

ChIPPeakAnno analysis

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Libraries

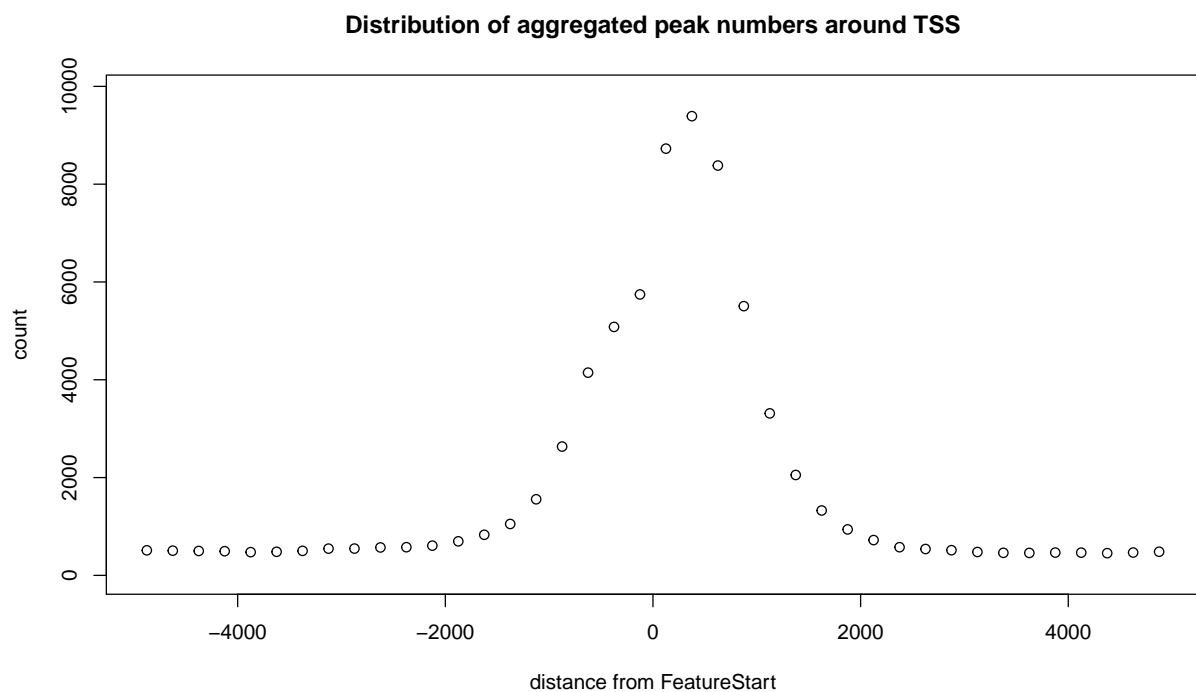
Settings

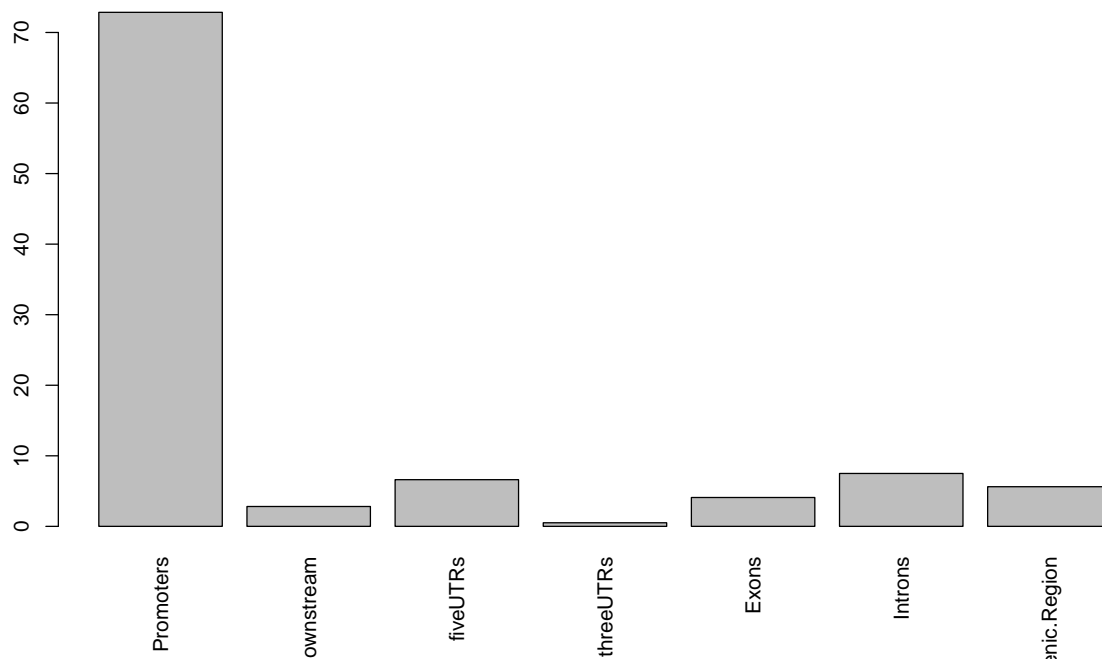
Prepare annotation data

Import data

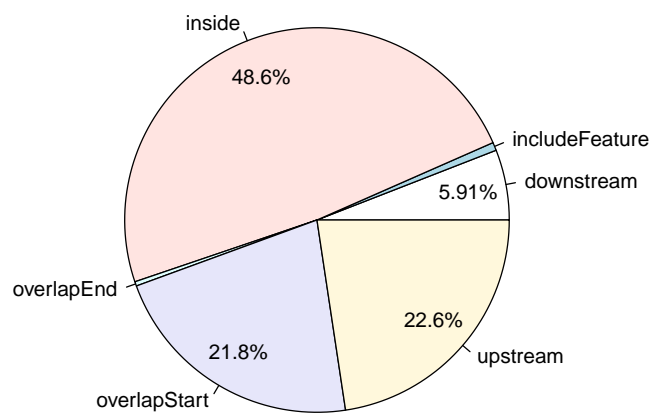
```
[1] "Total number of peaks: 14525"
```

Visualize binding site distribution relative to Transcription Start Sites





