**ATAC-seq data analysis**

Fastq reads were aligned to with UCSC mm10 with Botwie2 (L. Salzberg). PCR duplicates were removed by samtools. Peaks were called with MACS2 (X. S. Liu). Bigwig files for ATAC-seq signal visualization on UCSC genomebrowser was generated by converting MACS2 output read pileup file into bigwig files with bedgraphtobigwig from UCSC tools. Peaks from all samples were merged to create a common reference peak set using Homer. HTseq-count were used to calculate Tn5 insertion site number in peaks (W. Huber). Scikit-learn were used for t-sne analysis of Tn5 count matrix to visualize sample similarity (P. Fabian). For differential analysis, DEseq2 were used to compare Tn5 insertion site numbers in peaks for each condition (S. Anders). Motif enrichment were performed by Homer, with combination of Homer curated known motif set and motifs from MEME motif database. Family of transcription factors were characterized with information from TFclass database (J. Donitz). Footprint analysis were performed with RGT-hint (I. Costa). Scripts for analysis are deposited on Github: <https://github.com/ScrippsPipkinLab/JYC_DataAnalysis>.

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