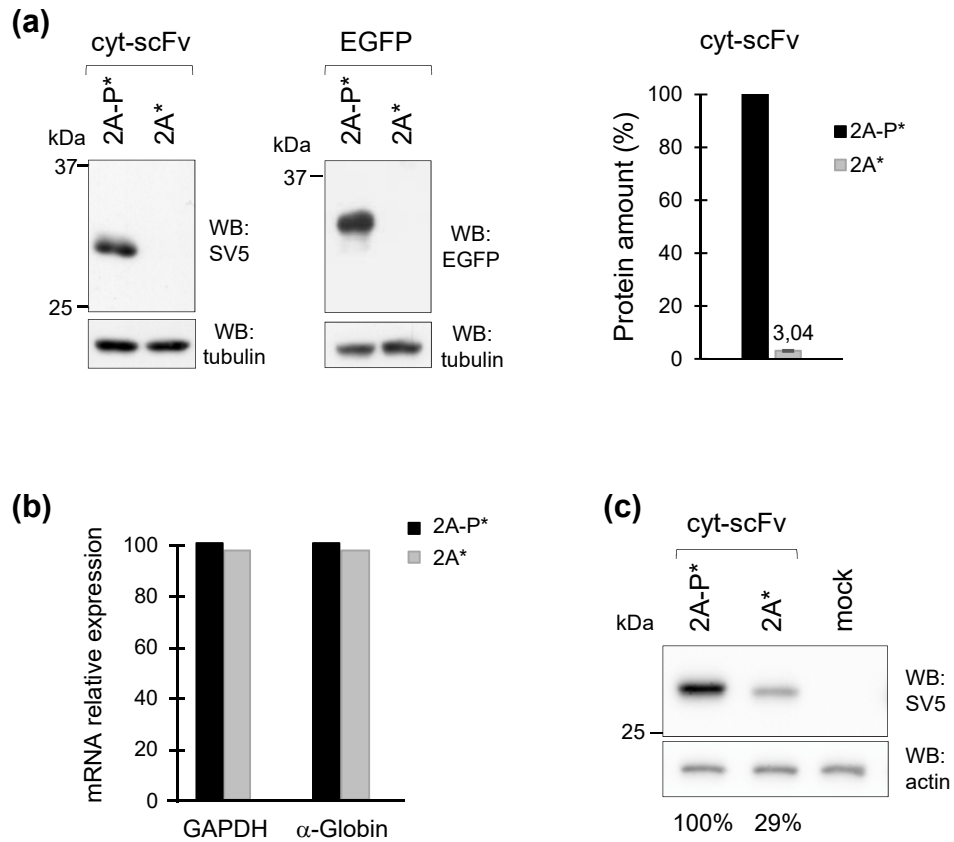
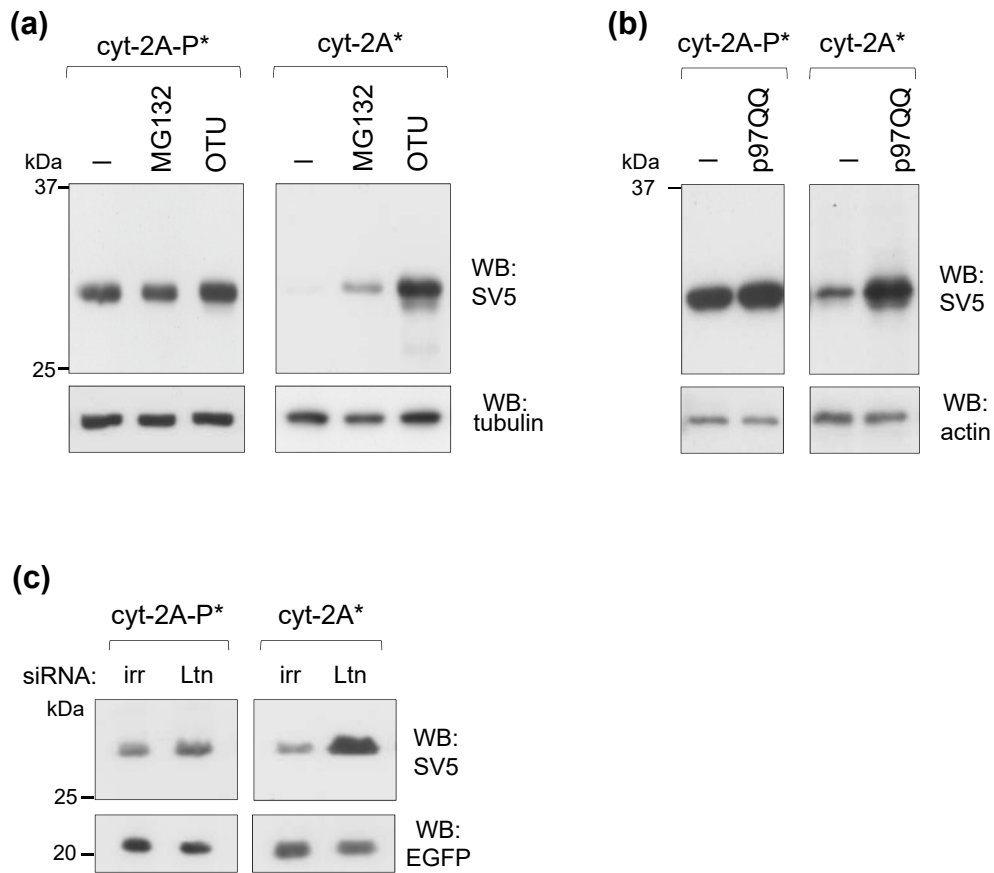


Supplementary Figure 1



C-terminal 2A* compromises the expression of cytosolic proteins. **(a)**, Western blot (left panel) and quantification (right panel, shown for cyt-scFv) of cell extracts transfected with reporters encoding the cytosolic proteins cyt-scFv or EGFP terminating in 2A-P* or 2A*, as indicated. Data presented as mean \pm S.E.M. of $n = 3$ independent experiments. **(b)**, RT-PCR quantification of mRNA levels in cells transfected with constructs 2A-P* (black) or 2A* (grey) and normalized to the endogenous GAPDH mRNA or to a co-transfected α -Globin encoding control plasmid. Representative of $n = 3$ independent experiments **(c)**, Western blot representative of $n = 3$ of the cytosolic reporter produced in a reticulocyte *in vitro* translation system.

Supplementary Figure 2



Proteasomal degradation of cytosolic 2A* proteins. (a-b), Western blots of the cytosolic constructs co-transfected, where indicated, with OTU, p97QQ or treated with MG132 for 4 h. Representative of $n = 3$ independent experiments. (c), Western blot of cells transfected with the indicated constructs in cells transfected 48 h before with the Ltn-specific or the irrelevant siRNA, as indicated. Representative of $n = 2$ independent experiments.

