All source data is linked in the references below. All the ChIP-seq datasets were processed with OccuPeak to generate genome-wide peak profiles.

References

- [GEO depository link:](#) CTCF ChIP-seq on human cardiomyocyte (HCM) cell line (Stamatoyannopoulous laboratory).
- [GEO depository link:](#) H3K27ac ChIP-seq on cerebellum tissue (Creyghton laboratory).
- [GEO depository link:](#) H3K27ac ChIP-seq on left and right ventricular tissue (Roadmap Epigenomics project).
- [GEO depository link:](#) various ChIP-seq on induced 14d cardiomyocytes (Murry laboratory).
- [GEO depository link:](#) various ChIP-seq on fetal heart tissue (BROAD Institute).
- [GEO depository link:](#) p300 and Pol2 ChIP-seq on heart tissue (Pennacchio laboratory).
- [GEO depository link:](#) Dnase1 hypersensitivity on frontal cortex tissue (ENCODE).
- [GEO depository link:](#) Dnase1 hypersensitivity on human cardiomyocyte (HCM) cell line (ENCODE).
- [Siepel et al. (PhastCon scores)](#) Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. Genome Research. 15: 1034-1050, 2005
- [de Boer and van Duijvenboden et al.](#) OccuPeak: ChIP-Seq Peak Calling Based on Internal Background Modelling. PLoS One. 9(6): e99844., 2014