

Motif Discovery (Homer)

[Homer](#) is a software for motif discovery and next-gen sequencing analysis [11]. We are going to use this tool to find enriched m6A motifs within peaks that has been found.

Install Homer

```
# Download and install following the instruction:
http://homer.ucsd.edu/homer/introduction/install.html
$ mkdir homer
$ cd homer
$ wget http://homer.ucsd.edu/homer/configureHomer.pl
$ perl configureHomer.pl -install

# Append to PATH environment variable
$ export PATH=$PATH:/path/to/homer/./bin/




# Verify installation
$ findMotifs.pl
```

Find Motifs




```
$ findMotifsGenome.pl Mod.bed /path/to/hg19_genome.fa /path/to/MotifOutput -rna
-p 10 -len 5,6
```

Note that Homer can analyze strand-specific genomic regions for motifs by running `findMotifsGenome.pl` with an `rna` option. Also note that filtering out the peaks longer than 1000bp can improve the reliability of motifs found by Homer.

The figure below shows the enriched motifs in peaks on hg19 transcripts.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background
1		1e-314	-7.239e+02	66.02%	44.91%
2		1e-89	-2.069e+02	51.22%	40.05%
3		1e-88	-2.030e+02	60.04%	48.90%

The figure below shows the enriched motifs in peaks on mm10 transcripts.

Rank	Motif	P-value	log P-pvalue	% of Targets	% of Background
1		1e-268	-6.186e+02	63.42%	45.31%
2		1e-72	-1.674e+02	28.97%	21.01%
3		1e-70	-1.620e+02	44.26%	35.29%