

Jump to: [Multiple Alignment](#) [Motif Tree](#) [Motif Matching](#)

Input file: 153 motifs loaded

Settings: Metric=PCC, Alignment=SWU, Gap-open=1000, Gap-extend=1000, -nooverlapalign

Multiple Alignment=IR, Tree=UPGMA, Matching against: ALL

Note: All results files are removed nightly at midnight EST. Please save your results by saving "Webpage, complete".

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Multiple Alignment

(Consensus sequence representations shown, but multiple alignment was carried out on the matrices)

```

6_bp_motif_1:  -----AGGTTCG-----
6_bp_motif_2:  -----GGGTCA-----
6_bp_motif_3:  -----GTTCGC-----
6_bp_motif_4:  -----CAGGGC-----
6_bp_motif_5:  -----CCAGGC-----
6_bp_motif_6:  -----TCGGGA-----
6_bp_motif_7:  -----GMGNCA-----
6_bp_motif_8:  -----CGGGTG-----
6_bp_motif_9:  -----GGAACG-----
6_bp_motif_10: -----CNGTGC-----
6_bp_motif_11: -----CCAGCT-----
6_bp_motif_12: -----TCGTGC-----
6_bp_motif_13: -----GTTTAC-----
6_bp_motif_14: -----CGGACA-----
6_bp_motif_15: -----CGTCTT-----
6_bp_motif_16: -----GTTCGT-----
6_bp_motif_17: -----GCAAGT-----
6_bp_motif_18: -----GGACTS-----
6_bp_motif_19: -----GGYATG-----
6_bp_motif_20: -----TCKTGG-----
6_bp_motif_pair_1: -----CAGGGCNNCGGG-----
6_bp_motif_pair_2: -----CCAGGCNNCGGG-----
6_bp_motif_pair_3: -----GCGNNSNNCGGG-----

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Stamp Results

09/05/08

6_bp_motif_pair_4: -----CAGGGCNCAGGC-----
6_bp_motif_pair_5: -----GCGNNSNCCAGGC-----
6_bp_motif_pair_6: -----CAGGGCNCACCCG-----
6_bp_motif_pair_7: -----GCGNNSNCAGGGC-----
6_bp_motif_pair_8: -----CGTCTTNSNCCG-----
6_bp_motif_pair_9: -----NCGGGNNCACCCG-----
6_bp_motif_pair_10: -----CGGGTGNGCCTGG-----
6_bp_motif_pair_11: -----NCGGGNNAGCTGG-----
6_bp_motif_pair_12: -----CCAGGCNAGCTGG-----
6_bp_motif_pair_13: -----CAGGGCNGCACGA-----
6_bp_motif_pair_14: -----CCAGGCNAAGACG-----
6_bp_motif_pair_15: -----CAGGGCNAAGACG-----
6_bp_motif_pair_16: -----CCAGGCNGCACGA-----
6_bp_motif_pair_17: -----TCGGGANGCACGA-----
6_bp_motif_pair_18: -----GCACNGNGCCTGG-----
6_bp_motif_pair_19: -----TCGGGANCTGTC-----
6_bp_motif_pair_20: -----TCGGGRNAAGACG-----
8_bp_motif_1: -----AGGTCA-----
8_bp_motif_2: -----CYGTTTGC-----
8_bp_motif_3: -----CCTGCGGS-----
8_bp_motif_4: -----CYKGGCWS-----
8_bp_motif_5: -----CAGAGCAA-----
8_bp_motif_6: -----CTGGAATG-----
8_bp_motif_7: -----ACAGCTGC-----
8_bp_motif_8: -----CTGGTTTG-----
8_bp_motif_9: -----CTTGGAGG-----
8_bp_motif_10: -----TCAGCAGA-----
8_bp_motif_11: -----ACAGTGAG-----
8_bp_motif_12: -----TGANTCAT-----
8_bp_motif_13: -----GGAAGAGG-----
8_bp_motif_pair_1: -----CCTGCGGSNCYKGGCWS-----
8_bp_motif_pair_2: -----CYKGGCWSNCCTCNCC-----
8_bp_motif_pair_3: -----CCTGCGGSNACAGCTGC-----
8_bp_motif_pair_4: -----AGGKCAGNCCTGCGGS-----
8_bp_motif_pair_5: -----CYKGGCWSNCAGRCAR-----
8_bp_motif_pair_6: -----CTTGGAGGNSCCGCAGG-----
8_bp_motif_pair_7: -----CCTGNNGSNCTCTTCC-----
8_bp_motif_pair_8: -----CCTGCGGSNCAGAGCAR-----
8_bp_motif_pair_9: -----AGGTCANNCYKGGCWS-----
8_bp_motif_pair_10: -----CYKGGCWSNACAGCTGC-----
8_bp_motif_pair_11: -----CYKGGCWSNCCTCCAAG-----
8_bp_motif_pair_12: -----NAGGKCAGNMCAGCTGC-----
8_bp_motif_pair_13: -----AGGTCASNCAGRCMR-----

Stamp Results

09/05/08

```

8_bp_motif_pair_14: -----CTKGGCWGNNCAGCARR-----
8_bp_motif_pair_15: -----CAGAGCNNNNCAGCARR-----
8_bp_motif_pair_16: -----CARRGCMRNCCTCCAAG-----
8_bp_motif_pair_17: -----CCTGCGGSNACAGTGAG-----
8_bp_motif_pair_18: -----TCTGCTGANGCAGCTGT-----
8_bp_motif_pair_19: -----GGAAGAGGNGCAGCTGT-----
8_bp_motif_pair_20: -----CYKGGCWSNCATTCCAG-----
10_bp_motif_1: -----GGTCANNSTG-----
10_bp_motif_2: -----TRAGYAAACA-----
10_bp_motif_3: -----CCYCAGGS-----
10_bp_motif_4: -----TGASTCAN-----
10_bp_motif_5: -----SCWGWGCTGN-----
10_bp_motif_6: -----CARRCWGGAR-----
10_bp_motif_7: -----CCTGGSANNG-----
10_bp_motif_8: -----CTGRCMTKTS-----
10_bp_motif_9: -----GGAGGGGCAG-----
10_bp_motif_10: -----TGACAKCAG-----
10_bp_motif_11: -----CMNTSYTGGS-----
10_bp_motif_12: -----RACTKGTTT-----
10_bp_motif_13: -----CCARGGAGCT-----
10_bp_motif_14: -----GATNNTNATC-----
10_bp_motif_15: -----GMNGCAGACA-----
10_bp_motif_16: -----TGGAATGTNA-----
10_bp_motif_17: -----CAGKYTNTNT-----
10_bp_motif_18: -----AGATAANATC-----
10_bp_motif_19: -----CTGGGAAAAC-----
10_bp_motif_20: -----AGAACAAGGT-----
10_bp_motif_pair_1: -----GGAGGGGNAGNSCTGGSANNS-----
10_bp_motif_pair_2: -----GGAGGGGNAGNNCCYCAGGS-----
10_bp_motif_pair_3: -----SCCTGRGGNNCNCNTSCCAGS-----
10_bp_motif_pair_4: -----GGAGGGGCAGNNCWGWSCTGN-----
10_bp_motif_pair_5: -----SCTGGSANNGNSCWGWSCTGN-----
10_bp_motif_pair_6: -----SCCTGRGGNNNCAGSWCWGN-----
10_bp_motif_pair_7: -----SCCTGNRGNNNCTSMNSYCA-----
10_bp_motif_pair_8: -----TGRNNKCAGNNSCWGWGCTGN-----
10_bp_motif_pair_9: -----TGRNNKSAGNNGGAGGGGCAG-----
10_bp_motif_pair_10: -----GGAGGGGNAGNYTCCWGCYTG-----
10_bp_motif_pair_11: -----SCCTGRGGNNCMNTSYKGRS-----
10_bp_motif_pair_12: -----CMARGRAGCTNSCTGGSANNG-----
10_bp_motif_pair_13: -----SCCAGSARKNGGTCANNNTG-----
10_bp_motif_pair_14: -----YTCCWGYTGNNCWWSCTGN-----
10_bp_motif_pair_15: -----SYCMRSANKNGGAGGGGMAG-----
10_bp_motif_pair_16: -----SCCTGRGGNNCARRCWGGAR-----

```

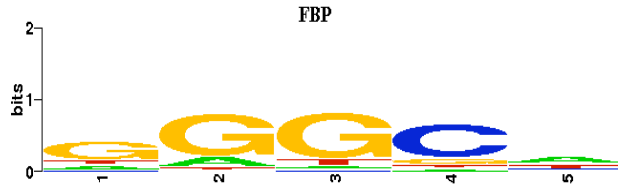
Stamp Results

09/05/08

10_bp_motif_pair_17: -----TKTCTGCNKCNSTGGSANNG-----
10_bp_motif_pair_18: -----SCTGGSANNNNYSCWGNKYG----
10_bp_motif_pair_19: ---CTGMNSTCANCCYTCTGGS-----
10_bp_motif_pair_20: -----SCTGGSARNNGGTCANNSTG-----
12_bp_motif_1: -----GGTCANNNTGAC-----
12_bp_motif_2: -----CWNWGYAAAYA-----
12_bp_motif_3: -----TGCCCCAGGGCA-----
12_bp_motif_4: -----NRRNTGASTCAN-----
12_bp_motif_5: -----CWGGKCAGGKCA-----
12_bp_motif_6: -----CAGRNCARMCAG-----
12_bp_motif_7: -----CCAGRGGNCWGS-----
12_bp_motif_8: -----CCAGCTKGGCTG-----
12_bp_motif_9: -----GGSTGGGGCWGG-----
12_bp_motif_10: -----RNGTGGCTCTGC-----
12_bp_motif_11: -----CAGGSWGNCAGN-----
12_bp_motif_12: -----CTGTGAGGTCAG-----
12_bp_motif_13: -----CCAGGTCWSCA-----
12_bp_motif_14: -----ANNNAAGGTCA-----
12_bp_motif_15: -----RARGSCTGKNTG-----
12_bp_motif_16: -----CTNTGGAATGTG-----
12_bp_motif_17: -----GCTGCTGGGAG-----
12_bp_motif_18: -----CCTGGGSTKKG-----
12_bp_motif_19: -----AGGTGACWKCTG-----
12_bp_motif_20: -----GSCAGRWGCAAA-----
12_bp_motif_pair_1: --RGCCNNGSCNNGNGGSTGGGGSWGG-----
12_bp_motif_pair_2: --YCTGCCWSCCTGNGGSTGGGGSWGG-----
12_bp_motif_pair_3: CCAGRGGNCWGSNCNNGSCNNGGCY-----
12_bp_motif_pair_4: -----GGSTGGGGSWGGNCCWGCTKGGCTG---
12_bp_motif_pair_5: -----NCYCTGNGCTCCNSCWGNCCYCWGG---
12_bp_motif_pair_6: -----GGSTGGGGSWGGNSCWGNCCYCTGG---
12_bp_motif_pair_7: -----CCWSCCCASCCNCAGGGCTGGRAN-----
12_bp_motif_pair_8: --SASAGCCMCAGNGGSTGGGGSWGG-----
12_bp_motif_pair_9: --GCAGAGCCASNYNGGSTGGGGSWGG-----
12_bp_motif_pair_10: -----CMNGSCNKGGCYNCCWGTNCCCWSM-----
12_bp_motif_pair_11: -CCCAGCCCAGNNCNGSCNNGGCY-----
12_bp_motif_pair_12: CCWSCCCASCCNRGNAGNAGGSA-----
12_bp_motif_pair_13: --TGMAGGAKGMCNGGSTGGGGSWGG-----
12_bp_motif_pair_14: --KSWGGNRCWGGNGGSWGGGGSWGG-----
12_bp_motif_pair_15: -----CCWGGGGSCWGSNCAGNSWGNCAGN--
12_bp_motif_pair_16: -----GGSTGGGGCWGGNCTGKYTGNYCTG---
12_bp_motif_pair_17: -----CWGGGCAGGKCANCCWSCCCASCC-----
12_bp_motif_pair_18: -----TGCCYCAGGGCANCCAGRGGNCWGS-----
12_bp_motif_pair_19: -----CAGNSWGNCAGNNCAGGGCTGNRAM-----

12_bp_motif_pair_20: -NCTGSCWSCCTGNCCWGCTKGGCTG-----

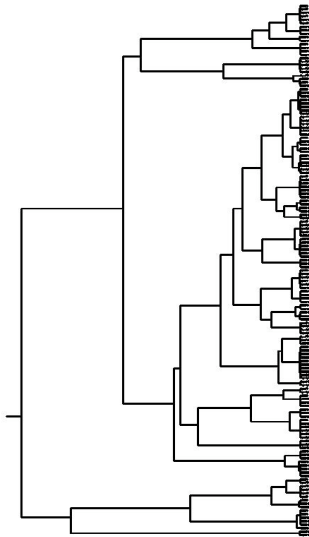
Familial Profile:
(click for matrix)







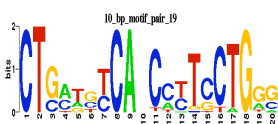

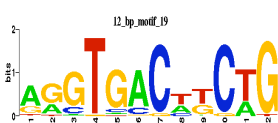


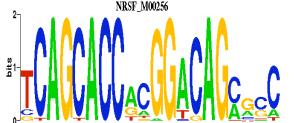



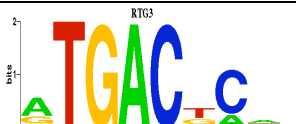


Motif Tree












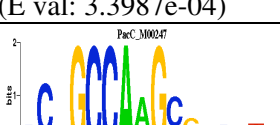

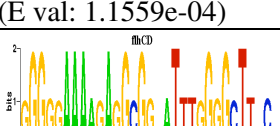

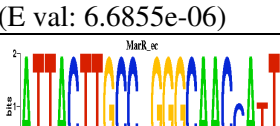
Tree (drawn by [Phylip](#))















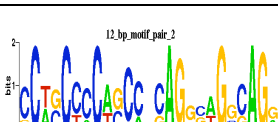

[Click here for Newick-format tree](#) (viewable with [MEGA](#))

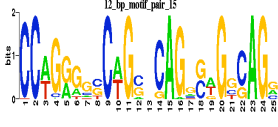

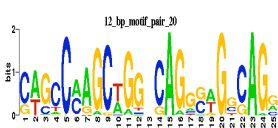

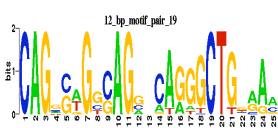

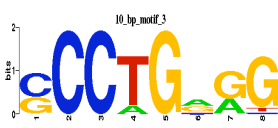

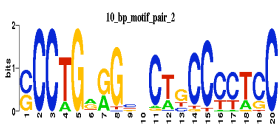
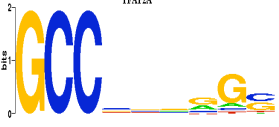
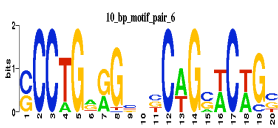

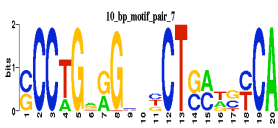


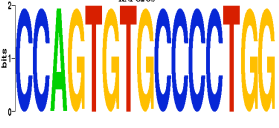


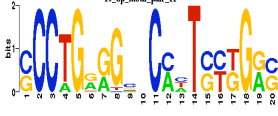
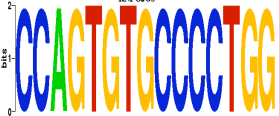








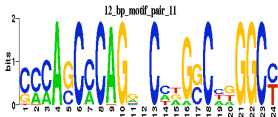

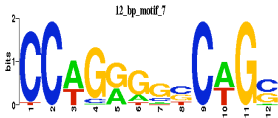

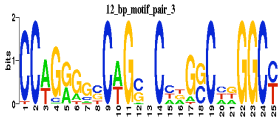

	Input Motif	Best match in ALL
	 6 bp motif 1	 QELEMENTZM13 QELEMENTZM13 (E val: 5.9379e-07)
	 6 bp motif 2	 CF1_M00112 CF1_M00112 (E val: 7.0080e-09)
	 12 bp motif 12	 QELEMENTZM13 QELEMENTZM13 (E val: 2.0490e-07)
	 8 bp motif 1	 QELEMENTZM13 QELEMENTZM13 (E val: 5.4849e-11)
	 12 bp motif 14	 RORA_1 RORA_1 (E val: 2.0705e-08)

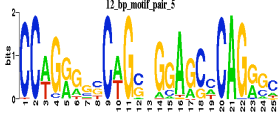

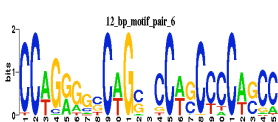

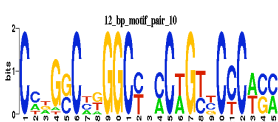
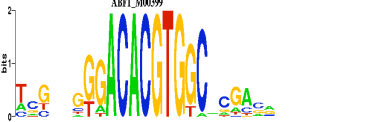
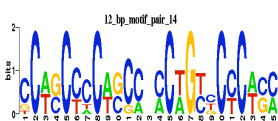
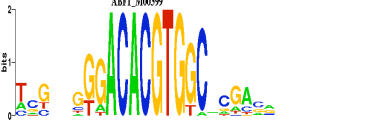


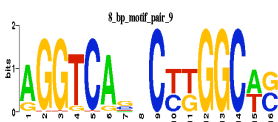



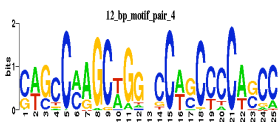

 <p>10 bp motif 8</p>	 <p>PPAR_M00762 PPAR_M00762 (E val: 1.0368e-06)</p>
 <p>10 bp motif 10</p>	 <p>ATF1_M00691 ATF1_M00691 (E val: 6.6765e-07)</p>
 <p>10 bp motif pair 19</p>	 <p>Tel-2_M00678 Tel-2_M00678 (E val: 2.0976e-04)</p>
 <p>12 bp motif 19</p>	 <p>ALF2NTPARB ALF2NTPARB (E val: 3.2161e-07)</p>
 <p>6 bp motif 14</p>	 <p>NRSF_M00256 NRSF_M00256 (E val: 6.4603e-06)</p>
 <p>6 bp motif 18</p>	 <p>GCN4OSGLUB1 GCN4OSGLUB1 (E val: 1.2242e-04)</p>
 <p>6 bp motif 7</p>	 <p>RTG3 RTG3 (E val: 1.1596e-07)</p>
 <p>8 bp motif 12</p>	 <p>GLMHVCHORD GLMHVCHORD (E val: 8.9669e-12)</p>

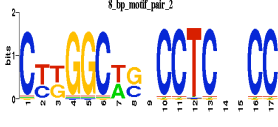

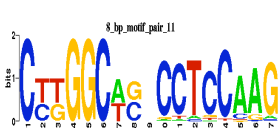
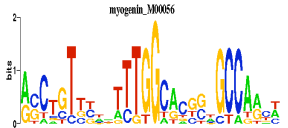
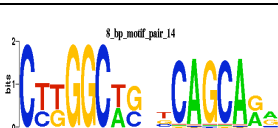
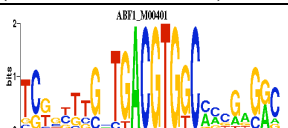


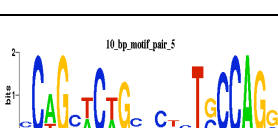
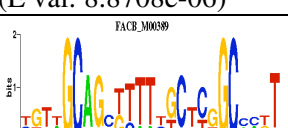

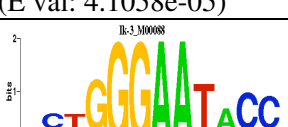


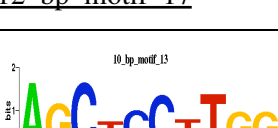
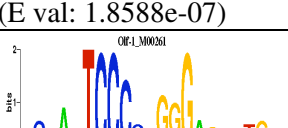
 <p>10 bp motif 4</p>	 <p>GCN4 (E val: 9.8410e-13)</p>
 <p>12 bp motif 4</p>	 <p>GLMHVCHORD (E val: 1.7434e-11)</p>
 <p>6 bp motif 15</p>	 <p>AAGACGTAGATACL12 (E val: 1.3539e-08)</p>
 <p>6 bp motif pair 8</p>	 <p>AAGACGTAGATACL12 (E val: 5.0338e-04)</p>
 <p>6 bp motif pair 14</p>	 <p>AtLEC2 (E val: 3.3987e-04)</p>
 <p>6 bp motif pair 15</p>	 <p>PacC_M00247 (E val: 1.1559e-04)</p>
 <p>6 bp motif pair 20</p>	 <p>flhCD (E val: 6.6855e-06)</p>
 <p>6 bp motif 17</p>	 <p>MarR_ec (E val: 6.3613e-06)</p>

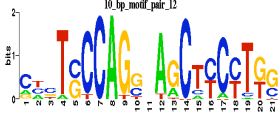

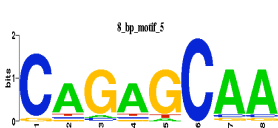



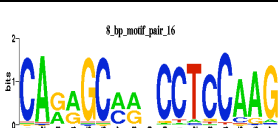
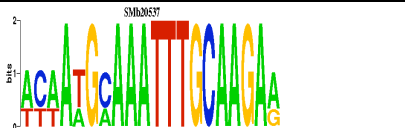


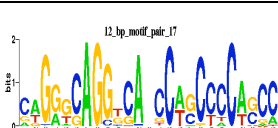

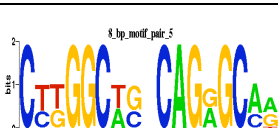
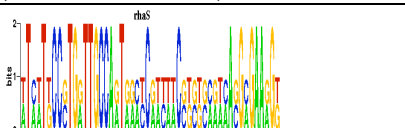


 <p>6 bp motif 20</p>	 <p>RbsR_SX (E val: 1.7536e-05)</p>
 <p>8 bp motif 9</p>	 <p>SBOXATRBCS (E val: 1.2177e-06)</p>
 <p>8 bp motif pair 6</p>	 <p>REGION1OSOSEM (E val: 3.5374e-06)</p>
 <p>6 bp motif 4</p>	 <p>MNF1ZMPPC1 (E val: 1.8833e-05)</p>
 <p>6 bp motif pair 1</p>	 <p>AMMORESVDCRNIA1 (E val: 9.1538e-08)</p>
 <p>6 bp motif pair 4</p>	 <p>AMMORESVDCRNIA1 (E val: 1.1915e-05)</p>