Supplementary Table 1

Mass Spectrometry analysis of 2A-P* termination

spectrum	log(e)	log(l)	m+h	delta	z	zeta	pre	start	sequence	end	post	modifications
656,1	-2,7	5,52	1381,689	-0,088	2	0,5	vatg	17	VHSDIVMTQSHK	28	fmst	
681,1	-2,4	7,22	1058,53	0,014	1	0,333	gvhs	20	DIVMTQSHK	28	fmst	
1214,1	-4,2	8,05	999,456	-0,114	2		qshk	29	FMSTSVGDR	37	vsit	
1291,1	-3,9	7,24	999,456	-0,14	2		qshk	29	FMSTSVGDR	37	vsit	
735,1	-3,6	7,01	1015,451	-0,022	2		qshk	29	FMSTSVGDR	37	vsit	M30#15.99492
1231,1	-2,7	8,37	999,456	-0,112	2		qshk	29	FMSTSVGDR	37	vsit	
1403,1	-2,6	6,48	999,456	-0,083	2		qshk	29	FMSTSVGDR	37	vsit	
1198,1	-2,4	7,4	999,456	-0,167	2		qshk	29	FMSTSVGDR	37	vsit	
772,1	-2,3	7,35	1015,451	-0,077	2		qshk	29	FMSTSVGDR	37	vsit	M30#15.99492
756,1	-2	7,37	1015,451	-0,102	2		qshk	29	FMSTSVGDR	37	vsit	M30#15.99492
1278,1	-1,9	7,65	999,456	-0,085	2		qshk	29	FMSTSVGDR	37	vsit	
1431,1	-1,3	6,1	999,456	-0,012	2		qshk	29	FMSTSVGDR	37	vsit	
785,1	-1,2	6,85	1015,451	-0,064	2		qshk	29	FMSTSVGDR	37	vsit	M30#15.99492
3144,1	-7,9	7,45	1681,818	-0,058	2		itck	44	ASQDVSTAVAWYQQK	58	pgqs	
3118,1	-7,5	7,67	1681,818	-0,023	2		itck	44	ASQDVSTAVAWYQQK	58	pgqs	
3096,1	-6,9	6,67	1681,818	-0,073	2		itck	44	ASQDVSTAVAWYQQK	58	pgqs	
3167,1	-6	6,6	1681,818	0,0061	2		itck	44	ASQDVSTAVAWYQQK	58	pgqs	
3143,1	-5,9	7,48	1681,818	-0,074	3	1,5	itck	44	ASQDVSTAVAWYQQK	58	pgqs	
3098,1	-4,6	6,82	1681,818	0,93	3	1,5	itck	44	ASQDVSTAVAWYQQK	58	pgqs	
3119,1	-3,7	7,54	1681,818	-0,023	3	1,5	itck	44	ASQDVSTAVAWYQQK	58	pgqs	
3168,1	-2,7	6,59	1681,818	0,967	3	1,5	itck	44	ASQDVSTAVAWYQQK	58	pgqs	
2683,1	-9,4	7,22	2277,115	2,196	2	0,667	itck	44	ASQDVSTAVAWYQQKPGQSPK	64	lly	Q46#0.98402
2718,1	-6	6,88	2277,115	-0,024	2	0,667	itck	44	ASQDVSTAVAWYQQKPGQSPK	64	lly	Q46#0.98402
2672,1	-5,6	6,77	2276,131	1,567	2	0,667	itck	44	ASQDVSTAVAWYQQKPGQSPK	64	lly	
2697,1	-3,6	7,37	2276,131	-0,036	2	0,667	itck	44	ASQDVSTAVAWYQQKPGQSPK	64	lly	
2840,1	-2	7,59	1085,599	-0,08	2		qspk	65	LLIYSASYR	73	ytgv	
2777,1	-1,7	8,14	1085,599	-0,027	2		qspk	65	LLIYSASYR	73	ytgv	
2794,1	-1,7	8,42	1085,599	-0,037	2		qspk	65	LLIYSASYR	73	ytgv	
2863,1	-1,4	6,84	1085,599	-0,008	2		qspk	65	LLIYSASYR	73	ytgv	
1041,1	-1,5	6,66	791,441	0,057	1	0,5	asyr	74	YTGVPVR	80	ftgs	
198,1	-6,8	5,14	1466,672	-0,074	2	0,667	leik	127	GSTSGSGKPGSGEGSSK	143	gevq	

Supplementary Table 1

309,1	-5,4	5,72	1466,672	-0,05	2	0,667	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
215,1	-5,2	5,69	1466,672	-0,12	2	0,667	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
244,1	-2,6	5,14	1466,672	0,863	3	1	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
321,1	-2,4	6,29	1466,672	-0,161	3	1	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
232,1	-1,8	5,72	1466,672	-0,167	3	1	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
336,1	-1,4	5,43	1466,672	-0,133	2	0,667	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
275,1	-1,1	5,24	1466,672	-0,09	3	1	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
204,1	-1,1	6,62	1466,672	-0,052	3	1	leik	127	GSTSGSGKPGSGEGSSK	143	gevq
1869,1	-6,9	6,9	2961,451	1,81	3	0,75	leik	127	GSTSGSGKPGSGEGSSKGEVQLQQSGAELVR	157	sgas
1883,1	-6,3	7,13	2961,451	-0,218	3	0,75	leik	127	GSTSGSGKPGSGEGSSKGEVQLQQSGAELVR	157	sgas
1909,1	-5,3	6,5	2961,451	2,385	3	0,75	leik	127	GSTSGSGKPGSGEGSSKGEVQLQQSGAELVR	157	sgas
1895,1	-2,5	8,16	2961,451	1,76	4	1	leik	127	GSTSGSGKPGSGEGSSKGEVQLQQSGAELVR	157	sgas
1860,1	-1,3	6,64	2961,451	-0,146	4	1	leik	127	GSTSGSGKPGSGEGSSKGEVQLQQSGAELVR	157	sgas
2292,1	-5,2	6,85	2300,148	-0,183	3	1	gsgk	135	PGSGEGSSKGEVQLQQSGAELVR	157	sgas
2307,1	-3,5	6,7	2300,148	-0,117	3	1	gsgk	135	PGSGEGSSKGEVQLQQSGAELVR	157	sgas
2637,1	-12,8	8,89	1513,797	0,023	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas
2657,1	-11,7	8,79	1513,797	-0,033	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas
2621,1	-10,9	6,92	1513,797	-0,032	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas
2829,1	-9,6	6,89	1514,781	-0,148	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q147#0.98402
2867,1	-8,4	7	1514,781	-0,043	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q150#0.98402
3033,1	-8,2	6,94	1514,781	-0,062	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q149#0.98402
2676,1	-8,2	8,55	1513,797	-0,041	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas
2558,1	-8,1	6,26	1513,797	-0,006	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas
2855,1	-7,4	6,56	1514,781	-0,127	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q149#0.98402
2664,1	-7,3	8,43	1513,797	-0,108	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas
3021,1	-6,9	6,94	1514,781	-0,055	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q149#0.98402
2890,1	-6,7	7,03	1514,781	-0,015	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q150#0.98402
2646,1	-6,6	8,52	1513,797	-0,006	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas
3003,1	-6,4	6,87	1514,781	-0,048	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q149#0.98402
2807,1	-6,2	6,69	1514,781	0,019	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q147#0.98402
2908,1	-6,1	6,36	1514,781	-0,098	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas Q150#0.98402
2628,1	-6	7,64	1513,797	-0,023	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas
2685,1	-5,8	8,14	1513,797	-0,057	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas
2886,1	-5,8	6,71	1514,781	-0,102	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas Q150#0.98402
2564,1	-5,2	6,27	1513,797	-0,092	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas
3031,1	-4,7	6,62	1513,797	-0,563	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas
3007,1	-4,7	6,54	1514,781	0,005	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas Q149#0.98402

