

Supplementary Information

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-102 gtccggtccgggttcgcttgctcgtcagcgtccgcttttctggcccccccaaccccccgacaggaccccccttgagctcgtccctcagctgctacc 0
1  atgagcgaccaagatcactccatggatgaaatgacagcagtggtgaagattgaaaaaggagttggtggcaataacgggggcaatggaaat 90
1  M S D Q D H S M D E M T A V V K I E K G V G G N N G G N G N 30
    acetylation site                                     Signal peptide
91  ggtagtggccttttctcaggctcgaagcggcagcgcagcagtagcagcagcagcggaggaggaggcaggaatcccagccatcccct 180
31  G S G A F S Q A R S G S A G S S S S S S G G G G Q E S Q P S P 60
181 ttgctctgctggcagcaacttgacagcaaatgagtcaccaatgaaaacagcaacaactcccagggcccaagccagtcagggggcaca 270
61  L A L L A A T C S R I E S P N E N S N N S Q G P S Q S G G T 90
271 ggtgagcttgacctcacagccacacaactttcccagggtgccaatggctggcagatcatcttctcctcctctggggctacctctacctcg 360
91  G E L D L T A T Q L S Q G A N G W Q I I S S S S G A T P T S 120
361 aaggaacagagtggtgagcagtagcaaacggcaacaatggcagtgagtcctcaagaatcgcacggctcctcgggtgggcagtagtgtgtggct 450
121 K E Q S G S S T N G N N G S E S S K N R T V S G G Q Y V V A 150
    glycosylation sites
451 gccacttccaacctcagaaccagcaagtcctaaccaggactacctggagtgatgcctaataattcagtatcaagtaatcccacagttccag 540
151 A T S N L Q N Q Q V L T G L P G V M P N I Q Y Q V I P Q F Q 180
541 accgttgatgggcaacagctgcagtttgctgccactggggcccaagtcagcagagtaggttcaggtcagatacagatcataccaggtgca 630
181 T V D G Q Q L Q F A A T G A Q V Q Q D G S G Q I Q I I P G A 210
631 aaccaacagatcatcaaatcgaggaagtggaggcaacatcattgctgctatgccaaacctactccagcaggtgtcccccttcaaggc 720
211 N Q Q I I T N R G S G G N I I A A M P N L L Q Q A V P L Q G 240
721 ctggctaataatgtactctcaggacagactcagtagtgaccaatgtaccagtgccctgaatgggaatatcaccttctgctcctgtcaac 810
241 L A N N V L S G Q T Q Y V T N V P V A L N G N I T L L P V N 270
811 agcgtttctgcagctaccttgactcctagctctcaagcagtcacgatcagcagctctgggtcccaggagagtggtcacacagctgtcacc 900
271 S V S A A T L T P S S Q A V T I S S S G S Q E S G S Q P V T 300
    glycosylation sites
901 tcagggactgccatcagttctgccagtttggtatcttcacaagccagttccagctcctttttaccaatgccaatagctactcaacaact 990
301 S G T A I S S A S L V S S Q A S S S S F F T N A N S Y S T T 330
991 actaccaccagcaacatgggagttatgaacttcaccaccagcggatcagcagggaccaactctcagagccagacaccccagagggtcagc 1080
331 T T T S N M G V M N F T T S G S A G T N S Q S Q T P Q R V S 360
1081 gggctacagggatctgatactctgaacatccagcagaaccagacatctggaggttactgcaagcaagtcaacaaaaagaggagagcaa 1170
361 G L Q G S D T L N I Q Q N Q T S G G S L Q A S Q Q K E G E Q 390
1171 aaccagcagacacagcagcaacaacaaattctcatccagcctcagctggttcaaggggacaggtcttccaggccctccaagccgccccca 1260
391 N Q Q T Q Q Q Q I L I Q P Q L V Q G G Q A L Q A L Q A A P 420
1261 ttgtcagggcagacctttacaactcaagctatctccaggaaacctccagaacctcagcttcaggctgttccaaactctggccccatc 1350
421 L S G Q T F T T Q A I S Q E T L Q N L Q L Q A V P N S G P I 450
1351 atcatccggacaccaacagtggggcccattggacaggtcagctggcagactcttcagctgcagaacctccaagttcagaaccacacaagcc 1440
451 I I R T P T V G P N G Q V S W Q T L Q L Q N L Q V Q N P Q A 480
1441 cagacaatcaccttgcccccaatgcagggtgtttctttggggcagaccagcagcagcaataccacccttacacctattgcctcagctgcc 1530

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Figure S1. Cont.