Annotate peaks by the nearest gene



Top 15 most frequent genes

.	Freq
RNA5-8SN3	10
RNA5-8SN1	10
EMB	10
RNA5-8SN2	8
MIR6724-4	7
SAMD11	5
NEMP1	5
LINC00682	5
KDM6B	5
HAND2-AS1	5
CLPTM1L	5
WDR60	4
TMEM161B-AS1	4
SMAD7	4
SLC25A4	4

KEGG pathway enrichment analysis

Uploading data to Enrichr... Done.

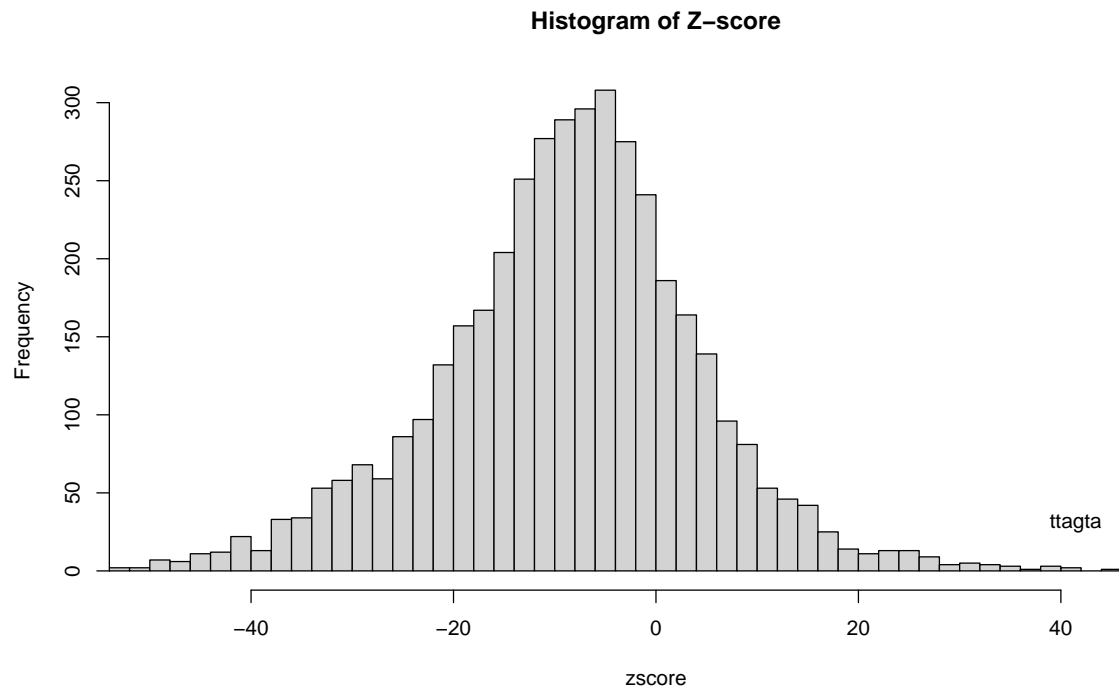
Querying KEGG_2019_Human... Done.

