| Gene | 95%CI | Cox model Wald test P value | Log rank test P value | FDR log rank test P value |
|---|---|---|---|---|
| **PIK3CA** | 2.53 (1.2~5.34) | 0.015 | 0.012 | 0.041 |
| **AKT3** | 3.83 (1.67~8.8) | 0.002 | 0.001 | 0.006 |
| **DDR2** | 3.3 (1.41~7.72) | 0.006 | 0.004 | 0.015 |
| **ESR1** | 3.78 (1.69~8.45) | 0.001 | 0.001 | 0.005 |
| **ATM** | 5.12 (2.2~11.94) | 0.0002 | 0.00003 | 0.001 |
| **AURKA** | 5.2 (2.06~13.13) | 0.0005 | 0.0001 | 0.002 |
| **MUC16** | 3.07 (1.22~7.7) | 0.017 | 0.012 | 0.041 |
| **BRCA2** | 4.25 (1.51~11.93) | 0.006 | 0.003 | 0.013 |
| **CCND1** | 4.13 (1.63~10.45) | 0.003 | 0.001 | 0.009 |
| **CCNE2** | 2.83 (1.06~7.58) | 0.038 | 0.031 | 0.084 |
| **DSP** | 5.39 (1.85~15.74) | 0.002 | 0.001 | 0.005 |
| **MYC** | 2.94 (1.01~8.59) | 0.049 | 0.040 | 0.105 |
| **PLCG1** | 12.9 (4.05~41.04) | 0.00001 | 0.0000001 | 0.000003 |
| **RB1** | 3.2 (1.04~9.85) | 0.042 | 0.031 | 0.084 |
| **RUNX1T1** | 4.45 (1.6~12.35) | 0.004 | 0.002 | 0.009 |
| **USH2A** | 4.51 (1.61~12.65) | 0.004 | 0.002 | 0.009 |
| **ZFHX3** | 4.27 (1.37~13.33) | 0.013 | 0.008 | 0.032 |

**Supplementary Table 3. Specific gene alterations are associated with shorter PFS.** Gene alterations (including SNVs and CNVs) were analyzed across 50 baseline samples using the PredicineWES™ assay. The presence of a genomic alteration in 17 genes was significantly associated with shorter PFS. Hazard ratios (alteration vs. no alteration) accompanied with 95% confidence intervals and Wald test P values were estimated from univariate Cox proportional hazards regression. Kaplan-Meier analysis was performed and P values were calculated using the log rank test. Raw P values were corrected for multiplicities using the post-hoc Benjamini-Hochberg procedure across all variants.