Supplementary Table 4. Simple nucleotide polymorphisms in *HOTAIR*

Name (SNP)	Function	Summary	Reference allele	Strand	Class	Position
rs1838169	nc-transcript variant	G>C/G	G	-	Single	Chr12:54357495–54357495 **(within CpG 1432)**
rs7958904	nc-transcript variant	G>G/C	C	+	Single	Chr12:54357552–54357552 **(within CpG 1432)**
rs17840857	nc-transcript variant	A/C/G/T	G	+	Single	Chr12:54357757–54357757 **(within CpG 1432)**
rs111434707	nc-transcript variant	-/G	G	+	Deletion	Chr12:54357757–54357757 **(within CpG 1432)**
rs200062983	nc-transcript variant	C>C/T	C	+	Single	Chr12:54357761–54357761 **(within CpG 1432)**
rs35951424	Intron variant	-/A	A	+	Deletion	Chr12:54357997–54357997 **(within HSMM cells DNase I hotspot:66574)**
rs201719283	Intron variant-Splice donor variant	-/C	C	+	Deletion	Chr12:54358048–54358014 **(within HSMM cells DNase I hotspot:66574)**
rs71227278	Intron variant nc-transcript variant	->TTAA	-	+	Insertion	Chr12:54358048–54358047 **(within HSMM cells DNase I hotspot:66574)**
rs58072355	Intron variant	A>A/G	A	+	Single	Chr12:54358443–54358443 **(within DNase I hypersensitivity peak clusters 8)**
rs139645979	Intron variant	-/ACGCACAAG	ACGCACAAG	+	Deletion	Chr12:54358629–54358629 **(within HSMM cells DNase I hotspot:66574)**
rs10783616	Intron variant	C>C/G	C	+	Single	Chr12:54359220–54359220 **(within active promoter of HSMM cells)**
rs10783617	Intron variant	G>G/T	G	+	Single	Chr12:54359387–54359387 **(within active promoter of HSMM cells)**
rs376812530	Intron variant	-/GAAG	-	+	Insertion	Chr12:54359525–54359525 **(within tandem repeat (AAAG)n)**
rs76084431	Intron variant	C>C/T	C	+	Single	Chr12:54359946–54359946 **(within CpG 1433)**
rs920778	Intron variant	C>C/T	C	-	Single	Chr12:54360232-54360232 **(within CpG1434 and CpG2.5(WE))**
rs920777	Intron variant	C>C/T	T	-	Single	Chr12:54360429–54360429 **(within CpG 25, CpG1434 and CpG2.5(WE))**
rs74089839	Intron variant	A>A/T	A	+	Single	Chr12:54360561–54360561 **(within CpG 25, CpG1434 and CpG2.5(WE))**
rs11301759	Intron variant	-/C	C	+	Deletion	Chr12:54360613–54360613 **(within CpG 25 ,CpG1434 andCpG2.5(WE))**
Rs1899663	Intron variant	G>G/T	G	-	Single	Chr12:54360994–54360994 **(within first active promoter based on Ensembl)**
rs4759314	Intron variant	A>A/G	G	+	Single	Chr12:54361835–54361835 **(within module025607)**
rs17105613	Intron variant	C>C/T	T	+	Single	Chr12:54362194–54362194 **(within CpG 1435)**
rs73313155	nc-transcript variant	C>C/T	C	+	Single	Chr12:54362432–54362432 **(within module025607)**
rs73313156	Intron variant	G>A/G	A	+	Single	Chr12:54362915–54362915 **(within module025608)**
rs5798292	Intron variant	-/G	G	+	Deletion	Chr12:54366274–54366274 **(within 4 strong Enhancers of NHEK cells)**
rs12427129	Intron variant	C>C/T	C	+	Single	Chr12:54367690–54367690 **(within CpG 165 and CpG1437)**
rs74089843	Intron variant	T>A/T	T	+	Single	Chr12:54368227–54368227 **(within CpG 165)**
rs78894992	Intron variant	G>A/G	A	+	Single	Chr12:54368400–54368400 **(within CpG 165 and CpG2.4(WE))**
rs75547142	Intron variant	C>C/T	C	+	Single	Chr12:54368560–54368560 **(within CpG 165 and CpG2.4(WE))**

Simple nucleotide polymorphisms (SNPs) were recognized by "dbSNP 147"and positions are based on UCSC hg19.