

Supplementary:

XM_031464240.1	TGCGAGGAGGAGTTGTCAGCTTCGCCAACCAGCTGCAGGCTCTGGGGCTGAAGCTGCGG	60
H	TGCGAGGAGGAGTTGTCAGCTTCGCCAACCAGCTGCAGGCTCTGGGGCTGAAGCTGCGG	60
M	TGCGAGGAGGAGTTGTCAGCTTCGCCAACCAGCTGCAGGCTCTGGGGCTGAAGCTGCGG	60

XM_031464240.1	GAGGTGCCGGGGGACGGCAATTGCCTATTTCAGAGCTCTTGGTGATCAATTGGAGGGACAT	120
H	GAGGTGCCGGGGGACGGCAATTGCCTATTTCAGAGCTCTTGGTGATCAATTGGAGGGACAC	120
M	GAGGTGCCGGGGGACGGCAATTGCCTATTTCAGAGCTCTTGGTGATCAATTGGAGGGACAT	120

XM_031464240.1	TCAAGAAATCATCTCAAGCACCGACAGGAGACAGTGGACTACATGATAAAGCAGCGGGAA	180
H	TCAAGAAATCATCTCAAGCACCGACAGGAGACAGTGGACTACATGATAAAGCAGCGGGAA	180
M	TCAAGAAATCATCTCAAGCACCGACAGGAGACAGTGGACTACATGATAAAGCAGCGGGAA	180

XM_031464240.1	GATTTTGAACCCCTTTGTAGAAGATGACGTTCCCTTTTGAGAAACATGTGGCCAGTTTGGCA	240
H	GATTTTGAACCCCTTTGTAGAAGATGACGTTCCCTTTTGAGAAACATGTGGCCAGTTTGGCA	240
M	GATTTTGAACCCCTTTGTAGAAGATGACGTTCCCTTTTGAGAAACATGTGGCCAGTTTGGCA	240

XM_031464240.1	AAGCCTGGAACATTTGCTGGCAATGATGCTATTGTAGCCTTTGCAAGAAATCATCAGTTG	300
H	AAGCCTGGAACATTTGCTGGCAATGATGCTATTGTAGCCTTTGCAAGAAATCATCAGTTG	300
M	AAGCCTGGAACATTTGCTGGCAATGATGCTATTGTAGCCTTTGCAAGAAATCATCAGTTG	300

XM_031464240.1	AATGTGGTGATTTCATCAACTTAATGCCCTTTGTGGCAGATCCGCGGTACAGAGAAGAGC	360
H	AATGTGGTGATTTCATCAACTTAATGCCCTTTGTGGCAGATCCGCGGTACAGAGAAGAGC	360
M	AATGTGGTGATTTCATCAACTTAATGCCCTTTGTGGCAGATCCGCGGTACAGAGAAGAGC	360

XM_031464240.1	AACGTGCGGGAGTTGCACATCGCGTACCGGTGTGGCGAGCACTATGACAGCGTCCGGAGG	420
H	AACGTGCGGGAGTTGCACATCGCGTACCGGTGTGGCGAGCACTATGACAGCGTCCGGAGG	420
M	AACGTGCGGGAGTTGCACATCGCGTACCGGTGTGGCGAGCACTATGACAGCGTCCGGAGG	420

XM_031464240.1	ATCAACGACAACTCGGAAGCACCTGCGCACCT	452
H	ATCAACGACAACTCGGAAGCACCTGCGCACCT	452
M	ATCAACGACAACTCGGAAGCACCTGCGCACCT	452

Figure S1. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_031464240.1| and *OTUD3* marker (452-bp) sequences.

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MW557315.1 TCAGGCCCATTCTCTGTCTTGTGACCCCACTGGCGTCTGTGATGGCCGTGCCAGATCTTT 60
H TCAGGCCCATTCTCTGTCTTGTGACCCCACTGGCGTCTGTGATGGCCGTGCCAGATCTTT 60
M TCAGGCCCATTCTCTGTCTTGTGACCCCACTGGCGTCTGTGATGGCCGTGCCAGATCTTT 60
*****

MW557315.1 AAACGCCATCCCCCAGGGCTCACGGCAGCTGTGAAAAGCCTTGACCTGTCCGATAACAA 120
H AAACGCCATCCCCCAGGGCTCACGGCAGCTGTGAAAAGCCTTGACCTGTCCGATAACAA 120
M AAACGCCATCCCCCAGGGCTCACGGCAGCTGTGAAAAGCCTTGACCTGTCCAATAACAA 120
*****

MW557315.1 GATCACCTATGTCGGCAACAATGACCTGCAGAGGTGTGTGGGCCTCAAGGCCTTGAGGCT 180
H GATCACCTATGTCGGCAACAATGACCTGCAGAGGTGTGTGGGCCTCAAGGCCTTGAGGCT 180
M GATCACCTATGTCGGCAACAATGACCTGCAGAGGTGTGTGGGCCTCAAGGCCTTGAGGCT 180
*****

MW557315.1 GGGGTCCAATGGAGTCCACACAATAGAGGAAGATTCCCTTTTTTCCCCTGAGGAGCCTCGA 240
H GGGGTCCAATGGAGTCCACACAATAGAGGAAGATTCCCTTTTTTCCCCTGAGGAGCCTCGA 240
M GGGGTCCAATGGAGTCCACACAATAGAGGAAGATTCCCTTTTTTCCCCTGAGGAGCCTCGA 240
*****