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2998,1	-4,3	6,87	1514,781	1,919	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas	Q147#0.98402
2708,1	-4	7,13	1513,797	-0,137	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas	
3050,1	-3	6,37	1514,781	-0,109	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas	Q149#0.98402
2873,1	-2,6	6,74	1514,781	-0,041	3	1,5	gssk	144	GEVQLQQSGAELVR	157	sgas	Q150#0.98402
2764,1	-1,8	6,55	1513,797	0,836	2	1	gssk	144	GEVQLQQSGAELVR	157	sgas	
2603,1	-3	7,39	1141,514	-0,048	2	0,667	fnik	175	DYYMHVVK	182	qrpe	
2643,1	-2,5	7,47	1141,514	0,011	2	0,667	fnik	175	DYYMHVVK	182	qrpe	
2624,1	-1,6	7,96	1141,514	-0,074	2	0,667	fnik	175	DYYMHVVK	182	qrpe	
1936,1	-1,4	6,46	1157,508	-0,23	2	0,667	fnik	175	DYYMHVVK	182	qrpe	M178#15.99492
5096,1	-12	8,76	2959,39	1,798	3	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	Q183#-
4968,1	-7,9	7,89	2976,416	1,849	3	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	
4980,1	-6,6	8,79	2976,416	0,211	3	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	
5027,1	-6,1	8,35	2977,4	-0,134	3	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	N199#0.98402
5070,1	-5,6	7,9	2977,4	-0,02	3	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	N199#0.98402
5015,1	-4,8	7,18	2976,369	2,052	4	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	Q183#- 17.02655, Q187#0.98402, W191#15.99492 Q183#-
5116,1	-4,8	7,14	2960,374	1,944	3	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	17.02655, N199#0.98402
5002,1	-4,7	8,6	2976,416	-0,124	3	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	
5100,1	-4,3	8,02	2959,39	-0,049	4	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	Q183#-
4974,1	-1,7	8,04	2976,416	-0,118	4	1	hwvk	183	QRPEQGLEWIGWIDPENGYTEYAPK	207	fqgk	
4470,1	-14,3	7,38	2311,051	-0,055	2	1	fyyr	247	YDAFDYWGQGTTTLTVSSGASGK	268	pipn	
4432,1	-12,2	6,56	2311,051	1,106	2	1	fyyr	247	YDAFDYWGQGTTTLTVSSGASGK	268	pipn	
4453,1	-11,5	7,32	2311,051	-0,284	2	1	fyyr	247	YDAFDYWGQGTTTLTVSSGASGK	268	pipn	
4442,1	-5,9	7,54	2311,051	-0,142	3	1,5	fyyr	247	YDAFDYWGQGTTTLTVSSGASGK	268	pipn	
4486,1	-5,8	7,21	2311,051	-0,076	3	1,5	fyyr	247	YDAFDYWGQGTTTLTVSSGASGK	268	pipn	
4465,1	-2,7	7,87	2311,051	-0,042	3	1,5	fyyr	247	YDAFDYWGQGTTTLTVSSGASGK	268	pipn	
1527,1	-4,7	6,3	1323,669	-0,058	2	0,667	eaqk	291	IEWHEG GTAPVK	302	qtln	
1511,1	-2,6	6,3	1323,669	-0,041	2	0,667	eaqk	291	IEWHEG GTAPVK	302	qtln	
5106,1	-1,3	8,07	1074,583	0,024	1	0,5	apvk	303	QTLNFDLLK	311	lagd	Q303#-
1112,1	-2,5	8,24	958,448	-0,022	2	1	dllk	312	LAGDVESNPG	321]	
1131,1	-2,1	7,94	958,448	-0,068	2	1	dllk	312	LAGDVESNPG	321]	
1097,1	-1,8	7,59	958,448	-0,058	2	1	dllk	312	LAGDVESNPG	321]	
1126,1	-1,5	7,95	958,448	-0,046	1	1	dllk	312	LAGDVESNPG	321]	

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1168,1	-1,4	6,33	958,448	-0,083	2	1 dIlk	312 LAGDVESNPG	321]
1152,1	-1,1	7,14	958,448	-0,151	2	1 dIlk	312 LAGDVESNPG	321]
1747,1	-3,3	6,85	1055,5	0,017	2	1 dIlk	312 LAGDVESNPGP	322]
1671,1	-3,3	7,15	1055,5	-0,093	2	1 dIlk	312 LAGDVESNPGP	322]
1705,1	-3,1	8,14	1055,5	-0,083	2	1 dIlk	312 LAGDVESNPGP	322]
1730,1	-2,7	7,02	1055,5	1,007	1	1 dIlk	312 LAGDVESNPGP	322]
1687,1	-2,4	7,97	1055,5	-0,223	2	1 dIlk	312 LAGDVESNPGP	322]
1826,1	-1,7	6,15	1055,5	-0,122	2	1 dIlk	312 LAGDVESNPGP	322]
1725,1	-1,6	7,72	1055,5	-0,131	2	1 dIlk	312 LAGDVESNPGP	322]
1842,1	-1,2	6,19	1056,484	-0,127	2	1 dIlk	312 LAGDVESNPGP	322]

N319#0.98402

Supplementary Table 2A

Mass Spectrometry Analysis of BioID-2A*

rank	log(e)	log(l)	% measured	% corrected	unique	total	Mr	Accession	Description
1	-125.6	8.00	23	41	10	79	46.5	ENSP00000347005	LUC7L2:p , LUC7 like 2, pre-mRNA splicing factor [Source:HGNC Symbol;Acc: HGNC:21608]
2	-110.4	7.23	19	25	13	28	77.5	ENSP00000325376	HNRNPM:p , heterogeneous nuclear ribonucleoprotein M [Source:HGNC Symbol;Acc: HGNC:5046]
3	-105.6	7.36	28	42	11	32	49.6	ENSP00000339001	TUBB:p , tubulin beta class I [Source:HGNC Symbol;Acc: HGNC:20778]
4	-91.0	7.23	17	32	9	23	59.3	ENSP00000253363	RBM39:p , RNA binding motif protein 39 [Source:HGNC Symbol;Acc: HGNC:15923]
5	-88.3	6.74	5.2	7	11	12	269.8	ENSP00000344789	ACACA:p , no protein text annotation available
6	-86.4	7.43	33	52	9	25	27.7	ENSP00000258962	SRSF1:p , serine and arginine rich splicing factor 1 [Source:HGNC Symbol;Acc: HGNC:10780]
7	-83.4	7.53	7.4	12	2	6	38.4	ENSP00000337507	LUC7L:p , LUC7 like [Source:HGNC Symbol;Acc: HGNC:6723]
8	-75.9	7.87	37	71	8	26	19.3	ENSP00000362820	SRSF3:p , serine and arginine rich splicing factor 3 [Source:HGNC Symbol;Acc: HGNC:10785]
9	-75.2	7.23	43	65	9	20	17.7	ENSP00000393241	RPS18:p , ribosomal protein S18 [Source:HGNC Symbol;Acc: HGNC:10401]
10	-71.2	7.16	3.2	5	1	1	49.6	ENSP00000264071	TUBB4:p , tubulin beta 4A class Iva [Source:HGNC Symbol;Acc: HGNC:20774]
11	-48.1	7.17	20	37	4	6	27.4	ENSP00000325905	SRSF7:p , serine and arginine rich splicing factor 7 [Source:HGNC Symbol;Acc: HGNC:10789]
12	-47.3	7.01	16	24	6	14	50.1	ENSP00000336799	TUBA1B:p , tubulin alpha 1b [Source:HGNC Symbol;Acc: HGNC:18809]
13	-45.9	6.57	23	41	6	8	21.4	ENSP00000339566	HIST1H1C:p , histone cluster 1 H1 family member c [Source:HGNC Symbol;Acc: HGNC:4716]
14	-45.4	6.64	18	32	5	10	23.7	ENSP00000441406	ADP ribosylation factor like GTPase 6 interacting protein 4 [Source:HGNC Symbol;Acc: HGNC:18076]
15	-35.8	6.51	8.7	16	1	1	21.9	ENSP00000307705	HIST1H1E:p , histone cluster 1 H1 family member e [Source:HGNC Symbol;Acc: HGNC:4718]

