

Table S1

Primer	Sequence (5'---->3')
<i>CHIP analysis</i>	
1_d	GCCTCTGCTTCTGGACCTATGCTTTATT
1_r	TTTAGCCCTGCGAAGATATG
2_d	GGTGCAGTAGTAAATATAAGCAAAGAG
2_r	GCGTGCGGTTCTCTTATCAC
3_d	GTCGCAAGAACTTCACAACAG
3_r	GCCATCATGGATGTGAAAGA
4_d	TTCCGCCGACGGCATT
4_r	GAACATCAGTTTCGTATGCGAGTTATAG
$\gamma$ Tub37C_d	GCTTTCCAAGAAGCTCATAACA
$\gamma$ Tub37C_r	GGTTCAGTGCGGTATTATCCAG
hsp70_d	GACAGAGTGAGAGAGCATTAG
hsp70_r	GGTTATTGTGGTAGGTCATTTG
PREeng_d	AGATGGCATGTGGCTCTCCC
PREeng_r	AACTGTGTCCCAGCGAACTG
<i>Probes for EMSA</i>	
dHS1	CAAAGAGCGACACGTGAACAGGTGCAGTAGTAAATATAAGCAAAGAGAGTTGGAAAGAG TATTGGCTAAGAGCGTCCGCTCACTAACACATAGATAAATTAAGAGAGACGTGATAAGAG AACCGCACGCACACCACCGCAAAATCCAATTGGAAGAGAGCGACTGCTTGAGTGTATTGGT TAGCAAGAGAGCGGCTAAGGTTTGATGGTTTGATTGGAATTCAGTTGCCGTTTCG
dHS1 mut GAGA 3,4	ACCTCTATCACCGTGAACAGGTGCAGTAGTAAATATAAGCAAACAAATTGGAAAGAGT ATTGGCTAAGAGCGACCGCTCACTAACACATAGATAAATTAACAAAACGTGATAAGAG AACCGCACGCACACCACCGCAAAATCCAATTGGAAGAGAGCGACTGCTTGAATGTATTGGT AAGCAAGAGAGCGGCTAGGTTTGATGGTTTGATTGGAATTCAGTTGCCGTTTCG
dHS1 mut GAGA3-6	ACCTCTATCACCGTGAACAGGTGCAGTAGTAAATATAAGCAAACAAATTGGAAAGAGT ATTGGCTAAGAGCGACCGCTCACTAACACATAGATAAATTAACAAAACGTGATAAGAG AACCGCACGCACACCACCGCAAAATCCAATTGGAACAAAACGACTGCTTGAATGTATTGGT AAGCAAACAAAACGGCTAGGTTTGATGGTTTGATTGGAATTCAGTTGCCGTTTCG
HS3	CAGACGACGTCGCAGGTGAGTGGCGAGCAGAGCAGCATGGAGCGAGCATGGCCGCTGTGGAA TACCGCACTGTTCGTAGGCACGAGCGCGAGCGAGAGAGGCCAAGAGCACGCTCTCTTTCACAT CCATGATGGCTGCCGCTGTCTCGCCTCTTCTTCTTCATTTTCAGCTCGGCCATCATGGGGCTCC ATTAAATCCACT
HS3 mut GAGA	CAGACGACGTCGCAGGTGAGTGGCGAGCAGAGCAGCATGGAGCGAGCATGGCCGCTGTGGAA TACCGCACTGTTCGTAGGCACGAGCGCGAGCTTTTTAGGCCAAGAGCACGTTTTTTTCACATC CATGATGGCTGCCGCTGTCTCGCCTCTTCTTCTTCATTTTCAGCTCGGCCATCATGGGGCTCCA TTAAATCCACT
HS3 mut Pho	CAGACGACGTCGCAGGTGAGTGGCGAGCAGAGCAGCATGGAGCGAGCCGTACCGCTGTGGAA TACCGCACTGTTCGTAGGCACGAGCGCGAGCGAGAGAGGCCAAGAGCACGCTCTCTTTCACAT CCATGCGTACTGCCGCTGTCTCGCCTCTTCTTCTTCATTTTCAGCTCGGTACGCATGGGGCTCC ATTAAATCCACT
HS3 overlapping #1	ACGTCGCAAGAACTTCACAACAGACGACGTCGCAGGTGAGTGGCGAGCAGAGCAGCATGGA GCGAGCATGGCCGCTGTGGAATACCGCACTGTTCGTAGGC
HS3 overlapping #2	GTGGAATACCGCACTGTTCGTAGGCACGAGCGCGAGCGAGAGAGGCCAAGAGCACGCTCTCTT TCACATCCATGATGGCTGCCGCTGTCTCGCCTCTTCTT
HS3 overlapping #3	CACATCCATGATGGCTGCCGCTGTCTCGCCTCTTCTTCTTCATTTTCAGCTCGGCCATCATGGG GCTCCATTAATCCACTGCCTCTT
GAGA 3+4	CAAAGAGCGACACGTGAACAGGTGCAGTAGTAAATATAAGCAAAGAGAGTTGGAAAGAG TATTGGCTAAGAGCGTCCGCTCACTAACACATAGATAAATTAAGAGAGACGTGATAAGAG AACCGCACGCACACC
roX2	ACAATTGCCAAATAATACAGATCGATTTAGAGCGAGATGACAATAGAGAGGGCGATCTCTC TCGTATACGAGTCTTGAAAAGAAAGAGAAGGCGAACGGTGCTGGCTTAGAGAGAGATGGCA ATACTAATTAAGTCAATAATCCGCAATTTTGGTGGCGCTAAAAGTAACGGAAATTC GAGATGCTTTTAGGGCTG
GAGA 3	CAAAGAGCGACACGTGAACAGGTGCAGTAGTAAATATAAGCAAAGAGAGTTGGAAAGAGT ATTGG
GAGA 4	ATTGGCTAAGAGCGTCCGCTCACTAACACATAGATAAATTAAGAGAGACGTGATAAGAGA ACCGC
GAGA 3 + lacZ	CAAAGAGCGACACGTGAACAGGTGCAGTAGTAAATATAAGCAAAGAGAGTTGGAAAGAGT ATTGGGGCACCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCG GATAACAATTCACA