

All ChIP-seq data were generated by the White laboratory. The Dnase I hypersensitivity data were generated by the Karpen laboratory. All datasets were downloaded from the modENCODE depository. All the ChIP-seq datasets were subsequently processed with OccuPeak to generate genome-wide peak profiles.

## References

- [The modENCODE data depository](#). The source data and associated laboratories can be found on this website.
- [de Boer and van Duijvenboden et al.](#) OccuPeak: ChIP-Seq Peak Calling Based on Internal Background Modelling. PLoS One. 9(6): e99844., 2014