**Supplementary Table 1.** **PTEN mut and Wild type with Epirubicin IC50 Scatter plots in breast invasive carcinoma.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | PTEN mut | Wild type | MWW p value | Signif |
| Number of cell lines | 8 of 8 | 36 of 36 |  |  |
| Median | 0.36046 | 1.2345 |  |  |
| Geometric mean (red line) | 0.27432 | 1.3579 |  |  |
| BRCA | 8 | 36 | 0.0036612 | \*\* |

Screening concentration: 0.0039063 (lower brown line) - 1.0000 (upper brown line)

**Supplementary Table 2. HSF software impact prediction.**

|  |  |
| --- | --- |
| Type | Interpretation |
| 🞉Broken WT Acceptor Site | Alteration of the WT Acceptor site, most probably affecting splicing |
| Algorithm/Matix | position | sequences | variation |
| MaxEnt Acceptor site | chr10:87932993 | -REF: AGGTTATCTTTTTACCACAGTTG-ALT: AGGTTATCTTTTTACCACGGTTG | 5.35>-2.6 =>-148.6% |
| HSF Acceptor site (matrix AG) | chr10:87933001 | -REF: TTTTTACCACAGTT-ALT: TTTTTACCACGGTT | 89.48>61.61=>-31.15 |

**Supplementary Table 3.  Splice site predictions for 2 sequences with donor score cutoff 0.40, acceptor score cutoff 0.40 (exon/intron boundary shown in larger font).**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Start** | **End** | **Score** |  **Exon--Intron** |
| Donor site for wild seq | 310 | 324 | 0.56 | TGGGGAAGTAAGGAC |
| Donor site for wild seq | 331 | 345 | 1.00 | CAAAAAGGTAAGTTA |
| Acceptor site for wild seq | 78 | 118 | 0.83 | GAGGTTATCTTTTTACCACAGTTGCACAATATCCTTTTGAA |
| Donor site for mutation seq  | 310 | 324 | 0.56 | TGGGGAAGTAAGGAC |
| Donor site for mutation seq | 331 | 345 | 1.00 | CAAAAAGGTAAGTTA |
| Acceptor site for mutation seq | 60 | 100 | 0.41 | GTTTTTTTTTCTTATTCTGAGGTTATCTTTTTACCACGGTT |