**Table S6.** Ontological categories generated from common up-regulated and down-regulated genes in PPP tolerant Line2-T500 and Line3-T200 cells (by DAVID, from gene list U).

| ID | Name of GO category | No. of genes | p-value |
|---|---|---|---|
| ***UP-REGULATED GENES*** | | | |
| ***Biological processes*** | | | |
| GO:0008219 | cell death | 18 | 0.016 |
| ***Cellular components*** | | | |
| GO:0044424 | intracellular part | 134 | 0.005 |
| GO:0005622 | intracellular | 138 | 0.020 |
| GO:0005737 | cytoplasm | 88 | 0.021 |
| GO:0043229 | intracellular organelle | 110 | 0.048 |
| GO:0044431 | Golgi apparatus part | 11 | 0.011 |
| GO:0000139 | Golgi membrane | 9 | 0.038 |
| ***KEGG pathway*** | | | |
| hsa04510: | focal adhesion | 8 | 0.028 |
| ***SMART*** | | | |
| SM00165 | UBA | 4 | 0.006 |
| ***SP COMMENT*** | | | |
| similarity: | contains 1 UBA domain. | 4 | 0.003 |
| cofactor | magnesium | 7 | 0.039 |
| ***INTERPRO*** | | | |
| IPR000449 | Ubiquitin-associated/translation elongation factor EF1B, N-terminal | 4 | 0.013 |
| IPR015880 | Zinc finger, C2H2-like | 10 | 0.032 |
| IPR011992 | EF-Hand type | 8 | 0.018 |
| ***SP PIR KEYWORDS*** | | | |
| Keyword | apoptosis | 9 | 0.020 |
| ***UP SEQ FEATURE*** | | | |
| domain | UBA | 4 | 0.004 |
| ***DOWN-REGULATED GENES*** | | | |
| ***Biological processes*** | | | |
| GO:0008219 | cell death | 19 | 0.002 |
| GO:0048522 | positive regulation of cellular process | 21 | 0.002 |
| GO:0030154 | cell differentiation | 32 | 0.002 |
| GO:0043067 | regulation of programmed cell death | 14 | 0.003 |
| GO:0048518 | positive regulation of metabolic process | 22 | 0.004 |
| GO:0045595 | regulation of cell differentiation | 6 | 0.023 |
| GO:0051094 | positive regulation of developmental process | 4 | 0.036 |
| GO:0009611 | response to wounding | 11 | 0.010 |
| ***Molecular functions*** | | | |
| GO:0051213 | dioxygenase activity | 4 | 0.020 |
| GO:0016701 | oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | 4 | 0.021 |
| ***Cellular components*** | | | |
| GO:0005622 | intracellular | 119 | 0.042 |
| ***KEGG Pathway*** | | | |
| hsa00280 | valine, leucine and isoleucine degradation | 4 | 0.025 |
| ***INTERPRO*** | | | |
| IPR000742 | EGF-like, type 3 | 9 | 0.001 |

| | | | |
|---|---|---|---|
| IPR006210 | EGF | 8 | 0.007 |
| IPR013032 | EGF-like region | 9 | 0.015 |
| IPR001452 | Src homology-3 | 8 | 0.007 |
| IPR001715 | Calponin-like actin-binding | 4 | 0.031 |
| ***SP PIR KEYWORDS*** | | | |
| Key word | egf-like domain | 9 | 0.002 |
| Key word | apoptosis | 9 | 0.009 |
| Key word | SH3 domain | 7 | 0.017 |
| Key word | tyrosine-specific phosphatase | 3 | 0.036 |
| Key word | metalloprotease | 5 | 0.049 |
| Key word | DNA binding | 8 | 0.036 |
| ***UP SEQ FEATURE*** | | | |
| domain | EGF-like | 5 | 0.006 |
| domain | EGF-like 3 | 4 | 0.023 |
| active site | Phosphocysteine intermediate | 4 | 0.044 |
| metal ion-binding site | Zinc (catalytic) | 5 | 0.031 |
| **SP COMMENT** | | | |
| similarity | Contains 1 EGF-like domain | 5 | 0.007 |
| similarity | Contains 1 SH3 domain | 6 | 0.042 |
| catalytic activity | Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate | 4 | 0.050 |
| subcellular location | Membrane; Single-pass type I membrane protein | 11 | 0.017 |
| ***SMART*** | | | |
| SM00181 | EGF | 8 | 0.009 |
| SM00326 | SH3 | 8 | 0.009 |
| SM00033 | CH | 4 | 0.036 |