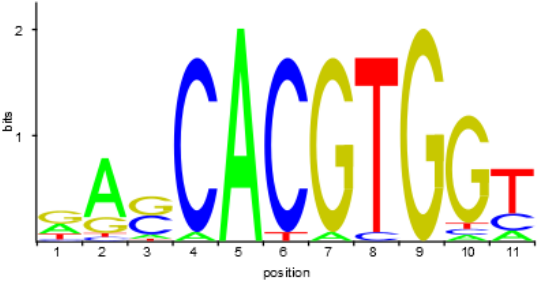
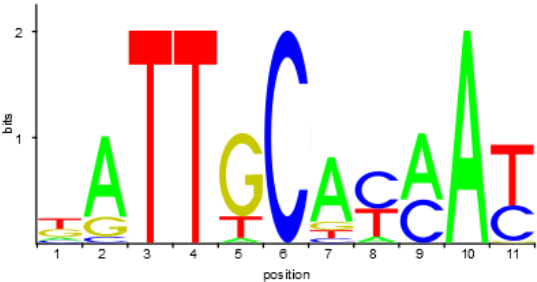
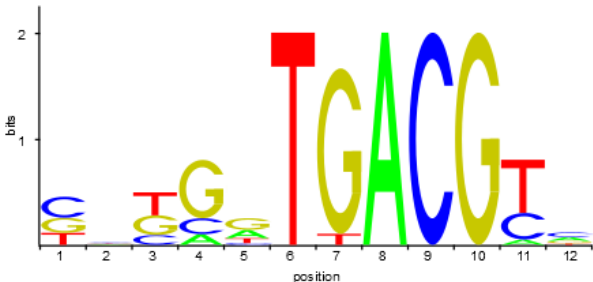
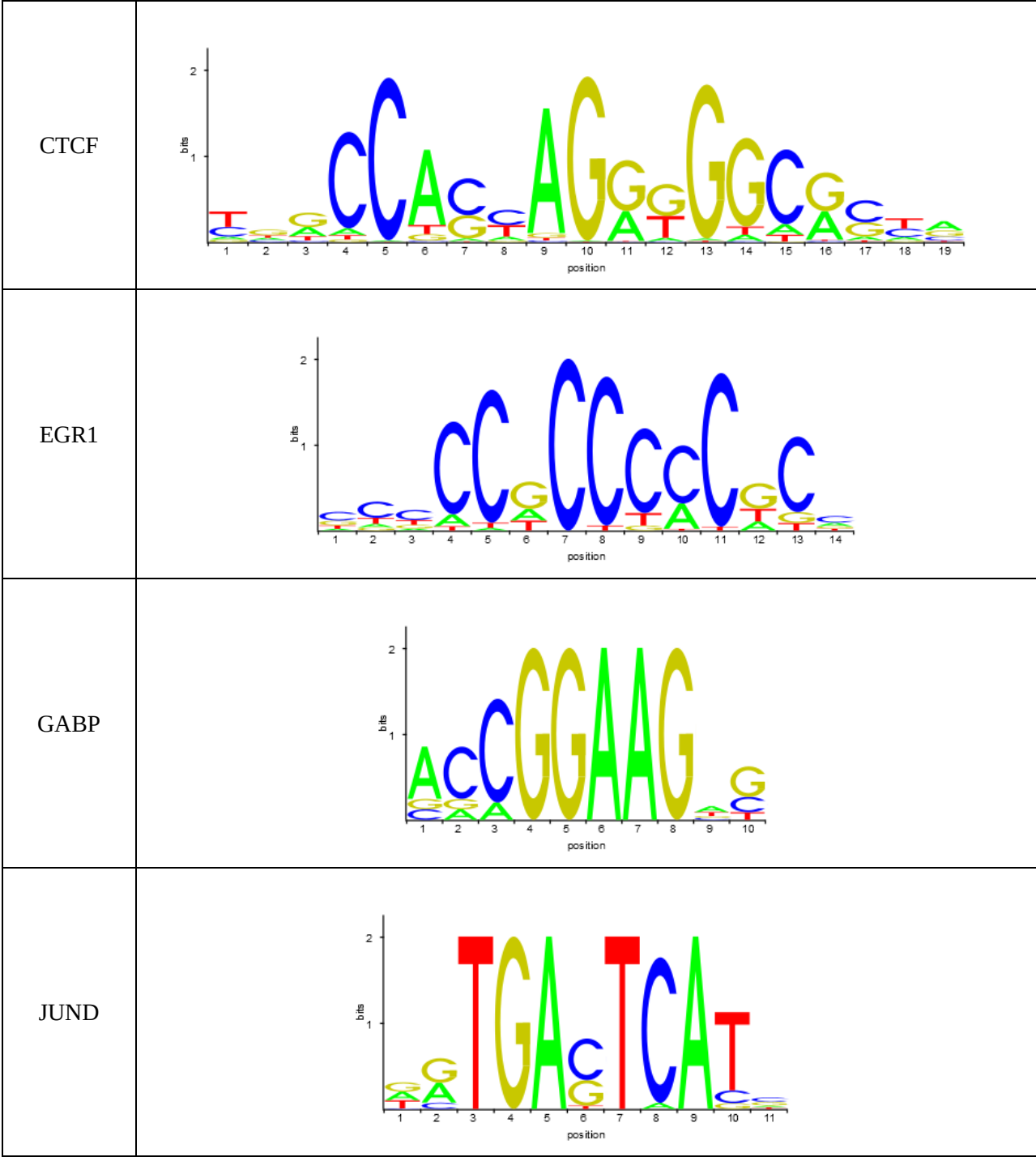