481 **Q** **T** **I** **T** **L** **A** **P** **M** **Q** **G** **V** **S** **L** **G** **Q** **T** **S** **S** **S** **N** **T** **T** **L** **T** **P** **I** **A** **S** **A** **A** 510
glycosylation sites

1531 tccatccctgccggcacagtcactgtgaatgtctcagctctcctccatgcctggcctccagaccattaacctcagtgcatgggtgct 1620
511 **S** **I** **P** **A** **G** **T** **V** **T** **V** **N** **A** **A** **Q** **L** **S** **S** **M** **P** **G** **L** **Q** **T** **I** **N** **L** **S** **A** **L** **G** **A** 540
1621 tcaggaatccagggtccaccagcttccaagcctgccttggcgatagcaaatgcctcagggtgatcatggagctcagcttggcctccatggg 1710
541 **S** **G** **I** **Q** **V** **H** **Q** **L** **P** **S** **L** **P** **L** **A** **I** **A** **N** **A** **S** **G** **D** **H** **G** **A** **Q** **L** **G** **L** **H** **G** 570
1711 gctggtggtgatggaatacatgatgacccaacaggtggagaggaaggagagaacagtcagatccccaacccaagctggtcggaggacc 1800
571 **A** **G** **G** **D** **G** **I** **H** **D** **D** **P** **T** **G** **G** **E** **E** **G** **E** **N** **S** **P** **D** **P** **Q** **P** **Q** **A** **G** **R** **R** **T** 600
1801 cggcggaagcatgcacttgcctcactgtaaagatagtgaaaggaagggtctctggggatcctggcaagaagaacagcacatttgtcac 1890
601 **R** **R** **E** **A** **C** **T** **C** **P** **Y** **C** **K** **D** **S** **E** **G** **R** **G** **S** **G** **D** **P** **G** **K** **K** **K** **Q** **H** **I** **C** **H** 630
1891 atgcaaggctgtggcaagtatatggcaagacctcacacctacgggcacacttgcctggcatacaggcgagagccttccatgtgtacc 1980
631 **M** **Q** **G** **C** **G** **K** **V** **Y** **G** **K** **T** **S** **H** **L** **R** **A** **H** **L** **R** **W** **H** **T** **G** **E** **R** **P** **F** **M** **C** **T** 660
1981 tggctattctgtgggaacgcttcacacgcttcagatgattacagaggcacaacgcacacacacaggtgagaagaaattgcctgcct 2070
661 **W** **S** **F** **C** **G** **K** **R** **F** **T** **R** **S** **D** **E** **L** **Q** **R** **H** **K** **R** **T** **H** **T** **G** **E** **K** **K** **F** **A** **C** **P** 690
2071 gagtgtcccaagccttcatgaggagtggccacctgtcaaagcatatcaagaccaccagaaataagaaggaggcccggtgtgaccctg 2160
691 **E** **C** **P** **K** **R** **F** **M** **R** **S** **G** **H** **L** **S** **K** **H** **I** **K** **T** **H** **Q** **N** **K** **K** **G** **G** **P** **G** **V** **A** **L** 720
2161 agtgtgggcacttggccctggacagtgaggcaggttcagaaggcagtggtactgcccaccttcagcccttattaccaccaacatggta 2250
721 **S** **V** **G** **T** **L** **P** **L** **D** **S** **G** **A** **G** **S** **E** **G** **S** **G** **T** **A** **T** **P** **S** **A** **L** **I** **T** **T** **N** **M** **V** 750