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16	-31.4	7.20	20	42	4	17	25.5	ENSP00000376276	SRSF2:p , serine and arginine rich splicing factor 2 [Source:HGNC Symbol;Acc: HGNC:10783]
17	-29.9	6.57	7.3	11	4	9	72.3	ENSP00000324173	HSPA5:p , heat shock 70kDa protein 5 glucose-regulated protein, 78kDa [Source:HGNC Symbol;Acc: HGNC:5238]
18	-27.5	6.73	17	26	4	6	29.4	ENSP00000272139	C1orf35:p , chromosome 1 open reading frame 35 [Source:HGNC Symbol;Acc: HGNC:19032]
19	-25.1	6.58	16	50	3	5	18.8	ENSP00000244227	SNRNP27:p , small nuclear ribonucleoprotein U4/U6.U5 subunit 27 [Source:HGNC Symbol;Acc: HGNC:30240]
20	-24.7	7.01	14	22	3	9	27.6	ENSP00000343557	ZCCHC17:p , zinc finger CCHC-type containing 17 [Source:HGNC Symbol;Acc: HGNC:30246]
21	-24.6	7.04	24	30	3	9	14.4	ENSP00000422078	SUB1:p , SUB1 homolog, transcriptional regulator [Source:HGNC Symbol;Acc: HGNC:19985]
22	-24.0	6.54	23	31	4	6	16.4	ENSP00000251453	RPS16:p , ribosomal protein S16 [Source:HGNC Symbol;Acc: HGNC:10396]
23	-22.8	6.62	17	35	3	7	22.9	ENSP00000448039	nascent polypeptide-associated complex alpha subunit [Source:HGNC Symbol;Acc: HGNC:7629]
24	-21.5	6.53	9.9	19	4	4	33.2	ENSP00000383059	ARGLU1:p , arginine and glutamate rich 1 [Source:HGNC Symbol;Acc: HGNC:25482]
25	-18.6	6.21	9.3	11	2	2	53.5	ENSP00000404372	HSPA8:p
26	-17.4	6.61	14	25	2	5	15.8	ENSP00000296674	RPS23:p , ribosomal protein S23 [Source:HGNC Symbol;Acc: HGNC:10410]
27	-10.6	5.89	1.8	3	2	2	117.4	ENSP00000416534	DDX46:p
28	-9.6	6.00	5.6	8	2	2	49.2	ENSP00000377082	HNRNPH1:p , heterogeneous nuclear ribonucleoprotein H1 [Source:HGNC Symbol;Acc: HGNC:5041]
29	-9.6	5.94	8.1	13	2	2	26.1	ENSP00000297157	RP9:p , RP9, pre-mRNA splicing factor [Source:HGNC Symbol;Acc: HGNC:10288]
30	-9.6	5.82	7.0	8	2	2	32.7	ENSP00000435905	PC:p
31	-9.2	5.62	20	34	2	2	14.8	ENSP00000346088	RPL22:p , ribosomal protein L22 [Source:HGNC Symbol;Acc: HGNC:10315]
32	-8.6	5.79	3.0	4	2	2	80.4	ENSP00000265594	MCCC1:p , methylcrotonoyl-CoA carboxylase 1 (alpha) [Source: HGNC 6936]
33	-8.6	5.76	8.7	14	2	2	37.5	ENSP00000305556	PCBP1:p , poly(rC) binding protein 1 [Source: HGNC 8647]
34	-8.6	6.25	2.4	3	2	2	163.0	ENSP00000397570	MAPKBP1:p

Supplementary Table 2A

35	-7.9	6.34	6.4	17	2	3	28.7	ENSP00000369757	RPS6:p , ribosomal protein S6 [Source:HGNC Symbol;Acc: HGNC:10429]
36	-7.1	5.96	12	29	2	2	13.7	ENSP00000435096	RPS25:p , ribosomal protein S25 [Source:HGNC Symbol;Acc: HGNC:10413]
37	-6.7	6.06	5.0	8	1	2	27.9	ENSP00000291552	U2AF1:p , U2 small nuclear RNA auxiliary factor 1 [Source:HGNC Symbol;Acc: HGNC:12453]
38	-5.4	5.91	14	18	1	2	9.5	ENSP00000357555	RPS27:p , ribosomal protein S27 [Source:HGNC Symbol;Acc: HGNC:10416]
39	-4.9	6.53	9.4	21	1	3	10.6	ENSP00000362671	RPL35:p , ribosomal protein L35 [Source:HGNC Symbol;Acc: HGNC:10344]
40	-4.6	5.60	2.3	4	1	1	47.7	ENSP00000311430	RPL4:p , ribosomal protein L4 [Source:HGNC Symbol;Acc: HGNC:10353]
41	-4.0	6.26	6.3	10	1	2	16.4	ENSP00000404375	RPL36A:p , ribosomal protein L36a [Source:HGNC Symbol;Acc: HGNC:10359]
42	-3.8	5.60	0.6	1	1	1	269.3	ENSP00000354085	ANKHD1:p , ankyrin repeat and KH domain containing 1 [Source:HGNC Symbol;Acc: HGNC:24714]
43	-3.7	5.47	5.2	11	1	2	33.6	ENSP00000416959	TRA2B:p , transformer 2 beta homolog [Source:HGNC Symbol;Acc: HGNC:10781]
44	-3.6	5.51	12	22	1	1	13.0	ENSP00000348849	RPS26:p , ribosomal protein S26 [Source:HGNC Symbol;Acc: HGNC:10414]
45	-3.5	6.58	6.8	14	1	3	16.6	ENSP00000346015	RPL27A:p , ribosomal protein L27a [Source:HGNC Symbol;Acc: HGNC:10329]
46	-3.5	5.51	6.6	22	1	1	16.3	ENSP00000385958	RPS14:p , ribosomal protein S14 [Source:HGNC Symbol;Acc: HGNC:10387]
47	-3.1	6.83	2.6	3	1	4	74.8	ENSP00000305107	GIMAP8:p , GTPase, IMAP family member 8 [Source:HGNC Symbol;Acc: HGNC:21792]
48	-3.1	6.02	6.4	8	1	1	14.9	ENSP00000420311	RPL23:p , ribosomal protein L23 [Source:HGNC Symbol;Acc: HGNC:10316]
49	-2.9	5.72	6.6	12	1	1	12.5	ENSP00000346012	RPL36AL:p , ribosomal protein L36a like [Source:HGNC Symbol;Acc: HGNC:10346]
50	-2.7	5.32	3.9	8	1	2	51.4	ENSP00000425092	LUC7L3:p , LUC7 like 3 pre-mRNA splicing factor [Source:HGNC Symbol;Acc: HGNC:24309]
51	-2.5	6.00	33	44	1	1	2.2	ENSP00000451870	T-cell receptor alpha joining 56 [Source:HGNC Symbol;Acc: HGNC:12088]
52	-2.5	6.22	5.5	10	1	3	22.2	ENSP00000342913	SRSF10:p
53	-2.4	7.05	3.0	4	1	6	24.4	sp TRYP_PIG	Trypsin; EC 3.4.21.4; Flags: Precursor

