

TABLE #2: A2058 CELLS; TRYPSIN DIGEST; TP MOTIF (CST# BL4180)

Index	Index in Detail	Normalized Fold Change			Gene Name	Protein Name	Site	Description	Accession	kD	Upstream Kinase	Downstream Target
		Cpd 1 : DMSO	Cpd 2 : DMSO	Cpd 1+2 : DMSO								
1	Adaptor/scaffold											
2	1	-1.3	-1.7	-1.3	AB11, AB11	Abi-1, Abi-1 iso3	\$182, \$183	abi-interactor 1 isoform b	Q81ZP0; Q81ZP0-3	55; 49		
3	3	1.3	1.7	1.1	AXIN1	axin 1	75, \$77	axin 1 isoform a	O15169	96		
4	4	-1.1	1.2	1.3	AXIN1	axin 1	75, \$77, 79	axin 1 isoform a	O15169	96		
5	6	-1.2	-1.6	-1.5	AXIN1	axin 1	75, 79	axin 1 isoform a	O15169	96		
7	8	-1.0	1.1	1.1	AXIN1	axin 1	79	axin 1 isoform a	O15169	96		
8	9	1.4	1.6	1.6	BCAR3	BCAR3	130	breast cancer antiestrogen resistance 3	O75815	93		
9	10	1.4	-1.2	1.1	BIN1, BIN1	BIN1; BIN1 iso2	348; 317	bridging integrator 1 isoform 8	O00499; O00499-2	65; 57		
11	12	-1.4	-1.2	1.0	EPB41L1; EPB41L1	EPB41L1; EPB41L1.1 iso2	\$79, \$17	erythrocyte membrane protein band 4.1-like 1 isoform a	Q9H4G0; Q9H4G0-2	99; 88		
12	13	-22.4	2.0	-16.3	FRS2	FRS2	124, 134, \$137	fibroblast growth factor receptor substrate 2	Q8WU20	57		
13	14	-4.0	1.9	-3.0	FRS2	FRS2	134, \$137	fibroblast growth factor receptor substrate 2	Q8WU20	57		
14	15	-1.2	-7.3	-6.0	IRS2	IRS-2	\$15, \$518, \$527	insulin receptor substrate 2	Q9Y4H2	137		
16	17	1.1	-8.0	-12.9	IRS2	IRS-2	\$518, \$523, \$527	insulin receptor substrate 2	Q9Y4H2	137		
18	19	1.1	-2.9	-5.8	IRS2	IRS-2	\$527	insulin receptor substrate 2	Q9Y4H2	137		
20	21	2.3	-1.1	-2.0	IRS2	IRS-2	\$577, \$580	insulin receptor substrate 2	Q9Y4H2	137		
21	22	1.0	-1.5	1.1	IRS2	IRS-2	\$779	insulin receptor substrate 2	Q9Y4H2	137		
25	27	1.1	1.2	1.1	RANBP2; RGPD1; RGPD2; RGPD3; RGPD4; LOC100133510	RanBP2; RGPD1; RGPD2; RGPD3; RGPD4; LOC100133510	\$796, \$799; 795; 798; 52; 55; 797, 800; 797, 800; 796; 799	RAN binding protein 2	P49792; NP_001019628; POC839; A6NK17; Q7ZJ33; XP_001719668	358; 197; 112; 198; 198; 116		
26	28	-2.5	-1.9	-1.2	RANBP2; RGPD1; RGPD2; RGPD3; RGPD4; LOC100133510	RanBP2; RGPD1; RGPD2; RGPD3; RGPD4; LOC100133510	\$799; 798; 55; 800; 800; 799	RAN binding protein 2	P49792; NP_001019628; POC839; A6NK17; Q7ZJ33; XP_001719668	358; 197; 112; 198; 198; 116		
27	Adhesion or extracellular matrix protein											
28	29	1.2	-1.1	-1.3	OCLN	occludin	376	occludin	O16625	59		
29	30	-1.2	-1.4	-1.1	ROBO1	ROBO1	\$1240	roundabout 1 isoform a	Q9Y6N7	181		
30	Apoptosis											
