**Supplementary Table 1**

**Primers for bisulfite analysis by Ion torrent PGM**

|  |  |  |  |
| --- | --- | --- | --- |
| **Reverse primera** | **Forward primera** | **Chromosomal positions in Human GRCh38** | **Region** |
| TAAAATTCCACCTATCTCTATACTGAGGTTCCACCTGTCTCTGTGC | GTATTGTAGGTGTATAGTTGTATAAGGTACTGCAGGTGCACAGCTGCATAAG | **Chr2**:11,333-11,460 | **Subtelomere 2p** |
| AAAAACCAAATAAAACAACAAAAGAGGCCAAATAGAACAACAAG | GAGGGTGGAATTTTAGTAATTTGAGGGTGGAACCTCAGCAATCT | **Chr5**:13,176-13,366 | **Subtelomere 5p** |
| CCATAAATAATCAAAATAAAAAACCCCATGAATAATCAAGGTGAGAGACC | TTATGTGTGTATTAGGAATGTTGTATCATGTGTGCATTAGGAATGCTGCA | **ChrX**:156,029,669-156,029,860**Chr9**:10,507-10,681 | **Subtelomeres 9p/Xq** |
| CTAACTTTTCAAATTACTAAAATTCCTGGCTTTTCAGATTACTGAGGTTC | TGGTGTAGATGTAGAGAAGATGGCGCAGACGCAGAGAAGA | **Chr4**:11,545-11,748 | **Subtelomere 4pb** |
| AAAACTATATTCTCATCAACAAAAACGAAGCTGTGTTCTCATCAGCAGAGAC | GTAAGGTTTGTGTTGATTAGGAGCAAGGTCTGTGCTGATCAGGA | **Chr18:** 10,732-10,916**Chr10:** 10,536-10,720 | **Subtelomeres 10p/18p** |
| TCTACACAACCTTTTAAAATACTCTGCACAGCCTTTTGGGGTAC | TTTTTAAGGTTTGTGTTGAGGCCCCCAAGGTCTGTGCTGAGG | **Chr7**: 159,335,309-159,335,467 | **Subtelomere 7q** |
| AAAAACAAACAATACCCCCAACAAAGGCAGGCAGTACCCCCAAC | GAGTAGAGTTTTTTTTAGGTTAGATTGAGCAGAGTTCTTCTCAGGTCAGACC | **Chr**[**10**:133,786,654-133,786,804](https://www.ensembl.org/Homo_sapiens/Location/View?r=10:133786646-133786811;tl=ZPHqcFp26x5GTtnv-4259339-693267756)**Chr**[**4**:190,204,097-190,204,247](https://www.ensembl.org/Homo_sapiens/Location/View?r=4:190204089-190204254;tl=ZPHqcFp26x5GTtnv-4259339-693267758)**Chr**[**2**:242,182,895-242,183,045](https://www.ensembl.org/Homo_sapiens/Location/View?r=2:242182887-242183052;tl=ZPHqcFp26x5GTtnv-4259339-693267757) | **Subtelomeres 2q/4q/10q** |
| AAACACTACAAAACCAACTTACCCGGGCACTACAGGACCAGCTTGCCC | TGTTGTTATTATAATGTGAGGAAGAGGTGCTGCCACTATAATGTGAGGAAGAGG | **Chr10**:133,785,955-133,786,173**Chr2**:242,182,046-242,182,264**Chr4**:190,203,253-190203,471**Chr13**:114,352,791-114,353,009**Chr1**:248,944,437-248,944,655**Chr21**:46,698,328-46,698,546 | **Subtelomeres 10q, 1q/21q, 2q/4q, and 13qc**  |
| ACTACG/ATTCTATTCAACACAAACGCTGCGTTCTGTTCAGCACAGAC | TAATTGGTTTTTGATTTTGATTTAACTGGTCTCTGACCTTGATT | **Chr10:**133,786,714-133,786,885**Chr2:**242,182,955-242,183,126 **Chr4:**190,204,157-190,204,328 | **Subtelomeres 10q, 2q/4qd** |
| TAAATAATTCCATTCG/AAATCCTAGATGATTCCATTCGGGTCC | TGGAATTATTTTTTAATGGAAATGGAATCATCTTCTAATGGAAA | **Chr1**: 125,180,136- 125,180,294**Chr1**: 143,215,669- 143,215,827**Chr1**: 143,192,699- 143,192,857 | **Satellite 2** |

**a**Bisulfite converted primers are in black. Sequence in gray depicts the genomic regions prior to bisulfite conversion

**b** These primers amplify an additional region in 4q- Chr4:190,120,841-190,121,044 positioned at least 30kb from chromosome end (based on UCSC)

**c** These different subtelomeres were told apart based on the following single nucleotide differences compared to subtelomere 10q (nucleotide number in amplicon):

|  |  |  |
| --- | --- | --- |
| Subtelomere | Nucleotide #1 | Nucleotide #2 |
| 1q/21q | 121C>G | 137G>A |
| 2q/4q | 128C>G | - |
| 13q | 162G>C | 179C>A |

**d** These primers were used following treatment with OICR9429. The different subtelomeres were told apart based on the following single nucleotide differences compared to subtelomere 10q (nucleotide number in amplicon):

|  |  |  |
| --- | --- | --- |
| Subtelomere | Nucleotide #1 | Nucleotide #2 |
| 2q/4q | 39G>A | - |