2251 gccatggaggccatttgtccagagggtattgccctcttgccaacagtggtcatcaatgtcatgaggtggcagatctgcagtcattaat 2340
751 **A** **M** **E** **A** **I** **C** **P** **E** **G** **I** **A** **R** **L** **A** **N** **S** **G** **I** **N** **V** **M** **Q** **V** **A** **D** **L** **Q** **S** **I** **N** 780
2341 atcagtgccaatggcttctgaggtcaggcacctggggccagagacatatgggccatacccatcaaccctgggatgcaaggtagcatgggt 2430
781 **I** **S** **G** **N** **G** **F** * 786
2431 ccaagagacgtgtgggagagtgcacctgagggcattaaaaatgcatgggtggggaagaattgggggtgggatacaaaagaagagatggg 2520
2521 gtccctggcaccacctgtatcatcagttacattctttaaagtgggaaacatagtgaaaattctgttgggtgccaccttggatgagcatttgtt 2610
2611 tgaccccaaacagtttcttaacacttcttaccaccagcctccccttctgctatttcccttctcagctccccatgatggatccccctt 2700
2701 cctaaagccatcatgccttgataaatatataatgatcattgaaatacttttaacaaaaacagattctatattatataatataataa 2790
2791 aagatataatagatgcatattgcaggggttggctgggaggaggaaggagaccattcgggtgacaaaataccttggctattttttatatt 2880
2881 gccttatttcttatggctgagccttgtgtgacacatcaagattttctatagatgtgtcttggcttcccaccagattaagcatttata 2970
2971 tgctctgcttttagttatatacatagataatgttttcttcttaattttgtcttttaatttgggatcagcttcttgcactcttcc 3060
3061 ctgactcaaccttctgtctccccttctctcacctgatcacttcatgttttggtttggtagtggctcctggatgaggcactctgtca 3150
3151 tgtttttataaagtcttagtcccagcagcagaatggagaagccttgaagctcaggcgaatgcttgaggtagctgtgaagagagtgttca 3240
3241 aaatactactgacgcaggcacccttttggctgagagtgcaaggcacctctctctcattagctgctcgaagcaggaatcagaag 3330
3331 tctttctatggaattgtacaagagaccttggtaagttagtctgggatcagtttgtgcaaacgtgaaaagatgggtcaataataggtg 3420
3421 ggagcttccaataggaataatgatgtgtcagaagtggaaagtactcaagtagtctcaggtcaggagttagtgagatattggaccttgtg 3510
3511 caactgtcttccaaggtagcttaagctttagatgtgtgggttctgagttcacgttctgaaaggaatacacttcccttttgaacatct 3600
3601 ccagtagttgcttcccatatgttgttatggagtgtcagccagtgactgttctggatttccattctgcagaactccagagcatggatca 3690
3691 gtggcaaggcagtggttctttagcttcccttaactcttctaggttggctcctgaggggaaaggaagcactcatgatcatgggagtg 3780
3781 atagcccagaaacaaaagaaatctgtcttaccactgtggcttataggggagaccagggaaaaccatctgcttttccatggcctgat 3870
3871 tccgtaagagactgatccaaaaattacagcggcaggaactcttagtgacttggcactgagatttaaatgcaaccagagttgtcctcaa 3960
3961 ggcccagccattaaaacattgtctcttctgacttctggtacctcgtcagagagcttctcactgtgaggaagtgtgaaatggctgtgtg 4050
4051 tatgtgtgtaactgttagattgggataggtttctgttagccaatactataagagacctgcaataaaaaattaccctaactctgtaga 4140
4141 aagtgaagtgttgtgtatgacctgtgtgaatgtgtgtctgcttgtatatactacacagatgagaaattatattgaaattgtt 4230
4231 ggaaataaatcaaatcagatcaaaatgcaaaaaaaaaaaaaa 4273