31	33	1.1	-1.8	-2.6	ACIN1	acinus	\$240, \$243, \$254	apoptotic chromatin condensation inducer 1	Q9UKV3	152		
32	34	1.4	1.1	-1.4	ACIN1	acinus	\$240, \$254	apoptotic chromatin condensation inducer 1	Q9UKV3	152		
34	37	1.8	1.9	1.8	ACIN1	acinus	\$254	apoptotic chromatin condensation inducer 1	Q9UKV3	152		
35	38	-1.1	-1.5	1.0	DPF2	requiem	\$176	D4, zinc and double PHD fingers family 2	Q9Z785	44		
36	Cell cycle regulation											
37	40	1.2	1.4	1.7	BAT2D1; BAT2D1	BAT2D1; BAT2D1 iso8	\$2673, \$2673	HBxAg transactivated protein 2	Q9Y520; NP_055987	317; 309		
38	43	-1.4	1.7	-2.4	CEP170	KAB1	174	centrosomal protein 170kDa isoform beta	O5SW79	175		
39	44	1.3	2.5	1.3	CEP170	KAB1	914, 920	centrosomal protein 170kDa isoform beta	O5SW79	175		
40	45	2.4	4.8	1.6	CEP170	KAB1	920	centrosomal protein 170kDa isoform beta	O5SW79	175		
41	47	4.1	4.3	2.0	CLASP1; CLASP1	CLASP1; CLASP1 iso3	\$1091, \$1099, \$1086, \$1094	CLIP-associating protein 1	Q7Z460; Q7Z460-3	169; 165		
42	48	-1.5	-1.1	1.1	CUL4B	CUL4B	\$31	cullin 4B isoform 2	O13620	102		
43	50	-1.2	1.2	1.4	MDC1	MDC1	\$1696	mediator of DNA damage checkpoint 1	O14676	227		
44	53	2.7	2.4	2.4	MDC1	MDC1	\$1696, \$1702, \$1711	mediator of DNA damage checkpoint 1	O14676	227		
45	58	1.2	1.0	1.1	MDC1	MDC1	\$1696, \$1711	mediator of DNA damage checkpoint 1	O14676	227		
47	63	-1.1	-2.2	-2.0	MDC1	MDC1	\$1697	mediator of DNA damage checkpoint 1	O14676	227		
48	64	2.5	1.7	1.9	MDC1	MDC1	\$1697, \$1702, \$1711	mediator of DNA damage checkpoint 1	O14676	227		
50	68	1.9	1.0	1.1	MDC1	MDC1	\$1697, 1716	mediator of DNA damage checkpoint 1	O14676	227		
51	69	-1.0	-1.1	1.1	MDC1	MDC1	\$1702, 1706	mediator of DNA damage checkpoint 1	O14676	227		
52	70	-1.8	1.2	-1.5	MDC1	MDC1	\$763, \$780	mediator of DNA damage checkpoint 1	O14676	227		
53	71	1.9	1.9	1.2	Mki67	Ki-67	\$328	antigen identified by monoclonal antibody Ki-67	P46013	359		
54	72	2.6	2.4	1.9	NUMA-1	NUMA-1	\$200, \$203, \$211	nuclear mitotic apparatus protein 1	O14980	238		
55	73	4.6	3.3	2.3	NUSAP1	NUSAP1	\$182	nucleolar and spindle associated protein 1 isoform 3	O9BX56	49		
56	77	-1.1	-1.5	-1.8	PRC1; PRC1	PRC1; PRC1 iso2	\$470; \$440	protein regulator of cytokinesis 1 isoform 1	O43663; O43663-2	72; 67		PRC1; PRC1
58	79	1.1	1.4	1.5	RBBP6; RBBP6	RbBP6; RbBP6 iso2	\$516; \$516	retinoblastoma-binding protein 6 isoform 1	Q7Z6E9; Q7Z6E9-2	202; 197		
59	80	3.7	2.3	1.7	SEPT9	SEPT9	\$30, \$38, \$42	septin 9 isoform a	Q9UHD8	65		