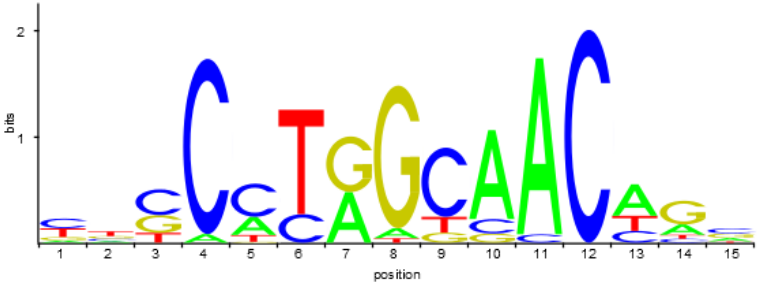
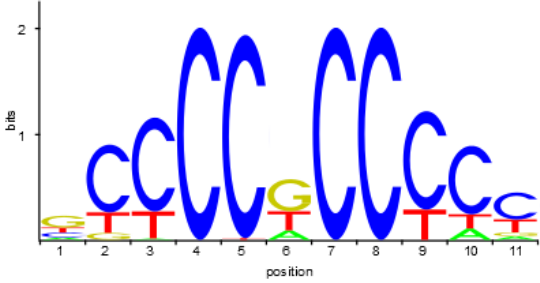
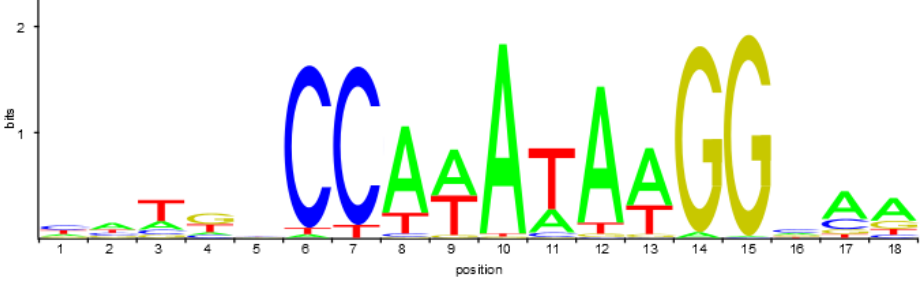
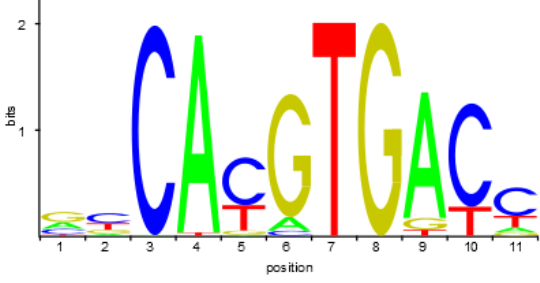
TFs and MOTIFS

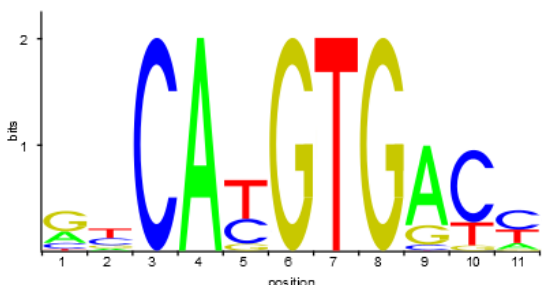
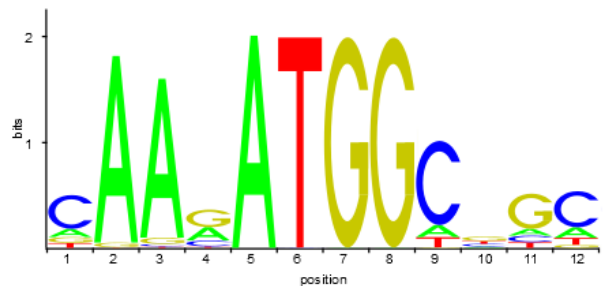
Below is the list of TFs for which a clear DNA-binding motif was available in the JASPAR database, along with the motif logos.