Figure S1. The nucleotide sequence of SP1 gene full-length cDNA and the deduced amino acid sequence of capra. An asterisk represents a termination codon. The grey bases represent predicted phosphorylation sites. The bold parts represent GLN rich region. The Italics parts represent SRE rich region. The underlined bases represent 3 zinc fingers. Other functional sites, such as acetylation site, glycosylation site, signal peptide, initiation codon, stop codon, poly A tail and “aacaaa” sequence are shown on the figure. The nucleotide sequence was submitted to the NCBI GenBank, accession no. HM_236311.

bos	MSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGSGAFSQAR--SSSAGSSSSSGGGGQESQFSP LALLAATCSRIESP NENS	78
goat	MSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGSGAFSQAR--SSSAGSSSSSGGGGQESQFSP LALLAATCSRIESP NENS	78
homo	MSDQDHSMDEMTAVVKIEKGVGGNNGGNGNGSGAFSQAR--SSSAGSSSSSGGGGQESQFSP LALLAATCSRIESP NENS	78
mus	MSDQDHSMDEVAVVKIEKDVGGNNGGSGNGGGAAFSQTRS SSII SSSSSGGGGQESQFSP LALLAATCSRIESP NENS	80
bos	NNSQGSPSQSGGTGELDLTATQLSQGANGWQI ISSSSGATPTSKEQSGS STNG NG SESSKNRTVSGGQYVVAATS NLQ NQ	158
goat	NNSQGSPSQSGGTGELDLTATQLSQGANGWQI ISSSSGATPTSKEQSGS STNG NG SESSKNRTVSGGQYVVAATS NLQ NQ	158
homo	NNSQGSPSQSGGTGELDLTATQLSQGANGWQI ISSSSGATPTSKEQSGS STNG NG SESSKNRTVSGGQYVVAAP NLQ NQ	158
mus	NNSQGSPSQSGGTGELDLTAAQLSQGANGWQI ISSSSGATPTSKEQSG STNG --- SESSKNRTVSGGQYVVAATP NLQ NQ	157
bos	QVLTGLPGVMPNIQYQVI PQFQTV DGQQLQFAATGAQVQD DGSGQIQI IPGANQOI I NRGSGGNI IAAMPNLLQ QAVPL	238
goat	QVLTGLPGVMPNIQYQVI PQFQTV DGQQLQFAATGAQVQD DGSGQIQI IPGANQOI I NRGSGGNI IAAMPNLLQ QAVPL	238
homo	QVLTGLPGVMPNIQYQVI PQFQTV DGQQLQFAATGAQVQD DGSGQIQI IPGANQOI I NRGSGGNI IAAMPNLLQ QAVPL	238
mus	QVLTGLPGVMPNIQYQVI PQFQTV DGQQLQFAATGAQVQD DGSGQIQI IPGANQOI I NRGSGGNI IAAMPNLLQ QAVPL	237
bos	QGLANNVLSGQTQYVTNVPVALNGNITLLPVNSVSAATLTPSSQAVTI ISSSGSQES GSQPVTSGTA ISSASLVSSQ ASSS	318
goat	QGLANNVLSGQTQYVTNVPVALNGNITLLPVNSVSAATLTPSSQAVTI ISSSGSQES GSQPVTSGTA ISSASLVSSQ ASSS	318
homo	QGLANNVLSGQTQYVTNVPVALNGNITLLPVNSVSAATLTPSSQAVTI ISSSGSQES GSQPVTSGTI ISSASLVSSQ ASSS	318
mus	QGLANNVLSGQTQYVTNVPVALNGNITLLPVNSVSAATLTPSSQAGTI ISSSGSQES SSQPVTSGTA ISSASLVSSQ ASSS	317
bos	SFFTANASYSTTTTTSNMGMNFTTSGSAGTSSQSGTPQRVSGLQSD LN IQNQTS GGSLQAS SOQKEGEQ QQTQ QQQ	398
goat	SFFTANASYSTTTTTSNMGMNFTTSGSAGTSSQSGTPQRVSGLQSD LN IQNQTS GGSLQAS SOQKEGEQ QQTQ QQQ	398
