SUPPLEMENTARY INFORMATION

GREGOR: Evaluating global enrichment of trait-associated variants in epigenomic features using a systematic, data-driven approach

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SUPPLEMENTARY METHODS

Data acquisition and pre-processing

DNase-seq ENCODE data for all available cell types were downloaded in the processed "narrowPeak" format. The local maxima of the tag density in broad, variable-sized "hotspot" regions of chromatin accessibility were thresholded at FDR 1% with peaks set to a fixed width of 150bp. Individual cell types were further grouped into 41 broad tissue categories (http://genome.ucsc.edu/ENCODE/cellTypes.html) by taking the union of DHSs for all related cell types and replicates (**Table S1**). We also obtained a set of BED files in hg19 assembly from the Integrative Analysis and original ENCODE analysis. These data include uniformly processed datasets in 125 cell types generated by the "Open Chromatin" (Duke University) and University of Washington (UW) ENCODE groups. Data processed during the ENCODE Integrative Analysis were downloaded for available tissues. Otherwise, data from the original ENCODE analysis were obtained. We examined the overlap of DHSs across different cell types, and found that as expected, cell types derived from related tissues generally clustered together. In addition, we examined chromatin state segmentation by HMM generated from ENCODE/Broad in nine human cell types, as well as transcription factor binding sites by ChIP-seq from the ENCODE Analysis Working Group (AWG) including ENCODE/HudsonAlpha (HAIB), ENCODE/Stanford/Yale/Davis/Harvard (SYDH), ENCODE/University of Chicago, ENCODE/Open Chrom (UT Austin), and ENCODE/University of Washington (UW). No datasets analyzed were under embargo.

Selecting matched control SNPs for GWAS index SNPs

For each GWAS locus, we selected a set of matched control SNPs based on 3 criteria: 1) number of variants in LD (r^2 > 0.7; ± 8 variants), 2) minor allele frequency (± 1%), and 3) distance to nearest gene (± 11,655 bp). To calculate the distance to the nearest gene, we calculated the distance to the 5' flanking gene (start and end position) and to the 3' flanking gene and then used the minimum of these 4 values. If the SNP fell within the transcribed region of a gene, the distance was 0.

Estimating probability of observed and expected overlap between a regulatory feature and GWAS locus

We estimated the probability that a set of GWAS loci overlap with a regulatory feature more often than we expect by chance using the following method. We considered a GWAS locus as the GWAS index SNP or a SNP in LD with the index SNP (r^2 > 0.7). For each regulatory feature, we counted the number of GWAS loci in which we observed physical overlap with at least one experimentally defined genomic region of the feature. The number of GWAS index SNPs in the ith matched control set that demonstrates positional overlap with a given epigenomic feature, written as s_i, follows a binomial distribution with parameters n_i and p_i. The parameter n_i is equal to the number of index SNPs present in the ith control set. The second parameter p_i is calculated as the number of variants in the ith control

set or their LD proxies that overlaps with the feature, divided by the total number of variants in the ith control set. If we assume there are r control sets in total, the number of index SNPs from all control sets that falls in a single feature is the sum of independent non-identical binomial random variables:

$$S = \sum_{i=1}^{r} s_i$$

In most cases only one index variant is assigned to a matched control set, but there are some exceptions where more than one index SNP could match on the same 3 properties. We estimate an enrichment P-value for any given s as $P(S \geq s)$. P is the cumulative right tail probability based on the distribution of S and is calculated using a saddlepoint approximation method (Te Grotenhuis, et al., 2013).

Permutation testing to evaluate estimated P-values

We performed up to 100,000 permutations to evaluate our enrichment P-value estimation method and found the results to be highly concordant for permutation P-values less than $1x10^{-5}$ that could be estimated (**Figure S3**). To assess the expected overlap with a regulatory domain, we generated 100,000 random permuted sets of non-associated matched control SNPs based on the criteria described above. We selected a control variant from the control pool for each locus and identified the variants in LD, resulting in 100,000 control sets. We evaluated the random SNP lists for overlap with each functional domain by averaging the number of SNPs that fell within the experimentally annotated regions from each control set that had at least one variant overlapping a regulatory element. This approach assumes that only one variant located in a regulatory region at each locus is responsible for the association signal. We calculated an empirical P-value for each regulatory dataset as the proportion of random sets with an equal or greater number of loci overlapping the regulatory domain than the observed set of trait-associated variants. For small P-values that could not be estimated (e.g. $P < 1x10^{-5}$ for 100,000 permutations), we used a normal approximation of the empirical overlap distribution to estimate P-values.

Luciferase expression constructs

To characterize the intergenic region around the candidate SNPs, 600-800 bp fragments containing the SNPs from human chromosomes were cloned into the pGL4-Promoter vector (Promega), in the 5'-to-3' orientation (toward the GWAS candidate gene), upstream of the firefly luciferase gene (**Table S6**). The QuikChange Site-Directed Mutagenesis Kit (Stratagene) was used to alter single nucleotides at the targeted SNP sites. All constructs were verified by DNA sequencing.

Luciferase expression assays

HepG2 cultured human hepatoma cells were transfected at roughly 50% confluence and maintained in DMEM with 10% FBS. The firefly luciferase constructs were co-transfected with either the C/EBP-β expression plasmid (pcDNA3.1-C/EBP-β) or empty pcDNA3.1 vector, together with the Renilla luciferase pRL-null Vector (Promega) as internal control, using the Lipofectamine 2000 transfection reagent (Invitrogen) in the ratio 0.25 µg:0.25ug:25 ng:2.5 µl mixed with Opti-MEM I Reduced Serum Medium

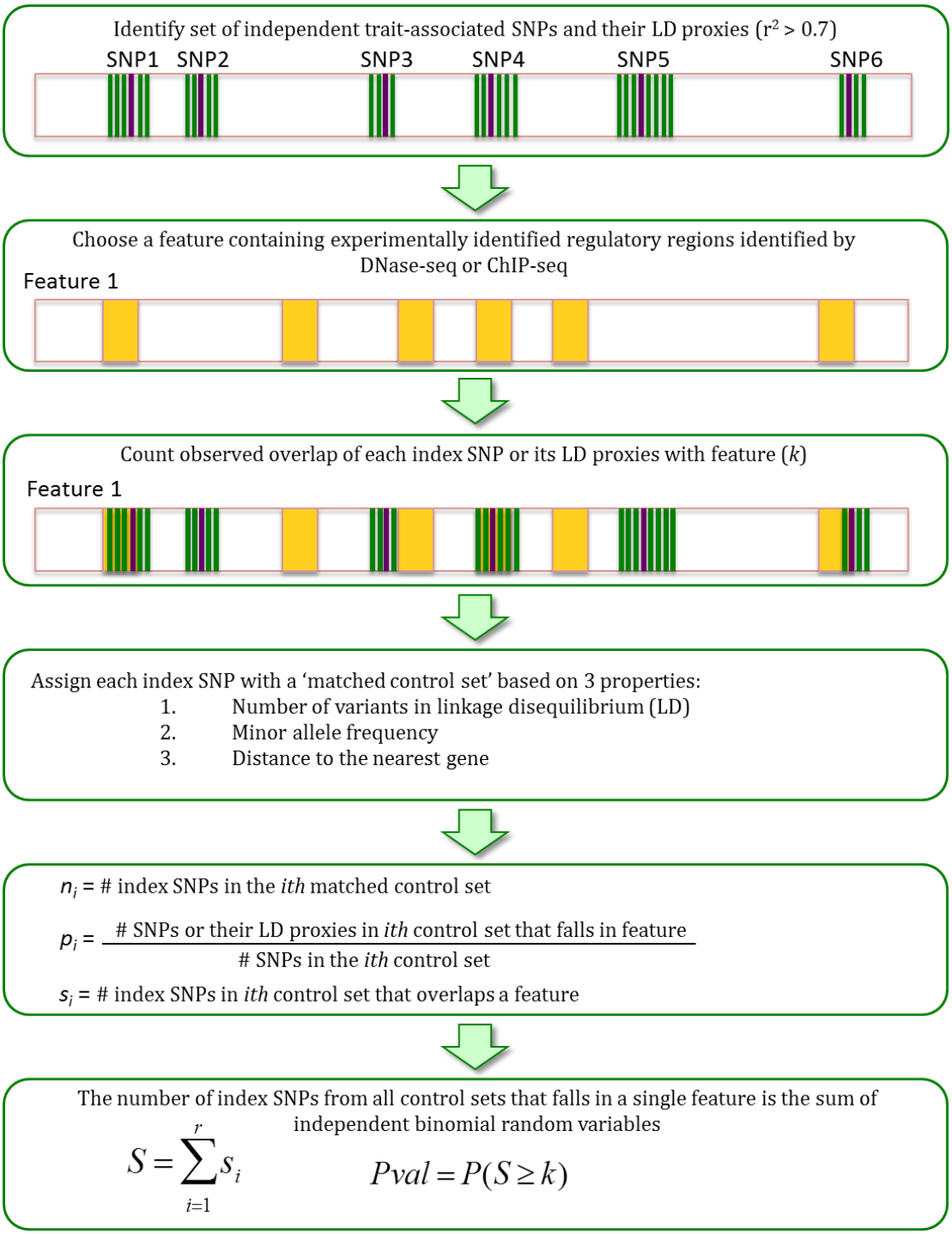
(Invitrogen) for a 50 µl mix used for each well of 24-well plates. Forty-eight hours after transfection, firefly and Renilla luciferase activities were measured using the Dual-Luciferase Reporter Assay System (Promega) according to the manufacturer's protocol, using untransfected cells to adjust for background activity.

Data Access

GREGOR documentation and software download, http://genome.sph.umich.edu/wiki/GREGOR; ENCODE Consortium, http://genome.ucsc.edu/ENCODE/dataMatrix/encodeDataMatrixHuman.html; Chromatin state segmentation by HMM from ENCODE/Broad in 9 human cell types, http://genome.ucsc.edu/cgi-bin/hgFileUi?g=wgEncodeBroadHmm&db=hg19; GWAS results for all traits and diseases including those studied here, http://www.genome.gov/gwastudies/. Data from the latest blood pressure study are not yet published; author CJW may be contacted at cristen@umich.edu.

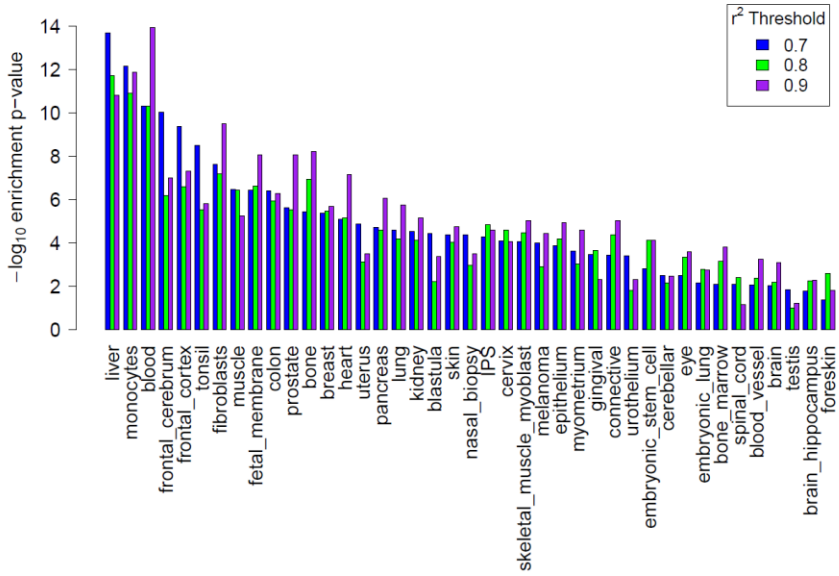
SUPPLEMENTARY FIGURES

Supplementary Figure 1. Summary of GREGOR variant enrichment method.

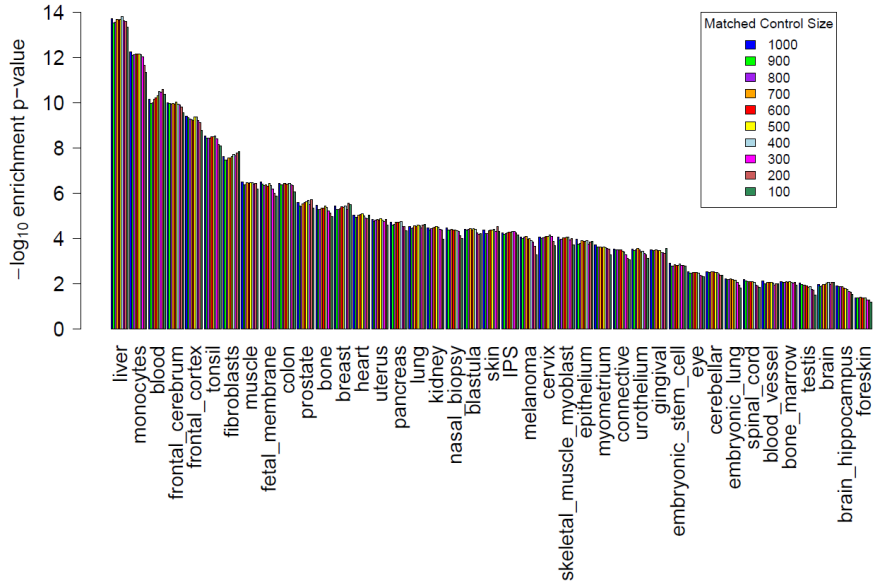


Supplementary Figure 2. Enrichment of lipid-associated variation in DNase hypersensitive sites using different parameter values. Tissues are ordered by decreasing *P*-value significance when using the parameters $r^2 = 0.7$ and matched control set size of 500.

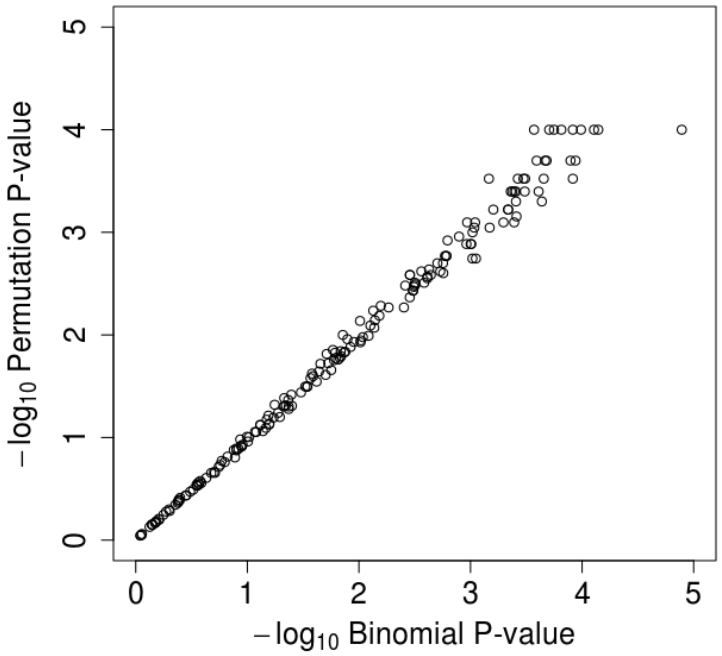
A. Magnitude of enrichment for a range of r^2 thresholds. The r^2 thresholds were used to select i. the potential functional variants in LD with index variants using 1000 Genomes CEU and ii. The control SNPs with approximately the same number of variants in LD as index variants (using the same threshold as in i). The higher the r^2 value, the fewer variants in LD would be selected.



B. Magnitude of enrichment for matched control sets of various sizes. Matched control sets contain variants that share the properties of 1) number of LD proxies, 2) minor allele frequency, and 3) gene proximity. The more variants selected as controls, the less close the matching.

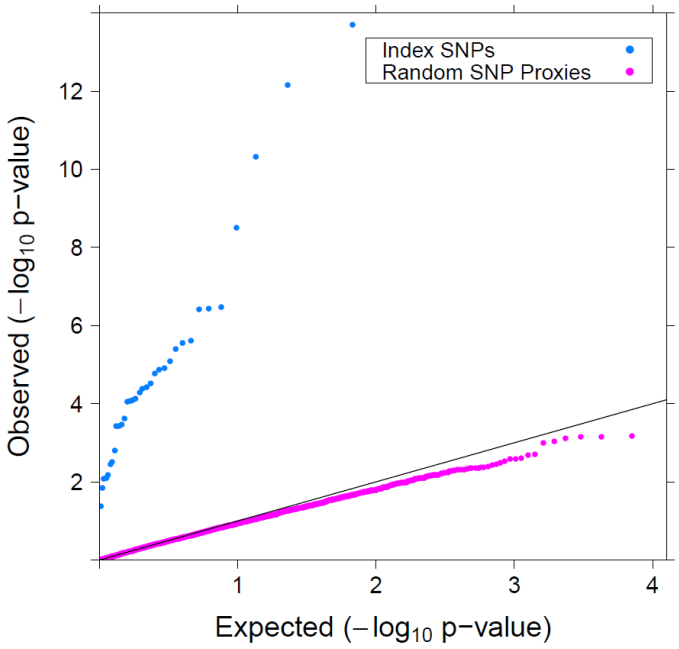


Supplementary Figure 3. Enrichment *P*-values estimated using 10,000 permutations (y-axis) and the sum of binomial trials as implemented in GREGOR (x-axis) show high concordance. *P*-values less than $1x10^{-5}$ cannot be precisely estimated by permutation testing, and so are excluded from the figure.

