SUPPLEMENTARY INFORMATION

Figure S1. Localization of key WNT/β-catenin signaling components in the HEK293T cell line.

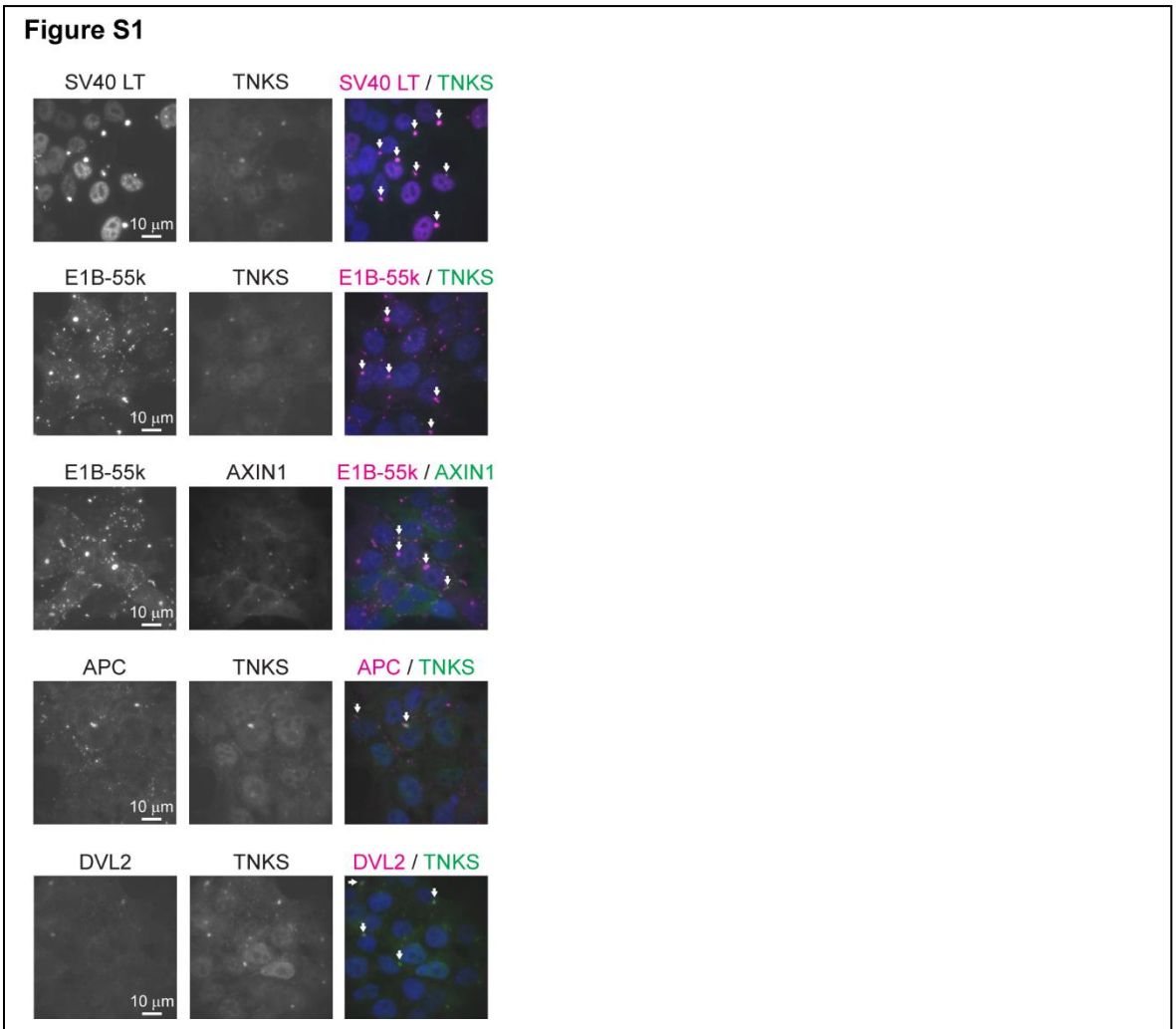


Figure S1. Localization of key WNT/β-catenin signaling components in the HEK293T cell line.

IF analysis (WF) of the localization of SV40-Large T antigen ((SV40 LT) not present in HEK293 cells), TNKS, E1B-55k, AXIN1, APC and DVL2 as indicated. In the merged color images co-localization is indicated with arrows and nuclear counterstaining is shown in blue.

Figure S2. Measurement of E1B-55k protein layer thickness.

Figure S2. Measurement of E1B-55k protein layer thickness.

The thickness of the E1B-55k protein layer was measured in a SIM image slice using the ZEN black software measurement tool. The histogram to the left shows the intensity plot of the E1B-55k (magenta) and TNKS (green) IF staining over the area covered by the red line in the image to the right. The white vertical lines in the histogram correspond to the center position of the aim crosses in the image. The measured distance between the lines and hence the thickness of the E1B-55k protein layer at the indicated position is 220 nm.

Figure S3. Western blot analysis of E1B-55k protein levels in siRNA treated HEK293 cells.

