

Meta Analysis Report for Bulk Data

Mahdi Eskandarian Boroujeni

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1 Datasets & Workflow

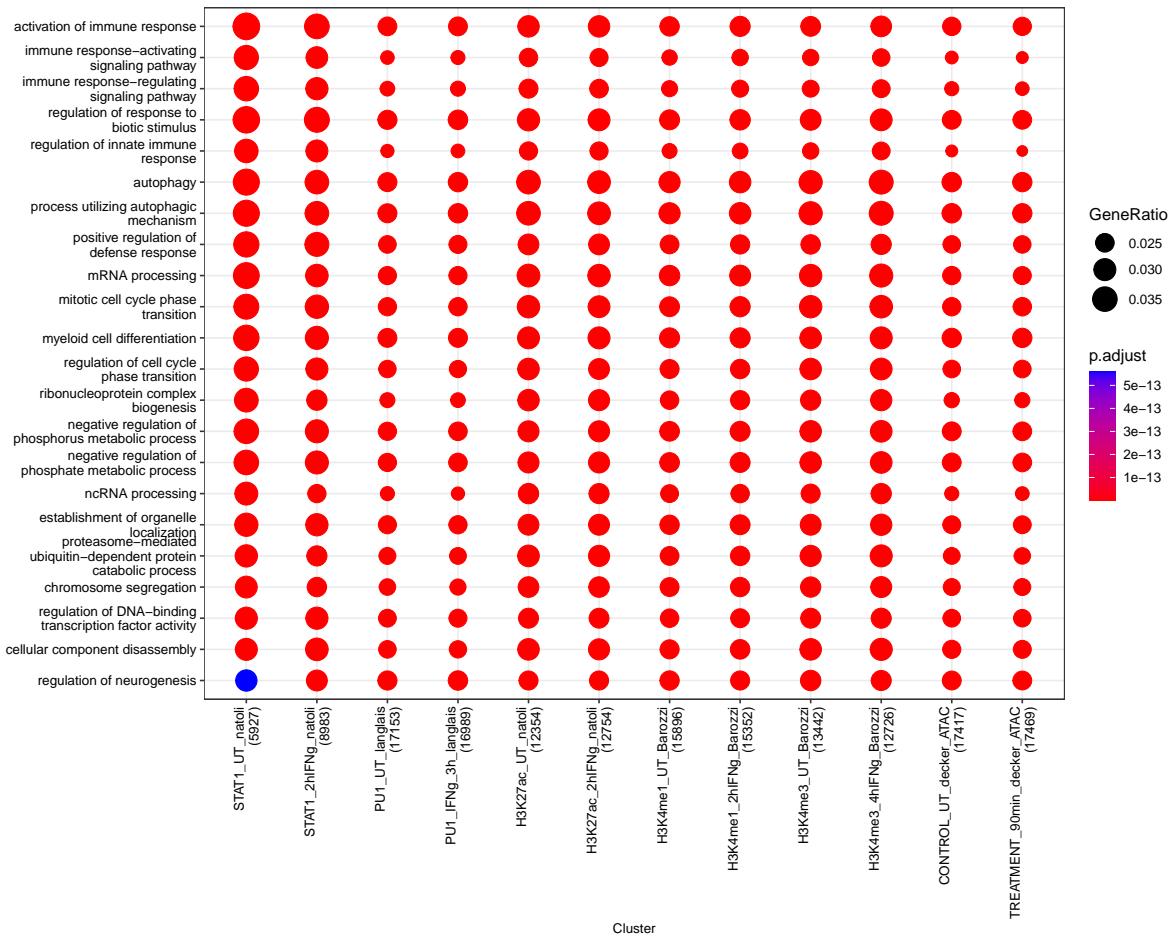
- Datasets including mouse macrophages and IFNg treatment:
 - **STAT1**: GEO Accession Number: GSE84518, [Article](#)
 - **PU1**: GEO Accession Number: GSE77886, [Article](#)
 - **H3K27ac**: GEO Accession Number: GSE84520, [Article](#)
 - **H3K4me1**: GEO Accession Number: GSE38377, [Article](#)
 - **H3K4me3** GEO Accession Number: GSE38377, [Article](#)
 - **ATAC-seq** GEO Accession Number: GSE115435, [Article](#)
 - **RNA-seq** GEO Accession Number: GSE115435, [Article](#)
- Workflows used for the Meta-analysis:
 - **Chip-seq**: ENCODE Transcription Factor and Histone ChIP-Seq processing pipeline
 - **ATAC-seq**: ATAC-seq peak-calling and QC analysis pipeline
 - **RNA-seq**: RNA sequencing analysis pipeline
- Softwares used for downstream Analysis:
 - [Homer](#)
 - R packages
 - * Peak annotation: ChIPseeker_1.36.0
 - * Enrichment Analysis: clusterProfiler_4.8.2
 - * Chip-seq/ATAT-seq count table: Rsubread_1.22.2
 - * For the full list of R packages and the codes see *Report_Meta_Analysis_Bulk.qmd*

2 Comparing all the peaks at one glance

2.1 Intro

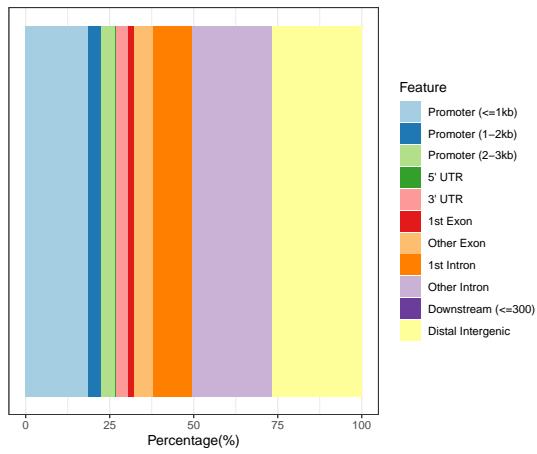
- Steps to prepare the high-quality peaks:
 - The raw sequencing data for each dataset were analysed using relevant pipelines(Encode/NF-core)
 - Peak calling is then performed on all replicates, pooled data, self-pseudoreplicates of each bio-replicate and the pooled pseudoreplicates. The workflow supports calling of two general types of peaks: narrow and region. The MACS2 and SPP methods are used for peak calling. The MACS2 software has a mode for narrow peak calling and can be used for both tf and histone pipeline type, while SPP is preferably used for region peak calling when analysing transcription factor binding sites.
 - As a way to assess concordance of peak calls between replicates, the IDR tool is used as the next step, along with Overlap, providing input peak files for the Reproducibility tool in order to obtain reproducibility QC. The basic idea is that if two replicates measure the same underlying biology, the most significant peaks, which are likely to be genuine signals, are expected to have high consistency between replicates, whereas peaks with low significance, which are more likely to be noise, are expected to have low consistency.

Comparing enrichment results of multiple peak list for Biological Process

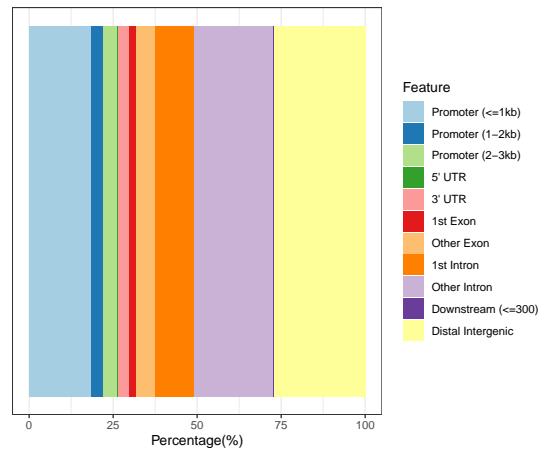


3 Annotation of all peaks

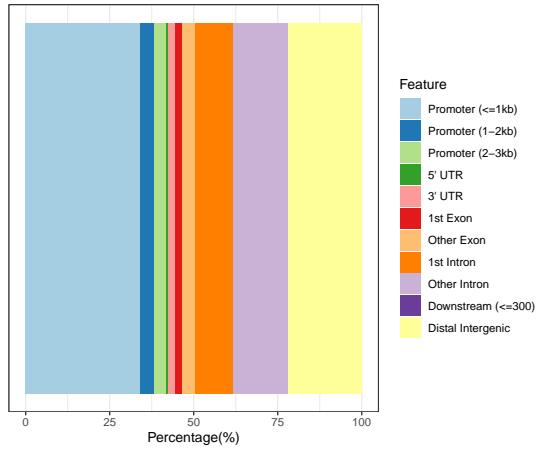
ATAC_UT



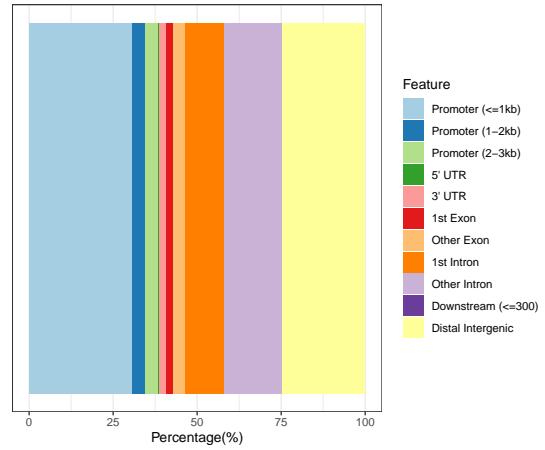
ATAC_IFNg



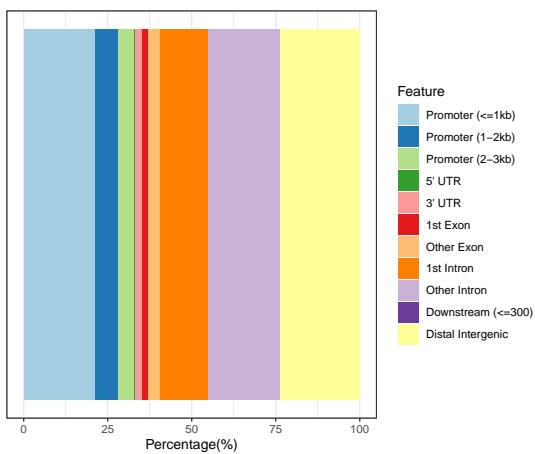
H3K27ac_UT



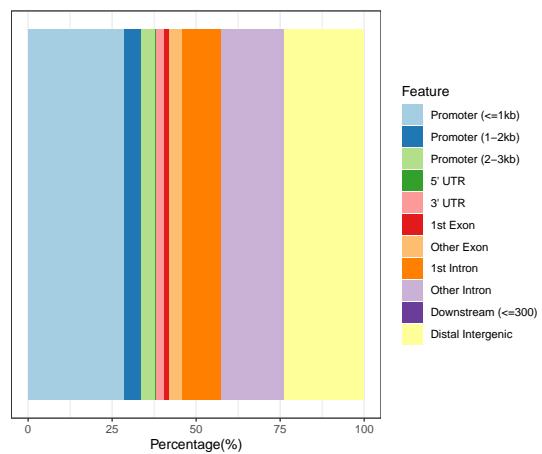
H3K27ac_IFNg



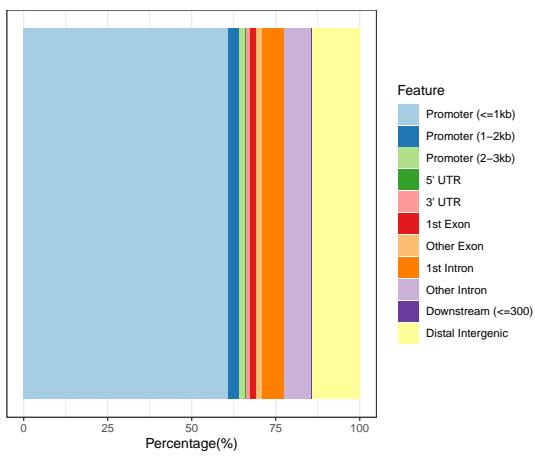
H3K4me1_UT



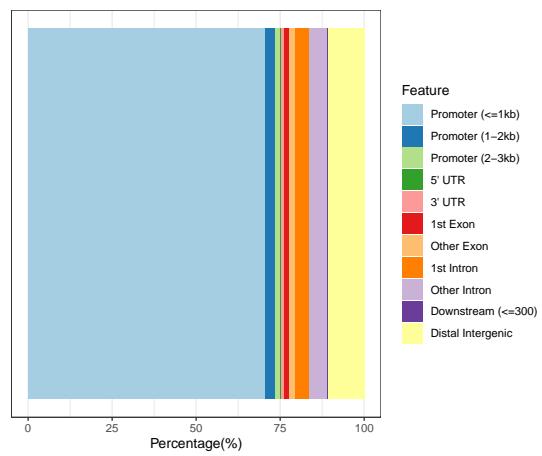
H3K4me1_IFNg

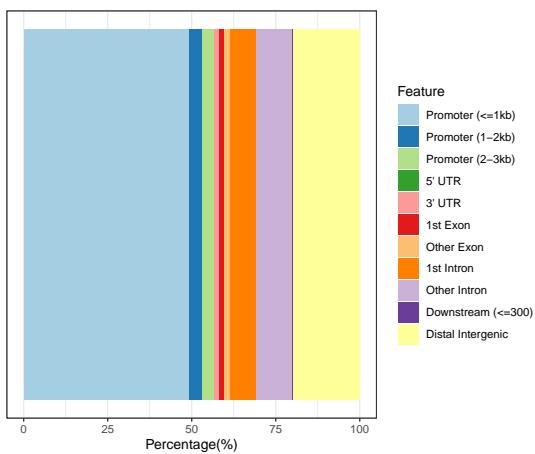
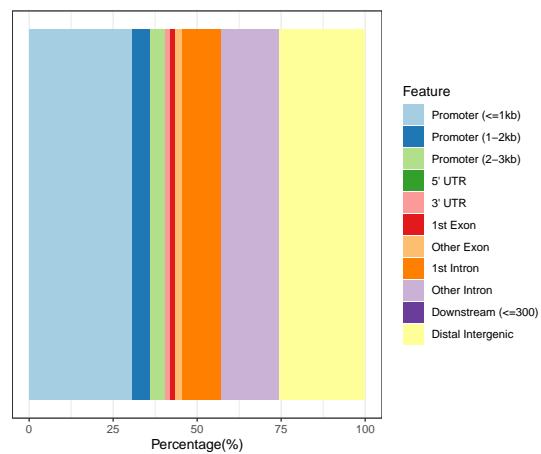
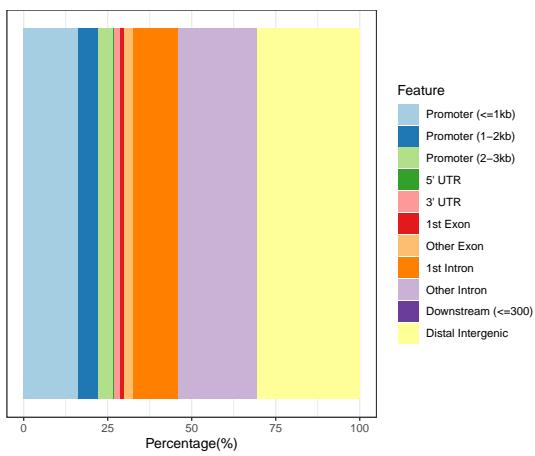
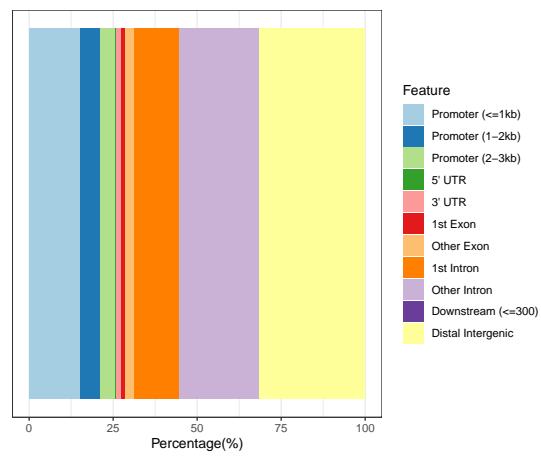


