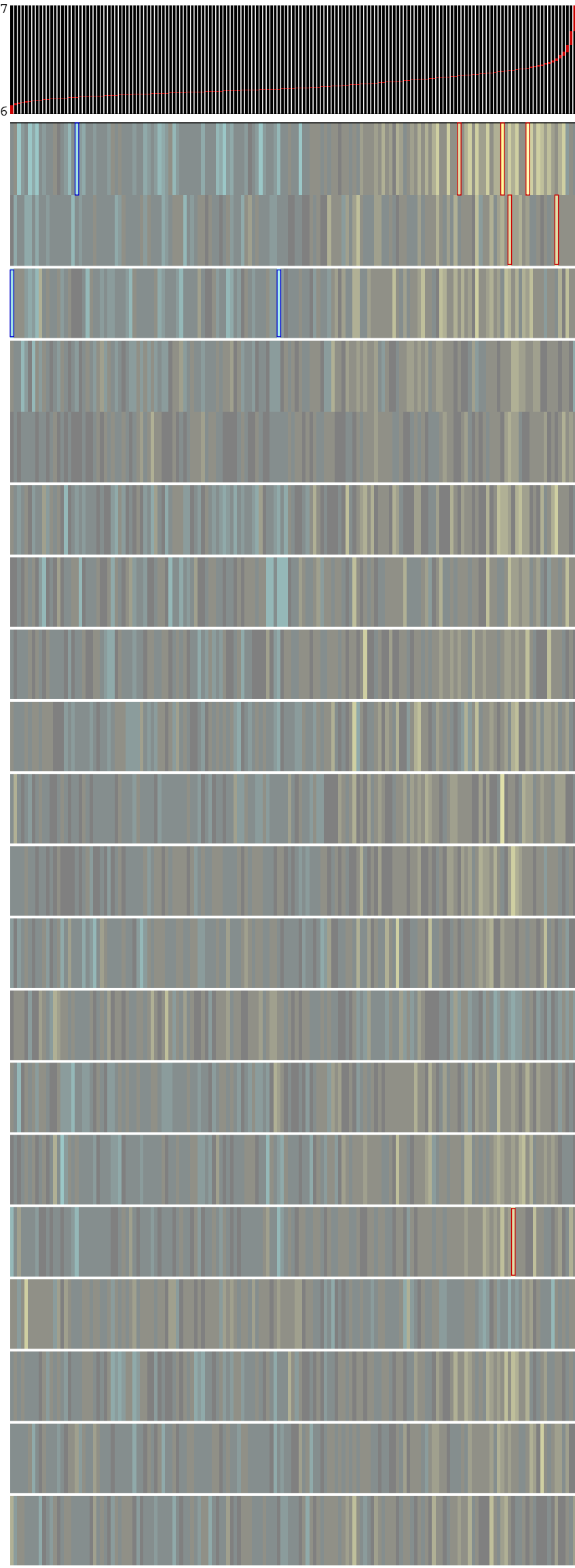


over-representation

under-representation



olfactory receptor activity, $p < 0.001$

complement activation, classical pathway, $p < 0.001$

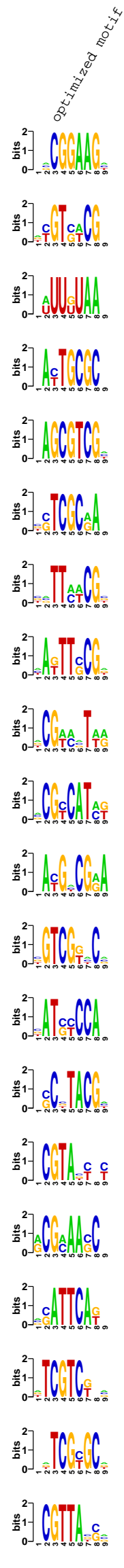
hormone metabolism, $p < 0.001$

ribosome biogenesis, $p < 0.001$

ribosome, $p < 0.001$

ribonucleoprotein complex, $p < 0.001$

endoplasmic reticulum part, $p < 0.01$



| optimized motif | location | MI (bits) | z-score | robustness | Position bias | orientation bias | conservation index | seed | motif name |
|-----------------|----------|-----------|---------|------------|---------------|------------------|--------------------|---------|------------|
| | 5' | 0.034 | 33.0 | 10/10 | Y | - | 1.00 | CCGGAAG | NRF-2 |
| | 5' | 0.015 | 10.2 | 10/10 | - | - | 0.91 | CGTCACG | - |
| | 3'UTR | 0.015 | 9.3 | 9/10 | - | → | 1.00 | UUUUUAA | - |
| | 5' | 0.015 | 9.2 | 9/10 | - | ← | 0.89 | ACTGCGC | - |
| | 5' | 0.014 | 6.4 | 6/10 | - | - | 0.25 | AGCGTCG | - |
| | 5' | 0.014 | 8.6 | 9/10 | - | - | 1.00 | CTCGCA | - |
| | 5' | 0.014 | 8.8 | 9/10 | - | → | 0.18 | CTTCACG | - |
| | 5' | 0.014 | 8.6 | 8/10 | - | - | 0.71 | AGTCCG | - |
| | 5' | 0.014 | 8.4 | 8/10 | - | → | 0.73 | CGAAGTA | - |
| | 5' | 0.014 | 7.7 | 7/10 | - | ← | 0.99 | CGTCATC | - |
| | 5' | 0.014 | 7.7 | 6/10 | - | → | 0.24 | ACGCCGG | - |
| | 5' | 0.013 | 7.6 | 8/10 | - | ← | 0.96 | GTCGCC | - |
| | 5' | 0.013 | 7.7 | 9/10 | - | - | 0.28 | ATGCCCA | - |
| | 5' | 0.013 | 7.5 | 10/10 | - | - | 0.94 | CCTACG | - |
| | 5' | 0.013 | 7.6 | 9/10 | - | → | 0.14 | CGTAGTC | - |
| | 5' | 0.013 | 7.6 | 9/10 | - | → | 0.69 | CGCAAGC | - |
| | 5' | 0.013 | 7.4 | 6/10 | - | - | 0.63 | CATTCA | - |
| | 5' | 0.013 | 7.0 | 6/10 | - | - | 0.89 | TCGTCG | - |
| | 5' | 0.013 | 7.2 | 7/10 | - | ← | 0.82 | ATCGCGC | E2F |
| | 5' | 0.013 | 6.5 | 6/10 | - | - | 0.84 | CGTTACC | v-Myb |