CentriMo
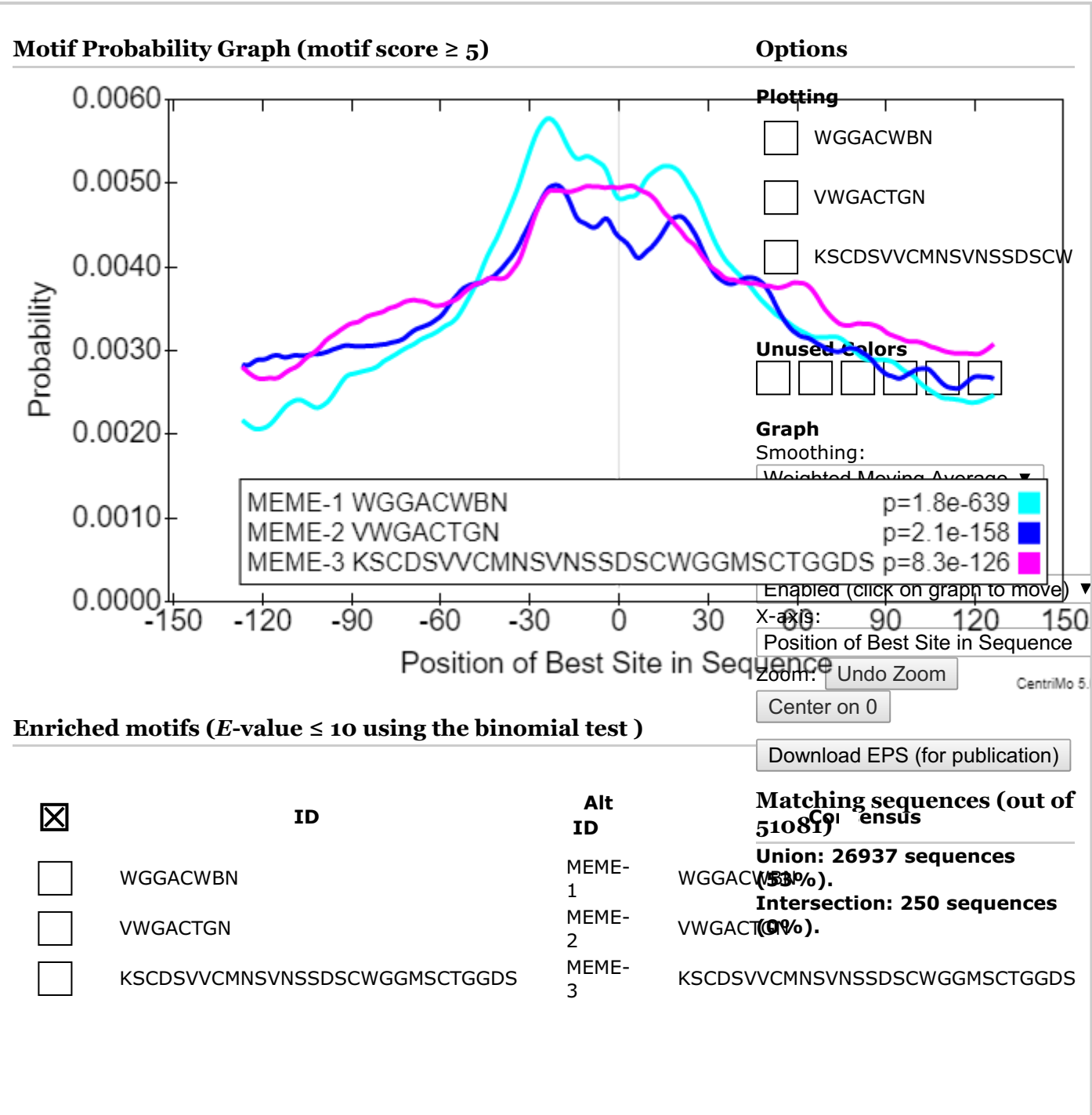## Local Motif Enrichment Analysis

For further information on how to interpret these results please access http://meme-suite.org/doc/centrimo-output-format.html.

To get a copy of the MEME software please access http://meme-suite.org.

