**Table S1.** Primer sequences and conditions used for PCR.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene | Exon | Forward primer sequence (5’🡪3’) | Reverse primer sequence (5’🡪3’) | Ta (°C) | Product size (bp) |
| *KRT3* | 1-1 | CTGGAACAAACTTATTGCCTTG | GCTGATGGAGATGCTCTTG | 54 | 388 |
| 1-2 [37] | TGGAACAAACTTATTGCCTTG | CACCAGGACTGCCCAAGC | 58 | 680 |
| 1-3 | CAGTCGCAGCCTCTACAAC | CCTCAACCCTGGATATCTTC | 60 | 640 |
| 2 | CCTAGTCCTACCTGAGTGAAG | GAACTGAATGAACCAAGCTG | 54 | 454 |
| 3 | AGATAGTAAAGAGGATGTGCTC | CAGTGGAGTGAGGAGATTC | 54 | 284 |
| 4 | GACAAGGACCATCACTGCAC | GGCTCATTCCAGATGTCTTC | 54 | 309 |
| 5 | GAGCAAGGAATCAGTGAATG | CAACTGAACCACCATTAGAAG | 60 | 420 |
| 6 | CAACTTGCTCAGGAACTACAG | CCTCCAGACGTCTATTCCAG | 54 | 438 |
| 7 | GAATAGACGTCTGGAGGTCA | GCTGGTAGAGGCAAATGCTT | 54 | 546 |
| 8 | GCTTCTCTGTTCAGCTCTG | CCACAGTACAGTCTTGATGAC | 54 | 415 |
| 9 | CTTGATCAGCTCTGGATAGTC | GAAGAGTTCTCCAGCTGCTC | 54 | 554 |
| *KRT12* | 1A | AGTGAACTTTTCAACTGCGA | TGCCCGAGAGAATACCTAGA | 52 | 430 |
| 1B | AGGACTGGGTGCTGGTTATG | CTGCAAGTACAGCTAAATTGGA | 60 | 447 |
| 2-1 | GATTGAAGACCTCAGGAATAAG | CAATGAAGGCAGGACAGTAG | 55 | 558 |
| 2-2 | CCAGGTTGTTTCACTCCAC | See reverse primer for *KRT12* Exon 2-1 | 58 | 407 |
| 3 | GAAGATCAGTGGCCTTGTTC | CCATACTTGTCCTGACTCCAG | 60 | 324 |
| 4, 5 | CACGAAAGTCACAATGGAC | AGGATGCTACGTCTGTTTG | 55 | 465 |
| 6-1 | CAACTTGCTCAGGAACTACAG | CCTCCAGACGTCTATTCCAG | 60 | 438 |
| 6-2 | CAGAATCGGAAGGACGCTGA | CCGTTGTCTGCTCACCCTT | 60 | 634 |
| 7 | GAGTCTGCACTAGTTGGAAG | AGTAGTCAATGAGGTCTTACAG | 60 | 276 |
| 8 | GATGGATTGTATCAACCAATG | GCTACAACCTTGATGAGCTTAC | 60 | 881 |

Note: letters indicate primer pairs amplifying different regions of an exon, whereas numbers indicate alternative primer pairs used to sequence the entirety of an exon.