Table S1. Differentially expressed proteins of *VHL*-wt (Caki-2) and *VHL*-mut (786-O) RCCs identified by database search (Mascot) and quantified by extracted peptide intensity (MS) features generated with Progenesis LC-MS. Minimum confidence scores: protein 99%, peptide 95% with a minimum of 2 peptides identified (validation by Scaffold). ANOVA was accepted at *P* < 0.05 with at least a 2-fold change in protein abundance.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Accession** | **Protein Name**a | **Molecular Weight****(kDa)** | ***P* ANOVA**  | **Max Fold Change** | ***VHL*-mutant (786-O) Average Normalized Abundance±Standard Deviation** | ***VHL*-wild type (Caki-2) Average Normalized Abundance±Standard Deviation**  | **Number of Unique Peptides** | **Sequence Coverage (%)** |
| **A) Up-regulated in VHL-mutant (786-O)** |  |  |  |  |  |  |  |
| IPI00003362 | 78 kDa glucose-regulated  Protein (*HSPA5*) | 72 | 0.04 | 3.4 | 2.71E+05 ± 1.36E+05 | 7.85E+04 ± 4.09E+04 | 13 | 22 |
| IPI00007765 | Stress-70 protein, mitochondrial (*HSPA9*) | 74  | 0.03 | 12.5 | 2.55E+04 ± 1.09E+04 | 2.04E+03 ± 1.10E+03 | 7 | 9 |
| IPI00008529 | 60S acidic ribosomal protein P2 (*RPLP2*) | 12  | 0.03 | 43.2 | 1.21E+05 ± 9.53E+04 | 2.81E+03 ± 9.21E+02 | 4 | 51 |
| IPI00011229 | Cathepsin D (*CTSD*) | 45  | 0.01 | 2.4 | 8.96E+04 ± 1.10E+04 | 3.77E+04 ± 1.98E+04 | 5 | 11 |
| IPI00013415 | 40S ribosomal protein S7 (*RPS7*) | 22  | 0.01 | 4.0 | 2.94E+04 ± 7.27E+03 | 7.28E+03 ± 3.82E+03 | 4 | 32 |
| IPI00020599 | Calreticulin (*CALR*) | 48  | 0.02 | 3.3 | 2.56E+05 ± 7.88E+04 | 7.85E+04 ± 3.76E+04 | 7 | 25 |
| IPI00024915  | Peroxiredoxin-5, mitochondrial (*PRDX5*) | 22  | 0.004 | 210.0 | 3.12E+04 ± 1.87E+04 | 1.49E+02 ± 8.87E+01 | 2 | 16 |
| IPI00025512 | Heat shock protein beta-1 (*HSPB1*) | 23  | 0.001 | 11.1 | 1.64E+06 ± 9.84E+05 | 1.47E+05 ± 6.13E+04 | 9 | 66 |
| IPI00171903  | Isoform 1 of heterogeneous nuclear ribonucleoprotein M (*HNRNPM*) | 78  | < 0.001 | 3.5 | 3.10E+05 ± 3.11E+04 | 8.75E+04 ± 1.82E+04 | 17 | 13 |
| IPI00216049  | Isoform 1 of heterogeneous nuclear ribonucleoprotein K (*HNRNPK*) | 51  | 0.03 | 6.3 | 2.51E+05 ± 1.57E+05 | 3.99E+04 ± 6.31E+03 | 13 | 23 |
| IPI00216691 | Profilin-1 (*PFN1*) | 15  | 0.005 | 11.4 | 2.09E+06 ± 1.42E+06 | 1.82E+05 ± 4.92E+04 | 9 | 56 |
| IPI00219365  | Moesin (*MSN*) | 68  | 0.002 | 4.4 | 4.29E+04 ± 5.28E+03 | 9.85E+03 ± 5.90E+03 | 18 | 25 |
