR.K
140	28	TNFAIP3 interacting protein 1	TNIP1	T431S435S442				18.3	59.2	K.ALEEALSIQT*PPSS*PPTAFGS*PEGAGALLR.K
150	30	TNFAIP3 interacting protein 1	TNIP1	S428S435S442				9.6	49.7	K.ALEEALS*IQTPSS*PPTAFGS*PEGAGALLR.K
160	32	TNFAIP3 interacting protein 1	TNIP1	S77				16.2	49.5	K.DNELLPPPS*PSLGSFDPLAELTGK.D
170	34	TNFAIP3 interacting protein 1	TNIP1	T431S434S442				11.2	30.4	K.ALEEALSIQT*PPS*SPPTAFGS*PEGAGALLR.K
180	36	TNFAIP3 interacting protein 1	TNIP1	T431S435				7.8	60.7	K.ALEEALSIQT*PPSS*PPTAFGSPEGAGALLR.K
190	38	TNFAIP3 interacting protein 1	TNIP1	S428S435				1.0	38.4	K.ALEEALS*IQTPSS*PPTAFGSPEGAGALLR.K
200	40	TNFAIP3 interacting protein 1	TNIP1	S79				7.9	30.8	K.DNELLPPPS*S*LSGFDPLAELTGK.D
210	42	TNFAIP3 interacting protein 1	TNIP1	T431S435T438				6.2	29.6	K.ALEEALSIQT*PPSS*PPT*AFGSPEGAGALLR.K
220	44	TNFAIP3 interacting protein 1	TNIP1	S82				3.9	14.3	K.DNELLPPPSPSLGS*FDPLAELTGK.D
230	46	TNFAIP3 interacting protein 1	TNIP1	S428S435T438				4.2	20.6	K.ALEEALS*IQTPPS*PPT*AFGSPEGAGALLR.K
240	48	TNFAIP3 interacting protein 1	TNIP1	S428S434S442				5.6	18.6	K.ALEEALS*IQTPPS*SPPTAFGS*PEGAGALLR.K
250	50	TNFAIP3 interacting protein 2	TNIP2	S333S339				100.0	59.2	K.VAS*LLHQVS*WR.Q
260	52	TOCA1	FNBP1L	S443				42.4	83.5	R.ES*PEGSYTDANQEV.R
270	54	TOCA1	FNBP1L	S430				48.7	39.6	R.RHS*SDINHLVTQGR.E
280	56	TOM1	TOM1	T154T164				25.6	19.0	K.GLEFPMT*DLDMLSPIHT*PQR.T
290	58	TOM1	TOM1	S160T164				41.7	24.9	R.KGLEFPMTDLDMLS*PIHT*PQR.T
300	60	TOM1	TOM1	S160				9.4	18.2	K.GLEFPMTDLDMLS*PIHTPQR.T
310	62	TOM20	TOMM20	S135				9.5	20.0	R.IV*S*AQSLAEDDVE.-
320	64	TOMM70A	TOMM70	S91				64.4	59.0	R.AS*PAPGSGHPGEGGAHDMNSLDR.A
330	66	TOMM70A	TOMM70	S96				7.8	51.6	R.ASPAPGS*GHPEGGAHDMNSLDR.A
340	68	Tomosyn	STXB5	S723				12.9	52.9	R.KLS*LPTDLKPOLDVK.D
350	70	Topoisomerase DNA II, beta	TOP2B	S1517S1519				40.2	72.0	K.VVEAVNS*DS*DSEFGIPK.K
360	72	Topoisomerase DNA II, beta	TOP2B	S1395S1419				24.1	31.4	K.VKAS*PITNDGEDEFVPSDGLDKDEYTF*S*PGK.S
370	74	Topoisomerase DNA II, beta	TOP2B	S1395S1408				38.1	50.2	K.VKAS*PITNDGEDEFVPS*DGLDKDEYTFSPGK.S
380	76	Topoisomerase DNA II, beta	TOP2B	S1395				39.0	63.7	K.AS*PITNDGEDEFVPSDGLDKDEYTFSPGK.S
390	78	Topoisomerase DNA II, beta	TOP2B	S1395S1408S1				29.5	39.4	K.VKAS*PITNDGEDEFVPS*DGLDKDEYTF*S*PGK.S
400	80	TOP2B	S1461					32.2	91.5	K.SEDDSAKFDS*NEEDSASVFSFSGLK.Q
410	82	TOP2B	S1517S1519S1					100.0	58.7	K.VVEAVNS*DS*DS*EFGIPK.K
420	84	TOP2B	T1398S1408					14.9	35.0	K.ASPIT*NDGEDEFVPS*DGLDKDEYTFSPGK.S
430	86	Topoisomerase DNA II, beta	TOP2B	T1366				-0.2	48.7	K.YT*FDFSEEDDADDDDDNNDLEELK.V
440	88	Topoisomerase DNA II, beta	TOP2B	S1370				17.5	142.9	K.YTFDF*S*EEEDDADDDDDNNDLEELK.V
450	90	Topoisomerase DNA II, beta	TOP2B	S1456S1461				18.3	61.4	K.SEDDS*AKFDS*NEEDSASVFSFSGLK.Q
460	92	Topoisomerase DNA II, beta	TOP2B	S1461S1466				4.3	22.4	K.SEDDSAKFDS*NEEDS*ASVFSFSGLK.Q
470	94	Topoisomerase DNA II, beta	TOP2B	S1331S1335S1				67.3	105.5	R.NPW*S*DES*KS*ES*DLEETEPWIPR.D
480	96	Topoisomerase DNA II, beta	TOP2B	S1456S1461S1				3.1	55.2	K.SEDDS*AKFDS*NEEDS*ASVFSFSGLK.Q
490	98	Topoisomerase DNA II, beta	TOP2B	T1570S1576				16.8	44.5	K.KT*SFDQDS*DVIDFSDFTPTEPPLR.T
500	100	Topoisomerase DNA II, beta	TOP2B	S1449				13.9	87.6	K.SQDFGNLFSFPSYS*QK.S
510	102	Topoisomerase DNA II, beta	TOP2B	S1576S1591				21.9	49.0	K.KTSFDQDS*DVIDFSDFTPTEPPLR.T
520	104	Topoisomerase DNA II, beta	TOP2B	S1576				11.5	65.5	K.TSFDQDS*DVIDFSDFTPTEPPLR.T
530	106	Topoisomerase DNA II, beta	TOP2B	S1436S1449				39.9	100.5	K.S*QDFGNLFSFPSYS*QK.S
540	108	Topoisomerase DNA II, beta	TOP2B	S1608				26.0	48.5	K.YFAES*DEEEDDVDFAMFN.-
550	110	Topoisomerase DNA II, beta	TOP2B	S1517S1521				30.3	72.6	K.VVEAVNS*DSDS*EFGIPK.K
560	112	TOP2B	S1395T1398					2.4	24.4	K.AS*PIT*NDGEDEFVPSDGLDKDEYTFSPGK.S
570	114	Topoisomerase DNA II, beta	TOP2B	T1570S1571				15.4	25.1	K.KT*S*FDQDSVDIFPSDFPTEPPLR.T
580	116	Topoisomerase DNA II, beta	TOP2B	S1571				-0.2	68.9	K.TS*FDQDSVDIFPSDFPTEPPLR.T
590	118	Topoisomerase DNA II, beta	TOP2B	S1571S1576				11.2	25.1	K.KT*S*FDQDS*DVIDFSDFTPTEPPLR.T
600	120	Topoisomerase DNA II, beta	TOP2B	T1570S1591				21.7	16.6	K.KT*SFDQDSVDIFPSDFPTEPPLR.T
610	122	Topoisomerase DNA II, beta	TOP2B	S1436S1444S1				18.6	42.2	K.S*QDFGNLFS*FPSYS*QK.S
620	124	Topoisomerase DNA II, beta	TOP2B	S1519S1521				7.6	26.2	K.KVVEAVNSDS*DS*EFGIPK.K

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
<10	0	Topoisomerase DNA II, beta	TOP2B	T1570				7.2	30.0	K.KT*SFDDQSDVDIFPSDFTEPPSLPR.T
10	2	Topoisomerase DNA II, beta	TOP2B	S1452S1461				4.1	12.3	K.S*EDDSAKFD*S*NEEDSASVFSFGLK.Q
20	4	Topoisomerase DNA II, beta	TOP2B	Y1365				7.6	68.0	K.Y*TFDFSEEDDDADDDDDNNDLLELK.V
30	6	Topoisomerase DNA II, beta	TOP2B	T1398S1408T14				8.5	13.5	K.ASPIT*NDGEDEFVPS*DGLDKDEYT*FSPGK.S
40	8	Topoisomerase DNA II, beta	TOP2B	S1444				14.9	40.4	K.SQDFGNLFS*FPSYSOK.S
50	10	Topoisomerase DNA II, beta	TOP2B	S1436				21.5	51.3	K.S*QDFGNLFSFPSYSOK.S
60	12	Topoisomerase DNA II, beta	TOP2B	S1447				14.9	13.7	K.SQDFGNLFSFPSYSOK.S
70	14	Topoisomerase DNA II, beta	TOP2B	S1337S1339				61.9	48.1	K.S*S*E*S*DELEETEPVVIPIR.D
80	16	Topoisomerase DNA II, beta	TOP2B	S1331S1335S1				12.0	44.4	R.NPWS*DDES*KSES*DELET*EPVVIPIR.D
90	18	TORC3	CRTC3	S62				53.0	64.6	R.LTQYHGS*LPNVSQLR.S
>100	>10	TORC3	CRTC3	S329				31.8	55.3	R.S*NPSIQATLNK.T
		TORC3	CRTC3	S391S396				22.6	38.8	R.RQPPVS*PLTLS*PGPEAHQGFSR.Q
		TORC3	CRTC3	S391T394				32.0	37.9	R.RQPPVS*PLT*LSPGPEAHQGFSR.Q
		TORC3	CRTC3	S443				14.0	44.1	R.SQLSFLPTEAQAQVS*PPPPYPAPQELTQPLLQOPRA
		Tousled like kinase 1	TLK1	S204T213				0.1	13.2	R.SPONSHSHSTPSSS*VRPNPSP*ALAFGDHPVQPK.Q
		Tousled like kinase 1	TLK1	S180				8.2	41.6	K.ISDYFEYQGGNGS*PVR.G
		Tousled like kinase 1	TLK1	S209S211				13.0	19.1	R.SPONSHSHSTPSSSVRPN*S*PTALAFGDHPVQPK.Q
		Tousled like kinase 1	TLK1	S191S195				24.1		R.S*PQN*S*HSHTPSSSVRPN*SPSPTALAFGDHPVQPK.Q
		Tousled like kinase 1	TLK1	S179				25.6	42.6	K.ISDYFEYQGGNGS*SPVR.G
		Tousled like kinase 1	TLK1	S199S209				-14.8	13.5	R.SPONSHSHS*TPSSSVRPN*SPSPTALAFGDHPVQPK.Q
		Tousled like kinase 1	TLK1	S199S202				7.1	16.0	R.SPONSHSHS*TPS*SSVRPN*SPSPTALAFGDHPVQPK.Q
		Tousled like kinase 1	TLK1	S204S211				10.8	14.0	R.SPONSHSHSTPSSS*VRPNP*S*PTALAFGDHPVQPK.Q
		Tousled like kinase 2	TLK2	S98				9.2	20.5	K.ISDYFEFAGGSAPGT*S*PGR.S
		Tousled like kinase 2	TLK2	T97				-0.4	35.1	K.ISDYFEFAGGSAPGT*SPGR.S
		TRA2A	TRA2A	S84S86T88				12.2	26.2	R.S*RS*YT*PEYR.R
		TRA2A	TRA2A	T202				50.5	79.1	R.AHT*PTPGIYMGRPTHSGGGGGGGGGGGGGGR.R
		TRA2A	TRA2A	Y87T88				15.1	32.5	R.S*Y*T*PEYR.R
		TRA2A	TRA2A	S16S18S20T24				28.1	26.6	R.S*QS*K*S*PTGT*PAR.V
		TRA2A	TRA2A	S98S100				29.0	19.5	R.S*HS*PMSNR.R
		TRA2A	TRA2A	S96S98S100				40.2	42.1	R.S*RS*HS*PMSNR.R
		TRA2A	TRA2B	S260S262				30.0	31.9	R.RR*S*P*PYYSR.Y
		TRA2A	TRA2B	S260Y264				16.6	29.4	R.RR*S*PSP*YYSR.Y
		TRA2A	TRA2A	S84S86Y87				25.7	25.8	R.S*RS*Y*TPEYR.R
		TRA2A	TRA2A	S86Y87				15.8	15.7	R.S*Y*TPEYR.R
		TRA2A	TRA2A	S16S18S20				28.1	23.4	R.S*QS*K*S*PTGT*PAR.V
		TRA2A	TRA2A	S86T88				20.2	27.6	R.S*Y*TPEYR.R
		TRA2A	TRA2A	S86Y87T88				10.9	34.1	R.SRS*Y*Y*TPEYR.R
		TRA2A	TRA2B	S260				44.9	29.5	R.S*PSP*YYSR.Y
		TRA2A	TRA2A	S98S103				17.5	15.4	R.S*HSFMS*NR.R
		TRA2A	TRA2A	T204				56.5	81.4	R.AHT*PT*PGIYMGRPTHSGGGGGGGGGGGGGGR.R
		TRAF1	TRAF1	S66				23.9	44.4	R.GEDLQSI*PGSR.L
		TRAF1	TRAF1	S172				7.3	81.0	R.APCSES*QEELALQFMK.E
		TRAF1	TRAF1	S170				20.7	76.3	R.APCS*ESQEELALQFMK.E
		TRAF1	TRAF1	S64				10.9	40.5	R.GEDLQSI*SPGSR.L
		TRAF3-interacting JNK-activating modulator	TRAF3IP3	S111				19.1	28.2	R.RIS*S*PR.E
		TRAF3-interacting JNK-activating modulator	TRAF3IP3	S110S111				100.0	20.2	R.RIS*S*PR.E
		Transcription elongation factor A protein-TCEAL1 like 1	TCEAL1	S41S42				100.0	17.2	R.RS*S*P*RR.R
		Transcription elongation factor A, 1	TCEA1	S100				80.1	69.8	K.KKEPAITSON*S*PEAR.E
		Transcription elongation factor B, 3	ELOA	T164S167				4.2	16.3	R.MSPT*YSS*DPRESSDYGHVQSPSCTSPHQMYVDHYR.S
		Transcription elongation factor B, 3	ELOA	S125				13.6	16.2	R.S*Y*S*PDHR.Q