H3K4me3_UT



H3K4me3_IFNg



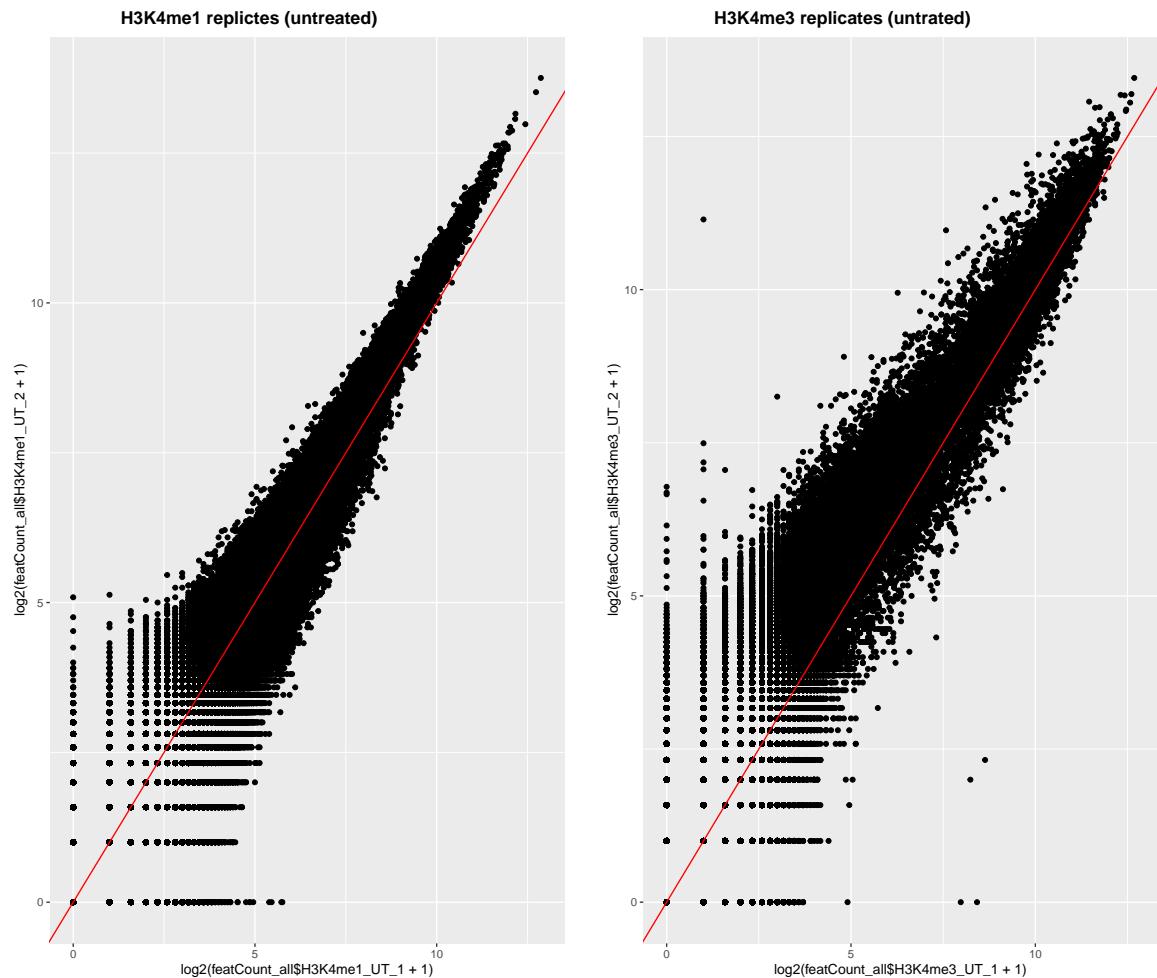
STAT1_UT**STAT1_IFNg****PU1_UT****PU1_IFNg**

4 Correlation

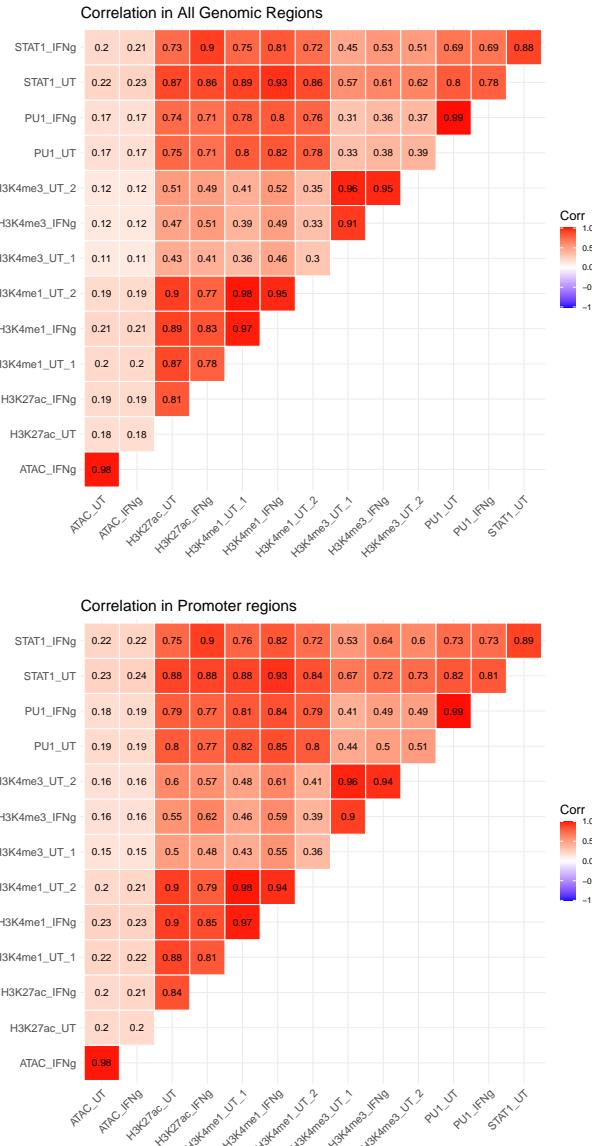
4.1 Intro

- **Steps to prepare correlation plots:**
 - All the bed files generated using respective pipelines(Encode/Nf-core) were merged together.
 - The peaks in merged file were counted in each dataset using featureCounts tool as described [here](#).
 - All the count table were merged into one for further analysis such as peak annotation, feature selection and correlation analysis.

4.2 Correlation between biological replicates



4.3 Correlation Plots



5 Differential Peaks

5.1 Intro

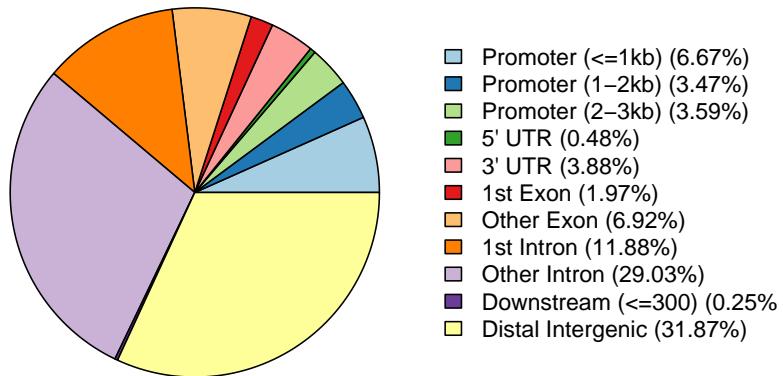
- Steps to prepare the differential peaks:
 - The raw sequencing data for each dataset were analysed using relevant pipelines(Encode/NF-core)
 - To standardize all sequence alignments from differet datasets, “Tag Directory” was created using the Homer function [makeTagDirectory](#)
 - To find peaks that are differentially enriched between two conditions, the Homer function [getDifferentialPeaks](#) were implemented. Next, these differential peaks were used for downstream analysis such peak annotation and KEGG enrichment analysis.

5.2 ATAC-seq

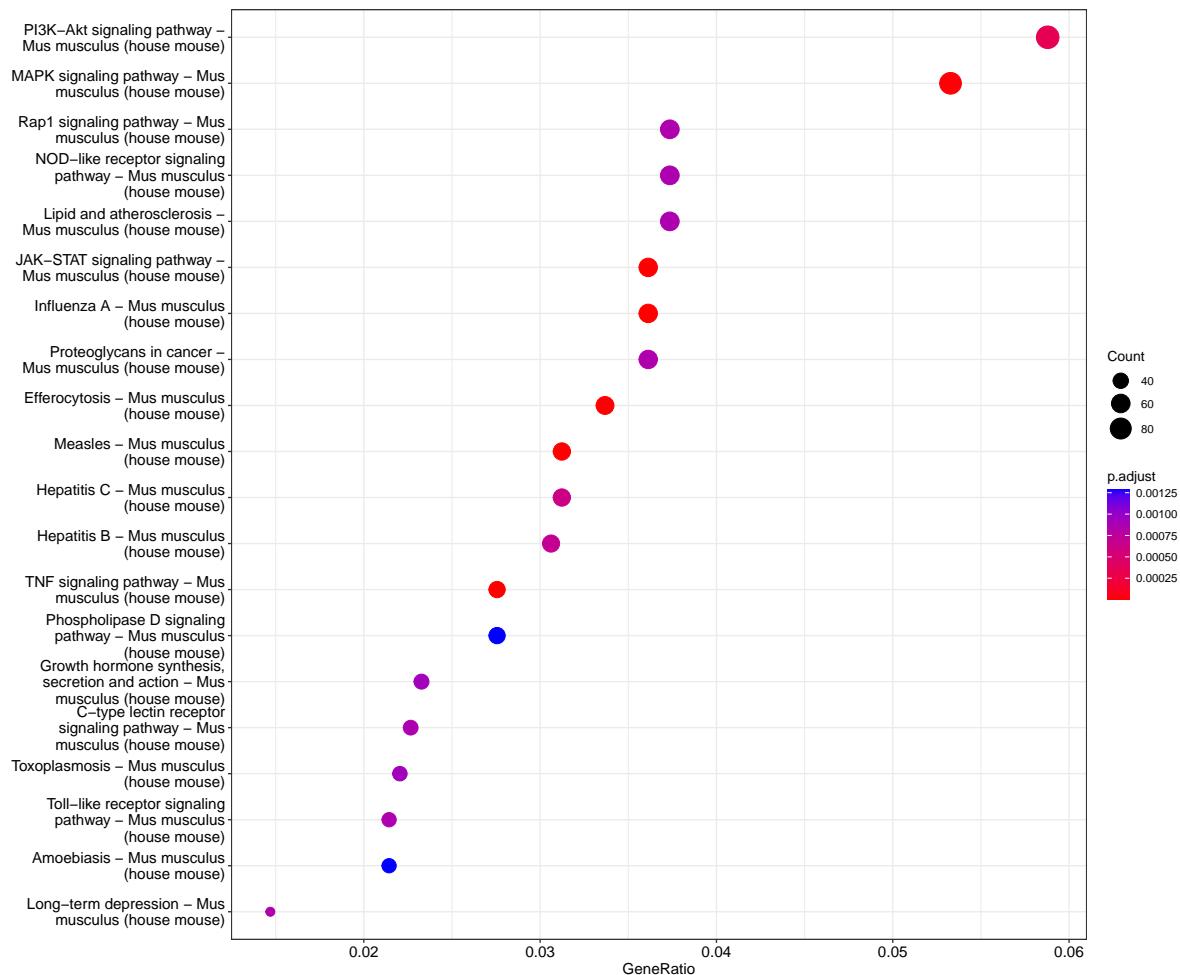
5.2.1 Differential Peak Annotation

Fold change cutoff is 2

```
>> preparing features information...           2023-12-28 01:04:45 AM
>> identifying nearest features...          2023-12-28 01:04:45 AM
>> calculating distance from peak to TSS... 2023-12-28 01:04:46 AM
>> assigning genomic annotation...         2023-12-28 01:04:46 AM
>> adding gene annotation...              2023-12-28 01:04:49 AM
>> assigning chromosome lengths        2023-12-28 01:04:49 AM
>> done...                                2023-12-28 01:04:49 AM
```



5.2.2 KEGG Enrichment Analysis

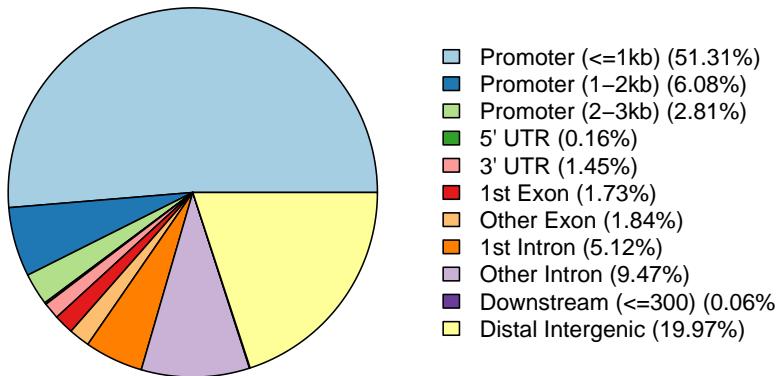


5.3 H3K4me1

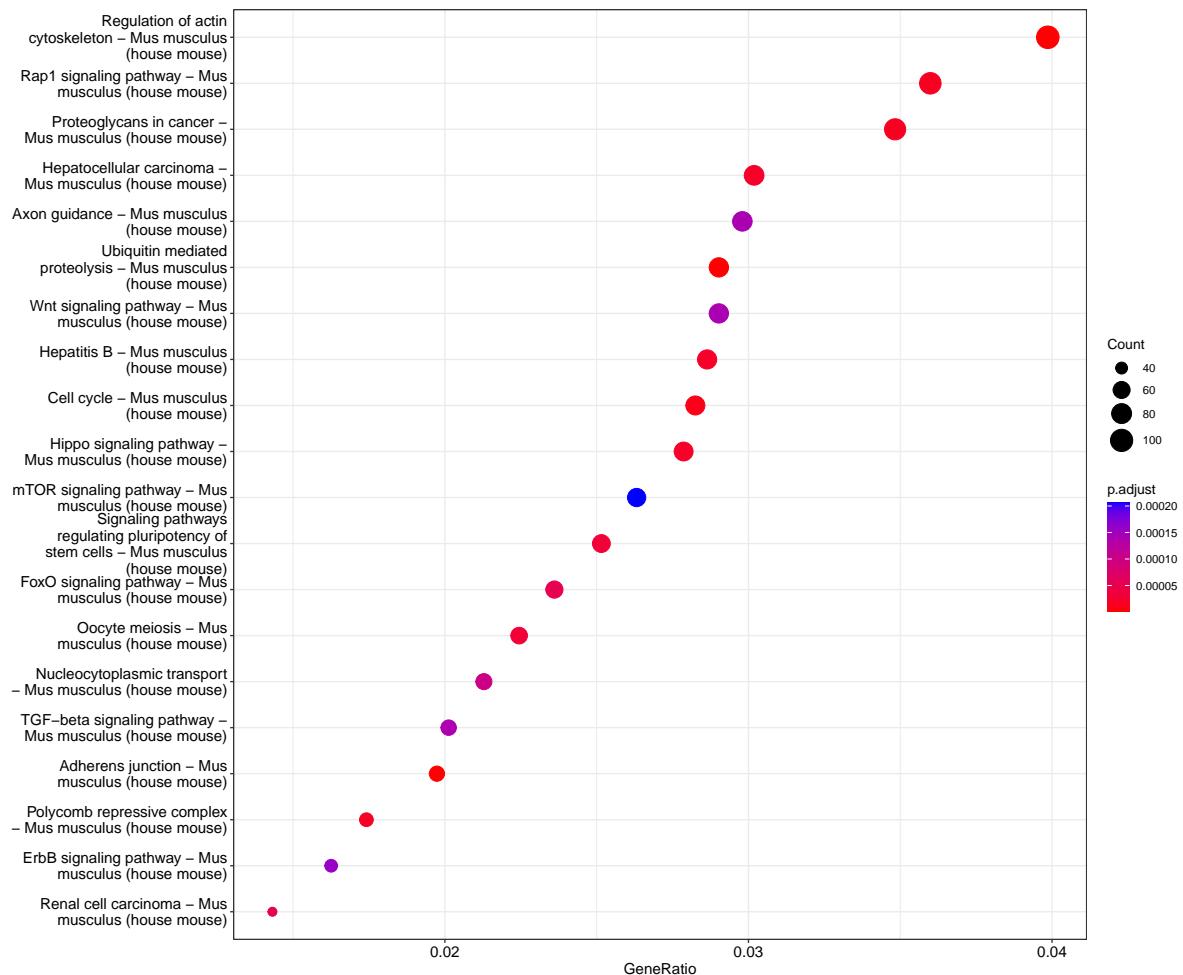
5.3.1 Differential Peak Annotation

Fold change cutoff is 2

```
>> preparing features information...           2023-12-28 01:04:57 AM
>> identifying nearest features...          2023-12-28 01:04:57 AM
>> calculating distance from peak to TSS... 2023-12-28 01:04:58 AM
>> assigning genomic annotation...         2023-12-28 01:04:58 AM
>> adding gene annotation...              2023-12-28 01:05:02 AM
>> assigning chromosome lengths        2023-12-28 01:05:02 AM
>> done...                                2023-12-28 01:05:02 AM
```