MW557315.1 ACATTTGGACTTATCCTATAATCGCTTGCTAACTTATCACCTTCCTGGTTCAGGACCCT 300
H ACATTTGGACTTATCCTATAATCGCTTGCTAACTTATCACCTTCCTGGTTCAGGACCCT 300
M ACATTTGGACTTATCCTATAATCGCTTGCTAACTTATCACCTTCCTGGTTCAGGACCCT 300
*****

MW557315.1 TTCTGCCTTGAAATTCTTAACTTGCTGGGAAATCCTTACAGAACACTTGGCGAAACGTC 360
H TTCTGCCTTGAAATTCTTAACTTGCTGGGAAATCCTTACAGAACACTTGGCGAAACGTC 360
M TTCTGCCTTGAAATTCTTAACTTGCTGGGAAATCCTTACAGAACACTTGGCGAAACGTC 360
*****

MW557315.1 TCTTTTTTCTCATCTCCCCAATCTGCGAATTCTGAAAGTAGGAAATAGTAACCCCTTCTC 420
H TCTTTTTTCTCATCTCCCCAATCTGCGAATTCTGAAAGTAGGAAATAGTAACCCCTTCTC 420
M TCTTTTTTCTCATCTCCCCAATCTGCGAATTCTGAAAGTAGGAAATAGTAACCCCTTCTC 420
*****

MW557315.1 CGAGATTGAGGAAAAGGATTTCTCTGGGCTCACTTTTCTTGAGGAACCTGAGATCGATGC 480
H CGAGATTGAGGAAAAGGATTTCTCTGGGCTCACTTTTCTTGAGGAACCTGAGATCGATGC 480
M CGAGATTGAGGAAAAGGATTTCTCTGGGCTCACTTTTCTTGAGGAACCTGAGATCGATGC 480
*****

MW557315.1 TTCAAATCTGCAGAGGTATGAGCCAAAGAGTTTGAGGTCAATTCAGAACATCACTCATCT 540
H TTCAAATCTGCAGAGGTATGAGCCAAAGAGTTTGAGGTCAATTCAGAACATCACTCATCT 540
M TTCAAATCTGCAGAGGTATGAGCCAAAGAGTTTGAGGTCAATTCAGAACATCACTCATCT 540
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Figure S2. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|MW557315.1| and *TLR2* marker (540-bp) sequences.

XM_010998333.2	TAGCTGTGGCTCTGATGACAGCCATGGCCTTTCTCTCCTGTCTGAGATCCGAGAGCTGGG	60
H	TAGCTGTGGCTCTGATGACAGCCATGGCCTTTCTCTCCTGTCTGAGATCCGAGAGCTGGG	60
M	TAGCTGTGGCTCTGATGACAGCCATGGCCTTTCTCTCCTGTCTGAGATCCGAGAGCTGGG	60

XM_010998333.2	AACCCTGTGTGCAGGTGGTTCCTAACATTAGTTACCAATGCATGGAGCTGAATCTCTACA	120
H	AACCCTGTGTGCAGGTGGTTCCTAACATTAGTTACCAATGCATGGAGCTGAATCTCTACA	120
M	AACCCTGTGTGCAGGTGGTTCCTAACATTAGTTACCAATGCATGGAGCTGAATCTCTACA	120

XM_010998333.2	AAGTCCCAGACAACATCCCCACATCGACCAAGATACTGGATCTCAGCTTTAACCACCTGA	180
H	AAGTCCCAGACAACATCCCCACATCGACCAAGATACTGGATCTCAGCTTTAACCACCTGA	180
M	AAGTCCCAGACAACATCCCCACATCGACCAAGATACTGGATCTCAGCTTTAACCACCTGA	180

XM_010998333.2	ATCATTTAGGCAGCCATAGCTTCTCCAGCTTCCAGAACTGCAGGTGCTGGATTTATCCA	240
H	ATCATTTAGGCAGCCATAGCTTCTCCAGCTTCCAGAACTGCAGGTGCTGGATTTATCCA	240
M	ATCATTTAGGCAGCCATAGCTTCTCCAGGTTCAGAACTGCAGGTGCTGGATTTATCCA	240

XM_010998333.2	GATGTGAAATTGAGATGATTGACGATAATGCGTATCAGGGGCTAAACCACCTTGCCACCT	300
H	GATGTGAAATTGAGATGATTGACGATAATGCGTATCAGGGGCTAAACCACCTTGCCACCT	300
M	GATGTGAAATTGAGATGATTGACGATAATGCGTATCAGGGGCTAAACCACCTTGCCACCT	300

XM_010998333.2	TGATATTGACGGGAAACCCTATCCAGAGTTTAGCCCTGAGAGCCTTTTCTGGAATACCGA	360
H	TGATATTGACGGGAAACCCTATCCAGAGTTTAGCCCTGAGAGCCTTTTCTGGAATACCGA	360
M	TGATATTGACGGGAAACCCTATCCAGAGTTTAGCCCTGAGAGCCTTTTCTGGAATACCGA	360

XM_010998333.2	GTTTACAGAAGCTGGTTGCTGTGGAGACAAACCTAGCATCTCTAG 405	
H	GTTTACAGAAGCTGGTTGCTGTGGAGACAAACCTAGCATCTCTAG 405	
M	GTTTACAGAAGCTGGTTGCTGTGGAGACAAACCTAGCATCTCTAG 405	

Figure S3. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_010998333.2| and *TLR4* marker (405-bp) sequences.

