

Cell-type Specificity of ChIP-predicted Transcription Factor Binding Sites

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Supplementary Table S2 - PWMs

The position weight-matrix identifiers of the PWMs taken from Transfac Professional [1] (6) and Jaspar [2] (1) databases. PWMs were not available for the TFs BDP1, BRF1, BRF2, RPC155, TAF1, and TFIIC-110. If more than one PWM was available for a given TF, the PWM with the highest information content after division by PWM length was chosen. Also shown are the sequence logos made from the motif sequences using WebLogo [3].

References

1. Matys V, Fricke E, Geffers R, Gossling E, Haubrock M, et al. (2003) TRANSFAC: Transcriptional regulation, from patterns to profiles. *Nucleic Acids Research* 31: 374.
2. Bryne J, Valen E, Tang M, Marstrand T, Winther O, et al. (2008) Jaspar, the open access database of transcription factor-binding profiles: new content and tools in the 2008 update. *Nucleic Acids Research* 36: D102–D106.
3. Crooks G, Hon G, Chandonia J, Brenner S (2004) Weblogo: a sequence logo generator. *Genome research* 14: 1188–1190.

