TableS1
Primer sequences used in this study

P75FP AAATAGATCTTGCCCAACAAAGCAGAGACC
P-1.0RP AATAAAGCTTGGCCTTAGCCTGTTGAAGC
P150FP AAATAGATCTTTAGCGGCCACTGGATTTT
P150_ALL MUT_FP
AAATAGATCTTTAGCGGCCACTGGATGTCAAGTCAAAGAAAAAAAAAAGTCAAGGTCAAGAGGTCGAGTCAATTTTCAGATAATGC
CCAACAAAGC
P150_MUT_GAR_FP
AAATAGATCTTTAGCGGCCACTGGATTTTCCAAAAAAGAAAAAAAAAAAATTCAGTCAAGAGGTCGAGTCAATTTTCAGATAATGC
CCAACAAAGC
P150_MUT_NS_FP AAATAGATCTTTAGCGGCCACTGGATGTCAAGTCAAAGAAAAAAAAAAATTCAAGATGAGTAAAGATG
P150_MUT_GA_FP
AAATAGATCTTTAGCGGCCACTGGATTTTCCAAAAAAGAAAAAAAAAAAATTCAGTCAAGAGGTCGATGTGGTTTTCAGATAATGC
CCCAA
P150_MUT_NFAT_FP AAATAGATCTTTAGCGGCCACTGGATGTCAAAAAAAAGAAAAAAAAAAATTCAAGATGAGTAAAGATG
P150_MUT_STAT5_FP AAATAGATCTTTAGCGGCCACTGGATTTTCCGTCAAAGAAAAAAAAAAAATTCAAGATGAGTAAAGATG
P150_MUT_HOXA5_FP
AAATAGATCTTTAGCGGCCACTGGATTTTCCAAAAAAGAAAAAAAAAAGTCAAGAGATGAGTAAAGATGTGGTTTTCAGATAA
P150_MUT_GATA2_FP
AAATAGATCTTTAGCGGCCACTGGATTTTCCAAAAAAGAAAAAAAAAAAATTCAGTCAAGGTAAAGATGTGGTTTTCAGATAATGC
CCC
P150_MUT_AP1_FP
AAATAGATCTTTAGCGGCCACTGGATTTTCCAAAAAAGAAAAAAAAAAAATTCAAGGTCAAGGTCGATGTGGTTTTCAGATAATGC
CCCAA
P150_MUT_RUNX1_FP
AAATAGATCTTTAGCGGCCACTGGATTTTCCAAAAAAGAAAAAAAAAAAATTCAAGATGAGTAAAGAGTCAATTTTCAGATAATGCC
CAACAAAGC
E+8.9FP AAATGCTAGCTGATCATGGTTCCTTATCTGGACC
E+8.9RP AAATCTCGAGTGGCATTTGGCACATTAGAAAAAAATATGTAAG
E+6.5(+6534)FP AATAGAGCTCAAGGAGGTCTCTCTTCCAGTCC
E+6.5(+8153)RP AAATGCTAGCAGAGAAACCCTGTCTCGAAAACAAAAA
E+6.5_6534FP AATAGAGCTCAAGGAGGTCTCTCTTCCAGTCC
E+6.5_6770FP AATAGAGCTCAAGCCGCTAAAGCTGACAGCAA
E+6.5_6970FP AATAGAGCTCCTGAGAGCCTGTGGTGAGTG
E+6.5_7170FP AATAGAGCTCAAACACAGTCACTTCAGGGGTTTC
E+6.5_7370FP AATAGAGCTCTCCTCTGAGATGGTGGCAGG
E+6.5_7570FP AATAGAGCTCCCACCCAAAAGCGACAGAGC
E+6.5_7770FP AATAGAGCTCGCCTAAGAAACTCCCCCAGC
E+6.5_7970FP AATAGAGCTCTGATTCCTGGCTGATTCCTAGCC
E+6.5_7370FP AATAGAGCTCTCCTCTGAGATGGTGGCAGG
E+6.5_7420FP AATAGAGCTCTCCTGACCATGGGGAACCCC
E+6.5_7470FP AATAGAGCTCGCCTAGAGCTGTGTCCATAGC
E+6.5_7520FP AATAGAGCTCGTGAAAACTAAAAGTCACGAGGCCTC
E+6.5_570RP AAAT CTCGAG GCCGAGAAATGAATGAAGA
E+6.5_7470-570_MUT_STREFP
AATAGGTACCGCCTAGAGCTGTGTCCATAGCCACCTTCCCCCACAGTGAGAACGGCGAAGGTGA
E+6.5_7470-570_MUT_EGR2FP AATAGGTACCGCCTAGAGCTGTGTCCATAGCAGAACGGCGAAGAACTGCCC
E+6.5_7470-570_MUT_FOXA2FP AATAGGTACCGCCTAGAAGAACGGCGAAGGCCACCTTCCCCCA
E+6.5_7470-570_MUT_EFSFP
AATAGGTACCGCCTAGAAGAACGGCGAAGGCAGAACGGCGAAGAACTGAGAACGGCGAAGGTGAAAA
E+2.5FPAATGGTACCGTTTCACAGGTCTCCAGCC
E+2.5RP AAATCTCGAGAAACAACAACAAAAGCAAAAAACCAACA
E+0.2FP AATAGGTACCAAGAGGTCATGAGCAGGCT
E+0.2RP AAATCTCGAGAGACCGTGAGTAGACCGGTAG
E-1.0FP AAATGCTAGCAGGAGAGAGGTGAGGAGGA
E-1.0RP AAATCTCGAGTGCCTATTGGGTAGTGATGTCAAG
E-1.0 _E+0.2FP
AAATGCTAGCCTGGCCTGAGGGAGGAAGTGGGTGAGGGTGCATCTTGACATCACTACCCAATAGGCAAAGAGGTCATGAGCA
GGCTGG
E+0.2RP AGACCGTGAGTAGACCGGTAG
E+6.5_E+0.2OLFP_CTACCGGTCTACTCACGGTCTTCCTCTGAGATGGTGGCAGG
E+6.5_FP AAATGCTAGCTCCTCTGAGATGGTGGCAGG
E+6.5_RP AGCCGAGAAATGAATGAAGA
P150_OLFP TCTTCATTCATTTCTCGGCTCCTTTAGCGGCCACTGGATTTT
P75_E+0.2OLFP CTACCGGTCTACTCACGGTCTTGCCCAACAAAGCAGAGACC
P-1.0BglIIRP AAATAGATCTGGCCTTAGCCTGTTGAAGC