XM_031462916.1	GACTGAGTGCCCAATCCTGCTCACTCAACTTTGGAATTAAGTGCCCAGATGGTTACACCAA	60
H	GACTGAGTGCCCAATCCTGCTCACTCAACTTTGGAATTAAGTGCCCAGATGGTTACACCAA	60
M	GACTGAGTGCCCAATCCTGCTCACTCAACTTTGGAATTAAGTGCCCAGATGGTTACACCAA	60

XM_031462916.1	GATTACCAATGGCACCCTAGGGATCCGAGACTGCAGGTACACCTTTGAGGTAAGAACATA	120
H	GATTACCAATGGCACCCTAGGGATCCGAGACTGCAGGTACACCTTTGAGGTAAGAACATA	120
M	GATTACCAATGGCACCCTAGGGATCCGAGACTGCAGGTACACCTTTGAGGTCAGAACATA	120

XM_031462916.1	CTCGCTGTCTCTCCCTGGATGCCGCCATATCTGCAGGAAGGACTATCTCCAGCCTCAGTG	180
H	CTCGCTGTCTCTCCCTGGATGCCGCCATATCTGCAGGAAGGACTATCTCCAGCCTCAGTG	180
M	CTCGCTGTCTCTCCCTGGATGCCGCCATATCTGCAGGAAGGACTATCTCCAGCCTCAGTG	180

XM_031462916.1	CTGTCCCGGCTACTGGGGCCCAGACTGCATGGAGTGCCCCGGAGGAGCGAGGTCCCCCTG	240
H	CTGTCCCGGCTACTGGGGCCCAGACTGCATGGAGTGCCCCGGAGGAGCGAGGTCCCCCTG	240
M	CTGTCCCGGCTACTGGGGCCCAGACTGCATGGAGTGCCCCGGAGGAGCGAGGTCCCCCTG	240

XM_031462916.1	CAGCGGCAGGGGCAGTTGTGCTGAAGGCATGGATGGAAACGGAAGCTGCTCCTGCCAAGA	300
H	CAGCGGCAGGGGCAGTTGTGCTGAAGGCATGGATGGAAACGGAAGCTGCTCCTGCCAAGA	300
M	CAGCGGCAGGGGCAGTTGTGCTGAAGGCATGGATGGAAACGGAAGCTGCTCCTGCCAAGA	300

XM_031462916.1	GGGGTTTGGTGAACAGCCTGTGAAGCCTGTGCTGATGACAACCTTATTTGGACCCAGCTG	360
H	GGGGTTTGGTGAACAGCCTGTGAAGCCTGTGCTGATGACAACCTTATTTGGACCCAGCTG	360
M	GGGGTTTGGTGAACAGCCTGTGAAGCCTGTGCTGATGACAACCTTATTTGGACCCAGCTG	360

XM_031462916.1	TTCAGCAGTGTGCACCTGTGTGCATGGCGTGTGCCGAGTGGAATTGATGGTGACGGGAC	420
H	TTCAGCAGTGTGCACCTGTGTGCATGGCGTGTGCCGAGTGGAATTGATGGTGACGGGAC	420
M	TTCAGCAGTGTGCACCTGTGTGCATGGCGTGTGCCGAGTGGAATTGATGGTGACGGGAC	420

XM_031462916.1	CTGTGAGTGCTACTCTGCATACACCGGCCCAATTGTGACAAACCCATCCCTGAATGTGC	480
H	CTGTGAGTGCTACTCTGCATACACCGGCCCAATTGTGACAAACCCATCCCTGAATGTGC	480
M	CTGTGAGTGCTACTCTGCATACACCGGCCCAATTGTGACAAACCCATCCCTGAATGTGC	480

XM_031462916.1	AACCTTGCTCTGCCCAGA498	
H	AACCTTGCTCTGCCCAGA498	
M	AACCTTGCTCTGCCCAGA498	

Figure S4. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_031462916.1| and STAB2 marker (498-bp) sequences.

XM_010975501.1	CGGCACGACTAATCATGTGTGCCTACTTCACCTTGTCCCTGCTTCCATCGCTCCTTCTCC	60
H	CGGCACGACTAATCATGTGTGCCTACTTCACCTTGTCCCTGCTTCCATCGCTCCTTCTCC	60
M	CGGCACGACTAATCATGTGTGCCTACTTCACCTTGTCCCTGCTTCCATCGCTCCTTCTCC	60

XM_010975501.1	TCCTCCTGATTGTGGTGACAGCATCTTGACAGAAACAGAAACTGTGAGAATGTCCAAA	120
H	TCCTCCTGATTGTGGTGACAGCATCTTGACAGAAACAGAAACTGTGAGAATGTCCAAA	120
M	TCCTCCTGATTGTGGTGACAGCATCTTGACAGAAACAGAAACTGTGAGAATGTCCAAA	120

