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| **MALDI-TOF MASS SPECTROMETRY PRIMERS TABLE** |

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| GENE | MUTATION | PRIMERS | AMPLICON (bp) |
| BRCA1 | C.1499insA | Fw\_ACGTTGGATGAAGAGTTCACTCCAAATCAG | 98 |
| Rev\_ACGTTGGATGGGCTTGCCTTCTTCCGATAG |
| Seq\_AGAGAGTAATATTGAAGACAAAATA |
| c.309 T>C | Fw\_ACGTTGGATGAGAAGAAAGGGCCTTCACAG | 121 |
| Rev\_ACGTTGGATGTTTCCTACTGTGGTTGCTTC |
| Seq\_CCTTCACAGTGTCCTTTA |
| c.5382insC | Fw\_ACGTTGGATGTTTGTCAACTTGAGGGAGGG | 95 |
| Rev\_ACGTTGGATGAAACCACCAAGGTCCAAAGC |
| Seq\_TACCTTTCTGTCCTGGG |
| c.1207delA | Fw\_ACGTTGGATGATCTGAATGCTGATCCCCTG | 115 |
| Rev\_ACGTTGGATGCCAAGGAACATCTTCAGTATC |
| Seq\_ACTGCCATGCTCAGAGA |
| c.2157\_2160delAGAA | Fw\_ACGTTGGATGTCTTCTCTTGGAAGGCTAGG | 94 |
| Rev\_ACGTTGGATGCCTGGTTCTTTTACTAAGTG |
| Seq\_TTCAAATACCAGTGAACTTAA |
| c.190 T>C | Fw\_ACGTTGGATGAGGCTCCTTTTGGTTATAC | 86 |
| Rev\_ACGTTGGATGTCTCAACCAGAAGAAAGGGC |
| Seq\_CCTTCACAGTGTCCTTTA |
| BRCA2 | c.3109 C>T | Fw\_ACGTTGGATGCAACACAAGCTAAACTAGTA | 112 |
| Rev\_ACGTTGGATGGGAAATCAAGCTCTCTGAAC |
| Seq\_CAAGCTAAACTAGTAGGATATT |
| c.771\_775delTCAAA | Fw\_ACGTTGGATGTTATCGCTTCTGTGACAGAC | 87 |
| Rev\_ACGTTGGATGGAGGACTTACCATGACTTGC |
| Seq\_CAGACAGTGAAAACACAAA |

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| **TAQMAN SNP GENOTYPING ASSAY** |
| **MUTATION** | **PRIMERS** | **Tm (°C)** | **CG****(%)** | **Length (bp)** | **FluorescentDye** |
| *BRCA2* | Fw\_GATAGATTTATCGCTTCTGTGACAGACA | 60 | 39 | 28 |  |
| c.771\_775delTCAAA | Rev\_ACCTGTAGTTCAACTAAACAGAGGACTT | 57,4 | 39 | 28 |  |
|  | Wild-type allele AAACACAAA**TCAAA**GAGAAG | 67 | 30 | 20 | FAM |
|   | Mutated allele TGAAAACACAAAGAGAAG | 66 | 33 | 18 | VIC |

**Supplementary Table 1**. Primers used for the matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) and SNP Genotyping assays.