5.3.2 KEGG Enrichment Analysis

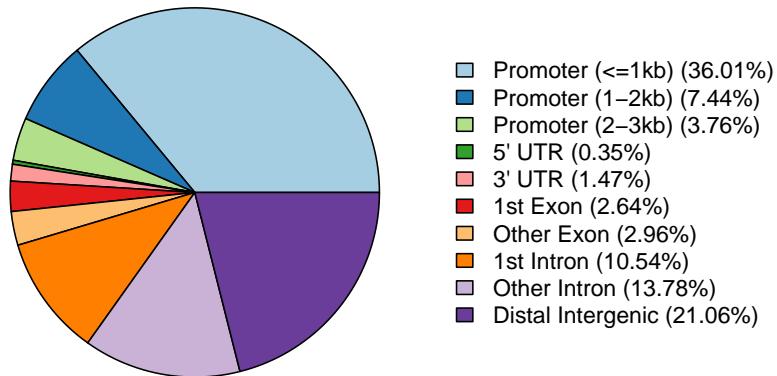


5.4 H3K4me3

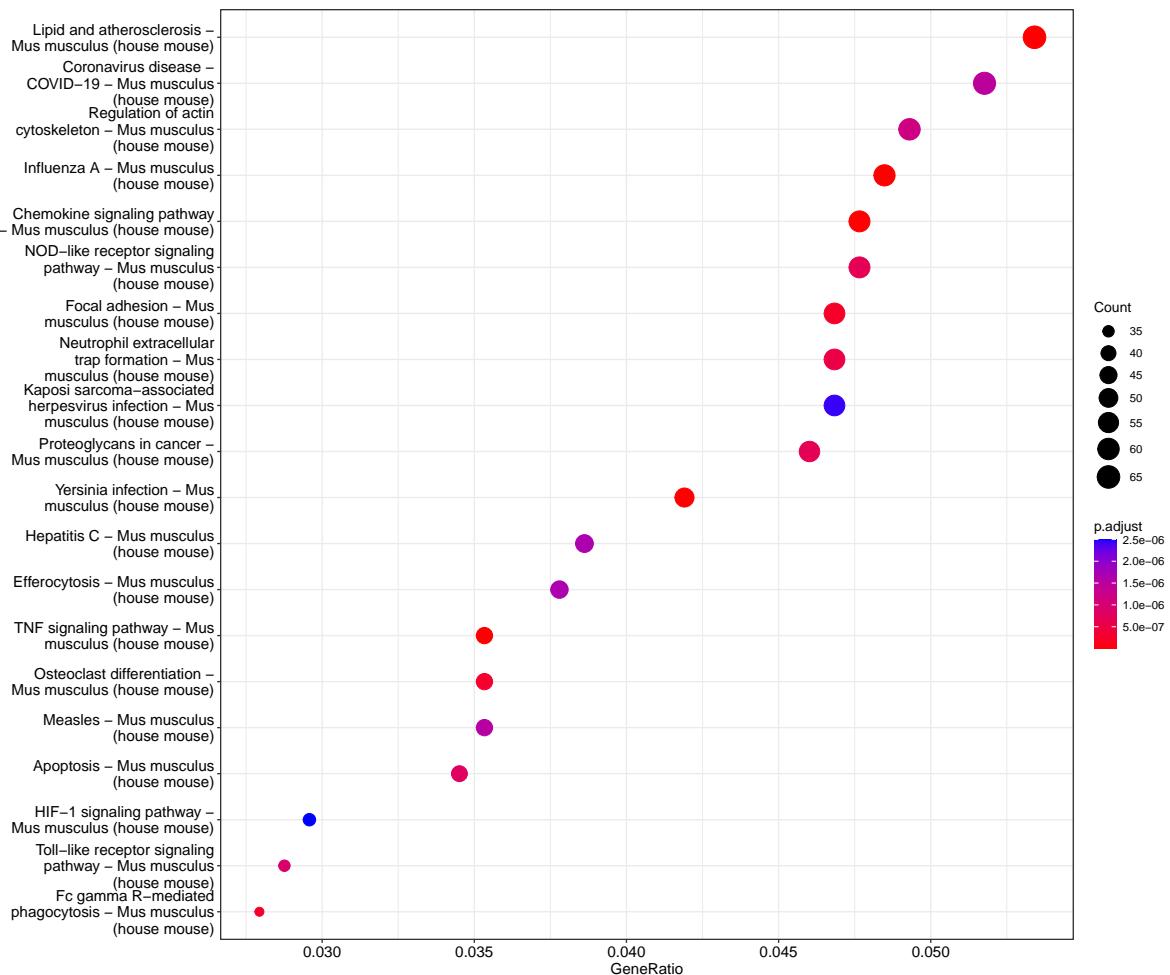
5.4.1 Differential Peak Annotation

Fold change cutoff is 2

```
>> preparing features information...           2023-12-28 01:05:03 AM
>> identifying nearest features...          2023-12-28 01:05:03 AM
>> calculating distance from peak to TSS... 2023-12-28 01:05:04 AM
>> assigning genomic annotation...         2023-12-28 01:05:04 AM
>> adding gene annotation...              2023-12-28 01:05:08 AM
>> assigning chromosome lengths        2023-12-28 01:05:08 AM
>> done...                                2023-12-28 01:05:08 AM
```



5.4.2 KEGG Enrichment Analysis

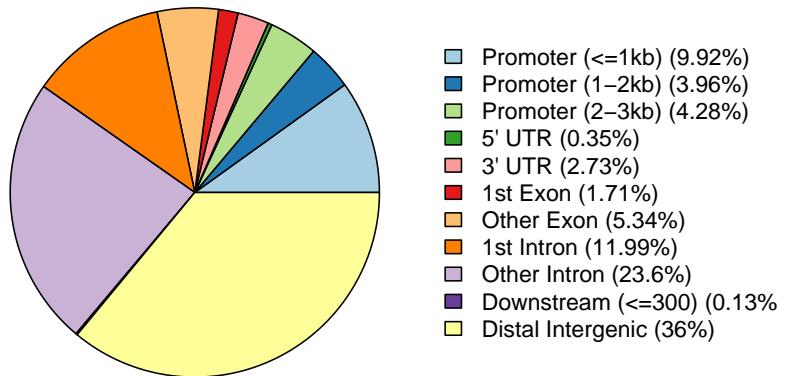


5.5 H3K27ac

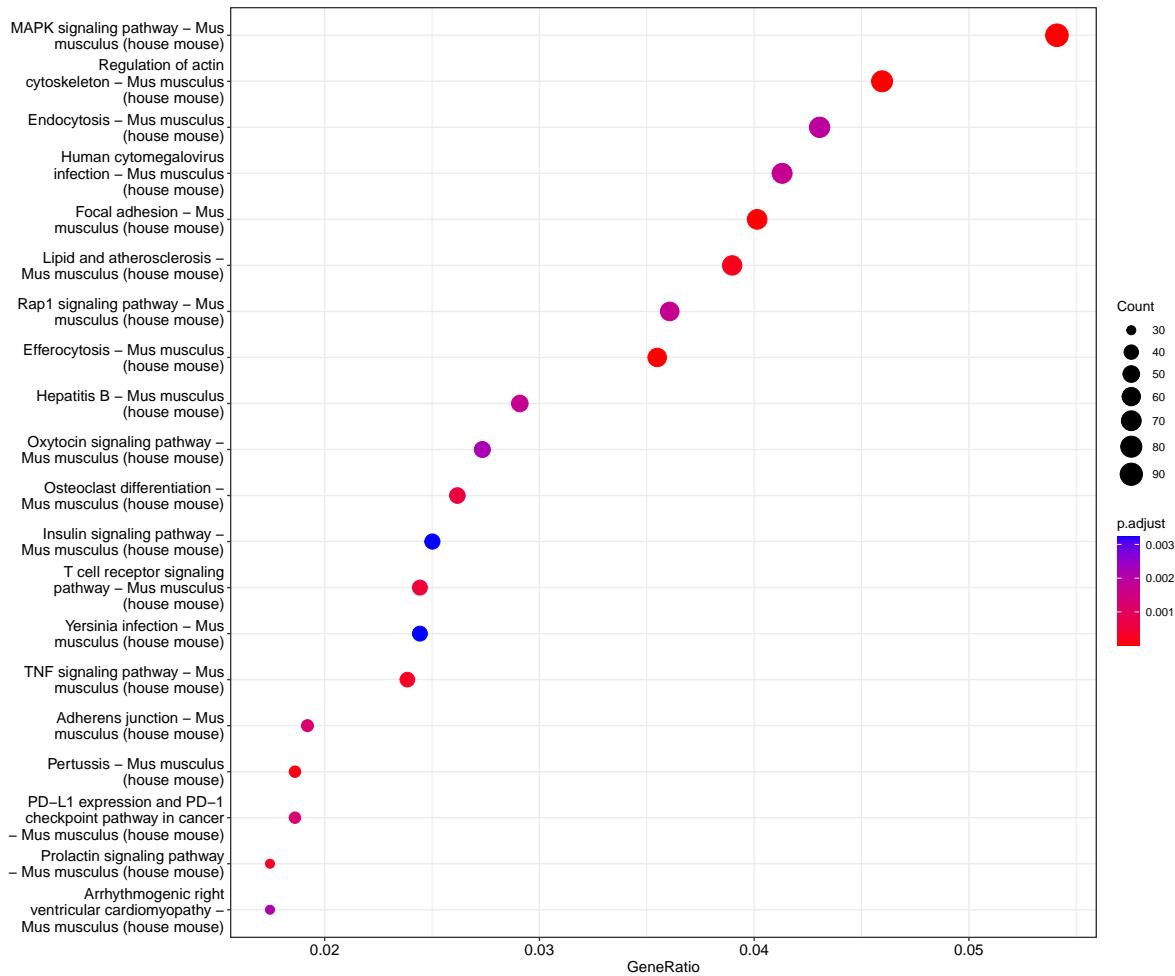
5.5.1 Differential Peak Annotation

Fold change cutoff is 4

```
>> preparing features information...           2023-12-28 01:05:10 AM
>> identifying nearest features...          2023-12-28 01:05:10 AM
>> calculating distance from peak to TSS... 2023-12-28 01:05:10 AM
>> assigning genomic annotation...         2023-12-28 01:05:10 AM
>> adding gene annotation...              2023-12-28 01:05:14 AM
>> assigning chromosome lengths        2023-12-28 01:05:14 AM
>> done...                                2023-12-28 01:05:14 AM
```



5.5.2 KEGG Enrichment Analysis

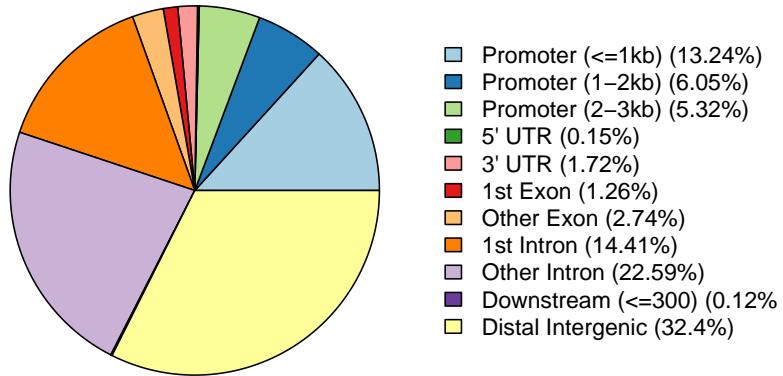


5.6 STAT1

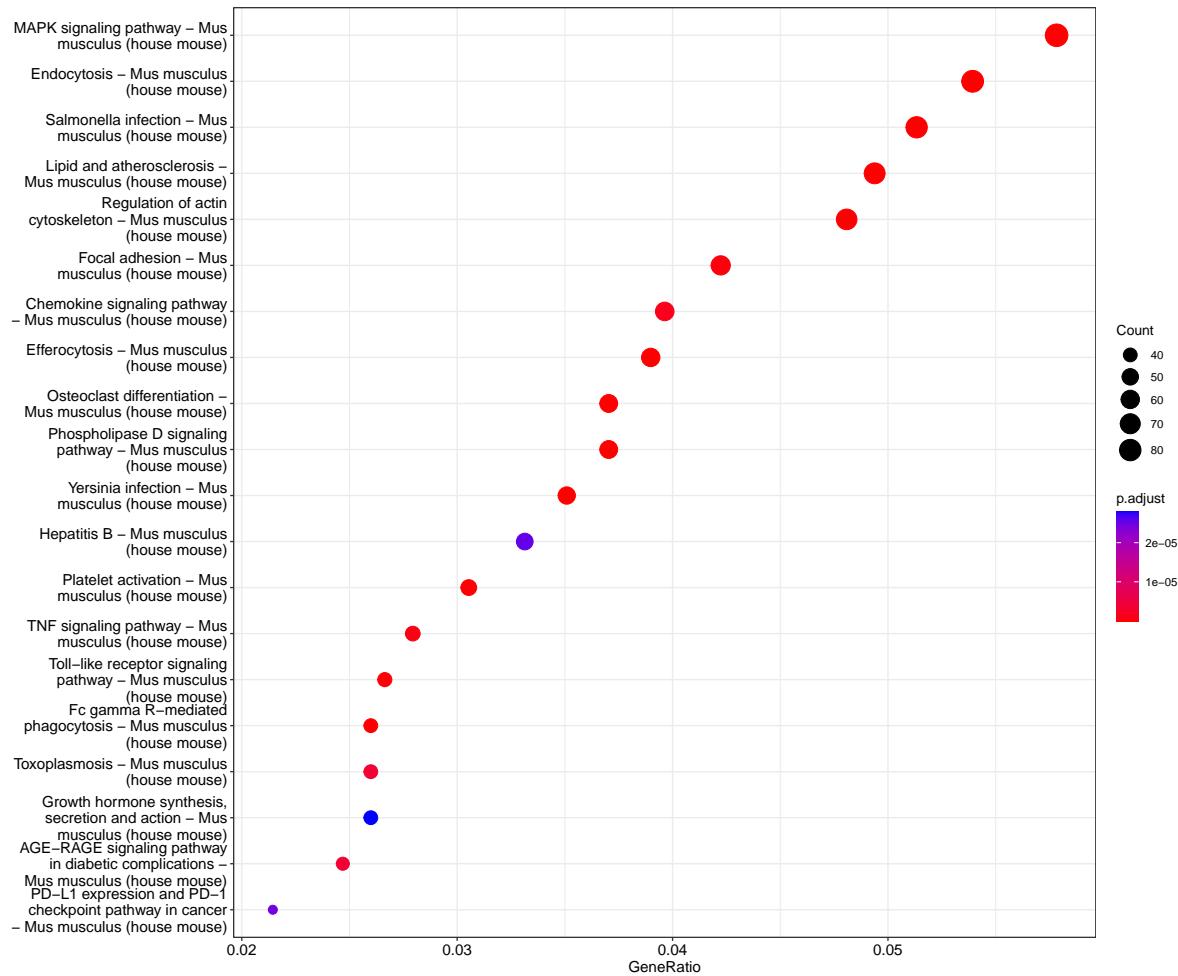
5.6.1 Differential Peak Annotation

Fold change cutoff is 4

```
>> preparing features information...           2023-12-28 01:05:16 AM
>> identifying nearest features...          2023-12-28 01:05:16 AM
>> calculating distance from peak to TSS... 2023-12-28 01:05:17 AM
>> assigning genomic annotation...         2023-12-28 01:05:17 AM
>> adding gene annotation...              2023-12-28 01:05:20 AM
>> assigning chromosome lengths        2023-12-28 01:05:21 AM
>> done...                                2023-12-28 01:05:21 AM
```



