

Supplementary Materials

IB: anti-Myc

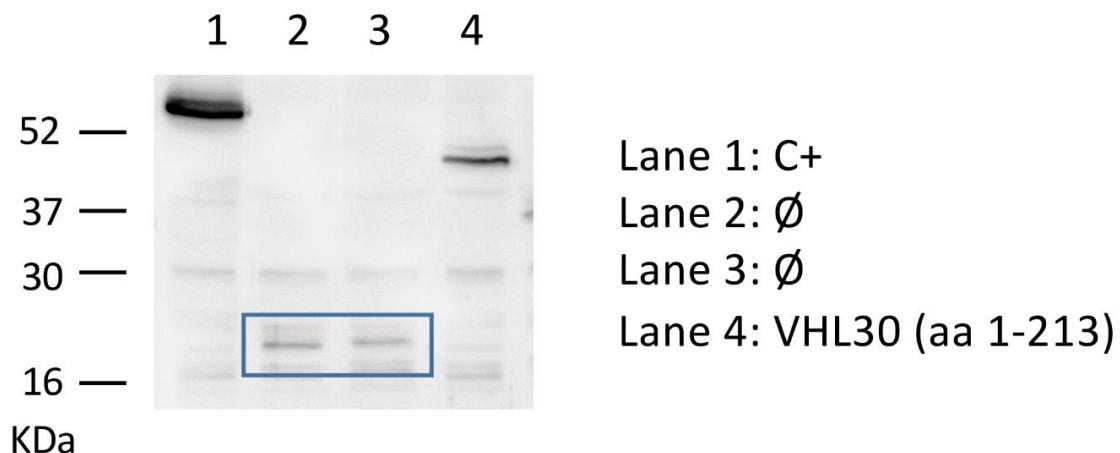


Figure S1. Western blot to confirm the expression of pVHL30 as bait in Y2H. Proteins were extracted as described in materials and methods section and visualized in Western Blot. The bait protein (i.e. pVHL30) is detected by anti-Myc (line 4). C+ and \emptyset correspond to positive (p53-Gal4BD) and negative control (Gal4-BD) respectively.