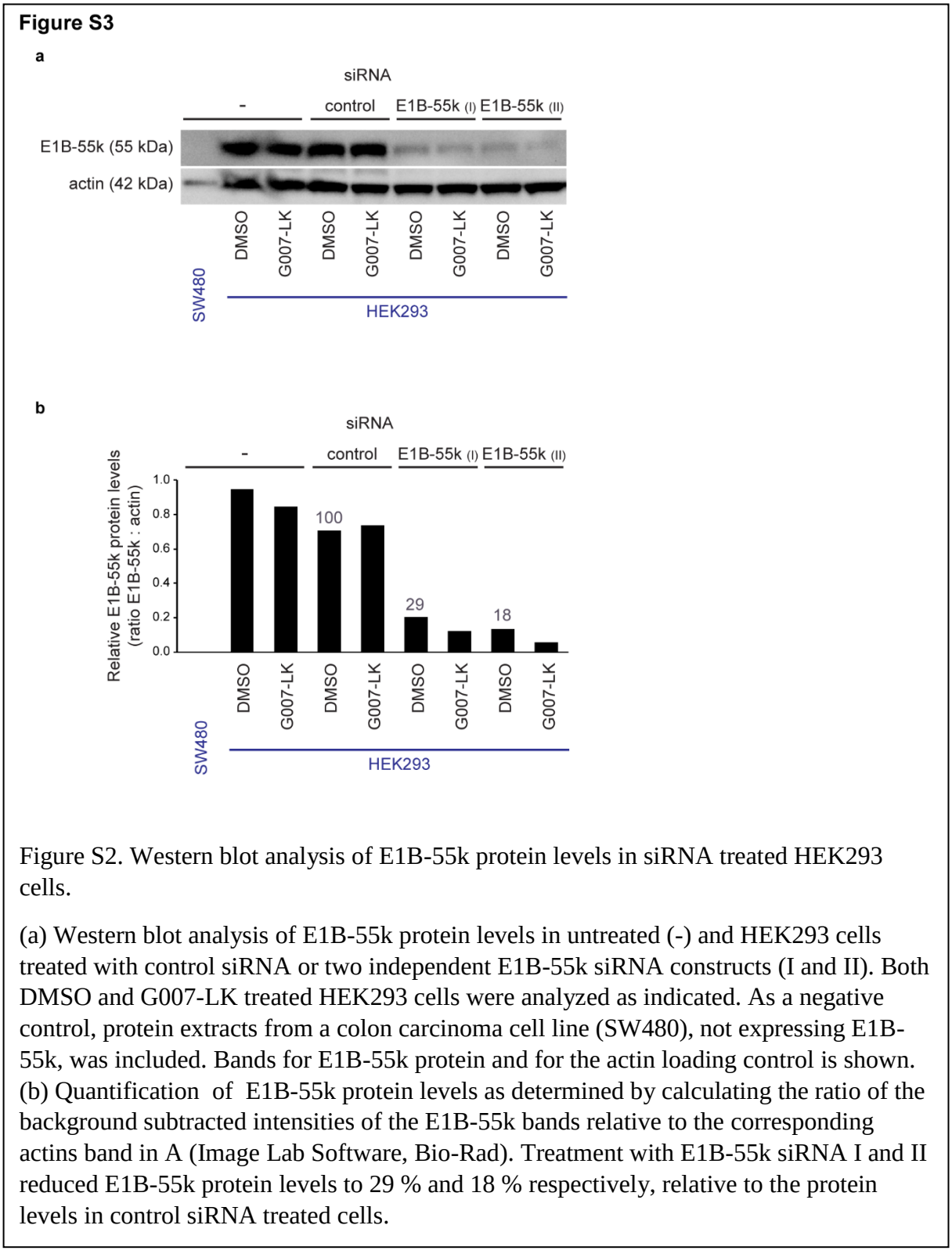


Figure S2. Western blot analysis of E1B-55k protein levels in siRNA treated HEK293 cells.

(a) Western blot analysis of E1B-55k protein levels in untreated (-) and HEK293 cells treated with control siRNA or two independent E1B-55k siRNA constructs (I and II). Both DMSO and G007-LK treated HEK293 cells were analyzed as indicated. As a negative control, protein extracts from a colon carcinoma cell line (SW480), not expressing E1B-55k, was included. Bands for E1B-55k protein and for the actin loading control is shown. (b) Quantification of E1B-55k protein levels as determined by calculating the ratio of the background subtracted intensities of the E1B-55k bands relative to the corresponding actins band in A (Image Lab Software, Bio-Rad). Treatment with E1B-55k siRNA I and II reduced E1B-55k protein levels to 29 % and 18 % respectively, relative to the protein levels in control siRNA treated cells.

Figure S4. In HEK293 cells with reduced E1B-55k protein levels the distribution of AXIN1, APC and DVL2 is changed from accumulation in aggregates to a more uniform cytoplasmic distribution.

