

Table S1. Summary of peaks

#samples	Num Peaks	Peaks Mean length	Peaks Median length	Peaks total length	Percentage of genomic length (%)
C13	110078	889.99	811	97968717	3.79
C14	86559	842.18	770	72898425	2.82
C7	121547	934.48	848	113583757	4.39
T10	93952	952.09	863	89450530	3.46
T5	116902	886.02	801	103577748	4
T8	105347	820.29	744	86415400	3.34
Merged	213392	1011.67	905	215883291	8.34

Table S2. Primers for BSP validation.

MDR	Gene	Forward(F)/Reverse(R)	Primer sequence
chr7:84219421-84219679	TGFB3	F	GAAATGGGTTCGGGTTAAT
		R	ATATATAACGCCGAAAACCT
chr19:42869604-42870470	ACOX2	F	AGTTAGGTAGTGGGTGTAGGTTGTG
		R	CCCCCTACAACCTATATAATCCTTC
chr26:13938540-13939276	ACSL1	F	ATTATTTGAGGGGAGGTGATTTTAG
		R	ATACAACCTCAACTTTTAACTTTCAC
chr13:38607690-38608423	RIN2	F	TTTTTTTTTTGGAATTTGGGT
		R	AATCACTTTATCCCAATTCCAC
chr21:25146996-25148088	ZDHHC13	F	TGTTTTAAATGTTGAATGATTGTA
		R	ATCACAAAACAACAAAAACAAC

Table S3. List of primers for real-time quantitative PCR

Gene name	Forward primer	Reverse primer
TGFB3	GCCACAGTCAGAGGAAGAAG	CCTGTCGGAAGTCAATGTAGAG
ACSL1	CGGAGGAGATTGTGGCTTAG	TGAGCGTGTTGGTTGGAAG
RYR1	GGTGCTGGATGTGCTATGT	AGTGATGAGGTCTTGGTTGG
ACOX2	GCGCTTGGCTGTTATGATGG	TCATAGGCAGGGTTCCCCTC
PPARG2	GCTGTGGAGTAATTCGCTGTC	CTACCTGCCGTGTCGCTAG
NTN1	TGCCCTTTCAGTTCTACTCC	CTCCTGCTCGTTCTGTTTG
RIN2	CCTGATTGGTGTCTCCTGTTC	CTCCTGCTCCTTGCTGTTG
MAPRE1	CTCTGAACAAACCGAAGAAACC	CTGCCTCGTCATCTCCATTC
ADAMTS2	TCTCAATACTTCCAGCACCA	TTTTGTAGGGCACATCCAC
MYOM1	TATGCTTCCGTTGTGGTAAA	ATTGTCTCGCCTTCTCTCC
ZDHHC13	TCCTGAACAATCTTAGCCAAC	TACCACACTTTCTCCATAATCG
SH3PHD2B	GATGAAATGAACCTGGAGAGA	TCTTTGCCCTGATACCTGA
β -action	CCCTGGAGAAGAGCTACGAG	GGTAGTTTCGTGAATGCCGC