Supplementary:

Table S1. Immune gene oligonucleotide primer sequence used in PCR-DNA sequencing.

Gene	Forward	Reverse	Annealing temperature (°C)	Length of PCR product (bp)	Source
SLC11A1	5′-GTGCCCGAGTCTGCAGTCCTCA-3′	5′-AGAGTGGGATTCGTCCGGCTGAG-3′	62	523	Present research
CD-14	5′-GTGTGCTTGCCCTGCCTGCTGC-3′	5′-AGTGTGCTTGGGCAATGTTCAGC-3′	64	538	Present research
CCL2	5′-GCCAGTCCAGAGGCCAACAGCT-3′	5′-AGTCACGGAAGATAAACTGAA-3′	62	534	Present research
TLR1	5′-ATGCCTGACATCCTCTCACTATC-3′	5′-AGACAGTTCCAGACTCACTGTG-3′	60	471	Present research
TLR7	5′-ATCTTCCTCCCAGCTTACAGCTG-3′	5′- AGAATTATTTTCACAGGGTGTG-3′	60	398	Present research
TLR8	5′-GCTTCTGACCTCCCTTTTCCTGC-3′	5′- GTGTATCTGAATTGAAGCACCT-3′	62	799	Present research
TLR9	5′-ATGGGCCCCTACTGTGCCCCGC-3′	5′-TGCTGGTGCGGCTCAGCGACAG-3′	62	460	Present research
β defensin	5′-CAGCATGAGGCTCCATCACCTG-3′	5′-CGAAGGCGGCAGTTTCTGACT-3′	62	253	Present research
SP110	5′-TCCTGTTTTGCCCACTGGTATC-3′	5′-AGACACGGCAATAGCAGGGTC-3′	58	537	Present research
SPP1	5′-ATGAGAATTGCAGTGATTTGCT-3′	5′-CATTCACCAACTAAGCTGAGAA-3′	60	943	Present research
BP1	5′-ATGGCCAGCGGCCCCGGCAGT-3′	5′-AGGTTGCAGCTTGGAGGACACA -3′	62	645	Present research
A2M	5′-AACCGCAATACATGGTGCTGGT-3′	5′-GGTTTGTCTGTCTGGACAAAGAC -3′	58	325	Present research
ADORA3	5′-CTACTCACCTGGGAAGCTTCTC-3′	5′- CCTTGACCTTCTCGTCCATGAC -3′	64	521	Present research
CARD15	5′-ATGTGCGCACAAGATGCTTTTCA-3′	5′-GCTGCTGTGTCAGGTCCAGCAC -3′	62	394	Present research
IRF3	5′-ACTCCTGGGAAGGATAAGCCCG-3′	5′-AGGGCAGAAGACAGTCTGCTGG-3′	60	468	Present research

SCART1	5'-CTGAGATCAGGAATGTGAACGG-3'	5'-ACAGCAGGGACTCGTTGCCCGC-3'	62	475	Present research

SLC11A1 = Solute Carrier Family 11 Member 1; *CD14* = cluster of differentiation 14; *CCL2*= C-C motif ligand 2; *TLR1* = Toll-like receptor 1; *TLR7* = Toll-like receptor 7; *TLR8* = Toll-like receptor 8; *TLR 9*= Toll-like receptor 9; *β defensin* = beta defensin; *SP110*= SP110 Nuclear Body Protein; *SPP 1*= Secreted Phosphoprotein 1; *BP1* = bactericidal/permeability-increasing protein; *A2M* = Alpha-2-Macroglobulin; *ADORA3* = the adenosine A3 receptor; *CARD15* = caspase recruitment domain-containing protein 15; *IRF3* = interferon regulatory factor 3; *SCART1* = Scavenger Receptor Family Member Expressed On T Cells 1.

Table S2. Sequence of the oligonucleotide primers used in real-time PCR for immunological genes under investigation.

Gene	Primer	Product length (bp)	Annealing temperature (°C)	Accession number	Source
SLC11A1	F5′- GGACATCCGAGAAGCCAACA -3 R5′- TGGGAAAGATCGTCGCGTAG -3′	182	60	KX151137.1	Present research
CD-14	F5′- CAGCTGCAACAAGCTAAGCA -3 R5′- CGGTCTGGAATCATACGGGA -3′	144	59	DQ457090.1	Present research
CCL2	F5′- ACATTCTGCTTCGGCACTCA -3′ R5′- AGACCTTCATGTTGCAGCGA - 3′	200	60	XM_005693218.3	Present research
TLR1	F5′- ATGCCTGACATCCTCTCACT -3′ R5′- GAGGTTCAGAGTAGGGTGGC - 3′	162	58	NM_001285605.1	Present research
TLR7	F5′- CTTCTCTGTGTCTTCCAGGGTC-3′ R5′- CTACCGTTTCCTCACCTTGC - 3′	194	59	NM_001285543.2	Present research
TLR8	F5′- CCCGAAGCTATCCTTGCGAT -3′ R5′- CCACTCTGGGACTTGGCATT - 3′	217	60	GU936189.1	Present research
TLR9	F5′- TTCACCTTGGACCTGTCACG -3′ R5′- ATTAACCGCCTGGGAGATGC - 3′	117	60	EU747825.1	Present research
β defensin	F5′- CTTCCTGGTCCTGTCTGCTG -3′ R5′- GTTTCTAGGGCACCTGTCCG - 3′	106	62	DQ532360.1	Present research
SP110	F5′- TGCCCACGATTCTTTCACGA -3′ R5′- CGGGCATAAATGAGCGAGGA - 3′	108	62	XM_018058530.1	Present research
SPP1	F5′- CGCCCTTCCAGTTAAACCGA -3′ R5′- GCTTCTGAGATGGGTCAGGC - 3′	110	62	NM_001285667.1	Present research
BP1	F5′- TTCAGCATGGTTATTCGAGGA-3′ R5′- TAGAGATGCCCTCCACACTCA - 3′	178	58	NM_001314172.1	Present research
A2M	F5′- TGCAGTTTGCCCCTCACGAT-3′ R5′- CACCGTCTCATTCAGGTGGC- 3′	192	62	XM_018048527.1	Present research
ADORA3	F5′- TGAGGCTCTTCATTCTGCTCT-3′ R5′- CCAGTACTTGGGGTGGTCTT - 3′	143	58	XM_013962543.2	Present research
CARD15	F5′- TCCTGAGCACCTACGATGGA -3′ R5′- AAATGGTCACGGGTGCTGAA - 3′	157	60	NM_001314291.1	Present research
IRF3	F5′- ACATGACTCCCGAGCAACTG -3′ R5′- TGGCAGCCTTCCACAATGAT - 3′	103	60	JQ308793.1	Present research
SCART1	F5′- CCACTGGGACTTGGCAGAC -3′ R5′- TGAGATCAGGAATGTGAACGGG -3′	151	62	XR_001917340.1	Present research
ß. actin	F5′- GCCCCTACAGGTCATGTACTTC-3′ R5′- GCACAGCCTGGATGGCCACATAC -3′	113	60	AF481159.1	Present research