60	81	1.3	1.4	1.6	SEPT9	SEPT9	\$30, \$42	septin 9 isoform a	Q9UHD8	65		
63	85	1.1	1.3	1.2	SEPT9	SEPT9	\$42	septin 9 isoform a	Q9UHD8	65		
64	86	-2.9	-1.1	-4.3	TNKS1BP1	TNKS1BP1	131	tankyrase 1-binding protein 1	Q9C0C2	182		
65	Cell development/differentiation											
66	87	1.6	1.4	2.1	ANKRD17	ANKRD17	732	ankyrin repeat domain protein 17 isoform a	O75179	274		
68	Chromatin, DNA-binding, DNA repair or DNA replication protein											
69	90	1.8	1.6	1.9	C14orf106	C14orf106	\$653	chromosome 14 open reading frame 106	O6P0N0	129		
70	91	-1.2	-1.1	1.1	CHAF1B	CAF-1B	\$429, \$433	chromatin assembly factor 1 subunit B	O13112	61		
71	92	1.6	1.6	1.1	CIC	capicua homolog	\$583	capicua homolog	Q96RK0	164		
72	94	1.7	1.5	-1.7	H2AFY	H2AFY	\$129	H2A histone family, member Y isoform 2	O75367	40		
73	95	-2.6	-2.1	-1.3	HP1BP3; HP1BP3	HP1BP3; HP1BP3 iso7	51; 51	HP1-BP74	Q9UHY0; Q5SSJ5	61; 61		
75	98	1.6	1.0	1.4	MYB8P1A	Myb8P1A	\$1241, \$1244	MYB binding protein 1a isoform 1	Q9BQGO	149		
78	102	1.1	-1.1	-1.2	ORC2L	ORC2L	228	origin recognition complex, subunit 2	O13416	66		
79	105	1.1	-1.3	-1.4	ORC6L	ORC6L	\$195	origin recognition complex subunit 6	Q9Y5N6	28		Cdc2
80	108	-1.0	-1.8	-2.1	PDSSB	APRIN	\$1394, \$1406	PDSS, regulator of cohesion maintenance, homolog B	Q9NTI5	168		Cdc2
81	109	-1.1	-1.2	-1.7	PDSSB	APRIN	\$1398, \$1406	PDSS, regulator of cohesion maintenance, homolog B	Q9NTI5	168		Cdc2
82	110	3.6	2.6	1.2	PRR12	PRR12	224	proline rich 12	Q9ULL5	211		
83	113	1.4	1.1	1.1	RIF1	Rif1	1210	RAP1 interacting factor 1	Q5UIP0	274		
84	Cytoskeletal protein											
85	114	3.0	2.4	1.9	ADD1; ADD2; ADD3	ADD1; ADD2; ADD3	724; 711; 691	adducin 1 (alpha) isoform a	P35611; P35612; Q9UEY8	81; 81; 79		
86	115	2.4	2.3	1.1	BICD2	Bicd2	\$821	bicaudal D homolog 2 isoform 1	Q8TD16	94		
87	116	-1.7	-1.4	-1.7	CAP1; CAP1	CAP1; CAP1 iso3	\$308; \$308	adenylyl cyclase-associated protein	Q01518; NP_001099000	52; 52		
92	122	1.2	1.3	-2.2	DYNC1L1	DNCL1	\$207	dynein, cytoplasmic 1, light intermediate chain 1	Q9Y6G9	57		Cdc2
93	124	2.0	2.5	2.8	DYNC1L1	DNCL1	\$405, \$408	dynein, cytoplasmic 1, light intermediate chain 1	Q9Y6G9	57		
94	125	-2.8	-1.6	-1.7	GAS2L1; HCN4; RGPD5; RGPD5; RGPD7; RGPD8; SRRM2	GAS2L1; HCN4; RanBP2L2; RGPD5; RGPD7; RGPD8; Srrm300	334; 996; 799; 799; 993	growth arrest-specific 2 like 1 isoform a	Q99501; Q9Y304; Q53T03; Q99666; Q9H0B2; O14715; Q9UQ35	73; 129; 199; 199; 103; 199; 300		
95	126	-1.1	1.2	-2.1	KATNB1	KATNB1	393	katanin p80 subunit B1	O9BVA0	72		
