Text S1. Primers and sequences

qPCR primers

mRNA: *Rps7*
upper primer: 5′-CCGGCTAGTTCGTGAATTGG-3′
lower primer: 5′-GAATCCTCCTCTGAGCAATGAAG-3′
TaqMan probe: 5′-/TEX615/AAAAGTTCAGTGGCAAGCACGTGG/3IABkFQ/-3′

mRNA: *Alpl*
upper primer: 5′-CCTGCCTTACCAACTCTTTTGTG-3′
lower primer: 5′-CAGGGCATTTTTCAAGGTCTCT-3′,
TaqMan probe: 5′-/Cy5/AGAGAAAGAGAGAGACCCCAGTTACTGGCGA/3IABkFQ/-3′

mRNA: *Dnmt1*
upper primer: 5′-TGGGTGACAGTGTGTACCTTCCT-3′
lower primer: 5′-ATCCTTCTTTGGGCGTTTCA-3′
TaqMan probe: 5′-/HEX/CCGAGGCCTTTACTTTCAACATCA/3IABkFQ/-3′

mRNA: *Dnmt3a*
upper primer: 5′-CCAGCCCTCGGGTCCTAA-3′
lower primer: 5′-ACCCACATGTCGGTGTAAACTTC-3′
TaqMan probe: 5′-/6-FAM/AGCCACCAG/ZEN/AAGAAGAGAAGAATCCTTACA/3IABkFQ/-3′

mRNA: *Dnmt3b*
upper primer: 5′-TGGAGTTCAGTAGGACAGCAAAGT-3′
lower primer: 5′-GTTTTTGCCCTGTCTGATGGA-3′
TaqMan probe: 5′-/HEX/AAAGAAAGTGCAGACAATAACCACCAAGTCGA/3IABkFQ/-3′

mRNA: *Dnmt3l*
upper primer: 5′-GAGTTACTGCACCATCTGCTGTTC-3′
lower primer: 5′-ACTCGAAACAGTAGCATCTGGTACA-3′
TaqMan probe: 5′-/6-FAM/TACCCTGTT/ZEN/CATCTGTGAGAGCCCCG/3IABkFQ/-3′

mRNA: *Rbl2*
upper primer: 5′-TGAGAGCAGAAGCCATCAGAATT-3′
lower primer: 5′-CCTCATCACTGGGCTGGAAT-3′
TaqMan probe: 5′-/6-FAM/TCCAACCGA/ZEN/ACTAAATACAGACAGAGCCAGTAGA/
3IABkFQ/-3′

Bisulphite sequencing primers

Chr 1 subtelomeric region, bases 197167907-197168572 NCBIM37
upper primer: 5′-AAGATGGTGAGTGTAGGTGTTAGTTGAG-3′
lower primer: 5′-TCTTTCTTCTAACTTCTATAACTTCCTATTACCTT-3′
amplicon size: 666 bp
CpGs analysed: 17

Chr 19 subtelomeric region, bases 61333524-61333949 NCBIM37
upper primer: 5′-AGGATTTGTTGATAAGTTTTGGGTTTTTGG-3′
lower primer: 5′-CTAATTCAAAAATAAAAATTTCTCCCCTAC-3′
amplicon size: 426 bp
CpGs analysed: 18

EpiTYPER primers

*Locus*_assay no.: *Xist*_1, Epipanel
upper primer:
5′-AGGAAGAGAGGTAGAGGATTAGGGGATAGGGTTTA-3′
lower primer:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTCACATTCAAAAACATATACCACCTCT-3′
amplicon size: 319 bp
CpG units analysed: 2, nos. 1/5.6; CpGs not analysed: CG
gene region analysed: exon 1, CpG-rich region 2
sequence:GCAGAGGACTAGGGGATAGGGCTCAGCGTGGGTGTGGGGATTGGGCAGGGTGTGTGTGCATA
TGGACCCCTGGCGCGGTCCCCCGTGGCTTTAAGGGCTGCTCAGAAGTCTATAAAATGGCGGCTCGGGGGCT
CCACCCGAGGCTCGACAGCCCAATCTTTGTTCTGGTGTGTAGCAATGGATTATAGGACATTTAGGTCGTAC
AGGAAAAGATGGCGGCTCAAGTTCTTGGTGCGGTATAACGCAAAGGGCTTTGTGTGTCACATGTCAGCTTC
ATGTCTGAGTTAGCCTGGAGAGGTGGCACATGCTCTTGAATGTG