SLC11A1 = Solute Carrier Family 11 Member 1; *CD14* = cluster of differentiation 14; *CCL 2*= C-C motif ligand 2; *TLR1* = Toll-like receptor 1; *TLR7* = Toll-like receptor 7; *TLR8* = Toll-like receptor 8; *TLR9* = Toll-like receptor 9; *β defensin* = beta defensin; *SP110*= SP110 Nuclear Body Protein; *SPP1* = Secreted Phosphoprotein 1; *BP1* = bactericidal/permeability-increasing protein; *A2M* = Alpha-2-Macroglobulin; *ADORA3* = the adenosine A3 receptor; *CARD15* = caspase recruitment domain-containing protein 15; *IRF3* = interferon regulatory factor 3; *SCART1* = Scavenger Receptor Family Member Expressed On T Cells 1.
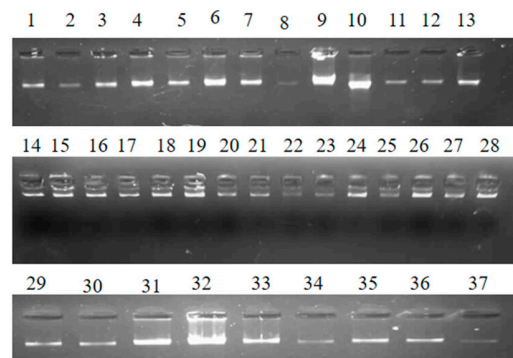
Figure S1: Representative gel electrophoresis for extracted DNA samples from the investigated does. Lanes from 1 to 37 are positive DNA samples.
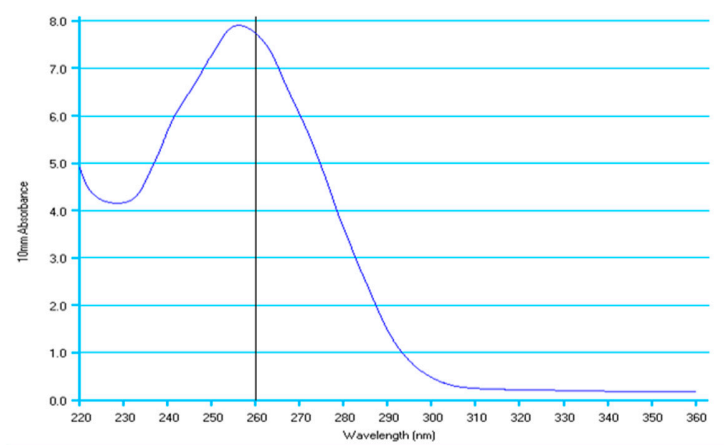
Figure S2: Nanodrop curve showing concentration of representative DNA extracted from the investigated does.

```
KX151137.1    GTGCCCGAGTCTGCAGTCCTCATGTCAGGTGACACGGGTACCCCAAACCAGGGAGGGACC 60
H             GTGCCCGAGTCTGCAGTCCTCATGTCAGGTGACACGGGTACCCCAAACCAGGGAGGGACC 60
P             GTGCCCGAGTCTGCAGTCCTCATGTCTGGTGACACGGGTACCCCAAACCAGGGAGGGACC 60
              ************************** *********************************
KX151137.1    AGATATGGCTCCATCTCCAGCCCACCCAGTCCAGGGCCACAGCAAGCACCTCCCGGAGGG 120
H             AGATATGGCTCCATCTCCAGCCCACCCAGTCCAGGGCCACAGCAAGCACCTCCCGGAGGG 120
P             AGATATGGCTCCATCTCCAGCCCACCCAGTCCAGGGCCACAGCAAGCACCTCCCGGAGGG 120
              ************************************************************
KX151137.1    ACCTACCTAAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTGCATTCAGCCTGCGG 180
H             ACCTACCTAAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTGCATTCAGCCTGCGG 180
P             ACCTACCTAAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTGCATTCAGCCTGCGG 180
              ************************************************************
KX151137.1    AAGCTGTGGGCCTTCACAGGGCCTGGATTCCTCATGAGCATAGCATTCCTGGACCCAGGA 240
H             AAGCTGTGGGCCTTCACAGGGCCTGGATTCCTCATGAGCATAGCATTCCTGGACCCAGGA 240
P             AAGCTGTGGGCCTTCACAGGGCCTGGATTCCTCATGAGCATAGCATTCCTGGACCCAGGA 240
              ************************************************************
KX151137.1    AACATCGAGTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACTGCTCTGGGTGCTG 300
H             AACATCGAGTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACTGCTCTGGGTGCTG 300
P             AACATCGAGTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACTGCTCTGGGTGCTG 300
              ************************************************************
KX151137.1    CTGTGGGCCACAGTGTTGGGCTTGCTCTGCCAGCGACTGGCTGCCCGGCTGGGCGTGGTG 360
H             CTGTGGGCCACAGTGTTGGGCTTGCTCTGCCAGCGACTGGCTGCCCGGCTGGGCGTGGTG 360
P             CTGTGGGCCACAGTGTTGGGCTTGCTCTGCCAGCGACTGGCTGCCCGGCTGGGCGTGGTG 360
              ************************************************************
KX151137.1    ACAGGCAAGGACTTGGGAGAGGTCTGCCATCTCTACTACCCTAAGGTGCCCCGCACTCTC 420
H             ACAGGCAAGGACTTGGGAGAGGTCTGCCATCTCTACTACCCTAAGGTGCCCCGCATTCTC 420
P             ACAGGCAAGGACTTGGGAGAGGTCTGCCATCTCTACTACCCTAAGGTGCCCCGCACTCTC 420
              ****************************************************** ****
KX151137.1    CTCTGGCTGACCATCGAGCTAGCCATCGTGGGCTCGGACATGCAGGAAGTCATTGGCACA 480
H             CTCTGGCTGACCATCGAGCTAGCCATCGTGGGCTCGGACATGCAGGAAGTCATTGGCACA 480
P             CTCTGGCTGACCATCGAGCTAGCCATCGTGGGCTCGGACATGCAGGAAGTCATTGGCACA 480
              ************************************************************
KX151137.1    GCTATTGCATTCAGTCTGCTCTCAGCCGGACGAATCCCACTCT 523
H             GCTATTGCATTCAGTCTGCTCTCAGCCGGACGAATCCCACTCT 523
P             GCTATTGCATTCAGTCTGCTCTCAGCCGGACGAATCCCACTCT 523
              *******************************************
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Figure S3: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|KX151137.1| and the *SLC11A1* gene (523-bp) demonstrating DNA sequence alignment.

```
NM_001361647.1    GTGTGCTTGCCCTGCCTGCTGCTGCTGCTGCTGCCGCCACTGCTGCGTGTGTCTGCGGAC    60
H                 GTGTGCTTGCCCTGCCTGCTGCTGCTGCTGCTGCCGCCACTGCTGCGTGTGTCTGCGGAC    60
P                 GTGTGCTTGCCCTGCCTGCTGCTGCTGCTGCTGCCGCCACTGCTGCGTGTGTCTGCGGAC    60
                  ************************************************************

NM_001361647.1    ACGACAGAGCCCTGCGAGCTGGACGACGACGATTTCCGCTGTGTCTGCAACTTCACGGAT   120
H                 ACGACAGAGCCCTGCGAGCTGGACGACGACGATTTCCGCTGTGTCTGCAACTTCACGGAT   120
P                 ACGACAGAGCCCTGCGAGCTGGACGACGACGATTTCCGCTGTGTCTGCAACTTCACGGAT   120
                  ************************************************************

NM_001361647.1    CCGAAGCCTGACTGGTCTAGCGCCGTTCAGTGTATGGTTGCCGTCGAGGTGGAGATCCGT   180
H                 CCGAAGCCTGACTGGTCTAGCGCCGTTCAGTGTATGGTTGCCGTCGAGGTGGAGATCCGT   180
P                 CCGAAGCCTGACTGGTCTAGCGCCGTTCAGTGTATGGTTGCCGTCGAGGTGGAGATCCGT   180
                  ************************************************************

NM_001361647.1    GGCGGCGGCCACAGCCTGGACCAGTTTCTCAAGGGAGCCAACACCGACCCGAAGCAGTAT   240
H                 GGCGGCGGCCACAGCCTGGACCAGTTTCTCAAGGGAGCCAACACCGACCCGAAGCAGTAT   240
P                 GGCGGCGGCCACAGCCTGGACCAGTTTCTCAAGGGAGCCAACACCGACCCGAAGCAGTAT   240
                  ************************************************************

NM_001361647.1    GCTGACACAATCAAGGCTCTGCGCGTTCGGCGACTCAAGCTGGGCGCTGCACAGGTTCCT   300
H                 GCTGACACAATCAAGGCTCTGCGCGTTCGGCGACTCAAGCTGGGCGCTGCACAGGTTCCT   300
P                 GCTGACACAATCAAGGCTCTGCGCGTTCGGCGACTCAAGCTGGGCGCTGCACAGGTTCCT   300
                  ************************************************************

NM_001361647.1    GCTCAGCTTCTGGTCGCCGTTCTGCGCGCGCTCGGGTACTCTCGTCTCAAGGAACTGACG   360
H                 GCTCAGCTTCTGGTCGCCGTTCTGCGCGCGCTCGGGTACTCTCGTCTCAAGGAACTGACG   360
P                 GCTCAGCTTCTGGTCGCCGTTCTGCGCGCGCTCGGGTACTCTCGTCTCAAGGAACTGACG   360
                  ************************************************************

NM_001361647.1    CTTGAGGACCTGGAGGTAACTGGCCCAACGCCCCCGGCGCCTCTGGAAGCCACTGGGCCT   420
H                 CTTGAGGACCTGGAGGTAACTGGCCCAACGCCCCCGGCGCCTCTGGAAGCCACTGGGCCT   420
P                 CTTGAGGACCTGGAGGTAACTGGCCCAACGCCCCCGGCGCCTCTGGAAGCCACTGGGCCT   420
                  ************************************************************

NM_001361647.1    GCGCTCACCACCCTCAGTCTCCGTAACGTGTCGTGGGCAACAGGAGGTGCCTGGCTCGGC   480
H                 GCGCTCACCACCCTCAGTCTCCGTAACGTGTCGTGGACAACAGGAGGTGCCTGGCTCGGC   480
P                 GCGCTCACCACCCTCAGTCTCCGTAACGTGTCGTGGGCAACAGGAGGTGCCTGGCTCGGC   480
                  ************************************ ***********************

NM_001361647.1    GAACTGCAGCAGTGGCTCAAGCCTGGGCTCAGGGCGCTGAACATTGCCCAAGCACACT    538
H                 GAACTGCAGCGGTGGCTCAAGCCTGGGCTCAGGGCGCTGAACATTGCCCAAGCACACT    538
P                 GAACTGCAGCAGTGGCTCAAGCCTGGGCTCAGGGCGCTGAACATTGCCCAAGCACACT    538
                  ********** ***********************************************
```

Figure S4: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|NM_001361647.1| and the *CD14* gene (538-bp) demonstrating DNA sequence alignment.

