

Table S2. List of pyrosequencing assays used for validation

Assay	CG position	Functional annotation	Tool	Comparison	Primer 1 (5'-3')	Primer 2 (5'-3') biotinylated	Sequencing primer (5'-3')
<i>Aldh3b3</i>	19:3,955,095	3kb upstream of TSS, enhancer	MethylKit	XXF vs XYM	TTTTGGTGGTTGTAGATAGTGGT	TAATTACCCCCCCCCCTACAAT	GTAGATAGTGGTTGGTA
<i>Bcl6</i>	16:24,010,090	intergenic	MethylKit	XYF vs XYM	AGTAAGTATTTGAAGGTTTGTAGAGT	ATTCAAAAATTAAACCACTCATAAACATAC	GGTTTGTAGAGTTTATAGTATATT
<i>Caprin1</i>	2:103,766,583	exon	MethylKit	XXF vs XYM XXF vs XYF	TTAAGTAAGGGTGAGGAATTT	AAAAAACTATTTTCATCCCATAAAAACAA	TGTATTGTGTGTAAGGTTT
Ch6qA1	6:13,714,975	intergenic	MethylKit	XXF vs XYM XXF vs XYF	GTTATGGAGGTTGGTAATAATGTT	ACCAATAAAAAATCAAACAATTCACAAA	GGGGAATATATAGAAAGATATAAAA
<i>Comt</i>	16:18,407,984	exon enhancer	DSS	XXF vs XYM XYF vs XYM	AAGGGGAAGGTGTTTTAGTTGATAATG	TTCTCCAAACCCTCCACCATTTTCATA	GGTGTTTTTAGTTGATAATGT
<i>Cyp7b1</i>	3:18,239,446	intron	MethylKit and DSS	XXF vs XYM XYF vs XYM	GGTTATAAGGTTTGTGATATGTGTGTA	ATTCTTAACCAACTCTCTAATATACAAT	GGTTTGTGATATGTTGTATAG
<i>Ergic1</i>	17:26,634,198	intron	DSS	XYF vs XYM	AAAGAAGTATTAGGGATAATTTAGGGTAAG	TAACTCAAAATACACCCCTCACC	GGGATAATTTAGGGTAAGAG
<i>Esr1</i>	10:4,729,743	intron	MethylKit and DSS	XYF vs XYM	TTGGGGTTAATTATTTATTTGTGAGT	TCCCAAAAACACATTCCAATAAC	TGAGTTATTGGGTTGG
<i>Gstp1</i>	19:4,034,872	downstream	MethylKit and DSS	XXF vs XYM XYF vs XYM	GTTTTGGTTGTTTTGGAATTTATTATGT	AAATTTCTCTCCTTAACCTCAATATTCT	ATTTATTATGTAAATTAGGTTGG
<i>Hsd3b5</i>	3:98,626,053	intron	MethylKit	XXF vs XYM XYF vs XYM	TTGTAGATATTGAATAGATATTAGGGAATT	CTTCCCCAACTTACTTCTTAATCATA	ATTGAATAGATATTAGGGAATTTT
<i>Pgk1</i>	X:106,187,981	intron, promoter	DSS	XX ^{padF} vs XOF	TTAGTAATTTTTTTAGGTAAGGGAGAAGT	TTAAACTCCTAACCCTAAATTTACATCA	GTGAGGTTATAGGTTTTTAAT
<i>Snrpn</i>	7:60,005,146	promoter	n/a	n/a	TTGGTAGTTGTTTTTTGGTAGGAT	TCCACAAACCCAACCTAACCTTC	GTGTAGTTATTGTTTGGGAT
<i>Xist</i>	X:103,481,082	exon, promoter	DSS	XX ^{padF} vs XOF XXF vs XYM XXF vs XYF	GTAATAGTTATGGGGTAGATTTTGGA	CTTAACCTCTAATTTAACCACACTAA	ATTTAGTAGGTTTAGAGAAAT

CG position: UCSC genome browser - mouse GRCm38/mm10 Assembly

Functional annotation: Based on genomic region and histone marks enrichment (H3K4me1, H3k27ac for enhancers and H3k4me3 for promoters).

Information obtained from UCSC genome browser ([Bing Ren's laboratory](#) - LIRC histone track).