5.6.2 KEGG Enrichment Analysis

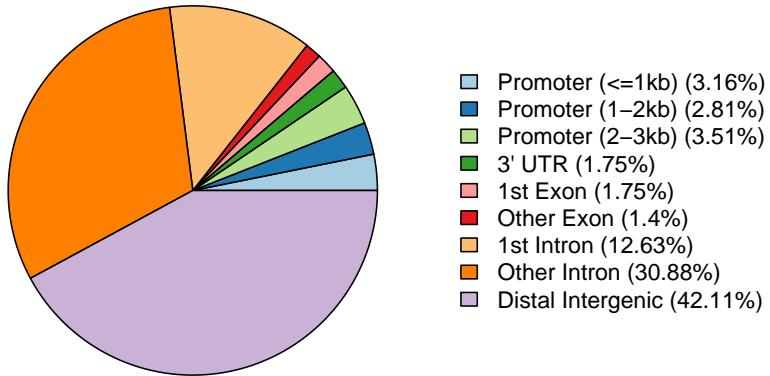


5.7 PU1

5.7.1 Differential Peak Annotation

Fold change cutoff is 4

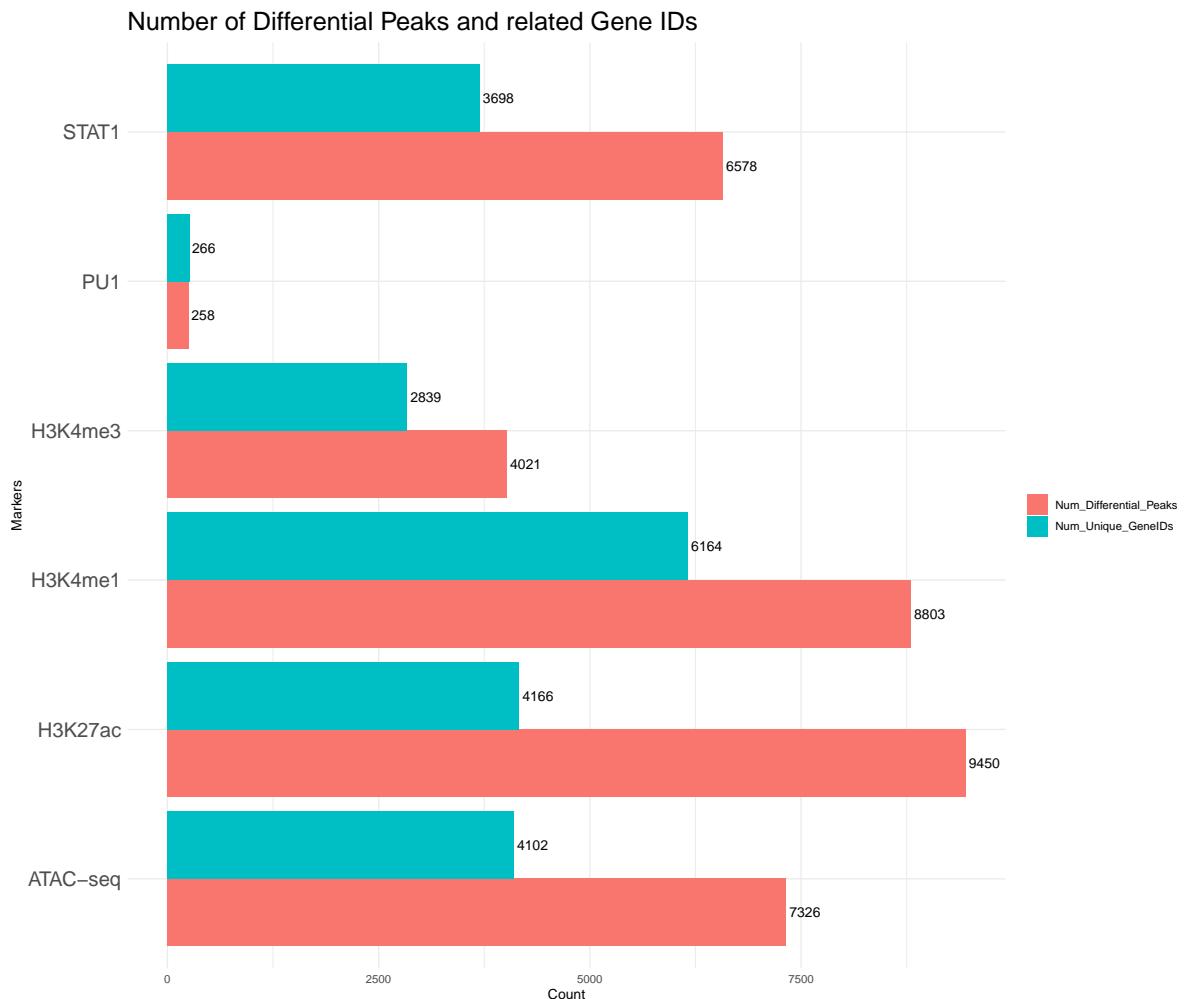
```
>> preparing features information...           2023-12-28 01:05:22 AM
>> identifying nearest features...          2023-12-28 01:05:22 AM
>> calculating distance from peak to TSS... 2023-12-28 01:05:23 AM
>> assigning genomic annotation...         2023-12-28 01:05:23 AM
>> adding gene annotation...              2023-12-28 01:05:26 AM
>> assigning chromosome lengths        2023-12-28 01:05:26 AM
>> done...                                2023-12-28 01:05:26 AM
```



5.7.2 KEGG Enrichment Analysis

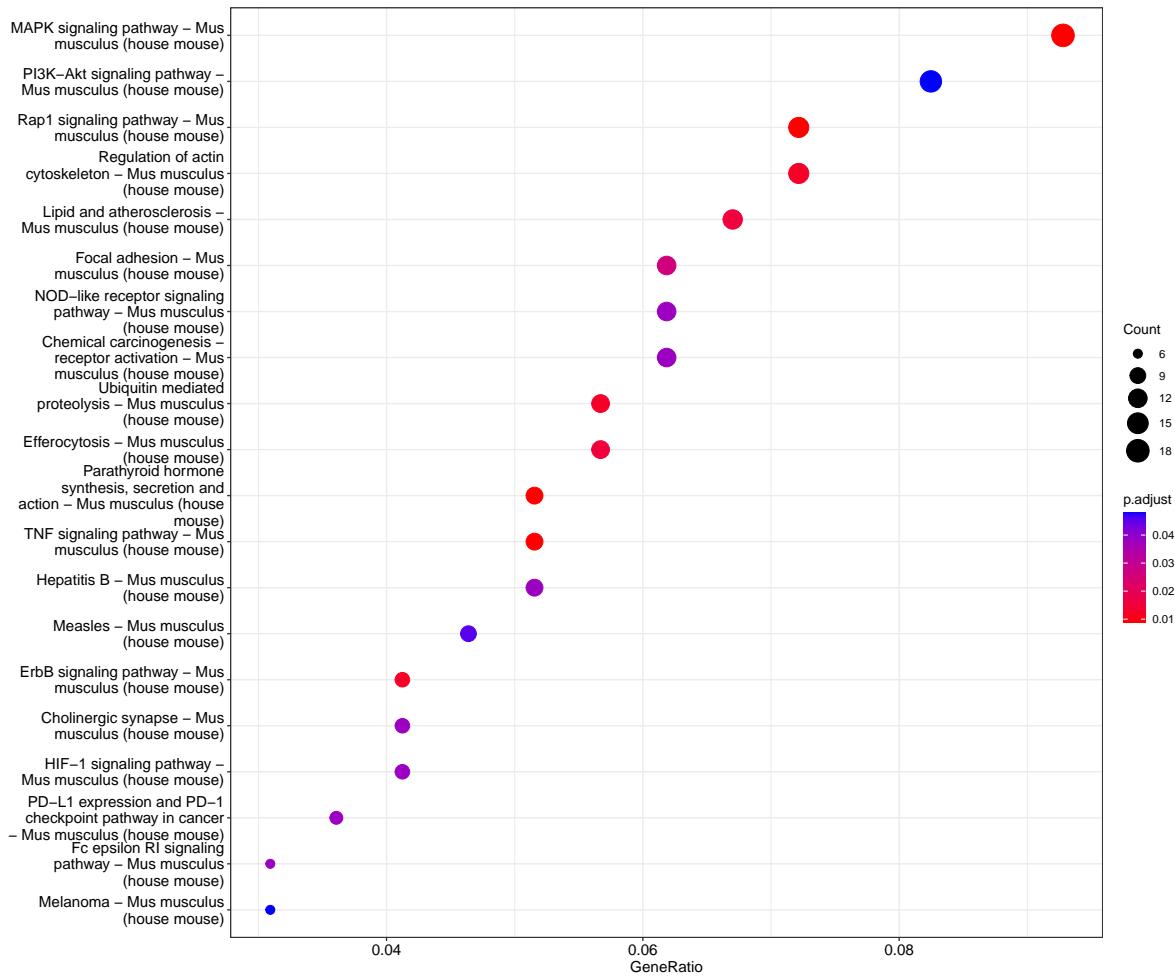
No KEGG enrichment for PU1 differential peaks

5.8 Summary of Differential Peaks in each Dataset

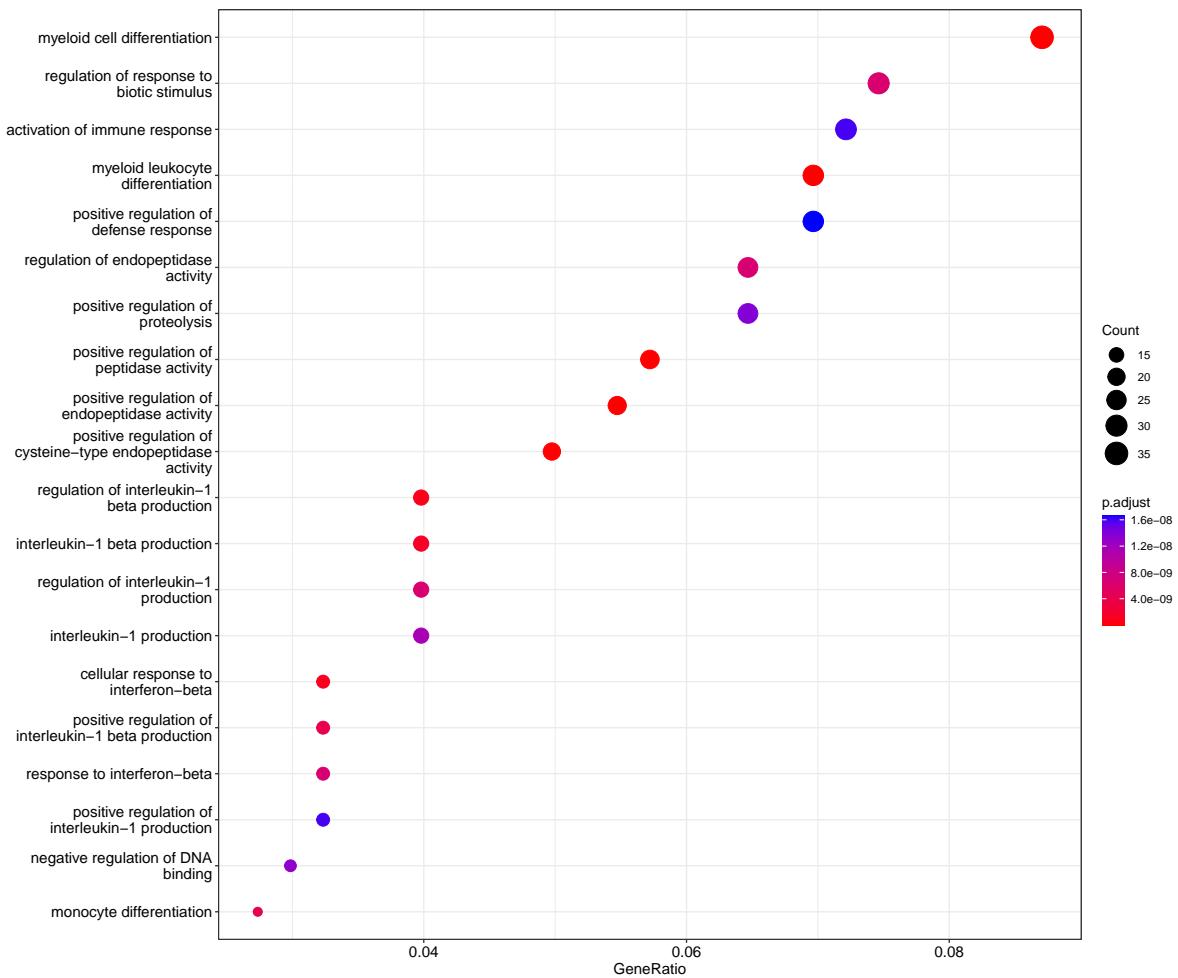


5.9 Enrichment analysis for overlapping differential peaks

5.9.1 KEGG Analysis



5.9.2 Biological Process Analysis



6 Merging Differential Peaks with RNA-seq dataset

6.1 Overlapping genes between Chip-seq, ATAC-seq & RNA-seq

[1] "The size of table is: 342"

Table 6.1: Full overlapping gene list. The genes are sorted based on log2FoldChange taken from RNA-seq data.

| gene | baseMean | log2FoldChange | padj | geneName |
|-----------|--------------|----------------|-----------|--|
| Serpina3g | 413.071001 | 12.2096933 | 0.0000000 | serine (or cysteine) peptidase inhibitor, clade A, member 3G |
| Serpina3f | 510.437561 | 11.5528438 | 0.0000000 | serine (or cysteine) peptidase inhibitor, clade A, member 3F |
| Selp | 173.331150 | 10.9569243 | 0.0000000 | selectin, platelet |
| Ifi205 | 117.339191 | 10.3941546 | 0.0000000 | interferon activated gene 205 |
| Gbp5 | 4190.462298 | 10.0602118 | 0.0000000 | guanylate binding protein 5 |
| Socs1 | 2671.065949 | 8.8008765 | 0.0000000 | suppressor of cytokine signaling 1 |
| Gm4951 | 570.938843 | 8.5122891 | 0.0000000 | predicted gene 4951 |
| Gbp4 | 270.390498 | 8.4344930 | 0.0000000 | guanylate binding protein 4 |
| Lipg | 24.946710 | 8.1606718 | 0.0000001 | lipase, endothelial |
| Gbp2 | 10619.152987 | 8.1441477 | 0.0000000 | guanylate binding protein 2 |
| Ch25h | 470.075801 | 6.9018842 | 0.0000000 | cholesterol 25-hydroxylase |
| F3 | 52.687178 | 6.7849443 | 0.0000000 | coagulation factor III |
| Nos2 | 17.099463 | 6.6412804 | 0.0000072 | nitric oxide synthase 2, inducible |
| Cish | 234.537957 | 6.4298654 | 0.0000000 | cytokine inducible SH2-containing protein |
| Gbp3 | 2168.178537 | 6.4234227 | 0.0000000 | guanylate binding protein 3 |
| Upp1 | 27.041170 | 6.4062552 | 0.0000001 | uridine phosphorylase 1 |
| Fgf9 | 12.696303 | 6.2040309 | 0.0000235 | fibroblast growth factor 9 |
| Batf2 | 955.412869 | 6.0498241 | 0.0000000 | basic leucine zipper transcription factor, ATF-like 2 |
| Serpina3i | 5.464133 | 5.9723181 | 0.0007875 | serine (or cysteine) peptidase inhibitor, clade A, member 3I |
| Nrg1 | 19.993485 | 5.9649237 | 0.0000021 | neuregulin 1 |
| Tnfsf10 | 107.078434 | 5.8163681 | 0.0000000 | tumor necrosis factor (ligand) superfamily, member 10 |
| Ifi203 | 2639.226408 | 5.4653712 | 0.0000000 | interferon activated gene 203 |
| Il18rap | 245.802923 | 5.1071061 | 0.0000000 | interleukin 18 receptor accessory protein |
| Gpr171 | 41.172334 | 4.8124015 | 0.0000000 | G protein-coupled receptor 171 |
| Nod1 | 982.767823 | 4.6225113 | 0.0000000 | nucleotide-binding oligomerization domain containing 1 |
| Gm12185 | 94.567259 | 4.5714614 | 0.0025934 | predicted gene 12185 |
| Epcam | 2.040421 | 4.5520034 | 0.1054329 | epithelial cell adhesion molecule |
| Mndal | 1713.561072 | 4.5423716 | 0.0000000 | myeloid nuclear differentiation antigen like |
| Tarm1 | 50.060741 | 4.4702825 | 0.0000000 | T cell-interacting, activating receptor on myeloid cells 1 |
| Ifit3 | 1428.365182 | 4.4451855 | 0.0000000 | interferon-induced protein with tetratricopeptide repeats 3 |
| Fgl2 | 1016.929465 | 4.2122742 | 0.0000000 | fibrinogen-like protein 2 |
| Ifi44 | 88.333213 | 4.2113817 | 0.0000000 | interferon-induced protein 44 |
| Rgl1 | 594.602833 | 4.1537089 | 0.0000000 | ral guanine nucleotide dissociation stimulator-like 1 |
| Prr5l | 579.813643 | 3.9927509 | 0.0000000 | proline rich 5 like |
| Rgs7bp | 8.610014 | 3.6532251 | 0.0033756 | regulator of G-protein signalling 7 binding protein |
| Gbp8 | 52.227025 | 3.6310916 | 0.0000007 | guanylate-binding protein 8 |