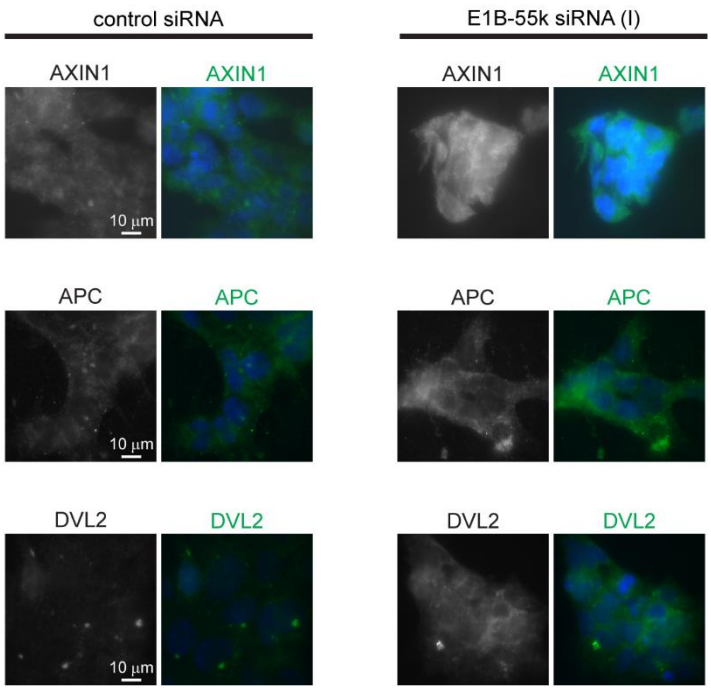


Figure S4. In HEK293 cells with reduced E1B-55k protein levels the distribution of AXIN1, APC and DVL2 is changed from accumulation in aggregates to a more uniform cytoplasmic distribution.

IF analysis (laser WF) of the localization of AXIN1, APC and DVL2 in HEK293 cells treated with control or E1B-55k siRNA. In the merged color images nuclear counterstaining is shown in blue.

Supplementary Table 1. E1B-55k interacting partners detected in Co-IP experiment 1.