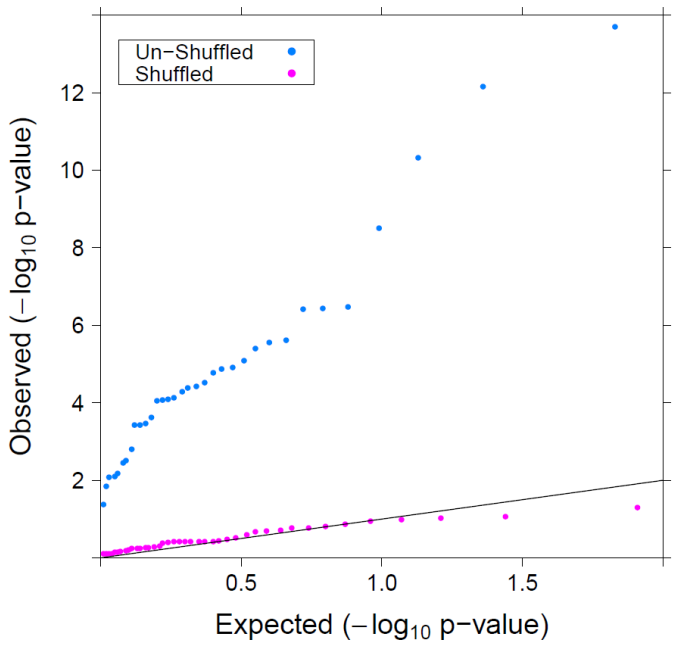


Supplementary Figure 4. QQ plots of enrichment performance for lipid-associated variation in DNase hypersensitive sites and control sets.

A. Permutation of index variants: A set of 50 lists of 'SNP proxies' was generated, where each list contained SNPs that match the lipid-associated SNPs on 3 properties: 1) number of LD proxies, 2) minor allele frequency, and 3) gene proximity but were otherwise randomly selected from across the genome. Enrichment *P*-values were calculated for each list and are shown in the pink distribution.

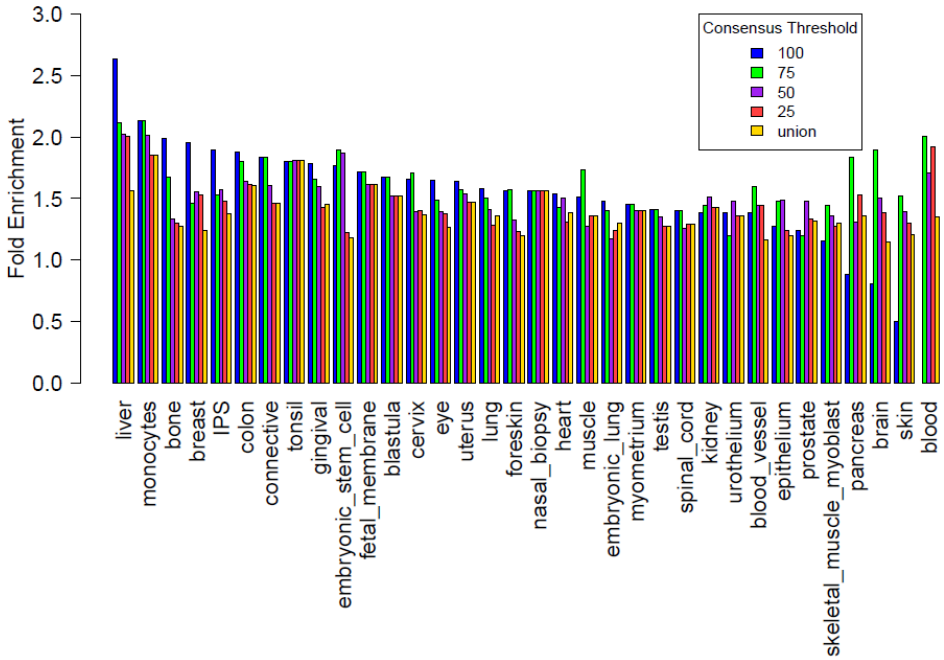


B. Shuffling of DHSs partitioned by genic landmark categories: We investigated type I error by categorizing DHSs using a hierarchical partitioning approach (Parker, et al., 2013). DHSs were partitioned into mutually exclusive genic landmark categories based on GENCODE annotation (e.g. 3'UTR, 5'UTR, intron, coding exons, intergenic TSS distal and proximal). We randomly shuffled DHSs within each of these categories, and then re-combined them for enrichment analysis. We evaluated the enrichment *P*-value distribution of lipid-associated variants in DHSs of these partitioned-then-shuffled DHSs (pink) and compared it with the *P*-value distribution in the original DHSs (blue). By this approach, we still see compelling type I error while maintaining the relationship between gene proximity and DHSs.

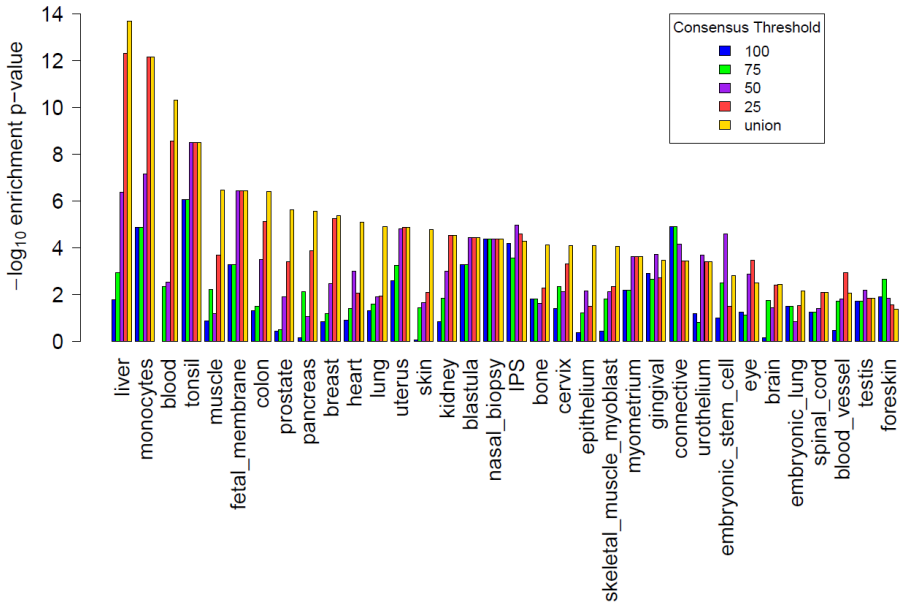


Supplementary Figure 5. Fold enrichment (A) and enrichment *P*-values (B) for lipid-associated variation in DNase hypersensitive sites (DHSs) of different tissues and at different 'consensus thresholds'. A consensus threshold is defined as the percentage of shared DHS regions among cell types derived from a given tissue.

A. Fold Enrichment

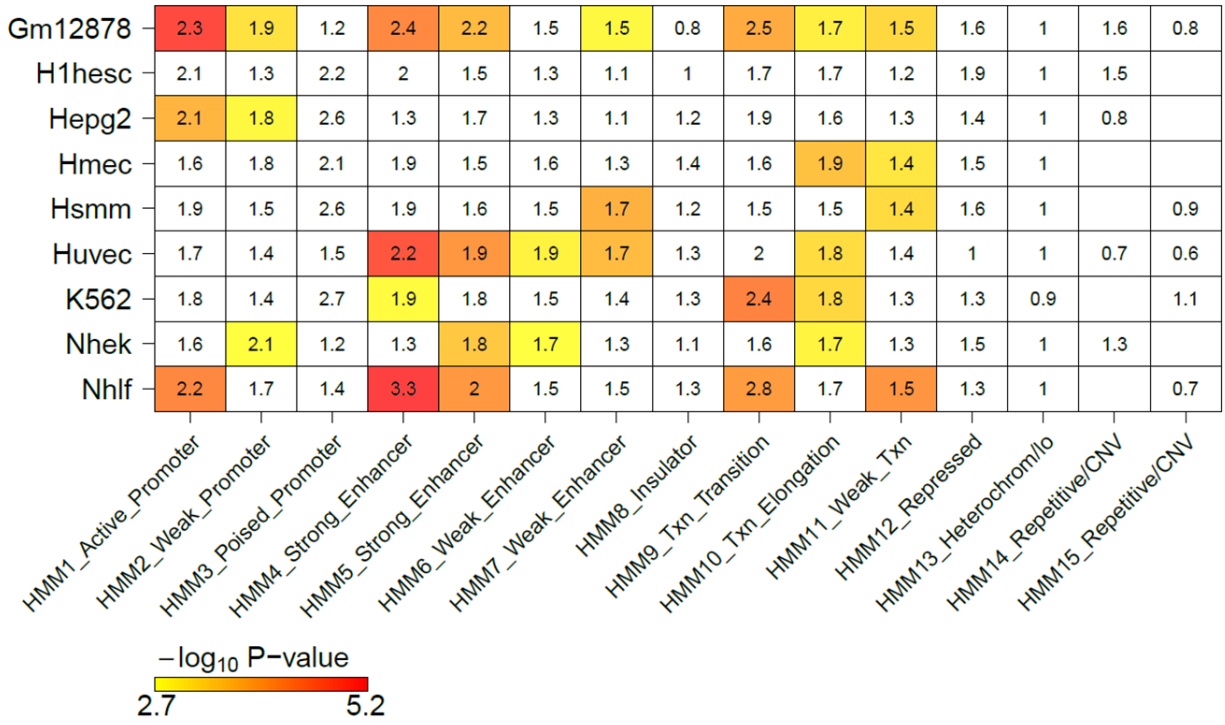


B. Enrichment *P*-values

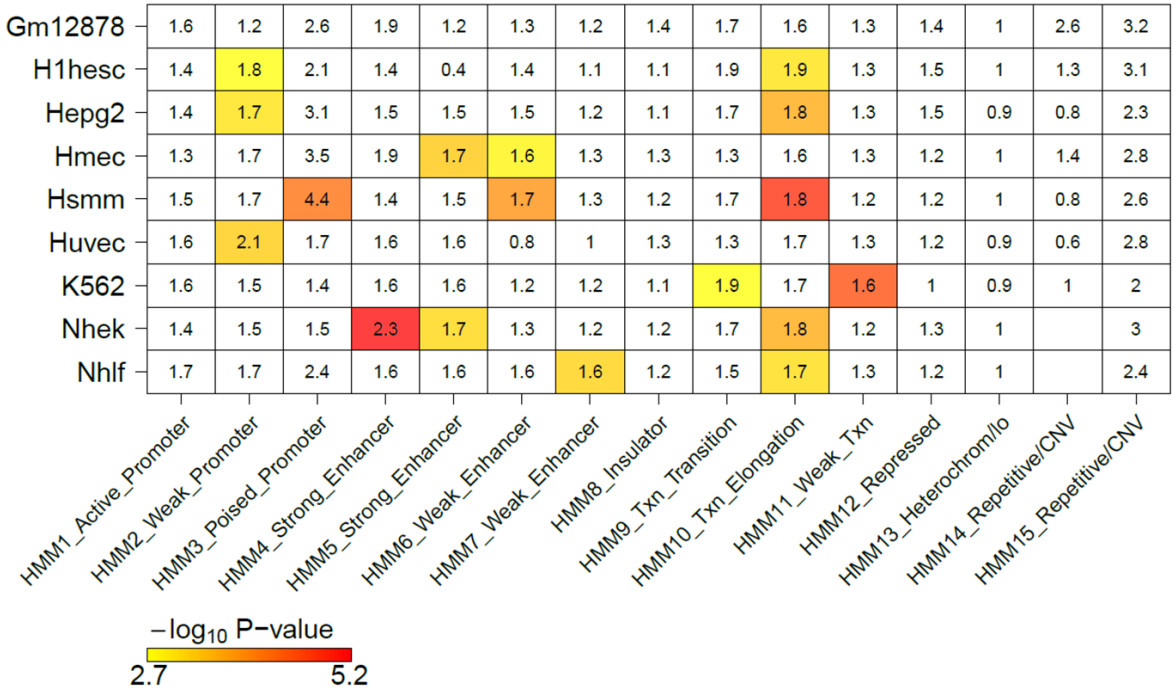


Supplementary Figure 6. Matrix of fold enrichment for five sets of trait-associated variants in predicted chromatin states in nine human cell types (HMM, hidden Markov model; txn, transcription; lo, low signal; CNV, copy number variation) (Ernst, et al., 2011). Boxes are colored by $-\log_{10}$ enrichment *P*-value. White color indicates not significant after Bonferroni correction for 15 chromatin states and 9 tissues.

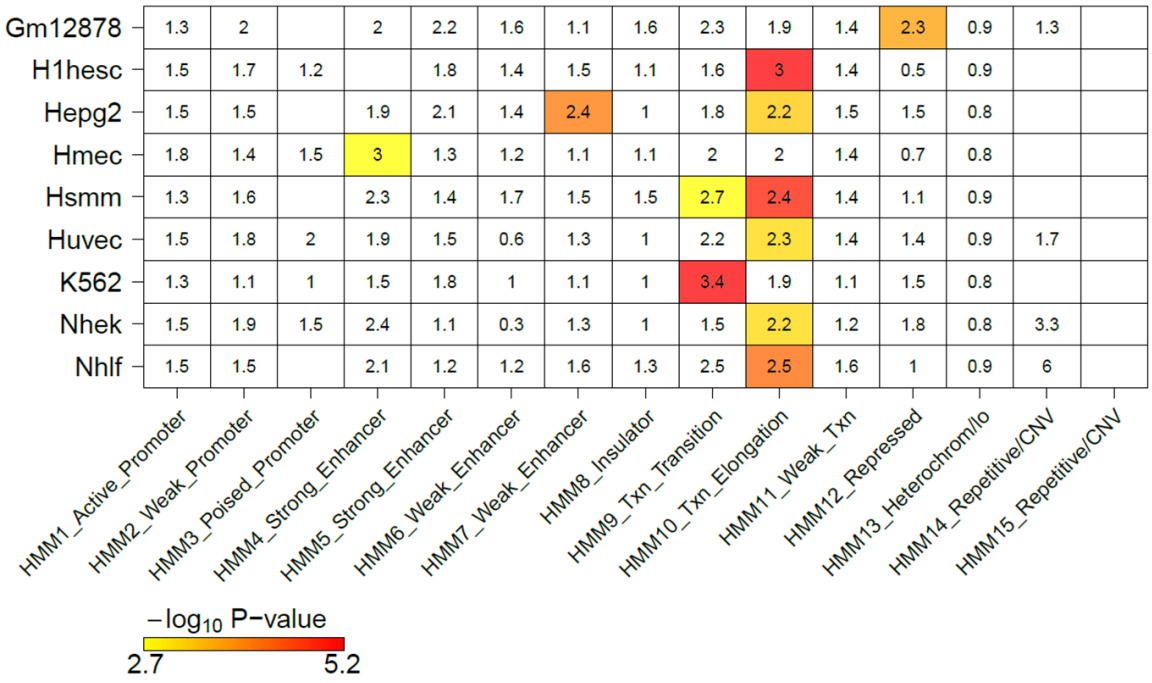
A. Blood Pressure GWAS variants (n=99)



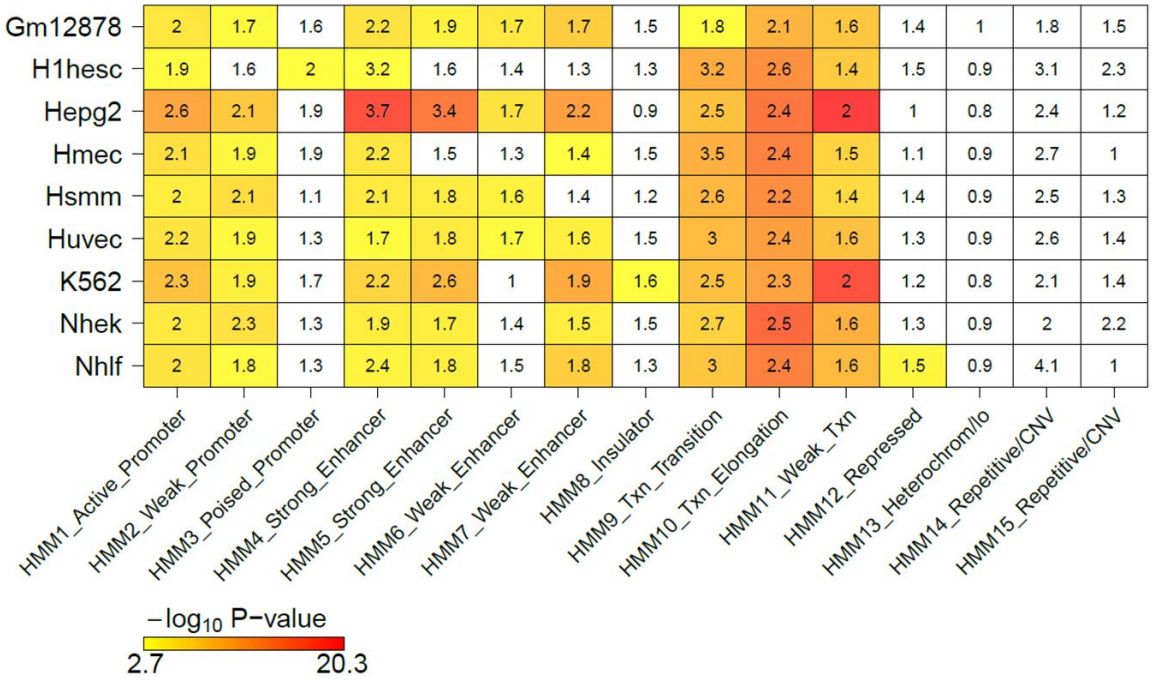
B. Body Mass Index GWAS variants (n=97)