If you use CentriMo in your research, please cite the following paper:

Timothy L. Bailey and Philip Machanick, "Inferring direct DNA binding from ChIP-seq", *Nucleic Acids Research*, **40**:e128, 2012. [full text]

MOTIF PROBABILITY GRAPH | **ENRICHED MOTIFS** | **INPUT FILES** | **PROGRAM INFORMATION** | **RESULTS IN TSV FORMAT**   🆕 | **SEQUENCE POSITION VS. NUMBER OF MATCHES FOR EACH MOTIF**   🆕

RESULTS

Motif Probability Graph (motif score ≥ 5)   Options

Plotting
- ☐ WGGACWBN
- ☐ VWGACTGN
- ☐ KSCDSVVCMNSVNSSDSCW

Unused Colors
☐ ☐ ☐ ☐ ☐ ☐

Graph
Smoothing:
Weighted Moving Average ▼

MEME-1 WGGACWBN	p=1.8e-639
MEME-2 VWGACTGN	p=2.1e-158
MEME-3 KSCDSVVCMNSVNSSDSCWGGMSCTGGDS	p=8.3e-126

Enabled (click on graph to move) ▼

X-axis:
Position of Best Site in Sequence

Zoom: Undo Zoom

Center on 0

Download EPS (for publication)

Enriched motifs (*E*-value ≤ 10 using the binomial test)

Matching sequences (out of 51081)

Union: 26937 sequences (53%).

Intersection: 250 sequences (0%).

☒	ID	Alt ID	Consensus
☐	WGGACWBN	MEME-1	WGGACWBN
☐	VWGACTGN	MEME-2	VWGACTGN
☐	KSCDSVVCMNSVNSSDSCWGGMSCTGGDS	MEME-3	KSCDSVVCMNSVNSSDSCWGGMSCTGGDS

```
chr1:3712371-3712672(-)
chr1:8415395-8415696(-)
chr1:8421244-8421545(-)
chr1:10713800-10714101(-)
chr1:10713800-10714101(-)
chr1:12568916-12569217(+)
chr1:16261866-16262167(+)
chr1:16551668-16551969(-)
chr1:16719688-16719989(-)
chr1:26758773-26759074(+)
```

Filter & Sort

Filters

☐ Top

10

☐ Database is [meme ▾]

☐ ID matches

.*

☐ Alt ID matches

.*

☐ *E*-value ≤ 1

☐ Region Width ≤

200

Sort

Motifs: [E-value   ▾]

[Update]

Columns to display

☐ Show Database

☑ Show ID

☑ Show Alt ID

☑ Show Consensus

☑ Show Concentration

☑ Show *E*-value

☐ Show *p*-value

☑ Show Region Width

☑ Show Region Matches

☐ Show Sequence Matches

☐ Show Max Probability

☐ Show Max Probability Location

☐ Show Multiple Tests

☐ Show Score Threshold

Input Files

Alphabet

Background source: built from the (primary) sequences

Name	Bg.			Bg.	Name
Adenine	0.22382	A	~	T	0.218976	Thymine
Cytosine	0.274676	C	~	G	0.282529	Guanine

Sequences

Database	Source	Se
m6A sig peaks summit	/public/home/xijf/project/MeRIP_seq/summitToMotif/results/m6A_sig_peaks_summit.fa	51

Motifs

Database	Source	Mo Cou
meme	/public/home/xijf/project/MeRIP_seq/motif_search/results/bestpeaks_meme/meme.txt	3

Other Settings

Objective Function	central region enrichment (CE)
Convert Motifs to Different Alphabet?	No
Motif Pseudo-Counts	0.1
Required sequence length	None
Site Scoring Method	log-odds scores
Score Threshold	5 (bits)
Optimize Score Threshold?	No
Minimum Region Size	0
Maximum Region Size	0
Strand Handling	scan given strands only
Plotting of Matches on Negative Strand	same as for positive strand
Sequence IDs Included in Output?	Yes

CentriMo version
5.0.5 (Release date: Mon Mar 18 20:12:19 2019 -0700)

Command line summary

```
centrimo --o /public/home/xijf/project/MeRIP_seq/summitToMotif/results/sig_peaks_motif_centrimo -
-norc /public/home/xijf/project/MeRIP_seq/summitToMotif/results/m6A_sig_peaks_summit.fa
/public/home/xijf/project/MeRIP_seq/motif_search/results/bestpeaks_meme/meme.txt
```