Supplementary Table 2A

54	-2.3	5.06	7.1	15	1	1	18.2	ENSP00000427401	SREK11P1:p
55	-2.2	5.52	14	17	1	1	10.5	ENSP00000215570	TIMM13:p
56	-2.1	5.54	0.8	3	1	1	161.0	ENSP00000420477	NACAD:p
57	-2.1	5.89	4.5	9	1	1	17.8	ENSP00000377640	RPL24:p , ribosomal protein L24 [Source:HGNC Symbol;Acc: HGNC:10325]
58	-1.9	5.52	2.7	5	1	1	72.9	ENSP00000356311	C1orf106:p
59	-1.9	5.39	1.4	4	1	1	103.9	ENSP00000345308	UBAP2L:p , ubiquitin associated protein 2 like [Source:HGNC Symbol;Acc: HGNC:29877]
60	-1.8	5.36	0.8	1	1	1	160.5	ENSP00000364979	COL4A1:p
61	-1.7	5.65	3.8	7	1	1	27.2	ENSP00000389783	FAM133B:p
62	-1.7	5.60	4.1	6	1	1	33.0	ENSP00000393746	FYTTD1:p
63	-1.6	5.61	12	21	1	1	6.7	ENSP00000245458	RPS29:p , ribosomal protein S29 [Source:HGNC Symbol;Acc: HGNC:10419]
64	-1.6	4.64	0.8	1	1	1	141.3	ENSP00000347730	ZNF536:p
65	-1.5	5.38	0.5	1	1	1	170.8	ENSP00000342434	BAZ1B:p
66	-1.5	5.45	6.5	13	1	1	17.7	ENSP00000366061	NMS:p
67	-1.5	6.01	0.5	1	1	1	150.7	ENSP00000303427	PDS5A:p
68	-1.5	5.52	1.8	3	1	1	116.6	ENSP00000382356	COL28A1:p
69	-1.4	5.31	1.1	2	1	1	110.6	ENSP00000353854	C15orf39:p
70	-1.4	5.54	1.5	3	1	2	53.5	ENSP00000307863	U2AF2:p , U2 small nuclear RNA auxiliary factor 2 [Source:HGNC Symbol;Acc: HGNC:23156]
71	-1.4	5.60	4.8	7	1	1	54.2	ENSP00000359160	CCDC76:p
72	-1.4	5.74	0.2	0	1	1	383.6	ENSP00000334714	IGFN1:p

Supplementary Table 2A

73	-1.4	5.38	4.1	11	1	1	23.5	ENSP00000225430	RPL19:p , ribosomal protein L19 [Source:HGNC Symbol;Acc: HGNC:10312]
74	-1.4	5.40	9.5	15	1	1	11.8	ENSP00000447415	no protein information available
75	-1.3	6.12	0.3	0	1	1	348.2	ENSP00000424243	EYS:p
76	-1.3	5.74	4.2	7	1	1	25.5	ENSP00000385298	MEI1:p
77	-1.3	5.34	1.8	2	1	1	163.9	ENSP00000379866	COL4A4:p , collagen, type IV, alpha 4 [Source: HGNC 2206]
78	-1.3	5.58	2.2	3	1	1	101.9	ENSP00000432728	TYK2:p
79	-1.3	5.55	3.5	5	1	1	54.4	ENSP00000260228	MMP20:p
80	-1.3	5.67	1.1	1	1	1	112.8	ENSP00000367787	LIG3:p
81	-1.3	5.45	12	31	1	1	23.6	ENSP00000242284	CLTA:p
82	-1.2	5.27	1.9	4	1	1	69.8	ENSP00000347451	LINGO1:p
83	-1.2	5.90	1.3	2	1	1	157.0	ENSP00000270238	LMTK3:p
84	-1.2	5.53	3.2	5	1	1	24.4	ENSP00000446215	RAN, member RAS oncogene family [Source:HGNC Symbol;Acc: HGNC:9846]
85	-1.2	5.58	18	90	1	1	6.4	ENSP00000355315	RPL39:p
86	-1.2	5.76	0.8	1	1	1	119.5	ENSP00000317614	ZNF518B:p
87	-1.2	5.32	1.9	3	1	1	67.8	ENSP00000359916	FRMD7:p
88	-1.2	6.00	0.4	1	1	1	237.9	ENSP00000276204	DOCK11:p
89	-1.2	5.89	4.6	6	1	1	45.1	ENSP00000384848	PRR5:p
90	-1.2	5.70	5.1	7	1	1	18.0	ENSP00000383981	RPS27A:p , ribosomal protein S27a [Source:HGNC Symbol;Acc: HGNC:10417]
91	-1.1	4.84	12	15	1	1	16.1	ENSP00000454239	no protein information available

Supplementary Table 2A

92	-1.1	5.35	0.2	0	1	1	256.1	ENSP00000418510	FLNB:p
93	-1.1	5.16	17	20	1	1	9.7	ENSP00000334644	LCE3C:p
94	-1.1	5.35	2.3	4	1	1	67.6	ENSP00000217429	FAM83D:p
95	-1.1	5.27	2.4	5	1	1	27.0	ENSP00000456266	no protein information available
96	-1.1	5.59	1.1	2	1	1	96.6	ENSP00000413812	ERN2:p
97	-1.1	5.50	2.7	4	1	1	34.6	ENSP00000354822	XAF1:p
98	-1.1	5.70	1.3	2	1	1	138.0	ENSP00000364798	ZBTB40:p
99	-1.1	5.86	0.9	1	1	1	161.0	ENSP00000303153	COL22A1:p , collagen type XXII alpha 1 chain [Source:HGNC Symbol;Acc: HGNC:22989]
100	-1.0	5.59	2.7	4	1	1	46.9	ENSP00000272224	GDF7:p
101	-1.0	6.23	1.2	2	1	1	89.7	ENSP00000206765	TGM1:p
102	-1.0	5.59	0.9	1	1	1	127.7	ENSP00000268296	ITGAX:p
103	-1.0	5.17	0.6	1	1	1	222.9	ENSP00000262450	CHD5:p

Supplementary Table 2B

Mass Spectrometry Analysis of BioID-2A-P*

rank	log(e)	log(l)	% measured	% corrected	unique	total	Mr	Accession	Description
1	-129.6	8.02	23	41	10	63	46.5	ENSP00000347005	LUC7L2:p , LUC7 like 2, pre-mRNA splicing factor [Source:HGNC Symbol;Acc: HGNC:21608]
2	-111.9	7.19	18	23	12	19	77.5	ENSP00000325376	HNRNPM:p , heterogeneous nuclear ribonucleoprotein M [Source:HGNC Symbol;Acc: HGNC:5046]
3	-88.0	7.62	7.4	12	2	5	38.4	ENSP00000337507	LUC7L:p , LUC7 like [Source:HGNC Symbol;Acc: HGNC:6723]
4	-83.6	7.30	23	35	9	24	49.6	ENSP00000339001	TUBB:p , tubulin beta class I [Source:HGNC Symbol;Acc: HGNC:20778]
5	-82.6	7.64	36	57	9	30	27.7	ENSP00000258962	SRSF1:p , serine and arginine rich splicing factor 1 [Source:HGNC Symbol;Acc: HGNC:10780]
6	-74.8	7.15	9.9	15	3	7	49.6	ENSP00000264071	TUBB4:p , tubulin beta 4A class IVa [Source:HGNC Symbol;Acc: HGNC:20774]
7	-74.0	7.19	2.5	4	1	1	49.8	ENSP00000341289	TUBB2C:p , tubulin beta 4B class Ivb [Source:HGNC Symbol;Acc: HGNC:20771]
8	-73.5	7.31	14	26	6	15	59.3	ENSP00000253363	RBM39:p , RNA binding motif protein 39 [Source:HGNC Symbol;Acc: HGNC:15923]
9	-60.3	8.11	34	65	6	34	19.3	ENSP00000362820	SRSF3:p , serine and arginine rich splicing factor 3 [Source:HGNC Symbol;Acc: HGNC:10785]
10	-56.2	6.67	3.6	5	8	9	269.8	ENSP00000344789	ACACA:p , no protein text annotation available
11	-52.0	7.14	30	46	6	13	17.7	ENSP00000393241	RPS18:p , ribosomal protein S18 [Source:HGNC Symbol;Acc: HGNC:10401]
12	-49.7	7.20	16	24	6	14	50.1	ENSP00000336799	TUBA1B:p , tubulin alpha 1b [Source:HGNC Symbol;Acc: HGNC:18809]
13	-36.3	7.47	11	21	3	4	27.4	ENSP00000325905	SRSF7:p , serine and arginine rich splicing factor 7 [Source:HGNC Symbol;Acc: HGNC:10789]
14	-32.2	7.11	14	22	3	10	27.6	ENSP00000343557	ZCCHC17:p , zinc finger CCHC-type containing 17 [Source:HGNC Symbol;Acc: HGNC:30246]
15	-31.8	6.56	19	28	4	5	29.4	ENSP00000272139	C1orf35:p , chromosome 1 open reading frame 35 [Source:HGNC Symbol;Acc: HGNC:19032]