 <p>12 bp motif 11</p>	 <p>CAC-binding_M00720 (E val: 6.8153e-07)</p>
 <p>12 bp motif pair 2</p>	 <p>UF1H3BETA_M01068 (E val: 5.8780e-07)</p>

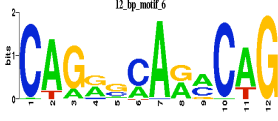
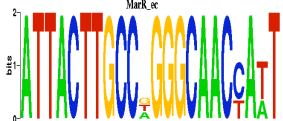


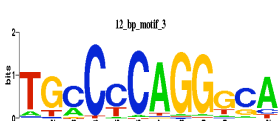

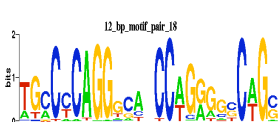


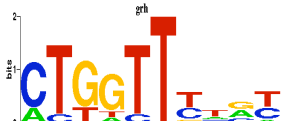


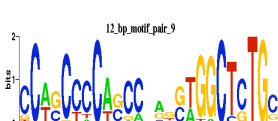



 <p>12 bp motif pair 15</p>	 <p>CAC-binding_M00720 (E val: 1.1027e-05)</p>
 <p>12 bp motif pair 20</p>	 <p>HEB_M00698 (E val: 1.1389e-06)</p>
 <p>12 bp motif pair 19</p>	 <p>CAC-binding_M00720 (E val: 3.9732e-06)</p>
 <p>10 bp motif 3</p>	 <p>AP-2alphaA_M01045 (E val: 1.3359e-07)</p>
 <p>10 bp motif pair 2</p>	 <p>TFAP2A (E val: 9.5223e-05)</p>
 <p>10 bp motif pair 6</p>	 <p>TFAP2A (E val: 9.5223e-05)</p>
 <p>10 bp motif pair 7</p>	 <p>HEN1_M00058 (E val: 1.6821e-04)</p>
 <p>10 bp motif pair 3</p>	 <p>RNFG2OS (E val: 1.3046e-07)</p>






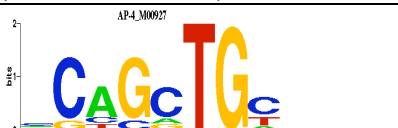



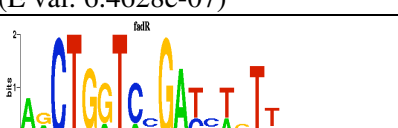

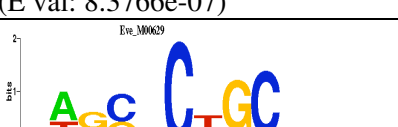
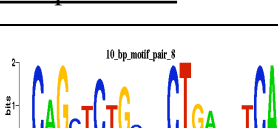
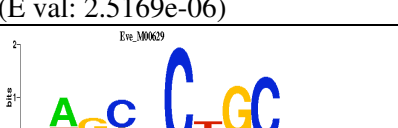
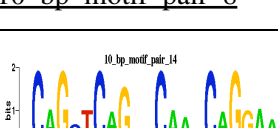
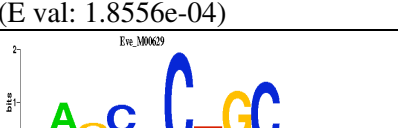
 <p>10 bp motif pair 11</p>	 <p>RNF205 (E val: 1.4185e-07)</p>
 <p>6 bp motif 5</p>	 <p>AP-2_M00915 (E val: 8.6298e-07)</p>
 <p>6 bp motif pair 2</p>	 <p>AMMORESVDCRNIA1 (E val: 4.6282e-09)</p>
 <p>12 bp motif 15</p>	 <p>Zec_M01081 (E val: 1.1421e-07)</p>
 <p>12 bp motif 18</p>	 <p>CAC-binding_M00720 (E val: 1.6676e-07)</p>
 <p>12 bp motif pair 11</p>	 <p>CAC-binding_M00720 (E val: 2.8114e-06)</p>
 <p>12 bp motif 7</p>	 <p>AMMORESVDCRNIA1 (E val: 2.1744e-06)</p>
 <p>12 bp motif pair 3</p>	 <p>AMMORESVDCRNIA1 (E val: 6.4637e-05)</p>

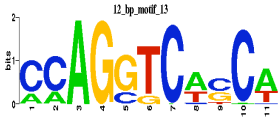




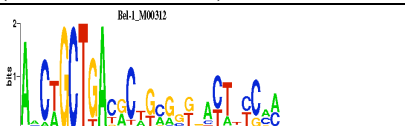


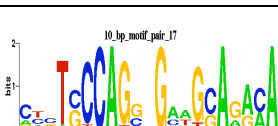





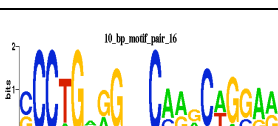

 <p>12 bp motif pair 5</p>	 <p>AtMYB-84_M00970 (E val: 4.6032e-05)</p>
 <p>12 bp motif pair 6</p>	 <p>UF1H3BETA_M01068 (E val: 5.0526e-08)</p>
 <p>12 bp motif pair 10</p>	 <p>ABF1_M00399 (E val: 7.8154e-07)</p>
 <p>12 bp motif pair 14</p>	 <p>ABF1_M00399 (E val: 3.0672e-06)</p>
 <p>8 bp motif 4</p>	 <p>RIM101 (E val: 3.2352e-08)</p>
 <p>8 bp motif pair 9</p>	 <p>QELEMENTZM13 (E val: 3.3174e-07)</p>
 <p>12 bp motif 8</p>	 <p>YY1_M00069 (E val: 1.4505e-10)</p>
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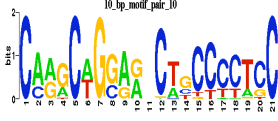










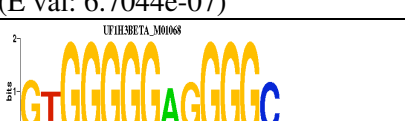



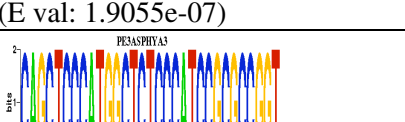
<p>8 bp motif pair 2</p>  <p>8 bp motif pair 2</p>	<p>RIM101</p>  <p>RIM101 (E val: 2.3339e-05)</p>
<p>8 bp motif pair 11</p>  <p>8 bp motif pair 11</p>	<p>myogenin_M00056</p>  <p>myogenin_M00056 (E val: 4.0010e-06)</p>
<p>8 bp motif pair 14</p>  <p>8 bp motif pair 14</p>	<p>ABF1_M00401</p>  <p>ABF1_M00401 (E val: 2.3310e-06)</p>
<p>10 bp motif 7</p>  <p>10 bp motif 7</p>	<p>MAZ_M00649</p>  <p>MAZ_M00649 (E val: 8.8708e-06)</p>
<p>10 bp motif pair 5</p>  <p>10 bp motif pair 5</p>	<p>FACB_M00389</p>  <p>FACB_M00389 (E val: 4.1058e-05)</p>
<p>10 bp motif 19</p>  <p>10 bp motif 19</p>	<p>Ik-3_M00088</p>  <p>Ik-3_M00088 (E val: 4.0042e-09)</p>
<p>12 bp motif 17</p>  <p>12 bp motif 17</p>	<p>ANAERO2CONSENSUS</p>  <p>ANAERO2CONSENSUS (E val: 1.8588e-07)</p>
<p>10 bp motif 13</p>  <p>10 bp motif 13</p>	<p>Olf-1_M00261</p>  <p>Olf-1_M00261 (E val: 4.6381e-06)</p>
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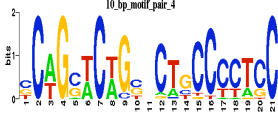
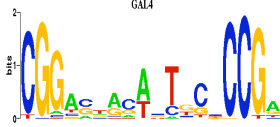


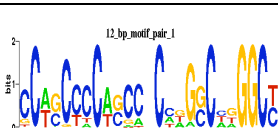
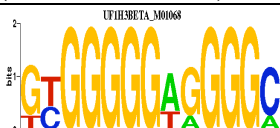


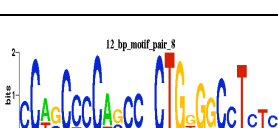

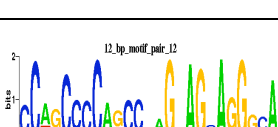

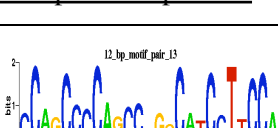
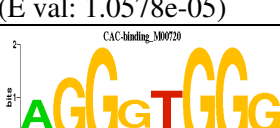


 <p>10 bp motif pair 12</p>	 <p>MAZ_M00649 (E val: 5.4899e-05)</p>
 <p>8 bp motif 5</p>	 <p>XPF-1_M00684 (E val: 6.2916e-06)</p>
 <p>8 bp motif pair 15</p>	 <p>HEB_M00698 (E val: 1.6251e-04)</p>
 <p>8 bp motif pair 16</p>	 <p>SMb20537 (E val: 6.1242e-05)</p>
 <p>12 bp motif 5</p>	 <p>QELEMENTZM13 (E val: 4.1080e-07)</p>
 <p>12 bp motif pair 17</p>	 <p>SMAD4_M00733 (E val: 1.4426e-06)</p>
 <p>8 bp motif pair 5</p>	 <p>rhaS (E val: 3.3835e-07)</p>
 <p>8 bp motif pair 13</p>	 <p>QELEMENTZM13 (E val: 1.0747e-06)</p>

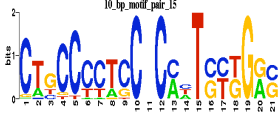

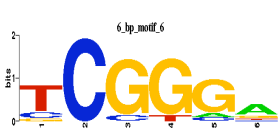

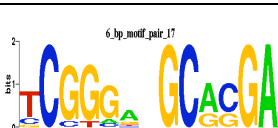






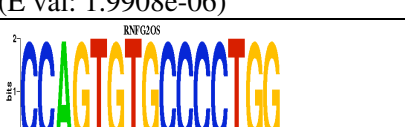
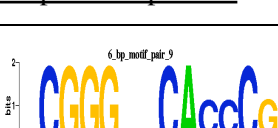
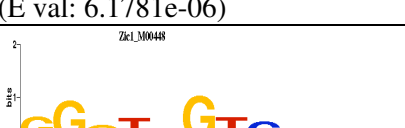


 <p>12 bp motif 6</p>	 <p>MarR_ec (E val: 1.5630e-06)</p>
 <p>12 bp motif pair 16</p>	 <p>CAC-binding_M00720 (E val: 6.8703e-06)</p>
 <p>12 bp motif 3</p>	 <p>TFAP2A (E val: 2.3702e-06)</p>
 <p>12 bp motif pair 18</p>	 <p>AMMORESVDCRNIA1 (E val: 6.4637e-05)</p>
 <p>10 bp motif 17</p>	 <p>grh (E val: 6.7987e-07)</p>
 <p>12 bp motif 10</p>	 <p>SORLIP1 (E val: 3.9455e-07)</p>
 <p>12 bp motif pair 9</p>	 <p>CAC-binding_M00720 (E val: 8.4158e-06)</p>
 <p>6 bp motif 11</p>	 <p>HEB_M00698 (E val: 7.5905e-09)</p>

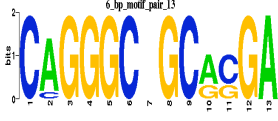




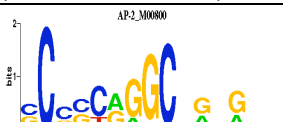




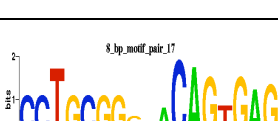



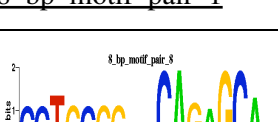
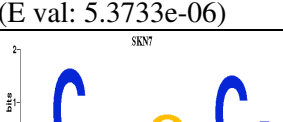
 <p>6 bp motif pair 11</p>	 <p>AtMYB-84_M00970 (E val: 2.9306e-07)</p>
 <p>6 bp motif pair 12</p>	 <p>LEGUMINBOXLEGA5 (E val: 2.6417e-06)</p>
 <p>8 bp motif 7</p>	 <p>AP-4_M00927 (E val: 2.0371e-09)</p>
 <p>8 bp motif pair 10</p>	 <p>myogenin_M00712 (E val: 6.4628e-07)</p>
 <p>8 bp motif pair 12</p>	 <p>fadR (E val: 8.3766e-07)</p>
 <p>10 bp motif 5</p>	 <p>Eve_M00629 (E val: 2.5169e-06)</p>
 <p>10 bp motif pair 8</p>	 <p>Eve_M00629 (E val: 1.8556e-04)</p>
 <p>10 bp motif pair 14</p>	 <p>Eve_M00629 (E val: 2.2152e-04)</p>

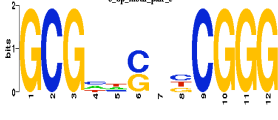

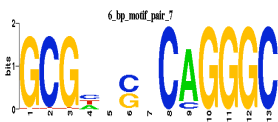

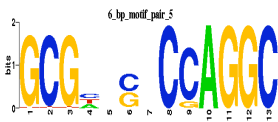
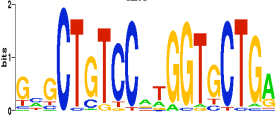
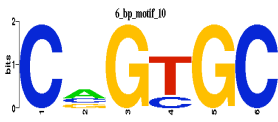
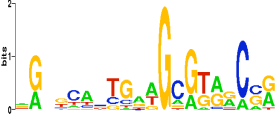

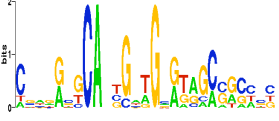
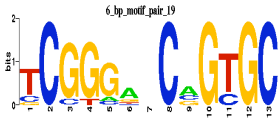
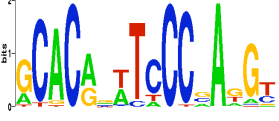
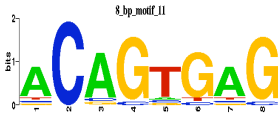

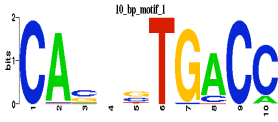
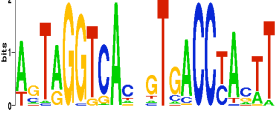
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 <p>8 bp motif 10</p>	 <p>LMAF_M01139 (E val: 4.8101e-10)</p>
 <p>8 bp motif pair 18</p>	 <p>Bel-1_M00312 (E val: 6.8351e-09)</p>
 <p>10 bp motif 15</p>	 <p>SMAD4_M00733 (E val: 6.8940e-06)</p>
 <p>10 bp motif pair 17</p>	 <p>MAZ_M00649 (E val: 5.4899e-05)</p>
 <p>12 bp motif 20</p>	 <p>sna (E val: 3.2668e-05)</p>
 <p>10 bp motif 6</p>	 <p>Barbie_M00238 (E val: 2.9175e-05)</p>
 <p>10 bp motif pair 16</p>	 <p>TFAP2A (E val: 9.5223e-05)</p>


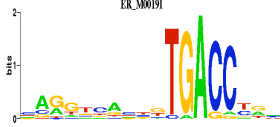
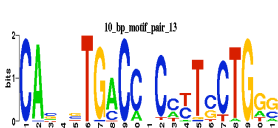

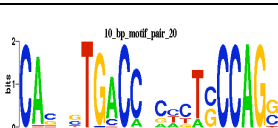
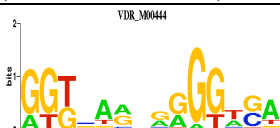




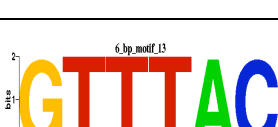


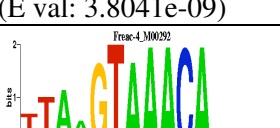

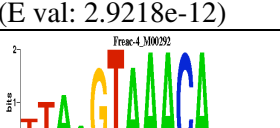
 <p>10 bp motif pair 10</p>	 <p>MAZ_M00649 (E val: 9.9365e-05)</p>
 <p>10 bp motif pair 18</p>	 <p>MAZ_M00649 (E val: 6.1165e-05)</p>
 <p>8 bp motif 13</p>	 <p>Nrf-2_M00108 (E val: 2.4532e-08)</p>
 <p>8 bp motif pair 7</p>	 <p>Nrf-2_M00108 (E val: 5.5746e-05)</p>
 <p>8 bp motif pair 19</p>	 <p>myogenin_M00712 (E val: 6.7044e-07)</p>
 <p>10 bp motif 9</p>	 <p>UF1H3BETA_M01068 (E val: 3.9237e-08)</p>
 <p>10 bp motif pair 9</p>	 <p>UF1H3BETA_M01068 (E val: 1.9055e-07)</p>
 <p>10 bp motif pair 1</p>	 <p>PE3ASPHYA3 (E val: 8.9793e-06)</p>










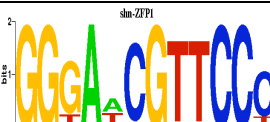





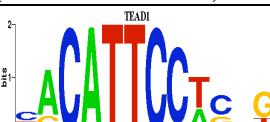
 <p>10 bp motif pair 4</p>	 <p>GAL4 (E val: 7.6524e-07)</p>
 <p>12 bp motif 9</p>	 <p>Alfin1_M00479 (E val: 3.5246e-08)</p>
 <p>12 bp motif pair 1</p>	 <p>UF1H3BETA_M01068 (E val: 8.8664e-06)</p>
 <p>12 bp motif pair 7</p>	 <p>UF1H3BETA_M01068 (E val: 7.2530e-07)</p>
 <p>12 bp motif pair 8</p>	 <p>CAC-binding_M00720 (E val: 8.4158e-06)</p>
 <p>12 bp motif pair 12</p>	 <p>CAC-binding_M00720 (E val: 1.0578e-05)</p>
 <p>12 bp motif pair 13</p>	 <p>CAC-binding_M00720 (E val: 9.3693e-06)</p>
 <p>10 bp motif 11</p>	 <p>LMAF_M01139 (E val: 7.0766e-05)</p>

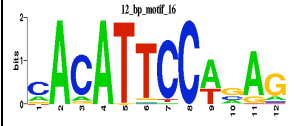
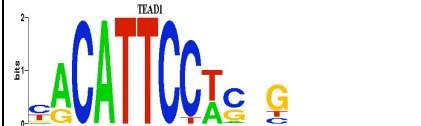



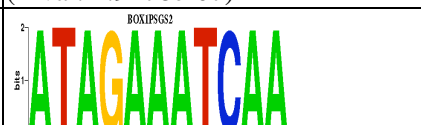


 <p>10 bp motif pair 15</p>	 <p>UF1H3BETA_M01068 (E val: 4.5768e-08)</p>
 <p>6 bp motif 6</p>	 <p>ANT_M00501 (E val: 8.1812e-07)</p>
 <p>6 bp motif pair 17</p>	 <p>ABRECE3ZMRAB28 (E val: 1.3223e-04)</p>
 <p>6 bp motif 8</p>	 <p>YDR026C (E val: 3.6408e-06)</p>
 <p>6 bp motif pair 6</p>	 <p>GCBP2ZMGAPC4 (E val: 1.9908e-06)</p>
 <p>6 bp motif pair 10</p>	 <p>RNFG2OS (E val: 6.1781e-06)</p>
 <p>6 bp motif pair 9</p>	 <p>Zic1_M00448 (E val: 2.9132e-06)</p>
 <p>6 bp motif 12</p>	 <p>RHERPATEXPA7 (E val: 2.1035e-06)</p>

 <p>6 bp motif pair 13</p>	 <p>GRAZMRAB28 (E val: 6.9807e-05)</p>
 <p>6 bp motif pair 16</p>	 <p>ABREMOTIFIIOSRAB16B (E val: 6.2461e-05)</p>
 <p>8 bp motif 3</p>	 <p>AP-2_M00800 (E val: 6.8282e-07)</p>
 <p>8 bp motif pair 4</p>	 <p>QELEMENTZMZM13 (E val: 4.3466e-06)</p>
 <p>8 bp motif pair 3</p>	 <p>myogenin_M00712 (E val: 6.7044e-07)</p>
 <p>8 bp motif pair 17</p>	 <p>SORLIP5 (E val: 2.1849e-05)</p>
 <p>8 bp motif pair 1</p>	 <p>RIM101 (E val: 5.3733e-06)</p>
 <p>8 bp motif pair 8</p>	 <p>SKN7 (E val: 8.3870e-05)</p>

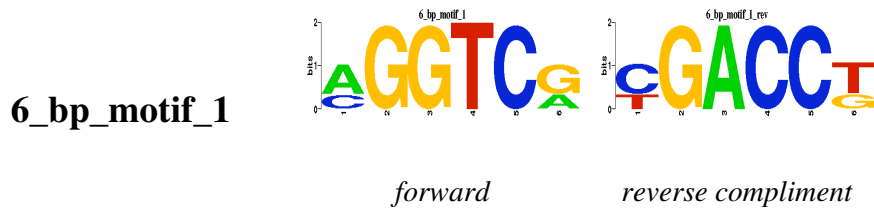
 <p>6 bp motif pair 3</p>	 <p>Mad (E val: 4.7888e-04)</p>
 <p>6 bp motif pair 7</p>	 <p>Mad (E val: 5.3676e-06)</p>
 <p>6 bp motif pair 5</p>	 <p>REST (E val: 1.6156e-04)</p>
 <p>6 bp motif 10</p>	 <p>Pax5 (E val: 3.3113e-05)</p>
 <p>6 bp motif pair 18</p>	 <p>Pax-5_M00143 (E val: 1.3153e-05)</p>
 <p>6 bp motif pair 19</p>	 <p>ANT (E val: 1.8102e-09)</p>
 <p>8 bp motif 11</p>	 <p>CIGMAUX28 (E val: 5.9954e-11)</p>
 <p>10 bp motif 1</p>	 <p>PPARgamma-RXRalpha_M00515 (E val: 3.4102e-11)</p>




 <p>12 bp motif 1</p>	 <p>ER_M00191 (E val: 4.6629e-15)</p>
 <p>10 bp motif pair 13</p>	 <p>NERF1a_M00531 (E val: 5.0020e-08)</p>
 <p>10 bp motif pair 20</p>	 <p>VDR_M00444 (E val: 1.2588e-05)</p>
 <p>6 bp motif 3</p>	 <p>AMMORESIVDCRNIA1 (E val: 9.1148e-06)</p>
 <p>6 bp motif 16</p>	 <p>AACACOREOSGLUB1 (E val: 4.4421e-06)</p>
 <p>6 bp motif 13</p>	 <p>FOXD1 (E val: 3.8041e-09)</p>
 <p>10 bp motif 2</p>	 <p>Freac-4_M00292 (E val: 2.9218e-12)</p>
 <p>12 bp motif 2</p>	 <p>Freac-4_M00292 (E val: 1.1626e-09)</p>

 <p>8 bp motif 2</p>	 <p>Sn_M00044 (E val: 2.6878e-07)</p>
 <p>8 bp motif 8</p>	 <p>Grainyhead-Elf-1-NTF-1_M00951 (E val: 8.6018e-11)</p>
 <p>10 bp motif 12</p>	 <p>Grainyhead-Elf-1-NTF-1_M00951 (E val: 2.6976e-09)</p>
 <p>10 bp motif 20</p>	 <p>RORA_1 (E val: 1.2075e-06)</p>
 <p>6 bp motif 9</p>	 <p>shn-ZFP1 (E val: 4.7754e-07)</p>
 <p>8 bp motif 6</p>	 <p>Opaque-2_M00010 (E val: 2.1242e-07)</p>
 <p>8 bp motif pair 20</p>	 <p>RIM101 (E val: 1.9865e-05)</p>
 <p>10 bp motif 16</p>	 <p>TEAD1 (E val: 9.1279e-08)</p>

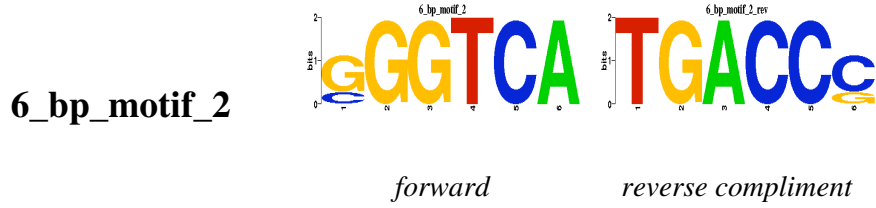
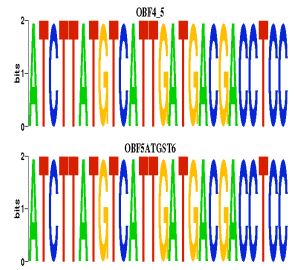