97	128	-2.5	-1.5	1.3	KIF1B	KIF1B iso3	1132	kinesin family member 1B isoform b	O60333-3	130		
98	130	1.6	1.3	1.3	KIF1C	KIF1C	\$1083	kinesin family member 1C	O43896	123		
100	134	-1.1	1.9	-1.5	MAP1A	MAP1A	1835	microtubule-associated protein 1A	P78559	306		
101	135	1.5	1.5	1.6	MAP1B	MAP1B	\$1067	microtubule-associated protein 1B	P46821	271		
103	138	-1.1	-1.2	-1.7	MARCKS	MARCKS	\$147, \$150	myristoylated alanine-rich protein kinase C substrate	P29966	32		
104	141	-1.5	-1.2	-1.0	MARCKS	MARCKS	\$150	myristoylated alanine-rich protein kinase C substrate	P29966	32		
106	147	1.4	1.1	1.2	PHACTR2	PHACTR2	25	phosphatase and actin regulator 2 isoform 1	O75167	70		
108	150	-1.6	3.0	1.5	PLEC1; PLEC1; PLEC1; PLEC1; PLEC1	plectin 1; plectin 1 iso2; plectin 1 iso6; plectin 1 iso10; plectin 1 iso11	\$4396; \$4286; \$4245; \$4263; \$4259	plectin 1 isoform 1	O15149; O15149-2; Q6S382; NP_958785; O15149-4	532; 518; 515; 516; 516		
109	152	-1.0	-1.1	-1.1	PHPLN1; PHPLN1	PHPLN1; PHPLN1 iso2	\$133; \$140	periphilin 1 isoform 1	Q8NEY8; Q8NEY8-2	53; 43		
110	154	5.0	3.7	2.0	SMTN	smothelin iso4	\$357, \$360	smothelin isoform c	P53814-4	99		

Peptide	Charge	Calc. m/z	Count in Details	Average RT	Intensity								Average Raw Intensity				Normalized Fold Change		
					DMSO (CS6142)	DMSO (CS6143)	Cpd 1 (CS6144)	Cpd 1 (CS6145)	Cpd 2 (CS6146)	Cpd 2 (CS6147)	Cpd 1 + 2 (CS6148)	Cpd 1 + 2 (CS6149)	DMSO	Cpd 1	Cpd 2	Cpd 1 + 2	Cpd 1 : DMSO	Cpd 2 : DMSO	Cpd 1+2 : DMSO
TNPPTQKPPS*PPMSGR	2	886.4138	2	58.18	472,118	354,308	416,587	471,934	186,276	300,664	247,830	421,352	413,213	444,261	243,470	334,591	-1.3	-1.7	-1.3
RSDDLGLGYEPGGS*AS*PTPPYLK	2	1276.5536	1	72.74	317,544	280,150	418,812	675,175	473,243	545,560	550,056	125,903	298,847	546,994	509,402	337,980	1.3	1.7	1.1
RSDDLGLGYEPGGS*AS*PT*PPYLK	3	878.0271	1	74.41	1,711,620	2,374,352	2,414,019	3,088,654	2,412,498	2,387,555	3,122,243	2,623,114	2,042,986	2,751,337	2,400,027	2,872,679	-1.1	1.2	1.3
RSDDLGLGYEPGGS*ASPT*PPYLK	3	851.3717	2	72.80	1,686,335	1,810,452	2,294,347	2,093,556	991,875	1,227,490	1,030,000	1,420,000	1,748,394	2,193,952	1,109,683	1,225,000	-1.1	-1.6	-1.5
RSDDLGLGYEPGGSASPT*PPYLK	3	824.7162	1	71.04	730,223	628,466	895,771	1,022,697	682,913	771,230	834,496	753,591	679,345	959,234	727,072	794,044	-1.0	1.1	1.1
HIMDRT*PEK	2	603.7707	1	48.03	103,542	134,216	215,000	248,000	212,000	166,126	199,997	200,916	118,879	231,500	189,063	200,457	1.4	1.6	1.6
