

Supplemental Table S3. The primer information of mRNA

Gene name	Sequence(5' to 3')
<i>CDK8</i>	F-ACGTTTTTGCCGGTTGTCAG
	R-TGATGAGTCCGCCTGAGGTA
<i>YBX1</i>	F-GAGAAGTGATGGAGGGTGCT
	R-GGTTGTCTTTGGCGAGGAG
<i>BCL-2</i>	F-GATCCAGGATAACGGAGGCT
	R-CCAGGAGAAATCAAATAGAGGC
<i>BAX</i>	F-CCTTTTGCTTCAGGGTTTCA
	R-GTTACTGTCCAGTTCATCTCCAAT
<i>GAPDH</i>	F-TGACCCCTTCATTGACCTCC
	R-TTCTCCGCCTTGACTGTGC

Supplemental Table S4. shRNA sequence and primer information

Gene	sequence (5' – 3')
<i>YBX1</i>	474F-CACCGGAGTTTGATGTTGTTGAAGGTTCAAGAGACCTTCAACAACATCAAACCTCCTTTTTTG

Negative control

474R- GATCCAAAAAAGGAGTTTGATGTTGTTGAAGGTCTCTTGAACCTTCAACAACATCAAACCTCC
614F- CACCGCAATTACCAGCAGAATTACCTTCAAGAGAGGTAATTCTGCTGGTAATTGCTTTTTTG
614R- GATCCAAAAAAGCAATTACCAGCAGAATTACCTCTCTTGAAGGTAATTCTGCTGGTAATTGC
986F- CACCGGTACCGCCGCAACTTCAATTTCAAGAGAATTGAAGTTGCGGCGGTACCTTTTTTG
986R- GATCCAAAAAAGGTACCGCCGCAACTTCAATTCTCTTGAAATTGAAGTTGCGGCGGTACC
F- CACCGTTCTCCGAACGTGTCACGTTTCAAGAGAACGTGACACGTTCCGGAGAATTTTTTG
R- GATCCAAAAAATTCTCCGAACGTGTCACGTTCTCTTGAAACGTGACACGTTCCGGAGAAC

Supplemental Table S5. Imputation accuracy and the number of SNPs calculated for each chromosome.

Chromosome	Before quality control		After quality control	
	Number of SNPs	Average accuracy	Number of SNPs	Average accuracy
1	1,356,375	0.71	477,856	0.97
2	1,052,192	0.71	303,923	0.96
3	866,093	0.71	300,641	0.97
4	783,586	0.72	274,087	0.96
5	691,083	0.72	183,287	0.96
6	943,353	0.72	301,818	0.96
7	844,634	0.73	229,335	0.96
8	900,494	0.73	294,289	0.96
9	892,768	0.73	300,569	0.96