 <p>12 bp motif 16</p>	 <p>TEAD1 (E val: 2.2411e-08)</p>
 <p>6 bp motif 19</p>	 <p>GRAZMRAB28 (E val: 4.9478e-07)</p>
 <p>10 bp motif 14</p>	 <p>BOX1PSGS2 (E val: 2.3721e-08)</p>
 <p>10 bp motif 18</p>	 <p>GLN3 (E val: 9.7500e-13)</p>

Motif Similarity Matches

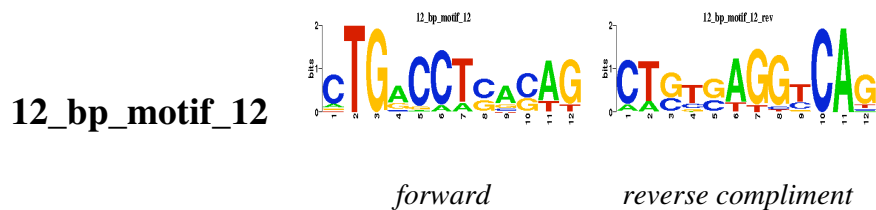


Name	E value	Alignment	Motif
QELEMENTZM13	5.9379e-07	CGACCT TGACCT	
DREB1B_twoSite	7.2123e-06	AGGTCG---- AKGTCCGYMR	
DREB1C_twoSite	7.2123e-06	AGGTCG---- AKGTCCGYMR	

OBF4_5	7.4322e-06	--AGGTCG----- GGAGGTCGTCATCAATGACATAAGAT
OBF5ATGST6	7.4322e-06	--AGGTCG----- GGAGGTCGTCATCAATGACATAAGAT

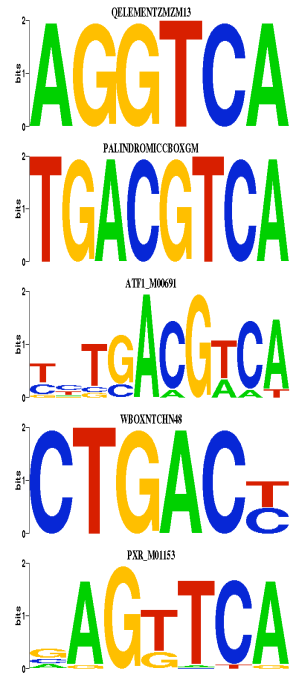


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CF1_M00112	7.0080e-09	--TGACCC NGTGACCC	
CF1_M00111	1.8889e-08	GGGTCA-- GGGTCANN	
usp	4.6742e-08	-GGGTCA--- GGGGTCACNN	
LF-A1_M00646	1.4653e-07	-TGACCC YWGASCC	
Hr46	3.9703e-07	----GGGTCA AATTGGGTCA	

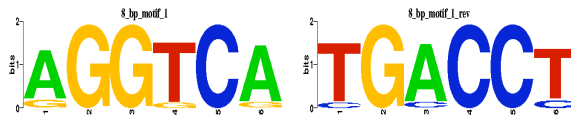


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
-------------	----------------	------------------	--------------

QELEMENTZM13	2.0490e-07	CTGACCTCACAG -TGACCT-----
PALINDROMICCBXGM	5.4993e-06	CTGACCTCACAG -TGACGTCA---
ATF1_M00691	7.4686e-06	CTGTGAGGTCAG-- ---TGACGTGANR
WBOXNTCHN48	7.6054e-06	CTGACCTCACAG CTGACY-----
PXR_M01153	1.1835e-05	CTGTGAGGTCAG ----NAGTTCA-



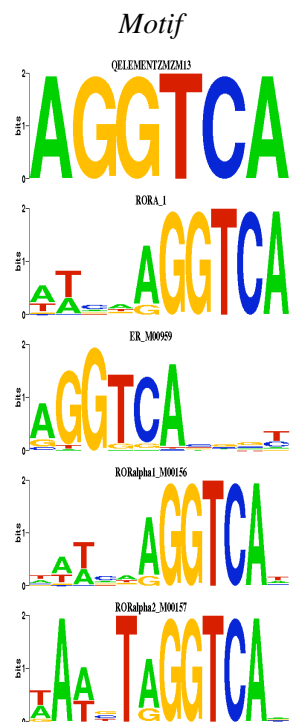
8_bp_motif_1

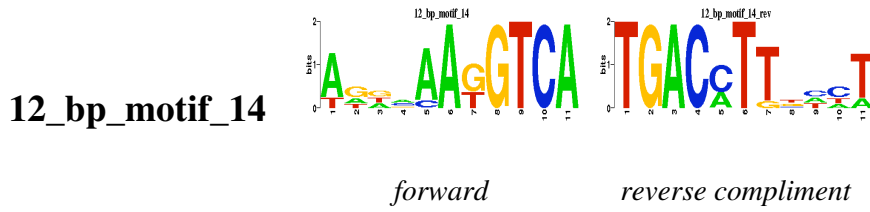


forward

reverse compliment

Name	E value	Alignment
QELEMENTZM13	5.4849e-11	TGACCT TGACCT
RORA_1	2.8358e-08	TGACCT---- TGACCTNNWW
ER_M00959	3.0117e-08	----TGACCT RNNNTGACCT
RORalpha1_M00156	9.4815e-08	-TGACCT----- NTGACCTNNWWN
RORalpha2_M00157	9.9510e-08	-TGACCT----- NTGACCTANTTW



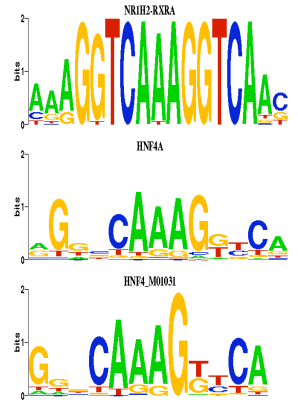


Name	E value	Alignment	Motif
RORA_1	2.0705e-08	TGACCTTNNNT TGACCTNNWW-	
ERR_M00511	8.8586e-08	ANNNAAAGGTCA-- NNNNAAGGTCANN	
QELEMENTZM3	2.0905e-07	TGACCTTNNNT TGACCT-----	
RORalpha1_M00156	4.5323e-07	-TGACCTTNNNT NTGACCTNNWWN	
PPAR,_M00762	1.6958e-06	TGACCTTNNNT- TGACCTTTGNCC	

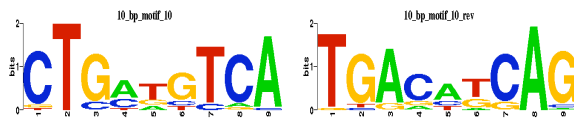


Name	E value	Alignment	Motif
PPAR,_M00762	1.0368e-06	CTGRCMTKTS--- -TGACCTTTGNCC	
HNF4alpha1_M00411	5.4272e-06	----SAMAKGYCAG RGGNCAAAGGTCAN	

NR1H2-RXRA	5.8201e-06	-----SAMAKGYCAG-- AAAGGTCAAAGGTCAS
HNF4A	6.0873e-06	CTGRCMTKTS----- -TGNMCTTTGNNCY
HNF4_M01031	1.1832e-05	CTGRCMTKTS--- NTGRMCTTTGNNC



10_bp_motif_10

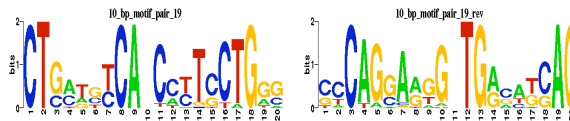


forward

reverse compliment




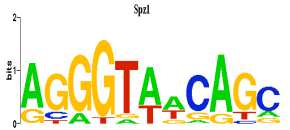
Name	E value	Alignment	Motif
ATF1_M00691	6.6765e-07	TGACAKCAG-- TGACGTCANR	
ATF3_M00513	1.0192e-06	-CTGMTGTCA--- NSTGACGTCANCS	
PALINDROMICCBOXGM	1.6003e-06	TGACAKCAG TGACGTCA-	
OBF4_5	2.9107e-06	-----TGACAKCAG-- GGAGGTCGTCATCAATGACATAAGAT	
OBF5ATGST6	2.9107e-06	-----TGACAKCAG-- GGAGGTCGTCATCAATGACATAAGAT	

10_bp_motif_pair_19

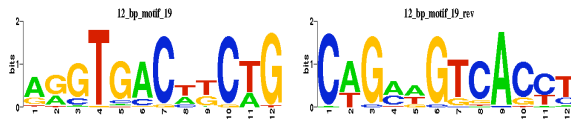


forward *reverse compliment*




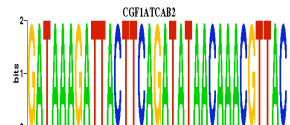
Name *E value* *Alignment* *Motif*

Tel-2_M00678	2.0976e-04	CTGMNSTCANCCYTCTGGS -----TACTTCTG--	
AMMORESIIUDCRNIA1	2.4286e-04	CTGMNSTCANCCYTCTGGS -----ACCCTWCC----	
Skn-1_M00229	2.8809e-04	SCCAGGARGGNTGASNKCAG -----NNNATGACAWN--	
AhR_M00139	3.9921e-04	-SCCAGGARGGNTGASNKCAG CYCNRNSTNGCGTGASA----	
Spz1	5.4892e-04	CTGMNSTCANCCYTCTGGS --GCTGWTACCCT-----	

12_bp_motif_19



forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ALF2NTPARB	3.2161e-07	----CAGMWGTCACCT-- ACCTCACAAGTCTCCTCA	
GLUTEBOX1OSGT2	3.7897e-05	----CAGMWGTCACCT-- ATATCATGAGTCACTTCA	
WBOXHVIS01	1.0335e-04	CAGMWGTCACCT ----AGTCA----	
CGF1ATCAB2	1.3249e-04	-----CAGMWGTCACCT----- GTAACGTTTGTTATATCTGAAGTAATCTTTATC	

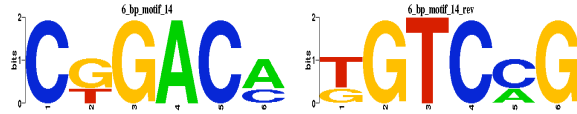
RBCSGBOXPS

1.4691e-04

CAGMWGTCACCT
CACATGGCACT-



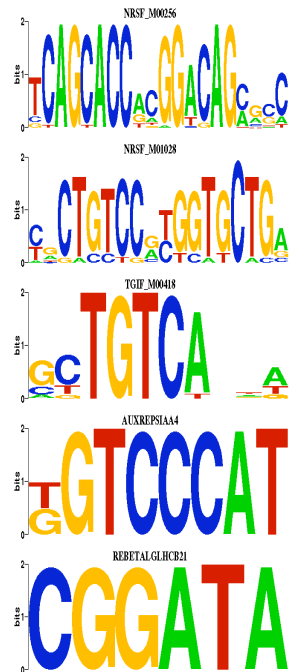
6_bp_motif_14



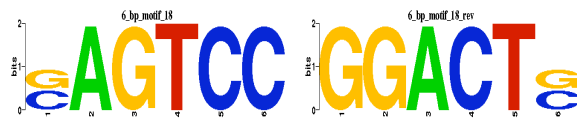
forward

reverse compliment

Name	E value	Alignment
NRSF_M00256	6.4603e-06	-----CGGACA----- TCAGCACCACGGACAGCRSC
NRSF_M01028	3.2919e-05	---TGTCCG----- YNCTGTCCRYGGTGCTGA
TGIF_M00418	6.2899e-05	--CGGACA-- WNNTGACAGC
AUXREPSIAA4	8.2349e-05	TGTCCG-- KGTCCCAT
REBETALGLHCB21	8.5096e-05	TGTCCG TATCCG



6_bp_motif_18



forward

reverse compliment

Name	E value	Alignment
GCN4OSGLUB1	1.2242e-04	GGACTS- TGACTCA



NF-kappaB_M00208 2.0445e-04

----SAGTCC--
NGGAAARTCCC



PALBOXAPC 2.5272e-04

SAGTCC
CCGTCC



ARG81 3.1250e-04

-SAGTCC-
NGAGTCAN

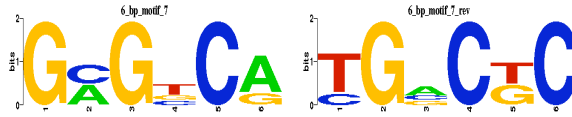


HNF4,_M00967 3.3510e-04

SAGTCC--
ARGTCCAN



6_bp_motif_7



forward

reverse compliment

Name

E value

Alignment

Motif

RTG3

1.1596e-07

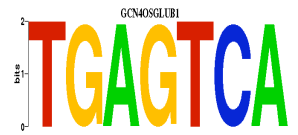
-GMGNCA-
NGMGTCAT



GCN4OSGLUB1

4.1637e-07

-GMGNCA
TGAGTCA



Bach2_M00490

1.2403e-06

--TGNCKC--
NNTGACTCAY



ARG81

1.8686e-06

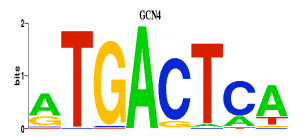
-GMGNCA-
NGAGTCAN



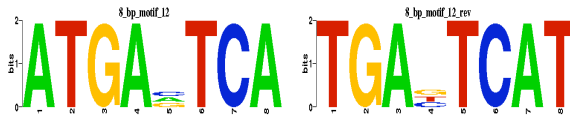
GCN4

2.2593e-06

-GMGNCA-
TGAGTCAT



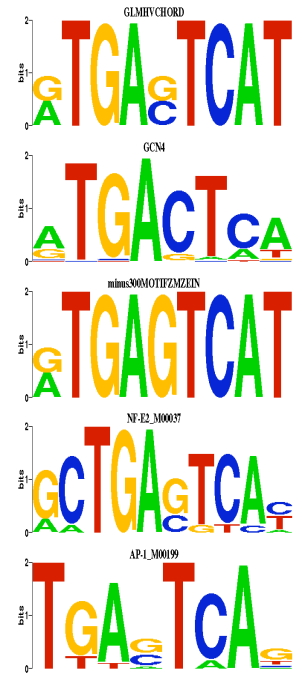
8_bp_motif_12



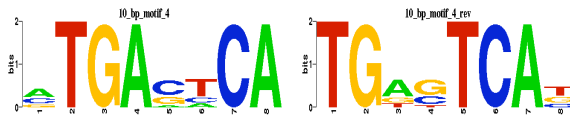
forward

reverse compliment

Name	E value	Alignment
GLMHVCHORD	8.9669e-12	ATGANTCA- ATGASTCAY
GCN4	2.2985e-11	TGANTCAT TGAGTCAT
minus300MOTIFZMZEIN	9.6750e-11	-TGANTCAT RTGAGTCAT
NF-E2_M00037	4.4288e-09	ATGANTCA-- RTGACTCAGC
AP-1_M00199	5.5423e-09	-TGANTCAT NTGASTCA-



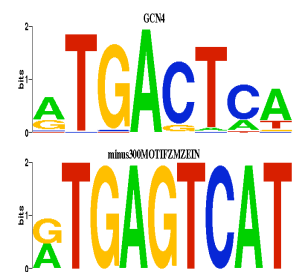
10_bp_motif_4



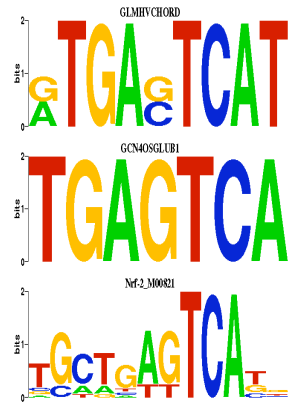
forward

reverse compliment

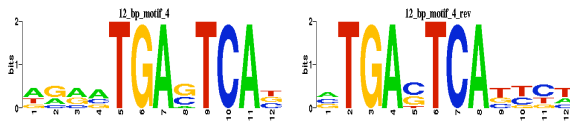
Name	E value	Alignment
GCN4	9.8410e-13	TGASTCAN TGAGTCAT
minus300MOTIFZMZEIN	1.1107e-11	NTGASTCA- ATGACTCAY



GLMHVCHORD	1.2949e-11	NTGASTCA- ATGASTCAY
GCN4OSGLUB1	7.8854e-11	NTGASTCA -TGACTCA
Nrf-2_M00821	8.1284e-11	-NTGASTCA--- NNTGACTCAGCA



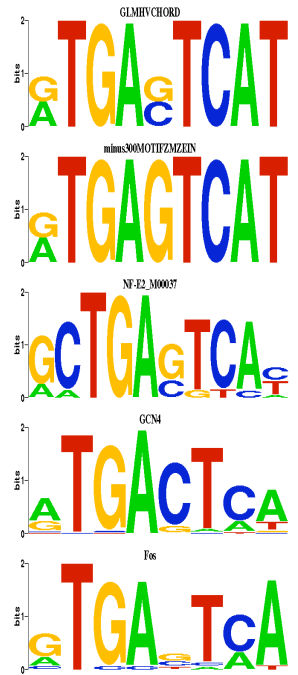
12_bp_motif_4



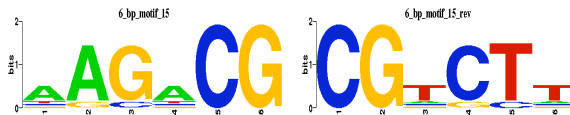
forward


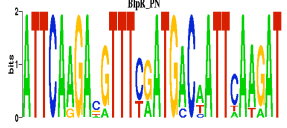



reverse compliment

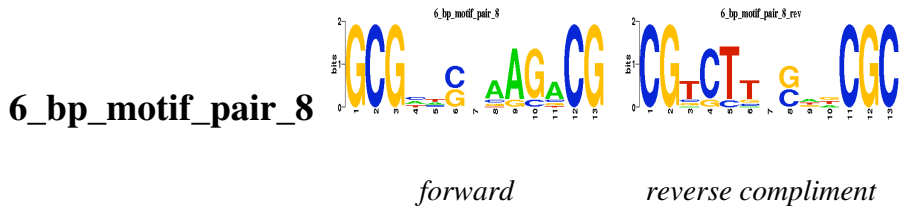
Name	E value	Alignment	Motif
GLMHVCHORD	1.7434e-11	NRRNTGASTCAN ---ATGASTCAY	GLMHVCHORD TGA TCA
minus300MOTIFZMZEIN	1.3206e-09	NTGASTCANYYN ATGACTCAY---	minus300MOTIFZMZEIN TGAGTCA
NF-E2_M00037	2.1445e-09	NTGASTCANYYN RTGACTCAGC--	NF-E2_M00037 GCTGAGTCA
GCN4	2.8144e-09	NRRNTGASTCAN ----TGAGTCAT	GCN4 TGACTCA
Fos	6.3829e-09	NRRNTGASTCAN ----TGANTCAC	Fos TGA TCA







6_bp_motif_15



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AAGACGTAGATACL12	1.3539e-08	---CGTCTT CTACGTCTT	
BlpR_PN	1.0736e-06	-----CGTCTT----- ATCTTGAATWGTTCATCGAAACNTCTTGAAT	
ABREBZMRAB28	7.4257e-05	AAGACG---- GAGACGTGGA	
PEND_M01015	1.3418e-04	-CGTCTT ACTTCTT	
CDA1ATCAB2	2.4447e-04	-CGTCTT- GCGTTTTG	

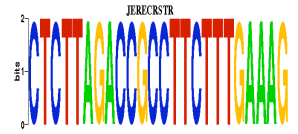


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AAGACGTAGATACL12	5.0338e-04	GCGNNSNAAGACG--- -----AAGACGTAG	
LS5	2.3295e-03	GCGNNSNAAGACG- ----TCTATGACGT	
LS7ATPR1	2.3295e-03	GCGNNSNAAGACG- ----TCTATGACGT	
STE11_M01005	2.5639e-03	CGTCTTNSNNCGC TTTCTTTGTTTC--	

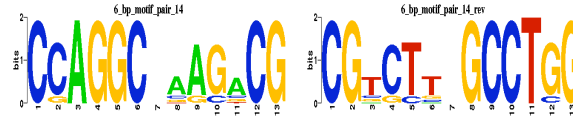
JERECRSTR

2.7998e-03

-----GCGNNSNAAGACG
CTTTCAAAGAAGGCGGTCTAAGAG-



6_bp_motif_pair_14



forward

reverse compliment

Name

E value

Alignment

Motif

AtLEC2

3.3987e-04

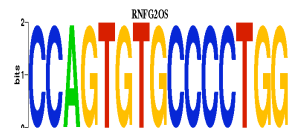
CGTCTTNGCCTGG-
----TTGCATGNN



RNFG2OS

4.5838e-04

CCAGGCNAAGACG--
CCAGGGGCACACTGG



AAGACGTAGATACL12 5.0338e-04

CCAGGCNAAGACG---
-----AAGACGTAG



SOK2

7.5902e-04

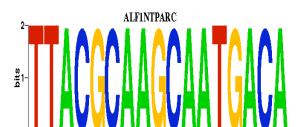
CGTCTTNGCCTGG
-----TTKCCTRN



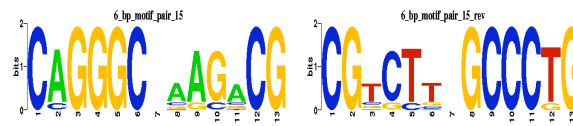
ALFINTPARC

8.9819e-04

CGTCTTNGCCTGG----
TGTCATTGCTTGCGTAA



6_bp_motif_pair_15



forward

reverse compliment

Name

E value

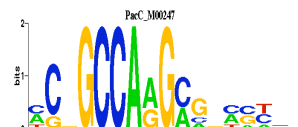
Alignment

Motif

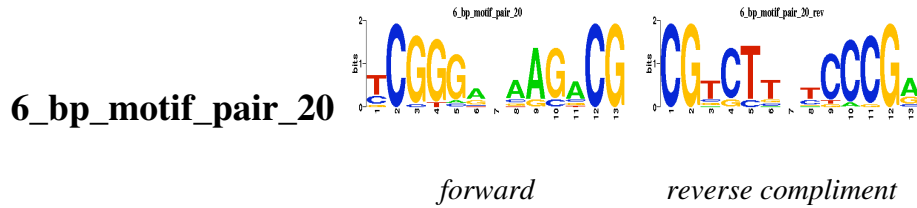
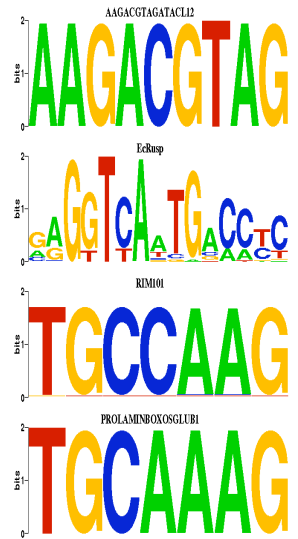
PacC_M00247

1.1559e-04

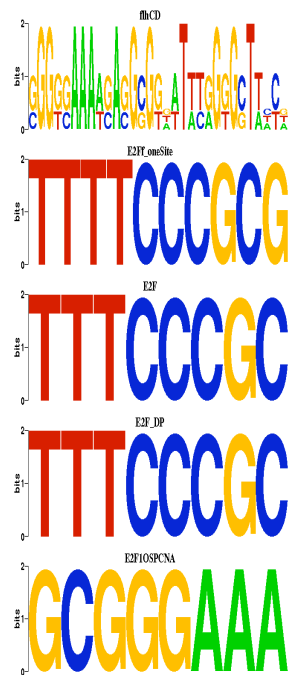
----CGTCTTNGCCCTG
NNNNNNKCYTGCGNGN-



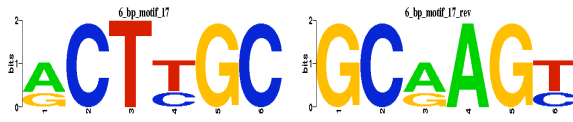
AAGACGTAGATAACL12	5.0338e-04	CAGGGCNAAGACG--- -----AAGACGTAG
EcRusp	1.6221e-03	CAGGGCNAAGACG-- RAGGTCAATGACCYC
RIM101	2.3171e-03	CGTCTTNGCCCTG ---CTTGCA---
PROLAMINBOXOSGLUB1	2.3171e-03	CAGGGCNAAGACG ---TGCAAAG---



Name	E value	Alignment	Motif
flhCD	6.6855e-06	-----CGTCTTNYCCCGA NGNAAGCCCCAAATNCCGCCTCTTTTCCCC	
E2Ff_oneSite	1.6747e-05	CGTCTTNYCCCGA- ----TTTTCCCGCG	
E2F	1.0837e-04	TCGGGRNAAGACG GCGGGAAA-----	
E2F_DP	1.0837e-04	TCGGGRNAAGACG GCGGGAAA-----	
E2F1OSPCNA	1.0837e-04	CGTCTTNYCCCGA -----TTTCCCGC	



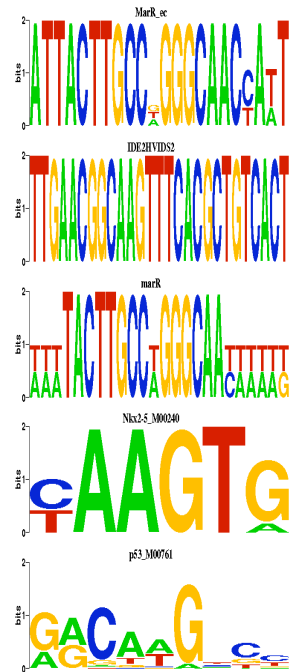
6_bp_motif_17



forward

reverse compliment

Name	E value	Alignment
MarR_ec	6.3613e-06	---ACTTGC----- ATTACTTGCCNGGGCAACCATT
IDE2HVIDS2	7.4322e-06	-----ACTTGC----- AGTGACAGCGTGAAACTTGCCGTTCAA
marR	7.4322e-06	-----GCAAGT----- MWWWWRTTGCCWGGCAAGTAWWW
Nkx2-5_M00240	5.5626e-05	-ACTTGC CACTTR-
p53_M00761	6.8288e-05	--ACTTGC- NGNCWTGYC



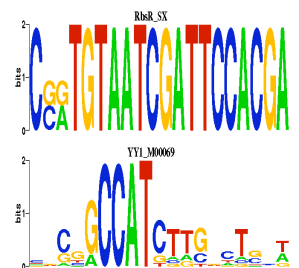
6_bp_motif_20



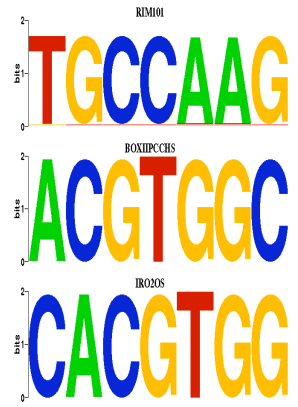
forward

reverse compliment

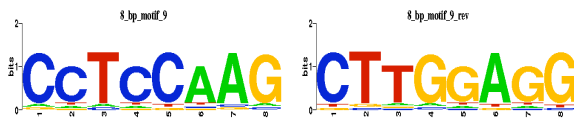
Name	E value	Alignment
RbsR_SX	1.7536e-05	TCKTGG----- TCGTGGAATCGATTACAYSG
YY1_M00069	8.7095e-05	-----CCAMGA----- WNSANNCAAGATGGCNGNN



RIM101	1.2242e-04	TCKTGG-- -CTTGGCA
BOXIIPCCHS	1.2242e-04	-CCAMGA GCCACGT
IRO2OS	1.2242e-04	CCAMGA- CCACGTG

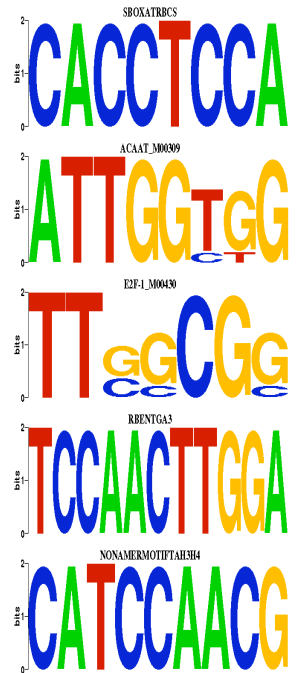


8_bp_motif_9

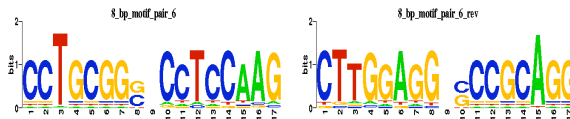


forward *reverse compliment*

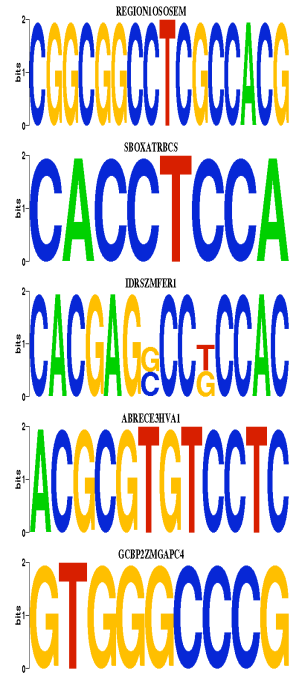
Name	E value	Alignment	Motif
SBOXATRBCS	1.2177e-06	--CCTCCAAG CACCTCCA--	CACCTCCA
ACAAT_M00309	1.9806e-05	CCTCCAAG CCACCAAT	ATTGGTGG
E2F-1_M00430	1.9826e-05	CCTCCAAG CCGCSAA-	TTGGCGG
RBENTGA3	2.6591e-05	CCTCCAAG----- --TCCAAGTTGGA	TCCAACTTGA
NONAMERMOTIFTAH3H4	4.2744e-05	-CTTGGAGG CGTTGGATG	CATCCAACG



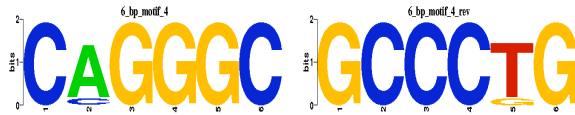
8_bp_motif_pair_6



	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
REGION1OSOSEM	3.5374e-06	CCTGCGGSNCCTCCAAG -CGGCGGCTCGCCACG
SBOXATRBCS	8.7571e-06	CCTGCGGSNCCTCCAAG -----CACCTCCA--
IDRSZMFER1	2.2810e-04	CCTGCGGSNCCTCCAAG --CACGAGSCKCCAC-
ABRECE3HVA1	2.4160e-04	CCTGCGGSNCCTCCAAG -ACGCGTGTCTC----
GCBP2ZMGAPC4	2.9716e-04	CCTGCGGSNCCTCCAAG ----CGGGCCCAC----

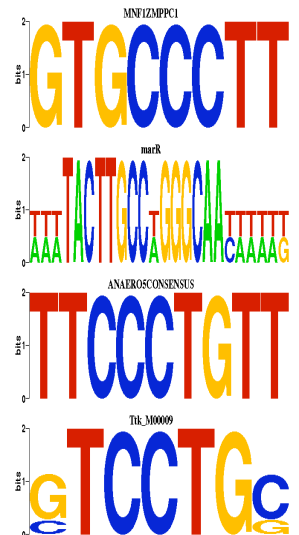


6_bp_motif_4



forward *reverse compliment*

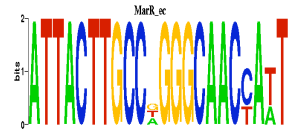
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
MNF1ZMPPC1	1.8833e-05	CAGGGC-- AAGGGCAC
marR	4.0921e-05	-----GCCCTG----- MWWWWRTTGCCCWGGCAAGTAWWW
ANAERO5CONSENSUS	4.1712e-05	--CAGGGC- AACAGGGAA
Ttk_M00009	1.0615e-04	-CAGGGC GCAGGAC



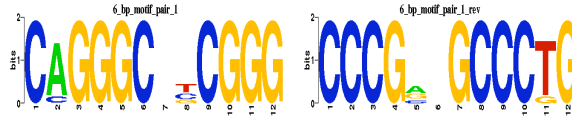
MarR_ec

2.9316e-04

-----GCCCTG-----
AATGGTTGCCCNCGCAAGTAAT



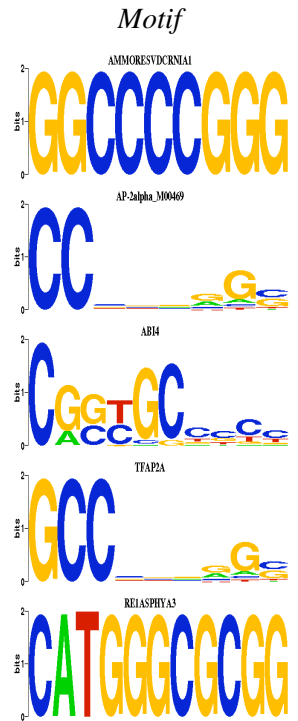
6_bp_motif_pair_1



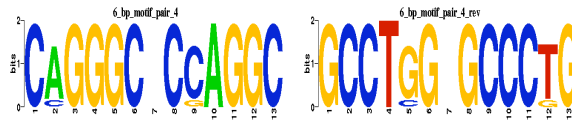
forward

reverse compliment

Name	E value	Alignment
AMMORESVDCRNIA1	9.1538e-08	CAGGGCNNCGGG ---GGCCCCGGG
AP-2alpha_M00469	1.4662e-04	CAGGGCNNCGGG ----SCNNNNGG
ABI4	6.7828e-04	CAGGGCNNCGGG NGNNGCRSCG--
TFAP2A	7.2791e-04	CAGGGCNNCGGG- ----SCNNNNGGC
RE1ASPHYA3	9.5537e-04	CCCGNNGCCCTG -CCGCGCCCATG



6_bp_motif_pair_4



forward

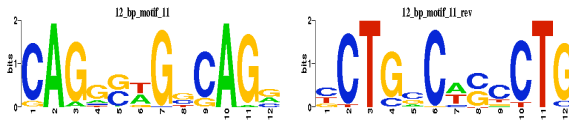
reverse compliment

Name	E value	Alignment
AMMORESVDCRNIA1	1.1915e-05	CAGGGCNCAGGC ---GGCCCCGGG-



brk	2.5673e-05	CAGGGCNCAGGC ---RGCGCCRS--	
MNF1ZMPPC1	6.8275e-05	CAGGGCNCAGGC AAGGGCAC-----	
SZF1-1_M01109	7.1448e-05	-GCCTGGNGCCCTG CNGCTGWTACCTG	