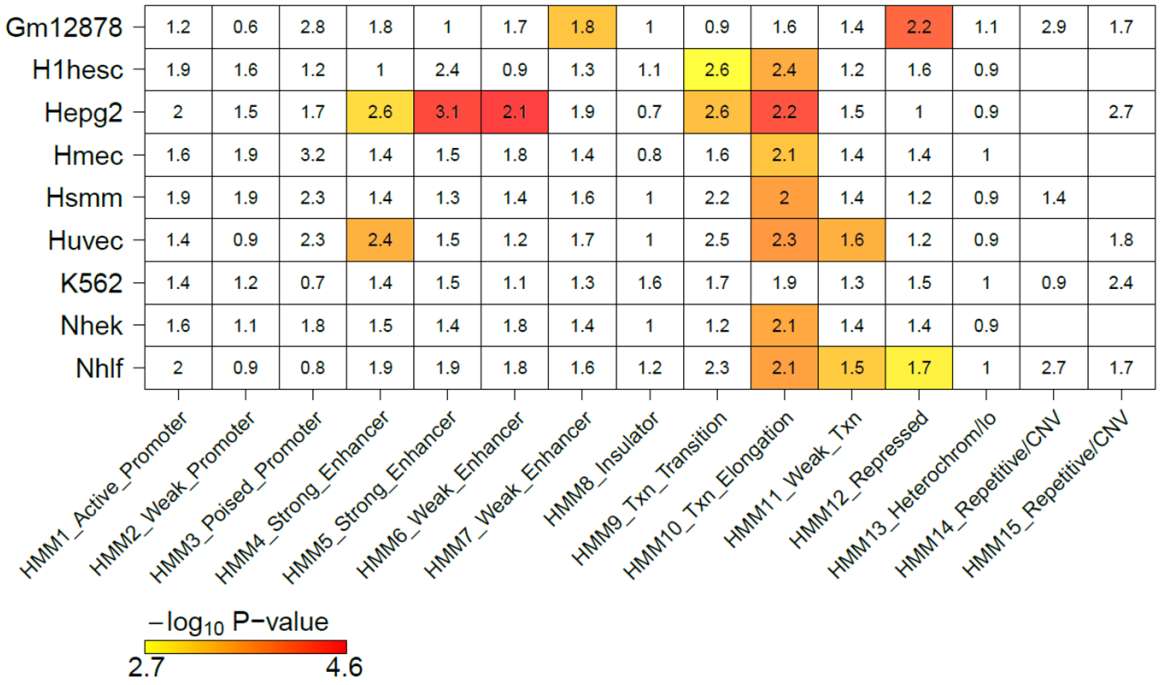
C. Coronary Artery Disease GWAS variants (n=36)



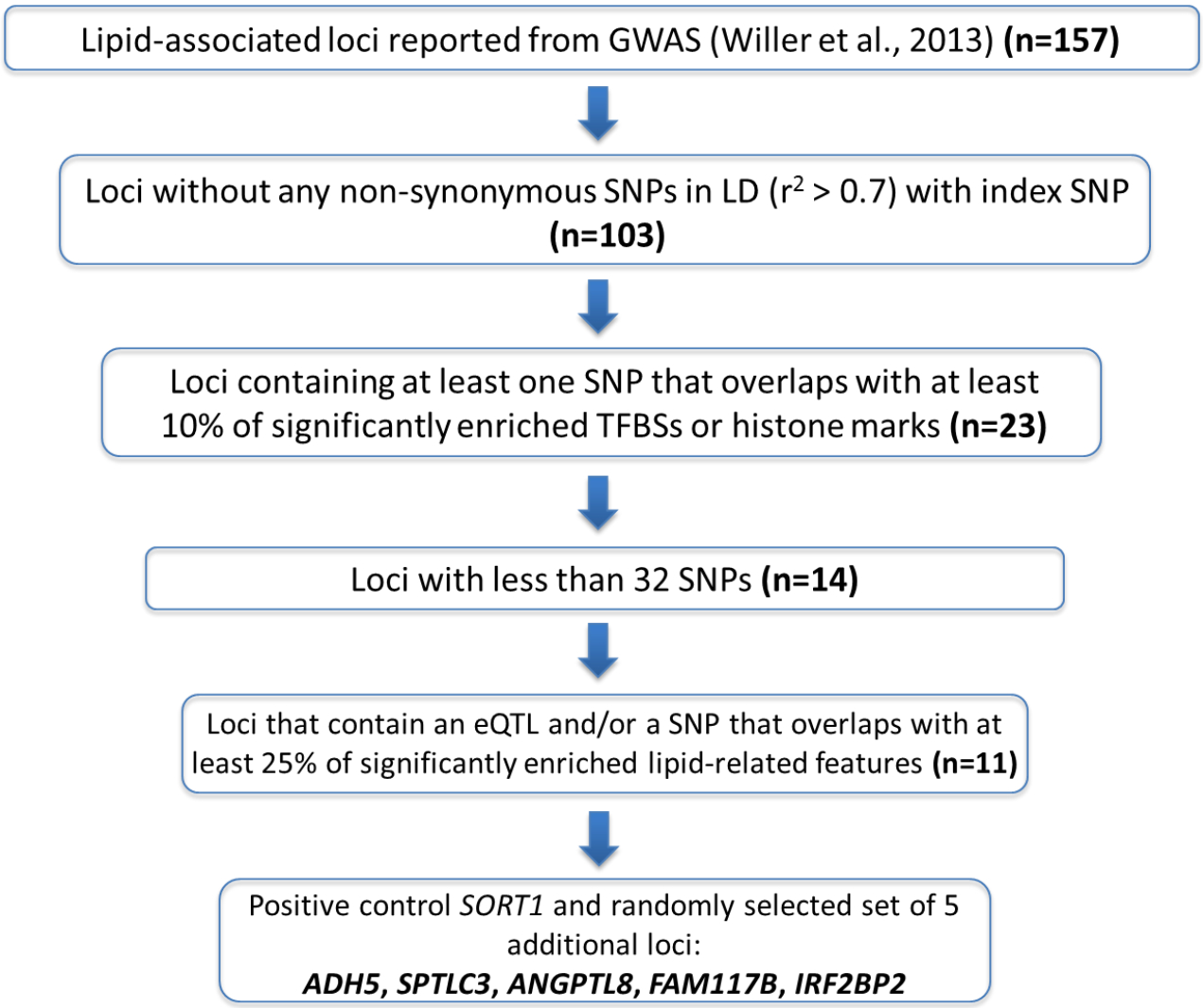
D. Lipids GWAS variants (n=157)



E. Type 2 Diabetes GWAS variants (n=65)

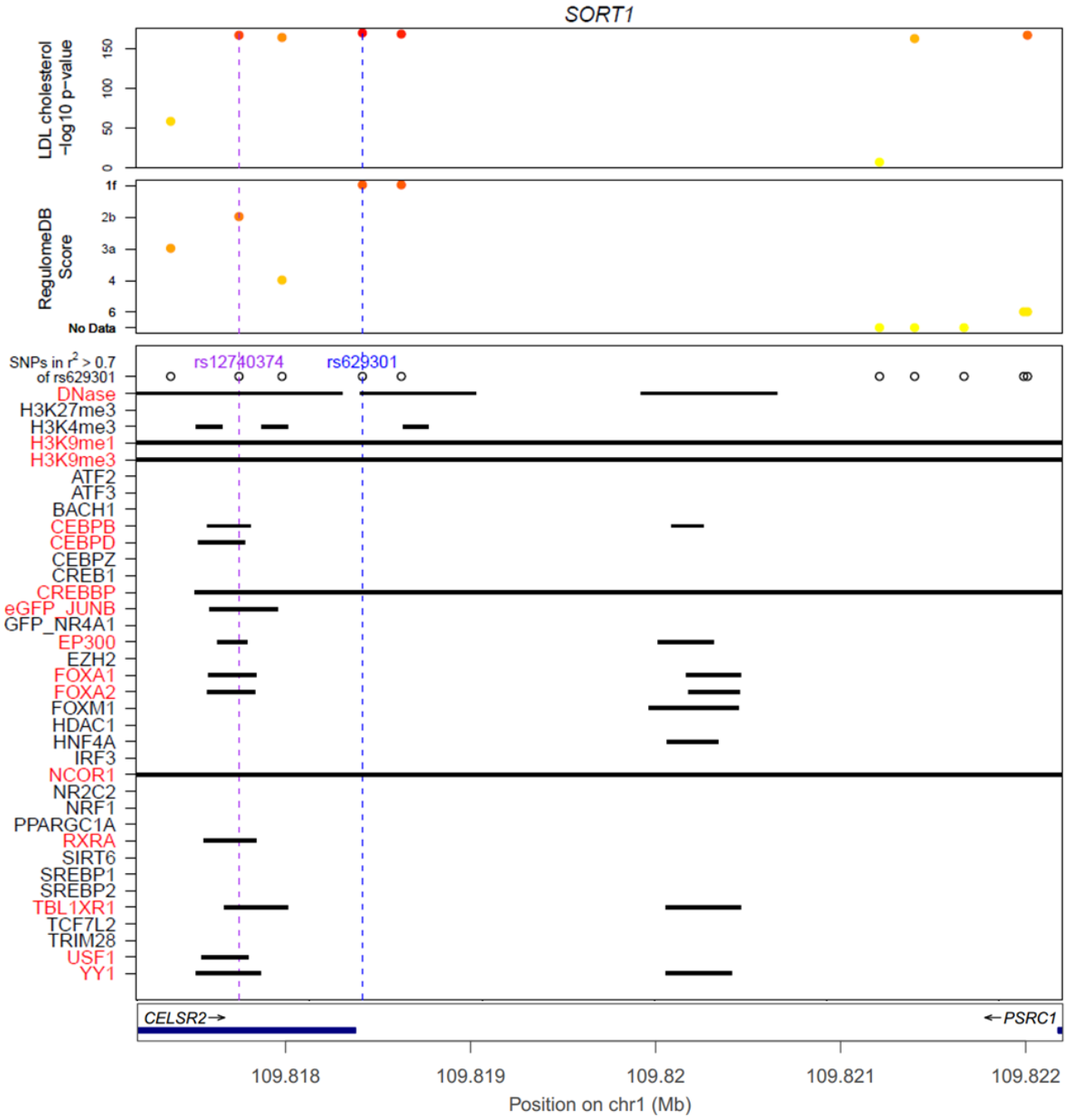


Supplementary Figure 7. Prioritization of lipid-associated loci for functional follow-up. Prioritization is based on functional annotation, physical overlap with regulatory domains, and association with transcript levels in relevant tissues. Each expression quantitative trait locus (eQTL) contains at least one variant associated with expression level changes in either liver, omental fat, or subcutaneous fat (eQTL $P < 1x10^{-3}$).

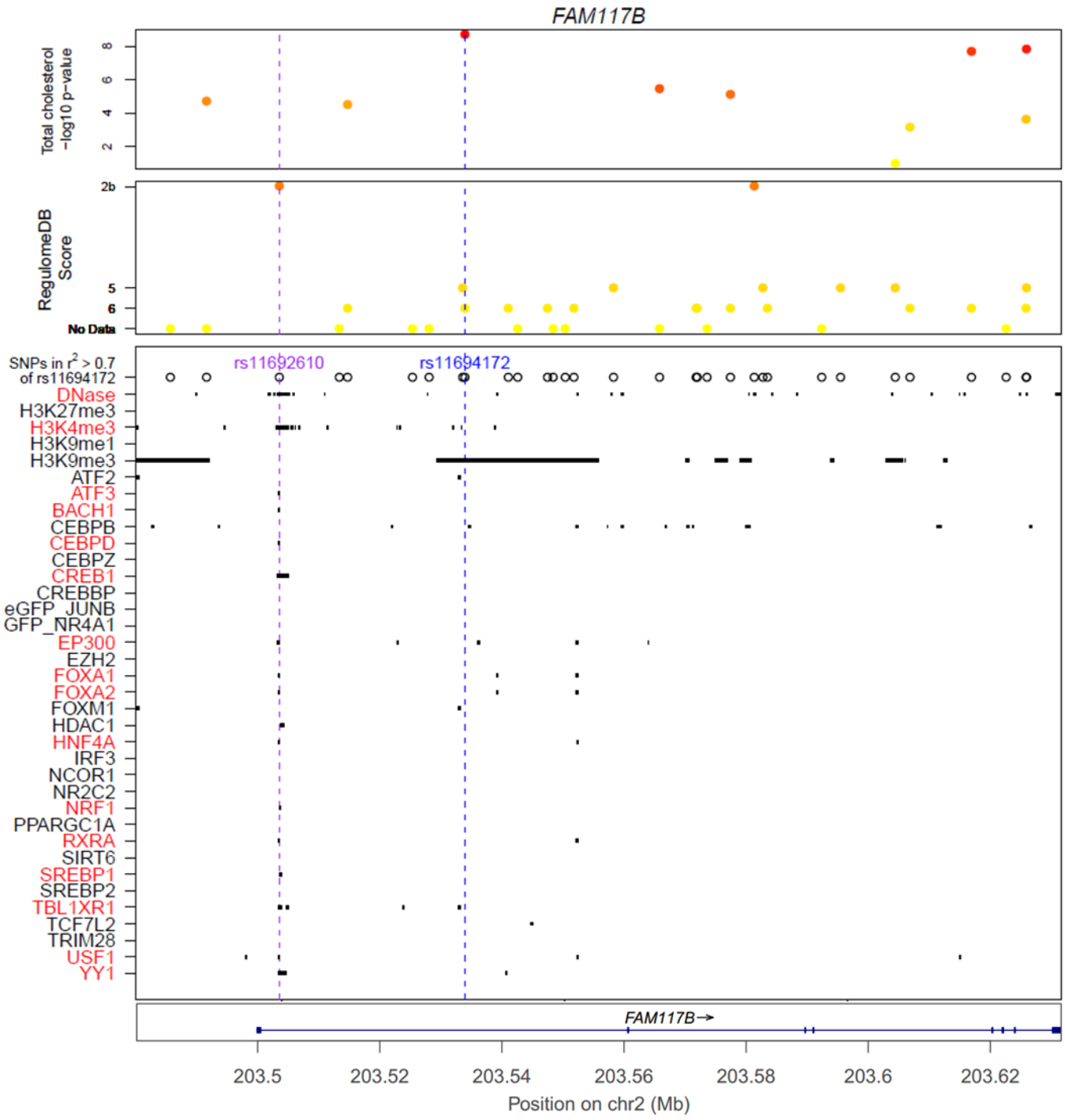


Supplementary Figure 8. Physical overlap of variants at six lipid loci (SNPs within $r^2 > 0.7$ of the GWAS index SNP) with ChIP-seq or DNase-seq binding sites for lipid-related ENCODE features (The ENCODE Project Consortium, 2012). GWAS $-\log_{10}$ *P*-values are plotted in the top panel (Teslovich, et al., 2010). RegulomeDB SNP annotation scores of predicted regulatory elements are shown in the second panel (Boyle, et al., 2012). Purple dotted lines annotate the hypothesized functional variant based on physical overlap prediction. Blue dotted lines annotate the control SNP, which is usually the top most significant GWAS SNP. Regulatory elements highlighted in red annotate overlap with the candidate functional variant.

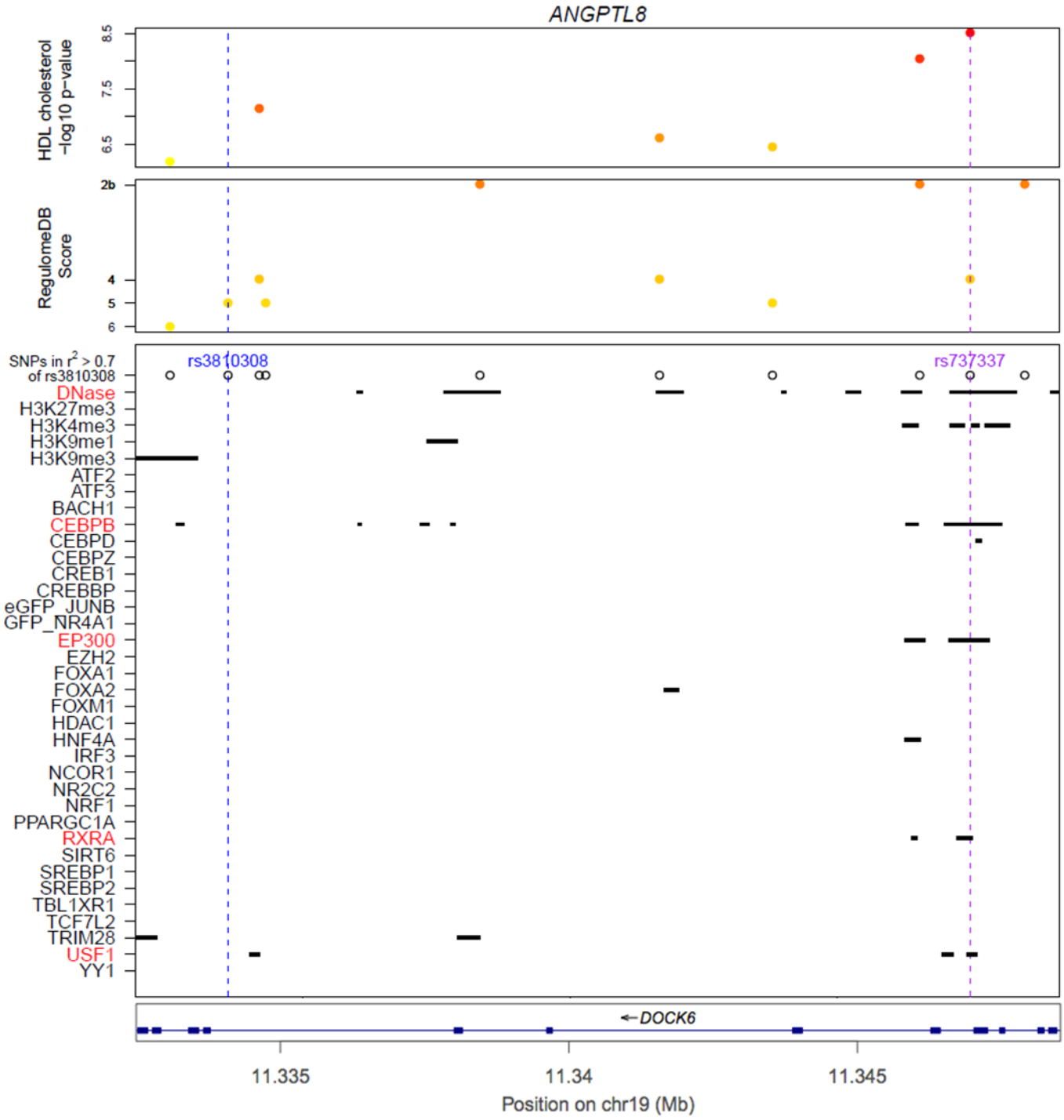
A. ***SORT1* (sortilin 1)**. GWAS index SNP rs629301 is associated with LDL cholesterol and total cholesterol.