		Transcription elongation factor B, 3	ELOA	S162S167				2.7	16.4	R.MS*PTYSS*DPRESSDYGHVQSPSCTSPHQMYVDHYR.S
		Transcription elongation factor B, 3	ELOA	S162T164					13.0	R.MS*PT*YSSDPRESSDYGHVQSPSCTSPHQMYVDHYR.S
		Transcription factor 12	TCF12	S559				15.0	95.2	R.TSS*TNEDDLNPEQK.I
		Transcription factor 12	TCF12	T560				-0.3	91.4	R.TSST*NEDEDLNPEQK.I
		Transcription factor 12	TCF12	S98				13.1	51.0	R.LGAHEGLS*PTPFMNSNLMGK.T
		Transcription factor 12	TCF12	T100				4.2	50.8	R.LGAHEGLSPT*PFMNSNLMGK.T
		Transcription factor 12	TCF12	S67				14.7	79.3	R.GGTTSWGTSQGPS*PSYDSSR.G
		Transcription factor 2B related factor	BRF2	S385				19.3	78.8	R.ICPVPPVSTVTGDENIS*DSEIEQYLR.T
		Transcription factor 3	TCF3	S354S359				33.5	76.2	K.ALASIYSPDHSSNNFSSSPS*TPVGS*PQGLAGTSQWPR.A
		Transcription factor 3	TCF3	S338Y340					73.5	K.ALAS*Y*Y*SPDHSSNNFSSSPS*TPVGS*PQGLAGTSQWPR.A
		Transcription factor 3	TCF3	S351T355S359				12.5	78.4	K.ALASIYSPDHSSNNFSSS*SPST*PVG*S*PQGLAGTSQWPR.A
		Transcription factor 3	TCF3	S346T355S359				9.3	74.4	K.ALASIYSPDHSS*NNFSSSPST*PVG*S*PQGLAGTSQWPR.A

Peak Area	<sup>14</sup> C	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM									
<div><div>&lt;10</div><div>10</div><div>20</div><div>30</div><div>40</div><div>50</div><div>60</div><div>70</div><div>80</div><div>90</div><div>&gt;100</div></div>	<div><div>0</div><div>2</div><div>4</div><div>6</div><div>8</div><div>10</div><div>12</div><div>14</div><div>16</div><div>18</div><div>20</div><div>22</div><div>24</div><div>26</div><div>28</div><div>30</div><div>32</div><div>34</div><div>36</div><div>38</div><div>40</div><div>42</div><div>44</div><div>46</div><div>48</div><div>50</div><div>52</div><div>54</div><div>56</div><div>58</div><div>60</div><div>62</div><div>64</div><div>66</div><div>68</div><div>70</div><div>72</div><div>74</div><div>76</div><div>78</div><div>80</div><div>82</div><div>84</div><div>86</div><div>88</div><div>90</div><div>92</div><div>94</div><div>96</div><div>98</div><div>100</div></div>	CarT	RajiB	Ascor	MOWSE	Sequence					
Protein Name	Gene	Phosphosites									
Transcription factor 3TCF3		S352T355S359					10.4	80.4			K.ALASIYSPDHSSNNFSS\$ <b>S</b> \$PST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		Y340S350S359					10.6	38.5			K.ALASIYSPDHSSNNF\$ <b>S</b> \$SSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S346S359					6.2	29.6			K.ALASIYSPDHS\$ <b>S</b> \$NNFSSSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		T355S359					24.1	94.4			K.ALASIYSPDHSSNNFSSSPST <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S338Y340S341						61.2			K.ALAS <b>IY</b> \$ <b>T</b> \$Y\$ <b>S</b> \$PDHSSNNFSSSPST <b>P</b> VGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		S352S354S359					5.7	76.4			K.ALASIYSPDHSSNNFSS\$ <b>S</b> \$P\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S341S350S359					9.2	47.6			K.ALASIY\$ <b>S</b> \$PDHSSNNF\$ <b>S</b> \$SSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		Y340S350S354					2.2	34.0			K.ALASIYSPDHSSNNF\$ <b>S</b> \$SP\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S350S354S359					7.9	55.7			K.ALASIYSPDHSSNNF\$ <b>S</b> \$SP\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S346S351S359					3.5	74.9			K.ALASIYSPDHS\$ <b>S</b> \$NNFSS\$ <b>S</b> \$PST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S350S351S359					5.8	49.1			K.ALASIYSPDHSSNNF\$ <b>S</b> \$S\$ <b>S</b> \$PST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S351S354S359					5.3	62.8			K.ALASIYSPDHSSNNFS\$ <b>S</b> \$SP\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S345S350S354					1.0	56.1			K.ALASIYSPDH\$ <b>S</b> \$NNF\$ <b>S</b> \$SP\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S346S351S354					4.2	62.0			K.ALASIYSPDHS\$ <b>S</b> \$NNFSS\$ <b>S</b> \$P\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		Y340S351S354					12.9	53.0			K.ALASIYSPDHSSNNFSS\$ <b>S</b> \$P\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S345S351T355					5.1	70.0			K.ALASIYSPDH\$ <b>S</b> \$NNFSS\$ <b>S</b> \$PST <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		Y340S345S354					2.3	46.1			K.ALASIYSPDH\$ <b>S</b> \$NNFSSSP\$ <b>S</b> \$TPVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S379					46.2	61.7			R.AGAPGAL\$ <b>S</b> \$PSYDGGHLGQSK.I
Transcription factor 3TCF3		S350S354					13.5	49.6			K.ALASIYSPDHSSNNF\$ <b>S</b> \$SSP\$ <b>T</b> PVGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		S351T355					4.4	84.0			K.ALASIYSPDHSSNNFS\$ <b>S</b> \$SPST <b>P</b> VGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		S345S350S359					-3.4	26.6			K.ALASIYSPDH\$ <b>S</b> \$NNF\$ <b>S</b> \$SSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S346S352					1.9	42.7			K.ALASIYSPDHS\$ <b>S</b> \$NNFSS\$ <b>S</b> \$PST <b>P</b> VGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		S346S354					5.5	38.5			K.ALASIYSPDHS\$ <b>S</b> \$NNFSSSP\$ <b>T</b> PVGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		S350T355S359					10.3	69.4			K.ALASIYSPDHSSNNF\$ <b>S</b> \$SSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S350S351S352					4.5	29.8			K.ALASIYSPDHSSNNF\$ <b>S</b> \$S\$ <b>S</b> \$PST <b>P</b> VGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		Y340T355S359					3.0	33.4			K.ALASIYSPDHSSNNFSSSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S345S359					-4.0	23.2			K.ALASIYSPDH\$ <b>S</b> \$NNFSSSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S351S354					7.2	56.5			K.ALASIYSPDHSSNNFS\$ <b>S</b> \$P\$ <b>T</b> PVGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		S350S359					2.5	27.1			K.ALASIYSPDHSSNNF\$ <b>S</b> \$SSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S352S354					9.8	54.1			K.ALASIYSPDHSSNNFSS\$ <b>T</b> \$P\$ <b>T</b> PVGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		S127S139					6.5	39.5			R.DAGVGGLTQAGFL\$ <b>S</b> \$GELALNSPGL\$ <b>S</b> \$PSGMK.G
Transcription factor 3TCF3		S134S139					10.5	60.1			R.DAGVGGLTQAGFLSGELALN\$ <b>S</b> \$PGL\$ <b>S</b> \$PSGMK.G
Transcription factor 3TCF3		S346S354S359					5.0	57.0			K.ALASIYSPDHS\$ <b>S</b> \$NNFSSSP\$ <b>T</b> PVG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S354T355					1.2	31.5			K.ALASIYSPDHSSNNFSSSPST <b>T</b> PVGSPQGLAGTSQWPR.A
Transcription factor 3TCF3		Y340S345S359					6.2	50.0			K.ALASIYSPDH\$ <b>S</b> \$NNFSSSPST <b>P</b> VG\$ <b>S</b> \$PQGLAGTSQWPR.A
Transcription factor 3TCF3		S346S350S354					3.3	25.6			K.ALASIYSPDHS\$ <b>S</b> \$NNF\$ <b>S</b> \$SP\$ <b>T</b> PVGSPQGLAGTSQWPR.A
Transcription factor AP-2 alpha (activating TFAP2A enhancer binding protein 2 alpha)	S181						15.1	21.6			K.KGPV\$ <b>S</b> \$LSK.S
Transcription factor Dp-2TFDP2	T40						3.5	43.9			K.GNISFVAFV\$ <b>S</b> \$NT\$ <b>N</b> SPTK.I
Transcription factor Dp-2TFDP2	S31T40						11.8	12.3			R.GFIDQNLSP\$ <b>T</b> KGNI\$ <b>S</b> \$FVAFV\$ <b>S</b> \$NT\$ <b>N</b> SPTK.I
Transcription factor Dp-2TFDP2	S31T44						6.0	14.7			R.GFIDQNLSP\$ <b>T</b> KGNI\$ <b>S</b> \$FVAFV\$ <b>S</b> \$NTNS\$ <b>P</b> T\$ <b>K</b> .I
Transcription factor E2-alphaTCF3	S479						13.6	90.7			R.T\$ <b>S</b> \$TDEVLSLEEK.D
Transcription factor E3TFE3	S568						8.9	12.2			R.R\$ <b>S</b> \$FSMEEES.-
Transcription factor E4F1E4F1	S642S643						100.0	19.6			R.R\$ <b>S</b> \$S\$RAPR.Q
Transcription factor EBTFEB	S109S122						56.9	24.2			K.FAAHIS\$ <b>P</b> AQGS\$ <b>P</b> KPPPAAS\$ <b>P</b> GVRA
Transcription factor EBTFEB	S467						12.1	61.3			R.R\$ <b>S</b> \$FSMEEGDVL.-
Transcription factor EBTFEB	S332						31.8	97.9			R.VHGLPTT\$ <b>S</b> \$PSGMMMAELAQOVVK.Q
Transcription factor EBTFEB	S133S134S142						12.9	56.5			R.AGHVLS\$ <b>S</b> \$S\$AGNSAPN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S122						66.9	28.5			K.FAAHISPAQGS\$ <b>P</b> KPPPAAS\$ <b>P</b> GVRA
Transcription factor EBTFEB	S138						4.3	75.2			R.AGHVLS\$ <b>S</b> \$SAGN\$ <b>S</b> \$APN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	T331						5.8	24.8			R.VHGLPTT\$ <b>S</b> \$PSGMMMAELAQOVVK.Q
