

**Supplemental Table S2.** Primer sequences used in this study.

<b>Name</b>	<b>Sequence</b>	<b>Application</b>
<i>Calr</i> R1 HindIII	TCATGAGTTCCCCACATCTTTG	Hi-C library QC
<i>Calr</i> R3 HindIII	CTGTGGGCACCAGATGTGTAAAT	Hi-C library QC
<i>Gapdh</i> (Belton et al. 2012)	TATCAAGGGTGCCCGTCACCTTCAGC	Hi-C library QC
<i>Gapdh</i> (Belton et al. 2012)	GGGCTTTTATAGCACGGTTATAAAGT	Hi-C library QC
<i>Hoxa7</i> fwd HindIII	GGAGGAGGGAAAAGGAGTGATT	Hi-C library QC
<i>Hoxa13</i> rev HindIII	CAGGCATTATTTGCTGAGAACG	Hi-C library QC
<i>Hist1h2ae</i> fwd HindIII	GGGTAATGGTGTCACTAACTGG	Hi-C library QC
<i>Hist1h3e</i> fwd HindIII	GGGTTTGATGAGTTGGTGAAG	Hi-C library QC
<i>Hist1h4i</i> fwd HindIII	TTGGGCCAAAGCCTATATGA	Hi-C library QC
<i>Hlf</i> fwd	GCGCAGAAAGAACAACATGG	RT-qPCR
<i>Hlf</i> rev	GCCCAGCTCCTTCCTTAAAT	RT-qPCR
<i>Sox4</i> fwd	AAGGACAGCGACAAGATTCC	RT-qPCR
<i>Sox4</i> rev	GCCCGACTTCACCTTCTTT	RT-qPCR
<i>Cxcr4</i> fwd	GTGGATGGTGGTGTTC AATTC	RT-qPCR
<i>Cxcr4</i> rev	CTTGGAGTGTGACAGCTTAGAG	RT-qPCR
<i>Myc</i> fwd	CGATTCCACGGCCTTCTC	RT-qPCR
<i>Myc</i> rev	TCTTCCTCATCTTCTTGCTCTTC	RT-qPCR
<i>Gapdh</i> fwd	CATGGCCTTCCGTGTTCCCTA	RT-qPCR
<i>Gapdh</i> rev	CCTGCTTCACCACCTTCTTGAT	RT-qPCR
<i>Hlf</i> promoter fwd	GAAGAGAGCACCGGGAAAG	ChIP-qPCR
<i>Hlf</i> promoter rev	CAGACCCGCAATTCACAAAG	ChIP-qPCR
<i>Hlf</i> enhancer fwd	GGCAGAGGCAATCTCTTCAT	ChIP-qPCR
<i>Hlf</i> enhancer rev	GGACTCGTGACATCGTAGTAATG	ChIP-qPCR
<i>Cxcr4</i> promoter fwd	GGGCAAACAGAAGTCCAAGA	ChIP-qPCR
<i>Cxcr4</i> promoter rev	CTCAAGTTCTCCACCCGTAAAC	ChIP-qPCR
<i>Spred1</i> enhancer fwd	GCAGAAAGTGGAAGTGTGAAAG	ChIP-qPCR
<i>Spred1</i> enhancer rev	GGCAGGAAGCTGGTATCATAAA	ChIP-qPCR
<i>Hlf</i> enhancer uSTAT5+ fwd	GGAGAGACAAAGGTCCCATAAG	ChIP-qPCR
<i>Hlf</i> enhancer uSTAT5+ rev	GCCTGGTATTCAGGGTAACAA	ChIP-qPCR
<i>Cxcr4</i> enhancer uSTAT5+ fwd	GGGCATCTAGCCAAGCATATC	ChIP-qPCR
<i>Cxcr4</i> enhancer uSTAT5+ rev	ACTAGAGTCGGAGGCTTTCA	ChIP-qPCR
<i>Sox4-1</i> uSTAT5+ fwd	TAGCAGGACTCCCAAGAAGA	ChIP-qPCR

Sox4-1 uSTAT5+ rev	CCGCAGTAACACACACCTAA	ChIP-qPCR
Sox4-2 uSTAT5+ fwd	CTGCTGCCGCTCTTAATACA	ChIP-qPCR
Sox4-2 uSTAT5+ rev	CACTTGAGAGGGAGCAAATCA	ChIP-qPCR

## References

Belton J, Mccord RP, Gibcus JH, Naumova N, Zhan Y, Dekker J. 2012. Hi-C : A comprehensive technique to capture the conformation of genomes. *EMBO J* **58**: 268–276.