| IPI00220642 | 14-3-3 protein gamma (*YWHAG*) | 28  | 0.006 | 5.2 | 1.04E+04 ± 3.70E+03 | 1.99E+03 ± 4.69E+02 | 6 | 32 |
| IPI00298547 | Protein DJ-1 (*PARK7*) | 20  | < 0.001 | 16.1 | 4.44E+04 ± 1.19E+04 | 2.75E+03 ± 7.48E+02 | 5 | 26 |
| aGene symbols are given in parentheses. |
| **Table S1** (cont.) |
| **Accession** | **Protein Name**a | **Molecular Weight****(kDa)** | ***P* ANOVA**  | **Max Fold Change** | ***VHL* mutant (786-O) Average Normalized Abundance±Standard Deviation** | ***VHL*-wild type (Caki-2) Average Normalized Abundance±Standard Deviation**  | **Number of Unique Peptides** | **Sequence Coverage (%)** |
| **A) Up-regulated in VHL-mutant (786-O)** |  |  |  |  |  |  |  |
| IPI00302927  | T-complex protein 1 subunit delta (*CCT4*) | 58  | 0.04 | 5.1 | 2.48E+04 ± 7.62E+03 | 4.88E+03 ± 1.86E+03 | 6 | 8 |
| IPI00453473 | Histone H4 (*HIST1H4C;HIST2H4B;HIST1H4A;HIST1H4L;HIST1H4J;HIST1H4E;HIST1H4D;HIST1H4I;HIST1H4F;HIST1H4B;HIST4H4;HIST2H4A;HIST1H4K;HIST1H4H*) | 11  | 0.009 | 5.8 | 4.76E+04 ± 1.27E+04 | 8.18E+03 ± 3.17E+03 | 5 | 34 |
| IPI00465028 | Triosephosphate isomerase isoform 2 (*TPI1P1*;*TPI1*) | 31  | 0.03 | 3.2 | 1.42E+06 ± 6.53E+05 | 4.46E+05 ± 1.97E+05 | 16 | 61 |
| IPI00555744  | Ribosomal protein L14 variant (*RPL14*) | 24  | 0.008 | 29.5 | 2.35E+04 ± 1.84E+04 | 7.96E+02 ± 7.94E+02 | 5 | 15 |
| **B) Down-regulated in VHL-mutant (786-O)** |  |  |  |  |  |  |  |
| IPI00009790 | 6-phosphofructokinase type C (*PFKP*) | 86  | 0.03 | 3.0 | 3.06E+04 ± 6.28E+03 | 9.29E+04 ± 2.32E+04 | 17 | 24 |
| IPI00010740 | Long isoform of proline and glutamine-rich splicing factor (*SFPQ*) | 76  | 0.002 | 5.5 | 5.02E+03 ± 1.68E+03 | 2.76E+04 ± 6.84E+03 | 6 | 10 |
| IPI00010779 | Isoform 1 of tropomyosin alpha-4 chain (*TPM4*) | 29  | 0.02 | 22.5 | 1.39E+03 ± 7.85E+02 | 3.13E+04 ± 1.74E+04 | 5 | 38 |
| IPI00010796 | Protein disulfide-isomerase (*P4HB*) | 57  | 0.04 | 10.2 | 6.27E+03 ± 1.82E+03 | 6.39E+04 ± 4.22E+04 | 13 | 19 |
| IPI00012069  | NAD(P)H dehydrogenase [quinone] 1 (*NQO1*) | 31  | 0.008 | 9.8 | 4.53E+03 ± 1.16E+03 | 4.44E+04 ± 2.14E+04 | 5 | 18 |
| IPI00012493  | 40S ribosomal protein S20 (*SNORD54;RPS20*) | 13  | 0.04 | 7.3 | 4.16E+03 ± 3.28E+03 | 3.04E+04 ± 1.93E+04 | 3 | 23 |
| aGene symbols are given in parentheses. |
| **Table S1** (cont.) |