Transcription factor EBTFEB	S138S142						22.4	52.2			R.AGHVLS\$ <b>S</b> \$SAGN\$ <b>S</b> \$APN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S114S122						26.5	21.6			K.FAAHISPAQGS\$ <b>P</b> KPPPAAS\$ <b>P</b> GVRA
Transcription factor EBTFEB	S133S134						10.4	86.0			R.AGHVLS\$ <b>S</b> \$S\$AGNSAPN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S133S134S151						14.7	46.0			R.AGHVLS\$ <b>S</b> \$S\$AGNSAPN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S134							83.7			R.AGHVLS\$ <b>S</b> \$S\$AGNSAPN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S134S138S142						6.8	16.5			R.AGHVLS\$ <b>S</b> \$SAGN\$ <b>S</b> \$APN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
TFEB	S134S138S142						16.3	61.4			R.AGHVLS\$ <b>S</b> \$SAGN\$ <b>S</b> \$APN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S133S134S138						9.9	49.7			R.AGHVLS\$ <b>S</b> \$SAGN\$ <b>S</b> \$APN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S133						15.6	78.3			R.AGHVLS\$ <b>S</b> \$SAGNSAPN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S142						3.9	16.8			R.AGHVLS\$ <b>S</b> \$SAGNSAPN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S133S151						21.2	77.8			R.AGHVLS\$ <b>S</b> \$SAGNSAPN\$ <b>S</b> \$PMAMLHIG\$ <b>S</b> \$NPER.E
Transcription factor EBTFEB	S109S114						85.4	22.9			K.FAAHIS\$ <b>P</b> AQGS\$ <b>P</b> KPPPAAS\$ <b>P</b> GVRA

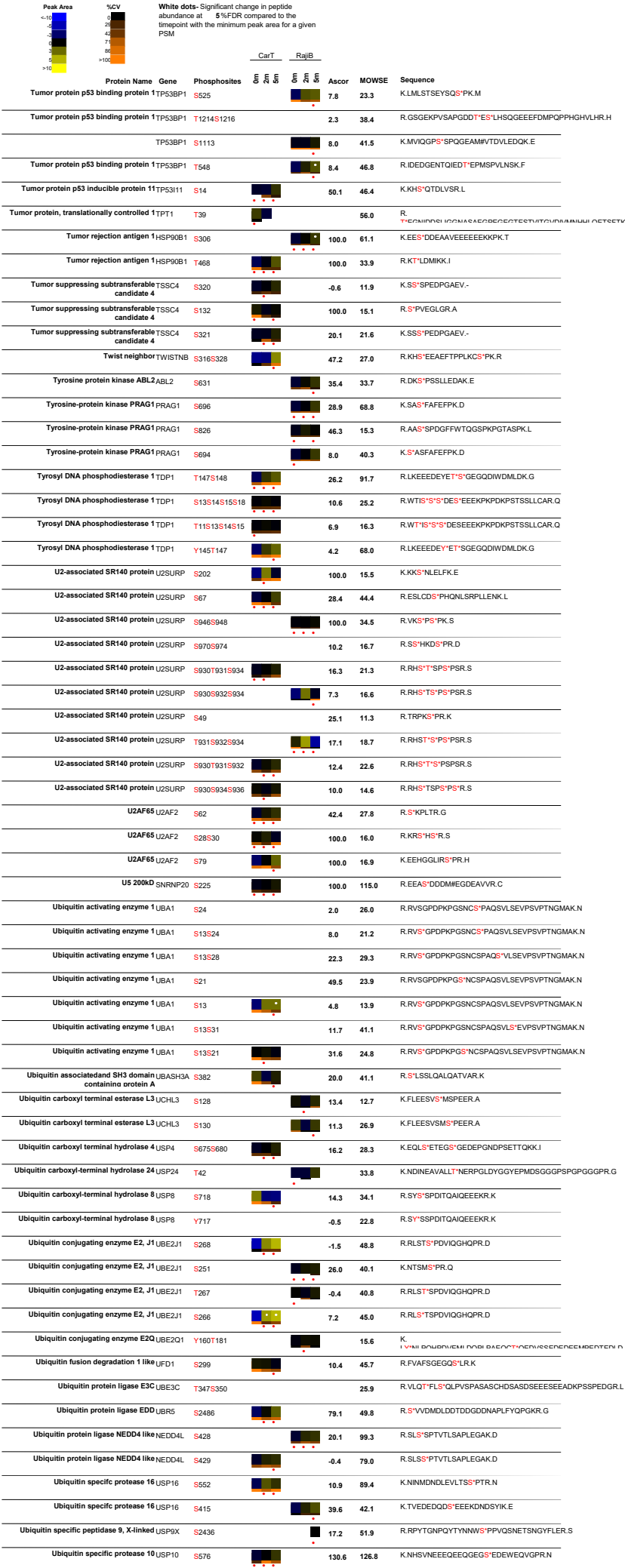


Peak Area	iCV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM									
<10	0										
10	1										
20	2										
30	3										
40	4										
50	5										
60	6										
70	7										
80	8										
90	9										
>100	>10										
		CarT		RajiB							
Protein Name	Gene	Phosphosites	5	6	7	8	9	10	11	12	13
Transcription factor EB TFEB		S133S138S142							6.4	38.8	R.AGHVLSS*SAGNS*APNS*PMAMLHIGS*NP.E.R
Transcription factor EB TFEB		S138S151							16.2	24.7	R.AGHVLSSSAGNS*APNSPMAMLHIGS*NP.E.R
Transcription factor EB TFEB		S334							2.3	40.1	R.VHGLPTTSP*SGM#NMAELAQOVVK.Q
Transcription factor EB TFEB		S466S467							13.8	15.5	R.RS*S*FSMEEGDVL.-
Transcription factor EB TFEB		S134S138							11.8	74.9	R.AGHVLSS*S*AGNS*APNSPMAMLHIGSNP.E.R
Transcription factor EB TFEB		S133S138S142							14.9	58.6	R.AGHVLSS*SAGNS*APNS*PMAMLHIGSNP.E.R
Transcription factor EB TFEB		S133S134S142							9.1	29.2	R.AGHVLSS*S*AGNSAPNS*PMAMLHIGSNP.E.R
Transcription factor ELF 1 ELF1		S187							21.9	16.8	K.TKPPRPDS*PATTPNISVK.K
Transcription factor ELYSAHCTF1		S1577							75.8	68.3	R.NLS*FNELYPSGTLK.L
Transcription factor ELYSAHCTF1		S1980							32.1	45.6	R.EVS*PSDVR.E
Transcription factor ELYSAHCTF1		S1195							26.9	25.6	R.SLPSSSQLKGS*PQAISR.A
Transcription factor IID TAF1		S328							7.6	12.3	K.SLWNYDYAPPPPPEQCLS*DDEITMAPVESK.F
Transcription factor IIF, alpha subunit GT2F1		S305S307S308							100.0	33.4	K.GVDEQS*DS*S*EES*EEEEKPEEDKEEEEEK.K
Transcription factor IIF, alpha subunit GT2F1		S385T389							31.9	76.1	R.GNS*RPQT*PSAEGGSTSSTLR.A
Transcription factor IIF, alpha subunit GT2F1		S217S218S221							100.0	36.4	R.IHLDLEDLEM*S*S*DAS*DAS*GEEGGRVPK.A
Transcription factor IIF, alpha subunit GT2F1		S385S391							12.8	52.0	R.GNS*RPQTPS*AEKGSTSSTLR.A
Transcription factor like nuclear regulator BDP1		S883							100.0	11.8	R.RAIS*PR.E
Transcription factor Sp3 SP3		S73							176.2	105.7	K.IGPPS*PGDDEEEAAAAAGAPAAAGATGOLASQLGAGNPR.W
Transcription factor Sp4 SP4		S770							21.4	17.3	R.IVTVAAISQDS*NPATPNVSTNMEEF.-
Transcription factor Sp4 SP4		T774							1.1	12.0	R.IVTVAAISQDSNPAT*PNVSTNMEEF.-
Transcription factor YY1 YY1		S118							100.0	82.2	R.EEVVGGDDS*DGLR.A
Transcription factor YY1 YY1		S247							67.5	87.9	K.DIDHETVVEEIGIENS*PPDYSEYMTGK.K
Transcription termination factor, RNA TTF1 polymerase 1		S64							18.4		K.DFOHLIS*SPLKK.S
Transcriptional coactivator CRSP70 MED26		S296S314T323							14.6	10.8	K.GS*VSPSPRQALDQVPS*PLPLAQPS*PPVR.R
Transcriptional coactivator MMS19 MMS19		S1027							11.8	36.9	R.GEWFLGS*PGS.-
Transcriptional intermediary factor 1 beta TRIM28		S473							94.5	79.0	R.S*GEGEVSGLMR.K
Transcriptional intermediary factor 1 beta TRIM28		S598							7.2	95.4	R.LASPSGS*TS SSGLEVVAEPTGSAPGGPGTLDOSATICR.V
Transcriptional intermediary factor 1 beta TRIM28		T599							5.3	105.6	R.LASPSGS*TS SSGLEVVAEPTGSAPGGPGTLDOSATICR.V
Transcriptional intermediary factor 1 beta TRIM28		S823							16.6	35.5	K.FSAVLVEPPM*SLPGAGLS*SQELSGGGPDGP.-
Transcriptional intermediary factor 1 beta TRIM28		S601							6.0	46.1	R.LASPSGSTS*GLEVVAEPTGSAPGGPGTLDOSATICR.V
Transcriptional intermediary factor 1 beta TRIM28		S33							31.8		R.S*TA*PSAAASASASAAAS*PAGGGAEALELLEHCGVCR.E
Transcriptional intermediary factor 1 beta TRIM28		S816							4.9	22.1	K.FSAVLVEPPM*SLPGAGLS*SQELSGGGPDGP.-
Transcriptional intermediary factor 1 beta TRIM28		T541							17.6	55.1	R.GAAAAATGQGP*TA*PAG*PGAPPLAGMAIVK.E
Transcriptional intermediary factor 1 beta TRIM28		S50							18.9	71.4	R.STAPSAASASASASAAAS*PAGGGAEALELLEHCGVCR.E
Transcriptional intermediary factor 1 beta TRIM28		S45							3.9	24.6	R.STAPSAASASASAS*AAAS*PAGGGAEALELLEHCGVCR.E
Transcriptional intermediary factor 1 beta TRIM28		S49							4.6	26.3	R.STAPSAASASASAAAS*SPAGGGAEALELLEHCGVCR.E
Transcriptional intermediary factor 1 beta TRIM28		S824							4.8	17.3	K.FSAVLVEPPM*SLPGAGLS*SQELSGGGPDGP.-
Transcriptional intermediary factor 1 beta TRIM28		S594							76.4		R.LAS*PSGSTSSSGLEVVAEPTGSAPGGPGTLDOSATICR.V
Transcriptional intermediary factor 1 beta TRIM28		T599S612							5.8	32.2	R.LASPSGS*TS SSGLEVVAEPTS*APGGPGTLDOSATICR.V
Transcriptional intermediary factor 1 TRIM33 gamma		T1102S1105							62.9	82.2	R.TFAPLPEFEQEEDDGEV*TEDS*DED*FIQPR.R
Transcriptional intermediary factor 1 TRIM33 gamma		S803S808T815							24.1	12.6	R.S*ACMLS*SPESSLY*PPLSTNLHSELDALASLENHVK.I
Transcriptional intermediary factor 1 TRIM33 gamma		S1119							100.0	12.1	R.LKS*DERPVHIK.-
Transcriptional intermediary factor 1, alpha TRIM24		S1019S1025							4.0	59.8	R.NES*EDNKFS*DDSDDFVQPR.K
Transcriptional intermediary factor 1, alpha TRIM24		S663S667							6.0	11.6	R.TVQSPNS*SVPS*PGLAGPVTMTSVHPPIR.S
Transcriptional intermediary factor 1, alpha TRIM24		S788S771							3.8	31.1	R.SILTSLLNS*QS*TSSEETVLR.S
Transcriptional intermediary factor 1, alpha TRIM24		S660S667							12.8	70.6	R.TVQS*PNSSVPS*PGLAGPVTMTSVHPPIR.S
Transcriptional intermediary factor 1, alpha TRIM24		T657S667							4.2	14.1	R.T*VQSPNSSVPS*PGLAGPVTMTSVHPPIR.S
Transcriptional intermediary factor 1, alpha TRIM24		S787S771							11.3	44.6	R.SILTSLLNS*SOS*TSSEETVLR.S
Transcriptional intermediary factor 1, alpha TRIM24		S1019S1028							11.7	73.3	R.NES*EDNKFSDS*DDDFVQPR.K
Transcriptional intermediary factor 1, alpha TRIM24		S788S770							-0.4	24.4	R.SILTSLLNS*QS*TSSEETVLR.S
Transcriptional intermediary factor 1, alpha TRIM24		S1025S1028							7.6	46.9	R.NESEDNKFS*DDS*DDDFVQPR.K
Transcriptional regulator protein HCN GP SAP30BP		S69S72S77							9.6	16.1	R.LGGDEDGYEEEDENS*RO*S*EDDS*ETEKPEADDPK.D
Transcriptional regulator protein HCN GP SAP30BP		Y46							1.2	20.6	K.GGLVSDA*GEDDFSRL
Transcriptional regulator protein HCN GP SAP30BP		S18S22							4.8	16.5	K.NVLSSLAVYAEDS*EPES*DGEAGIEAVGSAAEK.G
Transcriptional regulator protein HCN GP SAP30BP		S9S10							8.7	13.1	K.NVL*S*LVAYAEDSEPSDGEAGIEAVGSAAEK.G
Transcriptional regulator protein HCN GP SAP30BP		Y14S22							2.3	14.9	K.NVLSSLAV*AEDESEPS*DGEAGIEAVGSAAEK.G
Transcriptional repressor p66 alpha GATAD2A		S100S113							45.1	38.1	R.RPPS*PDVIVLSDNEQPS*SPR.V
Transcriptional repressor p66 alpha GATAD2A		S340							14.6	83.8	K.GTTATSAQANSTPTSVASVITSAES*PASR.Q
Transcriptional repressor p66 alpha GATAD2A		S100S107S114							33.4	40.0	R.RPPS*PDVIVLS*DNEQPS*PR.V
Transcriptional repressor p66 alpha GATAD2A		S100S107S113							45.1	20.0	R.RPPS*PDVIVLS*DNEQPS*SPR.V