*Locus*_assay no.: *Xist*_2, Epipanel
upper primer:
5′-AGGAAGAGAGTGTTGTGTGAGTGAATTTATGGTTT-3′
lower primer:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTCTAAACCCTATCCCCTAATCCTCTA-3′
amplicon size: 351 bp
CpG units analysed: 9, nos. 2/3.4.5/6/8/12.13/14.15/16/17/20.21.22
gene region analysed: exon 1, CpG-rich region 2
sequence:TGCTGTGTGAGTGAACCTATGGCTTAGAAAAACGACTTTGCTCTTAAACTGAGTGGGTGTTC
AGGGCGTGGAGAGCCCGCGTCCGCCATTATGGCTTCTGCGTGATACGGCTATTCTCGAGCCAGTTACGCCA
AGAATTAGGACACCGAGGAGCACAGCGGACTGGATAAAAGCAACCAATTGCGCTGCGCTAGCTAAAGGCTT
TCTTTATATGTGCGGGGTTGCGGGATTCGCCTTGATTTGTGGTAGCATTTGCGGGGTTGTGCTAGCCGGAA
GTAGAAAGCCAAGGAGTGCTCGTATTAGTGTGCGGTGTTGCGCGGAAGCCGCAGAGGACTAGGGGATAGGG
CTCAG

*Locus*_assay no.: *Xist*_4, EpiDesigner (antisense)
upper primer:
5′-AGGAAGAGAGTTATAAGGTTTGGTGGTAGGGGAAT-3′
lower primer:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTTCAAAATTACAATCTTTATAACCACTCC-3′

amplicon size: 196 bp
CpGs analysed: 3, nos. 5/7.8.9/10; CpGs not analysed: CG
gene region analysed: promoter; CpG-rich region 1; exon 1
sequence:CCATAAGGCTTGGTGGTAGGGGAACTAAAAATGTTCCCCCAAAGCTCCTTAGATGGAGAGAA
ACCACGGAAGAACCGCACATCCACGGGAAACGAGCAAACATGGCTGGAGCAAGCCGTTGCACGCCTTTAAC
TGATCCGCGGCGCTGAAGGCGGAGAGACCAGAAGAGGAGTGGCCACAAAGATTGCAATTCTGA

*Locus*_assay no.: *Gja8*_1 (EpiDesigner)
upper primer:
5′-AGGAAGAGAGGAGGGGTTTTTAGTTTTTAATTTTAGG-3′
lower primer:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTAAACACCCATTATAAACAACCCTTT-3′
amplicon size: 371 bp
CpGs analysed: 2, no. 2/3
gene region analysed: <1 kb upstream of AUG translation start site
sequence:GAGGGGTTTCCAGCTCTCAACCCCAGGAAAAGAAAGCATAAATTAGGACTGCAGAAGTCAGA
GAAACGTGTAGCCCACATCACAGGCAGTATTTCTTAATGGTTTGAGAATCCAACCTATGGGATCGGGTACA
GAACTGCTAGCTAGCATTTAGCTACCTGATCTTAGACCATCTGTTTAGCCTCAAAAGCCCCTGTTTTCTCA
CACATTGAAAGCAAGCTGGAAACAAACAAACACATCTGTGTGTGCGGGAATTGGCTATGCAGCTGTAACTA
CAATAGGCAGGTCCCTACCATCAGATAGCTAAGGTCTAACAGGACTAAGATAAACGAAATGATGCAACATC
AAAGGGCTGTCCATAATGGGTGTCC

*Locus*_assay no.: *Trpc1*_1, EpiDesigner
upper primer:
5′-AGGAAGAGAGTTGGTTTTATTTTGAGTTTTTTGGA-3′
lower primer:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTACCTCTCCTATTCAAACTACTTTATCCC-3′
amplicon size: 273 bp
CpGs analysed: 1, no. 3; CpGs not analysed: CG
gene region analysed: <1.5 kb upstream of AUG translation start site
CTGGCTTCACCTTGAGCCTCTTGGAAATTTCACCAAACTCATAAACTTGGAAGTGTATTAAACATTACACG
ACAACGGGGAGATCATTTAGAAACAAAAACTGGAGCAACTTGAGATTATCATTTACATCAAATACAGAAAA
CGTTTGAAAAGATGACTTCGACATCAAAGACTTTTAGAGAATATCTAAAGAGAACATTGATTTTTAAGAAT
TAGTAAGTTAAATGTTGAAAGAGAAACTAATGGGACAAAGTAGCCTGAATAGGAGAGGC