homo	SFFTANASYSTTTTTSNMGMNFTTSGSSTSSQSGTPQRVSGLQSD LN IQNQTS GGSLQAS SOQKEGEQ QQTQ QQQ	398
mus	SFFTANASYSTTTTTSNMGMNFTTSGSSTSSQSGTPQRVSGLQSD LN IQNQTS GGSLQAS SOQKEGEQ QQTQ QQQ	397
bos	QILIQPQLVQGGQALQALQAAPLSGQFTTTQAI Q ETLQNLQ LQAV NSGPI I IR PTVGPNGQVSW OTLQ LQNLQ VQNF	478
goat	QILIQPQLVQGGQALQALQAAPLSGQFTTTQAI S QETLQNLQ LQAV NSGPI I IR PTVGPNGQVSW OTLQ LQNLQ VQNF	478
homo	-ILIQPQLVQGGQALQALQAAPLSGQFTTTQAI S QETLQNLQ LQAV NSGPI I IR PTVGPNGQVSW OTLQ LQNLQ VQNF	477
mus	-ILIQPQLVQGGQALQALQAAPLSGQFTTTQAI S QETLQNLQ LQAV NSGPI I IR PTVGPNGQVSW OTLQ LQNLQ VQNF	476
bos	QAQTITLAPMQVSLGQTSSS NTLLTPIASAASIPAGTVVNAALSSMPGLQ TINLSALG ASGIQVH QLPS LPLA TANA	558
goat	QAQTITLAPMQVSLGQTSSS NTLLTPIASAASIPAGTVVNAALSSMPGLQ TINLSALG ASGIQVH QLPS LPLA TANA	558
homo	QAQTITLAPMQVSLGQTSSS NTLLTPIASAASIPAGTVVNAALSSMPGLQ TINLSALG ASGIQVH PL QLPLA TANA	557
mus	QAQTITLAPMQVSLGQTSSS NTLLTPIASAASIPAGTVVNAALSSMPGLQ TINLSALG ASGIQVH QLP LPLA TANT	556
bos	SGDHGAQLGLHCAGGDGIHDD PTAGGE E GENS FD PPQAGRRTRREACTCPYCKDSEGR SGDPGKKKOHICH MOGCGKVY	638
goat	SGDHGAQLGLHCAGGDGIHDD PTAGGE E GENS FD PPQAGRRTRREACTCPYCKDSEGR SGDPGKKKOHICH MOGCGKVY	638
homo	PGDHGAQLGLHCAGGDGIHDD PTAGGE E GENS FD PPQAGRRTRREACTCPYCKDSEGR SGDPGKKKOHICH MOGCGKVY	637
mus	PGDHGTQLGLHCSGGDGIHDD PTAGGE E GENS DL PPQAGRRTRREACTCPYCKDSEGR SGDPGKKKOHICH MOGCGKVY	635
bos	GKTSHLRAHLRWHTGERPFMC TWSFCGKRFRSDELQRHKRHTHTGEKKFACPECPKRFMRS DHLSKHIKTHQNKKG GPV	718
goat	GKTSHLRAHLRWHTGERPFMC TWSFCGKRFRSDELQRHKRHTHTGEKKFACPECPKRFMRS DHLSKHIKTHQNKKG GPV	718
homo	GKTSHLRAHLRWHTGERPFMC TWSYCGKRFRSDELQRHKRHTHTGEKKFACPECPKRFMRS DHLSKHIKTHQNKKG GPV	717
mus	GKTSHLRAHLRWHTGERPFMC TWSYCGKRFRSDELQRHKRHTHTGEKKFACPECPKRFMRS DHLSKHIKTHQNKKG GPV	715
bos	ALSVGTLPLDSGAGSE GS GTA TPSALITTNVAMEAICPEGIARLANSGINVMQVADLQ SINISGNGF	786
goat	ALSVGTLPLDSGAGSE GS GTA TPSALITTNVAMEAICPEGIARLANSGINVMQVADLQ SINISGNGF	786
homo	ALSVGTLPLDSGAGSE GS GTA TPSALITTNVAMEAICPEGIARLANSGINVMQVADLQ SINISGNGF	785
mus	ALSVGTLPLDSGAGSE -- GTA TPSALITTNVAMEAICPEGIARLANSGINVMQVTE LQ SINISGNGF	781

Figure S2. Alignment analysis of SP1 protein among various species. The similarity of the amino acid of goat shears is 99.3%, 96.9% and 95% with bovine (NM_001078027.1), human (NM_138473.2), and rattus (NM_013672.2) respectively. Activity sites prediction of SP1 are marked by the rectangular box.

