

**Supplementary Table 3.** The motifs sequences identified by MEME and Mast programs in *HOTAIR*

Motifs	Width	Best possible match (strand -)	p-value	Position
1	47	GCGAAAAAGGACCAAGAGGGCGAGACGAGGGAAGAGACCTAGAGAGA	0.00032	Chr12: 54357805-54357852 (within CpG1432)
2	40	TTTACTCTTTCTTTTCTCTCTTTCTTCCTCTCTTTTTTTT	0.00121	Chr12: 54360742-54360782 (within CpG143, CpG2.5(WE))
3	39	CCCTCTCCCTTTCCTCCCTCTCCCTCCCTCCCTTT	0.00048	Chr12: 54367746-54367785 (within CpG1437, CpG165)

The motifs sequences are predicted from antisense strand of *HOTAIR* locus and a specified p-value of the motifs are applied by Mast program.  
WE, Weizmann evolutionary.