

## TRANSFAC® release 2019.1

The TRANSFAC® database on transcription factors, their genomic binding sites and DNA-binding motifs (PWMs), contains these new data features:

- **Matrices for C2H2 zinc finger transcription factors**

130 matrices derived from CHIP-Seq experiments involving TFs from the C2H2 zinc finger family have been included. They were published in "Schnitges, F. W. et al, Multiparameter functional diversity of human C2H2 zinc finger proteins, *Genome Res.* 2016 26:1742-1752, Pubmed PMID: [27852650](https://pubmed.ncbi.nlm.nih.gov/27852650/)" alongside with 1,292 interactions of C2H2 factors with nuclear and cytoplasmic proteins.

- **Pig promoters added**

27,812 promoters for pig (*Sus scrofa*) have been included based on data from [Ensembl](#) version 94 and our [established](#) virtual transcription start site calculation. Experimentally verified transcription factor binding sites and 6 million SNPs from the dbSNP database have been mapped to the promoter sequences.

- **Interactions between *Arabidopsis thaliana* transcription factors**

8,456 new and 31 updated interactions between *Arabidopsis* transcription factors have been added based on data published in "Trigg, S. A. et al, CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. *Nat. Methods* 2017, 14(8):819-825, PubMed PMID: [28650476](https://pubmed.ncbi.nlm.nih.gov/28650476/)".

- **Ensembl version update**

Genomic information for genes, promoters, and CHIP fragments for the species human, mouse, rat, pig, macaque, and *Arabidopsis* is now based on Ensembl release 94.