**Supplementary Table S8. Novel variants in candidate suppressors of *Alu*-mediated recombination in high risk Ashkenazi Jewish breast cancer families.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Gene*** | ***Heterozygous Mutation*** | ***# of families with mutation*** | ***Frequency in controls*** |  ***SIFT del.a align.b*** |  ***PolyPhen Score  c prediction d*** | ***1000 Genomes*** | ***dbSNP*** | ***Secondary Structuree Prediction Confidence*** |
| PIF1f | L319P | 3 | 0 / 184 h  0 / 184 i | 0.00 | 0.99 | 2.139 | probably damaging | Not present | Not present | Helix | 9 |
| FANCMg | H1703R | 2 | 3 / 93 h | 0.83 | 0.13 | 1.888 | possibly damaging | Not present | Not present | Coil | 4 |
|  | I1742V | 3 | 8 / 94 h  8 / 196 i | 1.00 | 0.15 | 0.088 | benign | Not present | Not present | Coil | 5 |

a SIFT prediction probability of deleterious allele (<0.05 is deleterious)

b SIFT alignment score (1.00 is highest)

c PolyPhen Position-Specific Independent Counts (PSIC) profile score difference (large values may indicate that the studied substitution is rarely or never observed in the protein family)

d PolyPhen prediction

e Predicted secondary structure using PSIPRED (confidence level 0 = low; 9 = high)

f PIF1: gi for SIFT prediction is 82546872; protein identifier for PolyPhen prediction is Q330H5

g FANCM: gi for SIFT prediction is 78099254; protein identifier for PolyPhen prediction is Q8IYD8

h Ashkenazi Jewish control group

i Caucasian control group