Supplementary Table 2B

16	-29.9	6.80	22	40	4	7	21.9	ENSP00000307705	HIST1H1E:p , histone cluster 1 H1 family member e [Source:HGNC Symbol;Acc: HGNC:4718]
17	-29.1	7.39	17	36	3	22	25.5	ENSP00000376276	SRSF2:p , serine and arginine rich splicing factor 2 [Source:HGNC Symbol;Acc: HGNC:10783]
18	-28.9	6.79	7.0	12	1	2	21.4	ENSP00000339566	HIST1H1C:p , histone cluster 1 H1 family member c [Source:HGNC Symbol;Acc: HGNC:4716]
19	-27.9	6.49	21	38	4	5	12.5	ENSP00000346012	RPL36AL:p , ribosomal protein L36a like [Source:HGNC Symbol;Acc: HGNC:10346]
20	-27.1	6.81	6.3	10	2	5	16.4	ENSP00000404375	RPL36A:p , ribosomal protein L36a [Source:HGNC Symbol;Acc: HGNC:10359]
21	-26.6	6.27	9.0	10	3	3	42.0	ENSP00000355645	ACTA1:p , actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc: HGNC:129]
22	-26.1	6.44	16	28	3	4	23.7	ENSP00000441406	ADP ribosylation factor like GTPase 6 interacting protein 4 [Source:HGNC Symbol;Acc: HGNC:18076]
23	-26.1	7.00	16	50	3	7	18.8	ENSP00000244227	SNRNP27:p , small nuclear ribonucleoprotein U4/U6.U5 subunit 27 [Source:HGNC Symbol;Acc: HGNC:30240]
24	-23.8	6.73	16	45	4	6	28.7	ENSP00000369757	RPS6:p , ribosomal protein S6 [Source:HGNC Symbol;Acc: HGNC:10429]
25	-23.4	6.58	21	38	3	4	15.8	ENSP00000296674	RPS23:p , ribosomal protein S23 [Source:HGNC Symbol;Acc: HGNC:10410]
26	-22.8	6.23	7.3	11	3	3	49.2	ENSP00000377082	HNRNPH1:p , heterogeneous nuclear ribonucleoprotein H1 [Source:HGNC Symbol;Acc: HGNC:5041]
27	-22.5	7.02	24	30	3	8	14.4	ENSP00000422078	SUB1:p , SUB1 homolog, transcriptional regulator [Source:HGNC Symbol;Acc: HGNC:19985]
28	-15.8	6.08	3.0	4	3	3	163.7	ENSP00000361290	COL4A6:p , collagen type IV alpha 6 chain [Source:HGNC Symbol;Acc: HGNC:2208]
29	-15.3	6.65	7.3	14	3	3	33.2	ENSP00000383059	ARGLU1:p , arginine and glutamate rich 1 [Source:HGNC Symbol;Acc: HGNC:25482]
30	-15.3	6.04	11	19	3	3	34.9	ENSP00000352228	PCBP2:p , poly(rC) binding protein 2 [Source:HGNC Symbol;Acc: HGNC:8648]
31	-13.4	6.46	13	27	2	2	16.6	ENSP00000346015	RPL27A:p , ribosomal protein L27a [Source:HGNC Symbol;Acc: HGNC:10329]
32	-10.9	6.50	12	16	2	3	16.4	ENSP00000251453	RPS16:p , ribosomal protein S16 [Source:HGNC Symbol;Acc: HGNC:10396]
33	-10.7	5.90	8.5	14	2	2	24.2	ENSP00000307889	RPL13:p , ribosomal protein L13 [Source:HGNC Symbol;Acc: HGNC:10303]
34	-10.1	5.99	8.0	17	2	3	33.6	ENSP00000416959	TRA2B:p , transformer 2 beta homolog [Source:HGNC Symbol;Acc: HGNC:10781]

Supplementary Table 2B

35	-9.7	6.00	7.7	14	2	2	28.4	ENSP00000398401	FAM133B:p , family with sequence similarity 133 member B [Source:HGNC Symbol;Acc: HGNC:28629]
36	-9.1	6.16	19	34	2	2	13.0	ENSP00000348849	RPS26:p , ribosomal protein S26 [Source:HGNC Symbol;Acc: HGNC:10414]
37	-8.9	6.40	12	25	2	3	17.8	ENSP00000377640	RPL24:p , ribosomal protein L24 [Source:HGNC Symbol;Acc: HGNC:10325]
38	-8.7	6.12	4.5	7	2	2	26.1	ENSP00000297157	RP9:p , RP9, pre-mRNA splicing factor [Source:HGNC Symbol;Acc: HGNC:10288]
39	-8.5	7.09	4.4	6	2	2	70.0	ENSP00000364802	HSPA1A:p , heat shock protein family A (Hsp70) member 1A [Source:HGNC Symbol;Acc: HGNC:5232]
40	-8.2	6.10	3.6	5	2	2	61.3	ENSP00000343657	MCCC2:p , methylcrotonoyl-CoA carboxylase 2 [Source:HGNC Symbol;Acc: HGNC:6937]
41	-5.5	5.81	2.3	4	1	1	47.7	ENSP00000311430	RPL4:p , ribosomal protein L4 [Source:HGNC Symbol;Acc: HGNC:10353]
42	-5.2	5.88	9.6	11	1	1	12.3	ENSP00000451080	ERH, mRNA splicing and mitosis factor [Source:HGNC Symbol;Acc: HGNC:3447]
43	-4.8	5.68	4.1	11	1	1	23.5	ENSP00000225430	RPL19:p , ribosomal protein L19 [Source:HGNC Symbol;Acc: HGNC:10312]
44	-4.6	5.80	1.5	2	1	2	83.2	ENSP00000360709	HSP90AB1:p , heat shock protein 90 alpha family class B member 1 [Source:HGNC Symbol;Acc: HGNC:5258]
45	-4.5	4.96	3.9	8	1	1	51.4	ENSP00000425092	LUC7L3:p , LUC7 like 3 pre-mRNA splicing factor [Source:HGNC Symbol;Acc: HGNC:24309]
46	-4.4	4.99	3.9	6	1	1	42.4	ENSP00000360033	SERBP1:p , SERPINE1 mRNA binding protein 1 [Source:HGNC Symbol;Acc: HGNC:17860]
47	-4.4	5.79	4.6	8	1	2	34.2	ENSP00000380275	RNPS1:p , RNA binding protein with serine rich domain 1 [Source:HGNC Symbol;Acc: HGNC:10080]
48	-3.6	5.94	5.1	7	1	2	18.0	ENSP00000383981	RPS27A:p , ribosomal protein S27a [Source:HGNC Symbol;Acc: HGNC:10417]
49	-3.5	5.95	1.8	3	1	1	69.1	ENSP00000440276	DEAD-box helicase 5 [Source:HGNC Symbol;Acc: HGNC:2746]
50	-3.3	5.72	12	21	1	1	6.7	ENSP00000245458	RPS29:p , ribosomal protein S29 [Source:HGNC Symbol;Acc: HGNC:10419]
51	-3.2	6.21	14	18	1	3	9.5	ENSP00000357555	RPS27:p , ribosomal protein S27 [Source:HGNC Symbol;Acc: HGNC:10416]
52	-3.1	6.76	9.4	21	1	4	10.6	ENSP00000362671	RPL35:p , ribosomal protein L35 [Source:HGNC Symbol;Acc: HGNC:10344]
53	-2.8	5.27	5.0	8	1	1	27.9	ENSP00000291552	U2AF1:p , U2 small nuclear RNA auxiliary factor 1 [Source:HGNC Symbol;Acc: HGNC:12453]

