

Table S4. Association between frequency of aUPD and mutation status of *TP53*, *BRCA1*, *BRCA2*, homolog recombination (HR) and double-strand break (DSB) genes and aUPD regions at 17q (A-H), 22q (A-D), *TP53*, *BRCA1* and *BRCA2*.

Comparison	<i>p</i>	<i>q</i>
Somatic mutation at <i>TP53</i> vs no mutation*	0.004	0.008
Germline mutation at <i>BRCA1</i> vs no mutation	0.052	0.069
Germline mutation at <i>BRCA2</i> vs no mutation	0.101	0.127
Somatic mutation at <i>BRCA1</i> vs no mutation	0.871	0.871
Somatic mutation at <i>BRCA2</i> vs no mutation	0.290	0.331
Mutation at <i>BRCA1</i> (somatic & germline) vs no mutation	0.107	0.129
Mutation at <i>BRCA2</i> (somatic & germline) vs no mutation	0.046	0.069
Somatic mutation at HR and DSB genes vs no mutation	0.825	0.860
aUPD at <i>TP53</i> vs no aUPD	2.04 x 10 ⁻⁶	4.89 x 10⁻⁵
aUPD at <i>BRCA1</i> vs no aUPD	6.54 x 10 ⁻⁵	0.0003
aUPD at <i>BRCA2</i> vs no aUPD	0.021	0.0383
aUPD at 17qA vs no aUPD	8.84 x 10 ⁻⁵	0.0004
aUPD at 17qB vs no aUPD	1.76 x 10 ⁻⁵	0.0002
aUPD at 17qC vs no aUPD	2.27 x 10 ⁻⁵	0.0002
aUPD at 17qD vs no aUPD	0.0002	0.0007
aUPD at 17qE vs no aUPD	0.0005	0.0012
aUPD at 17qF vs no aUPD	0.0003	0.0008
aUPD at 17qG vs no aUPD	5.90 x 10 ⁻⁵	0.0003
aUPD at 17qH vs no aUPD	0.0003	0.0009
aUPD at 22qA vs no aUPD	0.0494	0.0688
aUPD at 22qB vs no aUPD	0.0021	0.0046
aUPD at 22qC vs no aUPD	0.0430	0.0688
aUPD at 22qD vs no aUPD	0.0239	0.0410

*Kruskal-Wallis test was performed to test association between frequency of aUPD and *TP53* mutation. The remaining comparisons were performed by using Wilcoxon-rank sum test. *q*, Benjamini-Hochberg's FDR. *q* < 0.05 was used to select features.