| **Accession** | **Protein Name**a | **Molecular Weight****(kDa)** | ***P* ANOVA**  | **Max Fold Change** | ***VHL* mutant (786-O) Average Normalized Abundance±Standard Deviation** | ***VHL*-wild type (Caki-2) Average Normalized Abundance±Standard Deviation**  | **Number of Unique Peptides** | **Sequence Coverage (%)** |
| **B) Down-regulated in VHL-mutant (786-O)** |
| IPI00013808 | Alpha-actinin-4 (*ACTN4*) | 105  | 0.03 | 3.7 | 4.57E+04 ± 2.13E+04 | 1.69E+05 ± 6.72E+04 | 32 | 37 |
| IPI00018352 | Ubiquitin carboxyl-terminal hydrolase isozyme L1 (*UCHL1*) | 25  | 0.04 | 10.4 | 1.45E+03 ± 9.44E+02 | 1.51E+04 ± 7.82E+03 | 8 | 44 |
| IPI00019502 | Isoform 1 of myosin-9 (*MYH9*) | 227  | 0.02 | 3.2 | 5.19E+04 ± 2.61E+04 | 1.66E+05 ± 4.83E+04 | 75 | 36 |
| IPI00021347  | Ubiquitin-conjugating enzyme E2 L3 (*UBE2L3*) | 18  | 0.003 | 3.1 | 3.19E+02 ± 3.19E+02 | 9.90E+02 ± 3.59E+02 | 3 | 24 |
| IPI00105407 | Aldo-keto reductase family 1 member B10(*AKR1B10*) | 36  | < 0.001 | 17.1 | 1.82E+04 ± 7.02E+03 | 3.11E+05 ± 8.75E+04 | 14 | 47 |
| IPI00216008  | Glucose-6-phosphate 1-dehydrogenase (*G6PD*) | 64  | < 0.001 | 8.3 | 3.77E+03 ± 1.63E+03 | 3.14E+04 ± 1.29E+04 | 5 | 5 |
| IPI00216298  | Thioredoxin (*TXN*) | 12  | 0.03 | 2.6 | 1.49E+04 ± 5.82E+03 | 3.92E+04 ± 9.25E+03  | 5 | 40 |
| IPI00216730 | Histone H2A type 2-B (*HIST2H2AB*) | 14  | 0.01 | 229.3 | 4.68E+01 ± 4.22E+01 | 1.07E+04 ± 5.71E+03 | 8 | 55 |
| IPI00217975 | Lamin-B1 (*LMNB1*) | 66  | 0.004 | 5.8 | 3.83E+03 ± 9.39E+02 | 2.22E+04 ± 5.32E+03 | 8 | 7 |
| IPI00291483 | Aldo-keto reductase family 1 member C3 (*AKR1C3*) | 37  | 0.006 | 30.5 | 1.60E+03 ± 7.83E+02 | 4.88E+04 ± 9.55E+03 | 3 | 35 |
| IPI00465439 | Fructose-bisphosphate aldolase A (*ALDOA*) | 39  | 0.005 | 6.1 | 1.46E+05 ± 2.24E+04 | 8.81E+05 ± 3.19E+05 | 23 | 44 |
| IPI00473014  | Destrin (*DSTN*) | 19  | < 0.001 | 19.9 | 3.60E+03 ± 1.50E+03 | 7.15E+04 ± 1.64E+04 | 3 | 22 |
| IPI00479217  | Short isoform of heterogeneous nuclear ribonucleoprotein U (*HNRNPU*) | 89  | 0.04 | 2.5 | 2.62E+04 ± 1.29E+04 | 6.54E+04 ± 1.96E+04 | 8 | 9 |
| IPI00554788 | Keratin, type I cytoskeletal 18 (*KRT18*) | 48  | 0.01 | 2.6 | 6.75E+04 ± 2.37E+04 | 1.74E+05 ± 3.55E+04 | 16 | 33 |
| IPI00643920  | cDNA FLJ54957, highly similar to transketolase (*TKT*) | 69  | 0.01 | 4.0 | 6.24E+04 ± 2.50E+04 | 2.48E+05 ± 9.43E+04 | 20 | 24 |
| IPI00744692 | Transaldolase (*TALDO1*) | 38  | 0.02 | 20.8 | 6.35E+02 ± 2.00E+02 | 1.32E+04 ± 5.62E+03 | 12 | 32 |

aGene symbols are given in parentheses.