**S4 Table: Variants identified in known CRC predisposing genes.a**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | Gene | Chr | Start | End | Ref | Var | PhyloP | Refseq. Accession | Protein effect | dbSNP | EVS MAF | Gene type |
| P022 | *MSH2* | 2 | 47635601 | 47635603 | TCT | - | N/A | NM\_000251 | p.D91del | - | - | CRC |
| P025 | *MSH6* | 2 | 48033981 | 48033981 | - | TTGA | N/A | NM\_000179 | p.T1355Tfs\* | - | - | CRC |
| 48032098 | 48032098 | A | T | 4.788 | NM\_000179 | p.E1163V | rs63750252 | - | CRC |
| P045 | *MSH6* | 2 | 48030685 | 48030685 | C | T | 4.398 | NM\_000179 | p.T1100M | rs63750442 | - | CRC |
| P017 | *PMS2* | 7 | 6043689 | 6043689 | T | G | 4.769 | NM\_000535 | p.D55A | - | - | CRC |

Abbreviations: Chr, chromosome; Ref, reference allele; Var, variant allele; EVS, exome variant server; MAF, minor allele frequency.

aAll variants were validated with Sanger sequencing.