XM_010975501.1	AGACTTGCCCTGTGATTGCCTGTGGTTCTCCAGGCATCAGCAGCTTCCCAGGCAAAGATG	180
H	AGACTTGCCCTGTGATTGCCTGTAGTTCTCCAGGCATCAGCAGCTTCCCAGGCAAAGATG	180
M	AGACTTGCCCTGTGATTGCCTGTGGTTCTCCAGGCATCAGCAGCTTCCCAGGCAAAGATG	180

XM_010975501.1	GGCATGATGGTGCCCAAGGAAGAAAAGGGAGAACCAGGCCAAGGACTCAGAGGCTTGCAAG	240
H	GGCATGATGGTGCCCAAGGAAGAAAAGGGAGAACCAGGCCAAGGACTCAGAGGCTTGCAAG	240
M	GGCATGATGGTGCCCAAGGAAGAAAAGGGAGAACCAGGCCAAGGACTCAGAGGCTTGCAAG	240

XM_010975501.1	GCCCTCCTGGAAGGCAGGGCCTCAAGGAATCCCAGGGACTCCTGGGTTACCAGGACCAG	300
H	GCCCTCCTGGAAGGCAGGGCCTCAAGGAATCCCAGGGACTCCTGGGTTACCAGGACCAG	300
M	GCCCTCCTGGAAGGCAGGGCCTCAAGGAATCCCAGGGACTCCTGGGTTACCAGGACCAG	300

XM_010975501.1	TGGGCCAAAAGGAGACCCTGGAGATGATTGGTTGACCATATTACCCTGGCTGCTTCAG	360
H	TGGGCCAAAAGGAGACCCTGGAGATGATTGGTTGACCATATTACCCTGGCTGCTTCAG	360
M	TGGGCCAAAAGGAGACCCTGGAGATGATTGGTTGACCATATTACCCTGGCTGCTTCAG	360

XM_010975501.1	AAAGAGCAGCCCTGCGATCAGAATTGGAC	389
H	AAAGAGCAGCCCTGCGATCAGAATTGGAC	389
M	AAAGAGCAGCCCTGCGATCAGAATTGGAC	389

Figure S5. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_010975501.1| and *MBL2* marker (389-bp) sequences.

XM_031439680.1	AGACTCTCCTCGTGGTGGTCCAGCCCGTGGGCATCGTATCGGAGGAGAACTTCTTCCGCA	60
H	AGACTCTCCTCGTGGTGGTCCAGCCCGTGGGCATCGTATCGGAGGAGAACTTCTTCCGCA	60
M	AGACTCTCCTCGTGGTGGTCCAGCCCGTGGGCATCGTATCGGAGGAGAACTTCTTCCGCA	60

XM_031439680.1	TCTACAAGCGGATCTCCTCCGTGAGCCAGGTGAGCGTGCGCGACTCCCAGCGGGTGCTCT	120
H	TCTACAAGCGGATCTCCTCCGTGAGCCAGGTGAGCGTGCGCGACTCCCAGCGGGTGCTCT	120
M	TCTACAAGCGGATCTCCTCCGTGAGCCAGGTGAGCGTGCGCGACTCCCAGCGGGTGCTCT	120

XM_031439680.1	ACATCCGCTACCGGCACCACTACCCGCCCGAGAACAACGAGTGGGGCGACTTCCAGACCC	180
H	ACATCCGCTACCGGCACCACTACCCGCCCGAGAACAACGAGTGGGGCGACTTCCAGACCC	180
M	ACATCCGCTACCGGCACCACTACCCGCCCGAGAACAACGAGTGGGGCGACTTCCAGACCC	180

XM_031439680.1	ACCGCAAGGTCGTGGGCCTCGTCACCATCACCGACTGCTTCTCGGCCAAGGACTGGCCGC	240
H	ACCGCAAGGTCGTGGGCCTCGTCACCATCACCGACTGCTTCTCGGCCAAGGACTGGCCGC	240
M	ACCGCAAGGTCGTGGGCCTCGTCACCATCACCGACTGCTTCTCGGCCAAGGACTGGCCGC	240

XM_031439680.1	AGACCTTTGAGAAGTTCCACGTGCAGAAGGAGCTGTATGGCGCCACGCTGTACGACTCGC	300
H	AGACCTTTGAGAAGTTCCACGTGCAGAAGGAGCTGTATGGCGCCACGCTGTACGACTCGC	300
M	AGACCTTTGAGAAGTTCCACGTGCAGAAGGAGCTGTATGGCGCCACGCTGTACGACTCGC	300

XM_031439680.1	GGCTCTTCGTCTTCGGGCTGCAGGGCGAGATCGCCGAGCAGCCGCGCACCGACGTGGCCT	360
H	GGCTCTTCGTCTTCGGGCTGCAGGGCGAGATCGCCGAGCAGCCGCGCACCGACGTGGCCT	360
M	GGCTCTTCGTCTTCGGGCTGCAGGGCGAGATCGCCGAGCAGCCGCGCACCGACGTGGCCT	360

XM_031439680.1	TCTACCCAGCTACGAGGACTGCGGGACGGTGGAGAAGAGGATCGAGGACTTCATCGAGT	420
H	TCTACCCAGCTACGAGGACTGCGGGACGGTGGAGAAGAGGATCGAGGACTTCATCGAGT	420
M	TCTACCCAGCTACGAGGACTGCGGGACGGTGGAGAAGAGGATCGAGGACTTCATCGAGT	420

XM_031439680.1	CGC	423
H	CGC	423
M	CGC	423

Figure S6. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_031439680.1| and *TRAPPC9* marker (423-bp) sequences.