GBOX10NT	1.6285e-04	CAGGGCNCAGGC ---GGCACGTGCC	

12_bp_motif_11

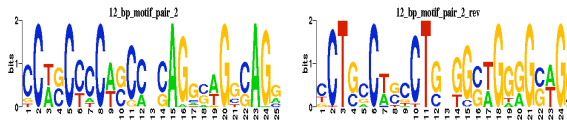


forward

reverse compliment

Name	E value	Alignment	Motif
CAC-binding_M00720	6.8153e-07	NCTGNCWSCCTG ---CCCASCCY-	
PSREGIONZM13	3.9562e-05	-----NCTGNCWSCCTG----- TTTGTCGGCTGCCCGTAGAAATAGTGCCGA	
SZF1-1_M01109	5.6895e-05	--NCTGNCWSCCTG CNGCTGWTACCTG	
Med	1.7322e-04	CAGGSWNCAGN GCGNCNGKSNT	
ABRECE1HVA22	2.3737e-04	CAGGSWNCAGN -CCGGTGGCA--	

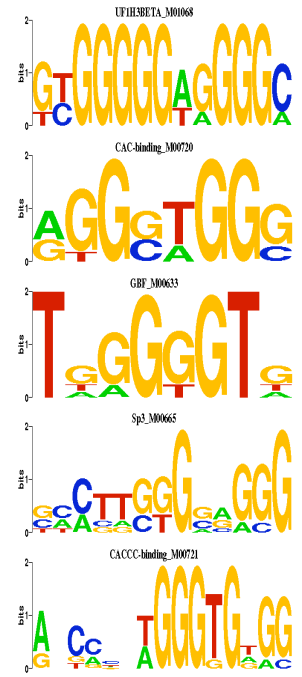
12_bp_motif_pair_2



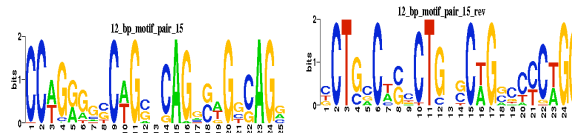
forward

reverse compliment

Name	E value	Alignment
UF1H3BETA_M01068	5.8780e-07	YCTGCCWSCCTGNGGSTGGGGSWGG -----GYGGGGGAGGGGC---
CAC-binding_M00720	1.1830e-05	CCWSCCCCASCCNCAGGSWGGCAGR -----RGGSTGGG---
GBF_M00633	2.1535e-05	CCWSCCCCASCCNCAGGSWGGCAGR -NACCCNA-----
Sp3_M00665	3.0378e-05	CCWSCCCCASCCNCAGGSWGGCAGR ----CCCYSCCAAGKS-----
CACCC-binding_M00721	3.8824e-05	YCTGCCWSCCTGNGGSTGGGGSWGG -----ANCMNNWGGGTGNGG----



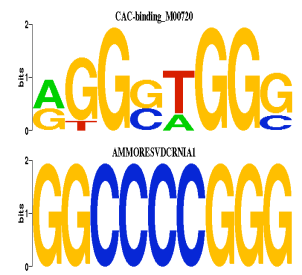
12_bp_motif_pair_15



forward




reverse compliment

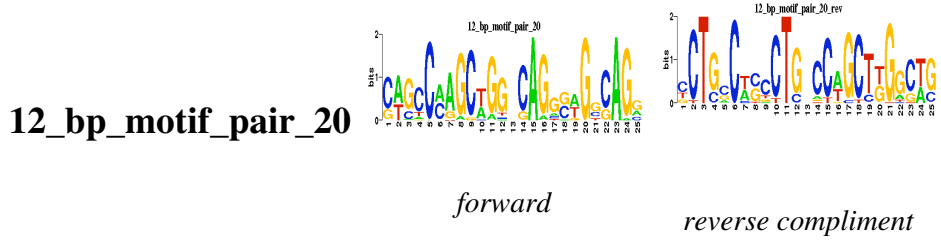
Name	E value	Alignment
CAC-binding_M00720	1.1027e-05	NCTGNCSNCTGNSCWGSCCCWGG ---CCASCY-----
AMMORESVDCRNIA1	6.1940e-05	CCWGGGSCWGSNCAGNSWGNCAGN CCCGGGGCC-----





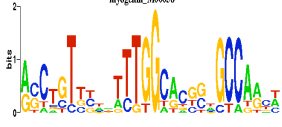


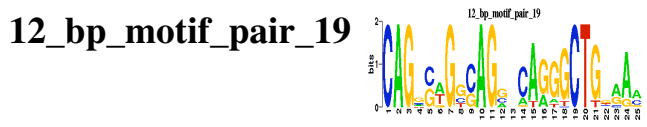
Stamp Results

09/05/08

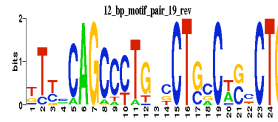
Egr_M00807	3.3475e-04	NCTGNCWSNCTGNSCWGSCCCCWGG -----NYYGCSCCCA--	
Tra-1_M01048	1.8579e-03	NCTGNCWSNCTGNSCWGSCCCCWGG ---ACCWCCC-----	
SITEIOSPCNA	3.2500e-03	NCTGNCWSNCTGNSCWGSCCCCWGG -----CCACCTGG	



<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
HEB_M00698	1.1389e-06	CAGCCMAGCWGGNCAGGSWGSCAGN -----CAGCWGG-----	
YY1_M00069	3.0764e-06	NCTGSCWSCCTGNCCWGCTKGGCTG-- -----NNCNGCCATCTTGNNTSNW	
CAC-binding_M00720	1.1719e-05	NCTGSCWSCCTGNCCWGCTKGGCTG ---CCCASCCY-----	
RIM101	1.7849e-04	NCTGSCWSCCTGNCCWGCTKGGCTG -----CTTGGCA--	
myogenin_M00056	1.8055e-04	-NCTGSCWSCCTGNCCWGCTKGGCTG-- NNYTGGCNSNGTGCCAAANNNNACAGST	

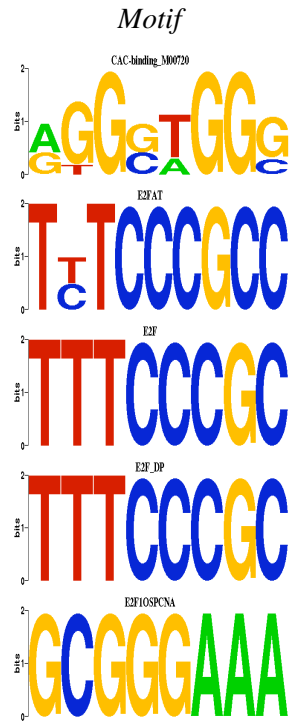


forward

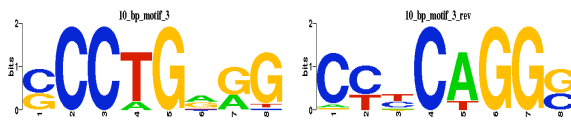


reverse compliment

Name	E value	Alignment
CAC-binding_M00720	3.9732e-06	KTYN CAGCCCTGNNCTGNCWSNCTG -----CC CASC CY-
E2FAT	3.1598e-05	KTYN CAGCCCTGNNCTGNCWSNCTG TYTCCCGCC-----
E2F	1.7928e-04	CAGNSWGN CAGNNCAGGGCTGNRAM -----GCGGGAAA
E2F_DP	1.7928e-04	CAGNSWGN CAGNNCAGGGCTGNRAM -----GCGGGAAA
E2F1OSPCNA	1.7928e-04	KTYN CAGCCCTGNNCTGNCWSNCTG TTTCCCGC-----



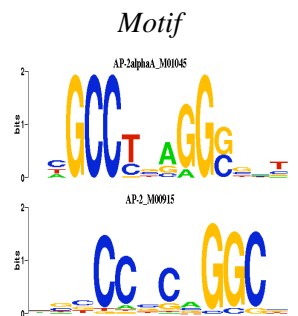
10_bp_motif_3



forward

reverse compliment

Name	E value	Alignment
AP-2alphaA_M01045	1.3359e-07	---SCCTGRGG--- NNNSCCTNAGGCNN
AP-2_M00915	1.6905e-06	---CCYCAGGS- NNNCCNCNGGCN



Stamp Results

09/05/08

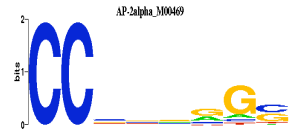
AP-2alphaA_M01047 3.8056e-06

---SCCTGRGG---
ANMGCCTNAGGCKN



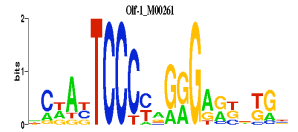
AP-2alpha_M00469 5.6738e-06

SCCTGRGG
SCNNNGG

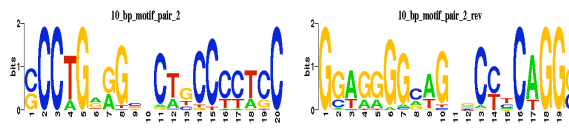


Olf-1_M00261 1.5368e-05

-----SCCTGRGG-----
NCMNNYTCCNRGGGANTNGN



10_bp_motif_pair_2



forward

reverse compliment

Name

E value

Alignment

Motif

TFAP2A

9.5223e-05

SCCTGRGGNCTNCCCCTCC
SCNNNGGC-----



MAZ_M00649

1.3023e-04

SCCTGRGGNCTNCCCCTCC-
-----CCCTCCC



UF1H3BETA_M01068 2.1169e-04

-----GGAGGGGAGNCCYCAGGS
GYGGGGGAGGGGC-----



Dde_M00304

2.8946e-04

SCCTGRGGNCTNCCCCTCC
-----GCTCAGCC-----

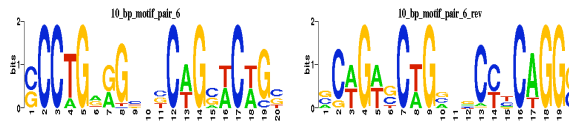


AP-2alphaA_M01047 3.2616e-04

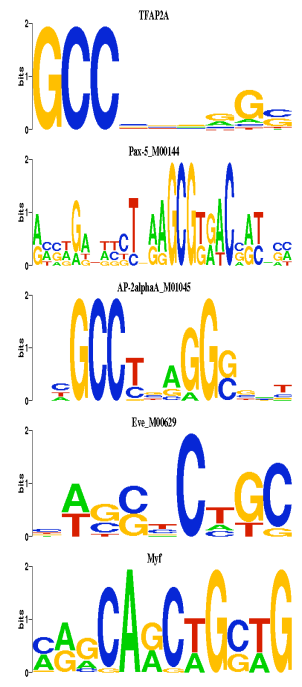
GGAGGGGAGNCCYCAGGS--
-----ANMGCCTNAGGCKN



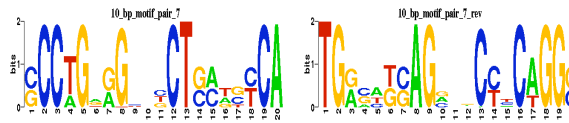
10_bp_motif_pair_6



	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
TFAP2A	9.5223e-05	SCCTGRGGNNNCAGSWCWGN SCNNNNGGC-----
Pax-5_M00144	1.0641e-04	NCWGWSTGNNNCCYCAGGS----- NNNRYNGTYMCGCTYNANNNNNNCNNNY
AP-2alphaA_M01045	4.4591e-04	---SCCTGRGGNNNCAGSWCWGN NNNSCCTNAGGCNN-----
Eve_M00629	4.5758e-04	NCWGWSTGNNNCCYCAGGS GCNGNSSWN-----
Myf	1.6832e-03	NCWGWSTGNNNCCYCAGGS ---CAGCAGYTGCYK-----

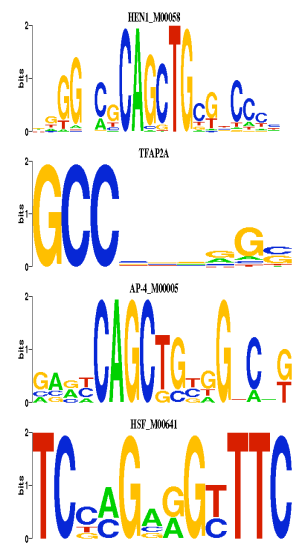


10_bp_motif_pair_7



forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
HEN1_M00058	1.6821e-04	SCCTGNRGNNNCTSMNSYCA- NNNGGNCGCAGCTGCGNCCNN
TFAP2A	2.3207e-04	SCCTGNRGNNNCTSMNSYCA SCNNNNGGC-----
AP-4_M00005	4.5096e-04	-TGRSNKSAGNNNCYNCAGGS MNGNCNNCAGCTGNNNN----
HSF_M00641	7.4432e-04	TGRSNKSAGNNNCYNCAGGS -----GAARCYNCKNGA



Stamp Results

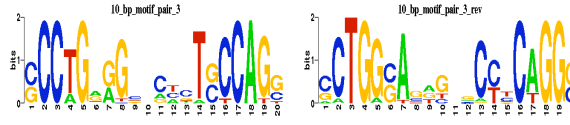
09/05/08

AP-2alphaA_M01045 8.4277e-04

---SCCTGNRGNNNCTSMNSYCA
NNNSCCTNAGGCNN-----



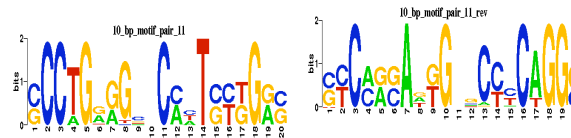
10_bp_motif_pair_3



forward *reverse compliment*

Name	E value	Alignment	Motif
RNFG2OS	1.3046e-07	SCCTGRGGNNC NNTSCCAGS -CCAGGGGCACACTGG----	
ANT	5.3016e-05	SCCTGRGGNNC NNTSCCAGS RCNTNGGGAWNTGTGC----	
TFAP2A	9.5223e-05	SCCTGRGGNNC NNTSCCAGS SCNNNGGC-----	
MAZ_M00649	9.9123e-05	SCCTGRGGNNC NNTSCCAGS -----CCCTCC-----	
NRSE_M00325	2.2171e-04	SCCTGRGGNNC NNTSCCAGS----- -----GGCRCTCTCCNGGTGCTGA	

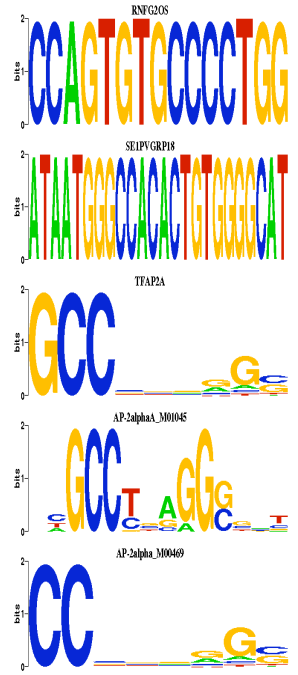
10_bp_motif_pair_11



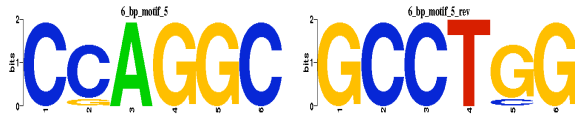
forward *reverse compliment*

Name	E value	Alignment	Motif
------	---------	-----------	-------

RNFG2OS	1.4185e-07	SCCTGRGGNNCMNTSYKGRS -CCAGGGGCACACTGG----
SE1PVGRP18	1.1974e-06	---SYCMRSANKGNCCYCAGGS- ATGCCCCACAGTGTGGCCATTAT
TFAP2A	2.8999e-05	SCCTGRGGNNCMNTSYKGRS SCNNNNGGC-----
AP-2alpha_M01045	4.5518e-04	---SCCTGRGGNNCMNTSYKGRS NNNSCTNAGGCNN-----
AP-2alpha_M00469	6.9137e-04	SCCTGRGGNNCMNTSYKGRS SCNNNNGG-----



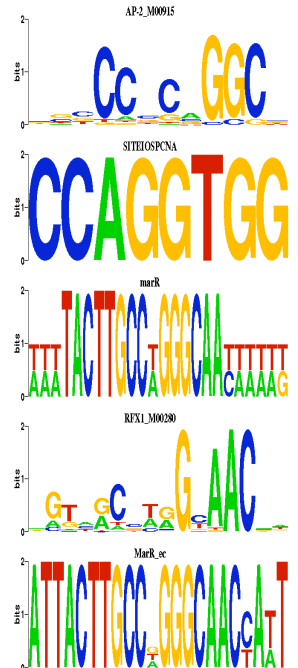
6_bp_motif_5

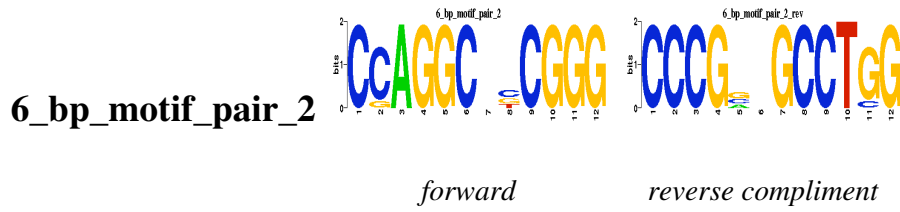


forward

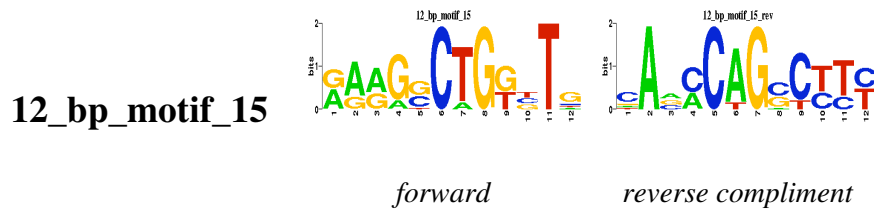
reverse compliment

Name	E value	Alignment
AP-2_M00915	8.6298e-07	-GCCTGG----- NGCCNGNGGNNN
SITEIOSPCNA	1.8811e-05	--GCCTGG CCACCTGG
marR	2.7644e-05	-----CCAGGC----- MWWWWRTTGCCCGGCAAGTAWWW
RFX1_M00280	9.2631e-05	-----CCAGGC----- NNGTTRCYWNGYNACN
MarR_ec	1.2847e-04	-----CCAGGC----- AATGGTTGCCCGGCAAGTAAT



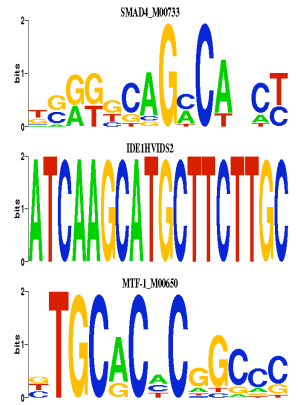


Name	E value	Alignment	Motif
AMMORESVDCRNIA1	4.6282e-09	CCAGGCNNCGGG ---GGCCCCGGG	AMMORESVDCRNIA1 GGCCCCGGGG
AP-2alpha_M00469	9.6236e-05	CCAGGCNNCGGG ----SCNNNNGG	AP-2alpha_M00469 CC
E12_M00693	1.9144e-04	CCCGNNGCCTGG --NNNCACCTGY	E12_M00693 CAGGTG
TFAP2A	4.4692e-04	-CCCGNNGCCTGG SCNNNNGGC----	TFAP2A GCC
NERF1a_M00531	7.4285e-04	----CCCGNNGCCTGG- SNNASNYRCTTCCTGNY	NERF1a_M00531 CAGGAG

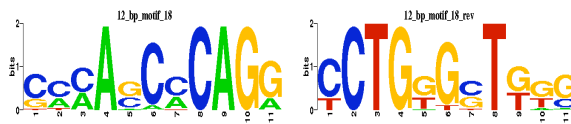


Name	E value	Alignment	Motif
Zec_M01081	1.1421e-07	-CANMCAGSCYTY GCAACCAACCTT-	Zec_M01081 AAGGTTGGTTGC
CAC-binding_M00720	1.1715e-05	RARGSCTGKNTG --RGGSTGGG--	CAC-binding_M00720 AGGTTGGG

SMAD4_M00733	3.7054e-04	RARGSCTGKNTG----- ---RGNTGKCTGNMYSN
IDE1HVIDS2	4.7555e-04	----RARGSCTGKNTG-- GCAAGAAGCATGCTTGAT
MTF-1_M00650	5.5027e-04	RARGSCTGKNTG--- --GGGCCGNGTGCAN



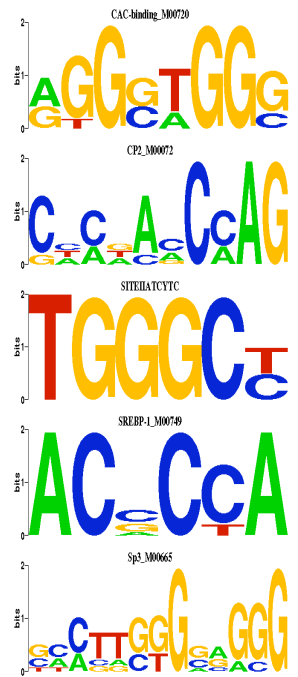
12_bp_motif_18



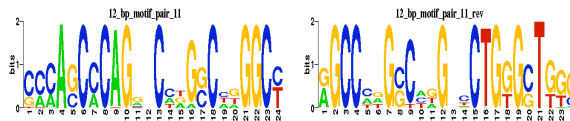
forward

reverse compliment

Name	E value	Alignment
CAC-binding_M00720	1.6676e-07	CMMASCCCAGG CCCASCCY---
CP2_M00072	1.3826e-06	CMMASCCCAGG CNCNAMCCAG-
SITEIIATCYTC	3.3757e-05	CCTGGGSTKKG --TGGGCY---
SREBP-1_M00749	1.5976e-04	CCTGGGSTKKG --TGGSGT---
Sp3_M00665	1.8043e-04	CMMASCCCAGG-- CCCYSCCAAGKS



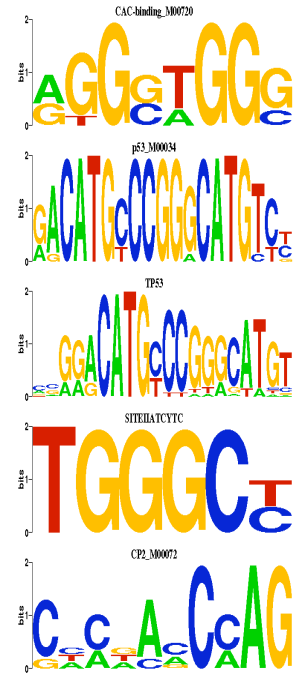
12_bp_motif_pair_11



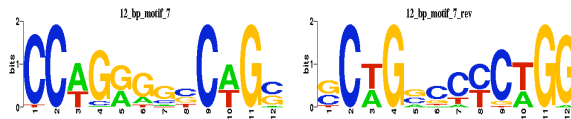
forward *reverse compliment*

Name *E value* *Alignment*

CAC-binding_M00720	2.8114e-06	CCCAGCCCAGNNCNGSCNNGGCY CCCASCCY-----
p53_M00034	3.8528e-06	RGCCNNGSCNNGNCTGGGCTGGG RGACATGCCCGGGCATGTC-----
TP53	1.2026e-04	CCCAGCCCAGNNCNGSCNNGGCY-- -----ACATGCCCGGGCATGTCCNN
SITEIIATCYTC	1.4423e-04	CCCAGCCCAGNNCNGSCNNGGCY ---RGCCA-----
CP2_M00072	2.7922e-04	RGCCNNGSCNNGNCTGGGCTGGG -----CTGGKTNGNG



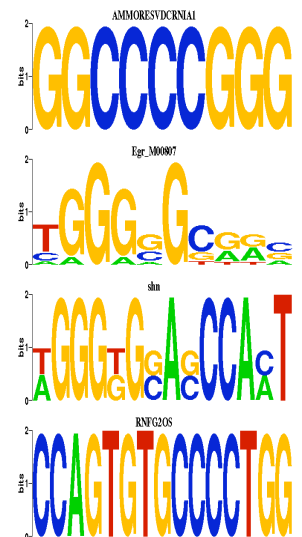
12_bp_motif_7



forward *reverse compliment*

Name *E value* *Alignment*

AMMORESVDCRNIA1	2.1744e-06	CCAGRGGNCWGS CCCGGGGCC---
Egr_M00807	3.4514e-05	CCAGRGGNCWGS --TGGGSGCRRN
shn	1.5434e-04	CCAGRGGNCWGS----- --WGGGKGSASCCAMT
RNFG2OS	1.8675e-04	CCAGRGGNCWGS--- CCAGGGGCACACTGG



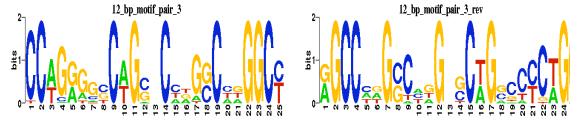
E12_M00693

2.3359e-04

SCWGNCCYCTGG
--NNNCACCTGY



12_bp_motif_pair_3

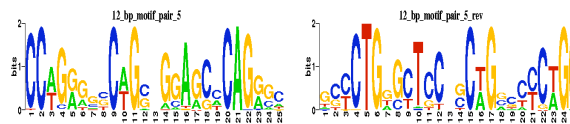


forward

reverse compliment

Name	E value	Alignment	Motif
AMMORESVDCRNIA1	6.4637e-05	CCAGRGGNCWGSNCNNGSCNNGGCY CCCCGGGCC-----	
p53_M00034	2.2341e-04	RGCCNNGSCNNGNSCWGNCCYCTGG RGACATGCCCGGGCATGTC-----	
shn	8.4280e-04	CCAGRGGNCWGSNCNNGSCNNGGCY --WGGGKSASCCAMT-----	
Egr_M00807	8.5401e-04	CCAGRGGNCWGSNCNNGSCNNGGCY --TGGGSGCRRN-----	
SITEIIATCYTC	1.0490e-03	RGCCNNGSCNNGNSCWGNCCYCTGG RGCCCA-----	

12_bp_motif_pair_5



forward

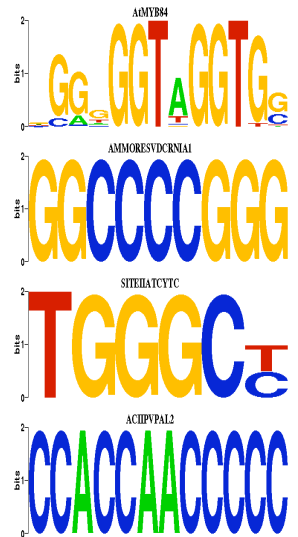
reverse compliment

Name	E value	Alignment	Motif
AtMYB-84_M00970	4.6032e-05	NCYCTGNGCTCCNSCWGNCCYCWGG -----SCACCTACCNCC---	

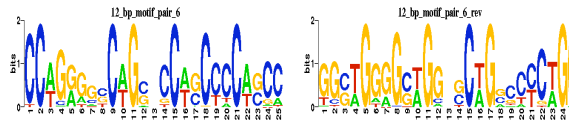
Stamp Results

09/05/08

AtMYB84	1.7757e-04	NCYCTGNGCTCCNSCWGNNCYCWGG -----SCACCTACCNCCN--
AMMORESVDCRNIA1	1.8225e-04	CCWGRGNNCWGSNNGAGCNCAGRGN CCCGGGGCC-----
SITEIIATCYTC	1.9894e-04	CCWGRGNNCWGSNNGAGCNCAGRGN -----RGCCCA-----
ACIIPVPAL2	4.0754e-04	CCWGRGNNCWGSNNGAGCNCAGRGN ---GGGGTTGGTG-----



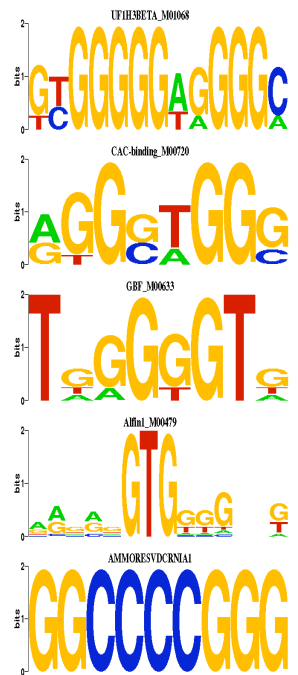
12_bp_motif_pair_6



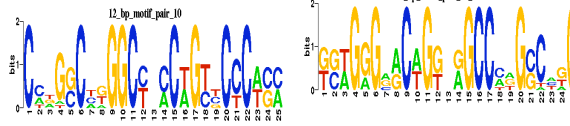
forward

reverse compliment

Name	E value	Alignment	Motif
UF1H3BETA_M01068	5.0526e-08	CCAGRGGNCWGSNCCWSCCCASCC -----GCCCTCCCCRC--	
CAC-binding_M00720	9.9149e-06	CCAGRGGNCWGSNCCWSCCCASCC- -----CCASCY	
GBF_M00633	1.5634e-05	GGSTGGGGSWGGNSCWGNCCYCTGG ---TNGGGGTN-----	
Alfin1_M00479	4.1222e-05	CCAGRGGNCWGSNCCWSCCCASCC -----MNNCCCCACNYNYN---	
AMMORESVDCRNIA1	6.4637e-05	CCAGRGGNCWGSNCCWSCCCASCC CCCGGGGCC-----	



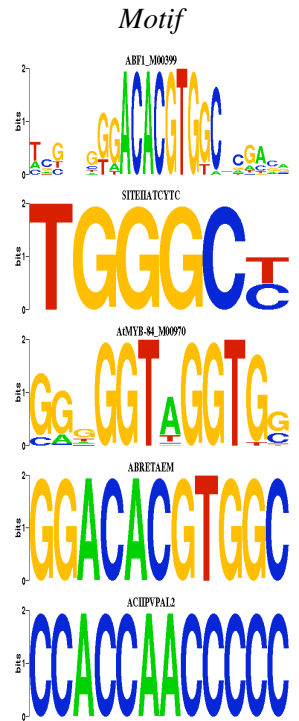
12_bp_motif_pair_10



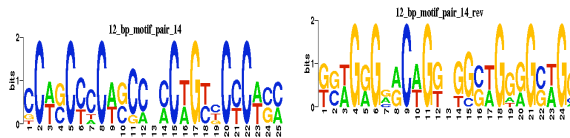
forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
ABF1_M00399	7.8154e-07	-KSWG GGNACWGGNRGCCMNGSCNKG WNNNNGGGACACGTGGC NNGANN----
SITEIIATCYTC	3.8402e-04	KSWG GGNACWGGNRGCCMNGSCNKG -----RGCCA-----
AtMYB-84_M00970	5.7979e-04	KSWG GGNACWGGNRGCCMNGSCNKG ---GGNGGTAGGTGS-----
ABRETAEM	7.2966e-04	CMNGSCNKGGCYNCCWGTNCCCWSM -----GCCACGTGTCC-----
ACIIPVPAL2	1.2457e-03	CMNGSCNKGGCYNCCWGTNCCCWSM -----CCACCAACCC--



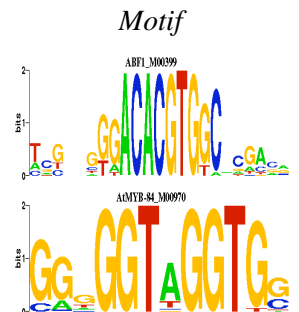
12_bp_motif_pair_14



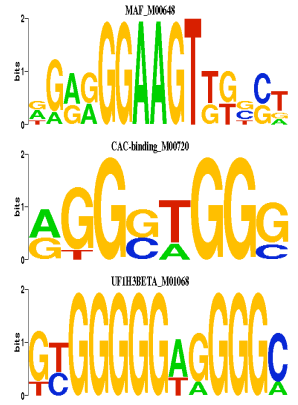
forward

reverse compliment

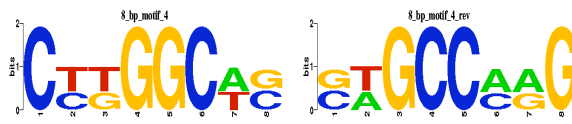
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
ABF1_M00399	3.0672e-06	CCWSCCCCWSSCNCCWGYNCCCWSM- ---NNTCNNGCCACGTGTCCNNNNW
AtMYB-84_M00970	1.0984e-05	CCWSCCCCWSSCNCCWGYNCCCWSM -----SCACCTACCNC--



MAF_M00648	1.7847e-05	CCWSCCCCWSCCNCCWGYNCCCWSM -----NSNMMACTTCCYYCN--
CAC-binding_M00720	2.6707e-05	CCWSCCCCWSCCNCCWGYNCCCWSM -----CCCASCCY-----
UF1H3BETA_M01068	2.9403e-05	CCWSCCCCWSCCNCCWGYNCCCWSM ---GCCCTCCCCRC-----



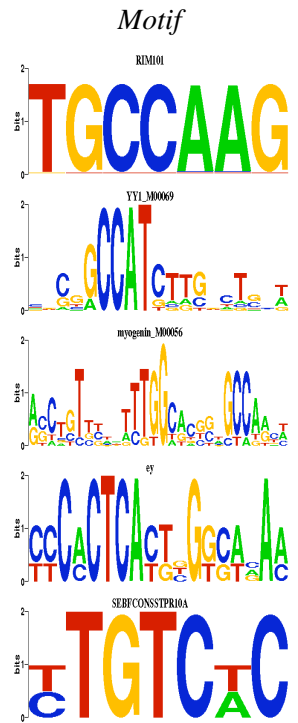
8_bp_motif_4



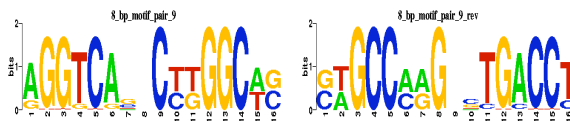
forward





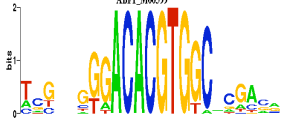
reverse compliment

Name	E value	Alignment	Motif
RIM101	3.2352e-08	SWGCCMRG -TGCCAAG	
YY1_M00069	5.1233e-06	-----CYKGGCWS-- NNCNGCCATCTGNNTSNW	
myogenin_M00056	4.2945e-05	-CYKGGCWS----- NNYTGGCNSNGTGCCAAANNNNACAGST	
ey	8.5762e-05	-----CYKGGCWS-- CCCACACTNGGCANAA	
SEBFCONSSTPR10A	2.4416e-04	CYKGGCWS -YTGTCWC	

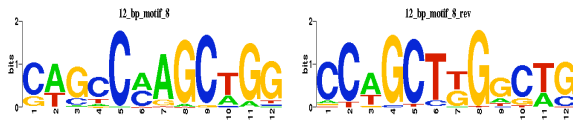






8_bp_motif_pair_9



