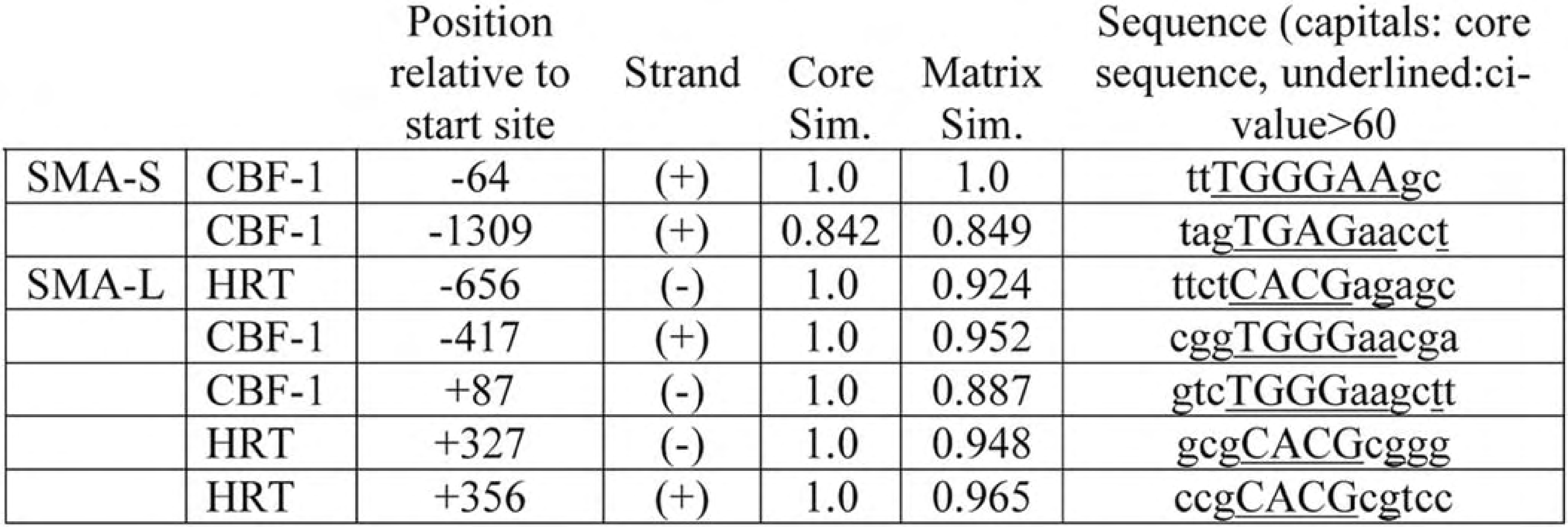
| Transcript | Forward primer | Reverse primer |
|---|---|---|
| HRT1 | CGTCGGGATCGGATAAATAA | GCACTCTCGGAATCCTATGC |
| HRT2 | CCAGAAAAAGACGGAGAGGA | GCGCGTCAAAGTAACCTTTC |
| β-actin | AGAAAATCTGGCACCACACC | GTCTCAAACATGATCTGGG |
| desmin | ATTGAATCTCTCAACGAGGA | ACACCTTCGACTTGTACCAC |
| myocardin | AATTCCATGAGCAAAGAAAA | GGTTACCTTTTATGGCCTCT |
| SM22α | AACAGCCTGTACCCTGATGG | CGGTAGTGCCCATCATTCTT |
| SM-MHC | GCTGGAAGACACACTGGACA | CCAGGTCTGCGTTCTCTTTC |
| GATA6 | AAAAAGAGGGAATTCAAACC | CCTATGTAGAGCCCATCTTG |
| SMA-L | CTGAGGGAAGGTCCTAACA | AGTGCTGTCCTCTTCTTCAC |
| SMA-S | AGCCAAGCACTGTCAGGA | ACAATGGATGGGAAAACAG |
| SMA-W | TCCCTTGAGAAGAGTTACGA | CCCCTGATAGGACATTGTTA |

**Supplemental Table 1. Primers used in this study.**



|  |  | Position relative to start site | Strand | Core Sim. | Matrix Sim. | Sequence (capitals: core sequence, underlined:ci-value>60 |
|---|---|---|---|---|---|---|
| SMA-S | CBF-1 | -64 | (+) | 1.0 | 1.0 | ttTGGGAAgc |
|  | CBF-1 | -1309 | (+) | 0.842 | 0.849 | tagTGAGaacct |
| SMA-L | HRT | -656 | (-) | 1.0 | 0.924 | ttctCACGagagc |
|  | CBF-1 | -417 | (+) | 1.0 | 0.952 | cggTGGGaacga |
|  | CBF-1 | +87 | (-) | 1.0 | 0.887 | gtcTGGGaagctt |
|  | HRT | +327 | (-) | 1.0 | 0.948 | gcgCACGcggg |
|  | HRT | +356 | (+) | 1.0 | 0.965 | ccgCACGcgtcc |

**Supplemental Table 2. Consensus CBF-1 and HRT binding sites in the SMA promoter.** Binding motif similarity scores are indicated. Perfect matches to core and matrix sequences get a score of 1.0, and hits with matrix scores lower than 0.8 are eliminated. Capital nucleotides indicate the core sequence, and the conservation index (ci) is given.