Transcriptional repressor p66 alpha GATAD2A		S100S114							42.8	16.7	R.RPPS*PDVIVLSDNEQPS*PR.V
Transducer of regulated cAMP response element binding protein 2		S171							-0.3	34.9	R.TSS*DSALHTSVMNPSQDQTYGPTTPPSILPSLR.R



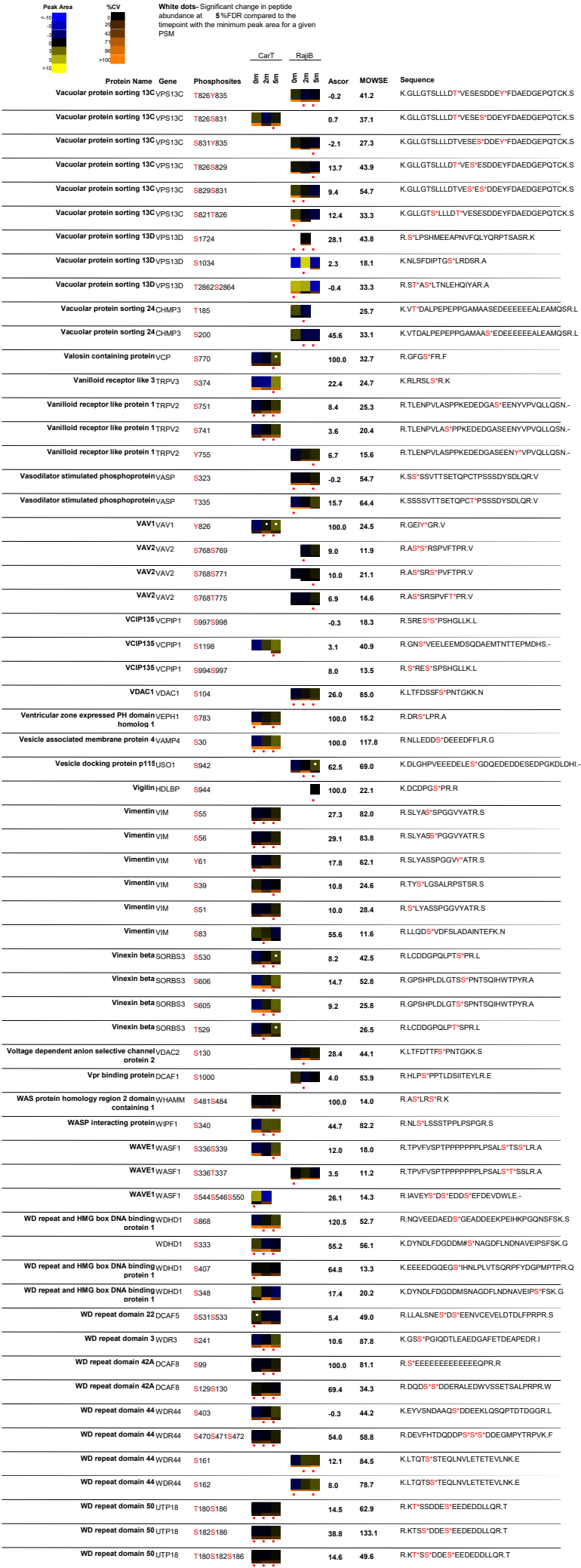
Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		Protein Name	Gene	Phosphosites						
		TRAP150	THRAP3	S534				-0.3	26.9	K.SS <sup>+</sup> SPPR.K
		TRAP150	THRAP3	S535				13.6	33.3	K.SS <sup>+</sup> PPPR.K
		TRAP150	THRAP3	S24S26S28S30				100.0	13.1	R.S <sup>+</sup> RS <sup>+</sup> FS <sup>+</sup> KS <sup>+</sup> R.S
		TRAP150	THRAP3	Y54S55				10.9	32.3	R.SY <sup>+</sup> S <sup>+</sup> PAHNR.E
		BCLAF1	S672					100.0	23.2	K.S <sup>+</sup> PEHRR.I
		TRAP150	THRAP3	S119				13.9	29.8	R.QAYS <sup>+</sup> PR.R
		TRAP150	THRAP3	S320				36.3	87.3	K.S <sup>+</sup> PPSTGSTYGSSQK.E
		TRAP150	THRAP3	S399S406				20.1	13.6	K.TDS <sup>+</sup> EKPFRGS <sup>+</sup> QSPK.R
		TRAP150	THRAP3	S315S320				56.7	75.4	K.S <sup>+</sup> PVGS <sup>+</sup> PPSTGSTYGSSQK.E
		TRAP150	THRAP3	S51S53S55				17.7	32.4	R.S <sup>+</sup> RS <sup>+</sup> YS <sup>+</sup> PAHNR.E
		TRAP150	THRAP3	S26S28S30				100.0	20.6	R.S <sup>+</sup> FS <sup>+</sup> KS <sup>+</sup> R.S
		TRAP150	THRAP3	S406S408				23.6	19.2	K.TDSEKPFRRGS <sup>+</sup> QS <sup>+</sup> PK.R
		TRAP150	ZNF318	S134S136				100.0	20.3	R.RS <sup>+</sup> PS <sup>+</sup> PR.R
		TRAP150	THRAP3	S53Y54S55				-0.1	15.2	R.SRS <sup>+</sup> YS <sup>+</sup> PAHNR.E
		TRAP150	THRAP3	S698				100.0	36.2	K.HGLAHDEMK <sup>+</sup> PR.E
		TRAP150	THRAP3	S928				5.8	29.4	K.FS <sup>+</sup> GEEGEIDDESGTENR.E
		TRAP150	THRAP3	S253				42.4	15.2	K.S <sup>+</sup> PLQSVVVR.R
		TRAP150	THRAP3	S51Y54S55				13.7	13.9	R.S <sup>+</sup> RSY <sup>+</sup> S <sup>+</sup> PAHNR.E
		TRAP150	THRAP3	S51S53Y54				1.9	11.4	R.S <sup>+</sup> RSY <sup>+</sup> SPAHR.E
		TRAP150	THRAP3	S377				7.2	72.4	K.GS <sup>+</sup> FSDTGLGDGK.M
		TRAP150	THRAP3	S24S26S28				100.0	11.5	R.S <sup>+</sup> RS <sup>+</sup> FS <sup>+</sup> KS
		TRAP150	THRAP3	S323				-20.9	87.8	K.SPPS <sup>+</sup> TGSTYGSSQK.E
		TRAP220	MED1	S120T71215				42.4	18.6	K.LAS <sup>+</sup> PMKPVPGT <sup>+</sup> PPSSK.A
		TRAP220	MED1	S1479S1482				17.7	18.7	K.SYQNS <sup>+</sup> PSS <sup>+</sup> DDGIRLPEYSTEK.H
		Treacle	TCOF1	S1301				13.9	97.9	K.LGAGEGGEASV <sup>+</sup> PEK.T
		Treacle	TCOF1	S270S272S273				65.8	46.2	R.AKKPEES <sup>+</sup> ES <sup>+</sup> S <sup>+</sup> EEGS <sup>+</sup> ES <sup>+</sup> EEEPAGTR.S
		Treacle	TCOF1	S1151				13.9	96.1	K.LDS <sup>+</sup> PSVSSTLAAK.D
		Treacle	TCOF1	S1073				6.5	13.5	K.KQEGPATQVDSAVGTLPA <sup>+</sup> SPQSTSVQAK.G
		Treacle	TCOF1	T785S791S794				5.2	33.3	K.AVATAAQAT <sup>+</sup> GPEEDS <sup>+</sup> GS <sup>+</sup> EEES <sup>+</sup> DS <sup>+</sup> EEEEATLQVKPSGK.T
		Treacle	TCOF1	T785S791S793				9.3	29.9	K.AVATAAQAT <sup>+</sup> GPEEDS <sup>+</sup> GS <sup>+</sup> SEES <sup>+</sup> DS <sup>+</sup> EEEEATLQVKPSGK.T
		Treacle	TCOF1	S1113S1114				25.4	77.0	R.TETLVEETAES <sup>+</sup> S <sup>+</sup> EDDVAPQSLLSGYMTPLTPANSQASK.A
		Treacle	TCOF1	T1102T1104				53.5		R.T <sup>+</sup> ET <sup>+</sup> LVEETAESSEDDVVAPQSLLSGYMTPLTPANSQASK.A
		Treacle	TCOF1	S1273				100.0	74.3	R.KLS <sup>+</sup> GDQPAAR.T
		Treacle	TCOF1	S304				24.2	55.5	K.TSQVGAASAPAKES <sup>+</sup> PR.K
		Treacle	TCOF1	S829				100.0	44.8	R.AALAPAKES <sup>+</sup> PR.K
		Treacle	TCOF1	S156				11.3	42.0	K.TVANLLSGKS <sup>+</sup> PR.K
		TCOF1	S505					10.9	33.4	K.SLGNILQAKPT <sup>+</sup> SPAKGPPQK.A
		Treacle	TCOF1	S426				72.1	71.0	K.S <sup>+</sup> PQVKPASTMGMPGLGK.G
		TCOF1	S506					3.5	37.3	K.SLGNILQAKPT <sup>+</sup> SPAKGPPQK.A
		Treacle	TCOF1	S1114S1122				3.3	51.0	R.TETLVEETAES <sup>+</sup> S <sup>+</sup> EDDVAP <sup>+</sup> QS <sup>+</sup> LLSGYMTPLTPANSQASK.A
		Treacle	TCOF1	S1114S1124				0.9	42.1	R.TETLVEETAES <sup>+</sup> S <sup>+</sup> EDDVAP <sup>+</sup> QS <sup>+</sup> LLSGYMTPLTPANSQASK.A
		Treacle	TCOF1	T504				79.5	29.8	K.SLGNILQAKPT <sup>+</sup> SSPAKGPPQK.A
		Treacle	TCOF1	T1072				10.3	36.0	K.KQEGPATQVDSAVGTLPA <sup>+</sup> SPQSTSVQAK.G
		Treacle	TCOF1	T1109S1122S11				1.0	15.6	R.TETLVEET <sup>+</sup> AAESSEDDVVAP <sup>+</sup> QS <sup>+</sup> LLSGYMTPLTPANSQASK.A
		Treacle	TCOF1	S1122S1124				0.9	44.2	R.TETLVEETAESSEDDVAP <sup>+</sup> RS <sup>+</sup> QS <sup>+</sup> LLSGYMTPLTPANSQASK.A
		Treacle	TCOF1	T779T785S791				54.3		K.AVAT <sup>+</sup> AAQAQT <sup>+</sup> GPEEDS <sup>+</sup> GS <sup>+</sup> S <sup>+</sup> EEESDSEEAETLAQVKPSGK.T
		Trinucleotide repeat containing 6 TNRC6A	Y1574					0.0	43.9	R.LEESPFPVY <sup>+</sup> DFMNSSTSPASPPGSIGDGWPRA
		Trinucleotide repeat containing 6 TNRC6A	S1585					26.0	47.7	R.LEESPFPVYDFMNSSTSPAS <sup>+</sup> PPGSIGDGWPRA
		Trinucleotide repeat containing 6 TNRC6A	Y1574S1585					14.6	39.6	R.LEESPFPVY <sup>+</sup> DFMNSSTSPAS <sup>+</sup> PPGSIGDGWPRA
		Trinucleotide repeat containing 6 TNRC6A	Y1574T1581					2.1	25.3	R.LEESPFPVY <sup>+</sup> DFMNSST <sup>+</sup> SPASPPGSIGDGWPRA
		Trinucleotide repeat containing 6 TNRC6A	S1579S1585					9.7	35.6	R.LEESPFPVYDFMNS <sup>+</sup> STSPAS <sup>+</sup> PPGSIGDGWPRA
		Trinucleotide repeat containing 6 TNRC6A	S1579S1580					5.5	11.9	R.LEESPFPVYDFMNS <sup>+</sup> S <sup>+</sup> TSPASPPGSIGDGWPRA
		Trinucleotide repeat containing 6 TNRC6A	T1581S1585					9.6	44.8	R.LEESPFPVYDFMNSST <sup>+</sup> SPAS <sup>+</sup> PPGSIGDGWPRA
		Trinucleotide repeat containing 6B TNRC6B	S1012					99.8	25.9	R.MGS <sup>+</sup> PAPLLPGDLLGGSDSL.-
		Trinucleotide repeat containing 6B TNRC6B	V630T640					4.5	11.5	R.GGSPY <sup>+</sup> NQFDIIPGDT <sup>+</sup> LGGHTPAGDSWLPAKSPPTNK.I
		Trinucleotide repeat containing 6B TNRC6B	V630S657					6.3	17.1	R.GGSPY <sup>+</sup> NQFDIIPGDTLGGHTGPAGDSWLPAK <sup>+</sup> SPTNK.I
		Trinucleotide repeat containing 6B TNRC6B	V630					9.8	15.8	R.GGSPY <sup>+</sup> NQFDIIPGDTLGGHTGPAGDSWLPAK.S
		Trinucleotide repeat containing 6B TNRC6B	T640					4.7	11.2	R.GGSPY <sup>+</sup> NQFDIIPGDT <sup>+</sup> LGGHTPAGDSWLPAK.S
		Trinucleotide repeat containing protein 15GIGYF2	S376					31.2	21.2	R.VGVEASEETPQTSS <sup>+</sup> SARPGTPSDHQSQEASQFER.K
		Trinucleotide repeat containing protein 15GIGYF2	S384					0.3	30.6	R.VGVEASEETPQTSSSARPGT <sup>+</sup> PS <sup>+</sup> DHQSQEASQFER.K
		Trinucleotide repeat containing protein 15GIGYF2	S26S30					23.1	37.2	R.ALSSGGIS <sup>+</sup> PPLS <sup>+</sup> PALPK.Y
		Trinucleotide repeat containing protein 15GIGYF2	S160					20.9	32.5	R.SQS <sup>+</sup> WEER.G

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT		RajiB		Ascor	MOWSE	Sequence
		5	6	5	6					
		Protein Name	Gene	Phosphosites						
Trinucleotide repeat containing protein 15GIGYF2										
		S236						100.0	49.2	R.VRPHS*PDGPR.S
Trinucleotide repeat containing protein 15GIGYF2										
		S26						23.9	87.6	R.ALSSGGIS*PPLSPALPK.Y
Trinucleotide repeat containing protein 15GIGYF2										
		T25S30						22.8	35.1	R.ALSSGGIS*SPPLS*PALPK.Y
Trinucleotide repeat containing protein 15GIGYF2										
		T373						7.4	16.8	R.VGVEASEETPQT*SSSARPGTPSDHQSEASQFER.K
Trinucleotide repeat containing protein 15GIGYF2										
		S374						0.3	16.8	R.VGVEASEETPQT*SSSARPGTPSDHQSEASQFER.K
Trinucleotide repeat containing protein 15GIGYF2										
		T25						17.8	18.4	R.ALSSGGIS*SPPLSPALPK.Y
Trinucleotide repeat-containing gene 6CTNRC6C protein										
		S1000						49.0	87.2	R.S*PLLPVSSGWGEMPNVHSK.T
TRIO TRIO										
		S1724						-0.3	26.2	R.SS*MEMEGIFNHK.D
Triosephosphate isomerase 1TP11										
		S21						108.0	119.5	R.KQS*LGLIGTLNAAK.V
Tripartite motif containing 46TRIM45										
		S451						100.0	12.1	K.KDS*PVR.T
tRNA modification GTPase GTPBP3, GTPBP3 mitochondrial										
		T22S23						100.0	17.9	R.RT*PRLR.R
tRNA-yW synthesizing protein 3 homolog TYW3										
		S236						14.1	15.0	K.ES*DELENDDDDLGINVTFPEDY.-
Tropomodulin 3TMOD3										
		S25						18.4	65.1	K.YKDLDEDELLGNLS*ETELK.Q
TRPC6 TRPC6										
		S14						8.9	20.0	R.RGSS*PR.G
Tryptophanyl tRNA synthetase WARS										