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
QELEMENTZM13	3.3174e-07	SWGCCMRGNNTGACCT -----TGACCT	
RIM101	4.2516e-06	SWGCCMRGNNTGACCT -TGCCAAG-----	
WBOXNTCHN48	1.9787e-05	AGGTCANNCYKGGCWS -RGTCAG-----	
YML081W	2.7564e-05	AGGTCANNCYKGGCWS --TTCAGACTGG----	
ABF1_M00399	1.9066e-04	----SWGCCMRGNNTGACCT---- NNTCNGCCACGTGTCCNNNNW	

12_bp_motif_8



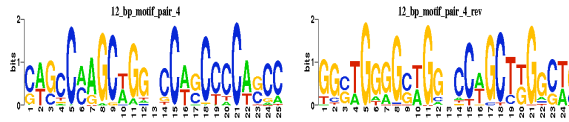
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
YY1_M00069	1.4505e-10	--CAGCCMAGCTGG----- WNSANNCAAGATGGCNGNN	
HEB_M00698	1.2534e-07	CCAGCTKGGCTG CCWGCTG-----	
RBENTGA3	9.6838e-06	-CCAGCTKGGCTG TCCAAC TTGGA--	
RIM101	2.0594e-05	CAGCCMAGCTGG -TGCCAAG-----	

SITEIOSPCNA 2.3403e-05

CCAGCTKGGCTG
CCACCTGG----



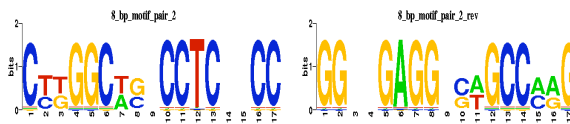
12_bp_motif_pair_4



forward *reverse compliment*

Name	E value	Alignment	Motif
HEB_M00698	1.6500e-06	CAGCCMAGCWGGNCCWSCCCASCC -----CAGCWGG-----	
CAC-binding_M00720	8.4158e-06	CAGCCMAGCWGGNCCWSCCCASCC- -----CCCASCCY	
YY1_M00069	8.5183e-06	--CAGCCMAGCWGGNCCWSCCCASCC WNSANNCAAGATGGCNGNN-----	
GBF_M00633	9.5902e-06	GGSTGGGGSWGGNCCWGCTKGGCTG ---TNGGGGTN-----	
UF1H3BETA_M01068	2.2835e-05	CAGCCMAGCWGGNCCWSCCCASCC -----GCCCTCCCCRC--	

8_bp_motif_pair_2



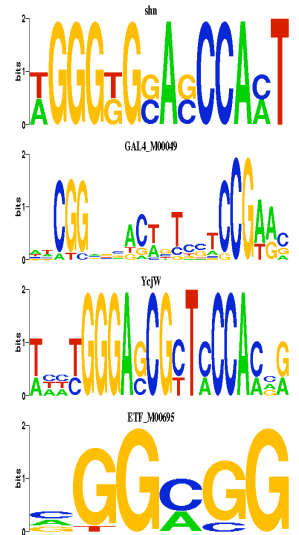
forward *reverse compliment*

Name	E value	Alignment	Motif
RIM101	2.3339e-05	CYKGGCWSNCTCNCC CTTGCA-----	

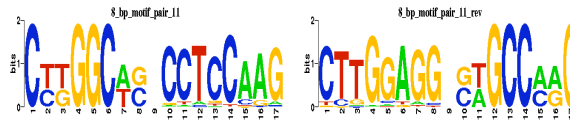
Stamp Results

09/05/08

shn	1.0992e-03	CYKGGCWSNCCTCNNCC AKTGGSTSCMCCCW---
GAL4_M00049	1.1061e-03	----CYKGGCWSNCCTCNNCC- NNCGGNNNACWNTNSTCCGAAS
YejW	1.6221e-03	--GGNNGAGGNSWGCCMRG- CNGTGGGAGCGCTCCCANNA
ETF_M00695	2.0792e-03	CYKGGCWSNCCTCNNCC -----CCGCCN--



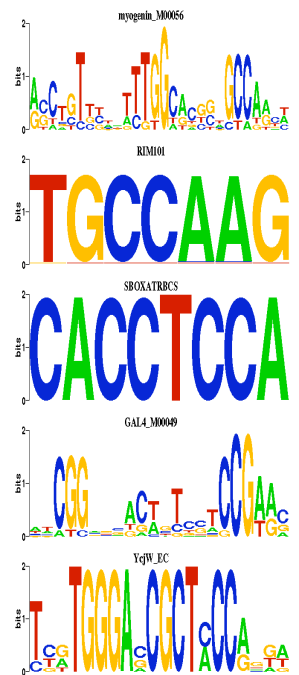
8_bp_motif_pair_11

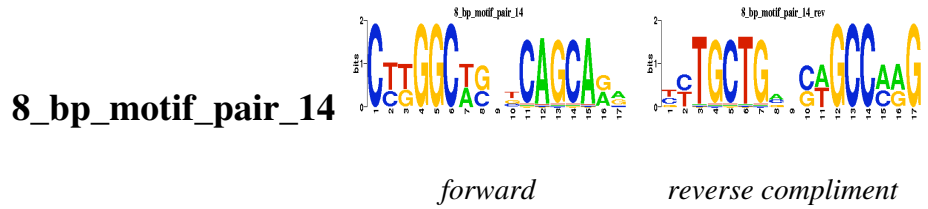


forward

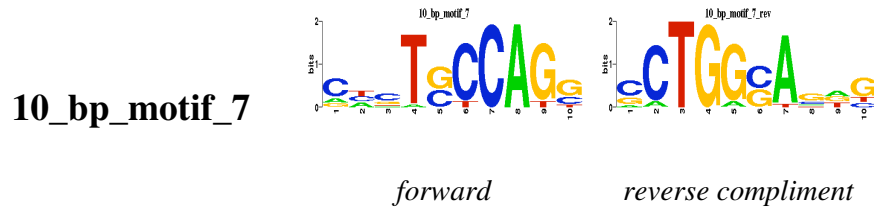
reverse compliment

Name	E value	Alignment
myogenin_M00056	4.0010e-06	-CYKGGCWSNCCTCCAAG----- NNYTGGCNSNGTGCCAAANNNNACAGST
RIM101	5.3733e-06	CTTGGAGGNSWGCCMRG -----TGCCAAG
SBOXATRBCS	7.4658e-06	CTTGGAGGNSWGCCMRG --TGGAGGTG-----
GAL4_M00049	9.0459e-05	-CTTGGAGGNSWGCCMRG---- STTCGGASNANWGTNNNCCGNN
YejW_EC	9.9494e-05	--CTTGGAGGNSWGCCMRG- WMNTGGKAGCGSTCCCAIRA



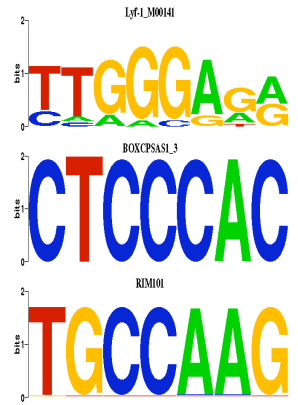


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ABF1_M00401	2.3310e-06	-----CTKGGCWGNNCAGCARR----- GYCNCNNKGCCACGTCANCNANNMGA	
RIM101	1.3440e-05	CTKGGCWGNNCAGCARR CTTGGCA-----	
LMAF_M01139	2.2791e-05	CTKGGCWGNNCAGCARR -----STCAGCAG-	
SMb20667	2.9473e-05	-CTKGGCWGNNCAGCARR-- GGTTGGCAGCGCTGCCAAAA	
myogenin_M00056	1.3140e-04	-CTKGGCWGNNCAGCARR----- NNYTGGCNSNGTGCCAAANNNACAGST	

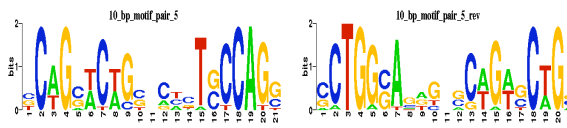


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAZ_M00649	8.8708e-06	CCTGGSANNG ---GGGAGGG	
TGIF_M00418	1.1810e-05	CNNTSCCAGG WNTTGACAGC	

Lyf-1_M00141	1.7915e-05	CNNTSCCAGG -YCTCCCAA-
BOXCPSAS1_3	6.0222e-05	CCTGGSANNG -GTGGGAG--
RIM101	2.3195e-04	CCTGGSANNG CTTGCA---

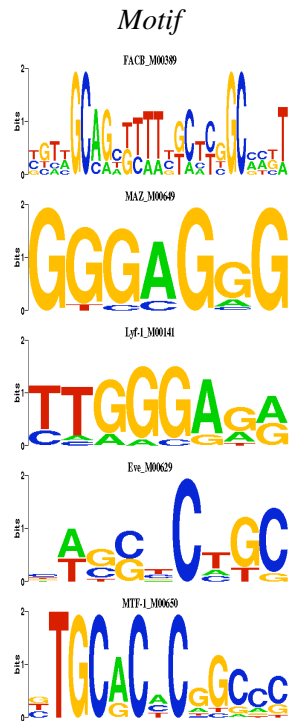


10_bp_motif_pair_5

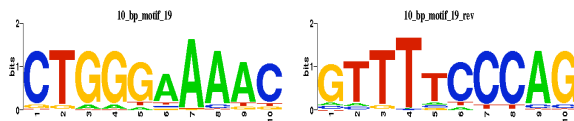


forward *reverse compliment*

Name	E value	Alignment
FACB_M00389	4.1058e-05	SCTGGSANNGNSCWGWSCTGN---- ANNNGCNRNGMNAAAMNCTGCNNNN
MAZ_M00649	8.7642e-05	NCAGSWCWGSNCNNTSCCAGS -----CCCTCCC---
Lyf-1_M00141	2.2747e-04	NCAGSWCWGSNCNNTSCCAGS -----YCTCCCAA-
Eve_M00629	3.0981e-04	SCTGGSANNGNSCWGWSCTGN -----GCNGSSWN-
MTF-1_M00650	4.6558e-04	SCTGGSANNGNSCWGWSCTGN --GGCCGNGTGCAN-----

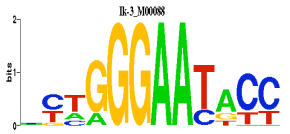






10_bp_motif_19

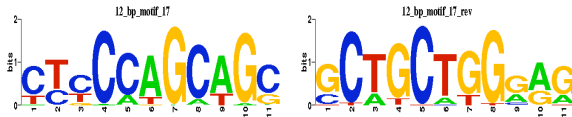


forward *reverse compliment*

Name *E value* *Alignment* *Motif*




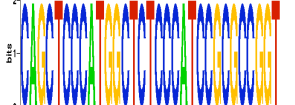
Ik-3_M00088	4.0042e-09	-CTGGGAAAAC- NYNGGGAAATACC	
dl	3.0991e-07	CTGGGAAAAC-- --NGGAAAAAYCC	
E2Ff_oneSite	5.8588e-07	GTTTTCCCAG- -TTTTCCCGCG	
dl_M00120	6.3839e-07	--GTTTTCCCAG NGNTTTCYC--	
dl_M00043	5.3707e-06	CTGGGAAAAC- -NGGAAAACC	

12_bp_motif_17



forward *reverse compliment*

Name *E value* *Alignment* *Motif*

ANAERO2CONSENSUS	1.8588e-07	GCTGCTGGGAG GCTGCT-----	
HEB_M00698	7.9932e-06	GCTGCTGGGAG -CAGCWGG---	
TAL1_M00993	1.8067e-05	-GCTGCTGGGAG RNCAGNTGG---	
PE3ASPHYA3	1.8685e-05	-----GCTGCTGGGAG----- ACCGGCGCGGATGGGAGAGCCATGGGAGCTG	

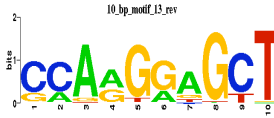
BOXCPSAS1_3

2.2854e-05

GCTGCTGGGAG
 ----GTGGGAG



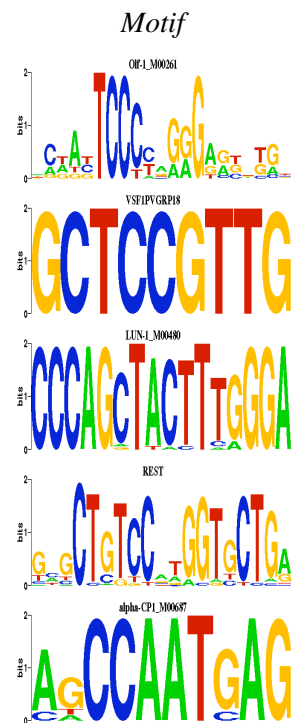
10_bp_motif_13



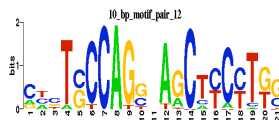
forward

reverse compliment

Name	E value	Alignment
Olf-1_M00261	4.6381e-06	---AGCTCCYTGG----- NCMNNYTCNCRGGGANTNGN
VSF1PVGRP18	1.0736e-05	CCARGGAGCT CAACGGAGC-
LUN-1_M00480	1.6897e-05	---CCARGGAGCT--- TCCCAAAGTAGCTGGG
REST	2.1974e-05	--AGCTCCYTGG----- TCAGCACCWNGGACAGCNC
alpha-CP1_M00687	5.8885e-05	AGCTCCYTGG-- --CTCATTGGCT



10_bp_motif_pair_12

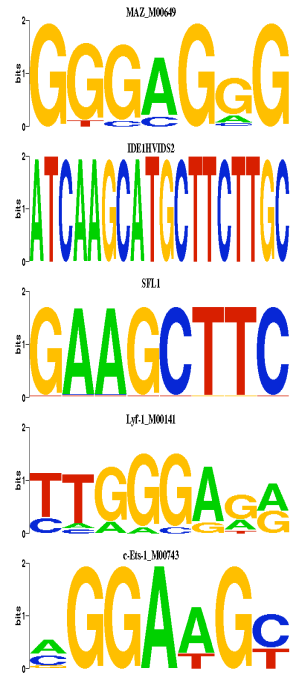


forward

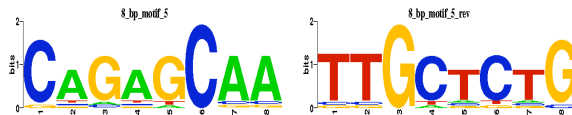
reverse compliment

Name	E value	Alignment	Motif
------	---------	-----------	-------

MAZ_M00649	5.4899e-05	CNNTSCCAGSNAGCTYCYTKG CCCTCCC-----
IDE1HVIDS2	5.6658e-05	CMARGRAGCTNSCTGGSANNG GCAAGAAGCATGCTTGAT---
SFL1	1.0766e-04	CNNTSCCAGSNAGCTYCYTKG -----GAAGCTTC----
Lyf-1_M00141	1.0823e-04	CNNTSCCAGSNAGCTYCYTKG -YCTCCCAA-----
c-Ets-1_M00743	1.3911e-04	CNNTSCCAGSNAGCTYCYTKG -----GCTTCK--



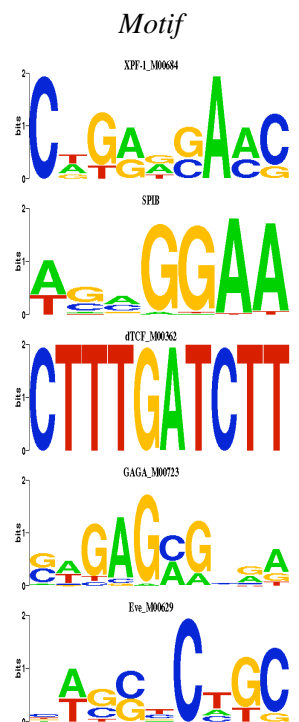
8_bp_motif_5

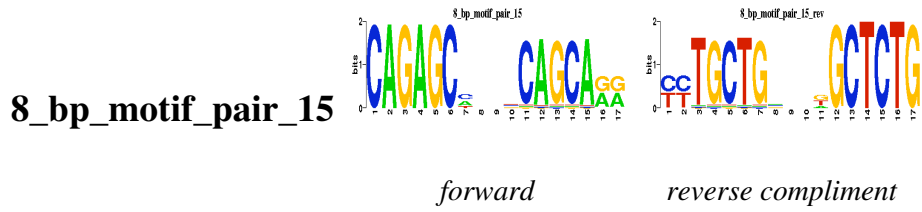


forward

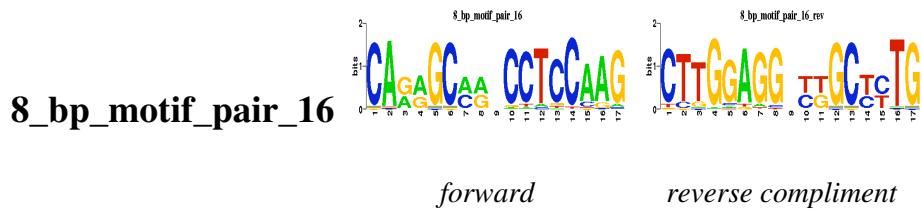
reverse compliment

Name	E value	Alignment
XPF-1_M00684	6.2916e-06	-TTGCTCTG GKTSNYCNG
SPIB	5.3064e-05	TTGCTCTG TTCKST-
dTCF_M00362	7.7097e-05	CAGAGCAA-- AAGATCAAAG
GAGA_M00723	9.5163e-05	TTGCTCTG-- TYNCKCTCWS
Eve_M00629	1.6344e-04	-CAGAGCAA GCNGNSSWN



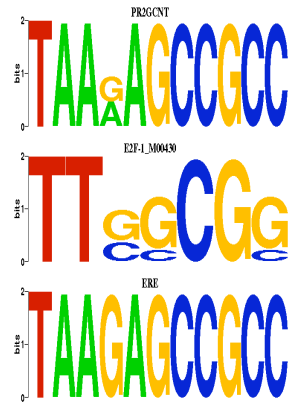


Name	E value	Alignment	Motif
HEB_M00698	1.6251e-04	CAGAGCNNNNCAGCARR -----CAGCWGG	
LMAF_M01139	2.6943e-04	YYTGCTGNNNNGCTCTG -CTGCTGAS-----	
fadR	4.0132e-04	--CAGAGCNNNNCAGCARR WANWNRTCNGACCAGYT--	
CP2-LBP-1c-LSF_M00947	5.5934e-04	-CAGAGCNNNNCAGCARR CNRGNNNNANCCAG----	
SMb20537	1.1700e-03	--YYTGCTGNNNNGCTCTG- TTCTTGCAAATTTGCATTGT	

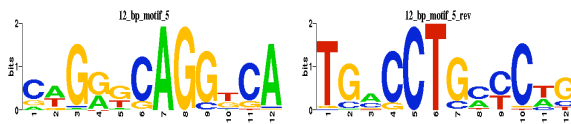


Name	E value	Alignment	Motif
SMb20537	6.1242e-05	--CTTGAGGNYKGCYYTG- TTCTTGCAAATTTGCATTGT	
SBOXATRBCS	2.3164e-04	CTTGAGGNYKGCYYTG --TGGAGGTG-----	

PR2GCNT	8.0193e-04	CTTGGAGGNYKGCYYTG- -----GGCGGCTYTTA
E2F-1_M00430	1.0160e-03	CTTGGAGGNYKGCYYTG -TTSGCGG-----
ERE	1.5300e-03	CTTGGAGGNYKGCYYTG- -----GGCGGCTCTTA



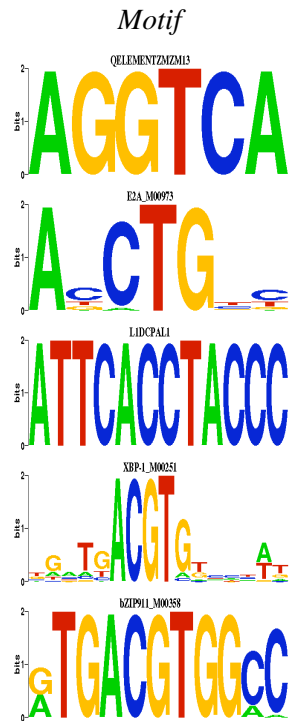
12_bp_motif_5



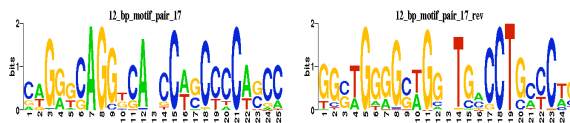
forward






reverse compliment

Name	E value	Alignment
QELEMENTZMZM13	4.1080e-07	TGMCCTGMCCWG TGACCT-----
E2A_M00973	4.7104e-06	TGMCCTGMCCWG --ANCTGNY---
L1DCPAL1	8.8197e-05	CWGGKCAGGKCA-- --GGGTAGGTGAAT
XBP-1_M00251	1.7425e-04	-CWGGKCAGGKCA--- NWNNNMCACGTCANCN
bZIP911_M00358	1.7861e-04	-TGMCCCTGMCCWG RTGACGTGGCC--

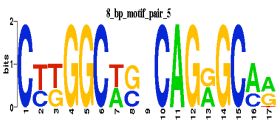


12_bp_motif_pair_17

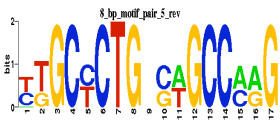


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD4_M00733	1.4426e-06	GGSTGGGGSWGGNTGMCCTGCCCWG -----RGNTGKCTGNMYSN-----	
PPARgamma-RXRalpha,_M00515	2.1745e-06	CWGGGCAGGKCANCCWSCCCASCSCC --AANTAGGTCACNGTGACCTAST--	
CAC-binding_M00720	8.4158e-06	CWGGGCAGGKCANCCWSCCCASCSCC- -----CCASCSCCY	
GBF_M00633	9.5902e-06	GGSTGGGGSWGGNTGMCCTGCCCWG ---TNGGGGTN-----	
PPARG	9.9465e-06	CWGGGCAGGKCANCCWSCCCASCSCC ---ANTRGGTCACNNTGACCTAN---	

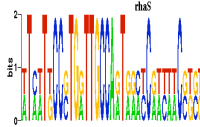

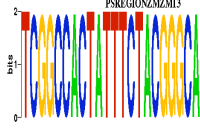

8_bp_motif_pair_5



forward



reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
rhaS	3.3835e-07	-----CYKGGCWSNCAGRGCAR----- MCYTTCKCSTKWKYSMSMSGWRRWYGRKYAYTGCAAYCASGGMAWKAW	
RIM101	1.9865e-05	CYKGGCWSNCAGRGCAR CTTGCA-----	
PSREGIONZMZM13	3.6899e-05	YTGCYCTGNSWGCCMRG----- TTTGTCTGGCTGCCCGTAGAAATAGTGGCCGA	
RFX1	1.2147e-04	-YTGCYCTGNSWGCCMRG GTINCCATGRCAAC----	

Stamp Results

09/05/08

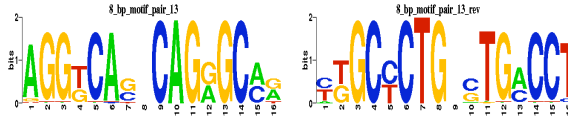
TGIF_M00418

1.9063e-04

YTGCYCTGNSWGCCMRG
 ---WNTGACAGC----



8_bp_motif_pair_13

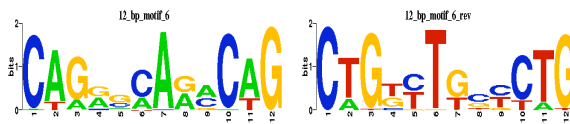


forward

reverse compliment

Name	E value	Alignment	Motif
QELEMENTZM3	1.0747e-06	AGGTCASNCAGRGC MR AGGTC A-----	
PSREGIONZM3	5.5893e-05	YKGCYCTGNSTGACCT----- TTTGTCTGGCTGCCCGTAGAAATAGTGGCCGA	
WBOXNTCHN48	1.1324e-04	YKGCYCTGNSTGACCT -----CTGACY-	
ESR1	1.2763e-04	YKGCYCTGNSTGACCT-- NNGGYCANNGTGACCTNN	
MYB1_twoSite	1.6552e-04	YKGCYCTGNSTGACCT ----YCTAACTGM---	

12_bp_motif_6

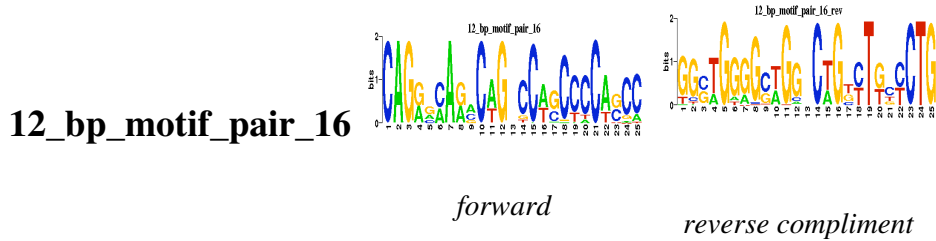
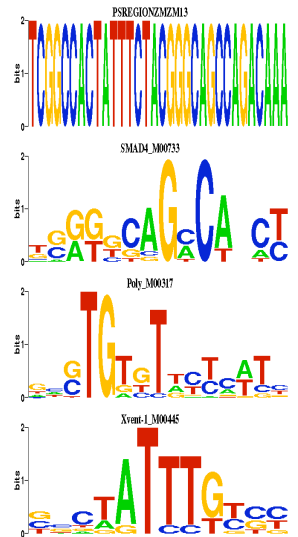


forward

reverse compliment

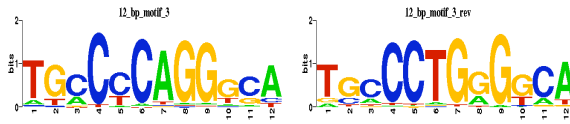
Name	E value	Alignment	Motif
MarR_ec	1.5630e-06	-CTGKYTGNYCTG----- AATGGTTGCCCGGCAAGTAAT	

PSREGIONZM3	6.8940e-06	-----CAGRNCARMCAG----- TCGGCCACTATTTCTACGGGCAGCCAGACAAA
SMAD4_M00733	2.2637e-05	--CTGKYTGNYCTG RGNTGKCTGNMYSN
Poly_M00317	2.7338e-05	--CTGKYTGNYCTG-- NNSTGKTNYMWTN
Xvent-1_M00445	6.7518e-05	CAGRNCARMCAG-- --RSRCAAATAGNN



<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CAC-binding_M00720	6.8703e-06	CAGRNCARMCAGNCCWCCCCASCC-- -----CCASCCY	
GBF_M00633	1.0385e-05	GGSTGGGGCWGGNCTGKYTGNYCTG ---TNGGGGTN-----	
Alfin1_M00479	4.3747e-05	---GGSTGGGGCWGGNCTGKYTGNYCTG NRNRNGTGGGGNNK-----	
RREB1	1.3217e-04	-GGSTGGGGCWGGNCTGKYTGNYCTG NGKKKGKGGTGKTTTGGG-----	
Bel-1_M00312	3.4916e-04	---GGSTGGGGCWGGNCTGKYTGNYCTG ANCTGCTGAYRCWGMGNKNACTNYCNM-	

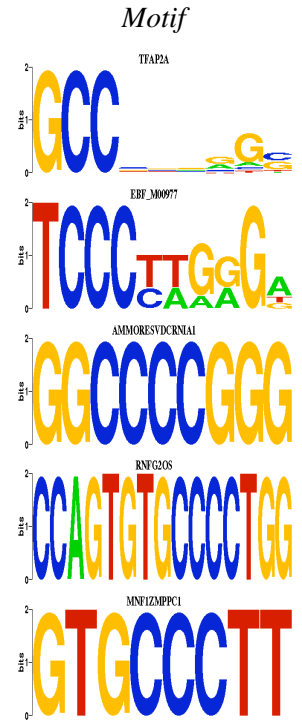
12_bp_motif_3



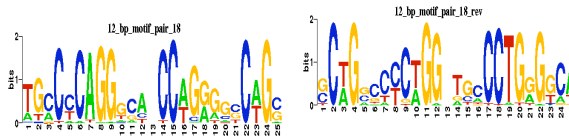
forward

reverse compliment

Name	E value	Alignment
TFAP2A	2.3702e-06	TGCCCCAGGGCA --SCNNNNGGC--
EBF_M00977	6.5711e-06	TGCCCCAGGGCA --NCYCWRGGGA
AMMORESVDCRNIA1	1.6370e-05	TGCCCCAGGGCA ---CCCGGGGCC
RNFG2OS	3.9118e-05	TGCCCTGGGGCA----- ---CCAGGGGCACACTGG
MNF1ZMPPC1	6.8460e-05	-TGCCCTGGGGCA GTGCCCTT-----



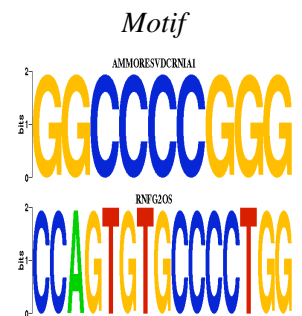
12_bp_motif_pair_18



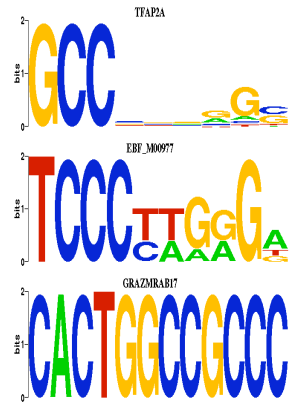
forward

reverse compliment

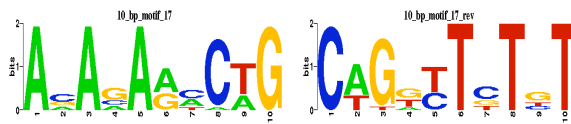
Name	E value	Alignment
AMMORESVDCRNIA1	6.4637e-05	TGCCYCAGGGCANCCAGRGGNCWGS -----CCCGGGGCC---
RNFG2OS	7.4941e-05	TGCCYCAGGGCANCCAGRGGNCWGS ---CCAGGGGCACACTGG-----



TFAP2A	9.7120e-05	TGCCYCAGGGCANCCAGRGGNCWGS --SCNNNGGC-----
EBF_M00977	2.3643e-04	TGCCYCAGGGCANCCAGRGGNCWGS --NCYCWRGGGA-----
GRAZMRAB17	3.2397e-04	SCWGNCCYCTGGNTGCCCTGRGGCA -----CACTGGCCGCC-----



10_bp_motif_17

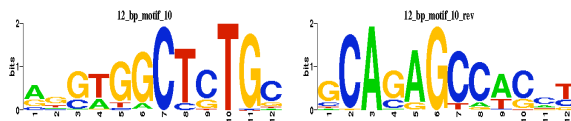


forward

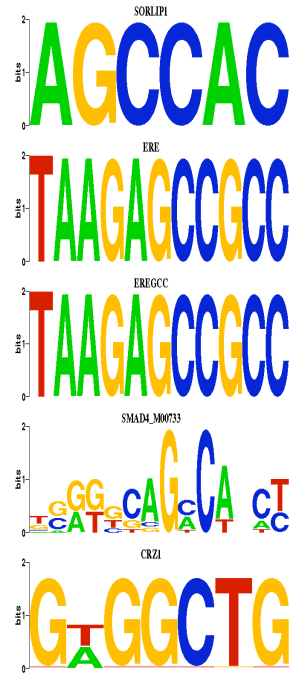
reverse compliment

Name	E value	Alignment	Motif
grh	6.7987e-07	ANANARMCTG RNNRAACCAG	
ICSBP_M00699	1.7047e-05	CAGKYTNTNT- CAGTTTCAYTT	
GARE2	1.1682e-04	-CAGKYTNTNT- CCRGANTYTGTAY	
HSF_M00168	2.7491e-04	--CAGKYTNTNT-- NGAANNTTCNNTTC	
rpoE	3.7531e-04	-----CAGKYTNTNT----- NNNTTNNTCAGANTGTNTTTTATCCTNAAGTTCCG	

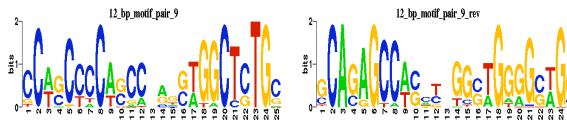
12_bp_motif_10



	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
SORLIP1	3.9455e-07	GCAGAGCCACNY ----AGCCAC--
ERE	4.4235e-06	RNGTGGCTCTGC -GGCGGCTCTTA
EREGCC	4.4235e-06	RNGTGGCTCTGC -GGCGGCTCTTA
SMAD4_M00733	1.4433e-05	RNGTGGCTCTGC-- RGNTGKCTGNMYSN
CRZ1	1.9905e-05	GCAGAGCCACNY ---CAGCCWC--

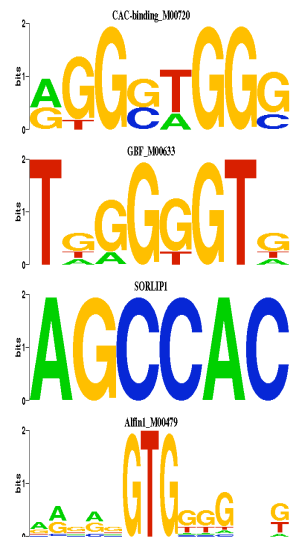


12_bp_motif_pair_9



forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
CAC-binding_M00720	8.4158e-06	CCWSCCCCASCCNRNSTGGCTCTGC -----CCCASCCY-----
GBF_M00633	9.5902e-06	GCAGAGCCASNYNGGSTGGGGSWGG -----TNGGGGTN--
SORLIP1	2.6696e-05	CCWSCCCCASCCNRNSTGGCTCTGC -----GTGGCT-----
