Supplementary file 6 Table: Mutprd results for the nsSNPs in TCGIR1 gene

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| --- | --- | --- | --- | --- | --- | --- | --- |
| Genes | Mutation |  | Score |  |  | Altrations |   |
| VPP3\_HUMAN | R56W |  | 0.591 |  |  | Altered Coiled coil (Pr = 0.87 | P = 1.5e-03); Loss of Helix (Pr = 0.28 | P = 0.02) |  ELME000012|ELME000102|ELME000108 |
| VPP3\_HUMAN | T570M |  | 0.527 |  |  | Altered Transmembrane protein (Pr = 0.27 | P = 5.2e-04) |  ELME000064|ELME000220|ELME000231|ELME000326|ELME000333|ELME000336|PS00006 |
| VPP3\_HUMAN | P572L |  | 0.89 |  |  | Altered Transmembrane protein (Pr = 0.24 | P = 1.5e-03) |  ELME000045|ELME000064|ELME000147|ELME000220|ELME000231|ELME000333|ELME000335|ELME000 |
| VPP3\_HUMAN | G405R |  | 0.938 |  |  | Gain of Helix (Pr = 0.27 | P = 0.04); Altered Metal binding (Pr = 0.22 | P = 0.01); Loss of Catalytic site at D406 (Pr = 0.20 | P = 0.01); Gain of Allosteric site at H409 (Pr = 0.19 | P = 0.04); Altered Transmembrane protein (Pr = 0.01 | P = 9.5e-03) |  None |
| VPP3\_HUMAN | R444L |  | 0.954 |  |  | Loss of Allosteric site at R444 (Pr = 0.43 | P = 3.8e-04); Altered Ordered interface (Pr = 0.36 | P = 2.1e-03); Altered Transmembrane protein (Pr = 0.20 | P = 5.2e-03) |  ELME000012|ELME000045|ELME000106|ELME000146|ELME000149|ELME000231|ELME000233 |
| VPP3\_HUMAN | M403I |  | 0.924 |  |  | Altered Metal binding (Pr = 0.20 | P = 0.02); Gain of Catalytic site at D406 (Pr = 0.18 | P = 0.02); Altered Transmembrane protein (Pr = 0.01 | P = 0.01) |  None |
| VPP3\_HUMAN | A417T |  | 0.841 |  |  | Altered Transmembrane protein (Pr = 0.01 | P = 0.01) |  ELME000336 |
| VPP3\_HUMAN | A778V |  | 0.584 |  |  | Altered Transmembrane protein (Pr = 0.15 | P = 0.01) |  None |
| VPP3\_HUMAN | S474W |  | 0.891 |  |  | Altered Ordered interface (Pr = 0.24 | P = 0.04); Altered Transmembrane protein (Pr = 0.19 | P = 7.3e-03) |  ELME000063|ELME000085|ELME000328 |
| VPP3\_HUMAN | G458S |  | 0.929 |  |  | Altered Ordered interface (Pr = 0.31 | P = 0.01); Gain of Allosteric site at F453 (Pr = 0.22 | P = 0.03); Altered Transmembrane protein (Pr = 0.18 | P = 8.1e-03); Gain of Catalytic site at E463 (Pr = 0.15 | P = 0.02); Altered Metal binding (Pr = 0.14 | P = 0.04) |  ELME000052|ELME000053|ELME000063|ELME000120|ELME000182 |
| VPP3\_HUMAN | R50C |  | 0.626 |  |  | Altered Coiled coil (Pr = 0.44 | P = 8.8e-03); Loss of Pyrrolidone carboxylic acid at Q48 (Pr = 0.04 | P = 0.04) |  ELME000012|ELME000102|ELME000108|ELME000233|ELME000300|ELME000328 |
| VPP3\_HUMAN | E321K |  | 0.795 |  |  | Loss of Catalytic site at E321 (Pr = 0.25 | P = 4.7e-03) |  None |
| VPP3\_HUMAN | R363C |  | 0.578 |  |  | Loss of Relative solvent accessibility (Pr = 0.30 | P = 8.8e-03); Altered Disordered interface (Pr = 0.28 | P = 0.03); Altered Transmembrane protein (Pr = 0.22 | P = 3.2e-03); Altered DNA binding (Pr = 0.20 | P = 0.02) |  ELME000053|ELME000336 |