KGGPPVPPPKHKT*PSK	3	548.6275	1	51.37	165,000	170,000	337,000	338,000	87,100	182,000	165,707	217,071	167,500	337,500	134,550	191,389	1.4	1.2	1.1
YDEADGLSERTI*PSK	2	918.3886	1	59.25	423,478	270,880	312,787	382,991	215,339	341,759	283,000	445,000	347,179	347,889	278,549	364,000	-1.4	-1.2	1.0
NHSHQ*ELFVLRIPTR*PTT*PGFAAQLNPNGVYR	4	954.1792	1	68.84	274,914	347,768	20,000	20,000	625,605	609,555	20,000	20,000	311,341	20,000	617,580	20,000	-22.4	2.0	-16.3
TPRT*PTT*PGFAAQLNPNGVYR	3	806.0334	1	67.58	223,617	229,351		82,600	434,587	405,632	82,500	74,600	226,484	82,600	419,810	78,550	-1.4	-1.9	-3.0
AFCS*HRS*NPITESAIET*PPAR	3	832.3220	1	61.37	771,044	642,201	814,904	861,912	99,621	92,009	97,300	148,000	706,623	638,408	95,815	122,650	-1.2	7.3	-6.0
SN*NPITES*IAET*PPAR	2	855.1439	1	59.74	707,943	578,810	995,143	1,055,010	98,184	61,224	58,707	45,600	643,377	1,025,077	79,704	52,154	-1.1	-8.0	-12.9
SNTPITESAIET*PPAR	2	775.3486	1	60.24	424,969	393,120	622,983	623,219	166,660	117,592	54,929	92,000	409,050	623,101	142,126	73,465	-1.1	-2.9	-5.8
TY5*LT*TPAR	2	585.2359	1	59.63	1,021,005	975,131	3,689,528	3,000,483	796,678	941,862	54,812	573,049	998,513	3,345,006	869,270	525,631	2.3	-1.1	-2.0
LLPNPGDLYLNPSPSDAVTGT*PPDFFSAALH PGGEPLR	3	1301.6264	1	79.76	136,168	112,459	205,653	159,116	85,870	79,022	164,637	112,809	124,314	182,385	82,446	138,723	1.0	-1.5	1.1
SYKYS*PKT*PPR	3	495.2179	2	56.69	6,332,002	6,206,826	9,457,905	10,425,899	7,689,369	6,987,934	7,201,896	7,636,234	6,269,414	9,941,902	7,338,652	7,419,065	1.1	1.2	1.1
YSKPT*PPR	2	513.2447	1	52.25	2,587,081	2,984,089	1,500,000	1,670,000	1,680,000	1,171,829	2,618,128	2,346,878	2,785,585	1,585,000	1,425,915	2,482,503	-2.5	-1.9	-1.2
YSSGGNFET*PSK	2	677.2718	1	56.41	234,754	208,970	447,618	312,279	187,919	215,271	188,637	165,972	221,862	379,949	201,595	177,305	1.2	-1.1	-1.3
MYLODELEEEEDERGPT*PPVR	3	914.0655	3	67.78	5,610,642	5,992,779	7,082,352	6,605,475	4,316,267	4,021,864	5,537,030	5,082,477	5,801,711	6,843,914	4,169,066	5,309,754	-1.2	-1.4	-1.1
AAKLS*EGS*QPAEEEDQET*PSR	3	876.6648	1	58.05	680,146	516,622	866,240	1,008,685	264,088	383,320	153,380	325,801	598,384	937,463	323,704	239,591	1.1	-1.8	-2.6
AAKLS*EGSQAPEEEDQET*PSR	3	850.0093	1	57.75	332,722	394,342	720,563	591,819	304,486	435,824	282,363	227,393	336,032	656,191	370,155	254,878	1.4	1.1	-1.4
SESGSQPAEEEDQET*PSR	3	733.2975	2	56.73	961,872	739,338	1,930,301	2,511,661	1,592,536	1,782,645	1,461,302	1,797,123	878,026	2,220,981	1,687,591	1,629,213	1.8	1.9	1.8
