**Supplementary Table S1**: List of PCR- and sequencing primer for bisulfite pyrosequencing

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | Chromosomal localizationa (bp) | Amplicon size (bp) | Forward primer | Reverse primer | Sequencing primer | No. of CpG sites | Reference |
| *BRCA1* | Chr17: 43,125,274-43,125,506 | 232 | ATTTAGAGTAGAGGGTGAAGG | \*TCTATCCCTCCCATCCTCTAATT | TGGGTGGTTAATTTAGAGT | 2 | [75] |
| *CDKN2A* | Chr9: 21,974,960-21,975,129 | 169 | GGTTGTTTTYGGTTGGTGTTTT | \*ACCCTATCCCTCAAATCCTCTAAAA | TTTTTGTTTGGAAAGAT | 2 | [76] |
| *TP53* | Chr17: 7,674,136 -7,674,298 | 162 | \*TTTTTTAGGTTGGTTTTGATTGTA | AAAACACAACAAACCAATATACA | TAATAATAAAAATAAACCTC | 2 | Designed for this study (Exon 6) |
| *APC* (part a) | Chr5: 112,737,67-112,737,871 | 193 | \*GGTTAGGGTTAGGTAGGTTGT | ACTACACCACTACAACCACATATC | CCACACCCAACCAA | 7 | Modified after [77] |
| *APC* (part b*)* | Chr5: 112,737,67-112,737,779 | 102 | GGGTTAGGGTTAGGTAGGT | TCCAACCAATTACACAACTACTTCTCTCT\* | AGGGTTAGGTAGGTT | 6 | Modified after [77]. |
| *RAD9A* | Chr11: 67,392,508-67,392,610 | 102 | GGTTTTTATGGGGAAAGGAGG | BioCCACAAACCCAACCCTCTAAC | TTTTATGGGGAAAGGA | 3 | Modified after [38] |
| *EFNA5* | Chr5: 107,670,85-107,670,957 | 104 | GAGGGTTTAGGAGGAAAAAGGAATTA | \*CCCCCCAAACACAACTTAAC | AATTATAAGATGGAGAGAAG | 5 | [33] |
| *FBN1* | Chr15: 48,417,049-48,417,285 | 236 | GTAGTAGGGTAGAAATTTATAGTTAGGTTT | \*CCACTTTTATCCACCTATTTTCTAAT | ATTATAGTGTTTTTTAAGAG | 1 | [78] |

a according to Ensemble NCBI human assembly GRCh37 (Ensembl release 92).

\* biotinylated

**Supplementary Table S2.** Primers for deep bisulfite sequencing.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene** | **Primer** | **Sequence (5′ to 3′)** | **CpG**  **No.** | **Chromosomal**  **localization (bp)** | **Amplicon**  **length** |
| *APC* | Forward | ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGTTAGGGTTAGGTAGGTTGT | 16 | 5:112737678-112737871 | 193bp |
| Reverse | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACTACACCACTACAACCACATATC |
| *CDKN2A* | Forward | ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGTTGTTTT**Y**GGTTGGTGTTTT | 10 | 9:21974960-21975129 | 169bp |
| Reverse | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTACCCTATCCCTCAAATCCTCTAAAA |
| *RAD9A* | Forward | ACACTCTTTCCCTACACGACGCTCTTCCGATCTGGTTTTTATGGGGAAAGGAGG | 3 | 11:67392508-67392610 | 102bp |
| Reverse | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCACAAACCCAACCCTCTAAC |
| *TP53* | Forward | ACACTCTTTCCCTACACGACGCTCTTCCGATCTTTTTTTAGGTTGGTTTTGATTGTA | 2 | 17:7674136-7674298 | 162bp |
| Reverse | GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTAAAACACAACAAACCAATATACA |

**Supplementary Table S3.** Deep bisulfite sequencing of EBV sample.

|  |  |  |
| --- | --- | --- |
|  | Deep bisulfite sequencing | |
| Gene | Mean (%) in EBV sample | Mean (%) of fibroblasts |
| *APC* | 0.6 | 0.4 |
| *BRCA1* | 0.4 | 0.4 |
| *CDKNA1* | 0.9 | 1.9 |
| *TP53* | 98.1 | 96.4 |
| ***RAD9A*** | **41.9** | 8.6 |