XM_031435000.1	TCTGCAGAAGCCCAGGTTGCTCCTGTTTTCTCCTTCTGTGGTTACCTAGGGGTCCCCCT	60
H	TCTGCAGAAGCCCAGGTTGCTCCTGTTTTCTCCTTCTGTGGTTACCTAGGGGTCCCCCT	60
M	TCTGCAGAAGCCCAGGTTGCTCCTGTTTTCTCCTTCTGTGGTTACCTAGGGGTCCCCCT	60

XM_031435000.1	GTCCGTGGTGGTGCAGCTCCAGGATGCTCCTCCCGGGCAGGTAGTGACAGGATCAGTGTT	120
H	GTCCGTGGTGGTGCAGCTCCAGGATGCTCCTCCCGGGCAGGTAGTGACAGGATCAGTGTT	120
M	GTCCGTGGTGGTGCAGCTCCAGGATGCTCCTCCCGGGCAGGTAGTGACAGGATCAGTGTT	120

XM_031435000.1	CCTGAGAAACCCGTCCAACCATCGTCACCTCTGTTCTGCGGAGGTGGATTTCACCCCTCAA	180
H	CCTGAGAAACCCGTCCAACCATCGTCACCTCTGTTCTGCGGAGGTGGATTTCACCCCTCAA	180
M	CCTGAGAAACCCGTCCAACCATCGTCACCTCTGTTCTGCGGAGGTGGATTTCACCCCTCAA	180

XM_031435000.1	CTCAGAGAAAGACTTCATACTTCTCAGCCTCCCGATCTCCCTGAAGGATGCAAAGGACTG	240
H	CTCAGAGAAAGACTTCATACTTCTCAGCCTCCCGATCTCCCTGAAGGATGCAAAGGACTG	240
M	CTCAGAGAAAGACTTCATACTTCTCAGCCTCCCGATCTCCCTGAAGGATGCGAAGGACTG	240

XM_031435000.1	TGGCCTCCATCTCCTCCGCAGAGCCCCGAGGTGCAGCTGGTGGTCCAGTCGTCATGGCT	300
H	TGGCCTCCATCTCCTCCGCAGAGCCCCGAGGTGCAGCTGGTGGTCCAGTCGTCATGGCT	300
M	TGGCCTCCATCTCCTCCGCAGAGCCCCGAGGTGCAGCTGGTGGTCCAGTCGTCATGGCT	300

XM_031435000.1	GAAGAACTATCTGTCCAAGCAGACTGACAGGCAGGGTGTCAACCTGTTCTTCTCCTCTCG	360
H	GAAGAACTATCTGTCCAAGCAGACTGACAGGCAGGGTGTCAACCTGTTCTTCTCCTCTCG	360
M	GAAGAACTATCTGTCCAAGCAGACTGACAGGCAGGGTGTCAACCTGTTCTTCTCCTCTCG	360

XM_031435000.1	CCGGGGCCACCTCTTTCTGCAGACTGACCAGCCCGTTTATAACCTGGCCAGCGCGTTTCG	420
H	CCGGGGACACCTCTTTCTGCAGACTGACCAGCCCGTTTATAACCTGGCCAGCGCGTTTCG	420
M	CCGGGGCCACCTCTTTCTGCAGACTGACCAGCCCGTTTATAACCTGGCCAGCGGGTTTCG	420
	***** *****	
XM_031435000.1	GTACCGAGTCTTTGCTCTGGATCA	444
H	GTACCGAGTCTTTGCTCTGGATCA	444
M	GTACCGAGTCTTTGCTCTGGATCA	444

Figure S7. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_031435000.1| and C4A marker (444-bp) sequences.

XM_011000575.2	CGGGATCCAGCCAGCGACCAGATGAAGCGCTGGAAGGAGCAGCGGGCCGCGCAGAAACCT	60
H	CGGGATCCAGCCAGCGACCAGATGAAGCGCTGGAAGGAGCAGCGGGCCGCGCAGAAACCT	60
M	CGGGATCCAGCCAGCGACCAGATGAAGCGCTGGAAGGAGCAGCGGGCCGCGCAGAAACCT	60

XM_011000575.2	GATGTCTTGACCACCGGGGGCGGCAATCCAGTAGGAGACAACTCAATGTTATGACAGCA	120
H	GATGTCTTGACCACCGGGGGCGGCAATCCAGTAGGAGACAACTCAATGTTATGACAGCA	120
M	GATGTCTTGACCACCGGGGGCGGCAATCCAGTAGGAGACAACTCAATGTTATGACAGCA	120

XM_011000575.2	GGGCCCCGCGGGCCCCCTCCTGGTTCAGGATGTGGTTTTCTACTGATGAAATGGCTCACTTC	180
H	GGGCCCCGCGGGCCCCCTCCTGGTTCAGGATGTGGTTTTCTACTGATGAAATGGCTCACTTC	180
M	GGGCCCCGCGGGCCCCCTCCTGGTTCAGGATGTGGTTTTCTACTGATGAAATGGCTCACTTC	180

