


Gene Expression Omnibus

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Scope: Format: Amount: GEO accession:

Series GSE109965

[Query DataSets for GSE109965](#)

Status	Public on May 17, 2018
Title	Analysis of genetically diverse macrophages reveals local and domain-wide mechanisms that control transcription factor binding and function
Organism	Mus musculus
Experiment type	Expression profiling by high throughput sequencing Genome binding/occupancy profiling by high throughput sequencing Methylation profiling by high throughput sequencing Other
Summary	Non-coding genetic variation is a major driver of phenotypic diversity and allows investigation of mechanisms that control gene expression. Here, we systematically investigated the effects of >50 million variations from five strains of mice on mRNA, nascent transcription, transcription start sites and transcription factor binding in resting and activated macrophages. We observed substantial differences associated with distinct molecular pathways. Evaluation of genetic variation provided evidence for roles of ~100 TFs in shaping lineage-determining factor binding. Unexpectedly, a substantial fraction of strain-specific factor binding could not be explained by local mutations. Integration of genomic features with chromatin interaction data provided evidence for hundreds of connected cis-regulatory domains associated with differences in transcription factor binding and gene expression. This system and the >250 data sets establish a substantial new resource for investigation of how genetic variation affects cellular phenotypes.
Overall design	5'GRO-Seq, GRO-Seq, ATAC-Seq, ChIP-seq, RNA-seq, Bisulfite-Seq, Hi-C and PLAC-Seq for diverse strains of mice: BALB/cJ, C57BL/6J, C57BL/6J x PWK/PhJ, C57BL/6J x SPRET/EiJ, NOD/ShiLtJ, PWK/PhJ, SPRET/EiJ Several of the Input samples have been used for multiple ChIP samples. Please see 'description' field for a list of the ChIP samples associated with the input sample.
Contributor(s)	Link VM , Glass CK
Citation(s)	Link VM , Duttke SH, Chun HB, Holtman IR et al. Analysis of Genetically Diverse Macrophages Reveals Local and Domain-wide Mechanisms that Control Transcription Factor Binding and Function. <i>Cell</i> 2018 Jun 14;173(7):1796-1809.e17. PMID: 29779944
Submission date	Jan 31, 2018
Last update date	Sep 28, 2018
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Platforms (2)	GPL19057 Illumina NextSeq 500 (Mus musculus) GPL21103 Illumina HiSeq 4000 (Mus musculus)
Samples (294)	GSM2974596 BALB_BMDM_5GRO_KLA_1h_rep1 More... GSM2974597 BALB_BMDM_5GRO_KLA_1h_rep2 GSM2974598 BALB_BMDM_5GRO_notx_rep1

Relations

BioProject	PRJNA432435
SRA	SRP131922

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- [MINiML formatted family file\(s\)](#)
- [Series Matrix File\(s\)](#)

Format

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- MINiML [?](#)
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Supplementary file	Size	Download	File type/resource
GSE109965_5GRO_processed_data.tar.gz	8.8 Mb	(ftp) (http)	TAR
GSE109965_ATAC-seq_processed_data.tar.gz	3.8 Mb	(ftp) (http)	TAR
GSE109965_BALBCJ_genome.tar.gz	830.1 Mb	(ftp) (http)	TAR
GSE109965_C57_BMDM_HiC_raw_interactions_1MB.txt.gz	6.7 Mb	(ftp) (http)	TXT
GSE109965_C57_cytosine_report.txt.gz	230.7 Mb	(ftp) (http)	TXT
GSE109965_ChIP-seq_processed_data.tar.gz	38.9 Mb	(ftp) (http)	TAR
GSE109965_GRO-Seq_processed_data.tar.gz	7.4 Mb	(ftp) (http)	TAR
GSE109965_GRO_Seq_all_strains_KLA_1h_TPM.txt.gz	2.0 Mb	(ftp) (http)	TXT
GSE109965_NODSHILTJ_genome.tar.gz	830.4 Mb	(ftp) (http)	TAR
GSE109965_PLAC_seq_consensus_interactions.txt.gz	1.3 Mb	(ftp) (http)	TXT
GSE109965_PWKPHJ_genome.tar.gz	837.1 Mb	(ftp) (http)	TAR
GSE109965_RNA-seq_processed_data.tar.gz	6.9 Mb	(ftp) (http)	TAR
GSE109965_SPRETEIJ_genome.tar.gz	845.7 Mb	(ftp) (http)	TAR

GSE109965_SPRET_BMDM_HiC_raw_interactions_1MB.txt.gz	6.4 Mb	(ftp) (http)	TXT
GSE109965_SPRET_cytosine_report.txt.gz	234.9 Mb	(ftp) (http)	TXT
GSE109965_mutations.bed.tar.gz	1.0 Gb	(ftp) (http)	TAR

Raw data are available in SRA
Processed data are available on Series record