Alfin1_M00479	8.3938e-05	CCWSCCCCASCCNRNSTGGCTCTGC -MNNCCCCACNYYN-----



Stamp Results

09/05/08

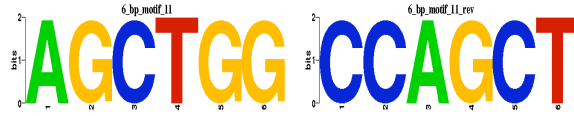
Roaz

1.0029e-04

GCAGAGCCASNYNGGSTGGGGSWGG
 -----GSMCCYARGGKNC-----



6_bp_motif_11

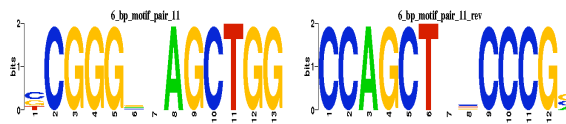


forward

reverse compliment

Name	E value	Alignment	Motif
HEB_M00698	7.5905e-09	-AGCTGG CAGCWGG	
AP-4_M00176	4.1156e-08	-CCAGCT-- NNCAGCTGN	
LBP-1_M00644	1.1346e-07	CCAGCT SCAGCN	
LUN-1_M00480	2.3287e-07	-----AGCTGG- TCCCAAAGTAGCTGGG	
TAL1_M00993	7.7875e-07	---AGCTGG RNCAGNTGG	

6_bp_motif_pair_11

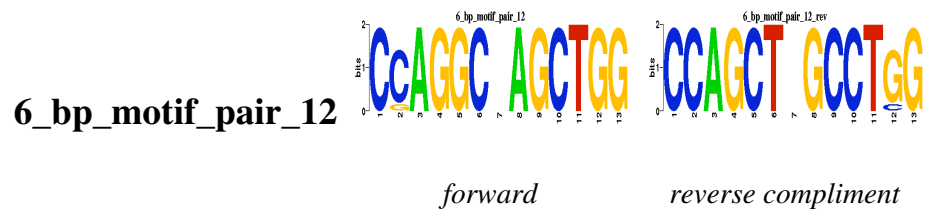
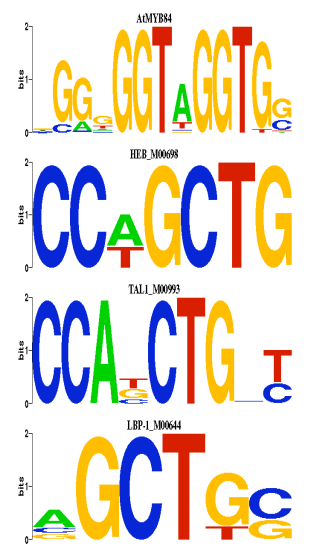


forward

reverse compliment

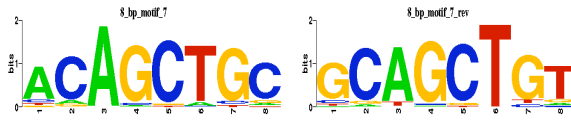
Name	E value	Alignment	Motif
AtMYB-84_M00970	2.9306e-07	NCGGGNNAGCTGG -GGNGGTAGGTGS	

AtMYB84	1.0492e-06	NCGGGNNAGCTGG NNGNGGTAGGTGS
HEB_M00698	2.4358e-05	NCGGGNNAGCTGG -----CAGCWGG
TAL1_M00993	2.8594e-05	NCGGGNNAGCTGG ----RNCAGNTGG
LBP-1_M00644	4.5927e-05	CCAGCTNNCCCGN SCAGCN-----



Name	E value	Alignment	Motif
LEGUMINBOXLEGA5	2.6417e-06	-----CCAGCTNGCCTGG----- GACATTCTKCAGYWTGCATGGCTATGGA	
LUN-1_M00480	1.7387e-05	--CCAGGCNAGCTGG-- TCCCAAAGTAGCTGGG	
AhR_M00139	2.3348e-05	--CCAGGCNAGCTGG-- TSTCACGCNASNYNGRG	
HEB_M00698	2.4358e-05	CCAGGCNAGCTGG -----CAGCWGG	
PE3ASPHYA3	3.4402e-05	CCAGCTNGCCTGG----- -CAGCTCCCATGGCTCTCCCATCCGCGCCGGT	

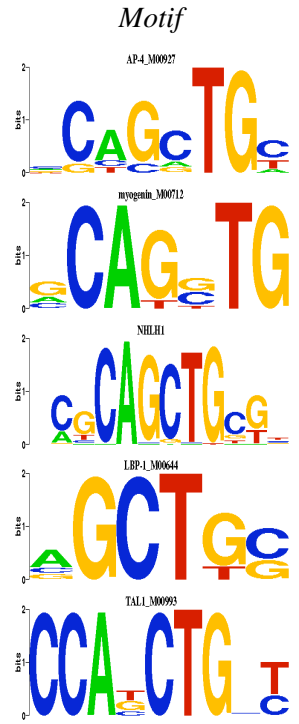
8_bp_motif_7



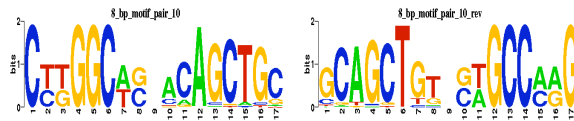
forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
AP-4_M00927	2.0371e-09	GCAGCTGT RCAGCTGN
myogenin_M00712	2.5841e-09	ACAGCTGC -CASCTGN
NHLH1	5.2790e-08	--GCAGCTGT-- NCGCAGCTGCGN
LBP-1_M00644	6.2764e-08	GCAGCTGT SCAGCN--
TAL1_M00993	1.4780e-07	-GCAGCTGT RNCAGNTGG



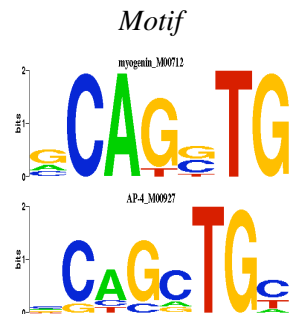
8_bp_motif_pair_10



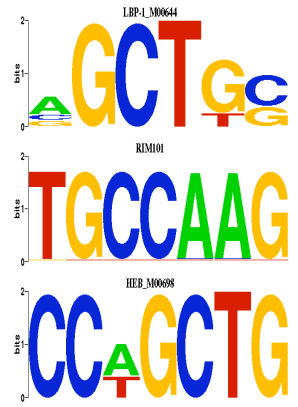
forward

reverse compliment

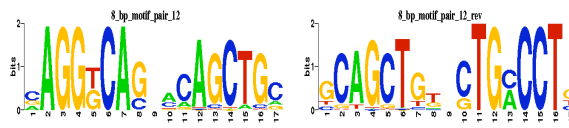
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
myogenin_M00712	6.4628e-07	GCAGCTGTNSWGCCMRG NCAGSTG-----
AP-4_M00927	2.5859e-06	GCAGCTGTNSWGCCMRG RCAGCTGN-----



LBP-1_M00644	2.8269e-06	GCAGCTGTNSWGCCMRG SCAGCN-----
RIM101	5.3733e-06	GCAGCTGTNSWGCCMRG -----TGCCAAG
HEB_M00698	6.4936e-05	GCAGCTGTNSWGCCMRG CCWGCTG-----



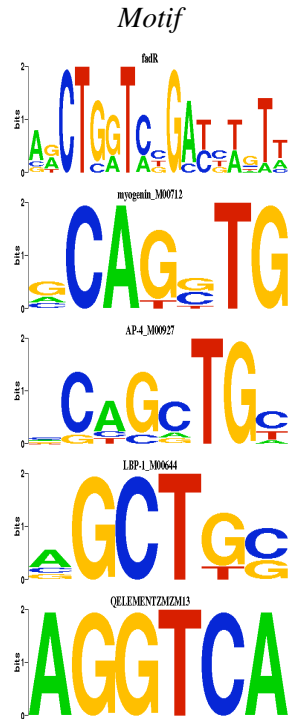
8_bp_motif_pair_12



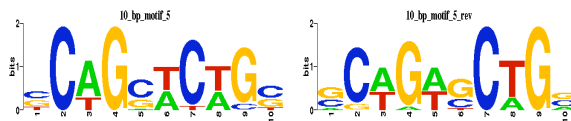
forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
fadR	8.3766e-07	GCAGCTGKNCTGMCCTN-- --ARCTGGTCNGAYNWNTW
myogenin_M00712	9.8346e-07	GCAGCTGKNCTGMCCTN NCAGSTG-----
AP-4_M00927	3.2181e-06	GCAGCTGKNCTGMCCTN RCAGCTGN-----
LBP-1_M00644	4.1196e-06	GCAGCTGKNCTGMCCTN SCAGCN-----
QELEMENTZM13	1.0424e-05	GCAGCTGKNCTGMCCTN -----TGACCT-

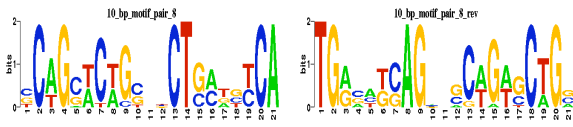


10_bp_motif_5



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Eve_M00629	2.5169e-06	SCWGWGCTGN GCNGNSSWN-	
Dde_M00304	2.4450e-05	NCAGCWCWGS- ---GCTCAGCC	
Sry-beta_M00666	3.5655e-05	NCAGCWCWGS GCATCWCT--	
SMb20667	5.0651e-05	-----NCAGCWCWGS----- GGTTGGCAGCGCTGCCAAAA	
D4GMAUX28	6.2154e-05	NCAGCWCWGS ACAGCACTA-	

10_bp_motif_pair_8



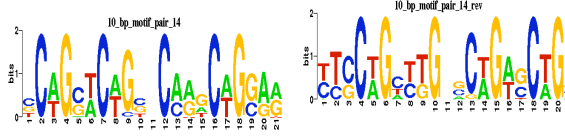
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Eve_M00629	1.8556e-04	TGRNNKCAGNNSCWGWGCTGN -----GCNGNSSWN-	
Myf	5.1490e-04	NCAGCWCWGSNNCTGMNNYCA -----CAGCAGYTGCYK---	
Dde_M00304	6.8358e-04	NCAGCWCWGSNNCTGMNNYCA ---GCTCAGCC-----	
Sry-beta_M00666	9.3272e-04	NCAGCWCWGSNNCTGMNNYCA GCATCWCT-----	

LBP-1_M00644 1.2135e-03

NCAGCWCWGSNNCTGMNNYCA
SCAGCN-----



10_bp_motif_pair_14

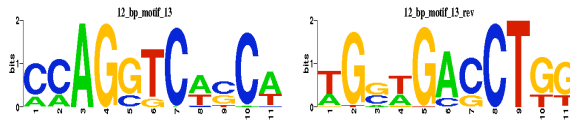


forward

reverse compliment

Name	E value	Alignment	Motif
Eve_M00629	2.2152e-04	YTCCWGYYTGNNCWGWSC TGN -----GCNGNSSWN-	
HEB_M00698	3.6926e-04	NCAGSWCWGNNCARRCWGGAR -----CAGCWGG--	
Dde_M00304	8.2179e-04	YTCCWGYYTGNNCWGWSC TGN -----GGCTGAGC---	
CDC5_M00361	9.5759e-04	YTCCWGYYTGNNCWGWSC TGN -----NSCGCTGAGS---	
LBP-1_M00644	1.2875e-03	YTCCWGYYTGNNCWGWSC TGN --SCAGCN-----	

12_bp_motif_13

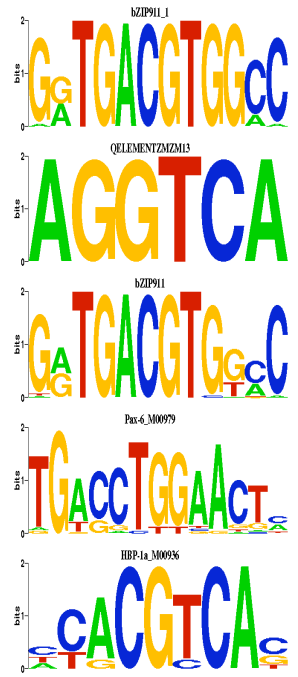


forward

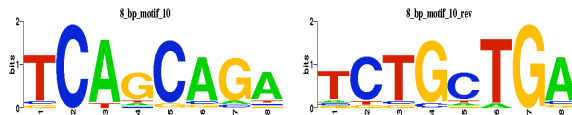
reverse compliment

Name	E value	Alignment	Motif
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bZIP911_1	3.6010e-07	TGSWGACCTGG-- -GRTGACGTGGCC
QELEMENTZM3	4.7185e-07	CCAGGTCWSCA --AGGTCA---
bZIP911	5.9518e-07	--CCAGGTCWSCA GGCCACGTCAYC-
Pax-6_M00979	8.1651e-07	-----CCAGGTCWSCA KAGTTCCAGGTCA---
HBP-1a_M00936	8.7844e-07	CCAGGTCWSCA NCACGTCAS--



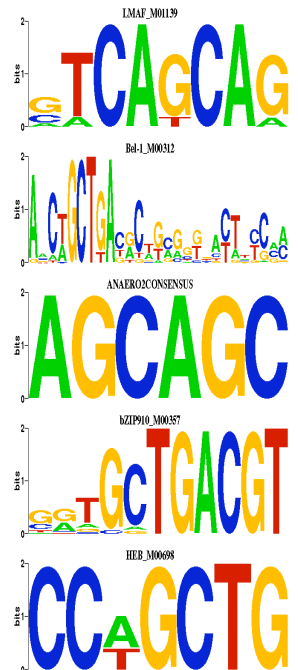
8_bp_motif_10

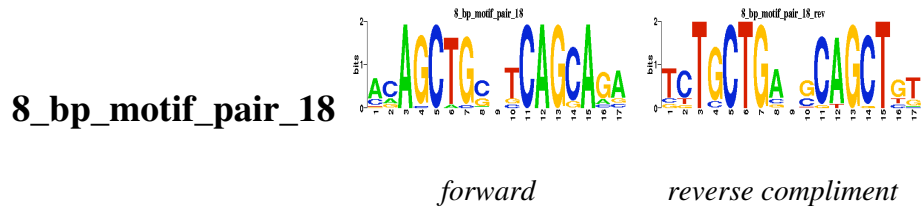


forward

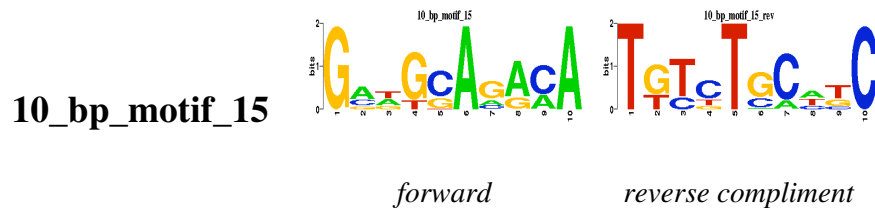
reverse compliment

Name	E value	Alignment	Motif
LMAF_M01139	4.8101e-10	-TCAGCAGA STCAGCAG-	
Bel-1_M00312	8.3565e-06	-TCTGCTGA----- ANCTGCTGAYRCWGMGNKNACTNYCNM	
ANAERO2CONSENSUS	1.9611e-05	TCTGCTGA GCTGCT--	
bZIP910_M00357	2.8962e-05	---TCAGCAGA ACGTCAGCAYS	
HEB_M00698	3.9071e-05	TCAGCAGA -CAGCWGG	



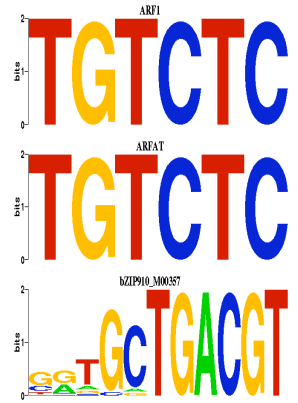


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Bel-1_M00312	6.8351e-09	-TCTGCTGANGCAGCTGT----- ANCTGCTGAYRCWGMGNKNACTNYCNM	
LMAF_M01139	6.8033e-07	ACAGCTGCNTCAGCAGA -----STCAGCAG-	
E2A_M00804	8.9024e-07	TCTGCTGANGCAGCTGT ---NMNGNGNCAGGTG-	
myogenin_M00712	9.3465e-07	ACAGCTGCNTCAGCAGA -CASCTGN-----	
LBP-1_M00644	1.1528e-06	ACAGCTGCNTCAGCAGA --NGCTGS-----	

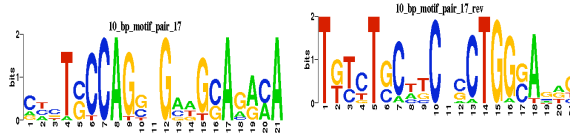


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SMAD4_M00733	6.8940e-06	---TGTCTGCNKC- RGNTGKCTGNMYSN	
ARF	1.9934e-04	GMNGCAGACA ----GAGACA	

ARF1	1.9934e-04	GMNGCAGACA ----GAGACA
ARFAT	1.9934e-04	GMNGCAGACA ----GAGACA
bZIP910_M00357	2.4184e-04	-TGTCTGCNKC ACGTCAGCAYS



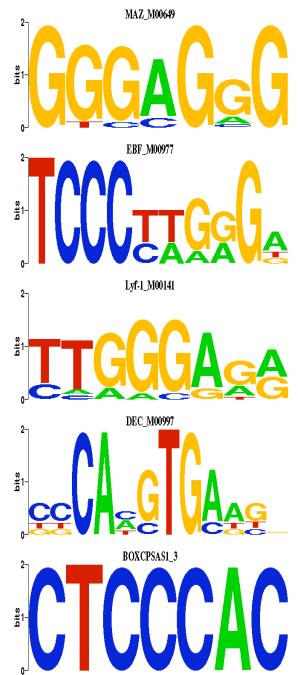
10_bp_motif_pair_17



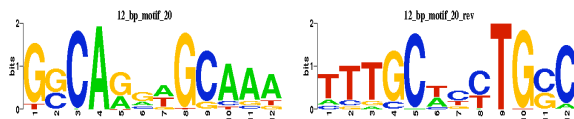
forward

reverse compliment

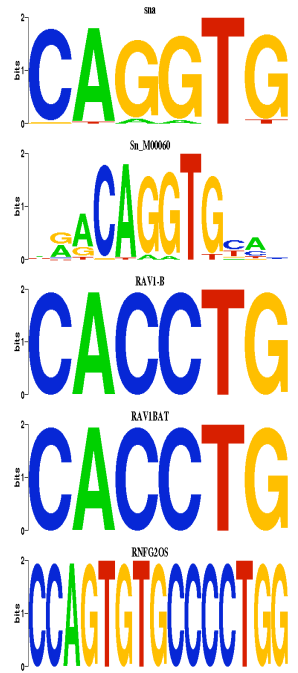
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
MAZ_M00649	5.4899e-05	CNNTSCCAGSNGMNGCAGAMA CCCTCCC-----	
EBF_M00977	6.1580e-05	TKTCTGCNKCNSCTGGSANNG -----TCCYWGRGN---	
Lyf-1_M00141	1.0823e-04	CNNTSCCAGSNGMNGCAGAMA -YCTCCAA-----	
DEC_M00997	2.7212e-04	TKTCTGCNKCNSCTGGSANNG -----NNNTCACNTGNN----	
BOXCPSAS1_3	4.7401e-04	TKTCTGCNKCNSCTGGSANNG -----GTGGGAG--	



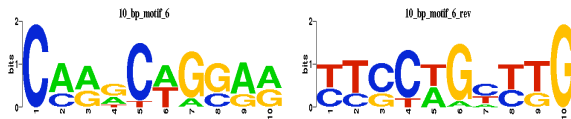
12_bp_motif_20



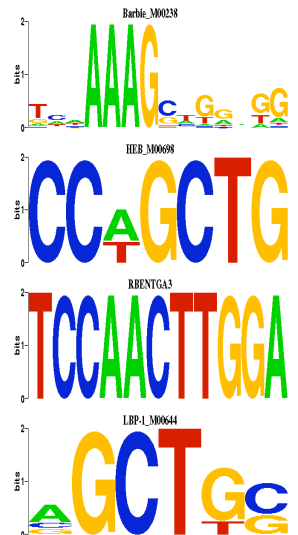
	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
sna	3.2668e-05	TTTGCWYCTGSC ----CACCTG--
Sn_M00060	4.3877e-05	TTTGCWYCTGSC- -NKRCACCTGTYN
RAV1-B	4.6503e-05	TTTGCWYCTGSC ----CACCTG--
RAV1BAT	4.6503e-05	TTTGCWYCTGSC ----CACCTG--
RNFG2OS	5.7789e-05	GSCAGRWGCAAA---- -CCAGGGGCACACTGG



10_bp_motif_6



	<i>forward</i>	<i>reverse compliment</i>
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
Barbie_M00238	2.9175e-05	-YTCCWGYITG--- CMNNCNSCTTTNNN
HEB_M00698	3.0153e-05	CARRCWGGAR -CAGCWGG--
RBENTGA3	3.7070e-05	--CARRCWGGAR TCCAAGTTGGA-
LBP-1_M00644	1.7282e-04	YTCCWGYITG --SCAGCN--



Stamp Results

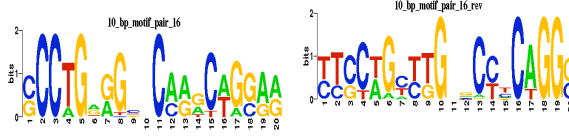
09/05/08

KAISO_M01119 2.7966e-04

CARRCWGGAR
NTNGCAGGA-



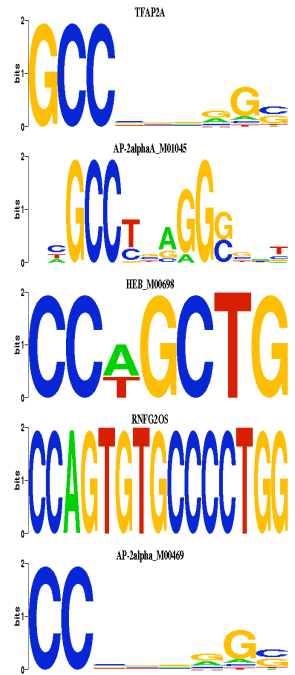
10_bp_motif_pair_16



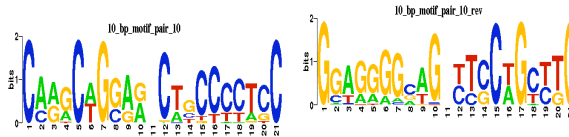
forward

reverse compliment

Name	E value	Alignment	Motif
TFAP2A	9.5223e-05	SCCTGRGGNNCARRCWGGAR SCNNNNGGC-----	
AP-2alphaA_M01045	4.4591e-04	---SCCTGRGGNNCARRCWGGAR NNNSCTNAGGCNN-----	
HEB_M00698	5.8862e-04	SCCTGRGGNNCARRCWGGAR -----CAGCWGG--	
RNFG2OS	6.8632e-04	SCCTGRGGNNCARRCWGGAR -CCAGGGGCACACTGG----	
AP-2alpha_M00469	1.7270e-03	SCCTGRGGNNCARRCWGGAR SCNNNNGG-----	



10_bp_motif_pair_10



forward

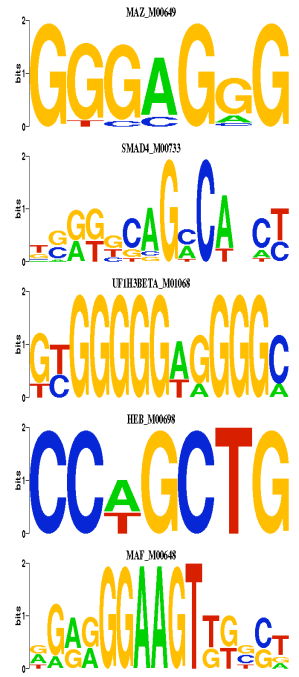
reverse compliment

Name	E value	Alignment	Motif
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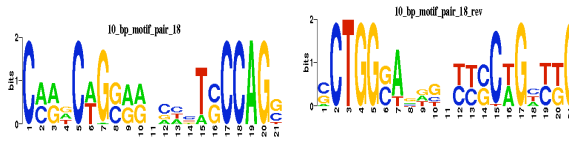
Stamp Results

09/05/08

MAZ_M00649	9.9365e-05	CARGCWGGARNCTNCCCCTCC- -----CCCTCCC
SMAD4_M00733	2.3887e-04	GGAGGGGNAGNYTCCWGCYTG --NSRKNCAGMCANCY-----
UF1H3BETA_M01068	2.8318e-04	-----GGAGGGGNAGNYTCCWGCYTG GYGGGGGAGGGGC-----
HEB_M00698	5.8854e-04	GGAGGGGNAGNYTCCWGCYTG -----CCWGCIG-
MAF_M00648	8.3733e-04	CARGCWGGARNCTNCCCCTCC -----NSNMMACTTCCYYCN-



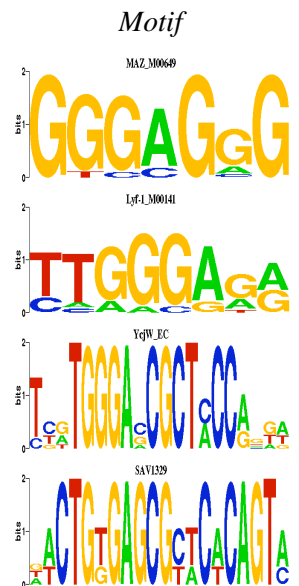
10_bp_motif_pair_18



forward

reverse compliment

Name	E value	Alignment
MAZ_M00649	6.1165e-05	CMRNCWGSRRNNNNTSCCAGS -----CCCTCCC---
Lyf-1_M00141	1.1725e-04	CMRNCWGSRRNNNNTSCCAGS -----YCTCCCAA-
YcjW_EC	2.7920e-04	-SCTGGSANNNNYSCWGNKYG WMNTGGKAGCGSTCCCAIRA--
SAV1329	4.4751e-04	CMRNCWGSRRNNNNTSCCAGS- --NACTGTGAGCGCTCACAGTA

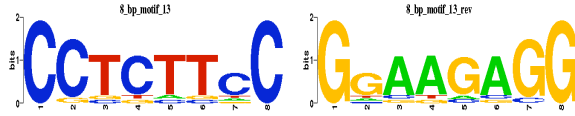


BOXCPSAS1_3 5.0975e-04

SCTGGSANNNNYSCWGNKYK
-GTGGGAG-----



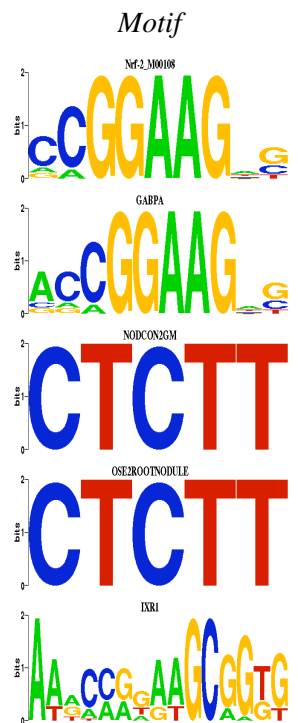
8_bp_motif_13



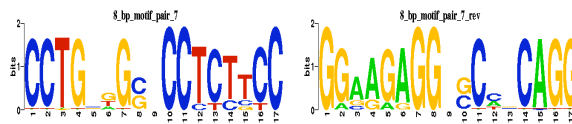
forward

reverse compliment

Name	E value	Alignment
Nrf-2_M00108	2.4532e-08	--GGAAGAGG CCGGAAGNS-
GABPA	8.2304e-08	---GGAAGAGG ACCGAAGNS-
NODCON2GM	2.0622e-06	GGAAGAGG --AAGAG-
OSE2ROOTNODULE	2.0622e-06	GGAAGAGG --AAGAG-
IXR1	2.3075e-05	-----GGAAGAGG-- AARCCGKAAGCGGTG



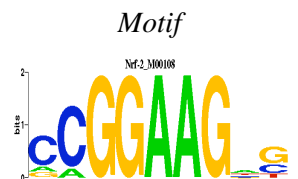
8_bp_motif_pair_7



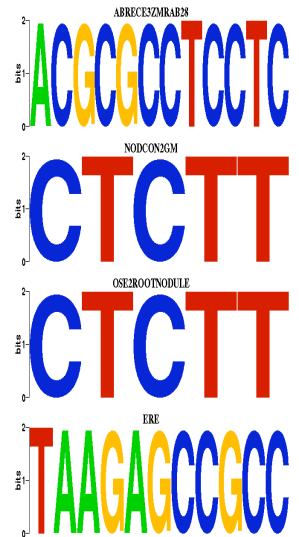
forward

reverse compliment

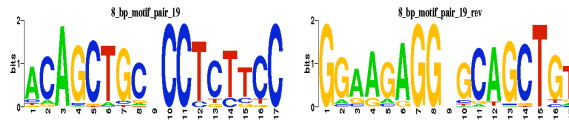
Name	E value	Alignment
Nrf-2_M00108	5.5746e-05	--GGAAGAGGNSCNNCAGG CCGGAAGNS-----



ABRECE3ZMRAB28	5.8515e-05	GGAAGAGGNSCNCAGG -GAGGAGGC GCGT----
NODCON2GM	6.5958e-05	GGAAGAGGNSCNCAGG --AAGAG-----
OSE2ROOTNODULE	6.5958e-05	GGAAGAGGNSCNCAGG --AAGAG-----
ERE	1.5383e-04	CCTGNNGSNCTCTTCC -----GCGGCTCTTA-



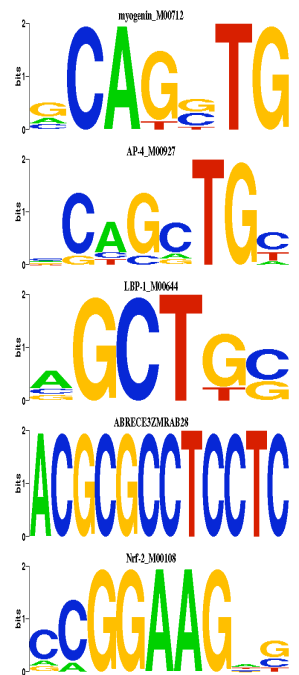
8_bp_motif_pair_19



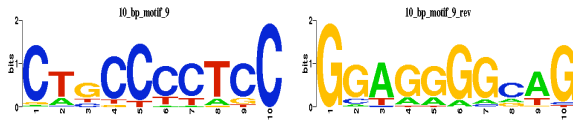
forward

reverse compliment

Name	E value	Alignment
myogenin_M00712	6.7044e-07	ACAGCTGCNCCTCTTCC -CASCTGN-----
AP-4_M00927	1.7800e-06	GGAAGAGGNGCAGCTGT -----RCAGCTGN
LBP-1_M00644	4.1953e-06	GGAAGAGGNGCAGCTGT -----SCAGCN--
ABRECE3ZMRAB28	1.5908e-05	GGAAGAGGNGCAGCTGT -GAGGAGGC GCGT----
Nrf-2_M00108	4.5578e-05	ACAGCTGCNCCTCTTCC-- -----SNCTTCCGG



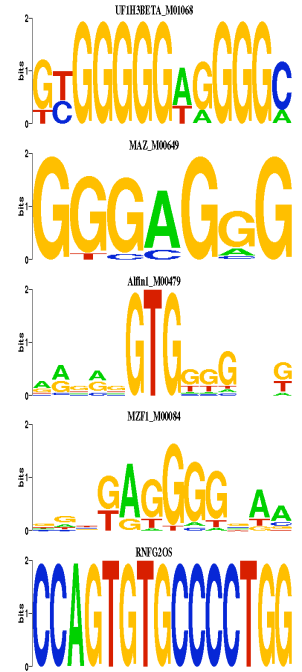
10_bp_motif_9



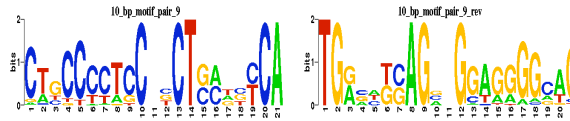
forward

reverse compliment

Name	E value	Alignment
UF1H3BETA_M01068	3.9237e-08	CTGCCCTCC----- --GCCCTCCCCRC
MAZ_M00649	2.4440e-06	-GGAGGGCAG GGGAGGG----
Alfin1_M00479	2.1940e-05	CTGCCCTCC---- MNNCCCCACNYNYN
MZF1_M00084	2.7952e-05	CTGCCCTCC-- TTNCCCCTCNNN
RNFG2OS	6.3639e-05	GGAGGGCAG----- CCAGGGGCACACTGG



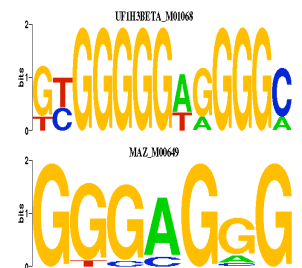
10_bp_motif_pair_9



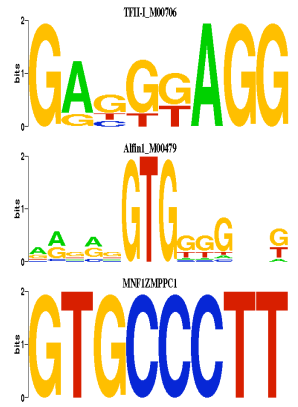
forward

reverse compliment

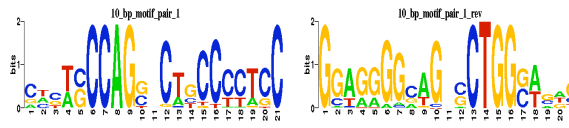
Name	E value	Alignment
UF1H3BETA_M01068	1.9055e-07	TGRNKSAGNNGGAGGGGCAG -----GYGGGGGAGGGGC--
MAZ_M00649	7.7234e-05	CTGCCCTCCNNTSMNNYCA ----CCCTCC-----



TFII-I_M00706	5.3432e-04	TGRNNKSAGNNGGAGGGGCAG -----GANGKAG-----
Alfin1_M00479	8.9603e-04	CTGCCCTCCNCTSMNNYCA MNNCCCCACNYNYN-----
MNF1ZMPPC1	1.4984e-03	TGRNNKSAGNNGGAGGGGCAG -----AAGGGCAC



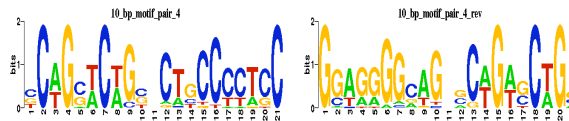
10_bp_motif_pair_1








forward *reverse compliment*

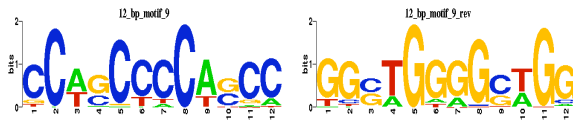
Name	E value	Alignment	Motif
PE3ASPHYA3	8.9793e-06	-----GGAGGGGNAGNSCTGGSANNS- ACCGGCGCGGATGGGAGGCCATGGGAGCTG	
SMb20667	7.4696e-05	GGAGGGGNAGNSCTGGSANNS -GGTTGGCAGCGCTGCCAAAA	
MAZ_M00649	9.9026e-05	SNNTSCCAGSNCTNCCCCCTCC- -----CCCTCCC	
UF1H3BETA_M01068	2.5424e-04	SNNTSCCAGSNCTNCCCCCTCC----- -----GCCCTCCCCRC	
Eve_M00629	6.1766e-04	GGAGGGGNAGNSCTGGSANNS -----GCNGNSWN-----	





10_bp_motif_pair_4