*Locus*_assay no.: *H19*_1, Epipanel (antisense)
upper primer:
5′-AGGAAGAGAGTTTGTTTGAGTTAGTTTTTTAGTTTTTTAA-3′
lower primer:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTACCACTCCAATTAAAAAAAACCC-3′
amplicon size: 198 bp
CpGs analysed: 4, no. 2/4/5.6/7; CpGs not analysed: CG
gene region analysed: promoter
sequence:TCTGCCTGAGCTAGCCCCTCAGTCCTTCAACATTCCTGCCAGACTCCAGATGCCGAGGTGCT
CCTCGGACCCCACGACTCTCCTCCAGCTCTCCCATCTTCCCCAGTTTCCCCGATACCCCCCACCCCCACCC
CCCACCCCCCTCCCACACCCGGTGCTTCGGGCCCTCTAGCCCGGGCTTTTTCTAACTGGAGTGGC

*Locus*_assay no.: *H19*_4, EpiDesigner
upper:
5′-AGGAAGAGAGTGTAAGGAGATTATGTTTTATTTTTGGA-3′
lower:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTCCCCCTAATAACATTTATAACCCC-3′
amplicon size: 203 bp
CpGs analysed: 3, no. 1/2.3/4.5; CpGs not analysed: CG
gene region analysed: imprinting control region; CTCF binding site
sequence:TGCAAGGAGACCATGCCCTATTCTTGGACGTCTGCTGAATCAGTTGTGGGGTTTATACGCGG
GAGTTGCCGCGTGGTGGCAGCAAAATCGATTGCGCCAAACCTAAAGAGCCCCCCCACCCCTGGTATTGGAA
TTCACAAATGGCAATGCTGTGGGTCACCCAAGTTCAGTACCTCAGGGGGGTCACAAATGCCACTAGGGGG

*Locus*_assay no.: *H19*_5, EpiDesigner (antisense)
upper primer:
5′-AGGAAGAGAGTTTATGATTATGGGATTATAGATGGTGA-3′
lower primer:
5′-CAGTAATACGACTCACTATAGGGAGAAGGCTACCTCAAAAAAATCACAAATACCAC-3′
amplicon size: 242 bp
CpGs analysed: 1, no. 4.5.6; CpGs not analysed: CG
gene region analysed: imprinting control region; CTCF binding site
sequence:CCCATGACTATGGGATCATAGATGGTGATAGGGGAGAAAACTCAATCAGTTGCAATCCGTTT
TAGGACTGCGATGTACGAGACTTCACTGCCGCCGTGCGGCAACCCTGGTCTTTACACACAAAGGATTCTTT
GCAGAGAGTAAGCCGACCTTGTTGATTTGGGAGTCCGAGTCCACGAGGTACCAGCCTAGAAAATGCATGTG
TCCTGCCCCCCTAGTGGCATTTGTGACCCCCCTGAGGT

Primers used to clone the stem-loop into inverted BsmBI sites

5′-TTTGAGTGTGTGAGGGAGAAATTCA AGAGATTTCTCCCTCACACACTCTTTTT....-3′
3′-....TCACACACTCCCTCTTTAAGTTCTCT AAAGAGGGAGTGTGTGAGAAAAAAGAG-5′

Sequence of the m*U6*pr cassette with inverted BsmBI sites for stem-loop cloning

CTCGAGATCCGACGCCGCCATCTCTAGGCCCGCGCCGGCCCCCTCGCACAGACTTGTGGGAGAAGCTCGGC
TACTCCCCTGCCCCGGTTAATTTGCATATAATATTTCCTAGTAACTATAGAGGCTTAATGTGCGATAAAAG
ACAGATAATCTGTTCTTTTTAATACTAGCTACATTTTACATGATAGGCTTGGATTTCTATAAGAGATACAA
ATACTAAATTATTATTTTAAAAAACAGCACAAAAGGAAACTCACCCTAACTGTAAAGTAATTGTGTGTTTT
GAGACTATAAATATCCCTTGGAGAAAAGCCTTGTTTGTGAGACGACTGCAGTCGTCTCTTCTCGACGGCGC
GCC.*Pgk1*>*sneo*>poly(A).GGCGCGCCGTCGAC