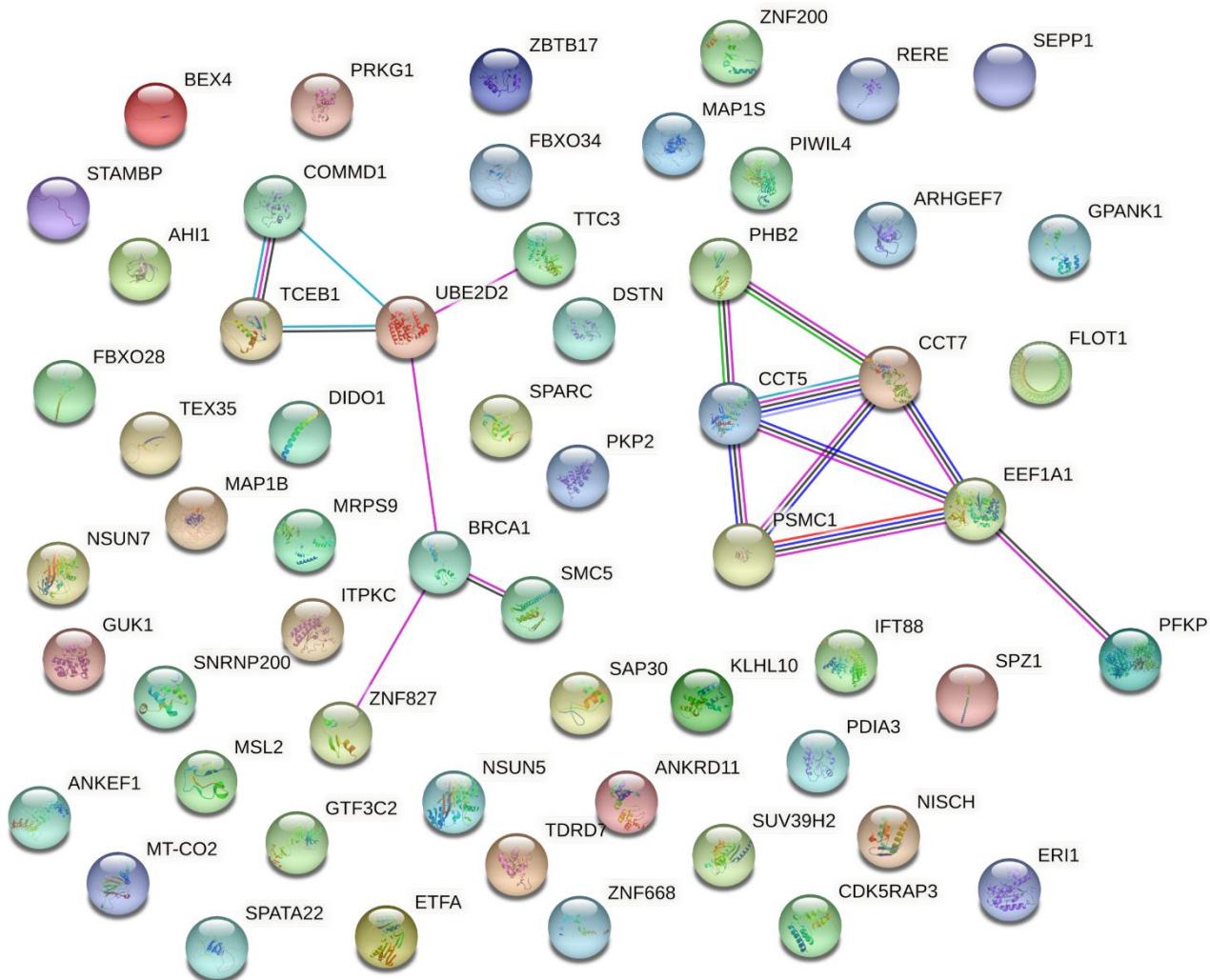


Figure S2. Single layer protein-protein interaction network generated with RING database. Proteins included in the network are presented with colored bubbles while edges are evidence of interactions reported in the literature. Edge coloring reflects different techniques, with green and blue showing in silico predictions while purple and pale blue are for experimentally validated interactions. Finally, black is used for proteins sharing similar co-expression levels.

Table S1. List of proteins interacting with pVHL30 identified testis library screening.

clone	protein name	protein size	binding fragment	function
cl 535	Joubertin	1196	978-1136	ciliogenesis
cl 338	Ankyrin repeat and EF-hand domain-containing protein 1	776	326-624	n.d.
cl 784	Ankyrin repeat and EF-hand domain-containing protein 1	776	325-624	n.d.
cl121	Ankyrin repeat domain-containing protein 11	2663	26-249	Chromatin regulator
cl 237	Ankyrin repeat domain-containing protein 11	2663	26-249	chromatin regulator
cl 491	Rho guanine nucleotide exchange factor 7	782	50-140	GEF apoptosis

cl 5	Protein BEX2	160	6-40	cell cycle regulator
cl 252	Protein BEX4	120	1-120	microtubule Dacetil.
cl 135	Protein BEX4	120	1-120	microtubule Dacetil.
cl 812	Breast cancer type 1 susceptibility protein	1863	1740-1863	E3-ub lig/DNA repair
cl 582	T-complex protein 1 subunit epsilon	541	1-230	actin/tubulin folding
cl 64	T-complex protein 1 subunit eta	543	145-368	actin/tubulin folding
cl 341	T-complex protein 1 subunit eta	543	146-474	actin/tubulin folding
cl 373	T-complex protein 1 subunit eta	543	203-536	actin/tubulin folding
cl 852	T-complex protein 1 subunit eta	543	145-472	actin/tubulin folding
cl 854	CDK5 regulatory subunit-associated protein 3	110	4-110	n.d.
cl 353	COMM domain-containing protein 1	190	1-190	protein ub regulator
cl 119	Copine-5	290	11-239	n.d.
cl 881	Cathepsin D (CTSD)	412	291-412	protease/prot degrad
cl 82	Death-inducer obliterator 1	2220	363-529	tumor suppressor
cl 95	Death-inducer obliterator 1	2220	363-529	tumor suppressor
cl 201	Death-inducer obliterator 1	2220	364-529	tumor suppressor
cl 131	Destrin	165	49-165	actin depolimerization
cl 75	Elongation factor 1-alpha 1	462	233-420	protein biosynthesis
cl 219	Elongation factor 1-alpha 1	462	295-462	protein biosynthesis
cl 175	Elongation factor 1-alpha 1	462	221-462	protein biosynthesis
cl 185	Elongation factor 1-alpha 1	462	295-462	protein biosynthesis
cl 239	Elongation factor 1-alpha 1	462	249-462	protein biosynthesis
cl 308	Elongation factor 1-alpha 1	462	297-462	protein biosynthesis
cl 332	Elongation factor 1-alpha 1	462	297-462	protein biosynthesis
cl 372	Elongation factor 1-alpha 1	462	213-462	protein biosynthesis
cl 900	Elongation factor 1-alpha 1	462	215-324	protein biosynthesis
cl 574	Elongation factor 1-alpha 1	462	165-434	protein biosynthesis
cl 138	Elongation factor 1-alpha 1	462	220-462	protein biosynthesis
cl 154	Elongation factor 1-alpha 1	462	197-434	protein biosynthesis
cl 476	Elongation factor 1-alpha 1	462	297-462	protein biosynthesis
cl 424	Elongation factor 1-alpha 1	462	231-462	protein biosynthesis
cl 324	Elongation factor 1-alpha 1	462	249-462	protein biosynthesis
cl 295	Elongation factor 1-alpha 1	462	288-462	protein biosynthesis
cl 655	Elongation factor 1-alpha 1	462	197-434	protein biosynthesis
cl 39	Elongin-C	112	1-112	protein degradation
cl 590	Elongin-C	112	1-112	protein degradation
cl 216	Elongin-C	112	1-112	protein degradation
cl 217	Elongin-C	112	1-112	protein degradation
cl 454	Elongin-C	112	1-112	protein degradation
cl 936	Elongin-C	112	1-112	protein degradation
cl 450	3'-5' exoribonuclease 1	349	35-209	histone mRNA degrad
cl 633	Electron transfer flavoprotein subunit alpha, mitochondrial	333	201-333	electron transport
cl 799	Electron transfer flavoprotein subunit alpha, mitochondrial	333	203-333	electron transport