		S467						100.0	36.6	R.KLS*FDFQ.-
Tryptophanyl tRNA synthetase WARS										
		S8						4.3	35.9	M.PNSEPAS*LLELFNSIATQGEIVR.S
TSC22 domain family 4 TSC22D4										
		S279						100.0	49.6	K.S*PDPFGAVAAQK.F
TSC22 domain family 4 TSC22D4										
		S165						23.2	90.8	R.S*FTGGLGQLVVP SKA
TSC22 domain family 4 TSC22D4										
		S260S263						11.4	12.0	R.MELGAPEEMGQVPPLDS*RP S*SPALYFTHDASLVHK.S
TSC22 domain family 4 TSC22D4										
		T167						-0.5	82.4	R.SFT*GGLGQLVVP SKA
TSC22 domain family 4 TSC22D4										
		T229						16.0	29.9	R.T*PPLSR.R
TTK protein kinase TTK										
		S455						16.9	54.2	K.TP S*NTLDDYMSCF.T
Tuberin TSC2										
		S1386						-0.1	87.8	K.SS*SPELQTLQDILGDPGDK.A
Tuberin TSC2										
		S1387S1411						22.0	21.6	K.SSS*SPELQTLQDILGDPGDKADVGRLS*PEVKA
Tuberin TSC2										
		S1388S1411						39.8	24.3	K.SSS*SPELQTLQDILGDPGDKADVGRLS*PEVKA
Tuberin TSC2										
		T1422						-0.5	86.4	R.SQSG*LDGESAAWSASGEDSR.G
Tuberin TSC2										
		S1387						9.5	40.8	K.SS*SPELQTLQDILGDPGDK.A
Tuberous sclerosis 1TSC1										
		T339T345							38.5	R.LIT*EPPQAT*LVSPSMVCGMTTPPTSPGNVPPDLSPHYK.V
Tubulin alpha 1TUBA1B										
		S340						104.7	72.4	R.S*IQFVDWCPTGFK.V
Tubulin tyrosine ligase-like family, member 4TLL4										
		S121S122						13.9	16.1	R.RS*S*YR.Q
Tubulin tyrosine ligase-like family, member 4TLL4										
		S122Y123						5.0	12.1	R.RS*S*YR.Q
Tubulin tyrosine ligase-like family, member 4TLL4										
		S121Y123						11.4	13.2	R.RS*S*YR.Q
Tubulin, alpha 2TUBA1C										
		S48						46.9	142.5	K.TIGGGDD S*NTFFSETGAGK.H
Tubulin, alpha, brain specificTUBA1B										
		S439						63.6	13.7	K.DYEEVGVD S*VEGEHEEEEEEY.-
Tubulin, betaTUBB										
		T55						12.7	30.3	R.ISVYYNEAT*GKK.Y
Tuftelin interacting protein 11TFIP11										
		S98						100.0	66.5	K.GAAEEAELED S*DDEKPVKODDFPK.D
Tuftelin interacting protein 11TFIP11										
		S210						86.3	85.7	R.TTQSMQDFPVVD S*EEEEEEFQK.E
TFIP11										
		S59						40.7	26.2	R.DS*DOERPSFGQK.R
Tuftelin interacting protein 11TFIP11										
		Y51						11.9	13.2	K.EEAT*GVWAERDSDDERPSFGQK.R
Tumor necrosis factor receptor superfamily, member 9										
		Y222						100.0	26.5	K.LLY*IFK.Q
Tumor protein D52TPD52										
		T180						7.4	47.6	K.VGGTKPAGDGFGEVLNANASATTTEPLPEKT*QESL.-
Tumor protein D52TPD52										
		S183						17.6	66.5	K.VGGTKPAGDGFGEVLNANASATTTEPLPEKTQES*L.-
Tumor protein D52 like 2TPD52L2										
		S21						32.1	100.2	K.GLLSD S*MTDVPDVGVAAR.T
Tumor protein p53 binding protein 1TP53BP1										
		S1094S1101						29.0	36.7	R.QSQQPMKPI S*PVKDPV S*PASQK.M
Tumor protein p53 binding protein 1TP53BP1										
		S1208S1219						7.6	13.5	R.GSGEKPV S*APGDDTESLH S*QGEEEFDMQPQPHGHVLR.H
Tumor protein p53 binding protein 1TP53BP1										
		T1214S1219						8.6	32.9	R.GSGEKPV S*APGDDTESLH S*QGEEEFDMQPQPHGHVLR.H
Tumor protein p53 binding protein 1TP53BP1										
		S1216S1219						19.2	37.7	R.GSGEKPV S*APGDDTESLH S*QGEEEFDMQPQPHGHVLR.H
Tumor protein p53 binding protein 1TP53BP1										
		S1202S1208						14.6		R.GS*GEKPV S*APGDDTESLH S*QGEEEFDMQPQPHGHVLR.H
Tumor protein p53 binding protein 1TP53BP1										
		S380						20.1	50.4	R.STPFIVPS*PTEQEGR.Q
Tumor protein p53 binding protein 1TP53BP1										
		S552						27.3	35.8	R.IDEDGENTQIEDTEPMS*PVLNSK.F
Tumor protein p53 binding protein 1TP53BP1										
		S500						104.3	117.8	K.NS*PEDLGLSLTGDSCK.L
Tumor protein p53 binding protein 1TP53BP1										
		S294						112.6	108.0	K.S*PEPEVLSTQEDLFDQSNK.T
Tumor protein p53 binding protein 1TP53BP1										
		S386						88.2	76.0	R.SLVQDSLSTNSSDLVARS*PDAFR.S
Tumor protein p53 binding protein 1TP53BP1										
		S1114						9.0	87.0	K.MVIQGPS*PQGEAMVTDVLEDQK.E
Tumor protein p53 binding protein 1TP53BP1										
		S1462						-0.5	96.3	R.SDS*PEIPFQAAAGPSDGLDASSPGNSFVGLR.V
Tumor protein p53 binding protein 1TP53BP1										
		S1460						7.2	52.6	R.S*DSPEIPFQAAAGPSDGLDASSPGNSFVGLR.V
Tumor protein p53 binding protein 1TP53BP1										
		S1758S1759						20.1	48.1	R.SKLPDQPTGS*S*EEEEFLEIPPNK.Q
Tumor protein p53 binding protein 1TP53BP1										
		S635S639S640						100.0	87.1	R.S*EAL S*S*VLDOEEAMEIK.E
Tumor protein p53 binding protein 1TP53BP1										
		S1462S1481						5.8	56.6	R.SDS*PEIPFQAAAGPSDGLDASS*PGNSFVGLR.V
Tumor protein p53 binding protein 1TP53BP1										
		S1426S1430						24.4	41.4	R.ETAVPGPLGIED S*PNL S*PDDKSFVR.V
Tumor protein p53 binding protein 1TP53BP1										
		S1462S1480						19.5	39.2	R.SDS*PEIPFQAAAGPSDGLDASS*PGNSFVGLR.V
Tumor protein p53 binding protein 1TP53BP1										
		S1460S1462						-0.5	16.3	R.S*DS*PEIPFQAAAGPSDGLDASSPGNSFVGLR.V

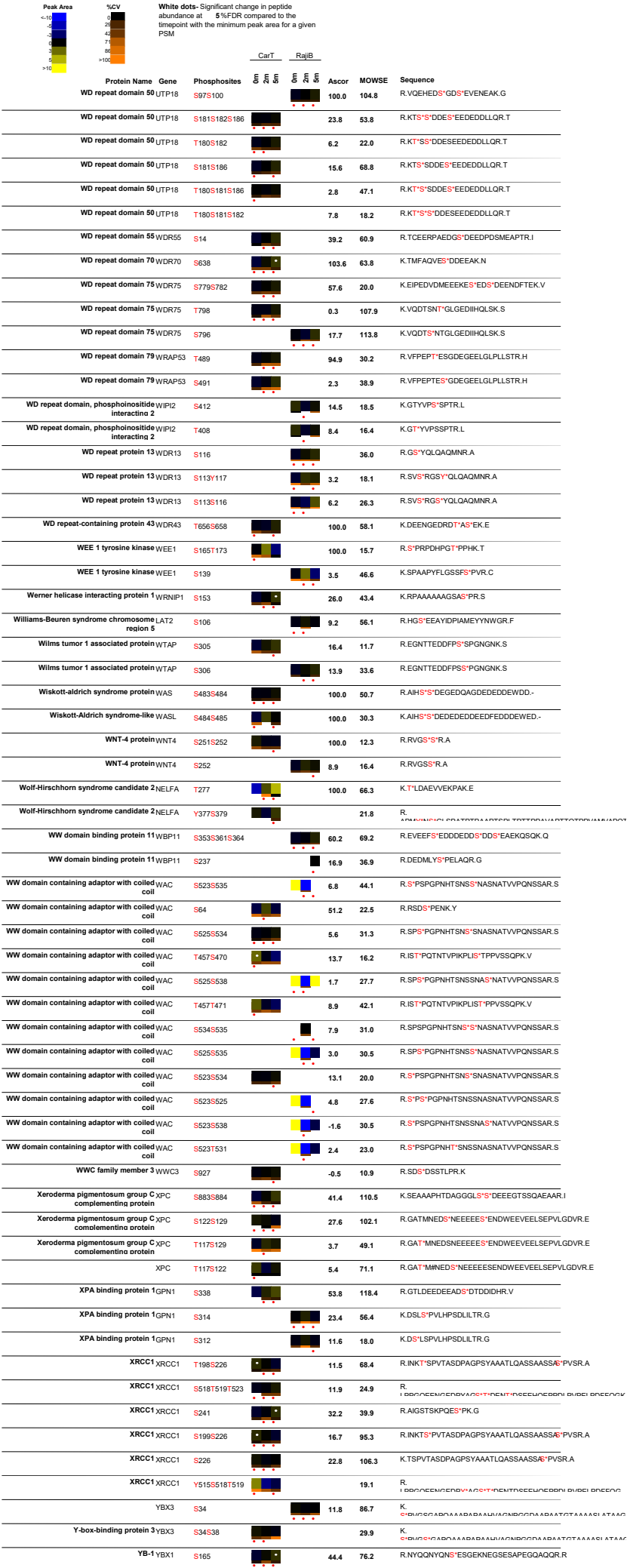


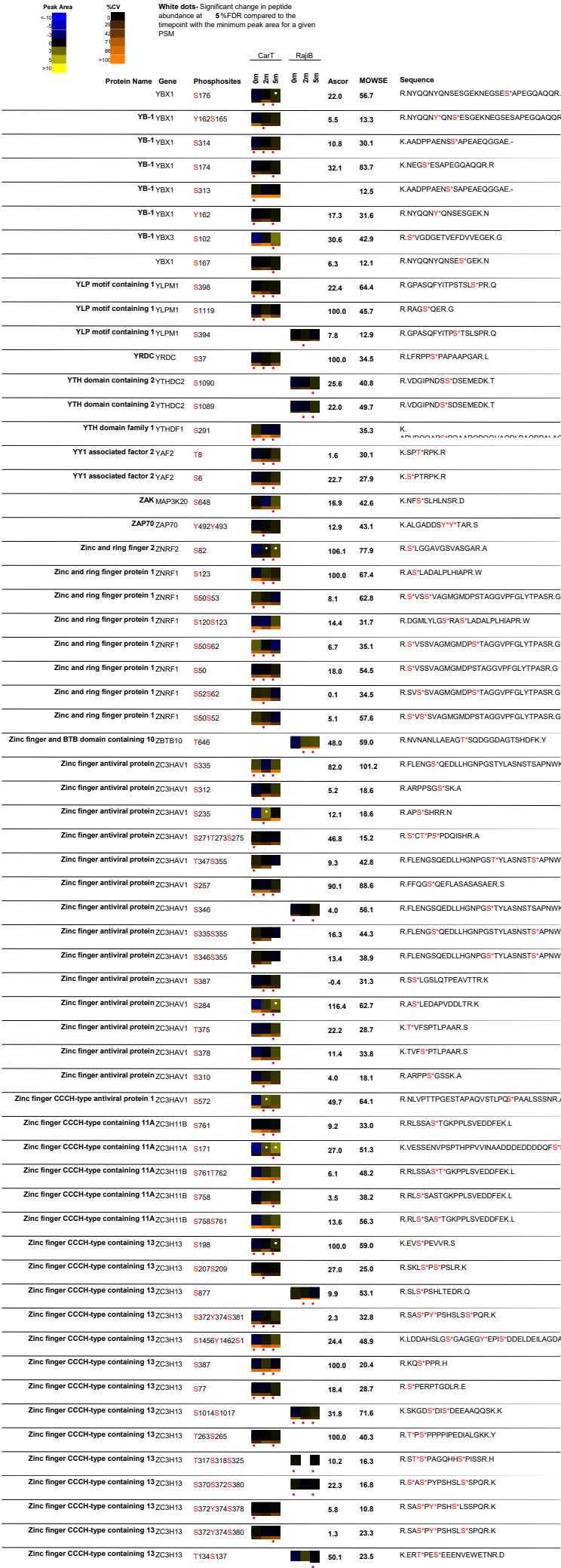
Peak Area	<div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>40</div> <div>70</div> <div>100</div> <div>&gt;100</div> </div> <div> <div>&lt;10</div> <div>10</div> <div>20</div> <div>40</div> <div>70</div> <div>100</div> <div>&gt;100</div> </div> </div>	<div> <div>White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM</div> </div>	<div> <div>CarT</div> <div>RajiB</div> </div>		Ascor	MOWSE	Sequence
			Phosphosites				
	Protein Name	Gene					
	Ubiquitin specific protease 10	USP10	S211		24.3	71.9	R.TCNS*PQNSTDVSDIVPDSFPFGALGSDTR.T
	Ubiquitin specific protease 10	USP10	S80		10.0	83.3	R.TPSYSIS*STLNPOAPEFILGCTASK.I
	Ubiquitin specific protease 10	USP10	T74		10.9	152.0	R.T*PSYSISSTLNPOAPEFILGCTASK.I
	Ubiquitin specific protease 10	USP10	T82		10.3	53.7	R.TPSYSISST*LNPOAPEFILGCTASK.I
	Ubiquitin specific protease 10	USP10	S76		17.7	68.4	R.TPS*YSISSTLNPOAPEFILGCTASK.I
	Ubiquitin specific protease 10	USP10	S211S215S220		7.5	52.6	R.TCNS*PQNS*TDVS*DIVPDSFPFGALGSDTR.T
	Ubiquitin specific protease 10	USP10	S81		12.2	29.7	R.TPSYSIS*STLNPOAPEFILGCTASK.I
	Ubiquitin specific protease 10	USP10	T216		0.2	20.3	R.TCNSPQNST*DSVSDIVPDSFPFGALGSDTR.T
	Ubiquitin specific protease 10	USP10	T208		2.5	26.1	R.T*CNSPQNSTDSVSDIVPDSFPFGALGSDTR.T
	Ubiquitin specific protease 10	USP10	S78		3.5	92.5	R.TPSYS*ISSTLNPOAPEFILGCTASK.I
	Ubiquitin specific protease 10	USP10	S211S215T216		1.7	44.8	R.TCNS*PQNS*TDVSDIVPDSFPFGALGSDTR.T
	Ubiquitin specific protease 10	USP10	S211S215S218		6.1	40.9	R.TCNS*PQNS*TD*SVDIVPDSFPFGALGSDTR.T
	Ubiquitin specific protease 10	USP10	S211S218S220		3.2	55.3	R.TCNS*PQNSTD*S*VSDIVPDSFPFGALGSDTR.T
	Ubiquitin specific protease 14	USP14	S143		16.3	85.8	R.AS*GEMASAQYITAAAL.R
	Ubiquitin specific protease 14	USP14	S148		18.5	67.9	R.ASGEMAS*AQYITAAAL.R
	Ubiquitin specific protease 15	USP15	S965		0.7	31.4	K.GASAATGIPLESD*NDNDNDIENENCMHTN.-
	Ubiquitin specific protease 15	USP15	S961		25.5	42.3	K.GASAATGIPLES*DEDSNDNDNDIENENCMHTN.-
	Ubiquitin specific protease 15	USP15	S961S965		25.3	32.9	K.GASAATGIPLES*DEDS*NDNDNDIENENCMHTN.-
	Ubiquitin specific protease 15	USP15	S229		42.4	29.0	K.S*PGASNFSTLPK.I
	Ubiquitin specific protease 20	USP20	S132S134		100.0	31.9	K.AVPIAVALDEGES*ES*EDDLKPR.G
	Ubiquitin specific protease 24	USP24	S1887		57.8	46.8	R.VSDQNS*PVLPK.K
	Ubiquitin specific protease 24	USP24	S250		33.6	141.1	R.TIS*AQDTLAYATALLNEK.E
	Ubiquitin specific protease 24	USP24	T254		14.2	86.5	R.TISAQDT*LAYATALLNEK.E
	Ubiquitin specific protease 34	USP34	S483S486S487		14.7	11.8	K.AQLS*KQS*S*FAS*LLNTNIPIGNKK.E
	Ubiquitin specific protease 34	USP34	S2488		46.9	58.7	K.GPENPQVEVL*S*EEEEEEEEEDILSLAEK.Y
	Ubiquitin specific protease 39	USP39	S82		100.0	28.6	R.EVDED*S*EPER.E
	Ubiquitin specific protease 47	USP47	T844		22.4	53.6	R.ELEQHIQ*T*SDPENFQSEER.S
	Ubiquitin specific protease 47	USP47	S744		22.4	18.4	R.LFVLLPEQS*PVYSKR.R
	Ubiquitin specific protease 6	USP6	S1214		100.0	31.1	R.LRLPQIGS*K.N
	Ubiquitin specific protease 7	USP7	S18		68.9	76.8	K.AGEQQLS*EPEDMEMEAGDTPDPR.I
	Ubiquitin-associated protein 2-like	UBAP2L	S478		18.0	49.6	K.STSAPQMS*PGSSDNQSSSPQPAQOK.L
	Ubiquitin-associated protein 2-like	UBAP2L	S478S488		20.8	42.4	K.STSAPQMS*PGSSDNQSS*PQPAQOK.L
