Additional Table 2. Links to databases used in this paper

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| --- | --- | --- | --- |
| **Database** | **Description** | **Link** | **Date** |
| ENCODE TF peaks (version 2) | All ENCODE proximal and distal TFs produced by combining original ENCODE TF ChiPseq data with ROADMAP DNAase1 data | <https://www.encodeproject.org/data/annotations/v2/>  Data file information:  <https://www.encodeproject.org/documents/a3631465-ac01-4a93-b257-88e344a4c3ef/@@download/attachment/ENCODEEncyclopediaV1README.pdf> | 2016/08/25 |
| ROADMAP | All 127 ROADMAP epigenomes (15 states) | <http://egg2.wustl.edu/roadmap/web_portal/chr_state_learning.html#core_15state> | 2016/08/25 |
| Cattle 92 RNASeq datasets | 79 different tissues from Dominette, the animal used for bTau genome sequence | <http://www.ncbi.nlm.nih.gov/Traces/study/?acc=SRP049415> | 2016/08/25 |
| FANTOM5 promoter atlas | All FANTOM phase 1 and phase 2 CAGE peaks | <http://fantom.gsc.riken.jp/5/datafiles/latest/extra/CAGE_peaks/hg19.cage_peak_phase1and2combined_coord.bed.gz> | 2016/08/25 |
| FANTOM5 enhancer atlas | All FANTOM5 permissive enhancers | <http://enhancer.binf.ku.dk/presets/permissive_enhancers.bed> | 2016/08/25 |
| SNP database | 99.5 Million Cattle RefSNP | <ftp://ftp.ncbi.nih.gov/snp/organisms/cow_9913/VCF/> | Build 146 (Nov 24, 2015) |
| Villar datasets | Peak files and Fastq files | <https://www.ebi.ac.uk/arrayexpress/files/E-MTAB-2633/E-MTAB-2633.processed.1.zip> (peak files)  <https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-2633/samples/> (FastQ files) | 2016/05/26 |
| liftOver chainfiles | Find relevant links for each species under the liftOver files | <http://hgdownload.soe.ucsc.edu/downloads.html> |  |
| …To be added | …To be added | …To be added | …To be added |