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| --- | --- | --- | --- | --- | --- |
| **Gene** | **Probe Up** | **Probe Down** | **Probe Start (hg19)** | **Probe End (hg19)** | **Length** |
| JAK2 | AGTTTACACTGACACCTAGCTGTGATC | CCATAATTTAAAACCAAATGCTTGTGAGAA | chr9:5073733 | chr9:5073887 | 155 |
| TP53-1 | TCATCTTGGGCCTGTGTTATCTCCTA | ATCCTCACCATCATCACACTGGAAGAC | chr17:7577504 | chr17:7577635 | 132 |
| TP53-2 | CCCTCAACAAGATGTTTTGCCAACTG | ATGAGCGCTGCTCAGATAGCGATGGT | chr17:7578369 | chr17:7578544 | 176 |
| TP53-3 | GGACAGGTAGGACCTGATTTCCTTACT | TGTCCTGGGAGAGACCGGCGCACAGA | chr17:7577084 | chr17:7577214 | 131 |
| NRAS-1 | CAATAGCATTGCATTCCCTGTGGTTTT | GTACAGTGCCATGAGAGACCAATACAT | chr1:115256496 | chr1:115256680 | 185 |
| NRAS-2 | GAAGGTCACACTAGGGTTTTCATTTCC | AAAAGCGCACTGACAATCCAGCTA | chr1:115258713 | chr1:115258897 | 185 |
| HRAS | TCCTTGGCAGGTGGGGCAGGAGACCC | GCAAGAGTGCGCTGACCATCCA | chr11:534258 | chr1:534385 | 128 |
| KRAS-1 | AGGTACTGGTGGAGTATTTGATAGTGT | CAAGAGTGCCTTGACGATACAGCTAATT | chr12:25398247 | chr12:25398415 | 169 |
| KRAS-2 | GACTGTGTTTCTCCCTTCTCAGGATTC | TACAGTGCAATGAGGGACCAGTACATG | chr12:25380242 | chr12:25380368 | 127 |
| TET2-1 | CCATGTTTTGGCTCATTCATGCTCTTA | ACGGCCACTCCCCCAATGTCAG | chr4:106197237 | chr4:106197405 | 169 |
| TET2-2 | CTTTTGAAAGAGTGCCACTTGGTGTCT | GGTGATGGTATCAGGAATGGACTTAGTC | chr4:106155137 | chr4:106155275 | 139 |
| DNMT3A | TGTGTGGTTAGACGGCTTCCGGGCA | AGGCAGAGACTGCTGGGCCGGTCA | chr2:25457211 | chr2:25457364 | 154 |
| IDH1 | CAAATGTGGAAATCACCAAATGGCACC | TGGGGATCAAGTAAGTCATGTTGGCA | chr2:209113077 | chr2:209113239 | 163 |
| IDH2 | GAAGAAGATGTGGAAAAGTCCCAATGG | CATGGCGACCAGGTAGGCCAGG | chr15:90631809 | chr15:90631969 | 161 |
| GATA1 | CTTCCAGCCATTTCTGAGATATCCTCA | CAGCTGCAGCGGTGGCTGTGCT | chrX:48649667 | chrX:48649849 | 183 |
| SF3B1 | GTGAACATATTCTGCAGTTTGGCTGAA | ACCATCAGTGCTTTGGCCATTGC | chr2:198266803 | chr2:198266967 | 165 |
| TIIIA | CATCTATTCTGTGCTAGGCATTGTGTG | CAGACCTAGCATCTGTGCCAGAC | chr1:115227814 | chr1:115227978 | 165 |
| TIIIB | CAGTCTGGGTTTTGGAGCAATGATATC | GCAGTGAGCTCAGCCTTGATTTT | chr2:223190674 | chr2:223190820 | 147 |
| TIIIC | CCTGGTGCTTAGTCCTGTTCTGAAATT | AGTCTTCTATAATGCCACAACCTGTAT | chr2:229041101 | chr2:229041289 | 189 |
| TIIID | GAACAGAACACTTGGTAGTTGACCATG | AGACAGGGAACTGGCATGAAGAGTTT | chr4:110541172 | chr4:110541302 | 131 |
| TIIIE | GCCTAGAACAGGCACCATACATTCAAT | AGATGGTGTTGCTGTGCCGGATAGGAG | chr4:112997214 | chr4:112997386 | 173 |
| TIIIF | TGGCACTATGTGGAGATGTTAGTACAG | GGATGTTGGTGCTATCAGTAGCCATA | chr4:121167756 | chr4:121167884 | 129 |
| TIIIG | CTCTAGGCTTAGTGGTCAAGGAATGAA | AGAAGCAGGACTGTGCTTCCAAACAA | chr4:123547743 | chr4:123547901 | 159 |
| TIIIH | CTTGGTGGTAGCCTAGGCAGTAATTAA | CACGTGGTTGGGAAGAGAAAGTG | chr4:124428637 | chr4:124428767 | 131 |
| TIIIJ | TTCTATAGCACTGGTGACCAGGACACT | CTGGCCACAGTGCCTGGTTTCC | chr11:2126256 | chr11:2126420 | 165 |
| TIIIK | AGACAGGAGGAAGGAGCAATTCAGAAG | CATGGAGATCTCGTCCCCTCAGA | chr11:2389983 | chr11:2390171 | 189 |
| TIIIL | TAGGCCAGAAAACACACAGTGTCGGG | AACTCCGGTAAGTGGCGGGTGGGGGT | chr11:2593889 | chr11:2594074 | 186 |
| TIIIM | ATCTGGGAACAGACCTTCCTCAGGCAT | GTTCTAAGTTACTCTGTGTACTTGACT | chr11:11486596 | chr11:11486728 | 133 |
| TIIIN | AGCCTAGTTACCATAGACGGATTCAAC | GAATATCTTCTAACTGGACTTAGAAAACC | chr15:92527052 | chr15:92527176 | 125 |
| TIIIO | CCAACATGTTCTAAATTCTGGCCACAG | TGGGTCTCAGCCATCCCATTACTG | chr16:73379656 | chr16:73379832 | 177 |
| TIIIP | CTAACATCTCACTTCTACCCTACGCTA | TAAGTGCCCACTACCCCATCCTTAAT | chr16:82455026 | chr16:82455164 | 139 |
| TIIIQ | TCATGACCCAGGCCTCCCAGAACTGAG | ATCTGTGAAGCCGGAGTGAAAACAAC | chr16:85949137 | chr16:85949299 | 163 |