cl 89	Electron transfer flavoprotein subunit alpha, mitochondrial	333	200-333	electron transport
cl 312	F-box only protein 28	368	1-126	ub/ prot degradation
cl 807	F-box only protein 34	711	1-53	SRP of E3-ub complex
cl 388	Flotillin-1	427	120-249	caveolae formation
cl 701	G patch domain and ankyrin repeat-containing protein 1	356	1-154	n.d.
cl 251	General transcription factor 3C polypeptide 2	911	1-290	DNA transcription
cl 348	Guanylate kinase (Fragment)	272	72-203	phosphorylation
cl 205	Guanylate kinase	197	21-197	phosphorylation
cl 313	Intraflagellar transport protein 88 homolog	833	39-282	ciliogenesis
cl 286	Inositol-trisphosphate 3-kinase	683	495-617	phosphorylation
cl 736	Kelch-like protein 10	608	472-608	ub/ prot degradation
cl 144	Microtubule-associated protein 1B	2468	2168-2468	microtub stabilization
cl 194	Microtubule-associated protein 1S	1059	778-1053	apoptosis
cl 287	Microtubule-associated protein 1S	1059	863-1059	apoptosis
cl 473	Microtubule-associated protein 1S	1059	677-932	apoptosis
cl 156	Microtubule-associated protein 1S	1059	815-1059	apoptosis
cl 630	28S ribosomal protein S9, mitochondrial	396	45-336	n.d.
cl 309	E3 ubiquitin-protein ligase MSL2	577	375-577	ub/ prot degradation
cl 102	Cytochrome c oxidase subunit 2	227	169-227	oxygen reduction
cl 235	Cytochrome c oxidase subunit 2	227	169-227	oxygen reduction
cl 561	Nischarin	1504	1386-1504	cell survival/migration
cl 236	Probable 28S rRNA (cytosine-C(5))-methyltransferase	429	291-428	methylation
cl 37	Putative methyltransferase NSUN7	718	510-696	methylation
cl 46	Putative methyltransferase NSUN7	718	510-523	methylation
cl 61	Putative methyltransferase NSUN7	718	510-718	methylation
cl 111	Putative methyltransferase NSUN7	718	510-718	methylation
cl 145	Putative methyltransferase NSUN7	718	510-701	methylation
cl 148	Putative methyltransferase NSUN7	718	510-687	methylation
cl 150	Putative methyltransferase NSUN7	718	510-718	methylation
cl 207	Putative methyltransferase NSUN7	718	510-630	methylation
cl 247	Putative methyltransferase NSUN7	718	510-718	methylation
cl 155	Putative methyltransferase NSUN7	718	510-718	methylation
cl 57	Putative methyltransferase NSUN7	718	510-718	methylation
cl 151	Putative methyltransferase NSUN7	718	510-718	methylation
cl 81	Protein disulfide-isomerase A3	505	343-500	protein folding
cl 124	Protein disulfide-isomerase A3	505	345-500	protein folding
cl 187	Protein disulfide-isomerase A3	505	345-500	protein folding
cl 198	Protein disulfide-isomerase A3	505	343-500	protein folding
cl 732	ATP-dependent 6-phosphofructokinase, platelet type	784	562-616	glycolysis
cl 381	Prohibitin-2	299	42-299	transcription inhibitor
cl 439	Prohibitin-2	299	42-290	transcription inhibitor
cl 218	Piwi-like protein 4	852	776-852	tumor enhancer
cl 815	Piwi-like protein 4	852	777-852	tumor enhancer