	Ubiquitin-associated protein 2-like	UBAP2L	S473S488		20.8	26.0	K.STS*APQMSPGSSDNQSS*PQPAQOK.L
	Ubiquitin-associated protein 2-like	UBAP2L	S473		8.7	26.7	K.STS*APQMSPGSSDNQSSSPQPAQOK.L
	Ubiquitin-associated protein 2-like	UBAP2L	S481		7.4	33.4	K.STSAPQMSPGS*SDNQSSSPQPAQOK.L
	Ubiquitin-associated protein 2-like	UBAP2L	S486S488		5.7	17.0	K.STSAPQMSPGSSDNQS*SS*PQPAQOK.L
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S231S232		4.6	35.5	R.LHNENAEMD*S*S*SGGTETDLHGSLR.V
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S229S231S232		19.9	77.7	R.LHNENAEMD*S*DS*S*S*SGTETDLHGSLR.V
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S229S231S232		15.1	38.6	R.LHNENAEMD*S*DS*S*S*S*GTETDLHGSLR.V
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S229S232		6.9	65.6	R.LHNENAEMD*S*DSS*SGGTETDLHGSLR.V
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S229S232S233		11.2	54.3	R.LHNENAEMD*S*DSS*S*SGTETDLHGSLR.V
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S229S231S232		21.9	74.0	R.LHNENAEMD*S*DS*S*SS*GTETDLHGSLR.V
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S229S232S233		13.5	20.9	R.LHNENAEMD*S*DSS*S*S*GT*ETDLHGSLR.V
	Ubiquitin-conjugating enzyme E2Z	UBE2Z	S231S232S233		10.6	33.6	R.LHNENAEMDSD*S*S*S*GTETDLHGSLR.V
	Ubiquitination factor E4B protein	UBE4B	S79		0.3	15.6	R.SQS*EGVSSLSSPSNLETQSQSLSR.S
	Ubiquitination factor E4B protein	UBE4B	S87		6.1	48.7	R.SQSSEGVSSL*S*SPNSLETQSQSLSR.S
	Ubiquitously transcribed TPR protein on X chromosome		S789		58.3	75.1	K.S*PGLLSSDNPQLSALLMGK.A
	UBX domain containing 7	UBXN7	S288		34.4	134.4	R.SESLIDASED*S*QLEAAIR.A
	UBX domain containing 7	UBXN7	S280S288		18.6	93.6	R.SES*LIDASED*S*QLEAAIR.A
	UBX domain containing 7	UBXN7	S350		100.0	42.5	K.S*PHKDLGHR.K
	UBX domain containing 7	UBXN7	S285		6.0	31.7	R.SESLIDAS*EDSQLEAAIR.A
	UBX domain containing 7	UBXN7	S280		13.6	29.4	R.SES*LIDASEDSQLEAAIR.A
	Inactive progesterone receptor 23KD	PTGES3	S113		75.8	100.0	K.DWEDDS*DEDMSNFDR.F
	Inactive progesterone receptor 23KD	PTGES3	S151		10.0	58.6	R.FSEMNNMGGDEDVDLPEVDGADDDSD*S*DOEKMPDLE.-
	Inactive progesterone receptor 23KD	PTGES3	S148		4.3	34.8	R.FSEMNNMGGDEDVDLPEVDGADDD*S*QDSDEKMPDLE.-
	Inactive progesterone receptor 23KD	PTGES3	S124		19.3		R.F*S*EMNNMGGDEDVDLPEVDGADDDSQDSDEKMPDLE.-
	Inactive progesterone receptor 23KD	PTGES3	S100		17.0	58.4	K.LNWLS*VDFNNWKDWEDSDSDMSNFDR.F
	Inactive progesterone receptor 23KD	PTGES3	S113S118		100.0	55.0	K.DWEDDS*DEDM*SNFDR.F
	Unc 51 like kinase 1	ULK1	S556		33.7	37.8	R.LHS*APNLSDLHVVRPK.L
	Unc 51 like kinase 1	ULK1	S638		16.9	101.3	K.TPS*SQNLALLAR.Q
	Unc 51 like kinase 1	ULK1	T709S716			42.9	K.AAFGT*QAPDPGS*TESLQEKPMEIAPSGFGGSLHPGAR.A
	Unc 51 like kinase 1	ULK1	S716S719		30.6	43.3	K.AAFGTQAPDPGS*TES*LQEKPMEIAPSGFGGSLHPGAR.A

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		Protein Name	Gene	Phosphosites					
		Unc 51 like kinase 1	ULK1	T660			31.4	12.8	R.TLPDLSEVGPFGHGQPLGPGLRPGEDPK.G
		Unc 93 homolog B1	UNC93B1	S547S550			27.8	25.1	R.YLEEDNSDESDAEHGDAQEEAAPAGPRPGPEAGLGR.R
		Unc 93 homolog B1	UNC93B1	Y541S547			19.4		R.YLEEDNSDESDAEHGDAQEEAAPAGPRPGPEAGLGR.R
		UNC112 related protein 2	FERMT3	S8			20.6	52.8	K.TASGDYIDSSWEI.R.V
		UNC112 related protein 2	FERMT3	S484			7.6	125.8	R.TGSGGPGNHPHGPDAEGLNPYQLVAPR.F
		UNC112 related protein 2	FERMT3	T482			5.5	44.6	R.TGSGGPGNHPHGPDAEGLNPYQLVAPR.F
		UNC119	UNC119	T12T14S16				12.5	K.VGGGASPTATCESADPSGCGUADIDPDASEENSESEEDAPD
		UNC119	UNC119	T12T14S16S21				13.0	K.VGGGASPTATCESADPSGCGUADIDPDASEENSESEEDAPD
		UNC13D	UNC13D	S150			12.8	61.0	K.DVSGFSDPYQLLIEQGVGVPGGS*PSGR.H
		Uncharacterized membrane protein C19orf24	C19orf24	T113S117			4.4	11.7	R.YGLLANTEDPT*EMIAS*LDSEETVFESR.N
		Uncharacterized membrane protein C19orf24	C19orf24	S120			24.4	84.9	R.YGLLANTEDPTEMASLDSEETVFESR.N
		Uncharacterized membrane protein C19orf24	C19orf24	S117S120			31.2	119.9	R.YGLLANTEDPTEMAS*LDSEETVFESR.N
		Uncharacterized membrane protein C19orf24	C19orf24	S117			12.0	97.0	R.YGLLANTEDPTEMAS*LDSEETVFESR.N
		Uncharacterized membrane protein C19orf24	C19orf24	T109S120			3.9	13.7	R.YGLLAN*EDPT*EMIASLDSEETVFESR.N
		Uncharacterized membrane protein C19orf24	C19orf24	T109T113			1.7	11.7	R.YGLLAN*EDPT*EMIASLDSEETVFESR.N
		Uncharacterized membrane protein C19orf24	C19orf24	T113S120			20.0	36.8	R.YGLLANTEDPT*EMIASLDSEETVFESR.N
		Uncharacterized protein		S101S102			100.0	23.4	R.RS*S*LPRR.G
		Uncharacterized protein (Fragment)		S96			6.5	24.2	R.RSS*GWPR.T
		Uncharacterized protein C11orf96	C11orf96	S86			12.1	45.5	K.SFLQS*LECLR.R
		Uncharacterized protein C6orf132	C6orf132	S1151			26.1	13.1	R.S*PYTTTR.Y
		Unconventional myosin-XVIIIa (Fragment)	MYO18A	S332			100.0	24.8	R.AAS*IRR.S
		UPF0505 protein C16orf62	C16orf62	T434			100.0	17.6	R.ALL*EMMER.C
		Upstream regulatory element binding protein 1	HUWE1	S2362S2365			44.1	107.4	R.DGGS*GNS*TIIVSR.S
		Upstream regulatory element binding protein 1	HUWE1	S1907			41.9	103.2	R.GSGTAS*DDEFNLRI
		Upstream regulatory element binding protein 1	HUWE1	S718				66.6	R.ENIWAACEASSECEEEEDVAMMSSESTQMETEDMVAIATEE
		Upstream regulatory element binding protein 1	HUWE1	S726S727			-3.7	46.5	R.ENIWAACEASSECEEEEDVAMMSSESTQMETEDMVAIATEE
		Upstream regulatory element binding protein 1	HUWE1	S3919T3924			35.3	25.7	K.DEPPPLS*PAPLT*PATPSSLDPFFSR.E
		Upstream regulatory element binding protein 1	HUWE1	S2619			40.5	102.1	R.S*DDELLDDFFHDQSTATSQAGTLSSIPTALTR.W
		Upstream regulatory element binding protein 1	HUWE1	S3373			22.2	83.6	K.ACS*PCSSQSSSSGICTDFWDLVLYKL
		Upstream regulatory element binding protein 1	HUWE1	S1395			100.0	51.2	R.AES*PEEVACR.K
		Upstream regulatory element binding protein 1	HUWE1	T3924			0.8	29.5	K.DEPPPLSAPALT*PATPSSLDPFFSR.E
		Upstream regulatory element binding protein 1	HUWE1	T2635			10.9	51.1	R.SDDELLDDFFHDQSTATSQAGTLSSIPTALTR.W
		Upstream regulatory element binding protein 1	HUWE1	S3919T3924T39			33.6	34.1	K.DEPPPLS*PAPLT*PATPSSLDPFFSR.E
		Upstream regulatory element binding protein 1	HUWE1	S740S743			6.8	66.1	R.ENIWAACEASSECEEEEDVAMMSSESTQMETEDMVAIATEE
		Upstream regulatory element binding protein 1	HUWE1	S649			12.1	95.9	R.RSS*DPLGDATSNLGSADVDELMRH
		Upstream regulatory element binding protein 1	HUWE1	S3379			5.8	25.0	K.ACSPCSSQS*SSSGICTDFWDLVLYKL
		Upstream regulatory element binding protein 1	HUWE1	S3919			1.6	45.0	K.DEPPPLS*PAPLT*PATPSSLDPFFSR.E
		Upstream regulatory element binding protein 1	HUWE1	S3757			41.9	112.7	R.LGSSGLGS*ASSIAQAVR.Q
		Upstream regulatory element binding protein 1	HUWE1	S740T744			-2.8	37.5	R.ENIWAACEASSECEEEEDVAMMSSESTQMETEDMVAIATEE
		Upstream regulatory element binding protein 1	HUWE1	S3919T3927			24.0	15.5	K.DEPPPLS*PAPLT*PATPSSLDPFFSR.E
		Upstream regulatory element binding protein 1	HUWE1	S3816			8.0	66.5	R.REESPMDVDQPS*PSAQDTQSIASDGTGQGEK.E
		Upstream regulatory element binding protein 1	HUWE1	S718S726				86.3	R.ENIWAACEASSECEEEEDVAMMSSESTQMETEDMVAIATEE
		Upstream regulatory element binding protein 1	HUWE1	S2377			3.9	66.3	R.SGEDES*QEDVLMDEAPSNLQASTLQANR.E
		Upstream regulatory element binding protein 1	HUWE1	S2632			2.4	22.8	R.SDDELLDDFFHDQS*ATSQAGTLSSIPTALTR.W
		Upstream regulatory element binding protein 1	HUWE1	S726T749			0.1	26.4	R.ENIWAACEASSECEEEEDVAMMSSESTQMETEDMVAIATEE
		Upstream regulatory element binding protein 1	HUWE1	T2633			16.0	74.4	R.SDDELLDDFFHDQS*ATSQAGTLSSIPTALTR.W
		Upstream regulatory element binding protein 1	HUWE1	S2636			-0.1	58.7	R.SDDELLDDFFHDQSTATSQAGTLSSIPTALTR.W
		Uracil DNA glycosylase	UNG	S23			34.3	45.7	R.HAPS*PEPAVQGTGVAGVPEESQDAAPAK.K
		Uracil DNA glycosylase	UNG	T60S63			19.6	56.7	K.KAPAGQEEPQT*PPS*PLSAEQLDR.I
		Uracil DNA glycosylase	UNG	T60S64			33.8	60.9	K.KAPAGQEEPQT*PPS*PLSAEQLDR.I
		Uridine monophosphate kinase	UCK2	S254			32.1	63.6	R.OAS*ESSSRPH.-
		USP6 N terminal like	USPNL	T276T279			100.0	11.8	R.T*PFT*LNLR.I
		UTP14A		S29S31			51.0	102.5	K.DYLLS*ES*EDEGNDGGR.K
		UTP14A		S341S343				37.5	K.LQVAS*ES*EEEEGGTDEVELLPDVVNEVQMADGPNPWMLR.