Accession	Gene name	Description	Coverage	# Peptides	# PSMs	# Unique Peptides	# Protein Groups	# AAs	MW [kDa]	calc. pI	Beads only control	Mouse IgG control	E1B-55k Ab	Protein FDR Confidence Mascot	Exp. q-value Mascot	Mascot Score	# Peptides Mascot
Q92878	RAD50	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	27,668	34	39	34	1	1312	153,797	6,89	Not Found	Not Found	High	High	0,000	236,18	4
P49959	MRE11	Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3	35,452	21	21	21	1	708	80,543	5,9	Not Found	Not Found	High	High	0,000	233,41	5
Q93008	USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	6,926	15	16	15	1	2570	292,094	5,8	Not Found	Not Found	High	High	0,000	230,37	6
P04637	TP53	Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4	26,209	10	10	10	1	393	43,625	6,79	Not Found	Not Found	High	High	0,000	228,01	2
Q96C92	SDCCAG3	Serologically defined colon cancer antigen 3 OS=Homo sapiens GN=SDCCAG3 PE=1 SV=3	17,931	6	7	6	1	435	47,932	5,14	Not Found	Not Found	High	High	0,000	223,93	3
Q8N1N4	KRT78	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 SV=2	11,731	6	8	4	1	520	56,83	6,02	Not Found	Not Found	High	High	0,000	221,95	6
Q5JSZ5	PRRC2B	Protein PRRC2B OS=Homo sapiens GN=PRRC2B PE=1 SV=2	1,660	3	3	3	1	2229	242,817	8,34	Not Found	Not Found	High	High	0,000	220,30	3
Q9NVI7	ATAD3A	ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A PE=1 SV=2	7,886	5	6	5	1	634	71,325	8,98	Not Found	Not Found	High	High	0,000	218,38	1
Q86SQ0	PHLDB2	Pleckstrin homology-like domain family B member 2 OS=Homo sapiens GN=PHLDB2 PE=1 SV=2	4,469	5	5	5	1	1253	142,07	7,43	Not Found	Not Found	High	High	0,000	215,79	3
P05089	ARG1	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	18,944	4	4	4	1	322	34,713	7,21	Not Found	Not Found	High	High	0,000	211,97	5
O60934	NBN	Nibrin OS=Homo sapiens GN=NBN PE=1 SV=1	4,244	3	3	3	1	754	84,906	6,9	Not Found	Not Found	High	High	0,000	206,41	5
Q08188	TGM3	Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens GN=TGM3 PE=1 SV=4	4,185	2	2	2	1	693	76,584	5,86	Not Found	Not Found	High	High	0,000	201,22	5
P31944	CASP14	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	13,223	3	3	3	1	242	27,662	5,58	Not Found	Not Found	High	High	0,000	200,38	4
A2RUB1	MEIOC	Meiosis-specific coiled-coil domain-containing protein MEIOC OS=Homo sapiens GN=MEIOC PE=2 SV=3	2,206	2	2	2	1	952	107,491	7,12	Not Found	Not Found	High	High	0,000	198,96	3
Q8NDV7	TNRC6A	Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	1,478	2	2	2	1	1962	210,169	7,01	Not Found	Not Found	High	High	0,000	197,88	3
O95816	BAG2	BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2 PE=1 SV=1	13,744	3	3	3	1	211	23,757	6,7	Not Found	Not Found	High	High	0,000	196,78	2
Q5VUA4	ZNF318	Zinc finger protein 318 OS=Homo sapiens GN=ZNF318 PE=1 SV=2	2,106	3	3	3	1	2279	250,958	7,2	Not Found	Not Found	High	High	0,000	191,71	3
O43663	PRC1	Protein regulator of cytokinesis 1 OS=Homo sapiens GN=PRC1 PE=1 SV=2	3,226	2	2	2	1	620	71,562	6,68	Not Found	Not Found	High	High	0,000	191,62	1
Q9UPQ9	TNRC6B	Trinucleotide repeat-containing gene 6B protein OS=Homo sapiens GN=TNRC6B PE=1 SV=4	1,200	2	2	2	1	1833	193,883	6,76	Not Found	Not Found	High	High	0,000	181,99	2
Q6Q0C0	TRAF7	E3 ubiquitin-protein ligase TRAF7 OS=Homo sapiens GN=TRAF7 PE=1 SV=1	1,493	1	1	1	1	670	74,561	7,15	Not Found	Not Found	High	High	0,000	181,43	3
Q13751	LAMB3	Laminin subunit beta-3 OS=Homo sapiens GN=LAMB3 PE=1 SV=1	1,280	1	1	1	1	1172	129,489	7,21	Not Found	Not Found	High	High	0,000	177,27	2
Q8WWI1	LMO7	LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=3	0,891	1	1	1	1	1683	192,576	8,09	Not Found	Not Found	High	High	0,000	175,38	5
Q14999	CUL7	Cullin-7 OS=Homo sapiens GN=CUL7 PE=1 SV=2	1,767	3	3	2	1	1698	191,04	5,87	Not Found	Not Found	High	High	0,000	174,62	4
P25311	AZGP1	Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	3,356	1	1	1	1	298	34,237	6,05	Not Found	Not Found	High	High	0,000	169,56	3
P84090	ERH	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	21,154	2	2	2	1	104	12,251	5,92	Not Found	Not Found	High	High	0,000	168,64	4
Q5T749	KPRP	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=1 SV=1	7,772	3	3	3	1	579	64,093	8,27	Not Found	Not Found	High	High	0,000	168,29	3
O43795	MYO1B	Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3	1,849	1	1	1	1	1136	131,902	9,38	Not Found	Not Found	High	High	0,000	168,12	6
O43823	AKAP8	A-kinase anchor protein 8 OS=Homo sapiens GN=AKAP8 PE=1 SV=1	1,879	1	1	1	1	692	76,061	5,15	Not Found	Not Found	High	High	0,000	167,47	5
P06733	ENO1	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	3,687	2	2	2	1	434	47,139	7,39	Not Found	Not Found	High	High	0,000	166,22	3
O75223	GGCT	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1	6,915	1	1	1	1	188	20,994	5,14	Not Found	Not Found	High	High	0,000	161,04	2
Q9UPN4	CEP131	Centrosomal protein of 131 kDa OS=Homo sapiens GN=CEP131 PE=1 SV=3	1,477	1	1	1	1	1083	122,075	8,69	Not Found	Not Found	High	High	0,000	160,86	4
Q8WVV4	POF1B	Protein POF1B OS=Homo sapiens GN=POF1B PE=1 SV=3	1,868	1	1	1	1	589	68,022	6,32	Not Found	Not Found	High	High	0,000	160,39	3
Q9ULV4	CORO1C	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	1,688	1	1	1	1	474	53,215	7,08	Not Found	Not Found	High	High	0,000	158,90	3
P14373	TRIM27	Zinc finger protein RFP OS=Homo sapiens GN=TRIM27 PE=1 SV=1	2,729	1	1	1	1	513	58,452	6,21	Not Found	Not Found	High	High	0,000	157,82	3
P52597	HNRNPF	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	4,096	1	1	1	1	415	45,643	5,58	Not Found	Not Found	High	High	0,000	155,60	4

