

TableS9_Reclassified_BRCA_varia

Table S9. Reclassified *BRCA* variants based on lack of phenotype in homozygotes

Column titled "SGP_score" includes number of screenings for that variant from gene panels and exomes, "SGP_C" includes number of occurrences of the variant, "SGP_C_hom" includes occurrences as hom, column titled "SGP_Freq" and "SGP_Freq_hom" include frequency for all and homozygous ones, "SGP_AF_Sitc" includes computation of allele frequency using formula given in the paper, column titled "SFT", "PolyPhen", "MutationTaster", "MetaSVF", and "cadd" provide pathogenicity predictions using respective tools. Columns titled "AngGen" and "AngGenL" include average quality scores for Ion and Illumina, and column titled "AngDepth" and "AngDepthL" include average depth for Ion and Illumina respectively.

[illegible]