ILEPDOLDLDDDEYEDT*PKR	3	959.7343	1	77.93	632,461	616,361	654,235	977,657	429,390	425,977	653,102	652,669	624,411	815,946	427,684	652,886	-1.1	-1.5	1.0
AFGSGIDIKPPT*PIAAGR	3	611.9805	4	78.30	66,870,552	53,583,464	89,391,696	126,175,744	76,275,272	85,718,404	94,391,304	122,540,184	60,227,008	107,783,720	80,996,656	108,420,744	1.2	1.4	1.7
PT*PLYGQPSWWGDDDEVEKIR	3	805.6815	1	62.06	696,715	569,907	690,024	556,159	1,056,208	1,081,817	231,642	314,000	633,311	643,982	1,069,013	272,821	-1.4	1.7	-2.4
LRQDNKT*DEGDPD*PSYNR	3	756.3506	1	55.77	29,599	39,008	61,227	65,925	81,648	91,745	46,440	46,100	34,304	63,576	86,697	46,270	1.3	2.5	1.3
LRQDNKTDEGDPD*PSYNR	3	729.6502	1	55.09	105,000	111,302	368,063	397,149	490,405	535,886	171,280	178,709	108,151	380,606	513,146	174,995	2.4	4.8	1.5
NSNSTSVGS*PSNTIGRT*PSR	3	726.9777	2	57.27	133,578	96,885	604,707	735,388	448,643	535,825	169,546	310,106	115,232	672,048	492,234	239,826	4.1	4.3	2.0
SATDGNSTIS*PPTSACK	2	808.3463	1	51.78	174,320	199,192	168,778	187,023	172,149	157,303	238,019	203,016	186,756	177,901	164,726	220,518	-1.5	-1.1	1.1
AMVPPT*TFEFSQPVTTDQIPISPEPITQPSCK	4	894.1782	4	75.17	193,007	329,992	202,132	453,704	360,424	276,571	480,000	329,000	261,500	327,918	318,498	368,500	-1.1	1.2	1.3
AMVPPT*TFEFSQ*PVTTDQIPIS*PEPITQPSCK	3	1245.2125	3	72.96	125,345	100,781	424,982	461,384	276,423	256,616	290,465	270,000	113,063	443,183	266,520	280,233	2.7	2.4	2.4
AMVPPT*TFEFSQPVTTDQIPIS*PEPITQPSCK	4	953.1950	3	71.58	214,073	205,165	351,704	395,160	303,733	121,432	218,284	247,526	209,629	373,432	215,583	232,905	1.2	1.0	1.1
AMVPPT*TFEFSQPVTTDQIPISPEPITQPSCKIR	4	933.2035	4	72.42	704,971	597,825	595,183	1,145,310	248,967	334,872	500,156	189,606	651,398	857,247	291,920	344,881	-1.1	-2.2	-2.0
AMVPPT*TFEFSQ*PVTTDQIPIS*PEPITQPSCK	4	973.1866	1	71.45	93,854	106,413	298,598	429,150	195,171	144,817	233,225	154,699	100,134	362,639	169,994	193,962	2.5	1.7	1.9
AMVPVPTT*PEFSQPVTTDQIPISPEPIT*QPSCK	3	1223.8887	2	72.54	141,305	212,881	489,978	463,069	182,238	175,000	249,000	169,000	177,093	476,524	178,619	209,000	1.9	1.0	1.1
AMVPVPTT*PEFSQ*PVT*TDQIPISPEPITQPSCK	4	914.1698	1	74.46	127,443	194,622	189,865	265,622	102,563	186,764	185,000	189,000	161,033	227,744	144,664	167,000	-1.0	-1.1	1.1
ESEDS*ETQPF0DTHL6AYG6CL5*PPR	3	1008.0669	1	73.39	266,518	344,862	219,943	281,684	477,962	252,675	270,000	163,000	305,690	250,364	365,319	216,500	-1.8	1.2	-1.5