```
XM_004012471.4    GCCAGTCCAGAGGCCAACAGCTCCCACGCTGAAGCTTGAATCCTCTCGCTGCAACATGAA    60
H                 GCCAGTCCAGAGGCCAACAGCTCCCACGCTGAAGCTTGAATCCTCTCGCTGCAACATGAA    60
P                 GCCAGTCCAGAGGCCAACAGCTCCCACGCTGAAGCTTGAATCCTCTCGCTGCAACATGAA    60
                  ************************************************************

XM_004012471.4    GGTCTCCGCTGCTCTCCTCTGCCTGCTACTCACAGTAGCTGCCTTCAGCACCGAGGTGCT    120
H                 GGTCTCCGCTGCTCTCCTCTGCCTGCTACTCACAGTAGCTGCCTTCAGCACCGAGGTGCT    120
P                 GGTCTCCGCTGCTCTCCTCTGCCTGCTACTCACAGTAGCTGCCTTCAGCACCGAGGTGCT    120
                  ************************************************************

XM_004012471.4    CGCTCAGCCAGATGCAATTAACTCCCAAATCGCCTGCTGCTATAAATTCAATAAGAAGAT    180
H                 CGCTCAGCCAGATGCAATTAACTCCCAAATCGCCTGCTGCTATAAATTCAATAAGAAGAT    180
P                 CGCTCAGCCAGATGCAATTAACTCCCAAATCGCCTGCTGCTATAAATTCAATAAGAAGAT    180
                  ************************************************************

XM_004012471.4    CCCCATACAGAGGCTGACAAACTACAGAAGAGTCACCACCAGCAAGTGTCCCAAAGAAGC    240
H                 CCCCATACAGAGGCTGACAAACTACAGAAGAGTCACCACCAGCAAGTGTCCCAAAGAAGC    240
P                 CCCCATACAGAGGCTGACAAACTACAGAAGAGTCACCACCAGCAAGTGTCCCAAAGAAGC    240
                  ************************************************************

XM_004012471.4    TGTGATTTTCAAGACCATCCTAGGCAAAGAGTTTTGTGCAGACCCCAACCTGAAATGGGT    300
H                 TGTGATTTTCAAGACCATCCTGGGCAAAGAGTTTTGTGCAGACCCCAACCTGAAATGGGT    300
P                 TGTGATTTTCAAGACCATCCTAGGCAAAGAGTTTTGTGCAGACCCCAACCTGAAATGGGT    300
                  *********************  *************************************

XM_004012471.4    CCAGGACGCCATAAACCATCTCAACAAGAAAAACCAAACTCCGAAGCCTTGAGCACTCAC    360
H                 CCAGGACGCCATAAACCATCTCAACAAGAAAAACCAAACTCCGAAGCCTTGAGCACTCAC    360
P                 CCAGGACGCCATAAACCATCTCAACAAGAAAAACCAAACTCCGAAGCCTTGAGCACTCAC    360
                  ************************************************************

XM_004012471.4    TCCACAACCCAAGAATCTAAAGACAATCTGTGTTCTTCTGGCTTCCCCTAACTGCCCTCT    420
H                 TCCACAACCCAAGAATCTAAAGACAATCTGTGTTCTTCTGGCTTCCCCTAACTGCCCTCT    420
P                 TCCACAACCCAAGAATCTAAAGACAATCTGTGTTCTTCTGGCTTCCCCTAACTGCCCTCT    420
                  ************************************************************

XM_004012471.4    GATATTACCTTATTATAATTTTGAAGAGTATAACTTTATTGATGTGAACATGATGCCTTA    480
H                 GATATTACCTTATTATAATTTTGAAGAGTATAACTTTATTGATGTGAACATGATGCCTTA    480
P                 GATATTACCTTATTATAATTTTGAAGAGTATAACTTTATTGATGTGAACATGATGCCTCA    480
                  **********************************************************  *

XM_004012471.4    AGTAATGTTAATATTATTTAAGTTATTGATGCTTTCAGTTTATCTTCCGTGACT    534
H                 AGTAATGTTAATATTATTTAAGTTATTGATGCTTTCAGTTTATCTTCCGTGACT    534
P                 AGTAATGTTAATATTATTTAAGTTATTGATGCTTTCAGTTTATCTTCCGTGACT    534
                  ******************************************************
```

Figure S5: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|XM_004012471.4| and the *CCL2* gene (534-bp) demonstrating DNA sequence alignment.

```
KJ210567.1    ATGCCTGACATCCTCTCACTATCAAAGCTGAAAATTTTGATAATTTCTCATAATAGAATC 60
H             ATGCCTGACATCCTCTCACTATCAAAGCTGAAAATTTTGATAATTTCTCATAATAGAATC 60
P             ATGCCTGACATCCTCTCACTATCAAAGCTGAAAATTTTGATAATTTCTCATAATAGAATC 60
              ************************************************************

KJ210567.1    CAGTATCTTGACGGTGTTTTTAAATTCAACCACAGACTGGAATACTTGGATTGTCCCAC 120
H             CAGTATCTTGACGGTGTTTTTAAATTCAACCACAGACTGGAATACTTGGATTGTCCCAC 120
P             CAGTATCTTGACGGTGTTTTTAAATTCAACCACAGACTGGAATACTTGGATTGTCCCAC 120
              ***********************************************************

KJ210567.1    AACAATTTGGAGAAGATTTCTTGCCACCCTACTCTGAACCTCAAGCACTTAGACCTCTCA 180
H             AACAATTTGGAGAAGATTTCTTGCCACCCTACTCTGAACCTCAAGCACTTAGACCTCTCA 180
P             AACAATTTGGAGAAGATTTCTTGCCACCCTACTCTGAACCTCAAGCACTTAGACCTCTCA 180
              ************************************************************

KJ210567.1    TTTAATGCATTTGATGCCCTGCCCATATGCCAAGAGTTTGGCAACATGTCTCAACTAGAA 240
H             TTTAATGCATTTGATGCCCTGCCCATATGCCAAGAGTTTGGCAACATGTCTCAACTAGAA 240
P             TTTAATGCTTTTGATGCCCTGCCCATATGCCAAGAGTTTGGCAACATGTCTCAACTAGAA 240
              ******** ***************************************************

KJ210567.1    TTTCTGGGGTTGAGTGCCACACAGTTACAAAAATCCAGTGTGCAGTCAATCACTCGTTTG 300
H             TTTCTGGGGTTGAGTGCCACACAGTTACAAAAATCCAGTGTGCACTCAATCACTCGTTTG 300
P             TTTCTGGGGTTGAGTGCCACACAGTTACAAAAATCCAGTGTGCAGTCAATCACTCGTTTG 300
              ******************************************** ***************

KJ210567.1    CACATCAGCAAGGTTTTATTGGTCTTAGGAGATACTTATGGGGAAAGAGAAGATGCTGAG 360
H             CACATCAACAAGGTTTTATTGGTCTTAGGAGATACTTATGGGGAAAGAGAAGATGCTGAC 360
P             CACATCAGCAAGGTTTTATTGGTCTTAGGAGATACTTATGGGGAAAGAGAAGATGCTGAG 360
              ******* ****************************************************

KJ210567.1    AGCCTTCAAGACCTTAAGACACAGAGCCTGCACGTTGTTTTCCCCACAGGAAAGGAATTC 420
H             AGCCTTCAAGACCTTAAGACACAGAGCCTGCACGTTGTTTTCCCCACAGGAAAGGAATTC 420
P             AGCCTTCAAGACCTTAAGACACAGAGCCTGCACTTTGTTTTCCCCACAGGAAAGGAATTC 420
              ********************************* **************************

KJ210567.1    CATTTAATTTGGACGTGTCAGTCAGCACCACAGTGAGTCTGGAACTGTCT 471
H             CATTTAATTTGGACGTGTCAGTCAGCACCACAGTGAGTCTGGAACTGTCT 471
P             CATTTAATTTGGACGTGTCAGTCAGCACCACAGTGAGTCTGGAACTGTCT 471
              **************************************************
```

Figure S6: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|KJ210567.1| and the *TLR1* gene (471-bp) demonstrating DNA sequence alignment.

```
GU289401.1    ATCTTCCTCCCAGCTTACAGCTGCTGAGCCTGGAGGCCAACAACATCTTCTTGATCATGA 60
H             ATCTTCCTCCCAGCTTACAGCTGCTGAGCCTGGAGGCCAACAACATCTTCTTGATCATGA 60
P             ATCTTCCTCCCAGCTTACAGCTGCTGAGCCTGGAGGCCAACAACATCTTCTTGATCATGA 60
              ************************************************************

GU289401.1    AGGAGAATCTAACAGAACTGGCCAACCTAGAAATACTCTACCTGGGCCAAAACTGTTACT 120
H             AGGAGAATCTAACAGAACTGGCCAACCTAGAAATACTCTACCTGGGCCAAAACTGTTACT 120
P             AGGAGAATCTAACAGAACTGGCCAACCTAGAAATACTCTACCTGGGCCAAAACTGTTACT 120
              ************************************************************

GU289401.1    ATCGTAACCCTTGTAATGTTTCATTTACTATCGAAAAAGATGCTTTCCTAAATATGAGAA 180
H             ATCGTAACCCTTGTAATGTTTCATTTACTATCGAAAAAGATGCTTTCCTAAATATGAGAA 180
P             ATCGTAACCCTTGTAATGTTTCATTTACTATCGAAAAAGATGCTTTCCTAAATATGAGAA 180
              ************************************************************

GU289401.1    ATTTAAAATTGCTCTCCCTAAAAGATAACAATATCTCAGCTGTCCCCACTGTTTTGCCAT 240
H             ATTTAAAATTGCTCTCCCTAAAAGATAACAATATCTCAGCTGTCCCCACTGTTTTGCCAT 240
P             ATTTAAAATTGCTCTCCCTAAAAGATAACAATATCTCAGCTGTCCCCACTGTTTTGCCAT 240
              ************************************************************

GU289401.1    CTAGTTTGACAGAACTCTATCTTTACAATAACATCATTACAAAAATCCAAGAAGATGATT 300
H             CTAGTTTGACAGAACTCTATCTTTACAATAACATCATTACAAAAATCCAAGAAGATGATT 300
P             CTAGTTTGACAGAACTCTATCTTTACAATAACATCATTACAAAAATCCAAGAAGATGATT 300
              ************************************************************

GU289401.1    TTAATAACCTCAGTCAACTACAAGTTCTTGATCTGAGTGGAAATTGCCCTCGTTGTTATA 360
H             TTAATAACCTCAGTCAACTACAAGTTCTTGATCTGAGTGGAAATTGTCCTCGTTGTTATA 360
P             TTAATAACCTCAGTCAACTACAAGTTCTTGATCTGAGTGGAAATTGCCCTCGTTGTTATA 360
              ********************************************** ************

GU289401.1    ATGTTCCATTTCCTTGCACACCCTGTGAAAATAATTCT      398
H             ATGTTCCATTTCCTTGCACACCCTGTGAAAATAATTCT      398
P             ATGTTCCATTTCCTTGCACACCCTGTGAAAATAATTCT      398
              **************************************
```

Figure S7: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|GU289401.1| and the *TLR7* gene (398-bp) demonstrating DNA sequence alignment.