| | | | | |
|--------------|-------------|-----------|-----------|--|
| Tfec | 807.975273 | 3.5698301 | 0.0000000 | transcription factor EC |
| Mir155hg | 2.042501 | 3.4806648 | 0.3858505 | Mir155 host gene (non-protein coding) |
| If204 | 2789.613603 | 3.4750426 | 0.0000000 | interferon activated gene 204 |
| Rmi2 | 7.462850 | 3.4303411 | 0.0214458 | RecQ mediated genome instability 2 |
| Epha4 | 6.644573 | 3.2459384 | 0.0257108 | Eph receptor A4 |
| Arhgef3 | 823.134474 | 3.2448113 | 0.0000000 | Rho guanine nucleotide exchange factor (GEF) 3 |
| Aqp9 | 11.467060 | 3.2416355 | 0.0001832 | aquaporin 9 |
| Fas | 186.853696 | 3.0728084 | 0.0000000 | Fas (TNF receptor superfamily member 6) |
| Pla2g4a | 339.653685 | 3.0701422 | 0.0000004 | phospholipase A2, group IVA (cytosolic, calcium-dependent) |
| Csrnp1 | 485.890401 | 3.0681834 | 0.0000000 | cysteine-serine-rich nuclear protein 1 |
| Mid1 | 857.745217 | 3.0458978 | 0.0000000 | midline 1 |
| Smkr-ps | 4.137886 | 2.9484670 | 0.1011484 | smal lysine rich protein 1, pseudogene |
| Ikzf2 | 42.096509 | 2.8871088 | 0.0000026 | IKAROS family zinc finger 2 |
| Dusp10 | 44.864183 | 2.7700868 | 0.0000000 | dual specificity phosphatase 10 |
| Dusp16 | 359.563445 | 2.7429549 | 0.0000000 | dual specificity phosphatase 16 |
| Hivep2 | 148.162104 | 2.6580257 | 0.0000000 | human immunodeficiency virus type I enhancer binding protein 2 |
| Il15 | 456.244607 | 2.6469781 | 0.0000000 | interleukin 15 |
| Jun | 3380.318613 | 2.6362999 | 0.0000000 | jun proto-oncogene |
| Pde4b | 762.549471 | 2.6243357 | 0.0000000 | phosphodiesterase 4B, cAMP specific |
| Nampt | 6120.458202 | 2.6002326 | 0.0000000 | nicotinamide phosphoribosyltransferase |
| Rapgef6 | 1050.733553 | 2.5722021 | 0.0000000 | Rap guanine nucleotide exchange factor (GEF) 6 |
| Samhd1 | 8725.412919 | 2.4786583 | 0.0000000 | SAM domain and HD domain, 1 |
| Zyx | 3502.165598 | 2.4774289 | 0.0000000 | zyxin |
| Gcnt2 | 87.865311 | 2.4482724 | 0.0000000 | glucosaminyl (N-acetyl) transferase 2, I-branching enzyme |
| Rbbp8 | 395.157940 | 2.2700957 | 0.0000211 | retinoblastoma binding protein 8, endonuclease |
| Homer1 | 235.085478 | 2.1196398 | 0.0000001 | homer scaffolding protein 1 |
| Ikzf1 | 2319.638152 | 2.1024429 | 0.0000000 | IKAROS family zinc finger 1 |
| Rap2c | 1343.990445 | 2.0905630 | 0.0000130 | RAP2C, member of RAS oncogene family |
| Ifih1 | 599.110689 | 1.9096837 | 0.0001719 | interferon induced with helicase C domain 1 |
| D16Erttd472e | 70.338137 | 1.8906825 | 0.0000006 | DNA segment, Chr 16, ERATO Doi 472, expressed |
| Spred1 | 1601.888930 | 1.8888303 | 0.0000078 | sprouty protein with EVH-1 domain 1, related sequence |
| Lyn | 3582.117255 | 1.8249210 | 0.0000000 | LYN proto-oncogene, Src family tyrosine kinase |
| Asb4 | 37.615437 | 1.8043738 | 0.0000097 | ankyrin repeat and SOCS box-containing 4 |
| Itga4 | 2861.148739 | 1.7540886 | 0.0018368 | integrin alpha 4 |
| Zfp800 | 278.027347 | 1.7333851 | 0.0057848 | zinc finger protein 800 |
| P2ry14 | 231.186549 | 1.7310964 | 0.0000000 | purinergic receptor P2Y, G-protein coupled, 14 |
| Fgf7 | 1.346767 | 1.7246680 | 0.7213626 | fibroblast growth factor 7 |
| Slamf6 | 17.713308 | 1.6520616 | 0.0269769 | SLAM family member 6 |
| Igf2bp2 | 446.077779 | 1.6462294 | 0.0000000 | insulin-like growth factor 2 mRNA binding protein 2 |
| Nrip1 | 281.277894 | 1.6358196 | 0.0000008 | nuclear receptor interacting protein 1 |
| Slc43a3 | 73.854210 | 1.5800953 | 0.0013317 | solute carrier family 43, member 3 |
| Nr3c1 | 1535.360028 | 1.5689132 | 0.0001389 | nuclear receptor subfamily 3, group C, member 1 |
| Fndc3a | 1380.369575 | 1.5549276 | 0.0001215 | fibronectin type III domain containing 3A |
| Klf7 | 35.810904 | 1.5532877 | 0.0006761 | Kruppel-like factor 7 (ubiquitous) |
| Slc31a1 | 1803.962867 | 1.5516839 | 0.0000000 | solute carrier family 31, member 1 |
| Slc31a2 | 1347.956254 | 1.5486740 | 0.0000000 | solute carrier family 31, member 2 |
| Klra2 | 9.736738 | 1.5428860 | 0.2023538 | killer cell lectin-like receptor, subfamily A, member 2 |
| Gm16675 | 26.127849 | 1.5110418 | 0.0028476 | predicted gene, 16675 |
| Trps1 | 776.533172 | 1.5079119 | 0.0004063 | transcriptional repressor GATA binding 1 |
| Cd86 | 191.382843 | 1.4364619 | 0.0090034 | CD86 antigen |
| Gpr141 | 91.891173 | 1.3942729 | 0.1924474 | G protein-coupled receptor 141 |
| Snx2 | 1934.596529 | 1.3819262 | 0.0000028 | sorting nexin 2 |
| Ctsc | 2519.856878 | 1.3786790 | 0.0006945 | cathepsin C |
| Fcho2 | 2223.783131 | 1.3598442 | 0.0350053 | FCH domain only 2 |
| Creb5 | 270.452587 | 1.3515666 | 0.0029660 | cAMP responsive element binding protein 5 |
| Htt | 1831.270243 | 1.3437941 | 0.0000000 | huntingtin |
| Mreg | 5.660576 | 1.3426284 | 0.4947682 | melanoregulin |
| Zfp608 | 169.379264 | 1.3405986 | 0.0000196 | zinc finger protein 608 |
| Msrb3 | 2.167804 | 1.3355768 | 0.7402845 | methionine sulfoxide reductase B3 |
| Birc3 | 1199.547468 | 1.3286893 | 0.0000185 | baculoviral IAP repeat-containing 3 |
| Cyp26b1 | 3.885981 | 1.3223280 | 0.5579284 | cytochrome P450, family 26, subfamily b, polypeptide 1 |
| Dhrs9 | 351.132776 | 1.3194461 | 0.0000031 | dehydrogenase/reductase (SDR family) member 9 |
| Acvr2a | 231.307422 | 1.2774174 | 0.0101104 | activin receptor II A |
| Malt1 | 546.282138 | 1.2767570 | 0.0011678 | MALT1 paracaspase |

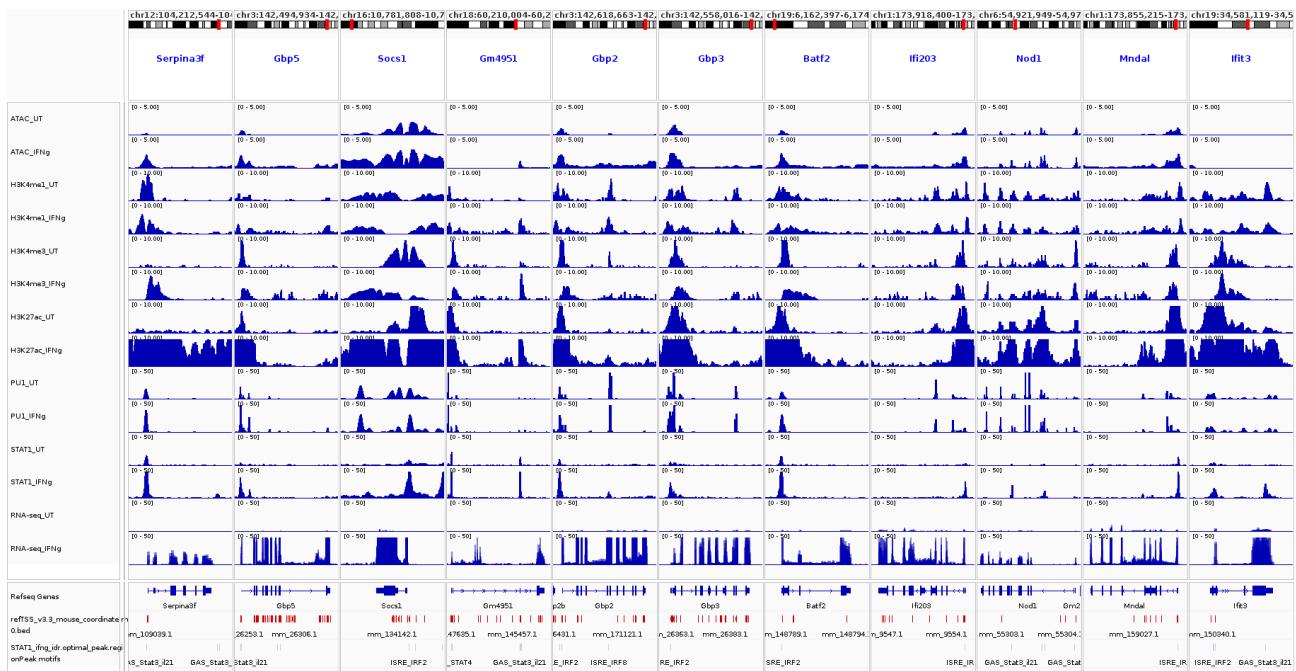
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|-----------|-------------|-----------|-----------|--|
| Bcas1 | 2.698263 | 1.2564326 | 0.6858828 | brain enriched myelin associated protein 1 |
| Pros1 | 687.333226 | 1.2486224 | 0.0000001 | protein S (alpha) |
| Ccdc39 | 15.304771 | 1.2434120 | 0.3026433 | coiled-coil domain containing 39 |
| Atp8a1 | 1149.607736 | 1.1765680 | 0.0048823 | ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1 |
| Snx10 | 1402.083267 | 1.1729119 | 0.0010468 | sorting nexin 10 |
| Tiparp | 335.595194 | 1.1649271 | 0.0857791 | TCDD-inducible poly(ADP-ribose) polymerase |
| Zranb3 | 676.743946 | 1.1455039 | 0.0000000 | zinc finger, RAN-binding domain containing 3 |
| Itgav | 5178.409908 | 1.0941165 | 0.0609244 | integrin alpha V |
| Ranbp2 | 1711.773394 | 1.0829160 | 0.0928100 | RAN binding protein 2 |
| Pkib | 404.691297 | 1.0788262 | 0.0036539 | protein kinase inhibitor beta, cAMP dependent, testis specific |
| Rap1gds1 | 1999.267781 | 1.0784309 | 0.0000002 | RAP1, GTP-GDP dissociation stimulator 1 |
| Spata13 | 556.027977 | 1.0737683 | 0.0071732 | spermatogenesis associated 13 |
| Baz2b | 889.304488 | 1.0664559 | 0.0072535 | bromodomain adjacent to zinc finger domain, 2B |
| Heatrl | 1223.405009 | 1.0504896 | 0.0000003 | HEAT repeat containing 1 |
| Chd7 | 551.259857 | 1.0350222 | 0.0056252 | chromodomain helicase DNA binding protein 7 |
| St7 | 83.920117 | 1.0229564 | 0.0005889 | suppression of tumorigenicity 7 |
| Tpx2 | 162.228284 | 1.0072705 | 0.0077993 | TPX2, microtubule-associated |
| Casp8 | 1071.663917 | 1.0024426 | 0.0002126 | caspase 8 |
| Pde4d | 82.134699 | 0.9295267 | 0.2100465 | phosphodiesterase 4D, cAMP specific |
| Filip1l | 297.181813 | 0.8947780 | 0.2499858 | filamin A interacting protein 1-like |
| Ankrnd50 | 569.467770 | 0.8844156 | 0.0000452 | ankyrin repeat domain 50 |
| Klf6 | 3808.944493 | 0.8767729 | 0.0041287 | Kruppel-like factor 6 |
| Extl3 | 2417.186812 | 0.8710837 | 0.0000273 | exostosin-like glycosyltransferase 3 |
| Aim2 | 312.280862 | 0.8651652 | 0.1071340 | absent in melanoma 2 |
| Rapgef2 | 401.011647 | 0.8496265 | 0.0007590 | Rap guanine nucleotide exchange factor (GEF) 2 |
| Ccdc71l | 1565.891119 | 0.8487009 | 0.0000079 | coiled-coil domain containing 71 like |
| Cmpk1 | 1985.997261 | 0.8411423 | 0.0059257 | cytidine monophosphate (UMP-CMP) kinase 1 |
| Cdk6 | 125.056541 | 0.8339580 | 0.2177764 | cyclin-dependent kinase 6 |
| Kitl | 339.464490 | 0.8307334 | 0.3625211 | kit ligand |
| Hipk1 | 3256.525597 | 0.8218165 | 0.0322666 | homeodomain interacting protein kinase 1 |
| Pcmtd1 | 630.450102 | 0.8212082 | 0.2349815 | protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1 |
| Lims1 | 1336.544882 | 0.7981153 | 0.2398502 | LIM and senescent cell antigen-like domains 1 |
| Tshz1 | 495.053053 | 0.7870213 | 0.0185865 | teashirt zinc finger family member 1 |
| Phip | 941.887681 | 0.7864389 | 0.4974667 | pleckstrin homology domain interacting protein |
| Jak2 | 481.321660 | 0.7770246 | 0.1408018 | Janus kinase 2 |
| Foxp1 | 901.881343 | 0.7751505 | 0.0110615 | forkhead box P1 |
| Tnrc6b | 947.083664 | 0.7630866 | 0.0601688 | trinucleotide repeat containing 6b |
| Zbtb18 | 618.556708 | 0.7623088 | 0.0219867 | zinc finger and BTB domain containing 18 |
| Clcc1 | 610.677246 | 0.7419651 | 0.0001225 | chloride channel CLIC-like 1 |
| Adgrl2 | 1177.230850 | 0.7377777 | 0.0000000 | adhesion G protein-coupled receptor L2 |
| Nup153 | 1081.172058 | 0.7371263 | 0.0656700 | nucleoporin 153 |
| Golph3l | 817.099410 | 0.7107983 | 0.1193930 | golgi phosphoprotein 3-like |
| Ppt1 | 1692.878280 | 0.6999368 | 0.0000405 | palmitoyl-protein thioesterase 1 |
| Dock10 | 1507.981410 | 0.6976968 | 0.4759601 | dedicator of cytokinesis 10 |
| Zfp287 | 68.540935 | 0.6934041 | 0.2612658 | zinc finger protein 287 |
| Btg1 | 4020.420233 | 0.6851406 | 0.0001443 | BTG anti-proliferation factor 1 |
| Tnfsf8 | 5.286350 | 0.6802200 | 0.8178935 | tumor necrosis factor (ligand) superfamily, member 8 |
| Hif1a | 1295.693353 | 0.6786006 | 0.3570285 | hypoxia inducible factor 1, alpha subunit |
| Vcan | 139.936002 | 0.6760107 | 0.5895203 | versican |
| Map2k6 | 14.645901 | 0.6687314 | 0.5514986 | mitogen-activated protein kinase kinase 6 |
| Hnrnph2 | 1238.499430 | 0.6664600 | 0.2167744 | heterogeneous nuclear ribonucleoprotein H2 |
| Lrp6 | 1328.096100 | 0.6339277 | 0.0260159 | low density lipoprotein receptor-related protein 6 |
| Tank | 422.447638 | 0.6189441 | 0.1669354 | TRAF family member-associated Nf-kappa B activator |
| Gramd1c | 10.229724 | 0.6147515 | 0.7520124 | GRAM domain containing 1C |
| Tlr5 | 10.524221 | 0.6120548 | 0.8823263 | toll-like receptor 5 |
| Rnaseh2b | 199.549215 | 0.5963251 | 0.0143562 | ribonuclease H2, subunit B |
| Slco3a1 | 89.641609 | 0.5931905 | 0.1266387 | solute carrier organic anion transporter family, member 3a1 |
| Zfp777 | 259.930243 | 0.5925482 | 0.0627753 | zinc finger protein 777 |
| Msh3 | 107.779823 | 0.5896687 | 0.3525700 | mutS homolog 3 |
| Pmepa1 | 97.948313 | 0.5887084 | 0.1341276 | prostate transmembrane protein, androgen induced 1 |
| Cd47 | 1653.331841 | 0.5719275 | 0.0020941 | CD47 antigen (Rh-related antigen, integrin-associated signal transducer) |
| Tcf4 | 1321.569092 | 0.5599529 | 0.4364645 | transcription factor 4 |
| Ust | 287.560286 | 0.5590742 | 0.2778126 | uronid-2-sulfotransferase |
| Secisbp2l | 1791.415260 | 0.5564515 | 0.3711217 | SECIS binding protein 2-like |