Supplementary Table 2B

54	-2.7	5.92	5.4	7	1	1	16.7	ENSP00000228140	RPS13:p , ribosomal protein S13 [Source:HGNC Symbol;Acc: HGNC:10386]
55	-2.5	7.12	3.0	4	1	6	24.4	sp TRYP_PIG	Trypsin; EC 3.4.21.4; Flags: Precursor
56	-2.3	5.51	1.8	2	1	1	80.0	ENSP00000365462	PCCA:p , propionyl-CoA carboxylase alpha subunit [Source:HGNC Symbol;Acc: HGNC:8653]
57	-2.3	5.52	1.4	4	1	1	103.9	ENSP00000345308	UBAP2L:p , ubiquitin associated protein 2 like [Source:HGNC Symbol;Acc: HGNC:29877]
58	-2.2	6.23	6.4	8	1	1	14.9	ENSP00000420311	RPL23:p , ribosomal protein L23 [Source:HGNC Symbol;Acc: HGNC:10316]
59	-2.1	6.05	33	44	1	1	2.2	ENSP00000451870	T-cell receptor alpha joining 56 [Source:HGNC Symbol;Acc: HGNC:12088]
60	-2.1	5.47	2.2	3	1	1	80.6	ENSP00000362929	GSN:p , gelsolin [Source:HGNC Symbol;Acc: HGNC:4620]
61	-2.0	5.45	0.7	1	1	1	211.0	ENSP00000356000	PLXNA2:p , plexin A2 [Source:HGNC Symbol;Acc: HGNC:9100]
62	-1.9	5.46	9.4	16	1	1	14.8	ENSP00000346088	RPL22:p , ribosomal protein L22 [Source:HGNC Symbol;Acc: HGNC:10315]
63	-1.9	5.64	5.5	10	1	1	22.2	ENSP00000342913	SRSF10:p
64	-1.9	6.07	1.7	3	1	1	50.1	ENSP00000339063	EEF1A1:p , eukaryotic translation elongation factor 1 alpha 1 [Source:HGNC Symbol;Acc: HGNC:3189]
65	-1.9	5.91	1.5	2	1	1	99.5	ENSP00000393313	EPS15L1:p
66	-1.9	5.57	1.9	2	1	1	58.9	ENSP00000263284	CCDC61:p
67	-1.9	6.29	6.8	18	1	1	14.4	ENSP00000435370	FAU:p , FAU, ubiquitin like and ribosomal protein S30 fusion [Source:HGNC Symbol;Acc: HGNC:3597]
68	-1.8	5.06	14	24	1	1	13.7	ENSP00000437206	ST3GAL3:p
69	-1.8	5.84	7.5	12	1	1	16.3	ENSP00000271843	JTB:p
70	-1.7	6.16	3.2	5	1	1	68.8	ENSP00000263663	TAF1B:p
71	-1.7	6.16	0.3	0	1	1	293.3	ENSP00000222270	Histone-lysine N-methyltransferase 2B
72	-1.7	5.64	1.1	2	1	1	131.8	ENSP00000384169	FBLN2:p

Supplementary Table 2B

73	-1.7	5.73	5.3	10	1	1	30.3	ENSP00000358731	ADORA3:p
74	-1.6	5.38	0.7	1	1	1	242.8	ENSP00000363215	MED12:p
75	-1.5	5.39	1.4	2	1	1	127.9	ENSP00000364973	COL4A1:p
76	-1.5	5.29	0.6	1	1	1	269.3	ENSP00000354085	ANKHD1:p , ankyrin repeat and KH domain containing 1 [Source:HGNC Symbol;Acc: HGNC:24714]
77	-1.5	5.51	4.8	12	1	1	13.7	ENSP00000435096	RPS25:p , ribosomal protein S25 [Source:HGNC Symbol;Acc: HGNC:10413]
78	-1.4	5.39	22	29	1	1	14.6	ENSP00000414803	LASP1:p
79	-1.4	5.74	6.0	11	1	1	17.0	ENSP00000268483	TXNL4B:p
80	-1.4	6.41	3.1	4	1	1	61.6	ENSP00000276211	ARHGAP36:p
81	-1.4	5.59	1.0	1	1	1	136.7	ENSP00000264229	KIAA1211:p
82	-1.4	5.82	6.5	12	1	1	21.6	ENSP00000342156	NCR3:p
83	-1.4	5.84	6.1	10	1	1	31.9	ENSP00000397385	DALRD3:p
84	-1.4	5.85	3.7	6	1	1	75.0	ENSP00000318429	CCDC114:p
85	-1.4	5.28	2.8	4	1	1	58.2	ENSP00000251654	PCCB:p , propionyl CoA carboxylase, beta polypeptide [Source: HGNC 8654]
86	-1.3	5.46	1.9	3	1	1	71.6	ENSP00000380557	AKAP8L:p
87	-1.3	5.48	0.9	1	1	1	295.0	ENSP00000332371	COL7A1:p , collagen type VII alpha 1 chain [Source:HGNC Symbol;Acc: HGNC:2214]
88	-1.3	5.51	0.7	1	1	1	222.1	ENSP00000383303	DSCAM:p
89	-1.3	4.25	2.2	4	1	1	73.0	ENSP00000348959	MAN1A2:p
90	-1.3	5.51	2.4	4	1	1	62.0	ENSP00000246662	KRT9:p , keratin 9 [Source:HGNC Symbol;Acc: HGNC:6447]
91	-1.3	5.33	0.9	2	1	1	116.9	ENSP00000265069	ZFR:p

Supplementary Table 2B

92	-1.2	5.63	1.0	2	1	1	160.5	ENSP00000323720	MED14:p
93	-1.2	5.97	2.4	4	1	1	82.8	ENSP00000410846	XPO5:p
94	-1.2	5.48	5.1	6	1	1	40.5	ENSP00000393189	EFCAB8:p
95	-1.2	5.48	4.1	6	1	1	33.0	ENSP00000393746	FYTTD1:p
96	-1.2	5.91	1.5	2	1	1	56.6	ENSP00000358417	PHGDH:p , phosphoglycerate dehydrogenase [Source:HGNC Symbol;Acc: HGNC:8923]
97	-1.2	5.57	1.1	2	1	1	83.1	ENSP00000435557	KIF21B:p
98	-1.2	5.62	0.4	1	1	1	213.5	ENSP00000352400	NUP214:p
99	-1.1	5.59	0.2	0	1	1	301.5	ENSP00000402033	PDZD2:p , PDZ domain containing 2 [Source: HGNC 18486]
100	-1.1	5.75	23	28	1	1	9.2	ENSP00000430824	CDK16:p
101	-1.1	5.50	20	21	1	1	9.5	ENSP00000436333	PARP10:p
102	-1.1	5.51	4.0	10	1	1	38.1	ENSP00000364265	FOXE1:p
103	-1.1	5.72	4.3	13	1	1	55.0	ENSP00000261622	SLC7A5:p
104	-1.1	5.28	1.9	3	1	1	42.2	ENSP00000298317	RPUSD4:p
105	-1.1	5.76	1.7	3	1	1	44.1	ENSP00000404464	CCBE1:p
106	-1.1	5.54	1.7	3	1	1	53.9	ENSP00000321835	ETV4:p
107	-1.1	5.44	3.7	4	1	1	26.7	ENSP00000413999	CKMT1B:p
108	-1.1	6.06	0.5	1	1	1	208.2	ENSP00000371994	NYNRIN:p
109	-1.1	5.55	1.2	2	1	1	111.5	ENSP00000435421	C11orf82:p
110	-1.1	5.79	1.2	2	1	1	102.4	ENSP00000453574	no protein information available
111	-1.1	5.70	1.1	1	1	1	112.8	ENSP00000367787	LIG3:p