```
GU936189.1    GCTTCTGACCTCCCTTTTCCTGCTCATCTCCGATTCCTGTGAGTTCTTCACTGAAGCCAG 60
H             GCTTCTGACCTCCCTTTTCCTGCTCATCTCCGATTCCTGTGAGTTCTTCACTGAAGCCAG 60
P             GCTTCTGACCTCCCTTTTCCTGCTCATCTCCGATTCCTGTGAGTTCTTCACTGAAGCCAG 60
              ************************************************************

GU936189.1    TTATCCCCGAAGCTATCCTTGCGATGTGAAAAACAATAATGGCTCTTTTATTGCAGAATG 120
H             TTATCCCCGAAGCTATCCTTGCGATGTGAAAAACAATAATGGCTCTTTTATTGCAGAATG 120
P             TTATCCCCGAAGCTATCCTTGCGATGTGAAAAACAATAATGGCTCTTTTATTGCAGAATG 120
              ************************************************************

GU936189.1    TAACAGTCGTCGATTACAGGAAGTACCCCAAACAGTGGACAAAGCTGTGACAGAAGTAGA 180
H             TAACAGTCGTCGATTACAGGAAGTACCCCAAACAGTGGACAAAGCTGTGACAGAAGTAGA 180
P             TAACAGTCGTCGATTACAGGAAGTACCCCAAACAGTGGACAAAGCTGTGACAGAAGTAGA 180
              ************************************************************

GU936189.1    CCTGTCTGATAATTTCATCACACGTATAACGAATGAATCCTTTCAAGGGCTGCAAAATCT 240
H             CCTGTCTGATAATTTCATCACACGTATAACGAATGAATCCTTTCAAGGGCTGCAAAATCT 240
P             CCTGTCTGATAATTTCATCACACGTATAACGAATGAATCCTTTCAAGGGCTGCAAAATCT 240
              ************************************************************

GU936189.1    GACTAAAATCAACCTGAACCATAATGCCAAGTCCCAGAGTGGAAATCCTGCTGTAAAGAA 300
H             GACTAAAATCAACCTGAACCATAATGCCAAGTCCCAGAGTGGAAATCCTGCTGTAAAGAA 300
P             GACTAAAATCAACCTGAACCATAATGCCAAGTCCCAGAGTGGAAATCCTGCTGTAAAGAA 300
              ************************************************************

GU936189.1    AGCTATGACTATTACAGACGGGGCATTTCTCAACCTCAAACACCTAAGGGAGTTGCTGCT 360
H             AGCTATGACTATTACAGACGGGGCATTTCTCAACCTCAAACACCTAAGGGAGTTGCTGCT 360
P             AGCTATGACTATTACAGACGGGGCATTTCTCAACCTCAAACACCTAAGGGAGTTGCTGCT 360
              ************************************************************

GU936189.1    GGAAGACAACCAGTTACAAGAAATACCGGCTGGTTTGCCAGAATCTTTGAAAGAACTTAG 420
H             GGAAGACAACCAGTTACAAGAAATACCGGCTGGTTTGCCAGAATCTTTGAAAGAACTTAG 420
P             GGAAGACAACCAGTTACAAGAAATACCGGCTGGTTTGCCAGAATCTTTGAAAGAACTTAG 420
              ************************************************************

GU936189.1    TCTAATTCAAAACAATATAATTACGTTAACGAAAAAGAACACTTCTGGACTTGGGAACCT 480
H             TCTAATTCAAAACAATATAATTACGTTAACGAAAAAGAACACTTCTGGACTTGGGAACCT 480
P             TCTAATTCAAAACAATATAATTACGTTAACGAAAAAGAACACTTCTGGACTTGGGAACCT 480
              ************************************************************

GU936189.1    GGAACGTCTCTATTTGGGCTGGAACTGTTATTTTGCTTGTAGTAAAAAATTTAGCATAGA 540
H             GGAACGTCTCTATTTGGGCTGGAACTGTTATTTTGCTTGTAGTAAAAAATTTAGCATAGA 540
P             GGAACGTCTCTATTTGGGCTGGAACTGTTATTTTGCTTGTAGTAAAAAATTTAGCATAGA 540
              ************************************************************

GU936189.1    AAATGGAGCATTCCAAAACCTTACCAAGTTGAAGGTGCTGTCATTATCTTTTAATCCCCT 600
H             AAATGGAGCATTCCAAAACCTTACCAAGTTGAAGGTGCTGTCATTATCTTTTAATCCCCT 600
P             AAATGGAGCATTCCAAAACCTTACCAAGTTGAAGGTGCTGTCATTATCTTTTAATCCCCT 600
              ************************************************************

GU936189.1    TCACAGCGTGCCACCGAGTCTGCCAAGCTCGCTAACAGAACTCTACCTTAGCAATACCCA 660
H             TCACAGCGTGCCACCGAGTCTGCCAAGCTCGCTAACAGAACTCTACCTTAGCAATACCCA 660
P             TCACAGCGTGCCACCGAGTCTGCCAAGCTCGCTAACAGAACTCTACCTTAGCAATACCCA 660
              ************************************************************

GU936189.1    TATTGGAAACGTCAGTGAAGAAGACTTCAAGGAACTGAGCAATTTAAGGGTACTAGATTT 720
H             TATTGGAAACGTCAGTGAAGAAGACTTCAAGGAACTGAGCAATTTAAGGGTACTAGATTT 720
P             TATTGGAAACGTCAGTGAAGAAGACTTCAAGGAACTGAGCAATTTAAGGGTACTAGATTT 720
              **************************************************  *********

GU936189.1    AAGTGGAAACTGCCCGAGATGTTTTAACGCTCCGTTTCCCTGTGTACCTTGCCAAGGAGG 780
H             AAGTGGAAACTGCCCGAGATGTTTTAACGCTCCGTTTCCCTGTGTACCTTGCCAAGGAGG 780
P             AAGTGGAAACTGCCCGAGATGTTTTAACGCTCCGTTTCCCTGTGTACCTTGCCAAGGAGG 780
              ************************************************************

GU936189.1    TGCTTCAATTCAGATACAC      799
H             TGCTTCAATTCAGATACAC      799
P             TGCTTCAATTCAGATACAC      799
              *******************
```

Figure S8: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|GU936189.1| and the *TLR8* gene (799-bp) demonstrating DNA sequence alignment.

```
EU747825.1    ATGGGCCCCTACTGTGCCCCGCACCCCCTTTCTCTTCTGGTGCAGGCAGCGGCGCTGGCA 60
H             ATGGGCCCCTACTGTGCCCCGCACCCCCTTTCTCTTCTGGTGCAGGCAGCGGCGCTGGCA 60
P             ATGGGCCCCTACTGTGCCCCGCACCCCCTTTCTCTTCTGGTGCAGGCAGCGGCGCTGGCA 60
              ************************************************************

EU747825.1    GCAGCCCTGGCCCAGGGCACCCTGCCTGCCTTCCTGCCCTGTGAGCTCCAGCCCCGGGGT 120
H             GCAGCCCTGGCCCAGGGCACCCTGCCTGCCTTCCTGCCCTGTGAGCTCCAGCCCCGGGGT 120
P             GCAGCCCTGGCCCAGGGCACCCTGCCTGCCTTCCTGCCCTGTGAGCTCCAGCCCCGGGGT 120
              ************************************************************

EU747825.1    CAGGTGAACTGCAACTGGCTGTTCCTGAAGTCTGTGCCGCGCTTTTCGGCCGGAGCCCCC 180
H             CAGGTGAACTGCAACTGGCTGTTCCTGAAGTCTGTGCCGCGCTTTTCGGCCGGAGCCCCC 180
P             CAGGTGAACTGCAACTGGCTGTTCCTGAAGTCTGTGCCGCGCTTTTCGGCCGGGGCCCCC 180
              *****************************************************  ******

EU747825.1    CGGGCCAATGTCACCAGCCTCTCCTTAATCTCCAACCGCATCCACCACTTGCACGACTCT 240
H             CGGGCCAATGTCACCAGCCTCTCCTTAATCTCCAACCGCATCCACCACTTGCACGACTCT 240
P             CGGGCCAATGTCACCAGCCTCTCCTTAATCTCCAACCGCATCCACCACTTGCACGACTCT 240
              ************************************************************

EU747825.1    GACTTCGTCCACCTGTCCAACCTGCGGGTCCTCAACCTCAAGTGGAACTGCCCGCCGGCC 300
H             GACTTCGTCCACCTGTCCAACCTGCGGGTCCTCAACCTCAAGTGGAACTGCCCGCCGGCC 300
P             GACTTCGTCCACCTGTCCAACCTGCGGGTCCTCAACCTCAAGTGGAACTGCCCGCCGGCC 300
              ************************************************************

EU747825.1    GGCCTCAGCCCCATGCACTTCCCCTGCCGCATGACCATTGAGCCCAACACCTTCCTGGCC 360
H             GGCCTCAGCCCCATGCACTTCCCCTGCCGCATGACCATTGAGCCCAACACCTTCCTGGCC 360
P             GGCCTCAGCCCCATGCACTTCCCCTGCCGCATGACCATTGAGCCCAACACCTTCCTGGCT 360
              *********************************************************** 

EU747825.1    GTGCCCACCCTGGAGGAGCTGAACCTGAGCTACAATGGCATCACGACCGTGCCTGCCCTG 420
H             GTGCCCACCCTGGAGGAGCTGAACCTGAGCTACAATGGCATCACGACCGTGCCTGCCCTG 420
P             GTGCCCACCCTGGAGGAGCTGAACCTGAGCTACAATGGCATCACGACCGTGCCTGCCCTG 420
              ************************************************************

EU747825.1    CCCAGTTCTCTCGTATCCCTGTCGCTGAGCCGCACCAGCA    460
H             CCCAGTTCTCTCGTATCCCTGTCGCTGAGCCGCACCAGCA    460
P             CCCAGTTCTCTCGTATCCCTGTCGCTGAGCCGCACCAGCA    460
              ****************************************
```

Figure S9: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|EU747825.1| and the *TLR9* gene (460-bp) demonstrating DNA sequence alignment.