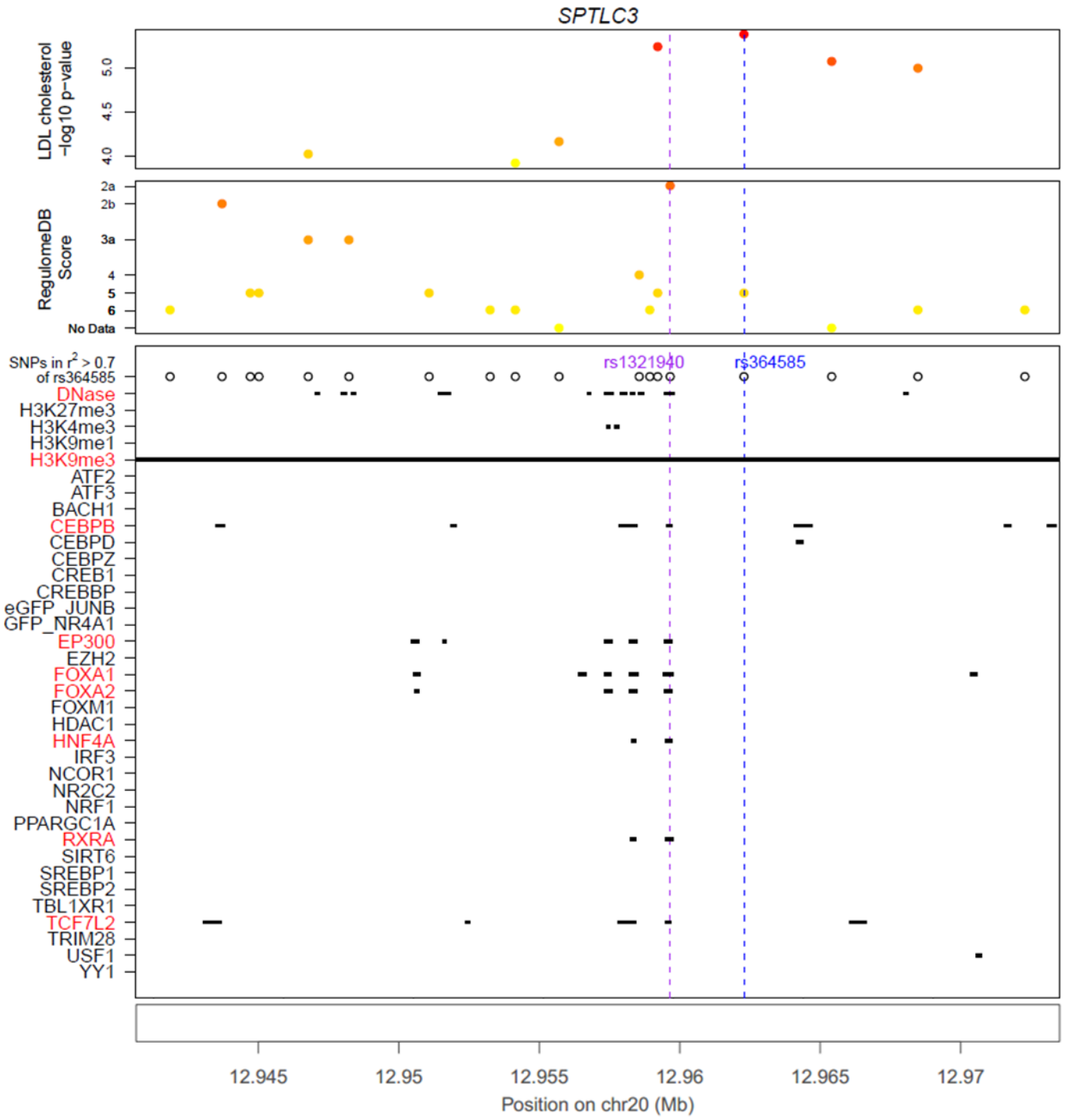
B. ***FAM117B* (family with sequence similarity 117, member B)**. GWAS index SNP rs11694172 is associated with total cholesterol.



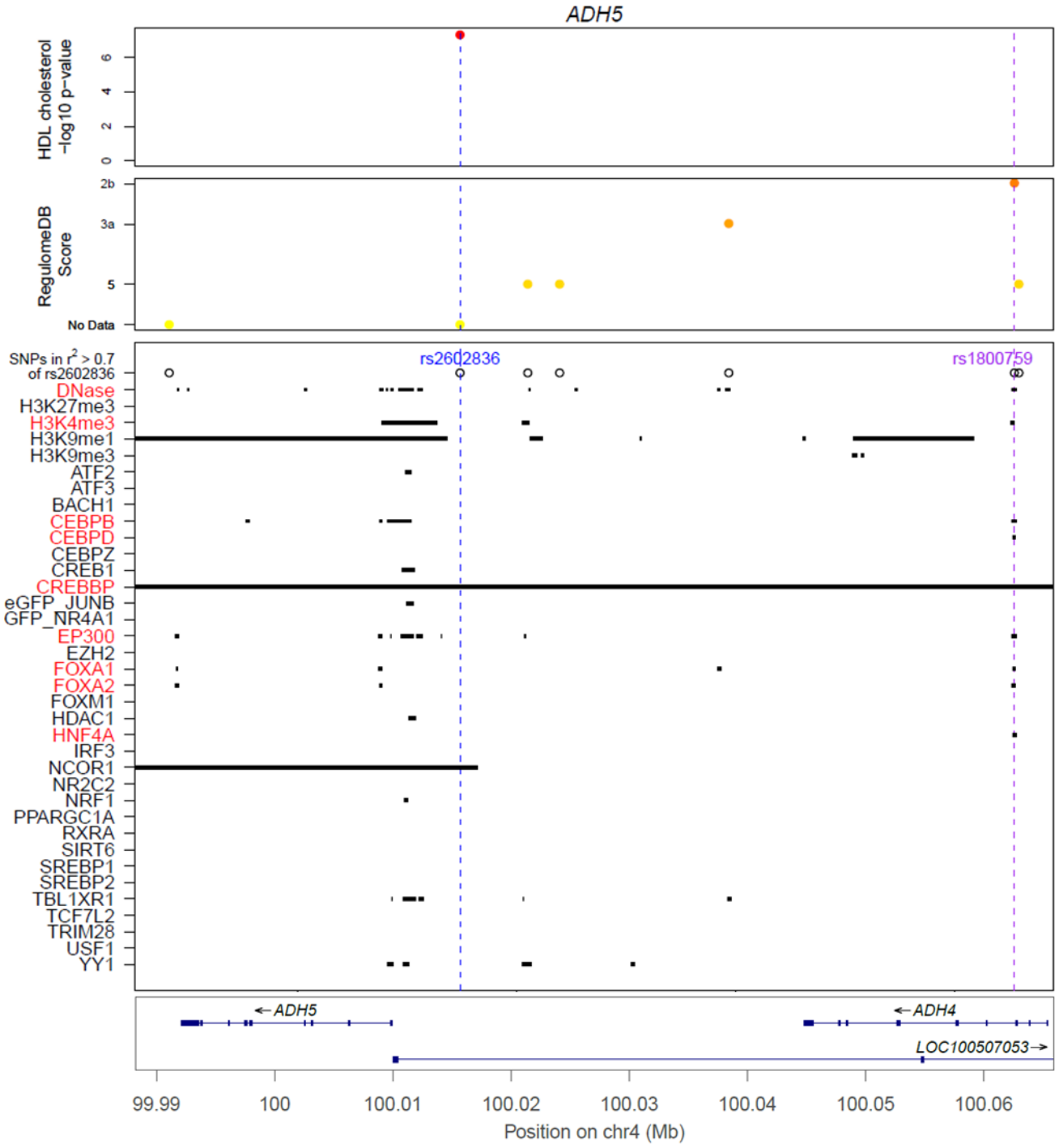
C. ***ANGPTL8* (Angiopoietin-like protein 8; C19orf80: chromosome 19 open reading frame 80)**. GWAS index SNP rs737337 is associated with HDL cholesterol, and the candidate functional SNP.



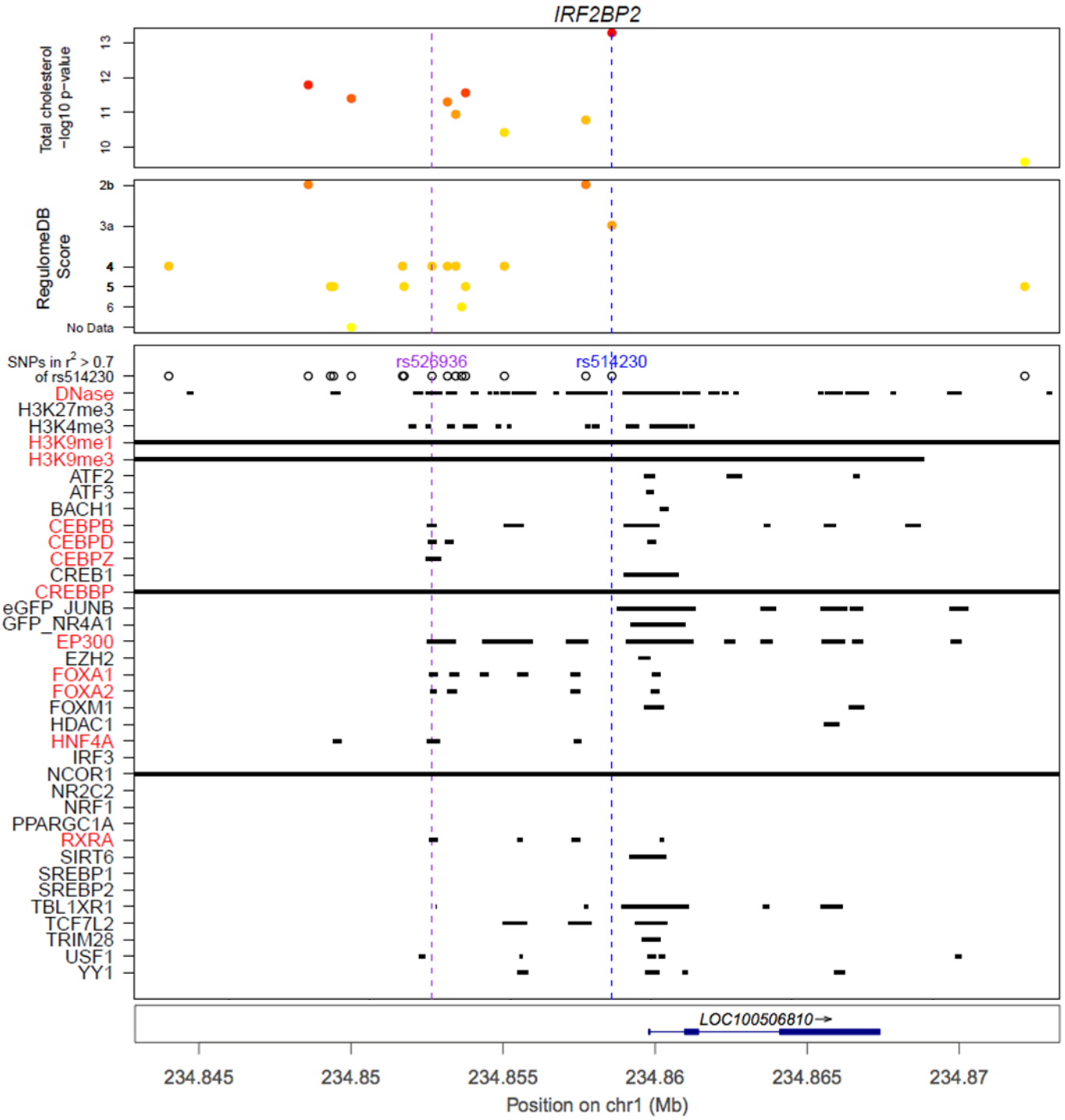
D. ***SPTLC3* (serine palmitoyltransferase, long chain base subunit 3)**. GWAS index SNP rs364585 is associated with LDL cholesterol.



E. ***ADH5* (alcohol dehydrogenase 5 (class III), chi polypeptide)**. GWAS index SNP rs2602836 is associated with HDL cholesterol. GWAS *P*-values here are reported from (Willer, et al., 2013).



F. ***IRF2BP2* (interferon regulatory factor 2 binding protein 2)**. GWAS index SNP rs514230 is associated with total cholesterol and LDL cholesterol.



SUPPLEMENTARY TABLES

Supplementary Table 1. ENCODE DNase hypersensitivity sites from various tissues are categorized into broader tissue groups for enrichment analysis.

broad_tissue_category	ENCODE_tissue_category	BED_File
blastula	blastula	wgEncodeAwgDnaseDukeHtr8svnUniPk.narrowPeak
blastula	blastula	wgEncodeOpenChromDnaseHtr8Pk.narrowPeak
blood	blood	wgEncodeAwgDnaseDukeCllUniPk.narrowPeak
blood	blood	wgEncodeAwgDnaseDukeGm12891UniPk.narrowPeak
blood	blood	wgEncodeAwgDnaseDukeGm12892UniPk.narrowPeak
blood	blood	wgEncodeAwgDnaseDukeGm18507UniPk.narrowPeak
blood	blood	wgEncodeAwgDnaseDukeGm19238UniPk.narrowPeak
blood	blood	wgEncodeAwgDnaseDukeGm19239UniPk.narrowPeak
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blood	blood	wgEncodeUwDnaseK562PkRep2.narrowPeak
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blood	blood	wgEncodeUwDnaseTh2PkRep2.narrowPeak
blood	blood	wgEncodeUwDnaseTh2wb33676984PkRep1.narrowPeak
blood	blood	wgEncodeUwDnaseTh2wb54553204PkRep1.narrowPeak
blood	blood	wgEncodeUwDnaseTregwb78495824PkRep1.narrowPeak
blood	blood	wgEncodeUwDnaseTregwb83319432PkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseDukeAosmcUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwAoafUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwdukeHuvecUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHbmecUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmvecdadUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmvecdbladUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmvecdblneoUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmvecdlyadUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmvecdlyneoUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmvecdneoUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmveclblUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHmvecllyUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHpaecUniPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeAwgDnaseUwHpafUniPk.narrowPeak

blood_vessel	blood_vessel	wgEncodeOpenChromDnaseAosmcSerumfreePk.narrowPeak
blood_vessel	blood_vessel	wgEncodeOpenChromDnaseHuvecPk.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseAoafPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseAoafPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHbmecPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHbmecPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHbvpPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHbvsmcPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHbvsmcPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdadPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdadPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdbladPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdbladPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdblneoPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdblneoPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdlyadPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdlyadPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdlyneoPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdlyneoPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdneoPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmvecdneoPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmveclblPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmveclblPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmveclly PkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHmveclly PkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHpaecPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHpafPkRep1.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHpafPkRep2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHuvecPkRep1V2.narrowPeak
blood_vessel	blood_vessel	wgEncodeUwDnaseHuvecPkRep2.narrowPeak
bone	bone	wgEncodeAwgDnaseDukeOsteoblUniPk.narrowPeak
bone	bone	wgEncodeOpenChromDnaseOsteoblPk.narrowPeak
bone_marrow	bone_marrow	wgEncodeUwDnaseHs27aPkRep1.narrowPeak

bone_marrow	bone_marrow	wgEncodeUwDnaseHs5PkRep1.narrowPeak
bone_marrow	bone_marrow	wgEncodeUwDnaseMscPkRep1.narrowPeak
bone_marrow	bone_marrow	wgEncodeUwDnaseMscPkRep2.narrowPeak
brain	brain	wgEncodeAwgDnaseDukeGlioblaUniPk.narrowPeak
brain	brain	wgEncodeAwgDnaseDukeMedulloUniPk.narrowPeak
brain	brain	wgEncodeAwgDnaseUwBe2cUniPk.narrowPeak
brain	brain	wgEncodeAwgDnaseUwNhaUniPk.narrowPeak
brain	brain	wgEncodeAwgDnaseUwSknmcUniPk.narrowPeak
brain	brain	wgEncodeAwgDnaseUwSknshraUniPk.narrowPeak
brain	brain	wgEncodeOpenChromDnaseGlioblaPk.narrowPeak
brain	brain	wgEncodeOpenChromDnaseMedullod341Pk.narrowPeak
brain	brain	wgEncodeOpenChromDnaseMedulloPk.narrowPeak
brain	brain	wgEncodeOpenChromDnaseSknshPk.narrowPeak
brain	brain	wgEncodeUwDnaseBe2cPkRep1.narrowPeak
brain	brain	wgEncodeUwDnaseBe2cPkRep2.narrowPeak
brain	brain	wgEncodeUwDnaseM059jPkRep1.narrowPeak
brain	brain	wgEncodeUwDnaseM059jPkRep2.narrowPeak
brain	brain	wgEncodeUwDnaseNhaPkRep1.narrowPeak
brain	brain	wgEncodeUwDnaseNhaPkRep2.narrowPeak
brain	brain	wgEncodeUwDnaseSknmcPkRep1.narrowPeak
brain	brain	wgEncodeUwDnaseSknmcPkRep2.narrowPeak
brain	brain	wgEncodeUwDnaseSknshraPkRep1.narrowPeak
brain	brain	wgEncodeUwDnaseSknshraPkRep2.narrowPeak
brain_hippocampus	brain_hippocampus	wgEncodeAwgDnaseUwHahUniPk.narrowPeak
brain_hippocampus	brain_hippocampus	wgEncodeUwDnaseHahPkRep1.narrowPeak
brain_hippocampus	brain_hippocampus	wgEncodeUwDnaseHahPkRep2.narrowPeak
breast	breast	wgEncodeAwgDnaseDukeMcf7hypoxiaUniPk.narrowPeak
breast	breast	wgEncodeAwgDnaseDukeT47dUniPk.narrowPeak
breast	breast	wgEncodeAwgDnaseUwdukeHmecUniPk.narrowPeak
breast	breast	wgEncodeAwgDnaseUwdukeMcf7UniPk.narrowPeak
breast	breast	wgEncodeOpenChromDnaseHmecPk.narrowPeak
breast	breast	wgEncodeOpenChromDnaseMcf7CtcfshrnaPk.narrowPeak
breast	breast	wgEncodeOpenChromDnaseMcf7HypoxlacconPk.narrowPeak