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GAL4	7.6524e-07	GGAGGGGCAGNNCWGWSCTGN -NCGGNGNANTNYNNTCCG--	
MAZ_M00649	9.2956e-05	-GGAGGGGCAGNNCWGWSCTGN GGGAGGG-----	
Eve_M00629	1.0850e-04	GGAGGGGCAGNNCWGWSCTGN -----GCNGNSSWN-----	
UF1H3BETA_M01068	2.2099e-04	NCAGSWCWGNNCTGCCCTCC----- -----GCCCTCCCCRC	
Dde_M00304	8.0321e-04	GGAGGGGCAGNNCWGWSCTGN -----GGCTGAGC-----	

12_bp_motif_9



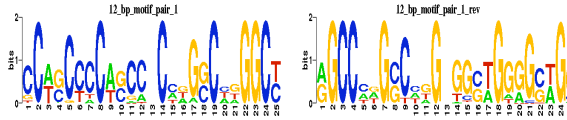
	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Alfin1_M00479	3.5246e-08	---GGSTGGGGCWGG NRNRNGTGGGGNNK-	
CAC-binding_M00720	2.8952e-07	CCWGCCCCASCC- -----CCCASCCY	
GBF_M00633	4.5652e-07	GGSTGGGGCWGG ---TNGGGGTN-	
KROX_M00982	2.2341e-06	-GGSTGGGGCWGG GNNNGGGGGCGG	

UF1H3BETA_M01068 3.4296e-06

GGSTGGGGCWGG---
 --GYGGGGGAGGGGC



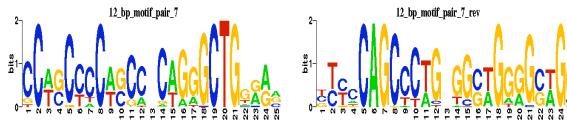
12_bp_motif_pair_1



forward *reverse compliment*

Name	E value	Alignment	Motif
UF1H3BETA_M01068	8.8664e-06	CCWSCCCASCNCNNGSCNNGGCY ---GCCCTCCCCRC-----	
CAC-binding_M00720	1.0578e-05	CCWSCCCASCNCNNGSCNNGGCY -----CCASCY-----	
GBF_M00633	1.8998e-05	CCWSCCCASCNCNNGSCNNGGCY -NACCCNA-----	
Alfin1_M00479	2.5117e-05	CCWSCCCASCNCNNGSCNNGGCY -MNNCCCCACNYNYN-----	
KROX_M00982	2.6734e-04	RGCCNNGSCNNGNGGSTGGGGSWGG -----GNNNGGGGGCGG-	

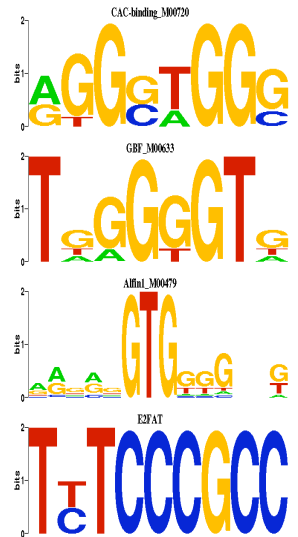
12_bp_motif_pair_7



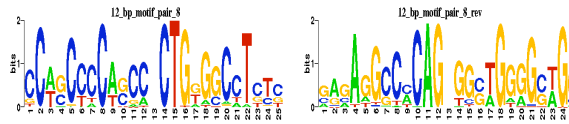
forward *reverse compliment*

Name	E value	Alignment	Motif
UF1H3BETA_M01068	7.2530e-07	NTYCCAGCCCTGNGGSTGGGGSWGG -----GYGGGGGAGGGGC---	

CAC-binding_M00720	1.8086e-05	CCWSCCCASCNCAGGGCTGGRAN -----CCCASCCY-----
GBF_M00633	3.3506e-05	NTYCCAGCCCTGNNGGSTGGGGSWGG -----TNGGGGTN-
Alfin1_M00479	8.8548e-05	CCWSCCCASCNCAGGGCTGGRAN -MNNCCCCACNYYN-----
E2FAT	1.7683e-04	CCWSCCCASCNCAGGGCTGGRAN -----GCGGGARA



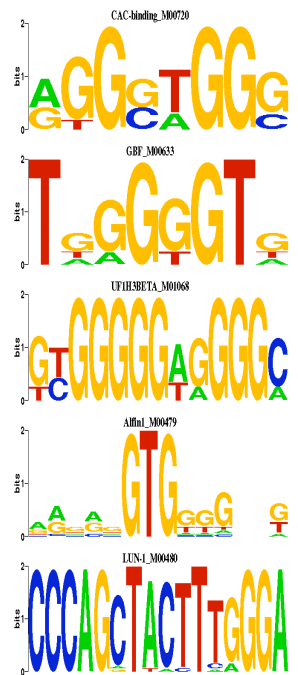
12_bp_motif_pair_8



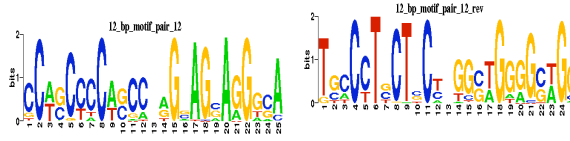
forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CAC-binding_M00720	8.4158e-06	CCWSCCCASCNCCTGKGGCCTSTS -----CCCASCCY-----	
GBF_M00633	9.5902e-06	SASAGCCMCAGNNGGSTGGGGSWGG -----TNGGGGTN-	
UF1H3BETA_M01068	1.0834e-05	CCWSCCCASCNCCTGKGGCCTSTS ---GCCCTCCCCRC-----	
Alfin1_M00479	1.1273e-05	CCWSCCCASCNCCTGKGGCCTSTS -MNNCCCCACNYYN-----	
LUN-1_M00480	3.7330e-05	SASAGCCMCAGNNGGSTGGGGSWGG ----TCCCAAAGTAGCTGGG-----	



12_bp_motif_pair_12

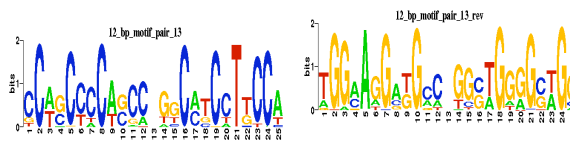


forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CAC-binding_M00720	1.0578e-05	CCWSCCCASCCNRGNAGNAGGGSA -----CCCASCCY-----	
GBF_M00633	1.8998e-05	CCWSCCCASCCNRGNAGNAGGGSA -NACCCNA-----	
TAL1_M00993	1.3493e-04	CCWSCCCASCCNRGNAGNAGGGSA -----RNCAGNTGG---	
Alfin1_M00479	1.7215e-04	CCWSCCCASCCNRGNAGNAGGGSA -MNNCCCCACNYYN-----	
UF1H3BETA_M01068	3.5286e-04	---CCWSCCCASCCNRGNAGNAGGGSA GCCCTCCCCRC-----	

12_bp_motif_pair_13

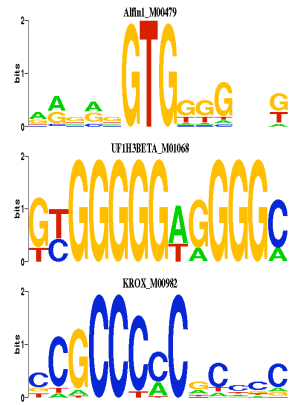


forward

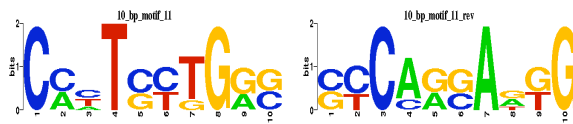
reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
CAC-binding_M00720	9.3693e-06	CCWSCCCASCCNGKCMTCCTKCCA -----CCCASCCY-----	
GBF_M00633	9.3929e-06	TGGMAGGAKGMCNGGSTGGGGSWGG -----TNGGGGTN-	

Alfin1_M00479	1.1001e-04	TGGMAGGAKGMCNGGSTGGGGSWGG -----NRNRNGTGGGGNNK--
UF1H3BETA_M01068	1.1231e-04	CCWSCCCASCNGKCMTCCTKCCA ---GCCCTCCCCRC-----
KROX_M00982	2.5091e-04	TGGMAGGAKGMCNGGSTGGGGSWGG -----GNNNGGGGGGCGG



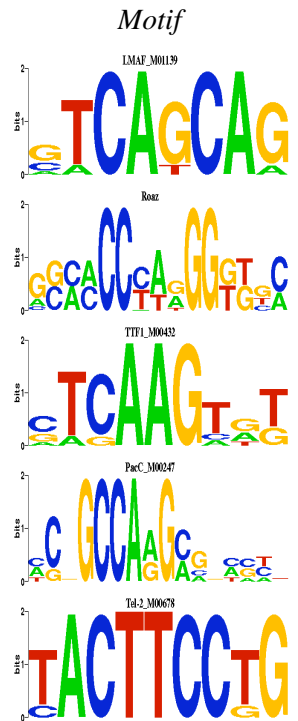
10_bp_motif_11



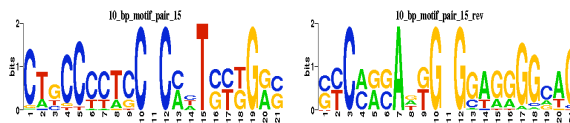
forward

reverse compliment





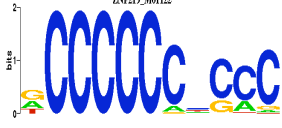
Name	E value	Alignment
LMAF_M01139	7.0766e-05	CMNTSYTGGS --CTGCTGAS
Roaz	3.1838e-04	-CMNTSYTGGS---- GNMMCCYTRGGKKSC
TTF1_M00432	3.3947e-04	CMNTSYTGGS -AYACTTGAS
PacC_M00247	3.4980e-04	---CMNTSYTGGS--- NNNNNNKCYTGCCNGN
Tel-2_M00678	4.7946e-04	-CMNTSYTGGS TACTTCCTG--



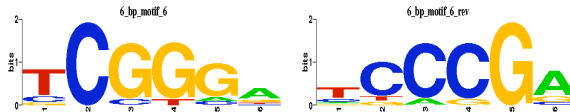
10_bp_motif_pair_15



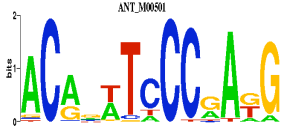
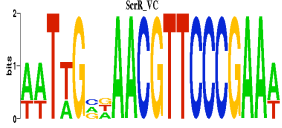
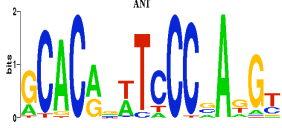

forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
UF1H3BETA_M01068	4.5768e-08	CTKCCCCTCCNCMNTSYKGRS --GCCCTCCCCRC-----	
MAZ_M00649	9.8262e-05	CTKCCCCTCCNCMNTSYKGRS ----CCCTCC-----	
Alfin1_M00479	3.4831e-04	CTKCCCCTCCNCMNTSYKGRS MNNCCCCACNYNYN-----	
ABRECE3ZMRAB28	3.9395e-04	CTKCCCCTCCNCMNTSYKGRS ACGCGCCTCCTC-----	
ZNF219_M01122	8.8127e-04	SYCMRSANKGNGGAGGGGMAG -----GGNGGGGGGN--	

6_bp_motif_6



forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ANT_M00501	8.1812e-07	-----TCCCGA-- ACANWTCCCRAG	
ScrR_VC	1.0918e-06	-----TCCCGA-- AATTGNNAACGTTCCCGAAA	
ANT	1.4262e-05	---TCGGGA----- RCNTNGGGAWNTGTGC	
E2F	2.2690e-05	TCGGGA-- GCGGAAA	

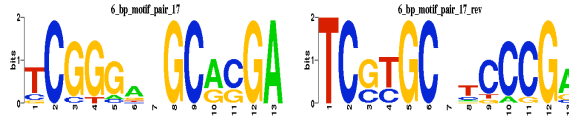
E2F_DP

2.2690e-05

TCGGGA--
GCGGGAAA



6_bp_motif_pair_17

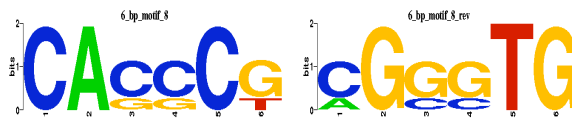


forward

reverse compliment

Name	E value	Alignment	Motif
ABRECE3ZMRAB28	1.3223e-04	TCGGGANGCACGA -GAGGAGGCGCGT	
RHERPATEXPA7	3.8609e-04	TCGTGCNTCCCGA WCGTGM-----	
ABI4_2	6.1755e-04	TCGGGANGCACGA ---GRNNGCACCG	
CCTCGTGTCTCGMGH3	8.0763e-04	--TCGTGCNTCCCGA CCTCGTGTCTC----	
PUT3	1.7706e-03	----TCGTGCNTCCCGA NNNNNNTGGCTTCCCG-	

6_bp_motif_8



forward

reverse compliment

Name	E value	Alignment	Motif
YDR026C	3.6408e-06	-CGGGTG CCGGGT-	

Stamp Results

09/05/08

Pax-4_M00378 1.4745e-05

CGGGTG-----
NGGGTGRNNNN



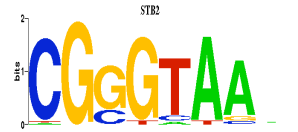
AFT2 1.7513e-05

CGGGTG--
-GGGTGCN



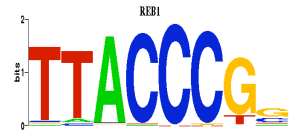
STB2 4.2368e-05

--CACCCG
NTTACCCG

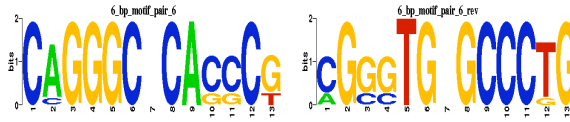


REB1 4.5052e-05

-CGGGTG-
SCGGGTAA



6_bp_motif_pair_6



forward

reverse compliment

Name

E value

Alignment

Motif

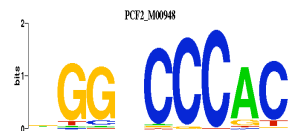
GCBP2ZMGAPC4 1.9908e-06

CAGGGCNCACCCG
-CGGGCCCAC---



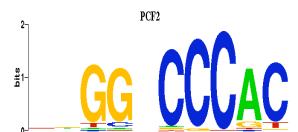
PCF2_M00948 3.6887e-06

CGGGTNGCCCTG
---GTGGGNCCN-



PCF2 2.2189e-05

CGGGTNGCCCTG
---GTGGGNCCNN



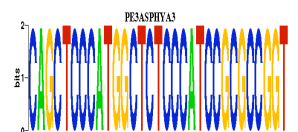
CACD_M01113 4.7511e-05

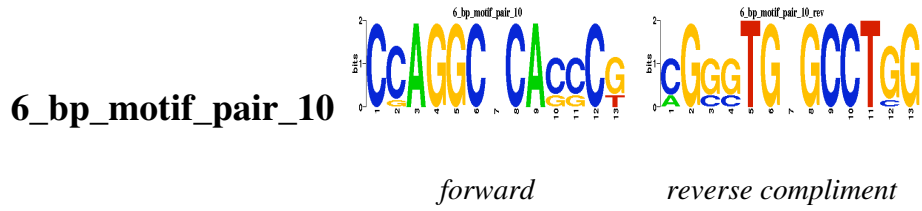
CGGGTNGCCCTG
-GGGYGTG-----



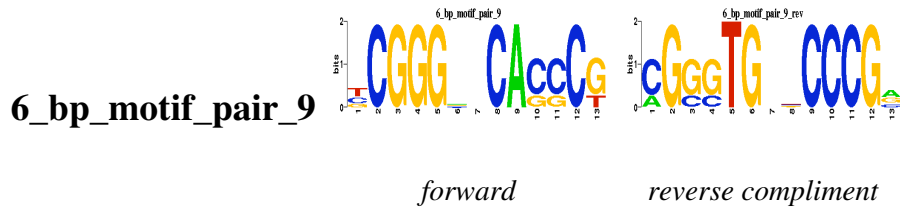
PE3ASPHYA3 6.0001e-05

-----CGGGTNGCCCTG-----
ACCGGCGCGGATGGGAGAGCCATGGGAGCTG





<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
RNFG2OS	6.1781e-06	--CGGGTGNCCCTGG CCAGTGTGCCCTGG	
GCBP2ZMGAPC4	1.6746e-05	CGGGTGNCCCTGG ---GTGGGCCCG--	
CACD_M01113	4.7494e-05	CGGGTGNCCCTGG -GGYGTG-----	
Dde_M00304	2.2921e-04	CCAGGCNACCCG ----GCTCAGCC--	
Alfin1_M00479	2.5765e-04	CCAGGCNACCCG-- -MNNCCCCACNYNYN	



<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
Zic1_M00448	2.9132e-06	NCGGGNNACCCG ----GACNACCC--	
Zic3_M00450	5.5308e-06	CGGGTGNCCCGN -GGKGNTC-----	

Stamp Results

09/05/08

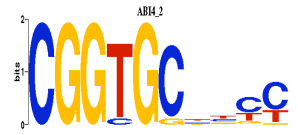
GCBP2ZMGAPC4 6.0127e-06

NCGGGNNCACCCG
-CGGGCCCAC---



ABI4_2 7.9049e-06

NCGGGNNCACCCG
--GRNNGCACCG--



DEAF1_M01001 8.1681e-06

-----NCGGGNNCACCCG-----
NNNNNNCGGAAAYNCCCGARNNNG



6_bp_motif_12



forward

reverse compliment

Name

E value

Alignment

Motif

RHERPATEXPA7 2.1035e-06

TCGTGC
WCGTGM



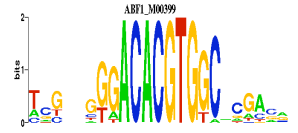
Ttk_M00009 6.8759e-06

-TCGTGC
GTCCGTC



ABF1_M00399 7.3116e-06

--TCGTGC-----
NNTCNNGCCACGTGTCCCNNNW



E2F-4-DP-2_M00739 1.0016e-05

GCACGA-
GCGSGAA

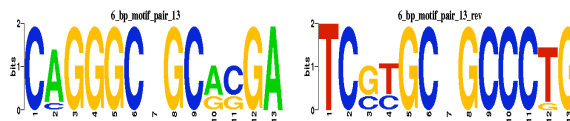


PE2FNTRNR1A 1.2692e-05

GCACGA--
GCGCGAAT

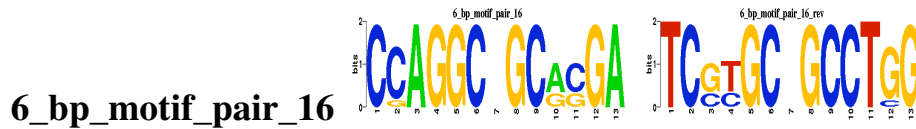


6_bp_motif_pair_13



forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GRAZMRAB28	6.9807e-05	CAGGGCNGCACGA ---GGCGGCATG-	
ERF1	2.0428e-04	CAGGGCNGCACGA ---GGCGGC----	
GCC-box	2.0428e-04	CAGGGCNGCACGA ---GGCGGC----	
GCCCORE	2.0428e-04	CAGGGCNGCACGA ---GGCGGC----	
ERF2_M01057	2.4526e-04	CAGGGCNGCACGA ---GGCGGC----	



6_bp_motif_pair_16

forward *reverse compliment*

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ABREMOTIFIIOSRAB16B	6.2461e-05	-CCAGGCNGCACGA GCCACGCGGC----	
GRAZMRAB28	6.9807e-05	CCAGGCNGCACGA ---GGCGGCATG-	
ABF1_M00399	1.1227e-04	--TCGTGCNGCCTGG----- NNTCNGGCCACGTGTCCNNNW	
ERF1	2.0428e-04	CCAGGCNGCACGA ---GGCGGC----	

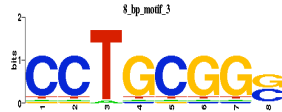
GCC-box

2.0428e-04

CCAGGCNGCACGA
 ---GGCGGC---



8_bp_motif_3

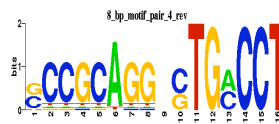
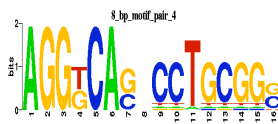


forward

reverse compliment

Name	E value	Alignment	Motif
AP-2_M00800	6.8282e-07	SCCGCAGG----- SCSSCRGGCNRNRNN	
AP-2_M00189	2.9052e-06	-SCCGCAGG-- NCCSCNNGGCG	
INTRONLOWER	1.7692e-05	CCTGCGGS CCTGCA--	
gcm	1.9621e-05	-SCCGCAGG ACCCGCAT-	
HIF1_M00466	2.0641e-05	SCCGCAGG--- NCNSCACGTM	

8_bp_motif_pair_4

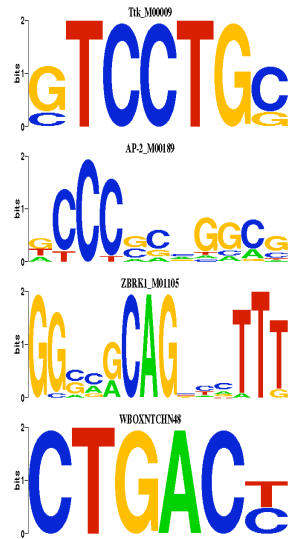


forward

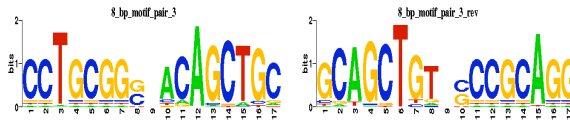
reverse compliment

Name	E value	Alignment	Motif
QELEMENTZM13	4.3466e-06	SCCGCAGGNCTGMCC -----TGACCT	

Ttk_M00009	3.0768e-05	SCCGCAGGNCTGMCCT ---GCAGGAC-----
AP-2_M00189	2.8997e-04	AGGKCAGNCCTGCGGS- -----CGCCNGSGGGN
ZBRK1_M01105	2.9899e-04	-SCCGCAGGNCTGMCCT GGSMGCAGNNNTTT---
WBOXNTCHN48	3.6331e-04	AGGKCAGNCCTGCGGS -RGTCAG-----



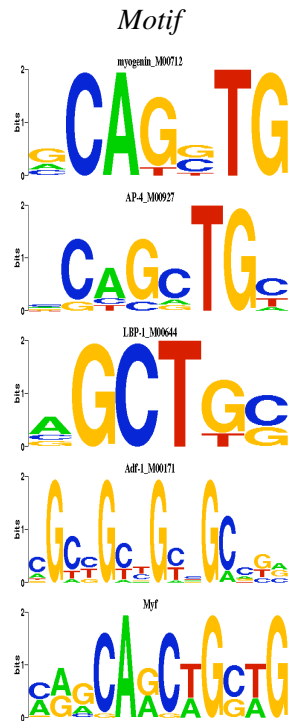
8_bp_motif_pair_3

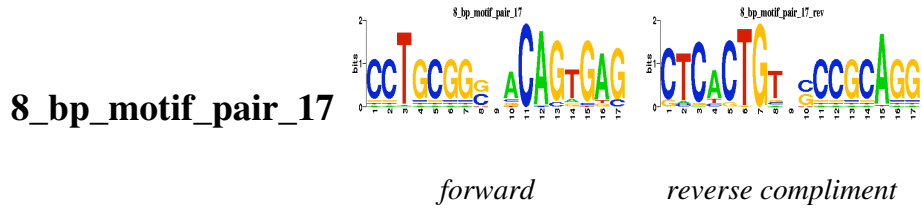


forward

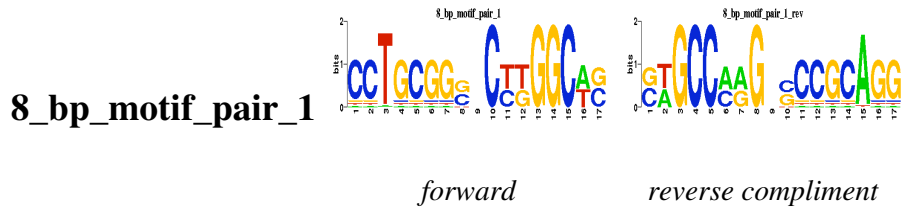
reverse compliment

Name	E value	Alignment
myogenin_M00712	6.7044e-07	CCTGCGGSNACAGCTGC -----CASCTGN
AP-4_M00927	1.7800e-06	GCAGCTGTNSCCGCAGG RCAGCTGN-----
LBP-1_M00644	4.1953e-06	GCAGCTGTNSCCGCAGG SCAGCN-----
Adf-1_M00171	8.5332e-06	CCTGCGGSNACAGCTGC NMNGCNRCRGRGCG--
Myf	8.6476e-06	GCAGCTGTNSCCGCAGG -CAGCAGYTGCYK----



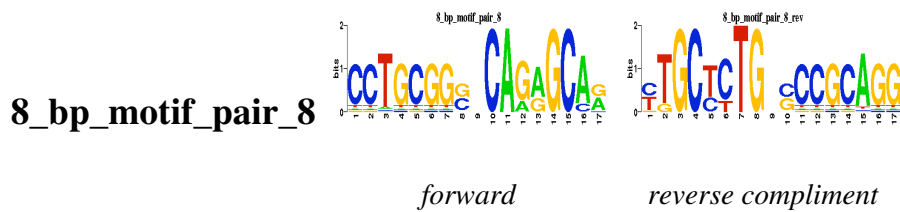
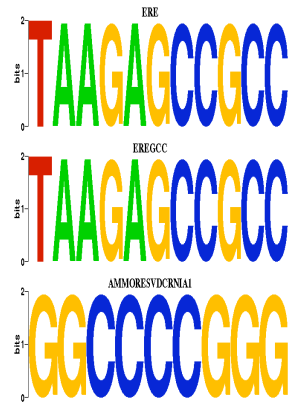


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
SORLIP5	2.1849e-05	CTCACTGTNSCCGCAGG CTCACTC-----	
SORLIP5AT	2.1849e-05	CTCACTGTNSCCGCAGG CTCACTC-----	
AhR_M00139	5.3848e-05	-CTCACTGTNSCCGCAGG TSTCACGCNASNYNGRG-	
Adf-1_M00171	7.0533e-05	CCTGCCGGSNACAGTGAG NMNGCNRRCRGCRGCG--	
E2F-1-DP-2_M00737	9.3779e-05	CCTGCCGGSNACAGTGAG ---GCCGGAA-----	

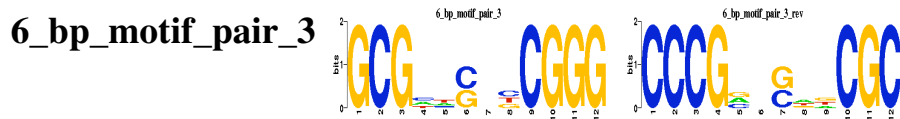
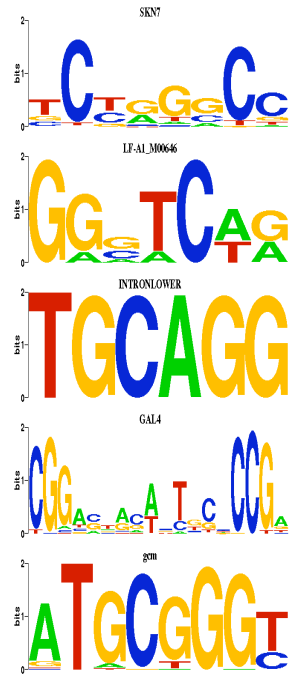


<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
RIM101	5.3733e-06	SWGCCMRGNSCCGCAGG -TGCCAAG-----	
GBOX10NT	2.1325e-04	CCTGCCGGSNCYKGGCWS -----GGCACGTGGC--	

ERE	2.2159e-04	CCTGCGGSNCYKGGCWS --GGCGGCTCTTA----
EREGCC	2.2159e-04	CCTGCGGSNCYKGGCWS --GGCGGCTCTTA----
AMMORESVDCRNIA1	2.3845e-04	SWGCCMRGNSCCGCAGG ---CCCGGGGCC-----



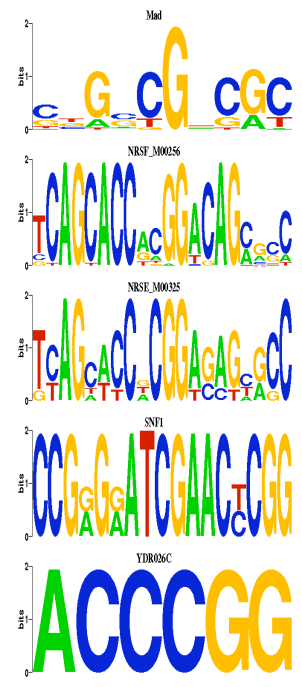
Name	E value	Alignment	Motif
SKN7	8.3870e-05	CCTGCGGSNCAGAGCAR -----GGSCYRGN-----	SKN7
LF-A1_M00646	2.2625e-04	YTGCTCTGNSCCGCAGG -----YWGASCC-----	LF-A1_M00646
INTRONLOWER	4.9523e-04	CCTGCGGSNCAGAGCAR CCTGCA-----	INTRONLOWER
GAL4	9.8797e-04	CCTGCGGSNCAGAGCAR----- ---NCGGNANTNYNNTCCG	GAL4
gcm	1.4741e-03	YTGCTCTGNSCCGCAGG -----ACCCGCAT-	gcm



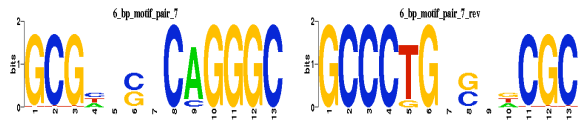
forward *reverse compliment*

Name *E value* *Alignment* *Motif*

Mad	4.7888e-04	GCGNNSNNCGGG GCGNCGNCNS--
NRSF_M00256	1.1320e-03	-GCGNNSNNCGGG----- GSYGCTGTCCGTGGTGCTGA
NRSE_M00325	1.5421e-03	-GCGNNSNNCGGG----- GGCRCTCTCCGNGGTGCTGA
SNF1	2.3653e-03	-----GCGNNSNNCGGG CCGRGTTTCGATYCYCGG-
YDR026C	3.3860e-03	GCGNNSNNCGGG- -----CCGGGT



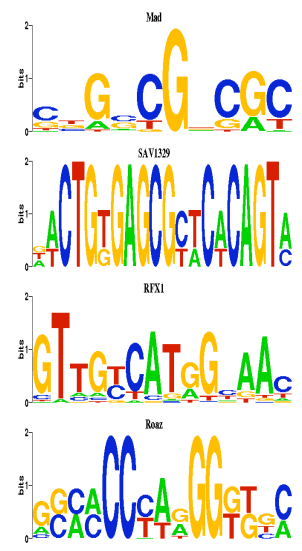
6_bp_motif_pair_7



forward *reverse compliment*

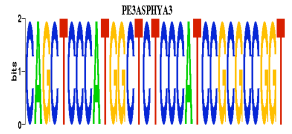
Name *E value* *Alignment* *Motif*

Mad	5.3676e-06	GCGNNSNCAGGGC GCGNCGNCNS---
SAV1329	2.0532e-04	GCCCTGNSNNCGC----- -TACTGTGAGCGCTCACAGTN
RFX1	2.3204e-03	GCGNNSNCAGGGC--- --GTTGYCATGGNAAC