| | | | | |
|---------------|--------------|-----------|-----------|---|
| Kdr | 334.444898 | 0.5556481 | 0.0361517 | kinase insert domain protein receptor |
| Slc4a7 | 703.512893 | 0.5363695 | 0.6527422 | solute carrier family 4, sodium bicarbonate cotransporter, member 7 |
| Runx2 | 59.528503 | 0.5221602 | 0.4288931 | runt related transcription factor 2 |
| Cited2 | 1288.425181 | 0.5212455 | 0.0812972 | Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2 |
| Cmtm6 | 2445.388543 | 0.5198865 | 0.0001097 | CKLF-like MARVEL transmembrane domain containing 6 |
| Crebrf | 876.326721 | 0.5102767 | 0.5472019 | CREB3 regulatory factor |
| Ssr3 | 2207.631011 | 0.5064376 | 0.2862583 | signal sequence receptor, gamma |
| Lilrb4a | 4744.323390 | 0.5044541 | 0.3966319 | leukocyte immunoglobulin-like receptor, subfamily B, member 4A |
| Vps54 | 609.500357 | 0.4994783 | 0.5090554 | VPS54 GARP complex subunit |
| Cd2ap | 588.989868 | 0.4982681 | 0.7266677 | CD2-associated protein |
| Akap13 | 2429.811836 | 0.4950523 | 0.0017067 | A kinase (PRKA) anchor protein 13 |
| 4930503L19Rik | 113.844927 | 0.4890968 | 0.5610281 | RIKEN cDNA 4930503L19 gene |
| Tax1bp1 | 1727.639501 | 0.4878963 | 0.6561469 | Tax1 (human T cell leukemia virus type I) binding protein 1 |
| Ascc3 | 372.861577 | 0.4843684 | 0.7255989 | activating signal cointegrator 1 complex subunit 3 |
| Syne2 | 45.177623 | 0.4801606 | 0.3985854 | spectrin repeat containing, nuclear envelope 2 |
| Csnk1g3 | 364.413391 | 0.4772956 | 0.4048026 | casein kinase 1, gamma 3 |
| Fmn1 | 878.619567 | 0.4726901 | 0.3909590 | formin 1 |
| Tnfaip3 | 289.545678 | 0.4668320 | 0.1895549 | tumor necrosis factor, alpha-induced protein 3 |
| Crkl | 1053.046533 | 0.4563966 | 0.0049513 | v-crk avian sarcoma virus CT10 oncogene homolog-like |
| Chn2 | 185.183132 | 0.4421177 | 0.4016988 | chimerin 2 |
| Vav3 | 469.056288 | 0.4366895 | 0.4618509 | vav 3 oncogene |
| Vps4b | 1606.698977 | 0.4318145 | 0.4968681 | vacuolar protein sorting 4B |
| Slc44a1 | 979.447628 | 0.4188947 | 0.3498643 | solute carrier family 44, member 1 |
| Anxa3 | 1550.170590 | 0.4075992 | 0.0011061 | annexin A3 |
| Fmn1l2 | 251.894578 | 0.4055761 | 0.6619212 | formin-like 2 |
| E230016M11Rik | 7.582015 | 0.4000324 | 0.9158477 | RIKEN cDNA E230016M11 gene |
| Msn | 13891.148209 | 0.3997157 | 0.0052507 | moesin |
| Man2a1 | 1392.695678 | 0.3834485 | 0.4425382 | mannosidase 2, alpha 1 |
| Srgap2 | 1702.946667 | 0.3794485 | 0.3043633 | SLIT-ROBO Rho GTPase activating protein 2 |
| St18 | 185.980705 | 0.3715900 | 0.8092669 | suppression of tumorigenicity 18 |
| Arl5a | 1033.906031 | 0.3707880 | 0.7453936 | ADP-ribosylation factor-like 5A |
| Mbip | 82.951191 | 0.3660252 | 0.7389355 | MAP3K12 binding inhibitory protein 1 |
| Akap6 | 7.118970 | 0.3567261 | 0.9373686 | A kinase (PRKA) anchor protein 6 |
| Dgki | 2.164798 | 0.3566757 | 0.9642067 | diacylglycerol kinase, iota |
| Skap2 | 3245.758734 | 0.3538093 | 0.0025433 | src family associated phosphoprotein 2 |
| Akap7 | 70.678598 | 0.3515925 | 0.6568805 | A kinase (PRKA) anchor protein 7 |
| Larp1 | 2128.547015 | 0.3393743 | 0.0693304 | La ribonucleoprotein 1, translational regulator |
| Lrrc8c | 188.571964 | 0.3312894 | 0.5323891 | leucine rich repeat containing 8 family, member C |
| Ank2 | 32.934646 | 0.3291563 | 0.8417265 | ankyrin 2, brain |
| Pik3r1 | 1149.143856 | 0.3284051 | 0.7133319 | phosphoinositide-3-kinase regulatory subunit 1 |
| Fyn | 794.487608 | 0.3279135 | 0.1544058 | Fyn proto-oncogene |
| Znrf1 | 1035.338573 | 0.3272375 | 0.0339092 | zinc and ring finger 1 |
| Stard3nl | 777.286492 | 0.3117537 | 0.0565516 | STARD3 N-terminal like |
| Ccnl1 | 535.180144 | 0.3107896 | 0.8522094 | cyclin L1 |
| Egfr | 14.273512 | 0.3030089 | 0.9280502 | epidermal growth factor receptor |
| Trio | 1295.377347 | 0.3027252 | 0.4524544 | triple functional domain (PTPRF interacting) |
| Hk2 | 1471.555055 | 0.3009760 | 0.0164070 | hexokinase 2 |
| Arhgap24 | 543.788957 | 0.2940300 | 0.2456450 | Rho GTPase activating protein 24 |
| Xpo6 | 1342.334513 | 0.2880536 | 0.2423260 | exportin 6 |
| Tmem135 | 590.449052 | 0.2785806 | 0.1784792 | transmembrane protein 135 |
| Med13l | 851.823536 | 0.2748985 | 0.5167443 | mediator complex subunit 13-like |
| Macrod2 | 7.306099 | 0.2722297 | 0.9581743 | mono-ADP ribosylhydrolase 2 |
| Inpp4b | 121.548158 | 0.2575354 | 0.9375937 | inositol polyphosphate-4-phosphatase, type II |
| Arhgap6 | 289.189029 | 0.2530956 | 0.6099571 | Rho GTPase activating protein 6 |
| Tpk1 | 82.690344 | 0.2530582 | 0.7040385 | thiamine pyrophosphokinase |
| Fat3 | 444.996230 | 0.2455980 | 0.5610549 | FAT atypical cadherin 3 |
| Dock4 | 635.843700 | 0.2431079 | 0.7646626 | dedicator of cytokinesis 4 |
| Ankrd17 | 1336.283498 | 0.2372411 | 0.7133319 | ankyrin repeat domain 17 |
| Arhgap15 | 229.867219 | 0.2312113 | 0.8900403 | Rho GTPase activating protein 15 |
| Stag2 | 1101.043860 | 0.2307548 | 0.9321744 | stromal antigen 2 |
| Mctp1 | 190.930703 | 0.2289210 | 0.9101028 | multiple C2 domains, transmembrane 1 |
| Ldlrad4 | 116.897634 | 0.2285860 | 0.7090934 | low density lipoprotein receptor class A domain containing 4 |
| Amz2 | 251.633722 | 0.2278971 | 0.4817312 | archaelysin family metallopeptidase 2 |

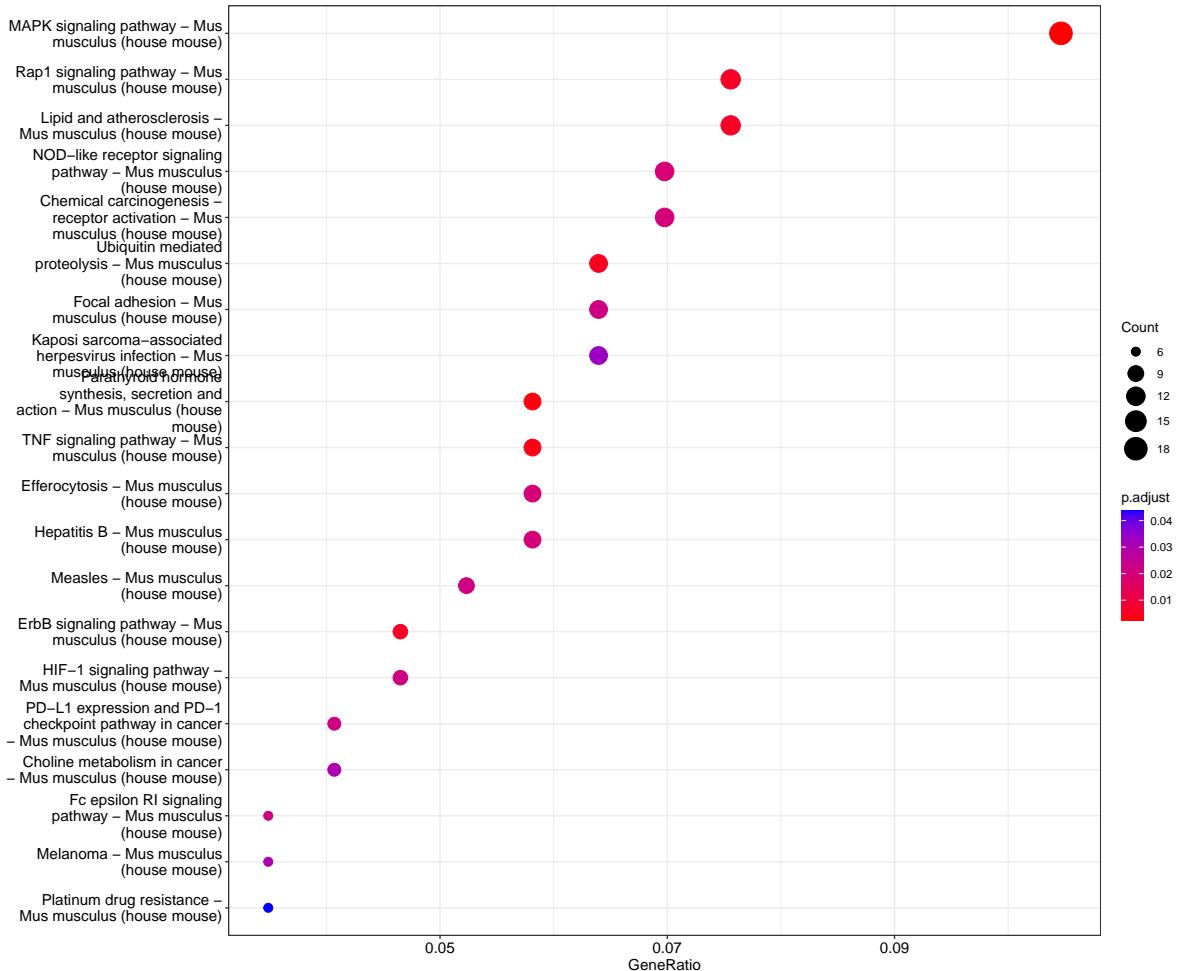
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|---------------|-------------|------------|-----------|--|
| Tnks | 758.687420 | 0.2278007 | 0.7098887 | tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase |
| Lpp | 377.441544 | 0.2204383 | 0.9051253 | LIM domain containing preferred translocation partner in lipoma |
| Atf2 | 365.474893 | 0.2195786 | 0.8956551 | activating transcription factor 2 |
| Slc25a12 | 520.945350 | 0.2185801 | 0.4940684 | solute carrier family 25 (mitochondrial carrier, Aralar), member 12 |
| Cdk14 | 937.656350 | 0.2169302 | 0.8028422 | cyclin-dependent kinase 14 |
| Mib1 | 528.228661 | 0.2124293 | 0.8624338 | MIB E3 ubiquitin protein ligase 1 |
| Acsll | 942.432093 | 0.2100877 | 0.4425382 | acyl-CoA synthetase long-chain family member 1 |
| Maf | 1953.451220 | 0.2050809 | 0.8813348 | MAF bZIP transcription factor |
| Huwe1 | 2651.108283 | 0.2032680 | 0.6004665 | HECT, UBA and WWE domain containing 1 |
| Foxn3 | 158.861376 | 0.1955525 | 0.8855933 | forkhead box N3 |
| Focad | 183.023546 | 0.1950634 | 0.7124616 | focadhesin |
| Kctd1 | 34.256538 | 0.1897577 | 0.9037307 | potassium channel tetramerisation domain containing 1 |
| Camk2d | 1235.016394 | 0.1889924 | 0.8067034 | calcium/calmodulin-dependent protein kinase II, delta |
| Procr | 206.560321 | 0.1832967 | 0.8097047 | protein C receptor, endothelial |
| Eif2s2 | 930.875427 | 0.1671322 | 0.8990194 | eukaryotic translation initiation factor 2, subunit 2 (beta) |
| Usp38 | 376.330458 | 0.1607826 | 0.8302798 | ubiquitin specific peptidase 38 |
| Zzef1 | 971.126470 | 0.1606886 | 0.6447933 | zinc finger, ZZ-type with EF hand domain 1 |
| Psd3 | 184.635768 | 0.1475675 | 0.9547418 | pleckstrin and Sec7 domain containing 3 |
| Fbxw7 | 256.464730 | 0.1427996 | 0.7660237 | F-box and WD-40 domain protein 7 |
| Zfp407 | 252.466446 | 0.1381762 | 0.9271355 | zinc finger protein 407 |
| Ahi1 | 42.523530 | 0.1316944 | 0.9442620 | Abelson helper integration site 1 |
| Marcks | 2562.217254 | 0.1289782 | 0.9130528 | myristoylated alanine rich protein kinase C substrate |
| Cep112 | 10.189901 | 0.1285657 | 0.9852525 | centrosomal protein 112 |
| Mbnl1 | 4992.217009 | 0.1237086 | 0.9581743 | muscleblind like splicing regulator 1 |
| Kcmf1 | 1138.913087 | 0.1227376 | 0.7099596 | potassium channel modulatory factor 1 |
| Acadl | 701.377036 | 0.1211521 | 0.8094838 | acyl-Coenzyme A dehydrogenase, long-chain |
| Tanc2 | 1180.829131 | 0.1188599 | 0.9426501 | tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2 |
| Phb | 1247.039768 | 0.1186042 | 0.8846606 | prohibitin |
| Bcas3 | 472.837951 | 0.1081709 | 0.8967396 | BCAS3 microtubule associated cell migration factor |
| Sf3b1 | 2855.493875 | 0.1042575 | 0.9581743 | splicing factor 3b, subunit 1 |
| Atxn1 | 498.690159 | 0.1034328 | 0.9613673 | ataxin 1 |
| Akr1e1 | 154.893849 | 0.1006667 | 0.9281860 | aldo-keto reductase family 1, member E1 |
| Adgb | 19.026828 | 0.0965787 | 0.9853709 | androglobin |
| Vps13a | 231.499957 | 0.0901070 | 0.9829878 | vacuolar protein sorting 13A |
| Rbx1 | 820.340395 | 0.0842208 | 0.9114668 | ring-box 1 |
| Sox5 | 1.640462 | 0.0807968 | 0.9933034 | SRY (sex determining region Y)-box 5 |
| Anxa4 | 4435.136208 | 0.0772623 | 0.9130528 | annexin A4 |
| Dennd1a | 952.819253 | 0.0766026 | 0.9442248 | DENN domain containing 1A |
| Frmd4b | 1120.961740 | 0.0735712 | 0.9073489 | FERM domain containing 4B |
| Nedd9 | 76.870036 | 0.0628922 | 0.9702110 | neural precursor cell expressed, developmentally down-regulated gene 9 |
| Ywhaz | 4904.269415 | 0.0564061 | 0.9416948 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide |
| Nt5e | 17.462573 | 0.0451238 | 0.9933034 | 5' nucleotidase, ecto |
| 5430437J10Rik | 4.422500 | 0.0376715 | 0.9933034 | RIKEN cDNA 5430437J10 gene |
| Macf1 | 5643.371656 | 0.0365398 | 0.9890696 | microtubule-actin crosslinking factor 1 |
| Cacnala | 709.385741 | 0.0270512 | 0.9902675 | calcium channel, voltage-dependent, P/Q type, alpha 1A subunit |
| Herc1 | 1499.209414 | 0.0219785 | 0.9901593 | HECT and RLD domain containing E3 ubiquitin protein ligase family member 1 |
| Smyd3 | 132.035669 | 0.0179241 | 0.9912629 | SET and MYND domain containing 3 |
| Kpnal2 | 660.079384 | 0.0163776 | 0.9903121 | karyopherin (importin) alpha 2 |
| Pcca | 338.629131 | 0.0151867 | 0.9901593 | propionyl-Coenzyme A carboxylase, alpha polypeptide |
| Uba1 | 4200.527000 | 0.0045948 | 0.9958964 | ubiquitin-like modifier activating enzyme 1 |
| Ssbp2 | 22.338876 | -0.0098106 | 0.9969441 | single-stranded DNA binding protein 2 |
| Prg4 | 7.981102 | -0.0104887 | 0.9986291 | proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein) |
| Rftnl | 1614.145766 | -0.0158432 | 0.9901593 | raftlin lipid raft linker 1 |
| Fam76b | 389.539889 | -0.0164573 | 0.9939265 | family with sequence similarity 76, member B |
| Spop | 1860.783346 | -0.0234688 | 0.9807272 | speckle-type BTB/POZ protein |
| Nav1 | 2225.300427 | -0.0266639 | 0.9767171 | neuron navigator 1 |
| Myof | 4545.269824 | -0.0282949 | 0.9679020 | myoferlin |
| Kpnbl1 | 2663.218057 | -0.0305781 | 0.9581743 | karyopherin (importin) beta 1 |
| Rasgef1b | 1239.876694 | -0.0358867 | 0.9705315 | RasGEF domain family, member 1B |
| Atp8b4 | 927.998454 | -0.0436209 | 0.9876054 | ATPase, class I, type 8B, member 4 |
| Mitf | 800.106425 | -0.0467953 | 0.9877495 | melanogenesis associated transcription factor |
| Eeal | 975.147947 | -0.0474874 | 0.9883991 | early endosome antigen 1 |
| Ube4b | 1242.295973 | -0.0596477 | 0.9250354 | ubiquitination factor E4B |