breast	breast	wgEncodeOpenChromDnaseMcf7HypoxlacPk.narrowPeak
breast	breast	wgEncodeOpenChromDnaseMcf7Pk.narrowPeak
breast	breast	wgEncodeOpenChromDnaseMcf7RandshrnaPk.narrowPeak
breast	breast	wgEncodeOpenChromDnaseT47dEst10nm30mPk.narrowPeak
breast	breast	wgEncodeOpenChromDnaseT47dPk.narrowPeak
breast	breast	wgEncodeUwDnaseHmecPkRep1.narrowPeak
breast	breast	wgEncodeUwDnaseHmecPkRep2.narrowPeak
breast	breast	wgEncodeUwDnaseMcf7Est100nm1hPkRep1.narrowPeak
breast	breast	wgEncodeUwDnaseMcf7Est100nm1hPkRep2.narrowPeak
breast	breast	wgEncodeUwDnaseMcf7Estctrl0hPkRep1.narrowPeak
breast	breast	wgEncodeUwDnaseMcf7Estctrl0hPkRep2.narrowPeak
breast	breast	wgEncodeUwDnaseMcf7PkRep1.narrowPeak
breast	breast	wgEncodeUwDnaseMcf7PkRep2.narrowPeak
breast	breast	wgEncodeUwDnaseT47dPkRep1.narrowPeak
breast	breast	wgEncodeUwDnaseT47dPkRep2.narrowPeak
breast	mammary	wgEncodeAwgDnaseUwHmfUniPk.narrowPeak
breast	mammary	wgEncodeUwDnaseHmfPkRep1.narrowPeak
breast	mammary	wgEncodeUwDnaseHmfPkRep2.narrowPeak
cerebellar	cerebellar	wgEncodeAwgDnaseUwHacUniPk.narrowPeak
cerebellar	cerebellar	wgEncodeUwDnaseHacPkRep1.narrowPeak
cerebellar	cerebellar	wgEncodeUwDnaseHacPkRep2.narrowPeak
cerebellar	cerebellum	wgEncodeOpenChromDnaseCerebellumocPk.narrowPeak
cervix	cervix	wgEncodeAwgDnaseDukeHelas3ifna4hUniPk.narrowPeak
cervix	cervix	wgEncodeAwgDnaseUwdukeHelas3UniPk.narrowPeak
cervix	cervix	wgEncodeOpenChromDnaseHelas3Ifna4hPk.narrowPeak
cervix	cervix	wgEncodeOpenChromDnaseHelas3Pk.narrowPeak
cervix	cervix	wgEncodeUwDnaseHelas3PkRep1.narrowPeak
cervix	cervix	wgEncodeUwDnaseHelas3PkRep2.narrowPeak
colon	colon	wgEncodeAwgDnaseUwCaco2UniPk.narrowPeak
colon	colon	wgEncodeAwgDnaseUwHct116UniPk.narrowPeak
colon	colon	wgEncodeUwDnaseCaco2PkRep1.narrowPeak
colon	colon	wgEncodeUwDnaseCaco2PkRep2.narrowPeak
colon	colon	wgEncodeUwDnaseHct116PkRep1.narrowPeak

colon	colon	wgEncodeUwDnaseHct116PkRep2.narrowPeak
connective	connective	wgEncodeAwgDnaseUwHvmfUniPk.narrowPeak
connective	connective	wgEncodeUwDnaseHvmfPkRep1.narrowPeak
connective	connective	wgEncodeUwDnaseHvmfPkRep2.narrowPeak
embryonic_lung	embryonic_lung	wgEncodeAwgDnaseUwWi38tamoxifentamoxifenUniPk.narrowPeak
embryonic_lung	embryonic_lung	wgEncodeAwgDnaseUwWi38UniPk.narrowPeak
embryonic_lung	embryonic_lung	wgEncodeUwDnaseWi38OhtamPkRep1.narrowPeak
embryonic_lung	embryonic_lung	wgEncodeUwDnaseWi38OhtamPkRep2.narrowPeak
embryonic_lung	embryonic_lung	wgEncodeUwDnaseWi38PkRep1.narrowPeak
embryonic_lung	embryonic_lung	wgEncodeUwDnaseWi38PkRep2.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeAwgDnaseDukeH9esUniPk.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeAwgDnaseUwdukeH1hescUniPk.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeAwgDnaseUwH7hescUniPk.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeOpenChromDnaseH1hescPk.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeOpenChromDnaseH7esPk.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeOpenChromDnaseH9esPk.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH1hescPkRep1.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esDiffa14dPkRep1.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esDiffa14dPkRep2.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esDiffa2dPkRep1.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esDiffa5dPkRep1.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esDiffa5dPkRep2.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esDiffa9dPkRep1.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esPkRep1V2.narrowPeak
embryonic_stem_cell	embryonic_stem_cell	wgEncodeUwDnaseH7esPkRep2.narrowPeak
epithelium	bronchial_epithelium	wgEncodeUwDnaseNhberaPkRep1.narrowPeak
epithelium	bronchial_epithelium	wgEncodeUwDnaseNhberaPkRep2.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseDukePhteUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwdukeA549UniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHaepicUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHcpepicUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHeepicUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHipepicUniPk.narrowPeak

epithelium	epithelium	wgEncodeAwgDnaseUwHnpcepicUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHpdlfUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHrcepicUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHreUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwHrpepicUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwRptecUniPk.narrowPeak
epithelium	epithelium	wgEncodeAwgDnaseUwSaecUniPk.narrowPeak
epithelium	epithelium	wgEncodeOpenChromDnaseA549Pk.narrowPeak
epithelium	epithelium	wgEncodeOpenChromDnasePhtePk.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseA549PkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseA549PkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHaePkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHaePkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHcpePkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHcpePkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHeePkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHeePkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHipePkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHipePkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHnpcePkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHnpcePkRep2V2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHpdlfPkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHpdlfPkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHrcePkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHrcePkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHrePkRep1V2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHrePkRep2V2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHrpePkRep1V2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseHrpePkRep2V2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseRptecPkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseRptecPkRep2.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseSaecPkRep1.narrowPeak
epithelium	epithelium	wgEncodeUwDnaseSaecPkRep2.narrowPeak

epithelium	luminal_epithelium	wgEncodeOpenChromDnaseEcc1Dm002p1hPk.narrowPeak
epithelium	luminal_epithelium	wgEncodeOpenChromDnaseEcc1Est10nm30mPk.narrowPeak
epithelium	pancreatic_duct	wgEncodeAwgDnaseDukeHpde6e6e7UniPk.narrowPeak
epithelium	pancreatic_duct	wgEncodeOpenChromDnaseHpde6e6e7Pk.narrowPeak
eye	eye	wgEncodeAwgDnaseUwHconfUniPk.narrowPeak
eye	eye	wgEncodeAwgDnaseUwWerirb1UniPk.narrowPeak
eye	eye	wgEncodeUwDnaseHconfPkRep1.narrowPeak
eye	eye	wgEncodeUwDnaseHconfPkRep2.narrowPeak
eye	eye	wgEncodeUwDnaseWerirb1PkRep1.narrowPeak
eye	eye	wgEncodeUwDnaseWerirb1PkRep2.narrowPeak
fetal_membrane	fetal_membrane	wgEncodeAwgDnaseDukeChorionUniPk.narrowPeak
fetal_membrane	fetal_membrane	wgEncodeOpenChromDnaseChorionPk.narrowPeak
fibroblasts	lung_fibroblast	wgEncodeOpenChromDnaseFibropag08396Pk.narrowPeak
fibroblasts	skin	wgEncodeAwgDnaseDukeFibroblUniPk.narrowPeak
fibroblasts	skin	wgEncodeAwgDnaseDukeFibropUniPk.narrowPeak
fibroblasts	skin	wgEncodeOpenChromDnaseFibroblgm03348LenticonPk.narrowPeak
fibroblasts	skin	wgEncodeOpenChromDnaseFibroblgm03348LentimyodPk.narrowPeak
fibroblasts	skin	wgEncodeOpenChromDnaseFibroblgm03348Pk.narrowPeak
fibroblasts	skin	wgEncodeOpenChromDnaseFibroblPk.narrowPeak
fibroblasts	skin	wgEncodeOpenChromDnaseFibropPk.narrowPeak
fibroblasts	skin_fibroblast	wgEncodeOpenChromDnaseFibropag08395Pk.narrowPeak
fibroblasts	skin_fibroblast	wgEncodeOpenChromDnaseFibropag20443Pk.narrowPeak
foreskin	foreskin	wgEncodeAwgDnaseUwHffmycUniPk.narrowPeak
foreskin	foreskin	wgEncodeAwgDnaseUwHffUniPk.narrowPeak
foreskin	foreskin	wgEncodeUwDnaseHffmycPkRep1.narrowPeak
foreskin	foreskin	wgEncodeUwDnaseHffmycPkRep2.narrowPeak
foreskin	foreskin	wgEncodeUwDnaseHffPkRep1.narrowPeak
foreskin	foreskin	wgEncodeUwDnaseHffPkRep2.narrowPeak
frontal_cerebrum	frontal_cerebrum	wgEncodeOpenChromDnaseCerebrumfrontalocPk.narrowPeak
frontal_cortex	frontal_cortex	wgEncodeOpenChromDnaseFrontalcortexocPk.narrowPeak
gingival	gingiva	wgEncodeAwgDnaseUwHgfUniPk.narrowPeak
gingival	gingiva	wgEncodeUwDnaseHgfPkRep1.narrowPeak
gingival	gingiva	wgEncodeUwDnaseHgfPkRep2.narrowPeak

gingival	gingival	wgEncodeAwgDnaseUwAg09319UniPk.narrowPeak
gingival	gingival	wgEncodeUwDnaseAg09319PkRep1V2.narrowPeak
gingival	gingival	wgEncodeUwDnaseAg09319PkRep2.narrowPeak
heart	heart	wgEncodeAwgDnaseUwHcfaaUniPk.narrowPeak
heart	heart	wgEncodeAwgDnaseUwHcfUniPk.narrowPeak
heart	heart	wgEncodeAwgDnaseUwHcmUniPk.narrowPeak
heart	heart	wgEncodeOpenChromDnaseHeartocPk.narrowPeak
heart	heart	wgEncodeUwDnaseHcfaaPkRep1.narrowPeak
heart	heart	wgEncodeUwDnaseHcfaaPkRep2.narrowPeak
heart	heart	wgEncodeUwDnaseHcfPkRep1.narrowPeak
heart	heart	wgEncodeUwDnaseHcfPkRep2.narrowPeak
heart	heart	wgEncodeUwDnaseHcmPkRep1.narrowPeak
heart	heart	wgEncodeUwDnaseHcmPkRep2.narrowPeak
IPS	induced_pluripotent_cell_iPS	wgEncodeOpenChromDnaseIpscwru1Pk.narrowPeak
IPS	induced_pluripotent_cell_iPS	wgEncodeOpenChromDnaseIpsnihi11Pk.narrowPeak
IPS	induced_pluripotent_cell_iPS	wgEncodeOpenChromDnaseIpsnihi7Pk.narrowPeak
IPS	induced_pluripotent_stem_cell	wgEncodeAwgDnaseDukeIpsUniPk.narrowPeak
IPS	induced_pluripotent_stem_cell	wgEncodeOpenChromDnaseIpsPk.narrowPeak
kidney	kidney	wgEncodeAwgDnaseUwHrgecUniPk.narrowPeak
kidney	kidney	wgEncodeOpenChromDnaseHek293tPk.narrowPeak
kidney	kidney	wgEncodeUwDnaseHrgecPkRep1.narrowPeak
kidney	kidney	wgEncodeUwDnaseHrgecPkRep2.narrowPeak
liver	liver	wgEncodeAwgDnaseDuke8988tUniPk.narrowPeak
liver	liver	wgEncodeAwgDnaseDukeHepatocytesUniPk.narrowPeak
liver	liver	wgEncodeAwgDnaseDukeHuh75UniPk.narrowPeak
liver	liver	wgEncodeAwgDnaseDukeHuh7UniPk.narrowPeak
liver	liver	wgEncodeAwgDnaseDukeStellateUniPk.narrowPeak
liver	liver	wgEncodeAwgDnaseUwdukeHepg2UniPk.narrowPeak
liver	liver	wgEncodeOpenChromDnase8988tPk.narrowPeak
liver	liver	wgEncodeOpenChromDnaseHepatocytesPk.narrowPeak
liver	liver	wgEncodeOpenChromDnaseHepg2Pk.narrowPeak
liver	liver	wgEncodeOpenChromDnaseHuh75Pk.narrowPeak
liver	liver	wgEncodeOpenChromDnaseHuh7Pk.narrowPeak

liver	liver	wgEncodeOpenChromDnaseStellatePk.narrowPeak
liver	liver	wgEncodeUwDnaseHepg2PkRep1.narrowPeak
liver	liver	wgEncodeUwDnaseHepg2PkRep2.narrowPeak
lung	lung	wgEncodeAwgDnaseUwAg04450UniPk.narrowPeak
lung	lung	wgEncodeAwgDnaseUwHpfUniPk.narrowPeak
lung	lung	wgEncodeAwgDnaseUwNhlfUniPk.narrowPeak
lung	lung	wgEncodeOpenChromDnaseImr90Pk.narrowPeak
lung	lung	wgEncodeUwDnaseAg04450PkRep1.narrowPeak
lung	lung	wgEncodeUwDnaseAg04450PkRep2.narrowPeak
lung	lung	wgEncodeUwDnaseHpfPkRep1.narrowPeak
lung	lung	wgEncodeUwDnaseHpfPkRep2.narrowPeak
lung	lung	wgEncodeUwDnaseNhlfPkRep1.narrowPeak
lung	lung	wgEncodeUwDnaseNhlfPkRep2.narrowPeak
melanoma	Melanoma_cell_line_derived_from_melanoma_metastasis	wgEncodeOpenChromDnaseMel2183Pk.narrowPeak
monocytes	monocytes	wgEncodeAwgDnaseUwMonocytescd14ro01746UniPk.narrowPeak
monocytes	monocytes	wgEncodeOpenChromDnaseMonocd14Pk.narrowPeak
monocytes	monocytes	wgEncodeUwDnaseMonocd14ro1746PkRep2.narrowPeak
muscle	muscle	wgEncodeAwgDnaseDukeHsmmembUniPk.narrowPeak
muscle	muscle	wgEncodeAwgDnaseUwdukeHsmmtubeUniPk.narrowPeak
muscle	muscle	wgEncodeAwgDnaseUwSkmcUniPk.narrowPeak
muscle	muscle	wgEncodeOpenChromDnaseHsmmembPk.narrowPeak
muscle	muscle	wgEncodeOpenChromDnaseHsmmfshdPk.narrowPeak
muscle	muscle	wgEncodeOpenChromDnaseHsmmtPk.narrowPeak
muscle	muscle	wgEncodeUwDnaseHsmmtPkRep1.narrowPeak
muscle	muscle	wgEncodeUwDnaseHsmmtPkRep2.narrowPeak
muscle	muscle	wgEncodeUwDnaseSkmcPkRep1.narrowPeak
muscle	muscle	wgEncodeUwDnaseSkmcPkRep2.narrowPeak
muscle	psoas_muscle	wgEncodeOpenChromDnasePsoasmuscleocPk.narrowPeak
myometrium	myometrium	wgEncodeAwgDnaseDukeMyometrUniPk.narrowPeak
myometrium	myometrium	wgEncodeOpenChromDnaseMyometrPk.narrowPeak
nasal_biopsy	nasal_biopsy	wgEncodeOpenChromDnaseOlfneurospherePk.narrowPeak
pancreas	pancreas	wgEncodeAwgDnaseDukePanisletdUniPk.narrowPeak
pancreas	pancreas	wgEncodeAwgDnaseDukePanisletsUniPk.narrowPeak

pancreas	pancreas	wgEncodeAwgDnaseUwPanc1UniPk.narrowPeak
pancreas	pancreas	wgEncodeOpenChromDnasePanisdPk.narrowPeak
pancreas	pancreas	wgEncodeOpenChromDnasePanisletsPk.narrowPeak
pancreas	pancreas	wgEncodeUwDnasePanc1PkRep1.narrowPeak
pancreas	pancreas	wgEncodeUwDnasePanc1PkRep2.narrowPeak
prostate	prostate	wgEncodeAwgDnaseDukeLncapandrogenUniPk.narrowPeak
prostate	prostate	wgEncodeAwgDnaseDukeRwpe1UniPk.narrowPeak
prostate	prostate	wgEncodeAwgDnaseUwdukeLncapUniPk.narrowPeak
prostate	prostate	wgEncodeAwgDnaseUwPrecUniPk.narrowPeak
prostate	prostate	wgEncodeOpenChromDnaseLncapAndroPk.narrowPeak
prostate	prostate	wgEncodeOpenChromDnaseLncapPk.narrowPeak
prostate	prostate	wgEncodeOpenChromDnaseRwpe1Pk.narrowPeak
prostate	prostate	wgEncodeUwDnaseLncapPkRep1.narrowPeak
prostate	prostate	wgEncodeUwDnaseLncapPkRep2.narrowPeak
prostate	prostate	wgEncodeUwDnasePrecPkRep1.narrowPeak
prostate	prostate	wgEncodeUwDnasePrecPkRep2.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeAwgDnaseUwdukeHsmmUniPk.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeOpenChromDnaseHsmmPk.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeUwDnaseHsmmPkRep1.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeUwDnaseHsmmPkRep2.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeUwDnaseLhcnm2Diff4dPkRep1.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeUwDnaseLhcnm2Diff4dPkRep2.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeUwDnaseLhcnm2PkRep1.narrowPeak
skeletal_muscle_myoblast	skeletal_muscle_myoblast	wgEncodeUwDnaseLhcnm2PkRep2.narrowPeak
skin	skin	wgEncodeAwgDnaseDukeMelanoUniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseDukeProgfibUniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseUwAg04449UniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseUwAg09309UniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseUwAg10803UniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseUwBjUniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseUwdukeNhekUniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseUwNhdfadUniPk.narrowPeak
skin	skin	wgEncodeAwgDnaseUwNhdfneoUniPk.narrowPeak