Supplementary Table 3

Sequences of Oligos for Cloning

2A* for: CGCCCCAGTCAAACAGACTCTCAACTTTGATCTACTCAAGCTGGCAGGTGATGTGGAATCTAACCCTGGATG
2A* rev: AATTCATCCAGGGTTAGATTCCACATCACCTGCCAGCTTGAGTAGATCAAAGTTGAGAGTCTGTTTGACTGGGGCGGTAC
2A-P* for: CGCCCCAGTCAAACAGACTCTCAACTTTGATCTACTCAAGCTGGCAGGTGATGTGGAATCTAACCCTGGACCATG
2A-P* rev: AATTCATGGTCCAGGGTTAGATTCCACATCACCTGCCAGCTTGAGTAGATCAAAGTTGAGAGTCTGTTTGACTGGGGCGGTAC
2A^M* for: CGCACCCGTTAAGCAAACATTAATTTTCGACCTCTTGAAACTCGCCGGCGACGTTGAGAGCAATCCAGGCTG
2A^M* rev: AATTCAGCCTGGATTGCTCTCAACGTCGCCGGCGAGTTTCAAGAGGTCGAAATTTAATGTTTGCTTAACGGGTGCGGTAC
2A^M-P* for: CGCACCCGTTAAGCAAACATTAATTTTCGACCTCTTGAAACTCGCCGGCGACGTTGAGAGCAATCCAGGCCCTG
2A^M-P* rev: AATTCAGGGCCCTGGATTGCTCTCAACGTCGCCGGCGAGTTTCAAGAGGTCGAAATTTAATGTTTGCTTAACGGGTGCGGTAC
T2A* for: CGCCACTAACTTTTCTCTACTCAAGCAGGCAGGTGATGTGGAAGAGAACCCTGGGTG
T2A* rev: AATTCACCCAGGGTTCTCTTCCACATCACCTGCCTGCTTGAGTAGAGAAAAGTTAGTGGCGGTAC
T2A-P* for: CGCCACTAACTTTTCTCTACTCAAGCAGGCAGGTGATGTGGAAGAGAACCCTGGGCCCTG
T2A-P* rev: AATTCAGGGCCCAGGGTTCTCTTCCACATCACCTGCCTGCTTGAGTAGAGAAAAGTTAGTGGCGGTAC
CD99L2* for: CCCTTTCTGTGTCTCTCTCCTTTCTCTTACAAAGATGCTTGTTAGTGGGTTTAAAGGCCACCTGGATAATCCAGGATG
CD99L2* rev: AATTCATCCTGGATTATCCAGGTGGGCCTTAAACCCACTAACAAGCATCTTTGTAAGAGAAAGGAGAGAGACACAGAAAGGGGTAC
CD99L2-P* for: CCCTTTCTGTGTCTCTCTCCTTTCTCTTACAAAGATGCTTGTTAGTGGGTTTAAAGGCCACCTGGATAATCCAGGACCATG
CD99L2-P* rev: AATTCATGGTCCTGGATTATCCAGGTGGGCCTTAAACCCACTAACAAGCATCTTTGTAAGAGAAAGGAGAGAGACACAGAAAGGGGTAC
POTE* for: CGTAATTTGCCAGTTACTTTCTGACTACAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGGTTG
POTE* rev: AATTC AACCTGGATTGCTGTTTTT CAGAAGAGATTTTTTAGCATCTGTTTTTCTTTGTAGTCAGAAAGTAAC TGGCAAATTACGGTAC
POTE-P* for: CGTAATTTGCCAGTTACTTTCTGACTACAAAGAAAAACAGATGCTAAAAATCTCTTCTGAAAACAGCAATCCAGGTCCATG
POTE-P* rev: AATTCATGGACCTGGATTGCTGTTTTT CAGAAGAGATTTTTTAGCATCTGTTTTTCTTTGTAGTCAGAAAGTAAC TGGCAAATTACGGTAC
TBCA* for: CGCCGATCCTCGCGTGAGACAGATCAAGATCAAGACCGGCGTGGTGAAGCGGCAGAGATCCTACAAGAATCCAGGATG
TBCA* rev: AATTCATCCTGGATTCTTGTAGGATCTCTGCCGCTTACCACGCCGGTCTTGATCTTGATCTGTCTCACGCGAGGATCGGCGGTAC
TBCA-P* for: CGCCGATCCTCGCGTGAGACAGATCAAGATCAAGACCGGCGTGGTGAAGCGGCAGAGATCCTACAAGAATCCAGGACCATG
TBCA-P* rev: AATTCATGGTCCTGGATTCTTGTAGGATCTCTGCCGCTTACCACGCCGGTCTTGATCTTGATCTGTCTCACGCGAGGATCGGCGGTAC
SPIRE2* for: CGGGGTACCGGGCTGCGGGGCTCGCCGGGCCGGCGCCTGCGGGATACCGGGGACCTCCTGCTGCGCGGGGACGGCTCGGTGCGGGCGCGG

Supplementary Table 3

SPIRE2* rev: CGGAATTCATCCTGGGTTTCTGACCTCTTCAACCGCGGCCTCGGGCTCCCGCGCCCCGACCGAGCCGTCCCCGCGCAGCAGGAGGTCCCC
SPIRE2-P* for: CGGGGTACCGGGCTGCGGGGCTCGCCGGGCCGGCGCCTGCGGGATACCGGGGACCTCCTGCTGCGCGGGGACGGCTCGGTTCGGGGCGCGG
SPIRE2-P* rev: CGGAATTCATGGTCCTGGGTTTCTGACCTCTTCAACCGCGGCCTCGGGCTCCCGCGCCCCGACCGAGCCGTCCCCGCGCAGCAGGAGGTTC
C-TAIL* for: CATGCACAGTGTAATATTTCTCCAAGTATCATCCAAAATTCCCCACAGACAAGGCTTTCGTCCTCATTAG
C-TAIL* rev: AATTCTAATGAGGACGAAAGCCTTGTCTGTGGGGAATTTGGATGATACTTGGAGAAATATTACACTGTGCATGGTAC
C-TAIL-P* for: CATGCACAGTGTAATATTTCTCCAAGTATCATCCAAAATTCCCCACAGACAAGGCTTTCGTCCTCATTAG
C-TAIL-P* rev: AATTCTAAGGATGAGGACGAAAGCCTTGTCTGTGGGGAATTTGGATGATACTTGGAGAAATATTACACTGTGCATGGTAC

Sequences of Oligos for qRT-PCR and RT-PCR

scFv for: CAAACAGACTCTCAACT
scFv rev: ATTTAGGTGACACTATAGAATA
 α -Globin for: GCCGACAAGACCAACGTCAA
 α -Globin rev: AGGTCGAAGTGCGGGAAGTA
GAPDH for: GGGCGCCTGGTCACCAGGGCTGC
GAPDH rev: GAGCCCCAGCCTTCTCCATGGTGG
Ltn for: TGGTGCTGCGGAACTTTCAAAG
Ltn rev: GCAGCTGGTGTGTAAGTATCAC