Q9NZT1	CALML5	Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	8,904	1	1	1	1	146	15,883	4,44	Not Found	Not Found	High	High	0,000	153,43	6
P48668	KRT6C	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 SV=3	52,305	35	108	2	1	564	59,988	8	Not Found	Not Found	Medium	High	0,001	112,04	2
Q14574	DSC3	Desmocollin-3 OS=Homo sapiens GN=DSC3 PE=1 SV=3	2,567	2	2	2	1	896	99,906	6,1	Not Found	Not Found	Medium	High	0,001	108,73	1
O75420	GIGYF1	PERQ amino acid-rich with GYF domain-containing protein 1 OS=Homo sapiens GN=GIGYF1 PE=1 SV=2	2,802	2	2	2	1	1035	114,531	5,39	Not Found	Not Found	Medium	High	0,001	108,60	2
Q8IWT3	CUL9	Cullin-9 OS=Homo sapiens GN=CUL9 PE=1 SV=2	0,874	2	2	1	1	2517	281,049	5,45	Not Found	Not Found	Medium	High	0,001	108,53	2
O00159	MYO1C	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	1,693	2	2	2	1	1063	121,606	9,41	Not Found	Not Found	Medium	High	0,001	107,00	2
P35580	MYH10	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	0,810	1	1	1	1	1976	228,858	5,54	Not Found	Not Found	Medium	High	0,001	106,08	2
O75342	ALOX12B	Arachidonate 12-lipoxygenase, 12R-type OS=Homo sapiens GN=ALOX12B PE=1 SV=1	1,712	1	1	1	1	701	80,304	7,64	Not Found	Not Found	Medium	High	0,001	104,66	1
P40939	HADHA	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	2,752	1	1	1	1	763	82,947	9,04	Not Found	Not Found	Medium	High	0,001	104,42	2
Q96P63	SERPINB12	Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	3,457	1	1	1	1	405	46,247	5,53	Not Found	Not Found	Medium	High	0,002	101,71	1
Q9H7T9	AUNIP	Aurora kinase A and ninein-interacting protein OS=Homo sapiens GN=AUNIP PE=1 SV=1	3,361	1	1	1	1	357	40,228	7,53	Not Found	Not Found	Medium	High	0,002	101,47	3
Q9UHB6	LIMA1	LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	1,449	1	1	1	1	759	85,173	6,84	Not Found	Not Found	Medium	High	0,002	95,88	2
Q7Z5K2	WAPL	Wings apart-like protein homolog OS=Homo sapiens GN=WAPL PE=1 SV=1	1,092	1	1	1	1	1190	132,863	5,44	Not Found	Not Found	Medium	High	0,002	90,14	1
P20930	FLG	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	0,837	2	2	2	1	4061	434,922	9,25	Not Found	Not Found	Medium	High	0,002	90,10	2
Q96QB1	DLC1	Rho GTPase-activating protein 7 OS=Homo sapiens GN=DLC1 PE=1 SV=4	0,654	1	1	1	1	1528	170,485	6,4	Not Found	Not Found	Medium	High	0,003	84,96	1
Q15058	KIF14	Kinesin-like protein KIF14 OS=Homo sapiens GN=KIF14 PE=1 SV=1	1,214	2	2	2	1	1648	186,375	7,91	Not Found	Not Found	Medium	High	0,003	82,61	3
Q92841	DDX17	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2	1,646	1	1	1	1	729	80,222	8,27	Not Found	Not Found	Medium	High	0,003	79,76	2
O60573	EIF4E2	Eukaryotic translation initiation factor 4E type 2 OS=Homo sapiens GN=EIF4E2 PE=1 SV=1	4,082	1	1	1	1	245	28,344	8,88	Not Found	Not Found	Medium	High	0,004	77,10	2
Q8NB66	UNC13C	Protein unc-13 homolog C OS=Homo sapiens GN=UNC13C PE=2 SV=3	0,361	1	1	1	1	2214	250,754	5,92	Not Found	Not Found	Medium	High	0,004	75,84	2
O14654	IRS4	Insulin receptor substrate 4 OS=Homo sapiens GN=IRS4 PE=1 SV=1	1,273	1	1	1	1	1257	133,685	8,44	Not Found	Not Found	Medium	High	0,004	75,77	1
Q9NYF8	BCLAF1	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2	1,522	1	1	1	1	920	106,059	9,98	Not Found	Not Found	Medium	High	0,004	74,43	2
P01861	IGHG4	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 PE=1 SV=1	2,752	1	1	1	1	327	35,918	7,36	Not Found	Not Found	Medium	High	0,004	74,19	2

Supplementary Table 2. E1B-55k interacting partners detected in Co-IP experiment 2.