skin	skin	wgEncodeOpenChromDnaseColo829Pk.narrowPeak
skin	skin	wgEncodeOpenChromDnaseMelanoPk.narrowPeak
skin	skin	wgEncodeOpenChromDnaseNhekPk.narrowPeak
skin	skin	wgEncodeOpenChromDnaseProgfibPk.narrowPeak
skin	skin	wgEncodeUwDnaseAg04449PkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseAg04449PkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseAg09309PkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseAg09309PkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseAg10803PkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseAg10803PkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseBjPkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseBjPkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseGm04503PkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseGm04503PkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseGm04504PkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseGm04504PkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseNhdfadPkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseNhdfadPkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseNhdfneoPkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseNhdfneoPkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseNhekPkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseNhekPkRep2.narrowPeak
skin	skin	wgEncodeUwDnaseRpmi7951PkRep1.narrowPeak
skin	skin	wgEncodeUwDnaseRpmi7951PkRep2.narrowPeak
spinal_cord	spinal_cord	wgEncodeAwgDnaseUwHaspUniPk.narrowPeak
spinal_cord	spinal_cord	wgEncodeUwDnaseHaspPkRep1.narrowPeak
spinal_cord	spinal_cord	wgEncodeUwDnaseHaspPkRep2.narrowPeak
testis	testis	wgEncodeAwgDnaseUwNt2d1UniPk.narrowPeak
testis	testis	wgEncodeUwDnaseNt2d1PkRep1.narrowPeak
testis	testis	wgEncodeUwDnaseNt2d1PkRep2.narrowPeak
tonsil	tonsil	wgEncodeOpenChromDnaseGcbcellPk.narrowPeak
tonsil	tonsil	wgEncodeOpenChromDnaseNaivebcellPk.narrowPeak
urothelium	urothelium	wgEncodeAwgDnaseDukeUrotheliaUniPk.narrowPeak

urothelium	urothelium	wgEncodeAwgDnaseDukeUrotheliaut189UniPk.narrowPeak
urothelium	urothelium	wgEncodeOpenChromDnaseUrothelPkV2.narrowPeak
urothelium	urothelium	wgEncodeOpenChromDnaseUrothelUt189PkV2.narrowPeak
uterus	uterus	wgEncodeAwgDnaseDukeIshikawaestradiolUniPk.narrowPeak
uterus	uterus	wgEncodeAwgDnaseDukeIshikawatamoxifenUniPk.narrowPeak
uterus	uterus	wgEncodeOpenChromDnaseIshikawaEst10nm30mPk.narrowPeak
uterus	uterus	wgEncodeOpenChromDnaseIshikawaTam10030Pk.narrowPeak

Supplementary Table 2. Enrichment of GWAS loci in DNase hypersensitive sites of common tissues.

A. Body Mass Index (BMI) and Blood Pressure (BP)

Bed_File	BMI_InBed_Index_SNP	BMI_ExpectNum_of_InBed_SNP	BMI_PValue	BP_InBed_Index_SNP	BP_ExpectNum_of_InBed_SNP	BP_PValue
heart	57	41.24	0.00029	64	39.56	0.00000
blood	64	60.63	0.25540	77	60.99	0.00016
liver	61	47.73	0.00250	64	48.20	0.00043
skin	69	59.97	0.02090	76	57.94	0.00002
IPS	52	38.09	0.00140	54	37.47	0.00023
blood_vessel	63	53.30	0.01750	78	51.61	0.00000
bone	49	37.55	0.00675	54	36.15	0.00007
frontal_cortex	39	22.99	0.00009	43	22.73	0.00000
fibroblasts	60	50.25	0.01857	66	49.20	0.00014
nasal_biopsy	40	23.46	0.00004	41	22.50	0.00001
breast	77	61.57	0.00014	75	60.98	0.00064
epithelium	70	63.04	0.05891	76	61.43	0.00035
muscle	66	49.82	0.00020	69	48.87	0.00001
skeletal_muscle_myoblast	60	44.95	0.00054	63	43.32	0.00001
myometrium	39	30.22	0.02555	49	29.35	0.00001
frontal_cerebrum	36	24.85	0.00503	42	24.83	0.00005
prostate	66	51.51	0.00071	66	49.48	0.00016

pancreas	55	42.27	0.00320	58	41.66	0.00025
fetal_membrane	43	28.17	0.00046	44	27.82	0.00020
monocytes	43	29.60	0.00152	44	29.24	0.00067
brain	75	60.89	0.00052	82	59.12	0.00000
cervix	53	37.42	0.00036	55	36.59	0.00004
connective	27	24.50	0.30142	38	22.95	0.00015
gingival	33	25.31	0.03684	39	23.75	0.00014
tonsil	35	24.54	0.00678	36	23.44	0.00164
colon	39	28.52	0.00806	40	26.45	0.00090
embryonic_stem_cell	67	57.77	0.02050	73	55.59	0.00005
cerebellar	50	36.12	0.00117	56	34.90	0.00000
melanoma	36	28.61	0.04666	32	27.03	0.13065
uterus	40	31.93	0.03721	40	29.81	0.01095
urothelium	43	33.81	0.02256	45	32.98	0.00416
kidney	45	33.92	0.00685	50	32.54	0.00005
lung	56	41.66	0.00091	59	39.68	0.00002
embryonic_lung	37	28.69	0.03081	41	26.96	0.00063
foreskin	40	31.28	0.02568	47	29.19	0.00002
blastula	34	26.40	0.04143	39	25.28	0.00078
bone_marrow	47	36.11	0.00757	49	33.81	0.00029
spinal_cord	42	29.09	0.00139	33	25.73	0.04523
brain_hippocampus	39	28.45	0.00756	33	25.83	0.04771
testis	32	28.13	0.19746	36	25.21	0.00509
eye	44	36.98	0.06586	46	34.49	0.00524

B. Coronary Artery Disease (CAD), Lipids, and Type 2 Diabetes (T2D)

Bed_File	CAD_InBed_Index_SNP	CAD_ExpectNum_of_InBed_SNP	CAD_PValue	lipids_InBed_Index_SNP	lipids_ExpectNum_of_InBed_SNP	lipids_PValue	T2D_InBed_Index_SNP	T2D_ExpectNum_of_InBed_SNP	T2D_PValue
heart	28	16.32	0.00002	90	65.14	0.00001	43	24.95	0.00000

blood	34	24.34	0.00006	133	98.38	0.00000	53	39.54	0.00014
liver	30	19.52	0.00012	121	77.57	0.00000	48	30.88	0.00001
skin	33	23.78	0.00013	116	94.69	0.00004	45	38.10	0.03792
IPS	25	15.18	0.00046	83	60.19	0.00005	33	23.20	0.00664
blood_vessel	30	20.93	0.00050	98	84.28	0.00844	47	32.67	0.00009
bone	24	14.61	0.00083	85	58.75	0.00000	37	22.80	0.00013
frontal_cortex	18	9.23	0.00084	71	37.41	0.00000	25	14.21	0.00119
fibroblasts	29	20.08	0.00089	111	79.99	0.00000	46	31.74	0.00010
nasal_biopsy	18	9.67	0.00134	58	37.15	0.00004	24	14.05	0.00207
breast	32	24.48	0.00170	122	98.18	0.00000	52	39.21	0.00025
epithelium	32	24.69	0.00210	119	99.73	0.00013	54	40.19	0.00005
muscle	28	19.90	0.00249	108	79.38	0.00000	46	30.98	0.00006
skeletal_muscle_myoblast	26	18.04	0.00312	93	71.36	0.00009	42	27.79	0.00012
myometrium	20	12.12	0.00338	68	48.54	0.00024	26	18.39	0.02075
frontal_cerebrum	18	10.26	0.00360	76	40.51	0.00000	24	15.41	0.00901
prostate	28	20.44	0.00392	107	81.16	0.00000	45	32.05	0.00041
pancreas	25	17.20	0.00431	92	68.16	0.00002	41	26.45	0.00010
fetal_membrane	19	11.47	0.00518	74	45.85	0.00000	32	17.70	0.00007
monocytes	19	11.74	0.00726	89	48.04	0.00000	33	18.16	0.00004
brain	30	23.82	0.01197	109	95.87	0.00945	53	38.38	0.00003
cervix	22	15.20	0.01209	81	59.09	0.00008	37	23.28	0.00021
connective	16	10.01	0.01448	56	38.41	0.00038	26	14.17	0.00026
gingival	16	10.05	0.01580	57	39.22	0.00034	26	14.64	0.00055
tonsil	16	9.96	0.01607	70	38.62	0.00000	25	14.05	0.00090
colon	17	11.25	0.02329	71	44.24	0.00000	29	16.70	0.00034
embryonic_stem_cell	28	22.55	0.02870	107	90.35	0.00156	53	36.17	0.00000
cerebellar	20	14.64	0.03683	74	58.41	0.00304	34	22.08	0.00092
melanoma	16	11.18	0.04524	64	43.98	0.00010	22	16.15	0.05325
uterus	17	12.01	0.04567	72	48.91	0.00001	32	18.02	0.00008
urothelium	18	13.33	0.06275	72	52.88	0.00038	31	20.44	0.00265
kidney	18	13.51	0.06817	75	52.58	0.00003	31	19.78	0.00141

lung	21	16.46	0.07114	89	65.70	0.00003	41	25.74	0.00004
embryonic_lung	16	11.72	0.07310	59	45.50	0.00682	30	16.83	0.00014
foreskin	17	12.81	0.08045	58	48.40	0.04169	30	18.05	0.00053
blastula	14	10.73	0.14100	63	41.54	0.00004	26	15.85	0.00239
bone_marrow	17	14.13	0.18233	69	55.72	0.00796	32	20.72	0.00125
spinal_cord	13	10.96	0.26115	57	44.25	0.00797	24	16.05	0.01249
brain_hippocampus	13	11.25	0.30365	56	44.53	0.01596	32	16.00	0.00000
testis	12	10.84	0.38860	54	42.32	0.01408	25	15.08	0.00225
eye	14	14.41	0.63104	73	57.72	0.00318	38	21.54	0.00001

Supplementary Table 3. Fold enrichment of lipid loci in DNase hypersensitive sites at different consensus thresholds.

Bed_File	InBed_Index_SNP_100	ExpectNum_of_InBed_SNP_100	PValue_100	InBed_Index_SNP_75	ExpectNum_of_InBed_SNP_75	PValue_75	InBed_Index_SNP_50	ExpectNum_of_InBed_SNP_50	PValue_50	InBed_Index_SNP_25	ExpectNum_of_InBed_SNP_25	PValue_25	InBed_Index_SNP_union	ExpectNum_of_InBed_SNP_union	PValue_union
blastula	36	21.47	0.00053	36	21.47	0.00053	63	41.54	0.00004	63	41.54	0.00004	63	41.54	0.00004
blood	0	NA	NA	16	7.99	0.00449	26	15.22	0.00301	63	32.85	0.00000	133	98.38	0.00000
blood_vessel	4	2.90	0.32853	20	12.49	0.01912	31	21.50	0.01522	50	34.62	0.00118	98	84.28	0.00844
bone	12	6.04	0.01578	19	11.38	0.01560	38	28.47	0.02371	60	46.12	0.00525	101	79.41	0.00008
brain	1	1.24	0.71722	13	6.86	0.01745	20	13.32	0.03740	49	35.46	0.00396	117	102.44	0.00357
breast	4	2.05	0.14653	17	11.62	0.06437	34	21.90	0.00328	68	44.39	0.00001	122	98.18	0.00000
cervix	14	8.43	0.03795	24	14.05	0.00458	42	30.08	0.00766	63	44.89	0.00047	81	59.09	0.00008
colon	9	4.79	0.04720	12	6.65	0.03071	40	24.35	0.00032	59	36.51	0.00001	71	44.24	0.00000
connective	42	22.90	0.00001	42	22.90	0.00001	50	31.15	0.00007	56	38.41	0.00038	56	38.41	0.00038
embryonic_lung	22	14.85	0.03232	28	20.03	0.03236	38	32.38	0.13776	52	41.83	0.02941	59	45.50	0.00682

embryonic_stem_cell	7	3.97	0.09952	20	10.54	0.00318	39	20.84	0.00002	56	45.67	0.03125	107	90.35	0.00156
epithelium	3	2.35	0.42011	17	11.53	0.06084	33	22.23	0.00718	50	40.27	0.03171	119	99.08	0.00008
eye	12	7.29	0.05668	15	10.10	0.07328	56	40.22	0.00129	68	49.47	0.00034	73	57.72	0.00318
fetal_membrane	35	20.40	0.00051	35	20.40	0.00051	74	45.85	0.00000	74	45.85	0.00000	74	45.85	0.00000
foreskin	25	16.00	0.01219	35	22.25	0.00214	45	33.98	0.01447	55	44.53	0.02679	58	48.40	0.04169
gingival	27	15.11	0.00126	30	18.08	0.00213	46	28.83	0.00019	49	34.29	0.00185	57	39.22	0.00034
heart	9	5.85	0.12673	24	16.79	0.03835	45	29.99	0.00101	54	41.39	0.00863	90	65.14	0.00001
IPS	35	18.44	0.00007	52	34.02	0.00028	64	40.82	0.00001	71	48.13	0.00003	83	60.19	0.00005
kidney	13	9.39	0.13796	31	21.48	0.01463	44	29.15	0.00099	75	52.58	0.00003	75	52.58	0.00003
liver	7	2.66	0.01629	19	8.99	0.00115	45	22.27	0.00000	78	38.84	0.00000	121	77.57	0.00000
lung	15	9.50	0.04747	23	15.32	0.02571	36	25.57	0.01241	55	42.78	0.01123	92	67.75	0.00001
monocytes	32	15.01	0.00001	32	15.01	0.00001	50	24.85	0.00000	89	48.04	0.00000	89	48.04	0.00000
muscle	9	5.96	0.13754	22	12.71	0.00613	34	26.70	0.06517	77	56.80	0.00021	108	79.38	0.00000
myometrium	37	25.52	0.00658	37	25.52	0.00658	68	48.54	0.00024	68	48.54	0.00024	68	48.54	0.00024
nasal_biopsy	58	37.15	0.00004	58	37.15	0.00004	58	37.15	0.00004	58	37.15	0.00004	58	37.15	0.00004
pancreas	4	4.55	0.67706	18	9.82	0.00723	25	19.16	0.08571	55	36.06	0.00013	100	73.80	0.00000
prostate	6	4.85	0.35503	11	9.19	0.30823	30	20.29	0.01235	74	55.50	0.00041	107	81.16	0.00000
skeletal_muscle_myoblast	10	8.64	0.36178	31	21.49	0.01585	47	34.61	0.00760	69	54.35	0.00446	93	71.36	0.00009
skin	1	1.99	0.87188	19	12.46	0.03690	32	22.94	0.02273	56	43.06	0.00807	126	104.57	0.00002
spinal_cord	22	15.67	0.05588	22	15.67	0.05588	43	34.25	0.04038	57	44.25	0.00797	57	44.25	0.00797
testis	32	22.66	0.01840	32	22.66	0.01840	49	36.30	0.00656	54	42.32	0.01408	54	42.32	0.01408
tonsil	54	30.03	0.00000	54	30.03	0.00000	70	38.62	0.00000	70	38.62	0.00000	70	38.62	0.00000
urothelium	22	15.90	0.06498	30	25.07	0.15255	59	39.96	0.00021	72	52.88	0.00038	72	52.88	0.00038
uterus	30	18.31	0.00261	42	26.70	0.00057	64	41.67	0.00002	72	48.91	0.00001	72	48.91	0.00001

Supplementary Table 4. Enrichment of GWAS loci for five traits or diseases (BMI; Body Mass Index, BP; Blood Pressure, CAD; Coronary Artery Disease, Lipids, T2D; Type 2 Diabetes) in predicted chromatin states.

