```
goat CDK8 (XP_005687614.1)   MDYDFKVKLSSERERVEDLFEYEGCKVGRGTYGHVYKAKRKDGKDDKDYALKQIEGTGIS 60
goat CDK19 (XP_017908559.1)  ------------------------------------------------------------ 1

goat CDK8 (XP_005687614.1)   MSACREIALLRELKHPNVISLQKVFLSHADRKVWLLFDYAEHDLWHIIKFHRASKANKKP 120
goat CDK19 (XP_017908559.1)  ...................A........S.............................. 60

goat CDK8 (XP_005687614.1)   VQLPRGMVKSLLYQILDGIHYLHANWVLHRDLKPANILVMGEGPERGRVKIADMGFARLF 180
goat CDK19 (XP_017908559.1)  M....S..................................................... 120

goat CDK8 (XP_005687614.1)   NSPLKPLADLDPVVVTFWYRAPELLLGARHYTKAIDIWAIGCIFAELLTSEPIFHCRQED 240
goat CDK19 (XP_017908559.1)  ............................................................ 180

goat CDK8 (XP_005687614.1)   IKTSNPYHHDQLDRIFNVMGFPADKDWEDIKKMPEHSTLMKDFRRNTYTNCSLIKYMEKH 300
goat CDK19 (XP_017908559.1)  ......F.........S.............R....YP..Q.....T..A.S......... 240

goat CDK8 (XP_005687614.1)   KVKPDSKAFHLLQKLLTMDPIKRITSEQAMQDPYFLEDPLPTSDVFAGCQIPYPKREFLT 360
goat CDK19 (XP_017908559.1)  .......V.L..........T........L.....Q......L................N 300

goat CDK8 (XP_005687614.1)   EEEPDDKGDKKNQQQQ----------------------PGNNHTNGTG-----HPG--- 389
goat CDK19 (XP_017908559.1)  .D..EE....NQ....NQHQQPTAPPQQAAAPPQAPPQQQNSTQ....AGGAGAG.AGAG 360

goat CDK8 (XP_005687614.1)   ---NQDSSHTQGPPLKKVRVVPPTTTSGGLIMTSDYQRSNPHAAYPNPGPSTSQPQSSMG 446
goat CDK19 (XP_017908559.1)  LQHS...GLN.V..N..P.LG.SG.N...PV.P....H.SSRLN.QSSVQGS..S..TL. 420

goat CDK8 (XP_005687614.1)   YSTTSQQPPQY--SHQTHRY 464
goat CDK19 (XP_017908559.1)  ..SS...SA..HP...A... 440
```

**Figure S1.** A protein sequence alignment between CDK8 and CDK19 in goat.

**Table S1.** Details of the primers in this study and their corresponding amplicon size.

| Genes | Reference | Primer pair with sequence (5′–3′)[a] | Primer length (nt) | TA[b] (℃) | Amplicon size[c] (bp) |
|---|---|---|---|---|---|
| circRNA-1926 | [16] | F: GGTGGCATCGATAATCCTGC | 20 | 55 | 182 |
| | | R: ACAGATCCCACATTTCAGAACT | 22 | | |
| *Keratin 6* | XM_018049019.1 in GenBank | F: CAGTCGCAGCCTCTACAACCT | 21 | 56 | 159 |
| | | R: CAAATGCCACCTCCATAACCA | 21 | | |
| *Keratin 7* | XM_005680100.3 in GenBank | F: GAGTTTGTGGTGTTGAAGAA | 20 | 56 | 194 |
| | | R: AAGTCCAGGGAGCGGTTGTT | 20 | | |
| *Keratin 8* | XM_005679931.3 in GenBank | F: TCCTTCAGCAGCCGCTCCTA | 20 | 58 | 160 |
| | | R: CTGTAATGCCCCCCAAACCT | 20 | | |
| *Keratin 16* | XM_013972083.2 in GenBank | F: CCTTTGTGGCTAGTGGTATG | 20 | 55 | 188 |
| | | R: CAGTTTCAGGGGTTGCTTAT | 20 | | |
| *Keratin 17* | XM_018065055.1 in GenBank | F: GGGGAATGGAAACAGAGGAG | 20 | 56 | 112 |
| | | R: GAGGAGAGAAGCCCAAGATG | 20 | | |
| *CDK19* | XM_005684572.3 in GenBank | F: TGAGAGGGGGAGAGTCAAAATA | 22 | 55 | 104 |
| | | R: ACCAGAAAGTCACAACTACAGG | 22 | | |
| *UBC* | [23] | F:GCATTGTTGGGTTCCTGTGT | 20 | 52 | 90 |
| | | R:TTTGCATTTTGACCTGTGAG | 20 | | |
| *YWHAZ* | [23] | F:TGTAGGAGCCCGTAGGTCATCT | 22 | 56 | 102 |
| | | R:TTCTCTCTGTATTCTCGAGCCATCT | 25 | | |
| *SDHA* | [23] | F:AGCACTGGAGGAAGCACAC | 19 | 53 | 105 |
| | | R:CACAGTCGGTCTCGTTCAA | 19 | | |
| *CDK19*[d] | The present study | F:TTGAATGTTTAGTTTTTGAAAT | 22 | 55 | 544 |
| | | R:ACAACTCCCATACTAACATAAA | 22 | | |
| miR-152-3p | MIMAT0000162 in miRBase | F:CGTCAGTGCATGACAGAACTTGG | 23 | 62 | N.A. |
| miR-148a-3p | MIMAT0035977 in miRBase | F:CGTCAGTGCACTACAGAACTTTGT | 24 | 60 | N.A. |
| miR-148b-3p | MIMAT0035979 in miRBase | F:CGTCAGTGCATCACAGAACTTTGT | 24 | 62 | N.A. |
| miR-642a-5p | MIMAT0003312 in miRBase | F:CGGTCCCTCTCCAAATGTGTCTTG | 24 | 63 | N.A. |
| let-7d-5p | [24] | F:CGAGAGGTAGTAGGTTGCATAGTT | 24 | 62 | N.A. |
| miR-26a-5p | [24] | F:CGTTCAAGTAATCCAGGATAGGCT | 24 | 61 | N.A. |
| miR-15a-5p | [24] | F: CGTAGCAGCACATAATGGTTTGTG | 24 | 63 | N.A. |

[a] F: forward, R:reverse; [b] TA annealing temperature; [c] N.A.: not available; [d] CDK19 was used for the designing of BSP primers.