```
DQ532360.1    CAGCATGAGGCTCCATCACCTGCTCCTCGCGCTCTTCTTCCTGGTCCTGTCTGCTGGGTC 60
H             CAGCATGAGGCTCCATCACCTGCTCCTCGCGCTCTTCTTCCTGGTCCTGTCTGCTGGGTC 60
P             CAGCATGAGGCTCCATCACCTGCTCCTCGTGCTCTTCTTCCTGGTCCTGTCTGCTGGGTC 60
              ***************************** ******************************

DQ532360.1    AGGATTTACTCAAGGAATAATAAATCATCGAAGCTGCCATAGGATTAAAGGCGTCTGTGC 120
H             AGGATTTACTCAAGGAATAATAAATCATCGAAGCTGCCATAGGATTAAAGGCGTCTGTGC 120
P             AGGATTTACTCAAGGAATAATAAATCATCGAAGCTGCCATAGGAATAAAGGCGTCTGTGC 120
              ******************************************* ***************

DQ532360.1    GCCGGACAGGTGCCCTAGAAACATGAGACAGATTGGCACCTGTTTCGGGCCCCCAGTAAA 180
H             GCCGGACAGGTGCCCTAGAAACATGAGACAGATTGGCACCTGTTTCGGGCCCCCAGTAAA 180
P             GCCGGACAGGTGCCCTAGAAACATGAGACAGATTGGCACCTGTTTCGGGCCCCCAGTAAA 180
              ************************************************************

DQ532360.1    ATGCTGCAGAAAGAAGTAACAGAAGGCGAAGACGCGGCCGGGACCGATGCGGAGTCAGAA 240
H             ATGCTGCAGAAAGAAGCAACAGAAGGCGAAGACGCGGCCGGGACCGATGCGGAGTCAGAA 240
P             ATGCTGCAGAAAGAAGTAACAGAAGGCGAAGACGCGGCCGGGACTGATGCGGAGTCAGAA 240
              *************** ************************** ***************

DQ532360.1    ACTGCCGCCTTCG          253
H             ACTGCCGCCTTCG          253
P             ACTGCCGCCTTCG          253
              *************
```

Figure S10: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|DQ532360.1| and the β defensin gene (253-bp) demonstrating DNA sequence alignment.

```
XM_013973239.2    TCCTGTTTTGCCCACTGGTATCTCTCTGCCCTTTTCTCAGTCTCCCAGGAGCCACCCCAG    60
H                 TCCTGTTTTGCCCACTGGTATCTCTCTGCCCTTTTCTCAGTCTCCCAGGAGCCACCCCAG    60
P                 TCCTGTTTTGCCCACTGGTATCTCTCTGCCCTTTTCTCAGTCTCCCAGGAGCCACCCCAG    60
                  ************************************************************

XM_013973239.2    AACAGCCCCTGGATCTGGAAGGGGACACGAACACCTAGTCATCTCAGCATCCAGGAAAGC    120
H                 ACCAGCCCCTGGATCTGGAAGGGGACACGAACACCTAGTCATCTCAGCATCCAGGAAAGC    120
P                 AACAGCCCCTGGATCTGGAAGGGGACACGAACACCTAGTCATCTCAGCATCCAGGAAAGC    120
                  * **********************************************************

XM_013973239.2    CACCATGACCAGGGCCTTGGAAGAGGCTCTTCTTCAGCACTTCATACATCAGAAGCTGGA    180
H                 CACCATGACCAGGGCCTTGGAAGAGGCTCTTCTTCAGCACTTCATACATCAGAAGCTGGA    180
P                 CACCATGACCAGGGCCTTGGAAGAGGCTCTTCTTCAGCACTTCATACATCAGAAGCTGGA    180
                  ************************************************************

XM_013973239.2    GATCGCTTATGCCATCAACAAGCCATTTCCCTTCTTCGAAGGCCTCCGAGACAACTCCTT    240
H                 GATTGCTTATGCCATCAACAAGCCATTTCCCTTCTTCGAAGGCCTCCGAGACAACTCCTT    240
P                 GATCGCTTATGCCATCAACAAGCCATTTCCCTTCTTCGAAGGCCTCCGAGACAACTCCTT    240
                  *** ********************************************************

XM_013973239.2    CATCACGGAGAGACTGTACAGGGAATCTATGGAAGCCTGGGAAAATCTGGTCCCTTTATG    300
H                 CATCACGGAGAGACTGTACAGGGAATCTATGGAAGCCTGGGAAAATCTGGTCCCTTTATG    300
P                 CATCACGGAGAGACTGTACAGGGAATCTATGGAAGCCTGGGAAAATCTGGTCCCTTTATG    300
                  ************************************************************

XM_013973239.2    CAGAGTTGTGTACAACATTCTTACCCAACTGGAGAAGACATTTAGTCTATCATTTCTGAA    360
H                 CAGAGTTGTGTACAACATTCTTACCCAACTGGAGAAGACATTTAGTCTATCATTTCTGAA    360
P                 CAGAGTTGTGTACAACATTCTTACCCAACTGGAGAAGACATTTAGTCTATCATTTCTGAA    360
                  ************************************************************

XM_013973239.2    GATATTGTTCAGCCGAATTAACCTGAAAGCATACCCCAACCTGATAACGGCTCTCAGTAG    420
H                 GATATTGTTCAGCCGAATTAACCTGAAAGCATACCCCAACCTGATAACGGCTCTCAGTAG    420
P                 GATATTGTTCAGCCGAATTAACCTGAAAGCATACCCCAACCTGATAACGGCTCTCAGTAG    420
                  ************************************************************

XM_013973239.2    CTTCACAAGAGTCGTCACTTCCCATGGAGGCTGGAGCAGAAACACAACCATCCCTCTTGA    480
H                 CTTCACAAGAGTCGTCACTTCCCATGGAGGCTGGAGCAGAAACACAACCATCCCTCTTGA    480
P                 CTTCACAAGAGTCGTCACTTCCCATGGAGGCTGGAGCAGAAACACAACCATCCCTCTTGA    480
                  ************************************************************

XM_013973239.2    AGCCCCAGCCAACCCAGCAGGAAAGAGCTCCTCGAGGACCCTGCTATTGCCGTGTCT      537
H                 AGCCCCAGCCAACCCAGCAGGAAAGAGCTCCTCGAGGACCCTGCTATTGCCGTGTCT      537
P                 AGCCCCAGCCAACCCAGCAGGAAAGAGCTCCTCGAGGACCCTGCTATTGCCGTGTCT      537
                  ********************************************************
```

Figure S11: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|XM_013973239.2|and the *SP110* gene (537-bp) demonstrating DNA sequence alignment.

```
NM_001285667.1    ATGAGAATTGCAGTGATTTGCTTCTGCCTCTTGGGCATTGCCTCCGCCCTTCCAGTTAAA    60
H                 ATGAGAATTGCAGTGATTTGCTTCTGCCTCTTGGGCATTGCCTCCGCCCTTCCAGTTAAA    60
P                 ATGAGAATTGCAGTGATTTGCTTCTGCCTCTTGGGCATTGCCTCCGCCCTTCCAGTTAAA    60
                  ************************************************************

NM_001285667.1    CCGACCAGTTCTGGCAGCTCTGAGGAAAAGCTGCTTAACAACAAATACCCAGATGCTGTA    120
H                 CCGACCAGTTCTGGCAGCTCTGAGGAAAAGCTGCTTAACAACAAATACCCAGATGCTGTA    120
P                 CCGACCAGTTCTGGCAGCTCTGAGGAAAAGCTGCTTAACAACAAATACCCAGATGCTGTA    120
                  ************************************************************

NM_001285667.1    GCCACATGGCTAAAGCCTGACCCATCTCAGAAGCAGACTTTCCTAGAACCCCAGAATTCT    180
H                 GCCACATGGCTAAAGCCTGACCCATCTCAGAAGCAGACTTTCCTAGAACCCCAGAATTCT    180
P                 GCCACATGGCTAAAGCCTGACCCATCTCAGAAGCAGACTTTCCTAGAACCCCAGAATTCT    180
                  ************************************************************

NM_001285667.1    GTGTCCTCTGAGGAAACTGATGACAACAAACAAAATACCCTCCCGAGTAAGTCCAATGAA    240
H                 GTGTCCTCTGAGGAAACTGATGACAACAAACAAAATACCCTCCCGAGTAAGTCCAATGAA    240
P                 GTGTCCTCTGAGGAAACTGATGACAACAAACAAAATACCCTCCCGAGTAAGTCCAATGAA    240
                  ************************************************************

NM_001285667.1    AGCCCTGAGCAAACAGACGATCTAGATGATGATGATGAAAACAGCCAGGAAGTCAACTCT    300
H                 AGCCCTGAGCAAACAGACGATCTAGATGATGATGATGAAAACAGCCAGGAAGTCAACTCT    300
P                 AGCCCTGAGCAAACAGACGATCTAGATGATGATGATGAAAACAGCCAGGAAGTCAACTCT    300
                  ************************************************************