Chromatin_State	BMI_InBed_Index_SNP	BMI_ExpectNum_of_InBed_SNP	BMI_PValue	BP_InBed_Index_SNP	BP_ExpectNum_of_InBed_SNP	BP_PValue	CAD_InBed_Index_SNP	CAD_ExpectNum_of_InBed_SNP	CAD_PValue	lipids_InBed_Index_SNP	lipids_ExpectNum_of_InBed_SNP	lipids_PValue	T2D_InBed_Index_SNP	T2D_ExpectNum_of_InBed_SNP	T2D_PValue
wgEncodeBroadHmmGm12878HMM_10_Txn_Elongation	28	17.42	0.00306	28	16.24	0.00119	14	7.30	0.00492	60	28.73	0.00000	16	9.73	0.02299
wgEncodeBroadHmmGm12878HMM_11_Weak_Txn	41	32.44	0.03254	47	31.80	0.00060	18	13.22	0.06184	86	53.30	0.00000	29	20.31	0.01284
wgEncodeBroadHmmGm12878HMM_12_Repressed	25	17.34	0.02940	27	17.37	0.00935	17	7.29	0.00020	38	26.86	0.01322	24	10.97	0.00006
wgEncodeBroadHmmGm12878HMM_13_Heterochrom	86	88.60	0.87378	88	87.57	0.52629	29	32.34	0.97732	135	140.64	0.94552	62	58.17	0.07573
wgEncodeBroadHmmGm12878HMM_14_Repetitive_CNV	6	2.30	0.02484	3	1.92	0.30015	1	0.76	0.54277	6	3.32	0.11233	3	1.04	0.08488
wgEncodeBroadHmmGm12878HMM_15_Repetitive_CNV	5	1.55	0.01683	1	1.26	0.73663	0	NA	NA	3	1.97	0.31591	1	0.60	0.46226
wgEncodeBroadHmmGm12878HMM_1_Active_Promoter	20	12.13	0.00978	25	10.70	0.00001	6	4.68	0.31572	37	18.76	0.00001	7	5.97	0.38554
wgEncodeBroadHmmGm12878HMM_2_Weak_Promoter	16	13.08	0.21245	22	11.42	0.00082	10	5.12	0.01570	34	20.25	0.00068	4	6.89	0.93479
wgEncodeBroadHmmGm12878HMM_3_Poised_Promoter	6	2.35	0.02863	3	2.43	0.44056	0	NA	NA	6	3.86	0.18785	4	1.44	0.05248
wgEncodeBroadHmmGm12878HMM_4_Strong_Enhancer	19	10.14	0.00367	22	9.27	0.00006	8	3.92	0.03291	34	15.45	0.00000	10	5.69	0.05065
wgEncodeBroadHmmGm12878HMM_5_Strong_Enhancer	14	11.62	0.26229	22	10.22	0.00025	10	4.60	0.00857	34	18.20	0.00011	6	6.09	0.58329
wgEncodeBroadHmmGm12878HMM_6_Weak_Enhancer	24	17.82	0.05573	24	16.29	0.02094	11	6.91	0.05770	48	27.74	0.00001	16	9.63	0.01943
wgEncodeBroadHmmGm12878HMM_7_Weak_Enhancer	29	24.99	0.18870	36	23.29	0.00157	11	9.82	0.38312	68	38.94	0.00000	26	14.43	0.00052

wgEncodeBroadHmmGm12878HMM_8_Insulator	20	13.90	0.04352	9	11.55	0.84645	8	4.89	0.09463	29	19.59	0.01381	7	6.69	0.51305
wgEncodeBroadHmmGm12878HMM_9_Txn_Transition	14	8.41	0.03222	18	7.24	0.00016	8	3.42	0.01316	25	13.65	0.00130	4	4.38	0.65457
wgEncodeBroadHmmH1hescHMM_10_Txn_Elongation	24	12.94	0.00099	21	12.17	0.00601	16	5.33	0.00001	56	21.66	0.00000	17	7.16	0.00030
wgEncodeBroadHmmH1hescHMM_11_Weak_Txn	61	47.37	0.00219	57	48.33	0.04144	26	19.06	0.01160	111	78.53	0.00000	39	31.34	0.03287
wgEncodeBroadHmmH1hescHMM_12_Repressed	15	10.18	0.07493	18	9.25	0.00393	2	3.86	0.91392	23	15.40	0.03117	10	6.16	0.08147
wgEncodeBroadHmmH1hescHMM_13_Heterochrom	86	87.44	0.76143	84	86.36	0.82505	29	32.05	0.96687	122	138.45	0.99997	53	57.06	0.95739
wgEncodeBroadHmmH1hescHMM_14_Repetitive_CNV	1	0.76	0.53915	1	0.68	0.50187	0	NA	NA	3	0.96	0.07081	0	NA	NA
wgEncodeBroadHmmH1hescHMM_15_Repetitive_CNV	1	0.33	0.28541	0	NA	NA	0	NA	NA	1	0.44	0.36135	0	NA	NA
wgEncodeBroadHmmH1hescHMM_1_Active_Promoter	12	8.67	0.13989	15	7.29	0.00325	5	3.35	0.22573	25	12.95	0.00049	8	4.19	0.04640
wgEncodeBroadHmmH1hescHMM_2_Weak_Promoter	22	12.16	0.00188	14	10.99	0.18914	8	4.58	0.06857	31	19.14	0.00241	11	6.95	0.06412
wgEncodeBroadHmmH1hescHMM_3_Poised_Promoter	13	6.27	0.00872	14	6.48	0.00432	3	2.45	0.44976	21	10.27	0.00115	5	4.03	0.37698
wgEncodeBroadHmmH1hescHMM_4_Strong_Enhancer	3	2.10	0.35106	4	2.00	0.13373	0	NA	NA	10	3.11	0.00097	1	0.97	0.63007
wgEncodeBroadHmmH1hescHMM_5_Strong_Enhancer	2	4.84	0.96092	7	4.69	0.18308	3	1.62	0.21815	13	8.19	0.06205	7	2.97	0.02528
wgEncodeBroadHmmH1hescHMM_6_Weak_Enhancer	31	22.84	0.02398	27	20.73	0.06259	12	8.80	0.12540	50	35.51	0.00225	11	12.46	0.73793
wgEncodeBroadHmmH1hescHMM_7_Weak_Enhancer	35	31.06	0.20953	33	29.29	0.22132	19	12.29	0.01116	62	47.85	0.00596	24	19.00	0.09911
wgEncodeBroadHmmH1hescHMM_8_Insulator	21	19.51	0.38530	17	16.85	0.52991	8	7.26	0.44264	37	29.15	0.05310	12	10.67	0.37223
wgEncodeBroadHmmH1hescHMM_9_Txn_Transition	13	6.98	0.01772	11	6.55	0.05705	4	2.56	0.24846	37	11.58	0.00000	11	4.21	0.00200

wgEncodeBroadHmmHepg2HMM_10_Txn_Elongation	31	17.48	0.00026	27	16.55	0.00367	16	7.41	0.00050	70	28.85	0.00000	23	10.23	0.00004
wgEncodeBroadHmmHepg2HMM_11_Weak_Txn	44	33.06	0.00980	42	32.94	0.02928	20	13.55	0.01699	110	55.50	0.00000	32	20.90	0.00229
wgEncodeBroadHmmHepg2HMM_12_Repressed	28	19.29	0.01999	29	20.15	0.02045	13	8.44	0.05695	33	32.12	0.46183	13	12.75	0.51995
wgEncodeBroadHmmHepg2HMM_13_Heterochrom	80	86.10	0.98158	85	84.57	0.52213	26	31.65	0.99803	103	136.22	1.00000	51	56.02	0.97414
wgEncodeBroadHmmHepg2HMM_14_Repetitive_CNV	1	1.22	0.71411	1	1.22	0.72606	0	NA	NA	4	1.69	0.08670	0	NA	NA
wgEncodeBroadHmmHepg2HMM_15_Repetitive_CNV	3	1.32	0.14164	0	NA	NA	0	NA	NA	2	1.68	0.50458	1	0.37	0.31435
wgEncodeBroadHmmHepg2HMM_1_Active_Promoter	17	12.11	0.07628	22	10.50	0.00021	7	4.67	0.16063	48	18.82	0.00000	12	6.11	0.01232
wgEncodeBroadHmmHepg2HMM_2_Weak_Promoter	27	15.46	0.00103	25	14.20	0.00158	9	5.99	0.11888	51	24.73	0.00000	13	8.51	0.06660
wgEncodeBroadHmmHepg2HMM_3_Poised_Promoter	9	2.92	0.00238	7	2.66	0.01681	0	NA	NA	9	4.65	0.04263	3	1.76	0.25667
wgEncodeBroadHmmHepg2HMM_4_Strong_Enhancer	13	8.58	0.07815	10	7.82	0.25040	6	3.10	0.08079	52	13.92	0.00000	13	5.01	0.00092
wgEncodeBroadHmmHepg2HMM_5_Strong_Enhancer	14	9.16	0.06308	13	7.67	0.03691	8	3.85	0.02441	46	13.37	0.00000	15	4.84	0.00003
wgEncodeBroadHmmHepg2HMM_6_Weak_Enhancer	33	22.02	0.00364	25	19.73	0.09967	12	8.29	0.08947	58	34.87	0.00000	26	12.42	0.00003
wgEncodeBroadHmmHepg2HMM_7_Weak_Enhancer	21	17.29	0.18249	18	16.22	0.34943	17	7.20	0.00009	63	28.14	0.00000	18	9.58	0.00384
wgEncodeBroadHmmHepg2HMM_8_Insulator	13	11.32	0.33648	12	9.83	0.26880	4	4.16	0.62164	16	17.34	0.68430	4	5.78	0.85090
wgEncodeBroadHmmHepg2HMM_9_Txn_Transition	17	10.05	0.01545	17	9.05	0.00574	7	3.88	0.07657	40	15.81	0.00000	14	5.37	0.00047
wgEncodeBroadHmmHmecHMM_10_Txn_Elongation	25	15.37	0.00515	28	15.10	0.00032	13	6.36	0.00440	65	26.64	0.00000	19	8.96	0.00054
wgEncodeBroadHmmHmecHMM_11_Weak_Txn	54	40.56	0.00237	56	40.89	0.00091	23	16.63	0.01961	97	66.27	0.00000	37	26.09	0.00353

wgEncodeBroadHmmHmecHMM_12_Repressed	17	13.75	0.20275	20	13.29	0.03616	4	5.49	0.82447	23	20.93	0.34458	12	8.41	0.12522
wgEncodeBroadHmmHmecHMM_13_Heterochrom	87	88.97	0.82918	87	87.80	0.68270	27	32.57	0.99888	126	140.80	0.99992	56	58.34	0.88127
wgEncodeBroadHmmHmecHMM_14_Repetitive_CNV	1	0.73	0.52615	0	NA	NA	0	NA	NA	3	1.12	0.09898	0	NA	NA
wgEncodeBroadHmmHmecHMM_15_Repetitive_CNV	2	0.71	0.15597	0	NA	NA	0	NA	NA	1	1.05	0.66251	0	NA	NA
wgEncodeBroadHmmHmecHMM_1_Active_Promoter	15	11.46	0.14897	16	9.70	0.02168	8	4.34	0.04599	36	17.18	0.000000	9	5.60	0.08990
wgEncodeBroadHmmHmecHMM_2_Weak_Promoter	16	9.40	0.01714	15	8.45	0.01533	5	3.64	0.28790	29	15.35	0.000025	9	4.80	0.04100
wgEncodeBroadHmmHmecHMM_3_Poised_Promoter	6	1.72	0.00726	4	1.87	0.11643	1	0.66	0.48777	5	2.70	0.13236	4	1.26	0.03566
wgEncodeBroadHmmHmecHMM_4_Strong_Enhancer	17	8.74	0.00376	16	8.54	0.00780	9	2.98	0.00166	32	14.52	0.000001	7	4.91	0.20969
wgEncodeBroadHmmHmecHMM_5_Strong_Enhancer	33	19.65	0.00052	28	18.55	0.00953	10	7.89	0.24007	44	30.10	0.00292	17	11.44	0.04839
wgEncodeBroadHmmHmecHMM_6_Weak_Enhancer	31	19.25	0.00151	28	17.10	0.00219	9	7.29	0.28634	39	29.48	0.02516	19	10.63	0.00441
wgEncodeBroadHmmHmecHMM_7_Weak_Enhancer	43	31.94	0.00744	40	30.41	0.01797	14	12.49	0.34892	66	48.85	0.00116	27	19.23	0.01963
wgEncodeBroadHmmHmecHMM_8_Insulator	16	12.11	0.13542	14	10.26	0.13111	5	4.50	0.47810	26	17.67	0.02093	5	6.30	0.77984
wgEncodeBroadHmmHmecHMM_9_Txn_Transition	7	5.27	0.27209	8	5.04	0.12514	4	1.99	0.13150	32	9.24	0.000000	5	3.17	0.20103
wgEncodeBroadHmmHsmmHMM_10_Txn_Elongation	38	20.79	0.00001	30	20.08	0.00805	20	8.51	0.00001	74	34.36	0.000000	24	12.10	0.00023
wgEncodeBroadHmmHsmmHMM_11_Weak_Txn	52	41.91	0.01883	57	41.37	0.00066	23	16.98	0.02663	97	67.66	0.000000	38	26.65	0.00253
wgEncodeBroadHmmHsmmHMM_12_Repressed	23	18.60	0.15206	31	19.88	0.00467	9	8.32	0.45763	44	31.29	0.00784	15	12.22	0.22691
wgEncodeBroadHmmHsmmHMM_13_Heterochrom	81	84.61	0.89963	82	83.24	0.70214	28	30.87	0.94424	117	133.22	0.99985	50	54.76	0.96265

wgEncodeBroadHmmHsmmHMM_14_Repetitive_CNV	1	1.33	0.74407	0	NA	NA	0	NA	NA	5	2.01	0.04890	1	0.73	0.52509
wgEncodeBroadHmmHsmmHMM_15_Repetitive_CNV	3	1.16	0.10728	1	1.07	0.67791	0	NA	NA	2	1.57	0.47121	0	NA	NA
wgEncodeBroadHmmHsmmHMM_1_Active_Promoter	16	10.99	0.06349	18	9.34	0.00275	5	3.87	0.34124	33	16.71	0.00003	10	5.27	0.02772
wgEncodeBroadHmmHsmmHMM_2_Weak_Promoter	18	10.80	0.01362	15	9.93	0.05604	7	4.28	0.11280	37	17.50	0.00000	11	5.86	0.02297
wgEncodeBroadHmmHsmmHMM_3_Poised_Promoter	10	2.25	0.00007	6	2.32	0.02798	0	NA	NA	4	3.55	0.47596	3	1.30	0.13899
wgEncodeBroadHmmHsmmHMM_4_Strong_Enhancer	15	10.79	0.10795	19	9.77	0.00265	9	3.99	0.01264	33	15.66	0.00002	9	6.26	0.16228
wgEncodeBroadHmmHsmmHMM_5_Strong_Enhancer	27	18.37	0.01576	26	16.43	0.00728	10	7.26	0.16368	47	26.82	0.00002	14	10.46	0.14401
wgEncodeBroadHmmHsmmHMM_6_Weak_Enhancer	35	20.34	0.00014	28	18.82	0.00996	13	7.55	0.01812	49	30.26	0.00008	16	11.07	0.06567
wgEncodeBroadHmmHsmmHMM_7_Weak_Enhancer	31	24.42	0.06768	38	22.82	0.00019	15	9.86	0.03500	51	36.97	0.00445	22	14.00	0.01203
wgEncodeBroadHmmHsmmHMM_8_Insulator	17	14.13	0.22879	15	12.35	0.23772	8	5.51	0.15601	25	20.92	0.18280	7	7.21	0.59872
wgEncodeBroadHmmHsmmHMM_9_Txn_Transition	17	9.97	0.01494	15	9.74	0.05134	10	3.66	0.00167	43	16.67	0.00000	12	5.55	0.00647
wgEncodeBroadHmmHuvecHMM_10_Txn_Elongation	25	14.96	0.00350	26	14.20	0.00068	14	6.00	0.00070	58	24.51	0.00000	19	8.29	0.00019
wgEncodeBroadHmmHuvecHMM_11_Weak_Txn	44	34.74	0.02386	47	33.96	0.00300	19	13.82	0.04670	91	56.69	0.00000	35	21.63	0.00034
wgEncodeBroadHmmHuvecHMM_12_Repressed	32	27.03	0.14665	28	27.98	0.53792	16	11.49	0.07308	60	44.52	0.00371	21	17.04	0.15885
wgEncodeBroadHmmHuvecHMM_13_Heterochrom	81	88.01	0.99411	84	87.05	0.87748	29	32.35	0.97855	127	139.56	0.99928	54	57.58	0.94331
wgEncodeBroadHmmHuvecHMM_14_Repetitive_CNV	1	1.56	0.79910	1	1.40	0.76423	1	0.59	0.46005	6	2.34	0.02866	0	NA	NA
wgEncodeBroadHmmHuvecHMM_15_Repetitive_CNV	5	1.78	0.02991	1	1.55	0.81037	0	NA	NA	3	2.09	0.34883	1	0.54	0.42469
wgEncodeBroadHmmHuvecHMM_1_Active_Pro	16	10.10	0.03150	15	8.71	0.01838	6	3.97	0.18168	33	15.29	0.00000	7	4.98	0.21588