Roaz	3.3222e-03	---GCCCTGNSNNCGC GNMMCCYTRGGKKSC-

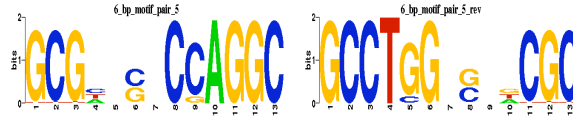


PE3ASPHYA3 5.0098e-03

-----GCCCTGNSNNCGC
ACCGGCGCGGATGGGAGAGCCATGGGAGCTG



6_bp_motif_pair_5

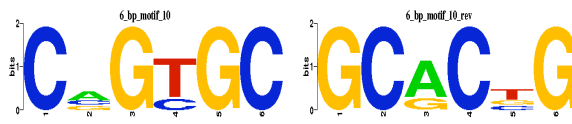


forward

reverse compliment

Name	E value	Alignment	Motif
REST	1.6156e-04	-----GCCTGGNSNNCGC TCAGCACCWNGGACAGCNC	
CGTGTSPHZMC1	3.3613e-04	--GCCTGGNSNNCGC-- ATGCATGGACGACACG	
Mad	1.0096e-03	GCGNNSNCCAGGC GCGNCGNCNS---	
MarR_ec	1.3902e-03	-----GCCTGGNSNNCGC-- ATTACTTGCCNGGGCAACCATT	
AP-2_M00915	1.7353e-03	GCGNNSNCCAGGC-- --NNNCCNCNGGCN	

6_bp_motif_10




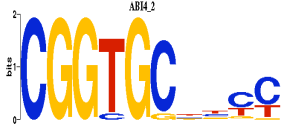


forward

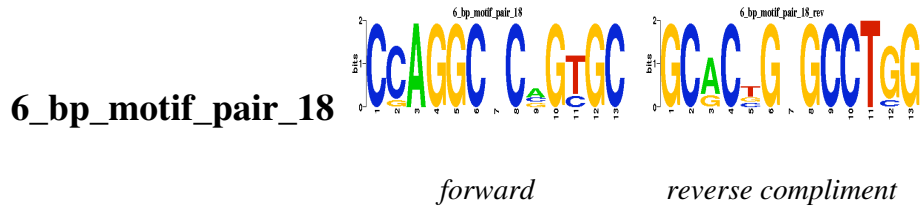
reverse compliment

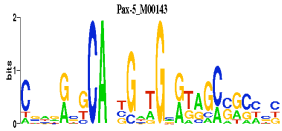
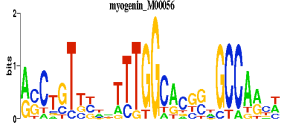
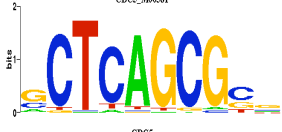


Name	E value	Alignment	Motif
Pax5	3.3113e-05	---GCACNG----- NGNNNNNYGNWGCGRRCR	

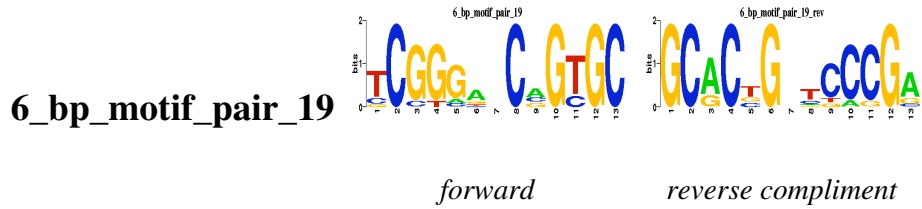
Stamp Results

09/05/08

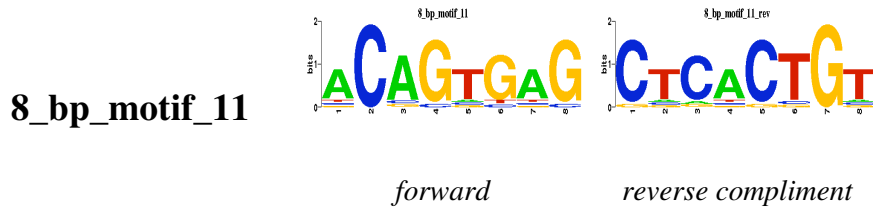
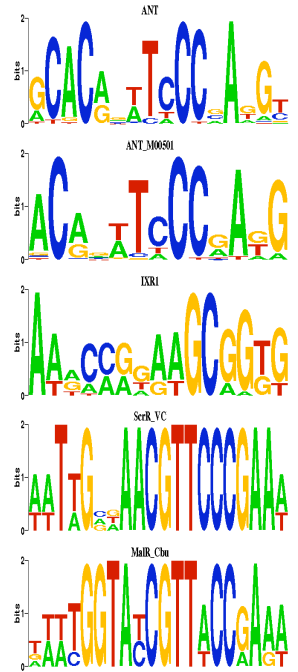
ABI4_M00958	6.9826e-05	---CNGTGC- GGGCGGTGCN	
ABI4_2	8.3601e-05	----GCACNG GRNNGCACCG	
ABI4	1.3811e-04	----GCACNG NGNNGCRSCG	
D4GMAUX28	1.8679e-04	---GCACNG ACAGCACTA	



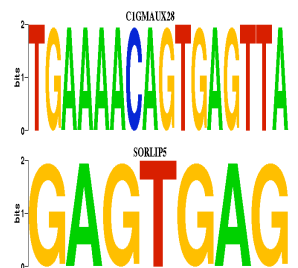
Name	E value	Alignment	Motif
Pax-5_M00143	1.3153e-05	-----GCACNGGCCTGG NNNSYSGCYMYNCWNCNNTGMNYNNG	
myogenin_M00056	6.7600e-05	-----GCACNGGCCTGG- ASCTGTNNNNTTGGCACNSNGCCARNN	
CDC5_M00361	1.0980e-04	-GCACNGGCCTGG NSCGTGAGS----	
CDC5	3.9320e-04	-GCACNGGCCTGG NSCGTGAGSN---	
SKN7	4.5094e-04	CCAGGCNCNGTGC ---GGSCYRGN--	



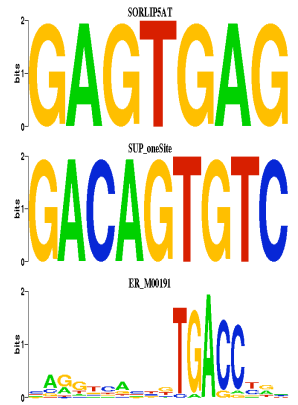
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
ANT	1.8102e-09	GCACNGNTCCCGA--- GCACANWTCCCNANGY
ANT_M00501	8.1829e-06	GCACNGNTCCCGA-- --ACANWTCCCRAKG
IXR1	2.8611e-04	GCACNGNTCCCGA--- -CACCGCTTMCGGYTT
ScrR_VC	6.5135e-04	--TCGGGANCNGTGC----- TTTCGGGAACGTTNNCAATT
MalR_Cbu	7.9497e-04	--TCGGGANCNGTGC----- TTTCGGTAACGRTACCAWWN



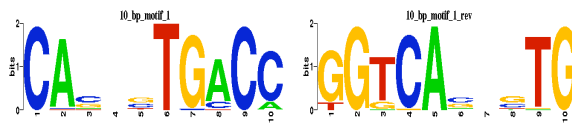
<i>Name</i>	<i>E value</i>	<i>Alignment</i>
C1GMAUX28	5.9954e-11	---CTCACTGT----- TAACTCACTGTTTTCA
SORLIP5	1.6201e-07	CTCACTGT CTCACTC-



SORLIP5AT	1.6201e-07	CTCACTGT CTCACTC-
SUP_oneSite	5.1999e-06	CTCACTGT- GACACTGTC
ER_M00191	7.1287e-06	-----ACAGTGAG--- NNNGGTCANNNNNNNYNN

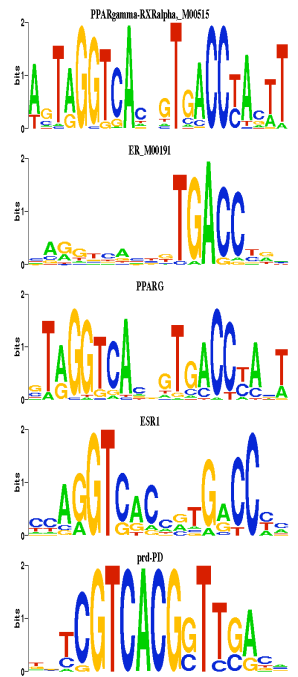


10_bp_motif_1

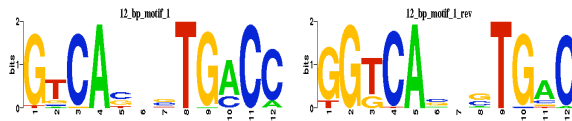


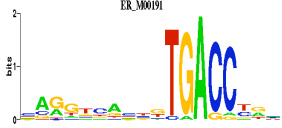


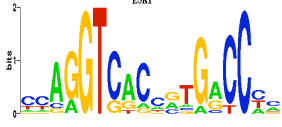
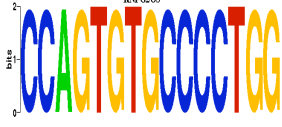
forward *reverse compliment*

Name	E value	Alignment	Motif
PPARgamma-RXRalpha,_M00515	3.4102e-11	-----CASNNTGACC----- AANTAGGTCACNGTGACCTAST	PPARgamma-RXRalpha,_M00515
ER_M00191	4.8677e-11	---GGTCANNSTG----- NNNGGTCANNNNNNNYNN	ER_M00191
PPARG	5.5354e-11	-----CASNNTGACC----- ANTRGGTCACNNTGACCTAN	PPARG
ESR1	2.1967e-10	--GGTCANNSTG----- NNGGYCANNGTGACCTNN	ESR1
prd-PD	1.2273e-06	----CASNNTGACC----- NNTCAACCGTGACGANN	prd-PD

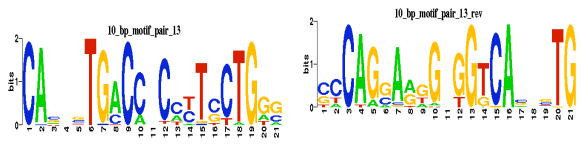



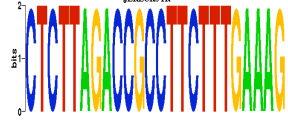

12_bp_motif_1



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
ER_M00191	4.6629e-15	---GGTCANNNTGAC--- NNNGGTCANNNNNNNNYNN	
PPARgamma-RXRalpha_M00515	7.9381e-14	-----GTCANNNTGACC----- AANTAGGTCACNGTGACCTAST	
PPARG	2.2649e-13	---GGTCANNNTGAC----- NTAGGTCANNGTGACCYANT	
ESR1	3.2419e-13	----GTCANNNTGACC-- NNAGGTCACNNTGRCCNN	
RNFG2OS	1.6051e-04	----GGTCANNNTGAC CCAGGGGCACACTGG-	

10_bp_motif_pair_13



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
NERF1a_M00531	5.0020e-08	CANNNTGACCNCMYTSTGGS ----SNNASNYRCTTCCTGNY	
JERECRSTR	2.9610e-05	CANNNTGACCNCMYTSTGGS--- CTCTTAGACCGCCTTCTTTGAAAG	
VDR_M00444	3.0295e-05	CANNNTGACCNCMYTSTGGS ----TSWCCYYNYTNMCC--	

Zic1_M00448

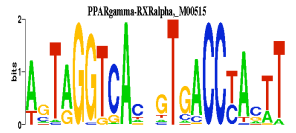
4.5619e-05

SCCAGSARKNGGTCANNNTG
-----GGTNGTC-----

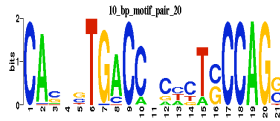


PPARgamma-RXRalpha,_M00515 7.1147e-05

-----CANNNTGACCNCMYTSC TGGS
AANTAGGTACNGTGACCTAST-----



10_bp_motif_pair_20

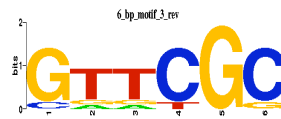


forward

reverse compliment

Name	E value	Alignment	Motif
VDR_M00444	1.2588e-05	CASNNTGACCNCNYTSCCAGS -----TSWCCYYNYTNMCC--	
ZNF219_M01122	1.4261e-05	SCTGGSARNGNGGTCANNSTG ---GGNGGGGGGN-----	
MAZ_M00649	2.0848e-05	CASNNTGACCNCNYTSCCAGS -----CCCTCCC---	
Zic1_M00448	3.3455e-05	CASNNTGACCNCNYTSCCAGS -----GACNACCC-----	
Zic3_M00450	5.2369e-05	SCTGGSARNGNGGTCANNSTG -----GGGKGNTC-----	

6_bp_motif_3



forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AMMORESIVDCRNIA1	9.1148e-06	--GTTTCGC AAGTTTCG--	
PE2FNTRNR1A	2.5012e-05	--GCGAAC GCGCGAAT	
E2F_M00425	2.9674e-05	GTTTCGC-- -TTCGCGC	
STB1	3.5856e-05	-GTTTCGC- TTTTTCGCG	
E2F_M00427	1.3905e-04	--GCGAAC SCGCSAA--	



<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
AACACOREOSGLUB1	4.4421e-06	GTTTCGT- GTTTGT	
AMMORESIVDCRNIA1	4.0948e-05	--GTTTCGT AAGTTTCG--	
CELLCYCLESC	1.0297e-04	-GTTTCGT- TTTTTCGTG	
GLUTAACAOS	1.2081e-04	-----GTTTCGT- ATAGAGTTTGT	

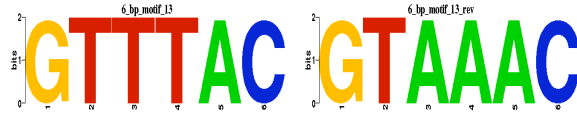
HFH4_M00742

1.3377e-04

---ACGAAC---
TAAACAAACAMW



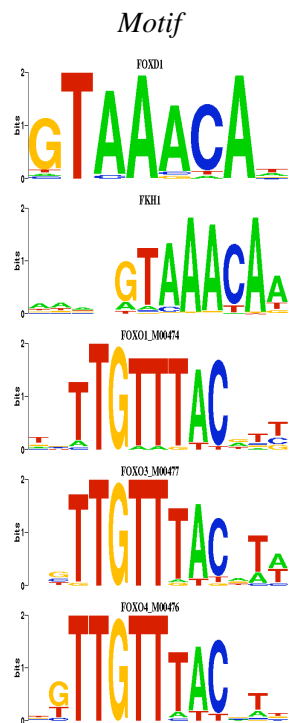
6_bp_motif_13



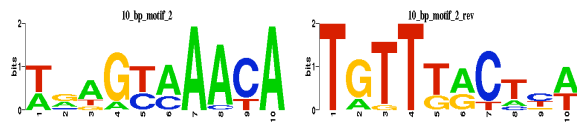
forward

reverse compliment

Name	E value	Alignment
FOXD1	3.8041e-09	--GTTTAC NTGTTTAC
FKH1	1.0861e-07	--GTTTAC---- TTGTTTACNNNN
FOXO1_M00474	1.2142e-07	---GTAAAC---- NNGTAAACAANN
FOXO3_M00477	1.2159e-07	---GTAAAC---- WANGTAAACAANN
FOXO4_M00476	1.3384e-07	---GTAAAC---- NANGTAAACAACN



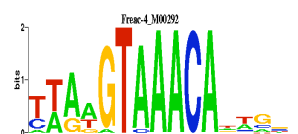
10_bp_motif_2



forward

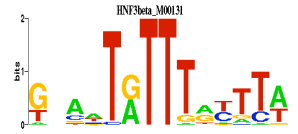
reverse compliment

Name	E value	Alignment
Freac-4_M00292	2.9218e-12	----TGTTTRCTYA- NNNNTGTTTACWTWR



HNF3beta_M00131 2.9936e-11

----TGTTTRCTYA
GNANTRITTRYTTW



FOX_M00809 4.5112e-10

TRAGYAAACA--
WAAAYAAACANT



HNF3alpha_M00724 3.7618e-09

-TRAGYAAACA
NWRARCAAAY-

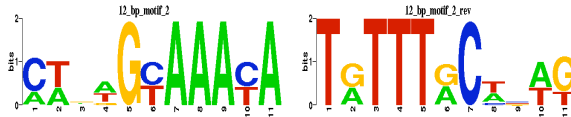


Foxa2 1.4741e-08

TRAGYAAACA---
-AARYAAATANTN



12_bp_motif_2



forward

reverse compliment

Name

E value

Alignment

Motif

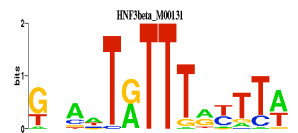
Freac-4_M00292 1.1626e-09

----TRTTTRCWNWG
NNNNTGTTTACWTWR



HNF3beta_M00131 1.2572e-09

----TRTTTRCWNWG
GNANTRITTRYTTW-



D3GMAUX28 1.2239e-08

TRTTTRCWNWG
TATTGCTTAA



HNF3alpha_M00724 1.2731e-08

CWNWGYYAAYA
NWRARCAAAY-

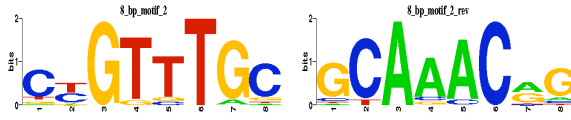


FOX_M00809 4.4116e-08

CWNWGYYAAYA--
-WAAAYAAACANT



8_bp_motif_2

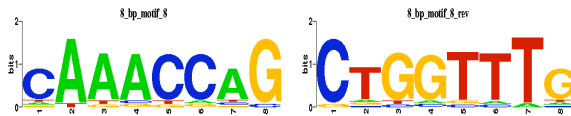


forward

reverse compliment

Name	E value	Alignment	Motif
Sn_M00044	2.6878e-07	----CYGTTTGC-- NNANNTGNTNNA	
DBP_M00624	9.2554e-07	CYGTTTGC --NWNATC	
2SSEEDPROTBANAPA	4.0844e-06	CYGTTTGC GIGTTTGC--	
PurR	6.3871e-06	-----CYGTTTGC-- AMGCAAACGTTTGCCT	
MalR_ST	1.3569e-05	-----CYGTTTGC----- TTATGCAANCGNTTGCCKWA	

8_bp_motif_8



forward

reverse compliment






Name	E value	Alignment	Motif
Grainyhead-Elf-1-NTF-1_M00951	8.6018e-11	CAAACCAG -AAACCRG	
CP2-LBP-1c-LSF_M00947	2.9219e-09	-----CAAACCAG CNRGNNNANCCAG	

MYB1AT	1.1906e-07	CAAACCAG -WAACCA-	
grh	3.2880e-07	--CAAACCAG RNNRAACCAG	
CP2_M00072	8.2667e-07	CTGGTTG-- CTGGKTNGNG	

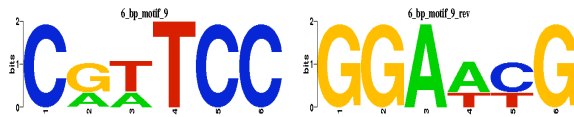



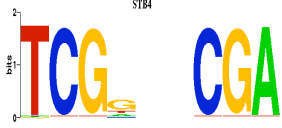

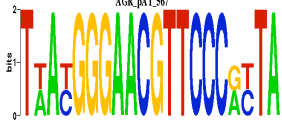
Name	E value	Alignment	Motif
Grainyhead-Elf-1-NTF-1_M00951	2.6976e-09	AAACMAGTY AAACCRG--	
MYB2	1.9794e-06	AAACMAGTY- -AACSAGTTA	
grh	2.5118e-06	---AAACMAGTY RNNRAACCAG--	
MYB1AT	4.0985e-06	RACTKGTTT ---TGGTTW	
ACE2	4.3820e-06	RACTKGTTT TRCKGGTT-	



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
RORA_1	1.2075e-06	--ACCTTGGTCT TGACCTNNWW--	
SF1_M00727	2.5131e-06	AGAACAAGGT- ----CAAGGTC	
GR_M00921	3.3177e-06	ACCTTGGTCT ---NIGTNCT	
PPARalpha-RXRalpha_M00242	3.5748e-06	-----ACCTTGGTCT TGACCTTTGNCTAGWTYW	
RORalpha1_M00156	1.0071e-05	---ACCTTGGTCT NTGACCTNNWWN-	

6_bp_motif_9

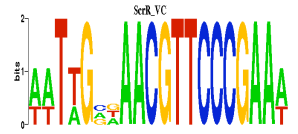


	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
shn-ZFP1	4.7754e-07	-----CGTTCC- GGGAACGWTCCC	
STB4	3.1813e-06	-CGTTCC-- TCGNNCGA	
Pax-1_M00326	3.8134e-06	-----GGAACG ATATCTAGAGCGGAACG	
AGR_pAT_567	5.1115e-06	-----CGTTCC----- TARYGGGAACGTTCCCRTWA	

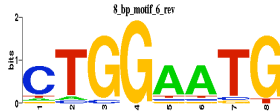
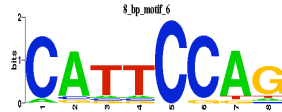
ScrR_VC

5.1115e-06

-----GGAACG-----
TTTCGGGAACGTTNNCAATT



8_bp_motif_6



forward

reverse compliment

Name

E value

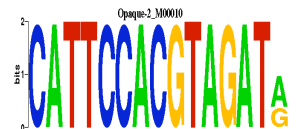
Alignment

Motif

Opaque-2_M00010

2.1242e-07

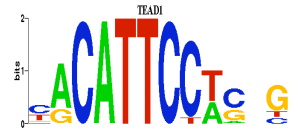
-----CTGGAATG
YATCTACGTGGAATG



TEAD1

8.8025e-07

--CATTCCAG--
YACATTCCWSNG



STAT5B_M00459

1.2865e-05

-CATTCCAG-----
NRNTTCCNGGAAWN



TE2F2NTPCNA

2.0984e-05

-CTGGAATG
GCGGGAAT-



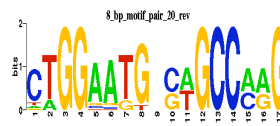
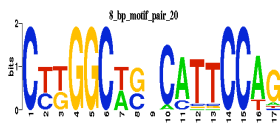
SV40COREENHAN

4.8024e-05

CATTCCAG
CNWWCCAC



8_bp_motif_pair_20



forward

reverse compliment

Name

E value

Alignment

Motif

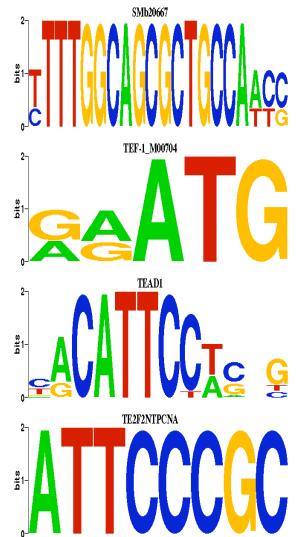
RIM101

1.9865e-05

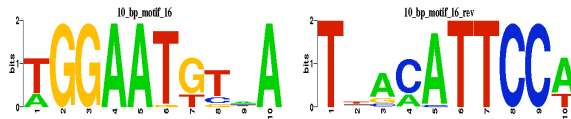
CYKGGCWSNCATTCCAG
CTTGGCA-----



SMb20667	1.2671e-04	--CTGGAATGNSWGCCMRG-- GGTTGGCAGCGCTGCCAAAA
TEF-1_M00704	8.7765e-04	CYKGGCWSNCATTCCAG -----CATYY---
TEAD1	2.1613e-03	CYKGGCWSNCATTCCAG-- -----YACATTCCWSNG
TE2F2NTPCNA	2.2611e-03	-CTGGAATGNSWGCCMRG GCGGGAAT-----



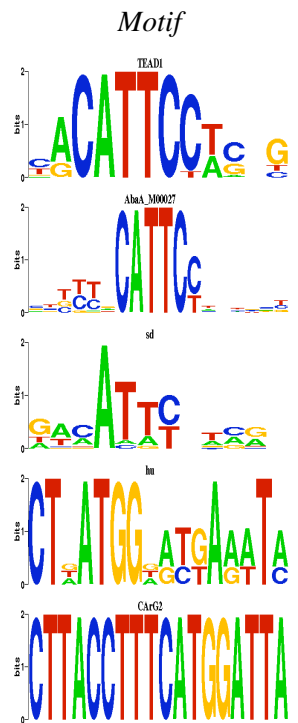
10_bp_motif_16



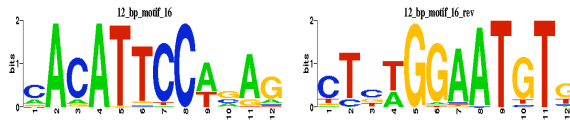
forward

reverse compliment

<i>Name</i>	<i>E value</i>	<i>Alignment</i>
TEAD1	9.1279e-08	TNACATTCCA--- -YACATTCCWSNG
AbaA_M00027	1.4757e-06	---TNACATTCCA----- NNNYNCATTCCNNNNNN
sd	5.8909e-06	---TGGAATGTNA NYNNNRAATKWN-
hu	9.4354e-06	--TNACATTCCA----- TATTCATNCCATNAG
CARg2	2.5397e-05	-TNACATTCCA----- CTTACCTTTCATGGATTA



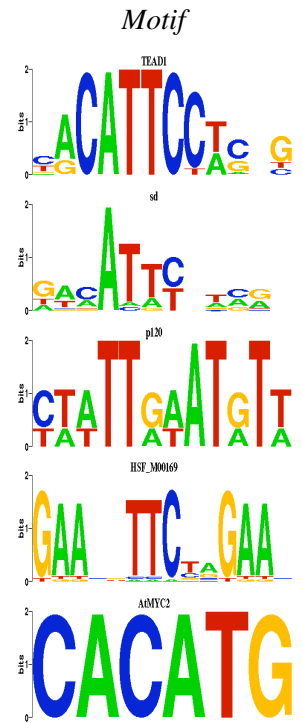
12_bp_motif_16



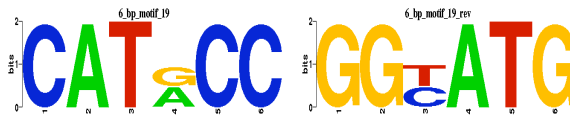
forward

reverse compliment

Name	E value	Alignment
TEAD1	2.2411e-08	CTNTGGAAATGTG CNSWGGAAATGTR
sd	8.8889e-08	CTNTGGAAATGTG NYNNNRAATKWN
p120	7.4549e-05	CACATTCCANAG AACATTCAATAG
HSF_M00169	1.2957e-04	-CACATTCCANAG- GAANNTTCNNGAAN
AtMYC2	2.1681e-04	CTNTGGAAATGTG -----CATGTG



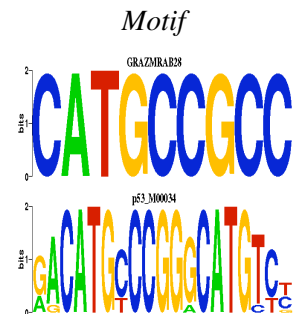
6_bp_motif_19

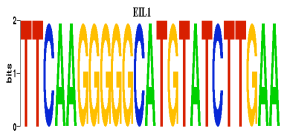
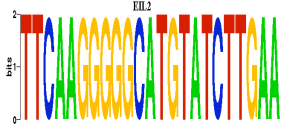
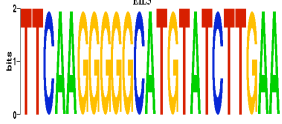


forward


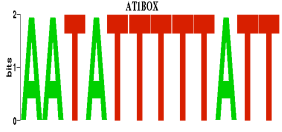



reverse compliment

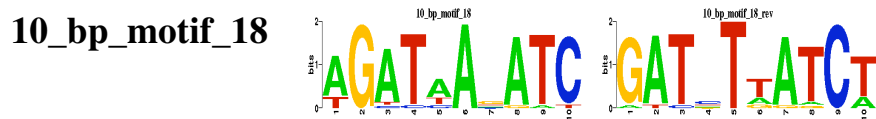
Name	E value	Alignment
GRAZMRAB28	4.9478e-07	---GGYATG GGCGGCATG
p53_M00034	1.1283e-05	---CATRCC----- RGACATGCCCGGGCATGTC








EIL1	2.3770e-05	-----CATRCC----- TTCAAGATACATGCCCCCTTGAA	
EIL2	2.3770e-05	-----CATRCC----- TTCAAGATACATGCCCCCTTGAA	
EIL3	2.3770e-05	-----CATRCC----- TTCAAGATACATGCCCCCTTGAA	



<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
BOX1PSGS2	2.3721e-08	GATNANNATC-- -ATAGAAATCAA	
AT1BOX	9.0339e-07	GATNANNATC-- AATAAAAATATT	
CCA1	3.1679e-06	GATNANNATC- ---AAMAATCT	
CCA1ATLHCB1	3.1679e-06	GATNANNATC- ---AAMAATCT	
Abd-B_M01094	8.1643e-06	GATNNTNATC ---TTTTAT-	



	<i>forward</i>	<i>reverse compliment</i>	
<i>Name</i>	<i>E value</i>	<i>Alignment</i>	<i>Motif</i>
GLN3	9.7500e-13	GATNTTATCT NATCTTATCN	
Evi-1_M00078	5.2360e-11	-GATNTTATCT---- TTATCTTATCTTRTC	
Evi1	7.2086e-11	---GATNTTATCT- NNTTATCTTRICTN	
GATA-3_M00350	3.2082e-10	GATNTTATCT- --TNTTATCTY	
GATA-2_M00349	3.2953e-10	GATNTTATCT- --TNTTATCTS	

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 STAMP is written by Shaun Mahony