Accession	Gene name	Description	Coverage	# Peptides	# PSMs	# Unique Peptides	# Protein Groups	# AAs	MW [kDa]	calc. pI	Beads only control	Mouse IgG control	E1B-55k Ab	Protein FDR Confidence Mascot	Exp. q-value Mascot	Mascot Score	# Peptides Mascot
Q92878	RAD50	DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1	33,99390244	41	50	41	1	1312	153,797	6,89	Not Found	Not Found	High	High	0,000	1521,70	41
Q93008	USP9X	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	13,46303502	24	26	24	1	2570	292,094	5,8	Not Found	Not Found	High	High	0,000	711,18	24
P49959	MRE11	Double-strand break repair protein MRE11 OS=Homo sapiens GN=MRE11 PE=1 SV=3	26,83615819	14	18	14	1	708	80,543	5,9	Not Found	Not Found	High	High	0,000	455,45	14
P04637	TP53	Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=4	25,95419847	7	12	4	1	393	43,625	6,79	Not Found	Not Found	High	High	0,000	436,61	7
Q5JSZ5	PRRC2B	Protein PRRC2B OS=Homo sapiens GN=PRRC2B PE=1 SV=2	1,973979363	3	4	3	1	2229	242,817	8,34	Not Found	Not Found	High	High	0,000	290,18	3
Q86SQ0	PHLDB2	Pleckstrin homology-like domain family B member 2 OS=Homo sapiens GN=PHLDB2 PE=1 SV=2	8,379888268	8	8	8	1	1253	142,07	7,43	Not Found	Not Found	High	High	0,000	216,19	8
O60934	NBN	Nibrin OS=Homo sapiens GN=NBN PE=1 SV=1	10,87533156	7	7	7	1	754	84,906	6,9	Not Found	Not Found	High	High	0,000	189,02	7
Q9Y5X1	SNX9	Sorting nexin-9 OS=Homo sapiens GN=SNX9 PE=1 SV=1	16,80672269	6	6	6	1	595	66,55	5,58	Not Found	Not Found	High	High	0,000	188,73	6
Q9H6S0	YTHDC2	Probable ATP-dependent RNA helicase YTHDC2 OS=Homo sapiens GN=YTHDC2 PE=1 SV=2	4,615384615	4	4	2	1	1430	160,147	8,4	Not Found	Not Found	High	High	0,000	143,30	4
P40939	HADHA	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	8,125819135	4	4	4	1	763	82,947	9,04	Not Found	Not Found	High	High	0,000	133,24	4
P25054	APC	Adenomatous polyposis coli protein OS=Homo sapiens GN=APC PE=1 SV=2	1,793879705	4	4	4	1	2843	311,455	7,8	Not Found	Not Found	High	High	0,000	132,09	4
Q7L804	RAB11FIP2	Rab11 family-interacting protein 2 OS=Homo sapiens GN=RAB11FIP2 PE=1 SV=1	8,0078125	3	3	3	1	512	58,243	9,32	Not Found	Not Found	High	High	0,001	115,78	3
Q7Z5K2	WAPL	Wings apart-like protein homolog OS=Homo sapiens GN=WAPL PE=1 SV=1	3,697478992	2	2	2	1	1190	132,863	5,44	Not Found	Not Found	High	High	0,001	114,53	2
Q02413	DSG1	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	4,671115348	3	4	3	1	1049	113,676	5,03	Not Found	Not Found	High	High	0,002	106,87	3
Q13428	TCOF1	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3	2,419354839	3	3	3	1	1488	152,015	9,04	Not Found	Not Found	High	High	0,002	106,12	3
P14373	TRIM27	Zinc finger protein RFP OS=Homo sapiens GN=TRIM27 PE=1 SV=1	5,068226121	2	2	2	1	513	58,452	6,21	Not Found	Not Found	High	High	0,002	105,73	2
Q96C92	SDCCAG3	Serologically defined colon cancer antigen 3 OS=Homo sapiens GN=SDCCAG3 PE=1 SV=3	6,436781609	2	2	2	1	435	47,932	5,14	Not Found	Not Found	High	High	0,002	97,60	2
O95816	BAG2	BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2 PE=1 SV=1	17,53554502	3	3	3	1	211	23,757	6,7	Not Found	Not Found	High	High	0,002	96,46	3
O14654	IRS4	Insulin receptor substrate 4 OS=Homo sapiens GN=IRS4 PE=1 SV=1	1,272871917	1	1	1	1	1257	133,685	8,44	Not Found	Not Found	High	High	0,003	93,65	1
Q9BQ70	TCF25	Transcription factor 25 OS=Homo sapiens GN=TCF25 PE=1 SV=1	6,952662722	2	2	2	1	676	76,619	6,35	Not Found	Not Found	High	High	0,003	93,08	2
Q13751	LAMB3	Laminin subunit beta-3 OS=Homo sapiens GN=LAMB3 PE=1 SV=1	1,279863481	1	1	1	1	1172	129,489	7,21	Not Found	Not Found	High	High	0,003	92,70	1
Q13263	TRIM28	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	5,508982036	2	2	2	1	835	88,493	5,77	Not Found	Not Found	High	High	0,003	90,57	2
Q7Z460	CLASP1	CLIP-associating protein 1 OS=Homo sapiens GN=CLASP1 PE=1 SV=1	1,88556567	2	2	2	1	1538	169,346	9,03	Not Found	Not Found	High	High	0,004	85,68	2
Q8NDV7	TNRC6A	Trinucleotide repeat-containing gene 6A protein OS=Homo sapiens GN=TNRC6A PE=1 SV=2	2,650356779	4	4	4	1	1962	210,169	7,01	Not Found	Not Found	High	High	0,004	83,93	4
P42357	HAL	Histidine ammonia-lyase OS=Homo sapiens GN=HAL PE=1 SV=1	6,849315068	2	2	2	1	657	72,652	6,95	Not Found	Not Found	High	High	0,004	79,82	2
Q99569	PKP4	Plakophilin-4 OS=Homo sapiens GN=PKP4 PE=1 SV=2	1,929530201	2	2	2	1	1192	131,787	8,94	Not Found	Not Found	High	High	0,004	78,86	2
A7E2V4	ZSWIM8	Zinc finger SWIM domain-containing protein 8 OS=Homo sapiens GN=ZSWIM8 PE=1 SV=1	1,741970604	2	2	2	1	1837	197,173	6,8	Not Found	Not Found	High	High	0,004	75,84	2
Q8IWT3	CUL9	Cullin-9 OS=Homo sapiens GN=CUL9 PE=1 SV=2	1,470003973	3	3	3	1	2517	281,049	5,45	Not Found	Not Found	Medium	High	0,004	75,06	3
Q5VUA4	ZNF318	Zinc finger protein 318 OS=Homo sapiens GN=ZNF318 PE=1 SV=2	1,360245722	2	2	2	1	2279	250,958	7,2	Not Found	Not Found	High	High	0,004	73,88	2
P38432	COIL	Coilin OS=Homo sapiens GN=COIL PE=1 SV=1	1,736111111	1	2	1	1	576	62,57	9,07	Not Found	Not Found	High	High	0,004	73,03	1
Q8WV41	SNX33	Sorting nexin-33 OS=Homo sapiens GN=SNX33 PE=1 SV=1	5,226480836	2	2	2	1	574	65,223	6,79	Not Found	Not Found	High	High	0,004	67,40	2
Q9BQS8	FYCO1	FYVE and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=FYCO1 PE=1 SV=3	0,947225981	1	1	1	1	1478	166,879	4,92	Not Found	Not Found	High	High	0,004	65,30	1
Q641Q2	WASHC2A	WASH complex subunit 2A OS=Homo sapiens GN=WASHC2A PE=1 SV=3	1,640566741	1	1	1	1	1341	147,095	4,81	Not Found	Not Found	High	High	0,010	60,50	1
Q15154	PCM1	Pericentriolar material 1 protein OS=Homo sapiens GN=PCM1 PE=1 SV=4	1,333992095	2	2	2	1	2024	228,392	5,02	Not Found	Not Found	Medium	High	0,010	60,23	2
Q9Y5Q9	GTF3C3	General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1	1,58013544	1	1	1	1	886	101,208	5,07	Not Found	Not Found	High	Medium	0,010	56,61	1