| VPP3\_HUMAN | A732T |  | 0.543 |  |  | Altered Ordered interface (Pr = 0.25 | P = 0.02); Loss of GPI-anchor amidation at N730 (Pr = 0.04 | P = 7.1e-03); Gain of N-linked glycosylation at N730 (Pr = 0.01 | P = 0.04) |  ELME000052|ELME000053|ELME000063|ELME000070|PS00001 |
| VPP3\_HUMAN | F51S |  | 0.892 |  |  | Altered Coiled coil (Pr = 0.36 | P = 0.01); Altered Stability (Pr = 0.35 | P = 4.0e-03); Loss of Pyrrolidone carboxylic acid at Q48 (Pr = 0.04 | P = 0.05) |  ELME000012|ELME000062|ELME000102|ELME000108|ELME000233|ELME000300|ELME000328|ELME000 |
| VPP3\_HUMAN | F610S |  | 0.938 |  |  | Altered Transmembrane protein (Pr = 0.40 | P = 0.0e+00) |  ELME000328|ELME000336 |
| VPP3\_HUMAN | R57H |  | 0.582 |  |  | Altered Coiled coil (Pr = 0.51 | P = 6.9e-03); Loss of Helix (Pr = 0.31 | P = 4.8e-03) |  ELME000012|ELME000102|ELME000108 |
| VPP3\_HUMAN | N730S |  | 0.617 |  |  | Altered Ordered interface (Pr = 0.25 | P = 0.02); Loss of GPI-anchor amidation at N730 (Pr = 0.04 | P = 7.0e-03) |  ELME000053|ELME000063|PS00008 |
| VPP3\_HUMAN | R56P |  | 0.848 |  |  | Altered Coiled coil (Pr = 0.85 | P = 1.7e-03); Loss of Helix (Pr = 0.36 | P = 3.5e-04) |  ELME000012|ELME000102|ELME000108|ELME000155 |
| VPP3\_HUMAN | M546V |  | 0.929 |  |  | Gain of Strand (Pr = 0.26 | P = 0.04); Altered Metal binding (Pr = 0.04 | P = 0.05); Altered Transmembrane protein (Pr = 0.01 | P = 0.01) |  None |
| VPP3\_HUMAN | R628W |  | 0.515 |  |  | Altered Transmembrane protein (Pr = 0.29 | P = 1.9e-04); Loss of Helix (Pr = 0.27 | P = 0.04); Gain of Strand (Pr = 0.26 | P = 0.04); Loss of Pyrrolidone carboxylic acid at Q629 (Pr = 0.08 | P = 0.02) |  ELME000117|ELME000163 |
| VPP3\_HUMAN | D517N |  | 0.891 |  |  | Loss of Catalytic site at D517 (Pr = 0.29 | P = 2.4e-03); Altered Metal binding (Pr = 0.28 | P = 5.5e-03); Altered Transmembrane protein (Pr = 0.28 | P = 4.0e-04); Altered Ordered interface (Pr = 0.28 | P = 0.03); Altered Disordered interface (Pr = 0.28 | P = 0.03); Loss of Allosteric site at W520 (Pr = 0.25 | P = 0.02) |  None |
| VPP3\_HUMAN | M783I |  | 0.654 |  |  | Altered Ordered interface (Pr = 0.23 | P = 0.05); Altered Transmembrane protein (Pr = 0.04 | P = 5.4e-04) |  ELME000041|ELME000052 |
| VPP3\_HUMAN | Y626S |  | 0.761 |  |  | Gain of Intrinsic disorder (Pr = 0.43 | P = 5.2e-03); Loss of Strand (Pr = 0.27 | P = 0.02); Altered Transmembrane protein (Pr = 0.26 | P = 9.5e-04); Altered Ordered interface (Pr = 0.24 | P = 0.05); Loss of Pyrrolidone carboxylic acid at Q629 (Pr = 0.08 | P = 0.02); Gain of GPI-anchor amidation at N622 (Pr = 0.02 | P = 0.02) |  ELME000106|ELME000136|ELME000159|ELME000163|PS00005 |
| VPP3\_HUMAN | G379S |  | 0.863 |  |  | Altered Ordered interface (Pr = 0.31 | P = 0.01); Gain of Relative solvent accessibility (Pr = 0.31 | P = 6.2e-03); Gain of Allosteric site at Y383 (Pr = 0.25 | P = 0.01); Altered Metal binding (Pr = 0.21 | P = 0.03); Altered DNA binding (Pr = 0.21 | P = 0.02); Gain of Catalytic site at Y383 (Pr = 0.19 | P = 0.01); Altered Transmembrane protein (Pr = 0.17 | P = 9.7e-03) |  ELME000293 |