XM_011000575.2	GACCGGGAGAGAAATTCCTGAGAGAGTTGTGCACGCTAAAGGAGCAGGGGCTTTTGGCTAC	240
H	GACCGGGAGAGAAATTCCTGAGAGAGTTGTGCACGCTAAAGGAGCAGGGGCTTTTGGCTAC	240
M	GACCGGGAGAGAAATTCCTGAGAGAGTTGTGCACGCTAAAGGAGCAGGGGCTTTTGGCTAC	240

XM_011000575.2	TTTGAGGTCACACATGACATTACTAGATACTCGAAGGCGAAGGTGTTTGAGCACATTGGA	300
H	TTTGAGGTCACACATGACATTACTAGATACTCGAAGGCGAAGGTGTTTGAGCACATTGGA	300
M	TTTGAGGTCACACATGACATTACTAGATACTCGAAGGCGAAGGTGTTTGAGCACATTGGA	300

XM_011000575.2	AAGAGGACGCCCAATTGCCGTTTCGCTTCTCCACTGTTGCTGGAGAATCAGGCTCACCTGAC	360
H	AAGAGGACGCCCAATTGCCGTTTCGCTTCTCCACTGTTGCTGGAGAATCAGGCTCACCTGAC	360
M	AAGAGGACGCCCAATTGCCGTTTCGCTTCTCCACTGTTGCTGGAGAATCAGGCTCACCTGAC	360

XM_011000575.2	ACCGTTCGTGACCCTCGTGGGTTTGCAGTGAAATTTTACACGGAGGATGGTAACTGGGAT	420
H	ACCGTTCGTGACCCTCGTGGGTTTGCAGTGAAATTTTACACGGAGGATGGTAACTGGGAT	420
M	ACCGTTCGTGACCCTCGTGGGTTTGCAGTGAAATTTTACACGGAGGATGGTAACTGGGAT	420

XM_011000575.2	CTTACTGGAATAACACCCCCATTTTCTTCATCAGGGATGCCATGTTGTTTCCATCCTTT	480
H	CTTACTGGAATAACACCCCCATTTTCTTCATCAGGGATGCCATGTTGTTTCCATCCTTT	480
M	CTTACTGGAATAACACCCCCATTTTCTTCATCAGGGATGCCATGTTGTTTCCATCCTTT	480

XM_011000575.2	ATCCACAGCCAAAAGAGAAACCTCAAACGCATCTAAAGGATCCAGATATGGTCTGGGAC	540
H	ATCCACAGCCAAAAGAGAAACCTCAAACGCATCTAAAGGATCCAGATATGGTCTGGGAC	540
M	ATCCACAGCCAAAAGAGAAACCTCAAACGCATCTAAAGGATCCAGATATGGTCTGGGAC	540

Figure S8. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_011000575.2| and CAT marker (540-bp) sequences.

XM_010963047.2	TGCTCTGTGCCTACCTGCTCACGGCGACACACGCCTCGGAAGCCTGGACCAACCCAGACC	60
H	TGCTCTGTGCCTACCTGCTCACGGCGACACACGCCTCGGAAGCCTGGACCAACCCAGACC	60
M	TGCTCTGTGCCTACCTGCTCACGGCGACACACGCCTCGGACGCCTGGACCAACCCAGACC	60

XM_010963047.2	CGCAGGACCCCGGCTTCGGCATGGAGGAGCAGATCCGCGACATGCACGCCAAGTGACGG	120
H	CGCAGGACCCCGGCTTCGGCATGGAGGAGCAGATCCGCGACATGCACGCCAAGTGACGG	120
M	CGCAGGACCCCGGCTTCGGCATGGAGGAGCAGATCCGCGACATGCACGCCAAGTGACGG	120

XM_010963047.2	AGATCTGGCAGGAGATGAAGCAGCGGCGGGCGGCGAGTGGCCAAGATGCTGCGCTGCACG	180
H	AGATCTGGCAGGAGATGAAGCAGCGGCGGGCGGCGAGTGGCCAAGATGCTGCGCTGCACG	180
M	AGATCTGGCAGGAGATGAAGCAGCGGCGGGCGGCGAGTGGCCAAGATGCTGCGCTGCACG	180

XM_010963047.2	CCGCCTGCCGCGTGCTGCCGTTCGGCCGCGCTGGCCGCGGCGCAGCCCCGGGTGAGGGGCC	240
H	CCGCCTGCCGCGTGCTGCCGTTCGGCCGCGCTGGCCGCGGCGCAGCCCCGGGTGAGGGGCC	240
M	CCGCCTGCCGCGTGCTGCCGTTCGGCCGCGCTGGCCGCGGCGCAGCCCCGGGTGAGGGGCC	240

XM_010963047.2	TCGTGCTCTTCCGGCAGCTCCGGCCCGGCGCCCTGCTCGAGGCCTTCTTCCACCTGGAGG	300
H	TCGTGCTCTTCCGGCAGCTCCGGCCCGGCGCCCTGCTCGAGGCCTTCTTCCACCTGGAGG	300
M	TCGTGCTCTTCCGGCAGCTCCGGCCCGGCGCCCTGCTCGAGGCCTTCTTCCACCTGGAGG	300

