

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](#): various general regulatory-DNA marking datasets (ENCODE).
- [GEO depository link](#): H3K27ac ChIP-seq on right atria and atrioventricular canal tissue (Christoffels laboratory).
- [GEO depository link](#): Nkx2-5 and Gata4 ChIP-seq on heart tissue (Christoffels laboratory).
- [GEO depository link](#): TBX3 ChIP-seq on heart tissue (Christoffels laboratory).
- [GEO depository link](#): Gata4 ChIP-seq on fetal and adult heart tissue (Pu laboratory).
- [GEO depository link](#): Tbx20 ChIP-seq on heart tissue (Evans laboratory).
- [GEO depository link](#): Tbx5 ChIP-seq on HL-1 cell line (Pu laboratory).
- [GEO depository link](#): H3K27ac ChIP-seq on heart tissue (Pennacchio laboratory).
- [GEO depository link](#): CoupTF2 ChIP-seq on E14.5 atrial tissue (Tsai laboratory).
- [GEO depository link](#): DNase1 hypersensitivity on heart and brain tissue (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