NM_001285667.1    GATGACTCCGACGATGCTAACCCTGATGACTCTGACCATTCCAACGAGTCTCACCATTCT    360
H                 GATGACTCCGACGATGCTAACCCTGATGACTCTGACCATTCCAACGAGTCTCACCATTCT    360
P                 GATGACTCCGACGATGCTAACCCTGATGACTCTGACCATTCCAACGAGTCTCACCATTCT    360
                  ************************************************************

NM_001285667.1    GATGAATCTGATGAAGCTGATTTTCCCACTGACATTCCAACAATCGCAGTTTTCACTCCA    420
H                 GATGAATCTGATGAAGCTGATTTTCCCACTGACATTCCAACAATCGCAGTTTTCACTCCA    420
P                 GATGAATCTGATGAAGCTGATTTTCCCACTGACATTCCAACAATCGCAGTTTTCACTCCA    420
                  ************************************************************

NM_001285667.1    CCTTTCCCTACGGAAAGCACAAATGATGGCCGAGGTGATAGTGTGGCTTATGGACTGAAG    480
H                 CCTTTCCCTACGGAAAGCACAAATGATGGCCGAGGTGATAGTGTGGCTTATGGACTGAAG    480
P                 CCTTTCCCTACGGAAAGCACAAATGATGGCCGAGGTGATAGTGTGGCTTATGGACTGAAG    480
                  ************************************************************

NM_001285667.1    TCAAAATCGAAGAAGTTCCGCCGATCTAACGTTGAGAGTCCAGATGCCACAGAGGAGGAC    540
H                 TCAAAATCGAAGAAGTTCCGCCGATCTAACGTTGAGAGTCCAGATGCCACAGAGGAGGAC    540
P                 TCAAAATCGAAGAAGTTCCGCCGATCTAACGTTGAGAGTCCAGATGCCACAGAGGAGGAC    540
                  ************************************************************

NM_001285667.1    TTCACATCACACATAGAGAGTGAGGAGATGCATGATGCACCTAAGAAGACGAGTCAGCTG    600
H                 TTCACATCACACATAGAGAGTGAGGAGATGCATGATGCACCTAAGAAGACGAGTCAGCTG    600
P                 TTCACATCACACATAGAGAGTGAGGAGATGCATGATGCACCTAAGAAGACGAGTCAGCTG    600
                  ************************************************************

NM_001285667.1    ACTGACCACAGCGAAGAAACCAACAGTGACGAGCTTTCCAAAGAACTCACACCAAAGGCC    660
H                 ACTGACCACAGCGAAGAAACCAACAGTGACGAGCTTTCCAAAGAACTCACACCAAAGGCC    660
P                 ACTGACCACAGCGAAGAAACCAACAGTGACGAGCTTTCCAAAGAACTCACACCAAAGGCC    660
                  ************************************************************

NM_001285667.1    CAGGAGGAGAGCAAGCATTCCAATCGGATCGAGAGTCAGGAAAATTCCAAACTCAGCCAA    720
H                 CAGGAGGAGAGCAAGCATTCCAATCGGATCGAGAGTCAGGAAAATTCCAAACTCAGCCAA    720
P                 CAGGAGGAGAGCAAGCATTCCAATCGGATCGAGAGTCAGGAAAATTCCAAACTCAGCCAA    720
                  ************************************************************

NM_001285667.1    GAATTCCATAGCCTTGAAGACAAGCTAGACCTAGATCATAAGAGTGAAGAAGACAAGCGC    780
H                 GAATTCCATAGCCTTGAAGACAAGCTAGACCTAGATCATAAGAGTGAAGAAGACAAGCGC    780
P                 GAATTCCATAGCCTTGAAGACAAGCTAGACCTAGATCATAAGAGTGAAGAAGACAAGCGC    780
                  ************************************************************

NM_001285667.1    CTGAAAATCCGCATTTCTCATGAATTAGATAGTGCCTCTTCTGAGGTCAACTGAAAGGAG    840
H                 CTGAAAATCCGCATTTCTCATGAATTAGATAGTGCCTCTTCTGAGGTCAACTGAAAGGAG    840
P                 CTGAAAATCCGCATTTCTCATGAATTAGATAGTGCCTCTTCTGAGGTCAACTGAAAGGAG    840
                  ************************************************************

NM_001285667.1    AAAATACAAGTTCTTACTTTGCTTTTAGTAAAAAGAAAAGGATATGTTAAAGCAGGGTGG    900
H                 AAAATACAAGTTCTTACTTTGCTTTTAGTAAAAAGAAAAGGATATGTTAAAGCAGGGTGG    900
P                 AAAATACAAGTTCTTATTTTGCTTTTAGTAAAAAGAAAAGGATATGTTAAAGCAGGGTGG    900
                  **************** *******************************************

NM_001285667.1    GAGACAATATGAAATGCGTATTTCTCAGCTTAGTTGGTGAATG    943
H                 GAGACAATATGAAATGCGTATTTCTCAGCTTAGTTGGTGAATG    943
P                 GAGACAATATGAAATGCGTATTTCTCAGCTTAGTTGGTGAATG    943
                  *******************************************
```

Figure S12: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|NM_001285667.1| and the *SPP1* gene (943-bp) demonstrating DNA sequence alignment.

```
KC894598.1    ATGGCCAGCGGCCCCGGCAGTGTGCGGAGGTGGGCAACCCTGGTGGTGCTGGTCGCCCTG 60
H             ATGGCCAGCGGCCCCGGCAGTGTGCGGAGGTGGGCAACCCTGGTGGTGCTGGTCGCCCTG 60
P             ATGGCCAGCGGCCCCGGCAGTGTGCGGAGGTGGGCAACCCTGGTGGTGCTGGTCGCCCTG 60
              ************************************************************

KC894598.1    GGCACGGCTGTGACAACGACGACCAACCCCGGCATCGTGGCCAGGGTCACCCAGAAAGGC 120
H             GGCACGGCTGTGACGACGACGACCAACCCCGGCATCGTGGCCAGGGTCACCCAGAAAGGC 120
P             GGCACGGCTGTGACAACGACGACCAACCCCGGCATCGTGGCCAGGGTCACCCAGAAAGGC 120
              ************** *********************************************

KC894598.1    CTGGACTACGCCTGCCAGCAGGGAGTGCTTACTCTGCAGAAAGAGTTGGAGAAGATAACA 180
H             CTGGACTACGCCTGCCAGCAGGGAGTGCTTACTCTGCAGAAAGAGTTGGAGAAGATAACA 180
P             CTGGACTACGCCTGCCAGCAGGGAGTGCTTACTCTGCAGAAAGAGTTGGAGAAGATAACA 180
              ************************************************************

KC894598.1    ATTCCCACTTTCTCAGGAAACTTTAAGATAAAATACCTCGGGAAAGGGCAATACAGCTTC 240
H             ATTCCCACTTTCTCAGGAAACTTTAAGATAAAATACCTCGGGAAAGGGCAATACAGCTTC 240
P             ATTCCCACTTTCTCAGGAAACTTTAAGATAAAATACCTCGGGAAAGGGCAATACAGCTTC 240
              ************************************************************

KC894598.1    TTCAGCATGGTTATTCGAGGATTCAATCTTCCCAATTCCCAGATCAGACCGTTGCCGGAT 300
H             TTCAGCATGGTTATTCAAGGATTCAATCTTCCCAATTCCCAGATCAGACCGTTGCCGGAT 300
P             TTCAGCATGGTTATTCGAGGATTCAATCTTCCCAATTCCCAGATCAGACCGTTGCCGGAT 300
              **************** *******************************************

KC894598.1    GAGGGCCTTGATCTCTCTATCAGAGATGCCAGTATCAAGATCAGAGGAAAATGGAAGGCA 360
H             GAGGGCCTTGATCTCTCTATCAGAGATGCCAGTATCAAGATCAGAGGAAAATGGAAGGCA 360
P             GAGGGCCTTGATCTCTCTATCAGAGATGCCAGTATCAAGATCAGAGGAAAATGGAAGGCA 360
              ************************************************************

KC894598.1    CGAAAGAACTTCATCAAACTCGGCGGCAACTTTGACCTGAGTGTGGAGGGCATCTCTATT 420
H             CGAAAGAACTTCATCAAACTCGGCGGCAACTTTGACCTGAGTGTGGAGGGCATCTCTATT 420
P             CGAAAGAACTTCATCAAACTCGGCGGCAACTTTGACCTGAGTGTGGAGGGCATCTCTATT 420
              ************************************************************

KC894598.1    TCGGCGGGTCTGAGTCTGGGCTATGACCCTGACTCAGGCCACTCCACTGTTACCTGCCCC 480
H             TCGGCGGGTCTGAGTCTGGGCTATGACCCTGACTCGGGCCACTCCACTGTTACCTGCCCC 480
P             TCGGCGGGTCTGAGTCTGGGCTATGACCCTGACTCAGGCCACTCCACTGTTACCTGCCCC 480
              *********************************** ************************

KC894598.1    AGATGCAGCAGCCACATCAACACCGTCCGCATACGCATCTCTGGCAGCAGCGTGGGGTGG 540
H             AGATGCAGCAGCCACATCAACACCGTCCGCATACGCATCTCTGGCAGCAGCGTGGGGTGG 540
P             AGATGCAGCAGCCACATCAACACCGTCCGCATACGCATCTCTGGCAGCAGCGTGGGGTGG 540
              ************************************************************

KC894598.1    TTGATCCAACTCTTCCACAAAAGAATCGAGTCTTCGCTCCAAAACTCCATGACCAGCAAG 600
H             TTGATCCAACTCTTCCACAAAAGAATCGAGTCTTCGCTCCAAAACTCCATGACCAGCAAG 600
P             TTGATCCAACTCTTCCACAAAAGAATCGAGTCTTCGCTCCAAAACTCCATGACCAGCAAG 600
              ************************************************************

KC894598.1    ATCTGCGAGGTGGTGACTAGTACTGTGTCCTCCAAGCTGCAACCT        645
H             ATCTGCGAGGTGGTGACTAGTACTGTGTCCTCCAAGCTGCAACCT        645
P             ATCTGCGAGGTGGTGACTAGTACTGTGTCCTCCAAGCTGCAACCT        645
              *********************************************
```

Figure S13: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|KC894598.1| and the *BP1* gene (645-bp) demonstrating DNA sequence alignment.