XM_010963047.2	GCTTCCCGACCGAGCCCAACGTACCCAGCCGCGCCATCCACGTGCACCAAGTTCGGGGACT	360
H	GCTTCCCGACCGAGCCCAACGTACCCAGCCGCGCCATCCACTTGCACCAAGTTCGGGGACT	360
M	GCTTCCCGACCGAGCCCAACGGCACCCAGCCGCGCCATCCACGTGCACCAAGTTCGGGGACT	360

XM_010963047.2	TGACCCAGGGCTGCGACACCACCGGGCCGCACTACAACCCGCTGGGGGTGCCGACCCGA	420
H	TGACCCAGGGCTGCGACACCACCGGGCCGCACTACAACCCGCTGGGGGTGCCGACCCGA	420
M	TGACCCAGGGCTGCGACACCACCGGGCCGCACTACAACCCGCTGGGGGTGCCGACCCGA	420

XM_010963047.2	AGCACCCGGGCGACTTCGGCAACTTCGCCGTGCGCGAC	458
H	AGCACCCGGGCGACTTCGGCAACTTCGCCGTGCGCGAC	458
M	AGCACCCGGGCGACTTCGGCAACTTCGCCGTGCGCGAC	458

Figure S9. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb| XM_010963047.2| and *SOD3* marker (458-bp) sequences.

XM_010984536.2	TCGAGGCCAATACTACCGTGGGCGCATCCGCTTCCACGACTATCTGGGAGACTCATGGG	60
H	TCGAGGCCAATACTACCGTGGGCGCATCCGCTTCCACGACTATCTGGGAGACTCATGGG	60
M	TCGAGGCCAATACTACCGTGGGCGCATCCGCTTCCACGACTATCTGGGAGACTCATGGG	60

XM_010984536.2	GCATTCTCTTCTCCCAACCCTCGGGACTTTACCCAGTGTGTACCACGGAGCTTGGCAGAG	120
H	GCATTCTCTTCTCCCAACCCTCGGGACTTTACCCAGTGTGTACCACGGAGCTTGGCAGAG	120
M	GCATTCTCTTCTCCCAACCCTCGGGACTTTACCCAGTGTGTACCACGGAGCTTGGCAGAG	120

XM_010984536.2	CAGCAAAGCTGGCACCAGAAATTTGCCAAGAGGAACGTGAAGATGATTGCCCTTTCAATAG	180
H	CAGCAAAGCTGGCACCAGAAATTTGCCAAGAGGAACGTGAAGATGATTGCCCTTTCAATAG	180
M	CAGCAAAGCTGGCACCAGAAATTTGCCAAGAGGAACGTGAAGATGATTGCCCTTTCAATAG	180

XM_010984536.2	ACAGTGTGGAAGACCATCTTGCTTGGAGCAAGGATATCAATGCTTACAATGGTAACGAGC	240
H	ACAGTGTGGAAGACCATCTTGCTTGGAGCAAGGATATCAATGCTTACAATGGTAACGAGC	240
M	ACAGTGTGGAAGACCATCTTGCTTGGAGCAAGGATATCAATGCTTACAATGGTAATGAGC	240

XM_010984536.2	CCACGGAAAAGTTACCTTTTCCCATCATTGATGACAAGAATCGGGACCTTGCCATCCAGT	300
H	CCACGGAAAAGTTACCTTTTCCCATCATTGATGACAAGAATCGGGACCTTGCCATCCAGT	300
M	CCACGGAAAAGTTACCTTTTCCCATCATTGATGACAAGAATCGGGACCTTGCCATCCAGT	300

XM_010984536.2	TGGGCATGCTGGACCCAGCAGAGAAGGACGAAAAGGGCATGCCTGTGACAGCTCGTGTGG	360
H	TGGGCATGCTGGACCCAGCAGAGAAGGACGAAAAGGGCATGCCTGTGACAGCTCGTGTGG	360
M	TGGGCATGCTGGACCCAGCAGAGAAGGACGAAAAGGGCATGCCTGTGACAGCTCGTGTGG	360

XM_010984536.2	TATTTATTTTGGTCCCTGATAAGAACTGAACTGTCCATCCTTTACCCAGCTACCACTG	420
H	TATTTATTTTGGTCCCTGATAAGAACTGAACTGTCCATCCTTTACCCAGCTACCACTG	420
M	TATTTATTTTGGTCCCTGATAAGAACTGAACTGTCCATCCTTTACCCAGCTACCACTG	420

XM_010984536.2	GCAGGAACCTTTGATGAGATTCTCAGAGTTATTATCTCTCTCCAGCTGACAG	471
H	GCAGGAACCTTTGATGAGATTCTCAGAGTTATTATCTCTCTCCAGCTGACAG	471
M	GCAGGAACCTTTGATGAGATTCTCAGAGTTATTATCTCTCTCCAGCTGACAG	471

Figure S10. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_010984536.2| and *PRDX6* marker (471-bp) sequences.