Parsing results... Done.

A total of 30 KEGG pathways were detected as significantly affected at FDR 0.3. Top 15 shown. If nothing is shown, nothing is significant.

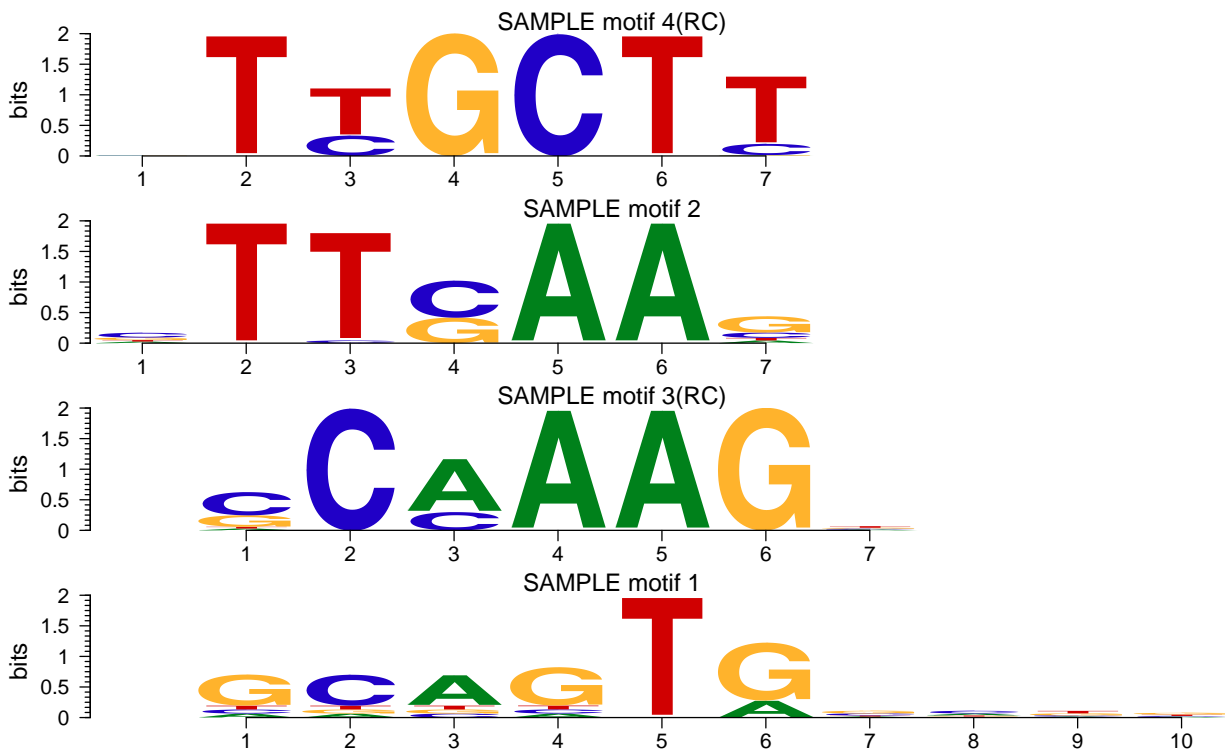
Term	Overlap	P.value	Adjusted.P.value	Old.P.value	Old.Adjusted.P.value
Spliceosome	99/134	0.0000000	0.0000006	0	
Autophagy	88/128	0.0000030	0.0004690	0	
Proteasome	36/45	0.0000148	0.0015242	0	
RNA degradation	57/79	0.0000178	0.0013732	0	
Protein processing in endoplasmic reticulum	107/165	0.0000181	0.0011149	0	
Endocytosis	151/244	0.0000191	0.0009804	0	
RNA transport	106/165	0.0000358	0.0015737	0	
SNARE interactions in vesicular transport	28/34	0.0000513	0.0019740	0	
Ribosome	95/153	0.0005295	0.0181203	0	
mRNA surveillance pathway	60/91	0.0006302	0.0194108	0	
Thermogenesis	137/231	0.0006727	0.0188347	0	
Phosphatidylinositol signaling system	64/99	0.0009313	0.0239029	0	
Longevity regulating pathway	65/102	0.0014808	0.0350834	0	
Neurotrophin signaling pathway	74/119	0.0019571	0.0430562	0	
Hedgehog signaling pathway	33/47	0.0022195	0.0455744	0	

Output a summary of consensus sequences in the peaks



Visualizing up to top 5 motifs, if any

```
[1] "Total number of motifs: 4"
```



Save the results