```
XM_018048527.1    AACCGCAATACATGGTGCTGGTCCCCTCCCTGCTCCGTACCAGAATCCCTGAGAAGGGTT    60
H                 AACCGCAATACATGGTGCTGGTCCCCTCCCTGCTCGGTACCAGAATCCCTGAGAAGGGTT    60
P                 AACCGCAATACATGGTGCTGGTCCCCTCCCTGCTCCGTACCAGAATCCCTGAGAAGGGTT    60
                  *********************************** ************************

XM_018048527.1    GCCTCCTTCTGAGCCACCTGAATGAGACGGTGACTGTCAGCGCCTCCTTGGAGTCCGTCA    120
H                 GCCTCCTTCTGAGCCACCTGAATGAGACGGTGACTGTCAGCGCCTCCTTGGAGTCCGTCA    120
P                 GCCTCCTTCTGAGCCACCTGAATGAGACGGTGACTGTCAGCGCCTCCTTGGAGTCCGTCA    120
                  ************************************************************

XM_018048527.1    GAGAGAACAGGAGCCTCTTCACTGATGTGGTGGCAGAGAAGGACTTATTCCACTGTGTCT    180
H                 GAGAGAACAGGAGCCTCTTCACTGATGTGGTGGCAGAGAAGGACTTATTCCACTGTGTCT    180
P                 GAGAGAACAGGAGCCTCTTCACTGATGTGGTGGCAGAGAAGGACTTATTCCACTGTGTCT    180
                  ************************************************************

XM_018048527.1    CCTTCAGCCTCCCAAGATCTCCAACCAGTCAAGAGGTAATGTTCCTCACCATCCAAGTTA    240
H                 CCTTCAGCCTCCCAAGATCTCCAACCAGTCAAGAGGTAATGTTCCTCACCATCCAAGTTA    240
P                 CCTTCAGCCTCCCAAGATCTCCAACCAGTCAAGAGGTAATGTTCCTCACCATCCAAGTTA    240
                  ************************************************************

XM_018048527.1    AAGGACCAACCCAAGAATTCAAGAAGCGGACCACAGTGTTGGTTAAAAATGAAGAGAGCC    300
H                 AAGGACCAACCCAAGAATTCAAGAAGCGGACCACAGTGTTGGTTAAAAATGAAGAGAGCC    300
P                 AAGGACCAACCCAAGAATTCAAGAAGCGGACCACAGTGTTGGTTAAAAATGAAGAGAGCC    300
                  ************************************************************

XM_018048527.1    TGGTCTTTGTCCAGACAGACAAACC    325
H                 TGGTCTTTGTCCAGACAGACAAACC    325
P                 TGGTCTTTGTCCAGACAGACAAACC    325
                  *************************
```

Figure S14: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|XM_018048527.1| and the *A2M* gene (325-bp) demonstrating DNA sequence alignment.

```
XM_013962543.2    CTACTCACCTGGGAAGCTTCTCCTGGAAAACGAGATGCCTGTCAACAGCACTGCCGTGTC    60
H                 CTACTCACCTGGGAAGCTTCTCCTGGAAAACGAGATGCCTGTCAACAGCACTGCCGTGTC    60
P                 CTACTCACCTGGGAAGCTTCTCCTGGAAAACGAGATGCCTGTCAACAGCACTGCCGTGTC    60
                  ************************************************************

XM_013962543.2    CTTGACCAGTGTCACCTACATCACTGTGGAGATCCTCATCGGGCTCTGCGCCATAGTGGG    120
H                 CTTGACCAGTGTCACCTACATCACTGTGGAGATCCTCATCGGGCTCTGCGCCATAGTGGG    120
P                 CTTGACCAGTGTCACCTACATCACTGTGGAGATCCTCATCGGGCTCTGCGCCATAGTGGG    120
                  ************************************************************

XM_013962543.2    CAACGTGCTGGTCATCTGGGTGGTCAAGCTGAACCCCAGCCTGCAGACCACCACCTTCTA    180
H                 CAACGTGCTGGTCATCTGGGTGGTCAAGCTGAACCCCAGCCTGCAGACCACCACCTTCTA    180
P                 CAACGTGCTGGTCATCTGGGTGGTCAAGCTGAACCCCAGCCTGCAGACCACCACCTTCTA    180
                  ************************************************************

XM_013962543.2    TTTCATTGTCTCCCTAGCCCTGGCTGACATTGCTGTCGGGGTGCTGGTTATGCCTCTGGC    240
H                 TTTCATTGTCTCCCTAGCCCTGGCTGACATTGCTGTCGGGGTGCTGGTTATGCCTCTGGC    240
P                 TTTCATTGTCTCCCTAGCCCTGGCTGACATTGCTGTCGGGGTGCTGGTTATGCCTCTGGC    240
                  ************************************************************

XM_013962543.2    CATTGTCATCAGCCTGGGTGTCACAATCCACTTTTATAGCTGCCTTTTCATGACCTGCTT    300
H                 CATTGTCATCAGCCTGGGTGTCACAATCCACTTTTATAGCTGCCTTTTCATGACCTGCTT    300
P                 CATTGTCATCAGCCTGGGTGTCACAATCCACTTTTATAGCTGCCTTTTCATGACCTGCTT    300
                  ************************************************************

XM_013962543.2    GATGCTGATCTTCACCCACGCATCCATCATGTCCTTGCTAGCCATTGCTGTGGACCGATA    360
H                 GATGCTGATCTTCACCCACGCATCCATCATGTCCTTGCTAGCCATTGCTGTGGACCGATA    360
P                 GATGCTGATCTTCACCCACGCATCCATCATGTCCTTGCTAGCCATTGCTGTGGACCGATA    360
                  ************************************************************

XM_013962543.2    CCTGCGGGTCAAGCTCACAGTCAGATCCAGGATTCCTAAGGCCCCTGGGTCCATCTGGTC    420
H                 CCTGCGGGTCAAGCTCACAGTCAGATCCAGGATTCCTAAGGCCCCTGGGTCCATCTGGTC    420
P                 CCTGCGGGTCAAGCTCACAGTCAGATACAGGATTCCTAAGGCCCCTGGGTCCATCTGGTC    420
                  ************************** *********************************

XM_013962543.2    ATCCCAGTTGAAGATTCACTTCTTTCCAGTCATGAGGCTCTTCATTCTGCTCTCTTTGAC    480
H                 ATCCCAGTTGAAGATTCACTTCTTTCCAGTCATGAGGCTCTTCATTCTGCTCTCTTTGAC    480
P                 ATCCCAGTTGAAGATTCACTTCTTTCCAGTCATGAGGCTCTTCATTCTGCTCTCTTTGAC    480
                  ************************************************************

XM_013962543.2    TGTCTTTTCAGATGCCATGGTCATGGACGAGAAGGTCAAGG    521
H                 TGTCTTTTCAGATGCCATGGTCATGGACGAGAAGGTCAAGG    521
P                 TGTCTTTTCAGATGCCATGGTCATGGACGAGAAGGTCAAGG    521
                  *****************************************
```

Figure S15: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|XM_013962543.2| and the *ADORA3* gene (521-bp) demonstrating DNA sequence alignment.

```
KJ001638.1    ATGTGCGCACAAGATGCTTTTCAGACACAGAGAAGCCAGCTGGTGGAGTTGCTGGTCTCG 60
H             ATGTGCGCACAAGATGCTTTTCAGACACAGAGAAGCCAGCTGGTGGAGTTGCTGGTCTCG 60
P             ATGTGCGCACAAGATGCTTTTCAGACACAGAGAAGCCAGCTGGTGGAGTTGCTGGTCTCG 60
              ************************************************************

KJ001638.1    GGGTCCCTGGAGAGCTTTGAGAGTATTGTGGACCGGCTGCTTTCCCGGGAAGTCCTCTCC 120
H             GGGTCCCTGGAGAGCTTTGAGAGTATTGTGGACCGGCTGCTTTCCCGGGAAGTCCTCTCC 120
P             GGGTCCCTGGAGGGCTTTGAGAGTATTGTGGACCGGCTGCTTTCCCGGGAAGTCCTCTCC 120
              ************ ***********************************************

KJ001638.1    TGGGAGGACTATGAGGGGCTTAGCCTCGTGGGCCAGCCCATCTCCCACTTGGCCAGGCGC 180
H             TGGGAGGACTATGAGGGGCTTAGCCTCGTGGGCCAGCCCATCTCCCACTTGGCCAGGCGC 180
P             TGGGAGGACTATGAGGGGCTTAGCCTCGTGGGCCAGCCCATCTCCCACTTGGCCAGGCGC 180
              ************************************************************