Q9UPW5	AGTPBP1	Cytosolic carboxypeptidase 1 OS=Homo sapiens GN=AGTPBP1 PE=1 SV=3	0,897226754	1	1	1	1	1226	138,361	6,15	Not Found	Not Found	High	Medium	0,011	55,71	1
Q9HCJ0	TNRC6C	Trinucleotide repeat-containing gene 6C protein OS=Homo sapiens GN=TNRC6C PE=1 SV=3	0,828402367	1	1	1	1	1690	175,857	6,96	Not Found	Not Found	High	Medium	0,012	54,00	1
Q16787	LAMA3	Laminin subunit alpha-3 OS=Homo sapiens GN=LAMA3 PE=1 SV=2	0,420042004	1	1	1	1	3333	366,414	7,24	Not Found	Not Found	High	Medium	0,013	53,17	1
O00468	AGRN	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=5	0,53217223	1	1	1	1	2067	217,092	6,39	Not Found	Not Found	High	Medium	0,013	52,88	1
P07942	LAMB1	Laminin subunit beta-1 OS=Homo sapiens GN=LAMB1 PE=1 SV=2	1,231802912	1	1	1	1	1786	197,909	4,94	Not Found	Not Found	High	Medium	0,013	52,29	1
P31944	CASP14	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	5,785123967	1	1	1	1	242	27,662	5,58	Not Found	Not Found	High	Medium	0,013	51,11	1
P62847	RPS24	40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	9,022556391	1	1	1	1	133	15,413	10,78	Not Found	Not Found	High	Medium	0,013	50,81	1
P36578	RPL4	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	2,576112412	1	1	1	1	427	47,667	11,06	Not Found	Not Found	High	Medium	0,013	50,62	1
Q6UWP8	SBSN	Suprabasin OS=Homo sapiens GN=SBSN PE=1 SV=2	3,050847458	1	1	1	1	590	60,505	7,01	Not Found	Not Found	High	Medium	0,013	50,43	1
P19823	ITIH2	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2	1,585623679	1	1	1	1	946	106,397	6,86	Not Found	Not Found	High	Medium	0,013	47,99	1
P04004	VTN	Vitronectin OS=Homo sapiens GN=VTN PE=1 SV=1	3,138075314	1	1	1	1	478	54,271	5,8	Not Found	Not Found	High	Medium	0,013	46,58	1
O43795	MYO1B	Unconventional myosin-Ib OS=Homo sapiens GN=MYO1B PE=1 SV=3	1,848591549	1	1	1	1	1136	131,902	9,38	Not Found	Not Found	Medium	Medium	0,016	43,67	1
P21333	FLNA	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	0,491122025	1	1	1	1	2647	280,564	6,06	Not Found	Not Found	Medium	Medium	0,016	43,12	1
Q9BWT7	CARD10	Caspase recruitment domain-containing protein 10 OS=Homo sapiens GN=CARD10 PE=1 SV=2	1,937984496	1	1	1	1	1032	115,859	5,95	Not Found	Not Found	Medium	Medium	0,017	42,85	1
A2RUB1	MEIOC	Meiosis-specific coiled-coil domain-containing protein MEIOC OS=Homo sapiens GN=MEIOC PE=2 SV=3	1,470588235	1	1	1	1	952	107,491	7,12	Not Found	Not Found	Medium	Medium	0,021	39,82	1
Q02978	SLC25A11	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3	5,095541401	1	1	1	1	314	34,04	9,91	Not Found	Not Found	Medium	Medium	0,023	38,81	1
Q5JTC6	AMER1	APC membrane recruitment protein 1 OS=Homo sapiens GN=AMER1 PE=1 SV=2	1,674008811	1	1	1	1	1135	123,952	4,84	Not Found	Not Found	Medium	Medium	0,023	38,28	1
Q9UDY2	TJP2	Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=2	1,428571429	1	1	1	1	1190	133,876	7,4	Not Found	Not Found	Medium	Medium	0,027	37,35	1
Q9UHR4	BAIAP2L1	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Homo sapiens GN=BAIAP2L1 PE=1 SV=2	2,935420744	1	1	1	1	511	56,847	8,68	Not Found	Not Found	Medium	Medium	0,030	35,57	1
P17040	ZSCAN20	Zinc finger and SCAN domain-containing protein 20 OS=Homo sapiens GN=ZSCAN20 PE=2 SV=3	1,821668265	1	1	1	1	1043	117,467	6,43	Not Found	Not Found	Medium	Medium	0,041	34,29	1
Q5T0W9	FAM83B	Protein FAM83B OS=Homo sapiens GN=FAM83B PE=1 SV=1	2,176063304	1	1	1	1	1011	114,729	8,97	Not Found	Not Found	Medium	Medium	0,047	34,04	1
A3KN83	SBNO1	Protein strawberry notch homolog 1 OS=Homo sapiens GN=SBNO1 PE=1 SV=1	0,502512563	1	1	1	1	1393	154,216	7,88	Not Found	Not Found	Medium	Medium	0,048	33,99	1
Q5TGY3	AHDC1	AT-hook DNA-binding motif-containing protein 1 OS=Homo sapiens GN=AHDC1 PE=1 SV=1	0,748596382	1	1	1	1	1603	168,245	9,04	Not Found	Not Found	Medium	Medium	0,048	33,70	1
P42766	RPL35	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2	8,130081301	1	1	1	1	123	14,543	11,05	Not Found	Not Found	Medium	Medium	0,048	33,59	1
P84090	ERH	Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=1 SV=1	10,57692308	1	1	1	1	104	12,251	5,92	Not Found	Not Found	Medium	Medium	0,048	33,47	1