TF Name	Sequence Motif Logo
CMYC	 A sequence motif logo for CMYC showing 11 positions. The y-axis is labeled 'bits' with a scale from 0 to 2. The x-axis is labeled 'position' from 1 to 11. The logo shows a conserved sequence: approximately GAGG CACG TGG. The 'C' at position 4 and 'G' at position 9 are the most conserved, with heights exceeding 2 bits.
CEBPB	 A sequence motif logo for CEBPB showing 11 positions. The y-axis is labeled 'bits' with a scale from 0 to 2. The x-axis is labeled 'position' from 1 to 11. The logo shows a conserved sequence: approximately TGG A T T G C A A T. The 'T' at positions 3 and 4 are the most conserved, with heights exceeding 2 bits.
CREB1	 A sequence motif logo for CREB1 showing 12 positions. The y-axis is labeled 'bits' with a scale from 0 to 2. The x-axis is labeled 'position' from 1 to 12. The logo shows a conserved sequence: approximately G G T G T G A C C G T. The 'T' at position 6 and 'G' at position 8 are the most conserved, with heights exceeding 2 bits.



MAFK	
MAX	
NRF1	
NRSF	

RFX5	 Sequence logo for RFX5. The binding site is 15 positions long. The sequence is approximately CCGCTGGCAACAG. The y-axis is labeled 'bits' from 0 to 2, and the x-axis is labeled 'position' from 1 to 15.
SP1	 Sequence logo for SP1. The binding site is 11 positions long. The sequence is approximately CCCCGCC. The y-axis is labeled 'bits' from 0 to 2, and the x-axis is labeled 'position' from 1 to 11.
SRF	 Sequence logo for SRF. The binding site is 18 positions long. The sequence is approximately CCAGAAAGGG. The y-axis is labeled 'bits' from 0 to 2, and the x-axis is labeled 'position' from 1 to 18.
USF1	 Sequence logo for USF1. The binding site is 11 positions long. The sequence is approximately CAGGTGAC. The y-axis is labeled 'bits' from 0 to 2, and the x-axis is labeled 'position' from 1 to 11.

USF2	 Sequence logo for USF2 binding site. The y-axis represents information content in bits (0 to 2), and the x-axis represents position (1 to 11). The sequence is approximately CAGTGGAC. <table><tr><th>Position</th><th>1</th><th>2</th><th>3</th><th>4</th><th>5</th><th>6</th><th>7</th><th>8</th><th>9</th><th>10</th><th>11</th></tr><tr><td>Consensus</td><td>G</td><td>T</td><td>C</td><td>A</td><td>C</td><td>G</td><td>T</td><td>G</td><td>A</td><td>C</td><td>C</td></tr><tr><td>Approx. Bits</td><td>0.2</td><td>0.2</td><td>1.8</td><td>1.9</td><td>0.5</td><td>1.9</td><td>1.9</td><td>1.8</td><td>0.8</td><td>0.8</td><td>0.2</td></tr></table>	Position	1	2	3	4	5	6	7	8	9	10	11	Consensus	G	T	C	A	C	G	T	G	A	C	C	Approx. Bits	0.2	0.2	1.8	1.9	0.5	1.9	1.9	1.8	0.8	0.8	0.2			
Position	1	2	3	4	5	6	7	8	9	10	11																													
Consensus	G	T	C	A	C	G	T	G	A	C	C																													
Approx. Bits	0.2	0.2	1.8	1.9	0.5	1.9	1.9	1.8	0.8	0.8	0.2																													
YY1	 Sequence logo for YY1 binding site. The y-axis represents information content in bits (0 to 2), and the x-axis represents position (1 to 12). The sequence is approximately CAAATGGGC. <table><tr><th>Position</th><th>1</th><th>2</th><th>3</th><th>4</th><th>5</th><th>6</th><th>7</th><th>8</th><th>9</th><th>10</th><th>11</th><th>12</th></tr><tr><td>Consensus</td><td>C</td><td>A</td><td>A</td><td>A</td><td>A</td><td>T</td><td>G</td><td>G</td><td>G</td><td>C</td><td>G</td><td>C</td></tr><tr><td>Approx. Bits</td><td>0.5</td><td>1.8</td><td>1.6</td><td>0.3</td><td>1.9</td><td>1.9</td><td>1.9</td><td>1.8</td><td>0.3</td><td>0.1</td><td>0.5</td><td>0.3</td></tr></table>	Position	1	2	3	4	5	6	7	8	9	10	11	12	Consensus	C	A	A	A	A	T	G	G	G	C	G	C	Approx. Bits	0.5	1.8	1.6	0.3	1.9	1.9	1.9	1.8	0.3	0.1	0.5	0.3
Position	1	2	3	4	5	6	7	8	9	10	11	12																												
Consensus	C	A	A	A	A	T	G	G	G	C	G	C																												
Approx. Bits	0.5	1.8	1.6	0.3	1.9	1.9	1.9	1.8	0.3	0.1	0.5	0.3																												