

Supplementary Information

TraPS-Varl: Identifying genetic variants altering phosphotyrosine based signalling motifs

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Scatter plots depicting genetic mutation data mapped to the domains of membrane proteins

Scatter plots for genetic mutations mapped to the coding regions of human membrane proteins. The chromosome position loci is plotted on the abscissa and normalized domain lengths along the ordinate axes. For each domains namely Signal, Extracellular, Transmembrane and Cytoplasm separate scatter plots are depicted. Each dots represents a genetic variant recorded in vcf files with colour coding namely, frameshift mutations (red), and missense mutations (blue) and stop created mutations (green). Genotyping datasets obtained from various sources namely dbSNP (Supplementary Fig. S4), Ensembl (Supplementary Fig. S5), NHLBI Exome Sequencing Project (Supplementary Fig. S6), Exome Aggregation Consortium, ExAC r0.3 (Supplementary Fig. S7), Ensembl 1000 genome phase 3 (Supplementary Fig. S8), Human HAPMAP (Supplementary Fig. S9), Cancer Cell Line Encyclopedia (Supplementary Fig. S10), Sanger COSMIC (Supplementary Fig. S11), the TCGA (Supplementary Fig. S12), and the Scripps Welllderly Project (Supplementary Fig. S13).

[Supplementary Fig. S4](#)

[Supplementary Fig. S5](#)

[Supplementary Fig. S6](#)

[Supplementary Fig. S7](#)

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[Supplementary Fig. S10](#)

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