**Data reference guide**

For each experiment type, bigWig files are provided for sequencing coverage depth and bed files (narrowPeak/broadPeak) are provided for called peaks, when relevant.

**Custom references sequences**

HPRT1\_HPRT1\_HPRT1~BigIN\_in\_pLM1110.fa – HPRT1 in pLM1110 YAC

HPRT1R\_hHPRT1R\_hHPRT1R\_in\_pLM1110.fa – HPRT1R in pLM1110 YAC

Mm10\_reformed\_HPRT1.fa – mm10 with HPRT1 integrated on chrX

Mm10\_reformed\_HPRT1R.fa – mm10 with HPRT1R integrated on chrX

Sc3\_reformed\_HPRT1.fa – SacCer3 with HPRT1 integrated on chrXI

Sc3\_reformed\_HPRT1R.fa – SacCer3 with HPRT1R integrated on chrXI

**Sample naming**

Samples are named in the format:

**CellType\_Locus\_Clone\_Replicate-Experiment-BS#\_CustomReference**

CellType = mESC or Yeast

Locus = HPRT1 or HPRT1R

Clone = clone1 or clone2 for independent mESC clones

 =YAC or Int for YAC or integrated loci in yeast

CustomReference:

MmHPRT1(R)pLM1110 – mm10 and HPRT1/R sequences separate

MmReform – reformed mm10 sequence with integrated HPRT1/R

ScHPRT1(R)pLM1110 – SacCer3 and HPRT1/R sequences separate

ScReform – reformed SacCer3 sequence with integrated HPRT1/R