DVESVQT*PSK	2	582.5852	1	53.34	32,344	43,112	89,463	115,483	67,526	75,430	55,275	36,000	37,728	102,473	71,478	45,638	1.9	1.9	1.2
VASSSSGNNFLGS*PAS*PMGDIGT*POFQMR	3	1151.1431	1	77.63	41,700	122,000	196,000	118,000	118,000	84,200	100,866	68,744	41,700	159,000	101,100	84,805	2.6	2.4	1.9
TAIT*PNKF	2	536.5767	2	62.14	1,883,359	1,198,690	11,145,829	9,268,120	5,652,039	4,533,224	3,315,565	4,090,000	1,541,025	10,206,975	5,092,632	3,702,783	4.6	3.3	2.3
QET9EMLYGASAPRT*PSK	3	659.2996	3	62.21	3,100,100	2,382,257	3,849,435	3,096,712	2,086,574	1,533,646	1,479,101	1,664,702	2,696,179	3,473,074	1,810,110	1,571,902	-1.1	-1.5	-1.8
LGVLVS*PQOIR	2	725.8766	1	71.35	836,000	605,000	1,097,235	1,172,464	1,171,101	820,289	893,000	1,290,000	720,500	1,134,850	995,695	1,091,500	1.1	1.4	1.4
SN*FEVEEET*PNST*PPR	2	1029.3810	1	66.77	113,133	105,923	559,998	596,052	234,698	264,283	183,065	202,228	109,528	578,025	249,491	192,647	3.7	2.3	1.7
SN*FEVEEET*PNST*PPR	2	989.3978	1	67.43	1,198,608	776,198	1,791,323	1,889,609	1,295,943	1,440,057	1,305,549	1,978,270	987,403	1,840,466	1,368,000	1,641,910	1.4	1.3	1.6
SN*FEVEEET*PNST*PPR	3	633.2790	1	65.03	8,313,348	5,447,295	8,474,806	12,981,820	9,622,152	8,092,688	8,640,408	8,969,677	6,880,322	10,728,313	8,857,420	8,805,043	1.1	1.3	1.2
PAVEASTGGEATQETGKEEAGKEPPPLT*PPAR	4	853.6546	1	62.95	445,368	503,284	246,129	233,002	483,742	389,861	121,000	111,000	474,326	239,556	439,802	116,000	-2.9	-1.1	-4.3
GGHTSVWCYLLDYPNNILSAPPDVLT*QLT PPSHDLNR	4	1035.2494	1	80.96	1,138,826	1,799,572	3,004,531	3,570,979	1,919,087	2,105,843	3,279,416	3,127,127	1,469,199	3,287,755	2,012,465	3,203,272	1.6	1.4	2.1
AYILVT*PLK	2	549.3042	1	70.37	649,322	538,745	1,129,716	1,944,843	787,399	1,119,079	936,000	1,480,000	594,034	1,537,280	953,239	1,208,000	1.8	1.6	1.9
TQDSS*PGT*PPQAR	2	850.3401	1	54.23	386,016	303,686	397,123	471,177	317,215	298,434	392,403	380,990	344,851	434,150	307,825	386,697	-1.1	-1.1	1.1
ADESGGSGTAGRLPPPPGAGGAP*PSK	3	884.0926	2	59.80	336,579	331,320	830,935	748,793	638,328	414,723	379,582	390,937	333,950	789,864	525,526	385,260	1.6	1.6	1.6
KL6LAIN*PPAK	2	707.8892	1	65.03	621,070	273,624	861,618	557,500	594,096	264,587	185,356	172,681	297,797	709,559	429,342	179,019	1.7	1.5	-1.7
TWNSTRET*PPK	2	655.3113	2	49.43	697,619	822,865	391,288	458,118	376,317	328,660	608,142	604,034	760,242	424,703	352,489	606,088	-2.6	-2.1	-1.3
SPAPAGTR*PS*PAK	2	841.3712	2	52.91	59,857	41,310	120,064	117,236</											