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| **Gene** | **Primer sequence (5´-3´)** | **Fragment Size, bp** | **Gene Bank Accession No.** |
| ***H2AFZ*** | AGGACGACTAGCCATGGACGTGTG  CCACCACCAGCAATTGTAGCCTTG | 209 | NM\_174809.2 |
| ***TP53*** | CTCAGTCCTCTGCCATACTA  GGATCCAGGATAAGGTGAGC | 364 | NM\_174201.2 |
| ***BAX*** | CTACTTTGCCAGCAAACTGG  TCCCAAAGTAGGAGAGGA | 158 | NM\_173894.1 |
| ***SHC1 SHC*** | GGTTCGGACAAAGGATCACC  GTGAGGTCTGGGGAGAAGC | 335 | NM\_001075305.1 |
| ***PLAC8*** | CGGTGTTCCAGAGGTTTTTCC  AAGATGCCAGTCTGCCAGTCA | 166 | NM\_001025325.1 |
| ***PTGS2*** | ATCTACCCGCCTCATGTTCCT  GGATTAGCCTGCTTGTCTGGA | 187 | NM\_174445.2 |
| ***DNMT3A*** | CTGGTGCTGAAGGACTTGGGC  CAGAAGAAGGGGCGGTCATC | 317 | XM\_867643.3 |
| ***IGF2R*** | GCTGCAGTGTGCCAAGTGAAAAAG  AGCCCCTCTGCCATTGTTACCT | 201 | NM\_174352.2 |
| ***SCL2A1*** | CTGATCCTGGGTCGCTTCAT  ACGTACATGGGCACAAAACCA | 68 | NM\_174602.2 |
| ***GAPDH*** | ACCCAGAAGACTGTGGATGG  AYGCCTGCTTCACCACCTTC | 247 | NM\_001034034.1 |
| ***G6PD*** | CGCTGGGACGGGGTGCCCTTCATC  CGCCAGGCCTCCCGCAGTTCATCA | 347 | XM\_583628.5 |