

Table S1. Amplicon characteristics of the PCR primers used in this study.

| Primers | Forward primer (5'→3') Reverse primer (5'→3') | Position # | Ta (°C) | Length (bp) | Mg²⁺ concentration (mM) | GC% |
|-----------------|--|-------------------|----------------|--------------------|---|------------|
| <i>SPRNA*</i> | AGGGACCACAGGATCGAACAGACG GGGACTAACCCCAGCAGGAGGCA | 568-2884 | 55 | 2317 | 3.0 | 73.03 |
| <i>SPRNB</i> | AGAGGCGTCTACAGCTACTGGGCGTGG CCCCGTGATGCTGGACCGAGACC | 2526-5387 | 60 | 2862 | 2.5 | 66.56 |
| <i>SPRNA †</i> | GGAGCAGTCGGGTCACAGATGGT AGCTGGGGTGGCCTGAACAGCCT | 804-2978 | 55 | 2172 | 3.0 | 73.70 |
| <i>SPRNA-b</i> | AGGGCTGGTGCTGCTCTG ACGGGA GGGAGGGGACA | 926-1302 | 54.3 | 377 | 3.0 | 70.03 |
| <i>SPRNA-c</i> | GGGTGCGAGGTGCTGAAG GACCAGAGGCGACCCCTG | 1146-1541 | 54.3 | 396 | 2.5 | 77.78 |
| <i>SPRNA-d</i> | CGCGGCTGGTAAGACCGG TGTGGAGCGTGGAGTGCG | 1458-1883 | 54.3 | 426 | 3.0 | 77.00 |
| <i>SPRNA-e</i> | CTCACCCGCTTCCTTTGG GACGGGGCACTCAGGAGCT | 1711-2155 | 54.3 | 446 | 2.5 | 70.85 |
| <i>SPRNA-g</i> | GACGGCAGTGCAGCCAAG GGACTAACCCCAGCAGGAGG | 2265-2883 | 55.4 | 619 | 3.0 | 76.58 |
| <i>SPRN-cds</i> | CCCGCG TACCACCCAATG TAACCCCAGCAGGAGGCA | 2041-2879 | 56 | 839 | 2.5 | 73.90 |
| Promoter 1* | CTCGAGCAGTCGGGTCACAGATGGTGGG AAGCTTGCAGGGAGC CTCGGTCGC TTTC | 808-1691 | 55 | 884 | 2.5 | 75.00 |
| Promoter 1† | CTCGAGCAGTCGGGTCACAGATGGTGGG AAGCTTGCAGGGAGCCTCGGTCGCTCTC | 808-1691 | 60 | 883 | 2.5 | 74.63 |
| Promoter 2 | CTCGAGGAGCAGTCGGGTCACAGATGG AAGCTTGAGGACTTGGGGAGGTAGGGAG | 805-2129 | 58 | 1325 | 3.0 | 73.66 |

* and † indicate the PCR primers for cattle and buffalo, respectively. Other primers are universal for the two species.

indicates position in sequence DQ058606 of GeneBank.

Ta = annealing temperature; GC% = the content of guanine plus cytosine.