| | | | | |
|----------|-------------|------------|-----------|---|
| Gmeb2 | 305.684006 | -0.0606980 | 0.9507849 | glucocorticoid modulatory element binding protein 2 |
| Mterf1a | 26.685377 | -0.0676236 | 0.9878493 | mitochondrial transcription termination factor 1a |
| Zeb2 | 3190.608664 | -0.0873159 | 0.9655572 | zinc finger E-box binding homeobox 2 |
| Trim24 | 139.798010 | -0.0961269 | 0.9482148 | tripartite motif-containing 24 |
| Dleu2 | 56.663672 | -0.1078983 | 0.9475373 | deleted in lymphocytic leukemia, 2 |
| Sipall1 | 286.498204 | -0.1113947 | 0.9280502 | signal-induced proliferation-associated 1 like 1 |
| Smg6 | 432.390577 | -0.1265593 | 0.7596003 | SMG6 nonsense mediated mRNA decay factor |
| Pde6a | 1.810285 | -0.1353319 | 0.9901593 | phosphodiesterase 6A, cGMP-specific, rod, alpha |
| Nedd4l | 596.595846 | -0.1483479 | 0.6396379 | neural precursor cell expressed, developmentally down-regulated gene 4-like |
| Pnrc1 | 953.493893 | -0.1600188 | 0.7140020 | proline-rich nuclear receptor coactivator 1 |
| Syne1 | 736.557323 | -0.1714561 | 0.8415333 | spectrin repeat containing, nuclear envelope 1 |
| Uaca | 119.168326 | -0.1759312 | 0.7970216 | uveal autoantigen with coiled-coil domains and ankyrin repeats |
| Arl4a | 121.316126 | -0.1765097 | 0.7844028 | ADP-ribosylation factor-like 4A |
| Rbpms | 76.564626 | -0.1790952 | 0.9379207 | RNA binding protein gene with multiple splicing |
| Nt5c2 | 686.957608 | -0.1838700 | 0.6600855 | 5'-nucleotidase, cytosolic II |
| Klf3 | 340.270347 | -0.1899967 | 0.8346818 | Kruppel-like factor 3 (basic) |
| Cdy12 | 186.132509 | -0.2015496 | 0.7402845 | chromodomain protein, Y chromosome-like 2 |
| Pik3cg | 799.707493 | -0.2096393 | 0.6820010 | phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma |
| Akap1 | 286.575823 | -0.2306454 | 0.5398729 | A kinase (PRKA) anchor protein 1 |
| Rest | 256.209330 | -0.2415618 | 0.7090088 | RE1-silencing transcription factor |
| Slx4ip | 38.208116 | -0.2421583 | 0.9347991 | SLX4 interacting protein |
| Med15 | 2126.030128 | -0.2543220 | 0.2463310 | mediator complex subunit 15 |
| Dapk1 | 2805.463586 | -0.2704344 | 0.2981619 | death associated protein kinase 1 |
| Rreb1 | 1245.671180 | -0.2743428 | 0.1306962 | ras responsive element binding protein 1 |
| Slc23a2 | 3326.747719 | -0.2848185 | 0.1174387 | solute carrier family 23 (nucleobase transporters), member 2 |
| Tbc1d9 | 1385.896631 | -0.3029572 | 0.5894208 | TBC1 domain family, member 9 |
| Mtus1 | 347.910229 | -0.3083919 | 0.6912394 | mitochondrial tumor suppressor 1 |
| Atad2b | 248.543560 | -0.3155036 | 0.8536423 | ATPase family, AAA domain containing 2B |
| Flrt3 | 10.011426 | -0.3195243 | 0.9457157 | fibronectin leucine rich transmembrane protein 3 |
| Sntb1 | 5.058952 | -0.3301067 | 0.9475373 | syntrophin, basic 1 |
| Pde7b | 107.180775 | -0.3696654 | 0.6473680 | phosphodiesterase 7B |
| Slc7a11 | 152.305563 | -0.3879933 | 0.7982656 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 11 |
| Mef2c | 504.986469 | -0.3946155 | 0.6706536 | myocyte enhancer factor 2C |
| Rgs1 | 166.602140 | -0.4302539 | 0.8015765 | regulator of G-protein signaling 1 |
| Pced1b | 42.970399 | -0.4447384 | 0.4590481 | PC-esterase domain containing 1B |
| Ldhal6b | 1.614842 | -0.4513752 | 0.9643660 | lactate dehydrogenase A-like 6B |
| Cped1 | 10.331720 | -0.4537691 | 0.8671383 | cadherin-like and PC-esterase domain containing 1 |
| Mir99ahg | 12.708712 | -0.4586051 | 0.8530261 | Mir99a and Mirlet7c-1 host gene (non-protein coding) |
| Arid1b | 1187.901822 | -0.4782144 | 0.0006051 | AT rich interactive domain 1B (SWI-like) |
| Hdac9 | 64.182024 | -0.5009593 | 0.6987333 | histone deacetylase 9 |
| Tusc1 | 196.497961 | -0.5247869 | 0.2820355 | tumor suppressor candidate 1 |
| Osbpl8 | 3901.686873 | -0.5407908 | 0.4231065 | oxysterol binding protein-like 8 |
| Cblb | 976.113631 | -0.5475697 | 0.1360422 | Casitas B-lineage lymphoma b |
| Tle1 | 645.174772 | -0.6151373 | 0.0081473 | transducin-like enhancer of split 1 |
| Mef2a | 3197.733608 | -0.6690459 | 0.1483341 | myocyte enhancer factor 2A |
| Tcf12 | 692.593772 | -0.6936269 | 0.0516439 | transcription factor 12 |
| Bcl6 | 1420.679905 | -0.6950283 | 0.0193094 | B cell leukemia/lymphoma 6 |
| Smad6 | 253.988009 | -0.7492200 | 0.0588300 | SMAD family member 6 |
| Nck2 | 241.731416 | -0.7630623 | 0.0000587 | non-catalytic region of tyrosine kinase adaptor protein 2 |
| Map3k9 | 478.433206 | -0.8926473 | 0.0013119 | mitogen-activated protein kinase kinase kinase 9 |
| Amer2 | 2.752414 | -1.1198616 | 0.7408885 | APC membrane recruitment 2 |
| Dusp6 | 161.448062 | -1.4533019 | 0.0000000 | dual specificity phosphatase 6 |

6.2 Top 10 Overlapping genes in IGV



6.3 KEGG Enrichment Analysis for Overlapping genes (342 genes)

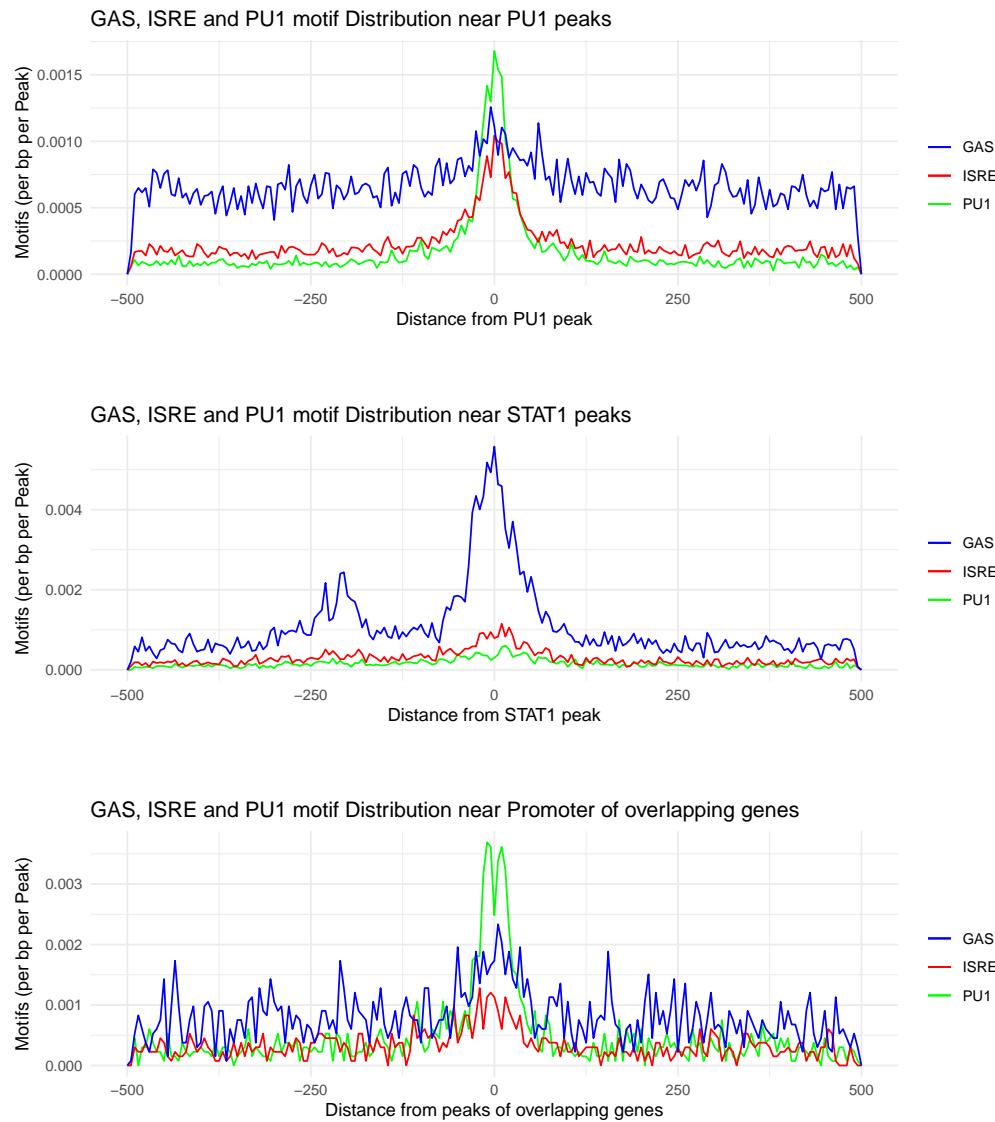


7 Finding Instances of Motifs near the binding Sites at Promoter

7.1 Intro

- Steps taken to quantify motif instances
 - The raw sequencing data for each dataset were analysed using relevant pipelines(Encode/NF-core)
 - The STAT1 and PU1 peaks, generated by a peak caller, were used to select those peaks that were in the immediate vicinity of *Promoter* region(-3000,3000).
 - The instances of GAS, ISRE & PU1 motifs in the promoter regions of STAT1 and PU1 binding sites were scanned and quantified using [annotatePeaks.pl](#).
 - The PU1 motifs were selected from [Homer Motif library](#).
 - The GAS & ISRE motifs were taken from this [paper](#).
 - For the overlapping gene list, only peaks located in the promoter region were selected.
 - For PU1 and STAT1, peaks in the IFNg-treated group were shown.

