|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Position | Mutation | Total Well Coverage | VAWF (%) | % Reads supporting the variant |
| Blood gDNA | PT2R gDNA |
| chr1:43050977 | C>T | 45 | 33.33% | 0.03 | 0.22 |
| chr1:84044398 | T>C | 14 | 78.57% | 0.02 | 0.85 |
| chr1:168274409 | C>G | 15 | 40.00% | 0.33 | 0.49 |
| chr2:33010682 | A>G | 36 | 58.33% | 0.00 | 0.77 |
| chr2:123789390 | C>T | 28 | 46.43% | 0.00 | 0.27 |
| chr3:121522102 | C>G | 46 | 43.47% | 0.19 | 0.30 |
| chr3:129524269 | G>A | 20 | 45.00% | 0.00 | 0.31 |
| chr4:76733361 | C>T | 11 | 27.27% | 0.03 | 0.03 |
| chr4:167932516 | T>C | 33 | 39.40% | 0.02 | 0.09 |
| chr6:73146508 | C>G | 33 | 45.45% | 0.12 | 0.12 |
| chr15:59093127 | G>A | 18 | 61.00% | 0.00 | 0.85 |
| chr17:66520311 | C>T | 18 | 38.89% | 0.06 | 0.46 |
| chr17:66521158 | C>T | 22 | 31.82% | 0.01 | 0.09 |
| chr17:66523728 | C>T | 33 | 39.39% | 0.02 | 0.35 |

**Figure 2-source data 2. Targeted sequencing of some of the clone-specific variants identified in run D1111.** Amplicon sequencing of the target sites was performed on the MiSeq platform. 3 out of the 14 targets appeared to have a high noise levels in the blood sample (highlighted in orange) and were therefore deemed inconclusive. Of the remaining 11 mutations only 1 did not seem to have any evidence in the bulk DNA sample of the PT2R tumor (highlighted in blue). VAWF: Variant Allele Well Fraction.