		UTP14A, U3 small nuclear ribonucleoprotein, homolog A	UTP14A	S40S407			38.7	24.3	K.EAATQEDPEQLPEAHGVS*ES*EGEERPVAEEILLR.E
		Utrophin	UTRN	S1866			-0.3	34.4	R.SS*LLPTDYLVINK.I
		Utrophin (Fragment)	UTRN	S21S213			10.1	19.5	R.LGYLPVQTVLEGDNLET*PS*QSPQLFHDDTHSR.I
		Utrophin (Fragment)	UTRN	T200S213			9.9	17.6	R.LGYLPVQTVLEGDNLET*PS*QSPQLFHDDTHSR.I
		Utrophin (Fragment)	UTRN	T209S211			8.3	24.2	R.LGYLPVQTVLEGDNLET*PS*QSPQLFHDDTHSR.I
		Utrophin (Fragment)	UTRN	T209S213			10.6	31.0	R.LGYLPVQTVLEGDNLET*PS*QSPQLFHDDTHSR.I
		Vac14 homolog	VAC14	S539S540			100.0	11.3	K.RFS*S*ERK.K
		Vacuolar protein sorting 13C	VPS13C	S829Y835			-0.2	51.1	K.GLLGTSLLDVTVE*ESDDEY*FDAEDGEPQTK.S









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		0	>10	0	>10	0	>10			
<10	<10									
10	10									
20	20									
30	30									
40	40									
50	50									
60	60									
70	70									
80	80									
90	90									
>100	>100									
Protein Name	Gene	Phosphosites								
Zinc finger CCH-type containing 13ZC3H13		S1453S1456S1						42.4	56.5	K.LDDAH*S*LGS*GAGEGYEPIS*YDDELDELAGDAEK.R
Zinc finger CCH-type containing 13ZC3H13		S643						6.5	18.4	R.DORPSS*PIR.H
Zinc finger CCH-type containing 13ZC3H13		S1010S1014S1						56.9	59.0	K.S*KGDS*DIS*DEEAQQSK.K
Zinc finger CCH-type containing 13ZC3H13		S875						13.8	47.1	R.S*LSPSHLTEDR.Q
Zinc finger CCH-type containing 13ZC3H13		S370S372S378						8.4	19.4	R.S*AS*PYPSHS*LSSPOR.K
Zinc finger CCH-type containing 13ZC3H13		S875S877						24.2	18.2	R.S*LS*PSHLTEDR.Q
Zinc finger CCH-type containing 13ZC3H13		S110						7.8	18.6	R.NTEESS*PVRK.E
Zinc finger DHHC domain containing 5ZDHHC5		S296S299						10.9	15.0	K.S*KGS*LEITESQSADAEPPPPKPDLSR.Y
Zinc finger DHHC domain containing 5ZDHHC5		S423						21.2	41.6	K.SFHFDPLSS*GSR.S
Zinc finger DHHC domain containing 5ZDHHC5		S429S432						11.6	64.3	R.SS*S*LKS*AQGTGFELGQLQIR.S
Zinc finger DHHC domain containing 5ZDHHC5		S428S429						4.4	65.3	R.SS*S*LKSAQGTGFELGQLQIR.S
Zinc finger DHHC domain containing 5ZDHHC5		S432						35.4	100.5	K.S*AQGTGFELGQLQIR.S
Zinc finger DHHC domain containing 5ZDHHC5		S422						37.2	36.0	K.SFHFDPLS*SGSR.S
Zinc finger DHHC domain containing 5ZDHHC5		S425						9.1	37.9	K.SFHFDPLSSG*S.RS
Zinc finger DHHC domain containing 5ZDHHC5		S429T436						1.9	50.0	R.SS*S*LKSAQGT*GFELGQLQIR.S
Zinc finger FYVE domain containing 26FYVE26		S1762						6.2	79.6	R.S*PSAEFSPAAPPGISIHPSLR.E
Zinc finger FYVE domain containing 26FYVE26		S1764						7.6	55.0	R.SP*S*AEFSPAAPPGISIHPSLR.E
Zinc finger protein 106ZNF106		S1370						78.7	42.1	R.AAHVPEN*S*DTEQDVLTVKPVRK.V
Zinc finger protein 106ZNF106		S1025S1026						20.7	53.1	R.ATGDGS*S*PELPSLER.K
Zinc finger protein 183RNF113A		S43545S46S47						36.4	27.0	R.KRPACDPEPGES*GS*S*S*DEGCTTVRPEK.K
Zinc finger protein 183RNF113A		S84S85						38.2	55.8	K.AAYGDL*S*EEEEENEPESLGVVYK.S
Zinc finger protein 183RNF113A		S253						87.6	107.2	R.YGVYEDENYEVGS*DOEEIPFK.C
Zinc finger protein 183RNF113A		Y80S84						25.5	13.7	K.AAY*GDL*S*EEEEENEPESLGVVYK.S
Zinc finger protein 206ZSCAN10		S333						-0.2	10.8	K.SFGRS*SILK.L
Zinc finger protein 22ZNF22		S49						43.5	22.1	R.S*LDDKPYK.C
Zinc finger protein 261ZMYM3		S256T257							28.6	R.RAEPKPEVVD*S*TESIPVSDSDAMVDDPNDEDVFVRPR.R
Zinc finger protein 261ZMYM3		S95T960						46.5	68.9	K.ASSDLCDLVS*NQS*AEGLEDCDLFGPAR.D
Zinc finger protein 261ZMYM3		S263S267						45.8	18.5	R.RAEPKPEVVDSTESIPVS*DED*S*DAMVDDPNDEDVFVRPR.R
Zinc finger protein 262ZMYM4		S122						12.7	46.2	R.VTQHE*S*DNENIQIKN.L
Zinc finger protein 262ZMYM4		S1542S1547						22.3	46.2	K.SEDS*DVELS*D.-
Zinc finger protein 262ZMYM4		S1088T1089						8.9	32.2	K.DQGS*TYSGDLESEAVSTPHSWEEELNHYALK.S
Zinc finger protein 262ZMYM4		S1088S1091						16.8	11.1	K.DQGS*TYSGDLESEAVSTPHSWEEELNHYALK.S
Zinc finger protein 265ZRANB2		S153						112.6	109.7	K.EVEDKE*S*EGEEDEDEDLSK.Y
Zinc finger protein 265ZRANB2		S305S307						53.8	36.9	R.S*RS*PESQVIGENTK.Q
ZRANB2		S188						46.5	77.4	K.YNLDA*S*EEEDSNK.K
Zinc finger protein 265ZRANB2		S120						49.2	74.7	R.EES*DGEYDEFGRK.K
Zinc finger protein 265ZRANB2		T303S305S307						31.6	29.7	R.T*RS*RS*PESQVIGENTK.Q
Zinc finger protein 265ZRANB2		S266S267						0.4	12.4	R.SHRGS*S*SPR.K
Zinc finger protein 265ZRANB2		S307						37.8	77.4	R.S*PESQVIGENTK.Q
Zinc finger protein 265ZRANB2		T303S307S310						12.3	11.5	R.T*RSR*S*PES*QVIGENTK.Q
Zinc finger protein 265ZRANB2		S305S307S310						10.5	11.9	R.TRS*RS*PES*QVIGENTK.Q
Zinc finger protein 272ZNF460		T492						9.8	19.6	R.RSPLT*R.H
Zinc finger protein 272ZNF460		S489						15.8	20.1	R.RS*PLTR.H
Zinc finger protein 28 (KOX 24)ZNF28		S427						100.0	14.2	R.OKS*HLER.H
Zinc finger protein 289, ID1 regulatedARFGAP2		S319						3.5	17.2	R.SSVSHS*VLESEMQIEQTPVSAK.S
Zinc finger protein 289, ID1 regulatedARFGAP2		S152							15.3	K. R.RPSTPLTADDAWDADTDEGTCADAPSTFESGLADPLKNT
Zinc finger protein 289, ID1 regulatedARFGAP2		S146						36.2	18.2	R.HGTDLWDNMSSAVPNH*S*PEKK.D
Zinc finger protein 295ZBTB21		S345						13.6	84.5	R.SLS*MDSQVPVYSPSIDLK.S
Zinc finger protein 316ZNF316		S112						100.0	14.1	K.S*PVLQEK.G
Zinc finger protein 318ZNF318		S136						74.0	59.2	R.S*PGLCSDSLEK.S
Zinc finger protein 318ZNF318		S173						138.9	58.0	R.LGS*PVDNLEMDRDDLTDSDSVFTR.S
Zinc finger protein 318ZNF318		S79S81						100.0	28.2	R.RVS*PS*PPR.A
Zinc finger protein 318ZNF318		S89S91						100.0	24.7	R.RGS*PS*PPR.G
Zinc finger protein 318ZNF318		S214						3.6	45.5	R.YISQEEGPLS*PFLGQLDEDYR.T
Zinc finger protein 318ZNF318		S69S71						100.0	18.1	R.RAS*PS*PPR.G
Zinc finger protein 318ZNF318		T686S698						24.7	16.7	R.EAHHSN*THSPEVSHPHPPS*PVDOPYLLTK.N
Zinc finger protein 318ZNF318		S684S698						26.3	16.9	R.EAHH*S*NTHSPEVSHPHPPS*PVDOPYLLTK.N
Zinc finger protein 318ZNF318		Y20S214						4.1	32.0	R.Y*ISQEEGPLS*PFLGQLDEDYR.T
Zinc finger protein 330ZNF330		S291						44.7	143.7	R.KDS*DTESSDLFTNLNLGR.T
Zinc finger protein 36ZKSCAN1		S208						100.0	14.7	R.ALPAAHIPAPHEGS*PR.D
Zinc finger protein 36 C3H type like 2ZFP36L2		S57						49.3	34.1	R.RHS*ASNHLALAHAPSPGSCSPK.F
Zinc finger protein 36 C3H type like 2ZFP36L2		S59S75						7.3	17.0	R.RHSAS*NLHALAHAPSPGSCS*PK.F

Peak Area	%CV	White dots: Significant change in peptide abundance at 5%FDR compared to the linepoint with the minimum peak area for a given PSM		CarT	RajiB	Ascor	MOWSE	Sequence	
		Protein Name	Gene	Phosphosites					
<10	0	Zinc finger protein 36 C3H type like 2 ZFP36L2		S59			4.6	15.7	R.RHSAS*NLHALAHAPSPGSCSPK.F
10-20	1	Zinc finger protein 363 RCHY1		S257			100.0	25.5	R.RIS*LDQQ.-
20-30	2	Zinc finger protein 40 HIVEP1		S536			32.1	83.5	K.SSFTPS*SPENVIGDFLLQDR.S
30-40	3	Zinc finger protein 40 HIVEP1		S537			15.2	55.3	K.SSFTPS*SPENVIGDFLLQDR.S
40-50	4	Zinc finger protein 40 HIVEP1		T569S577			6.4	15.1	K.VVVHHVT*VSPLRTDS*PK.A
50-60	5	Zinc finger protein 444 ZNF444		S104			33.0	63.2	R.QPOSGEEAAVLEEELWGPAAS*PDGSSATR.V
60-70	6	Zinc finger protein 483 ZNF483		T404S406			17.5	18.0	R.RST*LS*R.R
70-80	7	Zinc finger protein 483 ZNF483		S403S406			13.9	12.3	R.RS*TLS*R.R
80-90	8	Zinc finger protein 581 ZNF581		S305S36			49.5		R.S*PEGPSS*SSIGSPQASSPPRPNHYLLIDTQGVPTYVLVDEESQR.C
90-100	9	Zinc finger protein 581 ZNF581		S45T58			12.1	53.2	R.SPEPGPSSSIGSPQAS*SPRPNHYLLIDTQGVPTYVLVDEESQR.C
>100	10	Zinc finger protein 581 ZNF581		S45S46			7.1	24.5	R.SPEPGPSSSIGSPQAS*S*SPRPNHYLLIDTQGVPTYVLVDEESQR.C
		Zinc finger protein 581 ZNF581		Y53T58			-2.7	18.9	R.SPEPGPSSSIGSPQASSPPRPNHY*LLIDTQGVPTYVLVDEESQR.C
		Zinc finger protein 581 ZNF581		S46T58			-0.4	40.6	R.SPEPGPSSSIGSPQASS*PPRPNHYLLIDTQGVPTYVLVDEESQR.C
		Zinc finger protein 592 ZNF592		S142S145S146			9.9	26.4	K.SEPLPTFNQFS*PIS*S*PEPEDPIKNGFGIKPK.H
		Zinc finger protein 592 ZNF592		S689			4.3	42.0	K.HGLTSGS*ASPPPALPLYPDPVRL
		Zinc finger protein 592 ZNF592		T137S145S146			10.1	21.7	K.SEPLPT*FNQFSPIS*S*PEPEDPIKNGFGIKPK.H
		Zinc finger protein 592 ZNF592		S691			7.3	49.4	K.HGLTSGSAS*PPPALPLYPDPVRL
		Zinc finger protein 592 ZNF592		S132T137S142			21.5		K.S*EPLPT*FNQFS*PISSPEPEDPIKNGFGIKPK.H
		Zinc finger protein 609 ZNF609		S842Y845S849			22.1	58.7	K.TNS*PAY*SDIS*DAGEDGEGKVDVK.S