Table S1. Summary of genes, primers, and product sizes for RT-qPCR.

Gene	GenBank ID Number	Primer Name	Primer Sequence (5' to 3')	Size (bp)	Primer Source
<i>SPI</i>	HM236311	F. 1836 R. 1945	TAGTGAAGGAAGGGGCTCTGG AAGTGTGCCCGTAGGTGTGAG	110	this manuscript
<i>PPARγ</i>	HQ589347.1	F. 101 R. 245	CCTTCACCACCGTTGACTTCT GATACAGGCTCCACTTTGATTGC	145	[3]
<i>LXRα</i>	GU332719	F. 1005 R. 1167	CATCAACCCCATCTTCGAGTT CAGGGCCTCCACATATGTGT	163	[3]
<i>SREBP1</i>	HM443643.1	F. 73 R. 153	CTGCTGACCGACATAGAAGACAT GTAGGGCGGGTCAAACAGG	81	[3]
<i>CD36</i>	X91503	F. 743 R. 823	GTACAGATGCAGCCTCATTTC TGGACCTGCAAATATCAGAGGA	81	[3]
<i>LPL</i>	DQ997818	F. 161 R. 329	AGGACACTTGCCACCTCATTC TTGGAGTCTGGTTCCCTCTTGTA	169	[3]
<i>FASN</i>	DQ915966.3	F. 6850 R. 7075	GGGCTCCACCACCGTGTTC GCTCTGCTGGGCCTGCAGCTG	226	[3]
<i>ACACA</i>	NM174224.2	F. 3609 R. 3779	CTCCAACCTCAACCACTACGG GGGGAATCACAGAAGCAGCC	171	[3]
<i>FABP3</i>	NM174313.2	F. 214 R. 333	GATGAGACCACGGCAGATG GTCAACTATTTCCCGCACAAG	120	[3]
<i>ACSL1</i>	BC119914	F. 1929 R. 2047	TGACTGTTGCTGGAGACTGG CAGCCGTCTTTATCCAGAGC	220	[29]
<i>ACSS2</i>	BC134532	F. 1881 R. 1970	GGCGAATGCCTCTACTGCTT GGCCAATCTTTTCTAATCTGCTT	100	[29]
<i>GAPDH</i>	AJ431207	F. 59 R. 307	GCAAGTCCACGGCAGAG GGTTCACGCCATCACAA	249	[41]
<i>MRPL39</i>	NM017446	F. 493 R. 593	AGGTTCTCTTTTGTGGCATCC TTGGTCAGAGCCCCAGAAGT	101	[44]
<i>UXT</i>	NM_001037471	F. 134 R. 288	CAGCTGGCCAAATACCTTCAA GTGTCTGGGACCACTGTGTCAA	125	[44]

Table S2. Cloning primers sequences and related information.

Gene	Clone Area	Primer Name	Primer Sequence (5'→3')	Anneal Temperature (°C)	Product Length/bp
<i>SPI</i>	5'UTR	SP1-5Out	CCCCGTTATTGCCACCA	50	181
		SP1-5Inner	TGCCACCAACTCCTTTTCAA	54	172
	CDS	SP1-U	CCATGAGCGACCAAGATCACTCC	50	2432
		SP1-D	ACCCATGCTACCTTGCATCCC		
	3'UTR	SP1-3U	GTGGCATCAATGTCATGCAGGT	50	1436
		SP1-3D	GAAGAGTTAAGGGGAAAGATCAAAG	54	809
		SP1-3Out	TCAAGTAGTTCAGTTCAGGAGT	54	681
		SP1-3Inner	GAACATCTCCAGTAGTTGCTTTCCATT		