KJ001638.1    CTCCTGGACACCATCTGGAATAAGGGTGCTTGGGGCTGTGAACAACTGACTGCAGCTGTG 240
H             CTCCTGGACACCATCTGGAATAAGGGTGCTTGGGGCTGTGAACAACTGACTGCAGCTGTG 240
P             CTCCTGGACACCATCTGGAATAAGGGTGCTTGGGGCTGTGAACAACTGACTGCAGCTGTG 240
              ************************************************************

KJ001638.1    TGGGAGGCCCAGGCCGACAGCCAGCCCCCCGAGCTTCCCAGCTCCTGGGACCCCCACTCA 300
H             TGGGAGGCCCAGGCCGACAGCCAGCCCCCCGAGCTTCCCAGCTCCTGGGACCCCCACTCA 300
P             TGGGAGGCCCAGGCCGACAGCCAGCCCCCCGAGCTTCCCAGCTCCTGGGACCCCCACTCA 300
              ************************************************************

KJ001638.1    CCCCACCCAGCCCGTGACCTGCAGAGTCATCGGCCAGCCATCGTCAGGAGACTCTACGGC 360
H             CCCCACCCAGCCCGTGACCTGCAGAGTCATCGGCCAGCCATCGTCAGGAGACTCTACGGC 360
P             CCCCACCCAGCCCGTGACCTGCAGAGTCATCGGCCAGCCATCGTCAGGAGACTCTACGGC 360
              ************************************************************

KJ001638.1    CACGTGGAGGGTGTGCTGGACCTGACACAGCAGC         394
H             CACGTGGAGGGTGTGCTGGACCTGACACAGCAGC         394
P             CACGTGGAGGGTGTGCTGGACCTGACACAGCAGC         394
              **********************************
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Figure S16: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|KJ001638.1| and the *CARD15* gene (394-bp) demonstrating DNA sequence alignment.

```
JQ308793.1    ACTCCTGGGAAGGATAAGCCCGACCTGCCCACATGGAAGAGGAATTTCCGGTCTGCCCTG 60
H             ACTCCTGGGAAGGATAAGCCCGACCTGCCCACATGGAAGAGGAATTTCCGGTCTGCCCTG 60
P             ACTCCTGGGAAGGATAAGCCCGACCTGCCCACATGGAAGAGGAATTTCCGGTCTGCCCTG 60
              ************************************************************

JQ308793.1    AACCGGAAGGAAGTGTTGCGTTTAGCGGAGGACCACAGCAAGGACTCCCAAGACCCGCAC 120
H             AACCGGAAGGAAGTGTTGCGTTTAGCGGAGGACCACAGCAAGGACTCCCAAGACCCGCAC 120
P             AACCGGAAGGAAGTGTTGCGTTTAGCGGAGGACCACAGCAAGGACTCCCAAGACCCGCAC 120
              ************************************************************

JQ308793.1    AAGATCTATGAGTTTGTGAACTCAGGGGTCAGGGACATCCCTGAGACAGATACCGCTCAA 180
H             AAGATCTATGAGGTTGTGAACTCAGGGGTCAGGGACATCCCTGAGACAGATACCGCTCAA 180
P             AAGATCTATGAGTTTGTGAACTCAGGGGTCAGGGACATCCCTGAGACAGATACCGCTCAA 180
              ************ ***********************************************

JQ308793.1    GACAATGGCAGACACAGTACCTCTGATACCCAGGAAGACATTGTGCAGAAGTTACTGAGT 240
H             GACAATGGCAGACACAGTACCTCTGATACCCAGGAAGACATTGTGCAGAAGTTACTGAGT 240
P             GACAATGGCAGACACAGTACCTCTGATACCCAGGAAGACATTGTGCAGAAGTTACTGAGT 240
              ************************************************************

JQ308793.1    GACATGGACTTGAGCCCAGAAGGAGGGCCCTCCAATCTGACTATGACCTCTGAGAACCCC 300
H             GACATGGACTTGAGCCCAGAAGGAGGGCCCTCGAATCTGACTATGACCTCTGAGAACCCC 300
P             GACATGGACTTGAGCCCAGAAGGAGGGCCCTCCAATCTGACTATGACCTCTGAGAACCCC 300
              ******************************** ***************************

JQ308793.1    CCTCAGCTCTTACTGAGCCCCGAATCAGACATCCCTGCTCTTTGCCCAAACTCGGGACTC 360
H             CCTCAGCTCTTACTGAGCCCCGAATCAGACATCCCTGCTCTTTGCCCAAACTCGGGACTC 360
P             CCTCAGCTCTTACTGAGCCCCGAATCAGACATCCCTGCTCTTTGCCCAAACTCGGGACTC 360
              ************************************************************

JQ308793.1    TCTGAAAACCCCCTGAAGCAGCTGTTGGCGAACGAGGAAGATTGGGAGTTCGAGGTGACT 420
H             TCTGAAAACCCCCTGAAGCAGCTGTTGGCGAACGAGGAAGATTGGGAGTTCGAGGTGACT 420
P             TCTGAAAACCCCCTGAAGCAGCTGTTGGCGAACGAGGAAGATTGGGAGTTCGAGGTGACT 420
              ************************************************************

JQ308793.1    GCCTTCTACCGGGGCTGTCAAGTCTTCCAGCAGACTGTCTTCTGCCCT     468
H             GCCTTCTACCGGGGCTGTCAAGTCTTCCAGCAGACTGTCTTCTGCCCT     468
P             GCCTTCTACCGGGGCTGTCAAGTCTTCCAGCAGACTGTCTTCTGCCCT     468
              ************************************************
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Figure S17: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|JQ308793.1|and the *IRF3* gene (468-bp) demonstrating DNA sequence alignment.

```
XR_001917340.1    CTGAGATCAGGAATGTGAACGGGGTGGACCGCCTCTGTGGCCTGCACCGGGAGGAGGCCA    60
H                 CTGAGATCAGGAATGTGAACGGGGTGGACCGCCTCTGTGGCCTGCACCGGGAGGAGGCCA    60
P                 CTGAGATCAGGAATGTGAACGGGGTGGACCGCCTCTGTGGCTTGCACCGGGAGGAGGCCA    60
                  ***************************************** ******************

XR_001917340.1    CGGTGTTCTGCCAGGAGCTGGGGTGAGGCCCTGCCCTGCAGGTCCCCCGCCAAGATGGCA    120
H                 CGGTGTTCTGCCAGGAGCTGGGGTGAGGCCCTGCCCTGCAGGTCCCCCGCCAAGATGGCA    120
P                 CGGTGTTCTGCCAGGAGCTGGGGTGAGGCCCTGCCCTGCAGGTCCCCCGCCAAGATGGCA    120
                  ************************************************************

XR_001917340.1    GTGTCACCAGGAAGTACATGACCTGTAGGGGCGACGAGCTGACCATCCGGAACTGCAGAC    180
H                 GTGTCGCCAGGAAGTACATGACCTGTAGGGGCGACGAGCTGACCATCCGGAACTGCAGAC    180
P                 GTGTCACCAGGAAGTACATGACCTGTGGGGGCGACGAGCTGACCATCCGGAACTGCAGAC    180
                  ***** ******************** *********************************

XR_001917340.1    TGAACAAGTTCCGCAGCGGCTGCGACTTCCAGCGAGATGCCCAGGTGGTCTGCTCAGGGC    240
H                 TGAACAAGTTCCGCAGCGGCTGCGACTTCCAGCGAGATGCCCAGGTGGTCTGCTCAGGGC    240
P                 TGAACAAGTTCCGCAGCGGCTGCGACTTCCAGCGAGATGCCCAGGTGGTCTGCTCAGGGC    240
                  ************************************************************

XR_001917340.1    ACACGGAGGCCCGGCTGGCGGGTGGCGGGCACTCCTGTGCTGGGCGCCTGGAGGTGAGGC    300
H                 ACACGGAGGCCCGGCTGGCGGGTGGCGGGCACTCCTGTGCTGGGCGCCTGGAGGTGAGGC    300
P                 ACACGGAGGCCCGGCTGGCGGGTGGCGGGCACTCCTGTGCTGGGCGCCTGGAGGTGAGGC    300
                  ************************************************************

XR_001917340.1    GTGGCCTGACCTGGGGCACCGTCTGTGACGCTGACCTGGACCTGGCCACTGCCCACGTGG    360
H                 GTGGCCTGACCTGGGGCACCGTCTGTGACGCTGACCTGGACCTGGCCACTGCCCACGTGG    360
P                 GTGGCCTGACCTGGGGCACCGTCTGTGACGCTGACCTGGACCTGGCCACTGCCCACGTGG    360
                  ************************************************************

XR_001917340.1    TGTGCCGGGAGCTGCAGTGTGGTGTGGCCGTGTCCACACCCCAGGGCGCCCACTTTGGCC    420
H                 TGTGCCGGGAGCTGCAGTGTGGTGTGGCCGTGTCCACACCCCAGGGCGCCCACTTTGGCC    420
P                 TGTGCCGGGAGCTGCAGTGCGGTGTGGCCGTGTCCACACCCCAGGGCGCCCACTTTGGCC    420
                  ******************* ****************************************

XR_001917340.1    AGGGCTCGGGGCTCGTGTGGACCGAGGCCTTCCGCGGGCAACGAGTCCCTGCTGT   475
H                 AGGGCTCGGGGCTCGTGTGGACCGAGGCCTTCCGCGGGCAACGAGTCCCTGCTGT   475
P                 AGGGCTCGGGGCTCGTGTGGACCGAGGCCTTCCGCGGGCAACGAGTCCCTGCTGT   475
                  *******************************************************
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Figure S18: Comparison of healthy and pneumonia-affected Baladi goats using GenBank-sourced reference sequence gb|XR_001917340.1| and the *SCART1* gene (475-bp) demonstrating DNA sequence alignment.