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wgEncodeBroadHmmHuvecHMM_2_Weak_Promoter	19	8.98	0.00057	12	8.48	0.12478	6	3.41	0.10522	27	14.19	0.00040	4	4.28	0.63828
wgEncodeBroadHmmHuvecHMM_3_Poised_Promoter	5	2.86	0.15532	5	3.31	0.23304	2	1.01	0.26776	6	4.68	0.32608	4	1.72	0.08893
wgEncodeBroadHmmHuvecHMM_4_Strong_Enhancer	21	13.44	0.01763	27	12.01	0.00001	9	4.75	0.03485	34	19.98	0.00072	17	7.23	0.00034
wgEncodeBroadHmmHuvecHMM_5_Strong_Enhancer	27	16.59	0.00357	30	15.47	0.00008	10	6.48	0.08862	45	25.01	0.00002	14	9.21	0.06286
wgEncodeBroadHmmHuvecHMM_6_Weak_Enhancer	11	13.60	0.83641	22	11.74	0.00135	3	5.05	0.91056	35	20.80	0.00053	8	6.89	0.38235
wgEncodeBroadHmmHuvecHMM_7_Weak_Enhancer	24	23.87	0.53160	37	22.37	0.00026	12	9.42	0.19680	57	36.74	0.00005	23	13.53	0.00307
wgEncodeBroadHmmHuvecHMM_8_Insulator	17	13.51	0.17302	15	11.20	0.13812	5	4.94	0.57024	30	19.98	0.00999	7	6.72	0.51725
wgEncodeBroadHmmHuvecHMM_9_Txn_Transition	10	7.65	0.22563	13	6.47	0.00959	5	2.31	0.07353	34	11.31	0.00000	10	4.01	0.00468
wgEncodeBroadHmmK562HMM_10_Txn_Elongation	26	15.40	0.00224	26	14.13	0.00061	12	6.38	0.01160	58	25.28	0.00000	16	8.50	0.00622
wgEncodeBroadHmmK562HMM_11_Weak_Txn	52	33.39	0.00003	42	33.56	0.03989	15	13.59	0.36731	107	54.79	0.00000	27	20.96	0.06649
wgEncodeBroadHmmK562HMM_12_Repressed	26	26.00	0.53977	38	28.61	0.02441	16	10.95	0.05172	55	44.15	0.03239	26	17.76	0.01658
wgEncodeBroadHmmK562HMM_13_Heterochrom	79	83.70	0.94054	72	82.03	0.99751	26	30.71	0.99057	108	131.89	1.00000	53	54.46	0.75957
wgEncodeBroadHmmK562HMM_14_Repetitive_CNV	2	2.05	0.61663	0	NA	NA	0	NA	NA	6	2.88	0.06786	1	1.07	0.66296
wgEncodeBroadHmmK562HMM_15_Repetitive_CNV	4	1.96	0.12842	2	1.76	0.53543	0	NA	NA	4	2.79	0.30497	2	0.83	0.20096
wgEncodeBroadHmmK562HMM_1_Active_Promoter	19	12.11	0.02035	19	10.35	0.00354	6	4.66	0.31026	43	18.56	0.00000	8	5.78	0.20960
wgEncodeBroadHmmK562HMM_2_Weak_Promoter	17	11.26	0.04152	15	10.55	0.08612	5	4.41	0.45733	33	17.20	0.00006	7	5.79	0.35585
wgEncodeBroadHmmK562HMM_3_Poised_Promoter	3	2.19	0.37468	7	2.60	0.01347	1	0.96	0.62752	7	4.08	0.11276	1	1.49	0.78653

wgEncodeBroadHmmK562HMM_4_Strong_Enhancer	18	11.15	0.02121	20	10.26	0.00178	7	4.55	0.15212	40	18.03	0.00000	9	6.45	0.18388
wgEncodeBroadHmmK562HMM_5_Strong_Enhancer	17	10.50	0.02439	17	9.37	0.00885	8	4.35	0.04963	42	16.31	0.00000	9	5.83	0.11565
wgEncodeBroadHmmK562HMM_6_Weak_Enhancer	20	16.29	0.16977	20	13.71	0.03982	6	5.93	0.56655	25	24.89	0.52897	9	8.31	0.45355
wgEncodeBroadHmmK562HMM_7_Weak_Enhancer	30	25.19	0.14159	33	24.27	0.02225	11	10.06	0.42168	75	39.17	0.00000	19	14.35	0.09998
wgEncodeBroadHmmK562HMM_8_Insulator	17	15.63	0.38943	18	14.00	0.14298	6	5.92	0.56352	38	23.67	0.00089	13	8.04	0.04696
wgEncodeBroadHmmK562HMM_9_Txn_Transition	20	10.49	0.00197	22	9.36	0.00005	14	4.13	0.00001	41	16.57	0.00000	10	6.01	0.06522
wgEncodeBroadHmmNhekHMM_10_Txn_Elongation	30	16.53	0.00026	28	16.40	0.00140	15	6.69	0.00071	71	28.48	0.00000	21	9.99	0.00028
wgEncodeBroadHmmNhekHMM_11_Weak_Txn	46	37.85	0.04543	48	38.08	0.02125	18	15.56	0.24564	100	62.14	0.00000	35	24.18	0.00343
wgEncodeBroadHmmNhekHMM_12_Repressed	29	21.79	0.05078	32	22.05	0.01260	16	8.96	0.00741	45	34.85	0.03243	19	13.97	0.08596
wgEncodeBroadHmmNhekHMM_13_Heterochrom	85	87.43	0.85045	83	85.47	0.82461	25	31.95	0.99977	122	137.75	0.99992	52	56.68	0.97122
wgEncodeBroadHmmNhekHMM_14_Repetitive_CNV	0	NA	NA	1	0.77	0.54697	1	0.30	0.26567	2	0.99	0.25908	0	NA	NA
wgEncodeBroadHmmNhekHMM_15_Repetitive_CNV	1	0.34	0.29347	0	NA	NA	0	NA	NA	1	0.45	0.37221	0	NA	NA
wgEncodeBroadHmmNhekHMM_1_Active_Promoter	17	11.84	0.06250	17	10.56	0.02250	7	4.60	0.14893	36	18.45	0.00001	10	6.12	0.06757
wgEncodeBroadHmmNhekHMM_2_Weak_Promoter	13	8.95	0.09668	17	8.29	0.00195	7	3.62	0.05276	31	13.58	0.00000	5	4.37	0.44708
wgEncodeBroadHmmNhekHMM_3_Poised_Promoter	5	3.39	0.25070	4	3.22	0.40325	2	1.31	0.37839	7	5.22	0.26565	4	2.25	0.17985
wgEncodeBroadHmmNhekHMM_4_Strong_Enhancer	28	12.41	0.00001	16	11.88	0.12154	11	4.62	0.00323	37	19.42	0.00003	11	7.33	0.10129
wgEncodeBroadHmmNhekHMM_5_Strong_Enhancer	30	17.51	0.00075	30	16.78	0.00037	8	7.34	0.45680	46	26.86	0.00004	14	9.91	0.10164
wgEncodeBroadHmmNhekHMM_6_Weak_Enha	24	18.30	0.07473	27	16.01	0.00186	2	6.74	0.99652	38	27.52	0.01415	18	9.83	0.00449

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wgEncodeBroadHmmNhekHMM_7_Weak_Enhancer	35	28.09	0.06011	35	25.93	0.01945	14	10.44	0.11779	64	42.15	0.00003	23	15.96	0.02605
wgEncodeBroadHmmNhekHMM_8_Insulator	20	16.38	0.18127	15	14.11	0.44136	6	6.03	0.58342	36	24.78	0.00739	9	8.82	0.53272
wgEncodeBroadHmmNhekHMM_9_Txn_Transition	12	6.95	0.03933	10	6.37	0.09830	4	2.64	0.26818	31	11.47	0.00000	5	4.16	0.40400
wgEncodeBroadHmmNhlfHMM_10_Txn_Elongation	29	16.83	0.00086	27	16.16	0.00256	17	6.89	0.00006	68	28.36	0.00000	21	9.83	0.00024
wgEncodeBroadHmmNhlfHMM_11_Weak_Txn	47	37.41	0.02239	55	36.94	0.00008	24	15.43	0.00223	97	60.85	0.00000	37	24.21	0.00062
wgEncodeBroadHmmNhlfHMM_12_Repressed	31	25.33	0.10947	36	26.77	0.02373	11	10.55	0.49792	62	41.58	0.00019	28	16.72	0.00143
wgEncodeBroadHmmNhlfHMM_13_Heterochrom	83	86.70	0.92119	83	85.70	0.84432	27	31.72	0.99412	120	137.01	0.99997	54	56.38	0.86236
wgEncodeBroadHmmNhlfHMM_14_Repetitive_CNV	0	NA	NA	0	NA	NA	1	0.17	0.15724	4	0.97	0.01467	1	0.38	0.32084
wgEncodeBroadHmmNhlfHMM_15_Repetitive_CNV	4	1.69	0.08382	1	1.36	0.76471	0	NA	NA	2	2.01	0.60503	1	0.57	0.44501
wgEncodeBroadHmmNhlfHMM_1_Active_Promoter	20	11.78	0.00699	23	10.36	0.00006	7	4.61	0.15176	37	18.13	0.00000	12	5.94	0.00898
wgEncodeBroadHmmNhlfHMM_2_Weak_Promoter	18	10.52	0.01013	16	9.43	0.01845	6	4.07	0.20421	30	16.88	0.00063	5	5.45	0.65508
wgEncodeBroadHmmNhlfHMM_3_Poised_Promoter	5	2.07	0.05610	3	2.12	0.35538	0	NA	NA	5	3.92	0.35524	1	1.30	0.73465
wgEncodeBroadHmmNhlfHMM_4_Strong_Enhancer	9	5.56	0.09768	17	5.12	0.00001	5	2.33	0.07356	21	8.75	0.00012	6	3.21	0.09473
wgEncodeBroadHmmNhlfHMM_5_Strong_Enhancer	24	15.17	0.01013	28	13.86	0.00009	7	5.92	0.37745	41	22.68	0.00005	16	8.35	0.00575
wgEncodeBroadHmmNhlfHMM_6_Weak_Enhancer	27	16.73	0.00351	23	15.55	0.02289	8	6.82	0.36214	38	26.11	0.00564	16	9.12	0.01123
wgEncodeBroadHmmNhlfHMM_7_Weak_Enhancer	38	24.18	0.00065	34	22.99	0.00485	15	9.66	0.02947	66	37.50	0.00000	23	14.12	0.00594
wgEncodeBroadHmmNhlfHMM_8_Insulator	25	20.35	0.13187	24	17.83	0.05945	10	7.49	0.18780	39	30.63	0.04494	13	10.68	0.25547
wgEncodeBroadHmmNh	10	6.52	0.10	16	5.74	0.00	6	2.41	0.02	31	10.39	0.000	8	3.56	0.02

lfHMM_9_Txn_Transitio n			888			010			636			00			218

Supplementary Table 5. Enrichment of lipid loci in transcription factor binding sites and histone modifications from relevant Tier 1 and Tier 2 cell types.

Feature	InBed_Index_SNP	ExpectNum_of_InBed_SNP	PValue	Annotation
POLR2A	116	59.17	6.23E-24	
RCOR1	87	41.86	1.75E-16	
SP1	52	17.29	1.48E-15	
EP300	82	40.67	1.08E-14	literature
eGFP_JUND	86	43.98	2.20E-14	
H3K4me3	72	34.27	1.38E-13	literature
MXI1	62	26.53	2.79E-13	
MYC	71	33.76	5.75E-13	
H3K36me3	52	20.55	1.07E-12	
MYBL2	39	11.69	1.17E-12	
TBL1XR1	63	29.30	8.89E-12	lipid gene regulator
H3K9me1	111	70.65	2.11E-11	literature
SMC3	63	30.21	2.57E-11	
ARID3A	68	34.44	3.44E-11	
H3k4me1	74	38.57	4.82E-11	
H3K9ac	56	25.49	1.25E-10	
MAZ	70	37.11	3.52E-10	
BHLHE40	67	34.86	4.42E-10	
TBP	57	27.07	4.95E-10	
eGFP_GATA2	64	32.64	7.25E-10	
MAX	63	32.05	7.86E-10	
JUND	85	52.19	1.04E-09	
NCOR1	81	45.39	1.22E-09	lipid gene regulator
FOXA1	46	20.41	5.00E-09	lipid gene regulator

NFIC	48	21.88	6.26E-09	
TEAD4	44	19.11	7.09E-09	
TAL1	49	23.02	1.08E-08	
CEBPB	90	59.99	1.69E-08	lipid gene regulator
CCNT2	49	23.51	1.99E-08	
HDAC2	33	12.05	2.13E-08	
HNF4G	26	7.82	2.19E-08	
RFX5	48	23.02	2.20E-08	
eGFP_JUNB	52	25.73	2.39E-08	literature
RXRA	25	7.50	4.23E-08	lipid gene regulator
ELF1	40	17.21	4.38E-08	
JUN	61	34.37	1.08E-07	
CREB1	45	21.64	1.10E-07	literature
CHD2	47	23.26	1.65E-07	
eGFP_HDAC8	24	7.62	2.51E-07	
HMGN3	43	20.66	3.08E-07	
CUX1	40	18.64	4.04E-07	
ZNF143	51	27.20	4.49E-07	
CTCF	75	49.00	7.41E-07	
ZC3H11A	32	13.68	1.29E-06	
HNF4A	28	10.93	1.66E-06	lipid gene regulator
IRF1	49	26.87	1.71E-06	
YY1	42	21.34	2.22E-06	literature
TCF7L2	23	8.15	2.28E-06	literature
USF2	30	12.76	2.98E-06	
MBD4	16	4.26	3.52E-06	
ZNF384	47	25.87	3.84E-06	
SIN3AK20	28	11.66	3.93E-06	
NFYA	20	6.79	7.28E-06	
SPI1	37	18.56	8.45E-06	
BRCA1	22	8.21	9.76E-06	
RAD21	52	31.14	1.22E-05	

SREBP1	11	2.29	1.40E-05	lipid gene regulator
E2F6	35	17.56	1.48E-05	
HDAC1	22	8.52	1.85E-05	literature
ZBTB7A	25	10.54	2.06E-05	
UBTF	32	15.91	3.31E-05	
HCFC1	38	20.75	4.65E-05	
TAF1	29	13.98	4.65E-05	
TCF12	20	7.85	7.83E-05	
E2F4	23	10.14	8.46E-05	
CEBPD	16	5.54	8.69E-05	lipid gene regulator
EGR1	28	13.53	8.85E-05	
KDM5B	23	10.22	0.00010	
PML	32	17.10	0.00014	
RUNX3	40	23.82	0.00021	
USF1	26	12.74	0.00021	lipid gene regulator
FOS	15	5.37	0.00022	
EBF1	31	16.38	0.00023	
FOXA2	29	15.33	0.00029	lipid gene regulator
eGFP_FOS	30	16.04	0.00031	
REST	25	12.46	0.00033	
FOSL2	20	8.83	0.00036	
GTF2F1	24	11.97	0.00040	
CHD1	20	9.14	0.00046	
eGFP_NR4A1	11	3.50	0.00067	literature
ATF1	35	21.01	0.00069	
POU2F2	21	10.12	0.00074	
SAP30	17	7.44	0.00078	
CEBPZ	6	1.17	0.00095	literature
NR2F2	20	9.62	0.00101	
PHF8	25	13.65	0.00124	
MAFF	59	43.42	0.00130	
ELK1	20	10.04	0.00166	

MAFK	75	59.30	0.00170	
ATF3	16	7.46	0.00248	literature
SREBP2	2	0.08	0.00278	lipid gene regulator
GATA2	20	10.47	0.00284	
SIN3A	17	8.47	0.00337	
GTF2B	16	7.77	0.00338	
WRNIP1	16	7.77	0.00360	
ETS1	15	7.06	0.00366	
SIX5	9	3.16	0.00380	
KAP1	28	17.39	0.00417	
IRF4	16	8.10	0.00570	
CREBBP	87	70.93	0.00590	lipid gene regulator
ZEB1	8	2.80	0.00629	
GTF3C2	7	2.27	0.00698	
PAX5	22	13.06	0.00832	
GABPA	18	10.15	0.01012	
NR2C2	8	3.08	0.01097	literature
NFYB	24	15.13	0.01193	
STAT1	10	4.52	0.01362	
RBBP5	18	10.59	0.01497	
FOSL1	9	4.03	0.01757	
GATA1	17	10.02	0.02008	
MTA3	15	8.61	0.02249	
SMARCA4	7	2.90	0.02391	
NRF1	11	5.69	0.02427	lipid gene regulator
SIRT6	5	1.67	0.02492	lipid gene regulator
ATF2	20	12.81	0.02558	literature
STAT2	7	2.92	0.02602	
PBX3	8	3.77	0.03296	
H3k27me3	46	35.95	0.03437	literature
SP2	6	2.54	0.04047	
ZBTB33	7	3.23	0.04068	

NFE2	5	1.92	0.04189	
CTCFL	7	3.29	0.04599	
BCLAF1	11	6.32	0.04747	
RPC155	3	0.88	0.05834	
STAT5A	15	10.13	0.07479	
STAT3	7	3.71	0.07701	
GRp20	2	0.50	0.08754	
THAP1	5	2.46	0.09661	
ZNF274	9	5.55	0.10080	
MEF2A	13	8.91	0.10277	
BACH1	12	8.42	0.13021	literature
TAF7	5	2.74	0.13566	
IRF3	2	0.67	0.14483	literature
BATF	14	10.35	0.14632	
RELA	12	8.71	0.15678	
ESRRA	2	0.72	0.15937	
TCF3	10	7.04	0.16372	
EZH2	5	3.06	0.19139	literature
BCL3	10	7.33	0.19457	
IKZF1	8	6.00	0.25050	
MEF2C	6	4.34	0.26304	
SMARCB1	3	1.84	0.27931	
TRIM28	10	8.17	0.29765	literature
NFATC1	9	7.25	0.29894	
HSF1	2	1.15	0.31948	
FOXM1	15	13.35	0.35378	literature
SETDB1	8	6.90	0.38417	
RDBP	1	0.49	0.39523	
HDAC6	1	0.54	0.42744	
SRF	6	5.34	0.44601	
ZNF263	3	2.73	0.51755	
H3K9me3	116	119.25	0.77337	literature

BDP1	0	NA	NA	
BRF1	0	NA	NA	
POLR3G	0	NA	NA	
PPARGC1A	0	NA	NA	lipid gene regulator
XRCC4	0	NA	NA	
ZZZ3	0	NA	NA	

Supplementary Table 6: Primers used in luciferase expression constructs.

SPTLC3	Rs1321940F	GTGCTCACTGAAACGTGTCT
	Rs1321940R	CAGTGCACAATGTCAATATGGA
	Rs364585F	CACCTGACCATTTCTCCCCA
	Rs364585R	ACGAAACACCCCTGAAGACA
ANGPTL8	Rs3810308F	AGAGGAGGCAGAAGTGAAGG
	Rs3810308R	CCAGCTCTGAACTCTGGACA
	Rs737337F	GGGTAGGGATGTGGAGTGAG
	Rs737337R	ATTCCCATTGCCTCTCTGCT
FAM117B	Rs11692610F	TAAAAGCCCGAACGAGATGC
	Rs11692610R	GGGTTTTGTTGTTGTTGGGC
	Rs11694172F	TCCTGGGTTCAAGCAGTTCT
	Rs11694172R	ATCCCAAAGGCCTCCAAAGA
SORT1	Rs12740374F	ACACATTTTCAGGGGAGCCT

	Rs12740374R	AGGAGAGGTGGGGAGATGAT
	Rs629301F	TCTCCTCAGTTTTGCCGACT
	Rs629301R	CTCTCCCACCGTAGAAGTCC
IRF2BP2	Rs526936F	AAAACTAGCTGGGCGTGGTA
	Rs526936R	CCCCGAGTAAAACACCCTCT
	Rs514230F	CCCCAGACATGAGGACAAGT
	Rs514230R	GCAGGCCGGTTTTCTTCTTT
ADH5	Rs2602836F	GCCAGCAATGAACAAGTGGA
	Rs2602836R	CGCACATGTAACAAACCTGC
	Rs1800759F	CTGGCATAGGGGTCACTCAT
	Rs1800759R	AATGGGCGATTCTGAGGAGT

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