

Table 1. *MyHC-IIa* intron-exon boundaries

| Exon number | Exon size, bp | 3' splice site | 5' splice site | Intron number | Intron size, bp |
|-------------|------------------|------------------------------|-----------------------------|---------------|-----------------|
| 1 | 204* | | GGA GGA GCG gtgagtagaatccca | 1 | 98 |
| 2 | 144 | tttcctgtttaccag ACT CTG ACA | ATG ATC TAC gtgagtgtcccctgc | 2 | 1972 |
| 3 | 157 | ttttccttctcatag ACC TAT TCA | CTG ACT G.. gtgagttagccgaat | 3 | 1218 |
| 4 | 28 | taatttctttttag .AC CGA GAG | CTG ATC AC. gtaagtagattttat | 4 | 83 |
| 5 | 115 | gttttgatttgacag ..T GGA GAA | AAA ATA CAG gtgagtctgattgtc | 5 | 98 |
| 6 | 93 | ctcttgcccttgacag GGG ACT CTG | TCT CGC TTT gtaagtctctggac | 6 | 549 |
| 7 | 64 | agcttttatttcaag GGT AAA TTC | GAA ACA T.. gtaagtgttcagata | 7 | 124 |
| 8 | 99 | tttgtttccttccag .AT CTG CTA | CTT ATT G.. gtaagaaatgtcata | 8 | 2177 |
| 9 | 104 | gtttcctgtacttag .AA ATG CTT | GCC ACA GAT gtaagtagaacacaa | 9 | 527 |
| 10 | 139 | tggttatattgacag AGT GCT ATT | ACA GAA G.. gtatcaactaagtca | 10 | 365 |
| 11 | 119 | ctttcttctttttag .TT GCT GAC | GTA GAA CAG gtaggtgcataattc | 11 | 89 |
| 12 | 150 | attttgtcttttaag GTG TCC AAC | ATT TTT GAT gtgagttttagctg | 12 | 1369 |
| 13 | 171 | tatctatttatttag TTC AAC AGC | ATC GAG AAG gttggttttgcattt | 13 | 122 |
| 14 | 310 | tggtctgctttttag CCT ATG GGC | GAA GGA G.. gtaatgctcaaatgt | 14 | 626 |
| 15 | 77 | ttcctttttcttcag .AG GGA GCT | CTT TTC AGA gtaaggaagaaattg | 15 | 1164 |
| 16 | 88 | ttcctggttttacag GAG AAT TTG | ACT CCT G.. gtaagaaattccata | 16 | 87 |
| 17 | 118 | aatatgcatttttag .GT GCC ATG | AAA CAG AG. gtcagtttctcctga | 17 | 1440 |
| 18 | 124 | tatgtacttcaacag ..A TAC AAG | CAC ACC AAG gtaattttctgtaaa | 18 | 87 |
| 19 | 137 | tctttccattcacag GTC TTT TTC | GAG AGA AG. gtataaaaaatagt | 19 | 1396 |
| 20 | 256 | tcaattaaatttcag ..G GAG GCC | GTT CAG GCT gtgagttggaatc | 20 | 1558 |
| 21 | 243 | tgtttccaacttaag GAA GCC GAA | GAA AAC AAG gtatcaatcatattc | 21 | 91 |
| 22 | 177 | tcttcacctttag GTG AAA AAC | GTG GAT GAT gtaagtctggtatca | 22 | 82 |
| 23 | 146 | ataatttatatttag CTT GAA GGG | CTC AAA AA. gtaagtaagaaagaa | 23 | 83 |
| 24 | 91 | ctacttttctaaaag ..G AAA GAG | GAA TTG CAA gtaagtacatgattt | 24 | 82 |
| 25 | 390 | ttccaccattccag GCC CGC ATT | AAA GCC AAG gtactacaaattctg | 25 | 815 |
| 26 | 127 | ctttttcttctatag GGA AAC CTA | GAA TCT G.. gtaactctcccctct | 26 | 691 |
| 27 | 119 | tcttttgtccatcag .GT GAG TTT | GAG ATA AAA gtaattatgattcta | 27 | 142 |
| 28 | 197 | taactgcctccatag GCC AAG AAC | GAG GCC AA. gtatgtgcacagata | 28 | 722 |
| 29 | 184 | tgtataatattcaag ..G AAG AAG | TTC GAT AAG gtaattcctccagca | 29 | 76 |
| 30 | 166 | gtcttggtttttcag ATC CTG GCA | TTA CAG C.. gtaagtcctatcat | 30 | 102 |
| 31 | 126 | ttactcaaacaacag .AG GAG ATT | GAA GCA GAG gtacatgtaaaattg | 31 | 158 |
| 32 | 309 | cttgctgtcattaag GCA TCT CTT | ATC CTC AAG gtaaatatgtccaag | 32 | 87 |
| 33 | 204 | tggtttggtttcacag GAT ACC CAG | CAC ACC CAG gtgggattcagcaca | 33 | 581 |
| 34 | 126 | attctttttaaacag AAC ACC AGC | ATC ACT GAT gtgagtggcaggcac | 34 | 92 |
| 35 | 171 | ttatttgctatttag GCC GCC ATG | GAG GCC AGG gtgggtctccaata | 35 | 83 |
| 36 | 105 | cctacttatttgcag GTA CGG GAG | ACT TAC CAG gtacagccagtagtt | 36 | 122 |
| 37 | 96 | tttataatctttcag ACG GAA GAA | GAG GAG GCT gtaagtatttttaag | 37 | 1657 |
| 38 | 283 [†] | catttttattctcag GAG GAA CAA | | | |

*Calculated from the first A of the ATG initiating codon.

[†]Third base of stop codon is 153 bp after exon-intron junction.