

**Table S1**

| <b>Gene name</b>    | <b>Accession number</b>   | <b>Forward primer</b> | <b>Reverse primer</b> | <b>Use</b>     | <b>Length of riboprobe fragment (% of cDNA covered)</b> | <b>Start*</b> | <b>End*</b> |
|---------------------|---------------------------|-----------------------|-----------------------|----------------|---------------------------------------------------------|---------------|-------------|
| <i>Sum1/MyoD1</i>   | SPU_021119                | GCCGATGCAGAGGAGTAGTT  | CTTGTTTCTGCCGAGTCCAT  | WMISH template | 552 bp (44,6%)                                          | +5            | +557        |
| <i>MyoD2</i>        | SPU_006232                | GACAGTGCCAAGGTGGATTT  | TGGGGTTAATGAGAGGGATG  | WMISH template | 951 bp** (93%)                                          | -105          | +846        |
| <i>MyoR2</i>        | SPU_012008                | CAGTTCAATGAGGCCGACTT  | TCTTCCATCAAGCGAGTCATC | WMISH template | 477 bp (70,9%)                                          | +45           | +522        |
| <i>Twist</i>        | SPU_030059                | TGAATTCTCTGACGGGGTCT  | GTTGTCGTTCTCGCACATTG  | WMISH template | 609 bp (60,2%)                                          | -248          | +361        |
| <i>Maf</i>          | XM_003724131.1            | GACGGTGATCAGACCATGTG  | CTGTACTTTGCACCCGTCCT  | WMISH template | 2187 bp (27,8%)                                         | +988          | +3175       |
| <i>Eya</i>          | SPU_013869                | GTATTGGAAGAGGGCGTCAA  | ACTTGTTACCCGCCAGAATG  | WMISH template | 878 bp (83,1%)                                          | +127          | +1005       |
| <i>Capz</i>         | SPU_021007/<br>SPU_000461 | AAGAAGAAGCAACGCCAAGA  | GAGATCGCGACTCACAAACA  | WMISH template | 441 bp (29,7%)                                          | +271          | +712        |
| <i>MHC</i>          | SPU_010054                | TGTTCCCCAAGGCTACTGAC  | AAGTGGACAGCGTGCTTCTT  | qPCR           |                                                         |               |             |
| <i>Tropomyosin1</i> | SPU_000128                | TGAATCAACAGAGCGTGAGG  | TGCACCTCAGCTTCAAGAGA  | qPCR           |                                                         |               |             |
| <i>Tropomyosin2</i> | SPU_011034                | GGGGCTGATCCAGTCAGATA  | GTTGAGCGTCTTGGCTTGTT  | qPCR           |                                                         |               |             |
| <i>Myocardin</i>    | 577722                    | ACCAAGGTGACGAGTTCCAC  | AGGAGAAGCAGGGTCAGACA  | qPCR           |                                                         |               |             |
| <i>Ubq</i>          | SPU_021496                | CACAGGCAAGACCATCACAC  | GAGAGAGTGCGACCATCCTC  | qPCR           |                                                         |               |             |
| <i>Sum1/Myod1</i>   | SPU_021119                | ACGACTTCGAAAGGTGAACG  | CTTGTTTCTGCCGAGTCCAT  | qPCR           |                                                         |               |             |
| <i>MyoR2</i>        | SPU_012008                | GAATGCTCGTGAACGAATC   | GCTTGAAGCAAGTCGAAGTGT | qPCR           |                                                         |               |             |
| <i>Twist</i>        | SPU_030059                | TGAATTCTCTGACGGGGTCT  | TTGGTGGTGGTAGGGTAGGA  | qPCR           |                                                         |               |             |
| <i>Maf</i>          | XM_003724131.1            | GGGTTTGCTATGGCAGTGAT  | AGTGGAGAGAGGGAACAGCA  | qPCR           |                                                         |               |             |

\* Numbering refers to the translation start site (+1) based on the cDNA sequence with the exception of MyoD2 which is calculated based on the genomic sequence

\*\* Contains also 282 bp of intron fragment