

1 putative sites were predicted with these settings (80%) in sequence named **hg38_refGene_NR_002819**

| Model ID | Model name | Score | Relative score | Start | End | Strand | predicted site sequence |
|----------|------------|--------|-------------------|-------|------|--------|-------------------------|
| MA0112.2 | ESR1 | 14.677 | 0.836641411950213 | 1401 | 1420 | 1 | ctgcaaggtcagcctgagac |

11 putative sites were predicted with these settings (80%) in sequence named **hg38_refGene_NR_002819**

| Model ID | Model name | Score | Relative score | Start | End | Strand | predicted site sequence |
|----------|------------|--------|-------------------|-------|------|--------|-------------------------|
| MA0258.2 | ESR2 | 5.494 | 0.802348330490692 | 201 | 215 | -1 | gagccactgtgccca |
| MA0258.2 | ESR2 | 8.045 | 0.836048563338327 | 201 | 215 | 1 | tgggcacagtggctc |
| MA0258.2 | ESR2 | 9.320 | 0.852892074463664 | 263 | 277 | 1 | aggtcaggagatcca |
| MA0258.2 | ESR2 | 8.141 | 0.837316780646588 | 413 | 427 | -1 | ggctcaccgtaacct |
| MA0258.2 | ESR2 | 8.558 | 0.842825599579345 | 413 | 427 | 1 | aggttacggtgagcc |
| MA0258.2 | ESR2 | 11.006 | 0.875165140939992 | 809 | 823 | -1 | aggtcacctcgttc |
| MA0258.2 | ESR2 | 6.485 | 0.815440032079092 | 1194 | 1208 | -1 | aggtaggatggcaa |
| MA0258.2 | ESR2 | 8.745 | 0.845295981211061 | 1332 | 1346 | -1 | agggcacacaaagct |
| MA0258.2 | ESR2 | 5.919 | 0.807962834199138 | 1406 | 1420 | -1 | gtctcaggctgacct |
| MA0258.2 | ESR2 | 12.802 | 0.898891373082036 | 1406 | 1420 | 1 | aggtcagcctgagac |
| MA0258.2 | ESR2 | 10.067 | 0.862760390393568 | 1450 | 1464 | -1 | atgtcaccaggtctt |