cl 600	Plakophilin-2	504	472-504	cell-cell adhesion
cl 104	cGMP-dependent protein kinase 1	376	320-376	phosphorylation
cl 226	cGMP-dependent protein kinase 1	376	320-376	phosphorylation
cl 261	26S proteasome regulatory subunit 4	440	1-250	protein degradation
cl 318	26S proteasome regulatory subunit 4	440	1-294	protein degradation
cl 387	26S proteasome regulatory subunit 4	440	1-180	protein degradation
cl 911	Arginine-glutamic acid dipeptide repeats protein	1566	59-134	cell survival control
cl 378	Arginine-glutamic acid dipeptide repeats protein	1566	59-134	cell survival control
cl 182	Histone deacetylase complex subunit SAP30	220	61-210	deacetylation
cl 892	Histone deacetylase complex subunit SAP30	220	77-220	deacetylation
cl 637	Histone deacetylase complex subunit SAP30	220	64-220	deacetylation
cl 475	Selenoprotein P	382	119-299	selenium transport
cl 256	Structural maintenance of chromosomes protein 5	1101	1-113	DNA repair
cl 400	Structural maintenance of chromosomes protein 5	1101	1-114	DNA repair
cl 68	U5 small nuclear ribonucleoprotein 200 kDa helicase	2136	1229-1334	RNA splicing
cl 72	SPARC	303	133-303	cell growth
cl 96	Spermatogenesis-associated protein 22	363	1-249	germ cell division
cl 100	Spermatogenesis-associated protein 22	363	27-269	germ cell division
cl 137	Spermatogenesis-associated protein 22	363	58-324	germ cell division
cl 215	Spermatogenesis-associated protein 22	363	22-189	germ cell division
cl 231	Spermatogenesis-associated protein 22	363	20-326	germ cell division
cl 830	Spermatogenesis-associated protein 22	363	22-286	germ cell division
cl 97	Spermatogenesis-associated protein 22	363	62-363	germ cell division
cl 158	Spermatogenesis-associated protein 22	363	20-356	germ cell prolif and diff
cl 915	Spermatogenesis-associated protein 22	363	20-115	germ cell division
cl 393	Spermatogenesis-associated protein 22	363	24-294	germ cell division
cl 58	Spermatogenic leucine zipper protein 1	430	300-430	germ cell prolif and diff
cl 642	STAM-binding protein	424	151-424	protein degradation
cl 523	STAM-binding protein	424	151-370	protein degradation
cl 383	Histone-lysine N-methyltransferase SUV39H2	410	293-410	chromatin regulator
cl 880	Tudor domain-containing protein 7	1098	749-913	post-transcr regulator
cl 65	Testis-expressed protein 35	233	1-170	n.d.
cl 418	Testis-expressed protein 35	233	1-196	n.d.
cl 165	E3 ubiquitin-protein ligase TTC3	2025	998-1185	ub/ prot degradation
cl 166	E3 ubiquitin-protein ligase TTC3	2025	998-1185	ub/ prot degradation
cl 249	E3 ubiquitin-protein ligase TTC3	2025	998-1247	ub/ prot degradation
cl 691	Ubiquitin-conjugating enzyme E2 D2	147	8-147	protein ubiquitination
cl 533	Ubiquitin-conjugating enzyme E2 D2	147	8-112	protein ubiquitination
cl 48	Zinc finger and BTB domain-containing protein 17	803	459-662	cell cycle regulator

cl 56	Zinc finger and BTB domain-containing protein 17	803	306-450	cell cycle regulator
cl 74	Zinc finger and BTB domain-containing protein 17	803	459-723	cell cycle regulator
cl 524	Zinc finger and BTB domain-containing protein 17	803	459-711	cell cycle regulator
cl 78	Zinc finger and BTB domain-containing protein 17	803	459-711	cell cycle regulator
cl 426	Zinc finger and BTB domain-containing protein 17	803	460-741	cell cycle regulator
cl 757	Zinc finger and BTB domain-containing protein 17	803	461-793	cell cycle regulator
cl 754	Zinc finger and BTB domain-containing protein 17	803	487-757	cell cycle regulator
cl 270	Zinc finger and BTB domain-containing protein 17	803	461-789	cell cycle regulator
cl 141	Zinc finger protein 200	395	200-359	spermatogenesis
cl 22	Zinc finger protein 668	619	319-365	transcription regulator
cl 768	Zinc finger protein 827	1081	1013-1076	transcription regulator

Table S2. Regions shared among different clones of a same protein (* one clone was excluded from the mapping). Numbering refers to canonical sequences deposited in the UniProt database.

Protein	Nº hits	Shared region
EEF1A1	17	297-324
NSUN7	12	510-523
SPATA22	10	62-115
ZBTB17	9*	487-662
CCT7	4	203-368
PDIA3	4	345-500
MAP1S	4*	863-1053
DIDO1	3	363-529
PSMC1	3	1-180
SAP30	3	77-210
ETFA	3	203-333
TTC3	3	998-1185

Table S3. Amino acid sequences of the pseudo pVHL-binding fragments corresponding to 3'- or 5'-untranslated regions.

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>ID_66H176_1C_cl36
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