		Zinc finger protein 609 ZNF609		S842S846S849			17.8	75.8	K.TNS*PAYS*DIS*DAGEDGEGKVDVK.S
		Zinc finger protein 609 ZNF609		Y845S846S849			8.4	12.7	K.TNSPAY*S*DIS*DAGEDGEGKVDVK.S
		Zinc finger protein 638 ZNF638		S508S510			32.7	12.8	R.S*RS*PMHYMYRPR.S
		Zinc finger protein 638 ZNF638		S552			100.0	16.1	R.IRNPFRGS*PK.C
		Zinc finger protein 646 ZNF646		S930			54.7	123.2	R.S*PPLQSEAELLNQLQR.E
		Zinc finger protein 646 ZNF646		S936			8.2	89.0	R.SPPLQLS*EAELLNQLQR.E
		Zinc finger protein 687 ZNF687		S251			42.3	15.2	K.ATDIPAS*ASPPPVAGVPFFK.Q
		Zinc finger protein 687 ZNF687		S253			13.4	36.3	K.ATDIPASAS*PPPVAGVPFFK.Q
		Zinc finger protein 687 ZNF687		S1057			100.0	25.2	R.HGLQLGAOS*PGR.G
		Zinc finger protein 687 ZNF687		T191S197				11.9	R.EGALT*PPPPFS*SFELAQENGPMQPPVSSPPLGALK.Q
		Zinc finger protein 687 ZNF687		S198S215			17.8	11.1	R.EGALT*PPPPFS*FELAQENGPMQPPVSS*PPLGALK.Q
		Zinc finger protein 740 ZNF740		S44			100.0	50.4	R.AGS*PDVLR.C
		Zinc finger protein 800 ZNF800		S334			82.1	38.8	R.DSITPDIAIKPGQPLFLDS*ISPK.K
		Zinc finger protein 99		S2			13.2		-MIS*FWSEK.C
		Zinc finger protein A20 TNFAIP3		S381			46.9	54.3	R.EGHAQNPMEPSVPQLS*LMDVK.C
		Zinc finger protein A20 TNFAIP3		S376S381			100.0	45.0	R.EGHAQNPMEPS*VPQLS*LMDVK.C
		Zinc finger protein A20 TNFAIP3		T454			7.2	30.2	R.GEAYEPLAWNPEEST*GGPHSAPPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S645			32.1	13.9	K.VS*PTASR.F
		Zinc finger protein A20 TNFAIP3		S459			23.2	39.5	R.GEAYEPLAWNPEESTGGPHS*APPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		T463			7.1	45.2	R.GEAYEPLAWNPEESTGGPHSAPPT*APSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S453			4.2	45.9	R.GEAYEPLAWNPEES*TGPHSAPPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S573S575			37.5	37.8	R.S*PS*PHSCHRA
		Zinc finger protein A20 TNFAIP3		S453S471			10.1	17.0	R.GEAYEPLAWNPEES*TGPHSAPPTAPSPFLS*ETTAMK.C
		Zinc finger protein A20 TNFAIP3		S459S466			12.8	14.6	R.GEAYEPLAWNPEESTGGPHS*APPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		T454S459			1.5	35.3	R.GEAYEPLAWNPEEST*GGPHS*APPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S453S459			6.4	30.0	R.GEAYEPLAWNPEES*TGPHS*APPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S466				19.2	R.GEAYEPLAWNPEESTGGPHSAPPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S453T454			15.3	30.1	R.GEAYEPLAWNPEES*T*GGPHSAPPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S220			23.6	26.1	R.SLES*GSNFAPLK.V
		Zinc finger protein A20 TNFAIP3		T454S466			13.5	21.9	R.GEAYEPLAWNPEEST*GGPHSAPPTAPSPFLFSETTAMK.C
		Zinc finger protein A20 TNFAIP3		S453T463			0.6	37.1	R.GEAYEPLAWNPEES*TGPHSAPPT*APSPFLFSETTAMK.C
		Zinc finger protein AEBP2 AEBP2		S206			49.2	24.9	R.RGS*LEMSSDGEPLSR.M
		Zinc finger protein hR11 alph BCL11B		S375S381			26.8	51.2	R.ELAGNSS*TPPPVS*PGR.G
		Zinc finger protein hR11 alph BCL11B		T376S381			14.7	57.1	R.ELAGNSST*PPPVs*PGR.G
		Zinc finger protein hR11 alph BCL11B		S129			16.0	59.5	R.KVSEPVIEIQVTPDEDDHLLS*PTK.G
		Zinc finger protein hR11 alph BCL11B		S496S497			21.9	43.0	R.SDDGLSAAS*S*PEPGTSELAGEGLK.A
		Zinc finger protein hR11 alph BCL11B		S398			100.0	43.7	R.LLNPFQPS*PK.S
		Zinc finger protein hR11 alph BCL11B		T406T417			54.5	24.8	K.SPFLST*PPLPPMPGGT*PPQPAPK.S
		Zinc finger protein hR11 alph BCL11B		S493S496			6.6	25.6	R.SDDGLS*AA*S*PEPGTSELAGEGLK.A
		Zinc finger protein hR11 alph BCL11B		S493S496S497			1.1	25.5	R.SDDGLS*AA*S*PEPGTSELAGEGLK.A
		Zinc finger protein hR11 alph BCL11B		S401T417			56.4	19.0	K.S*PFLSTPPLPPMPGGT*PPQPAPK.S
		Zinc finger protein hR11 alph BCL11B		S401			30.6	19.4	K.S*PFLSTPPLPPMPGGT*PPQPAPK.S
		Zinc finger protein hR11 alph BCL11B		S488S493S496			25.2	30.6	R.S*DDGLS*AA*S*PEPGTSELAGEGLK.A

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<10	0								
10	2								
20	4								
40	6								
60	8								
70	10								
80	12								
90	14								
>100	>100								
Protein Name		Gene	Phosphosites						
Zinc finger protein hRIT1		alpBCL11B	S401S405T417				42.2	14.6	K.S*PFLS*TPPLPMPPGGT*PPQPPAK.S
Zinc finger protein, subfamily 1A, member 1		KZF1	S409				42.6	45.1	R.S*GLVLTNHIAPHAR.N
Zinc finger protein, subfamily 1A, member 1		KZF1	S17T23				11.7	39.5	K.ES*PPVSDT*PDEGDEPMPIDELSTTSGGQSSK.S
Zinc finger protein, subfamily 1A, member 1		KZF1	S361S364				32.1	69.0	R.S*NHS*AQDSAVENLLLLSK.A
Zinc finger protein, subfamily 1A, member 1		KZF1	S445				34.4	57.0	R.AASENS*QDALR.V
Zinc finger protein, subfamily 1A, member 1		KZF1	S364				8.7	49.9	R.SNHS*AQDSAVENLLLLSK.A
Zinc finger protein, subfamily 1A, member 1		KZF1	S21T23				1.0	48.9	K.ESPPVS*DT*PDEGDEPMPIDELSTTSGGQSSK.S
Zinc finger protein, subfamily 1A, member 1		KZF1	S361				9.2	71.3	R.S*NHSAQDSAVENLLLLSK.A
Zinc finger protein, subfamily 1A, member 1		KZF1	S63				39.7	47.1	K.VETQS*DEENGRA
Zinc finger protein, subfamily 1A, member 1		KZF1	S17S21T23				42.7	45.4	K.ES*PPVS*DT*PDEGDEPMPIDELSTTSGGQSSK.S
		IKZF2	S56				65.7	63.4	K.LEMQS*DEECDRKPLSR.E
Zinc finger protein, subfamily 1A, member 2		KZF2	S369T372S375				59.6	72.2	R.IERPIS*RET*ADS*HENNMDGPISLRPK.S
Zinc finger protein, subfamily 1A, member 2		KZF2	S433				20.3	27.5	R.KQS*PAYMK.E
Zinc finger protein, subfamily 1A, member 2		KZF2	S369				100.0	17.6	R.IERPIS*RE
Zinc finger protein, subfamily 1A, member 2		KZF2	S40				17.0	20.5	R.EHSNMAIDLTSSTPNGQHAS*PSHMTSTNSVK.L
Zinc finger protein, subfamily 1A, member 2		KZF2	S31S40				20.6	35.2	R.EHSNMAIDLTS*STPNGQHAS*PSHMTSTNSVK.L
Zinc finger protein, subfamily 1A, member 2		KZF2	T30S40				7.4	19.6	R.EHSNMAIDLTS*STPNGQHAS*PSHMTSTNSVK.L
Zinc finger protein, subfamily 1A, member 2		KZF2	S78S79				50.0	62.6	R.GHDEGS*S*LEEPIESSEVADNR.K
Zinc finger protein, subfamily 1A, member 2		KZF2	S32S40				7.3	39.0	R.EHSNMAIDLTS*TPNGQHAS*PSHMTSTNSVK.L
Zinc finger protein, subfamily 1A, member 2		KZF2	S23S40				23.7	32.6	R.EHS*NMAIDLTSSTPNGQHAS*PSHMTSTNSVK.L
Zinc finger protein, subfamily 1A, member 2		KZF2	S23T30				28.4		R.EHS*NMAIDLTSSTPNGQHASPSHMTSTNSVK.L
Zinc finger protein, subfamily 1A, member 2		KZF2	S23				27.9		R.EHS*NMAIDLTSSTPNGQHASPSHMTSTNSVK.L
Zinc finger protein, subfamily 1A, member 3		KZF3	S378S382S386				12.2		R.GLS*PNNS*GHDS*TT*DT*DS*NHEER.Q
Zinc finger, AN1-type domain 2B		ZFAND2B	S183				18.6	110.8	R.SPS*WTAPPVIALONGLSEDEALQRA
Zinc finger, AN1-type domain 2B		ZFAND2B	T185				6.0	78.8	R.SPS*WT*APPVIALONGLSEDEALQRA
Zinc finger, CCHC domain containing 6		ZCCHC6	T13				100.0	12.8	K.AT*KDR.G
Zinc finger, CW type with coiled-coil domain		MORC2	S681				50.7	32.6	R.SVAVS*DEEEVEEAER.R
Zinc finger, CW type with coiled-coil domain		MORC2	S553				100.0	17.6	R.S*PLPAVIR.N
Zinc finger, CW type with coiled-coil domain		MORC2	S715S717				29.4	62.4	K.KDSNELS*DS*AGEEDSADLKR.A
Zinc finger, FYVE domain containing 19		ZFYVE19	S344				133.0	99.6	R.LPDS*DDDEEETAIQR.V
Zinc finger, FYVE domain containing 19		ZFYVE19	S134				67.4	30.2	K.WS*PPQNYK.K
Znf HX		ATRX	Y1009S1012S1				2.3	36.6	K.MEQQY*ESS*S*DGTEKLPER.E
Znf HX		ATRX	T1989S1995				5.9	39.7	K.AT*SSSNP*S*SPAPDWYKDFVTDADAEVLEHSGK.M
Znf HX		ATRX	S1990S1991				19.3		K.ATS*S*SNPSSPAPDWYKDFVTDADAEVLEHSGK.M
Znf HX		ATRX	T1346S1352				20.3	58.4	R.HKLT*VSDGES*GEEKK.T
Znf HX		ATRX	S1348S1352				13.8	61.9	R.HKLT*VSDGES*GEEKK.T
Znf HX		ATRX	S1011S1012S10				10.2	41.7	K.MEQQYES*S*S*DGTEKLPER.E
Znf HX		ATRX	S729S731				61.1	71.1	K.QSETVDQNS*DS*DEMLAILK.E
Znf HX		ATRX	T724S731				9.3	18.1	K.QSET*VDQNS*DS*DEMLAILK.E
Znf HX		ATRX	Y1009S1011S10				10.1	17.6	K.MEQQY*ES*S*DGTEKLPER.E
Znf HX		ATRX	Y1009S1011S10				30.6	33.5	K.MEQQY*ES*S*SDGTEKLPER.E
Znf HX		ATRX	T1989Y2002				4.3	14.2	K.AT*SSSNPSSPAPDWY*KDFVTDADAEVLEHSGK.M
Znf HX		ATRX	S1991S1995				10.3	74.7	K.ATSS*SNP*S*SPAPDWYKDFVTDADAEVLEHSGK.M
Znf HX		ATRX	S1996Y2002				-2.0	25.6	K.ATSSSNPSS*PAPDWY*KDFVTDADAEVLEHSGK.M
ZNF635		POGZ	S746				100.0	15.8	R.KMS*VMGR.Q
Zuotin related factor 1		DNAJC2	S49				12.1	55.7	R.NASAS*FQELEDKK.E
Zuotin related factor 1		DNAJC2	S47				39.3	73.0	R.NAS*ASFQELEDK.K
Zuotin related factor 1		DNAJC2	S47S49				100.0	39.3	R.NAS*AS*FQELEDKK.E
Zyxin		ZYX	S308				15.7	44.6	K.LGHPEALSAGTGS*PQPPSFTYAQQR.E
Zyxin		ZYX	S344				54.8	40.8	R.S*PGAPGPLTLK.E