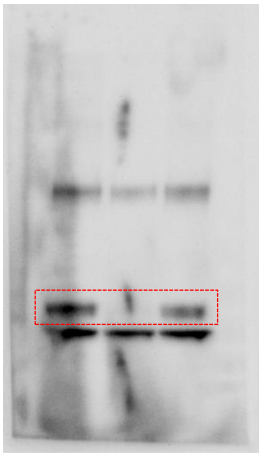
For both Supplementary Table 1 and 2:
Shown are
-proteins that were detected as "High" or "Medium"in the "E1B-55k Ab" sampe and "not found "in the "Beads only" nor "Mouse IgG"control samples.
-proteins with "Protein FDR Confidence Mascot" "High" or "Medium".

The proteins are sorted based on their "Mascot Score".

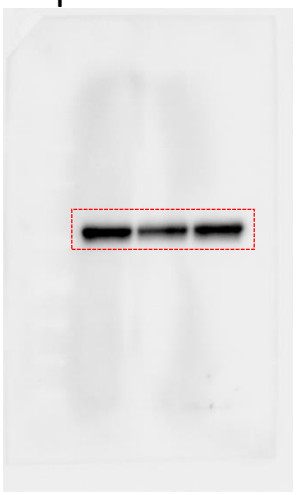
Uncropped images from Western blots

- **Blots used in Figure 4a**

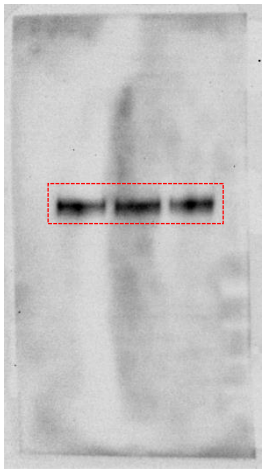
E1B-55k



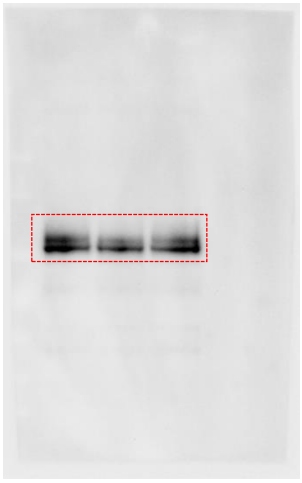
β-catenin



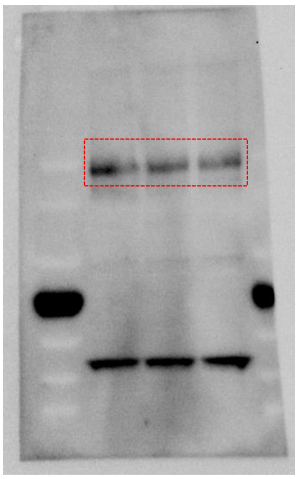
AXIN1



DVL2



TNKS



- **Blot used in Supplementary Figure S3a**

E1B-55k