7.2 Instances of GAS, ISRE and PU1 motifs near the binding sites at promoter

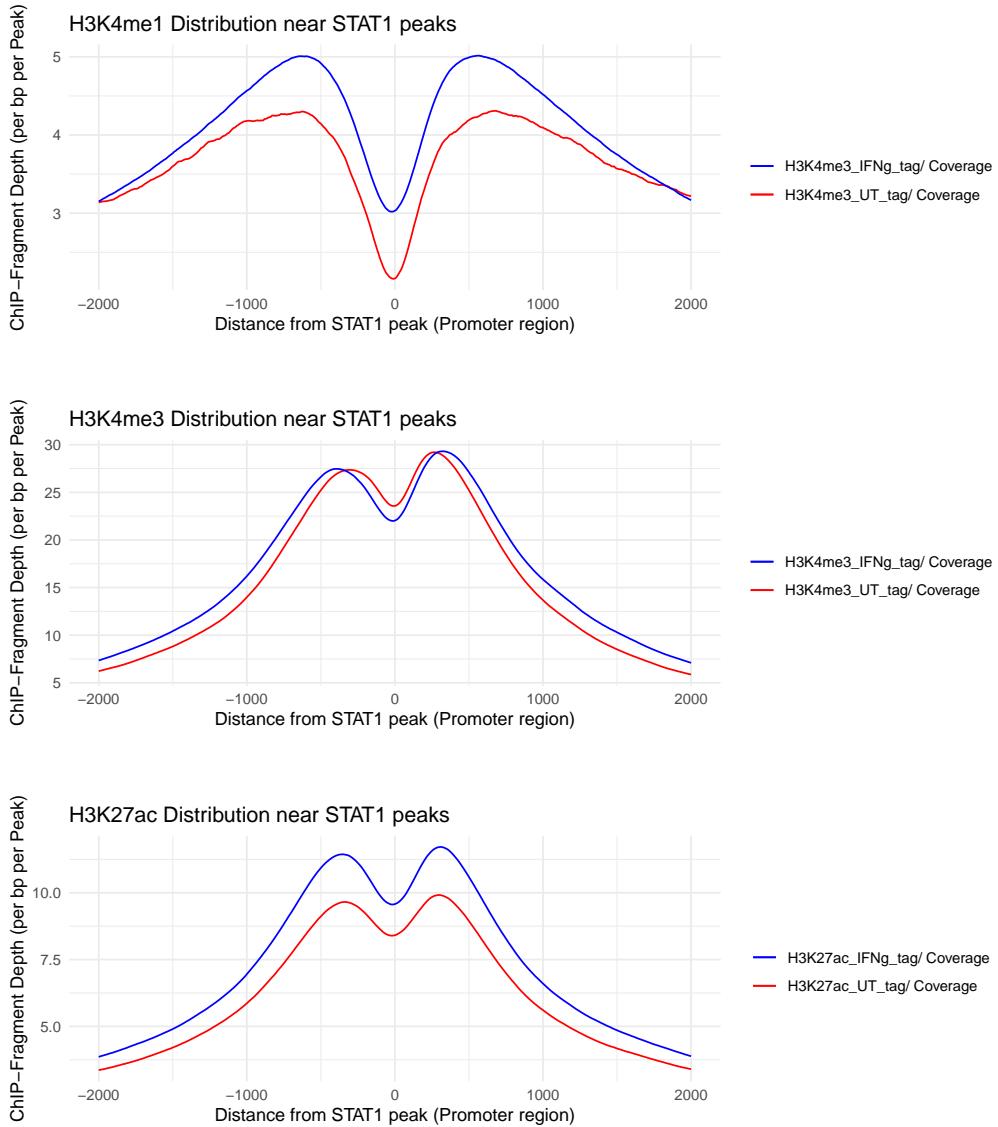


8 Distribution of Epigenetic markers near the binding sites at the Promoter

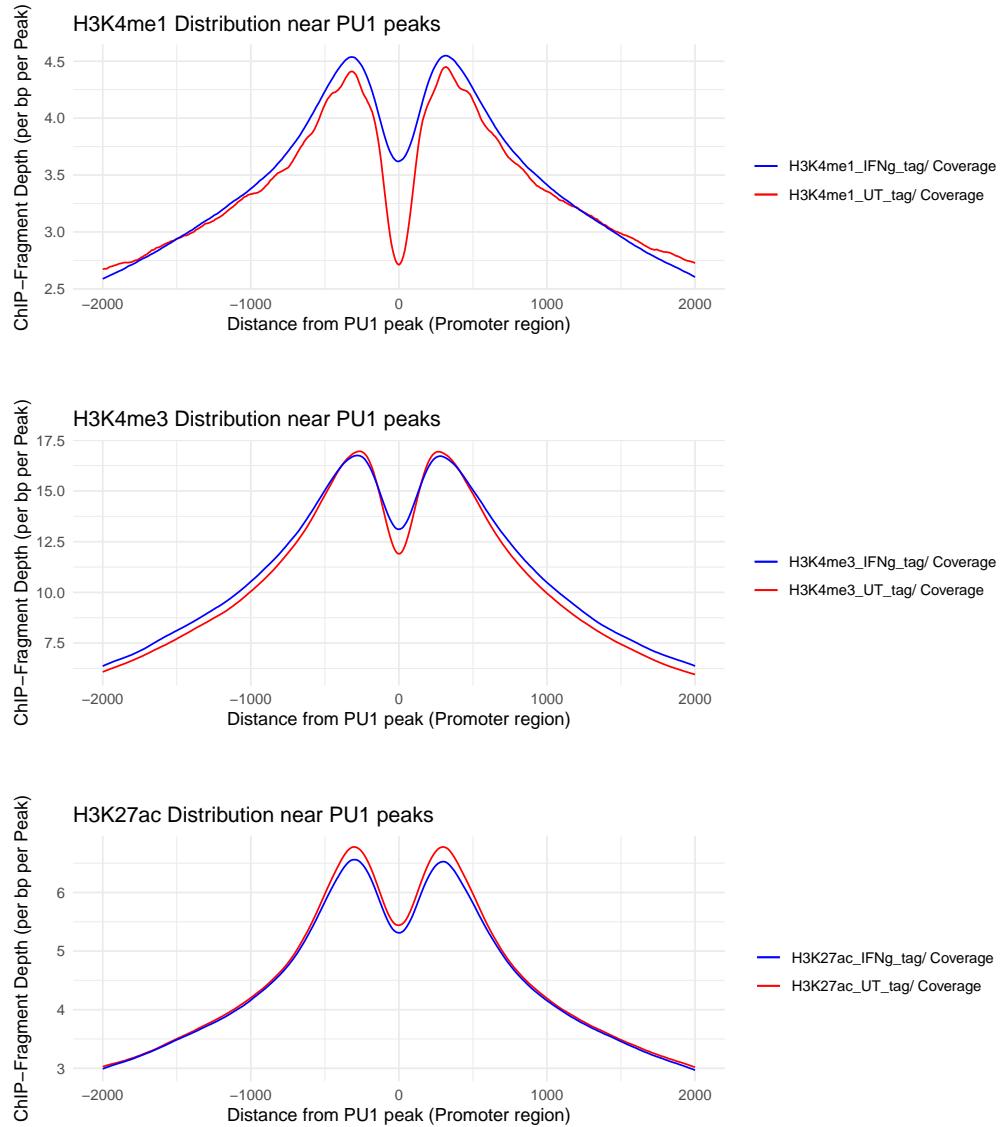
8.1 Intro

- Steps taken to quantify the distribution of epigenetic markers
 - The raw sequencing data for each dataset were analysed using relevant pipelines(Encode/NF-core)
 - The STAT1 and PU1 peaks, generated by a peak caller, were used to select those peaks that were in the immediate vicinity of *Promoter* region(-3000,3000).
 - The distribution of H3K4me1, H3K4me3 and H3K27ac in the promoter region were quantified using [annotatePeaks.pl](#).
 - For the overlapping gene list, only peaks located in the promoter region were selected.
 - For PU1 and STAT1, peaks in the IFNg-treated group were shown.

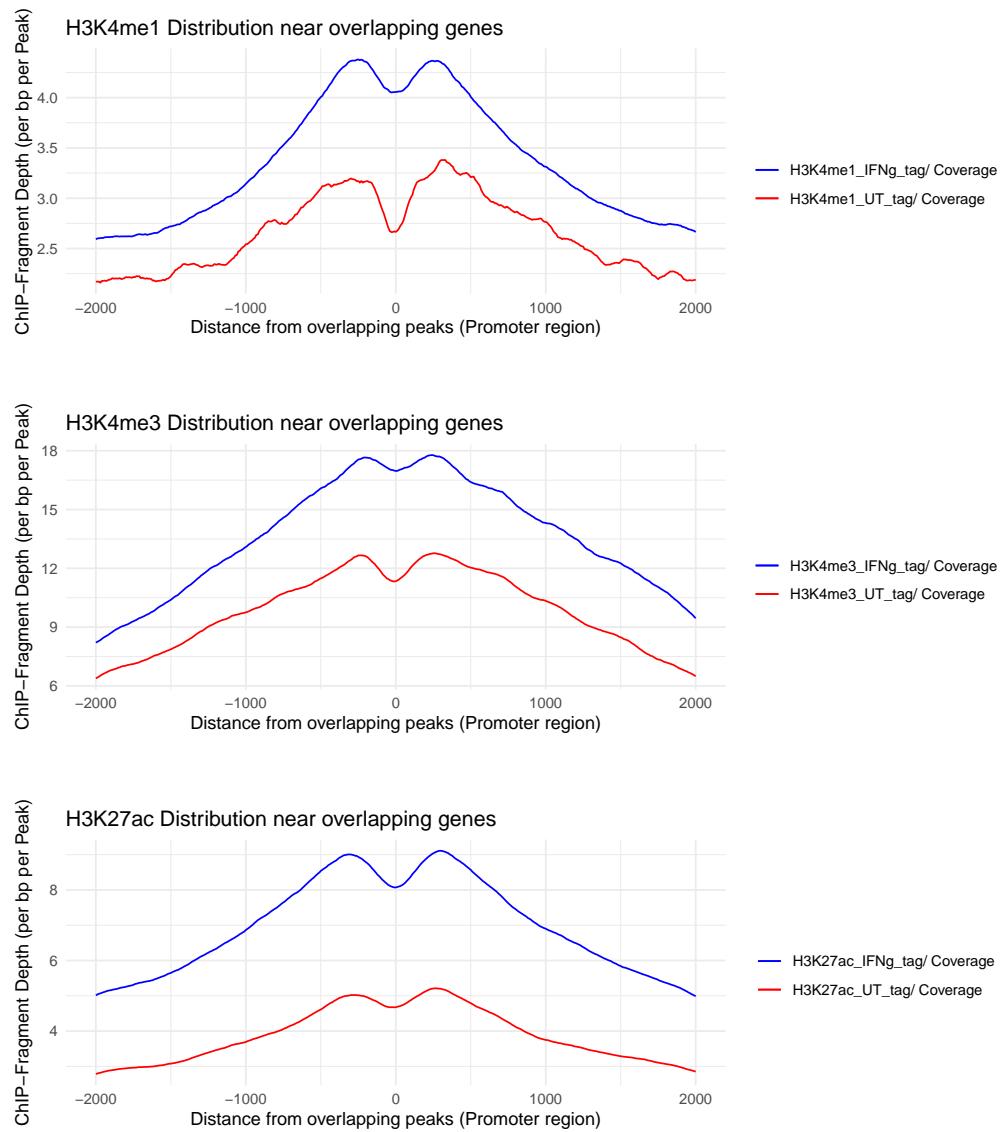
8.2 Epigenetic Markers Distribution near STAT1 binding sites



8.3 Epigenetic Markers Distribution near PU1 binding sites



8.4 Epigenetic Markers Distribution near the promoter regions of overlapping genes

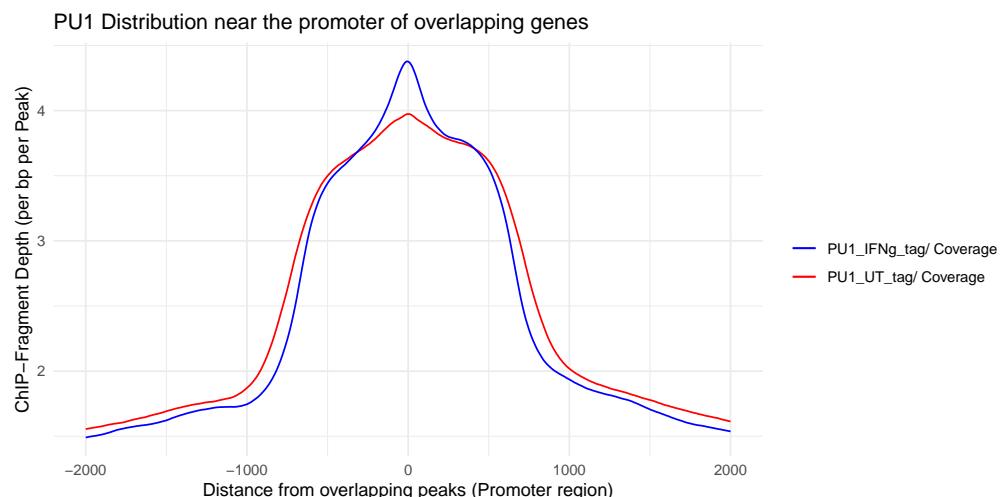
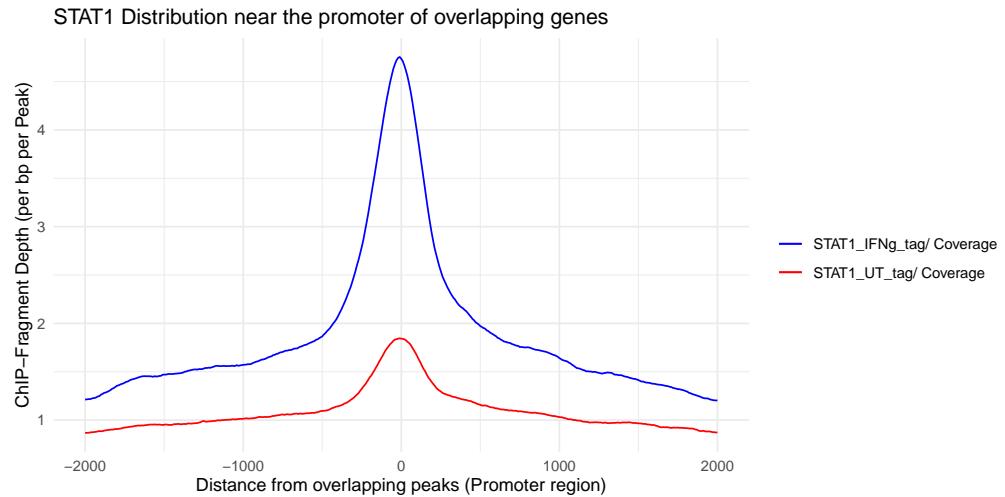


9 The Binding Site Profile of STAT1 and PU1 near the Promoter of overlapping genes

9.1 Intro

- Steps taken to quantify the binding site profile of STAT1 and PU1
 - The raw sequencing data for each dataset were analysed using relevant pipelines(Encode/NF-core)
 - The binding profile of STAT1 and PU1 in the promoter region were quantified using [annotatePeaks.pl](#).
 - For the overlapping gene list, only peaks located in the promoter region were selected.

9.2 The Binding Site Profile near the Promoter of overlapping genes



10 Distribution of Epigenetic markers near the Co-Bound Peaks (STAT1-PU1) at the Promoter

10.1 Intro

- Steps taken to quantify the distribution of epigenetic markers
 - The raw sequencing data for each dataset were analysed using relevant pipelines(Encode/NF-core)
 - The STAT1 and PU1 peaks, generated by a peak caller, were used to select those peaks that were in the immediate vicinity of *Promoter* region(-3000,3000).
 - To find the co-bound peaks between STAT1 and PU1 (overlapping bound peaks), `mergePeaks` was implemented.
 - The distribution of H3K4me1, H3K4me3 and H3K27ac in the co-bound peaks were quantified using `annotatePeaks.pl`.
 - For PU1 and STAT1, peaks in the IFNg-treated group were selected.

10.2 Epigenetic Markers near the promoter regions of Co-Bound Peaks (STAT1-PU1)