XM_045509732.1	CTGCATCTGTTGTTGTCATGTAGGAATAAGTCAAGAATTTTTCTCTTGTGTTAAATTTTGTA	60
H	CTGCATCTGTTGTTGTCATGTAGGAATAAGTCAAGAATTTTTCTCTTGTGTTAAATTTTGTA	60
M	CTGCATCTGTTGTTGTCATGTAGGAATAAGTCAAGAATTTTTCTCTTGTGTTAAATTTTGTA	60

XM_045509732.1	AGAATTAGAAATGCTTGTGTTTTATCTACCCATCTACTTATCTACTCATCTACATGTCTA	120
H	AGAATTAGAAATGCTTGTGTTTTATCTACCCATCTACTTATCTACTCATCTACATGTCTA	120
M	AGAATTAGAAATGCTTGTGTTTTATCTACCCATCTACTTATCTACTCATCTACATGTCTA	120

XM_045509732.1	TCTTTAGGGAGTGGAGCAACAGCTGTGGTCCAAGCAGCATATTGTATCCCTAAAAAGGAG	180
H	TCTTTAGGGAGTGGAGCAACAGCTGTGGTCCAAGCAGCATATTGTATCCCTAAAAAGGAG	180
M	TCTTTAGGGAGTGGAGCAACAGCTGTGGTCCAAGCAGCATATTGTATCCCTAAAAAGGAG	180

XM_045509732.1	AAAGTGGCAATCAAACGGATAAACCTCGAGAAATGTCAAAGTAGCATGGATGAACTCCTG	240
H	AAAGTGGCAATCAAACGGATAAACCTCGAGAAATGTCAAAGTAGCATGGATGAACTCCTG	240
M	AAAGTGGCGATCAAACGGATAAACCTCGAGAAATGTCAAAGTAGCATGGATGAACTCCTG	240

XM_045509732.1	AAAGAAATTCAAGCCATGAGTCAGTGCCATCATCCCAATATTGTGTCTTACTACACATCT	300
H	AAAGAAATTCAAGCCATGAGTCAGTGCCATCATCCCAATATTGTGTCTTACTACACATCT	300
M	AAAGAAATTCAAGCCATGAGTCAGTGCCATCATCCCAATATTGTGTCTTACTACACATCT	300

XM_045509732.1	TTTGTGGTAAAAGATGAGCTGTGGCTAGTCATGAAGCTGCTAAGTGGAGGTTCTGTTCTG	360
H	TTTGTGGTAAAAGATGAGCTGTGGCTAGTCATGAAGCTGCTAAGTGGAGGTTCTGTTCTG	360
M	TTTGTGGTAAAAGATGAGCTGTGGCTAGTCATGAAGCTGCTAAGTGGAGGTTCTGTTCTG	360

XM_045509732.1	GATATTATTAAGCACATTGTGGCAAAGGGGGAACATAAAAGTGGAGTCCTAGATGAAGCT	420
H	GATATTATTAAGCACATTGTGGCAAAGGGGGAACATAAAAGTGGAGTCCTAGATGAAGCT	420
M	GATATTATTAAGCACATTGTGGCAAAGGGGGAACATAAAAGTGGAGTCCTAGATGAAGCT	420

Figure S11. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_045509732.1| and *OXSRI* marker (420-bp) sequences.

XM_031442846.1	CGCCCGGTGCTTCGGGGTGCGGACCTCGCCGTCCGGGGAGAAGGTCACGCATACCGGCCA	60
H	CGCCCGGTGCTTCGGGGTGCGGACCTCGCCGTCCGGGGAGAAGGTCACGCATACCGGCCA	60
M	CGCCCGGTGCTTCGGGGTGCGGACCTCGCCGTCCGGGGAGAAGGTCACGCATACCGGCCA	60

XM_031442846.1	GGTTTATGAGGATGAAGACTACAGAAAAGTTCGATTGTAGGTCGCCAGAAAGAGGTGAA	120
H	GGTTTATGAGGATGAAGACTACAGAAAAGTTCGATTGTAGGTCGCCAGAAAGAGGTAAA	120
M	GGTTTATGAGGATGAAGACTACAGAAAAGTTCGATTGTAGGTCGCCAGAAAGAGGTGAA	120
	***** **	
XM_031442846.1	TGAGAACTTTGCCATCGATCTGATAGCAGAGCAGCCTGTGAGCGAAGTCGGGAGTCGAGT	180
H	TGAGAACTTTGCCATCGATCTGATAGCAGAGCAGCCTGTGAGCGAAGTCGGGAGTCGAGT	180
M	TGAGAACTTTGCCATCGATCTGATAGCAGAGCAGCCTGTGAGCGAAGTCGGGAGTCGAGT	180

XM_031442846.1	CATATCGTGTGACGGCGGGCGGGGGCGCCCTGGGCCACCCGCGAGTCTACATAAACCTGGA	240
H	CATATCGTGTGACGGCGGGCGGGGGCGCCCTGGGCCACCCGCGAGTCTACATAAACCTGGA	240
M	CATATCGTGTGACGGCGGGCGGGGGCGCCCTGGGCCACCCGCGAGTCTACATAAACCTGGA	240

XM_031442846.1	CAAAGAAACAAAGACAGGGACGTGCGGCTACTGTGGCCTGCAGTTCAGACAGCACCACCA	300
H	CAAAGAAACAAAGACAGGGACGTGCGGCTACTGTGGCCTGCAGTTCAGACAGCACCACCA	300
M	CAAAGAAACAAAGACAGGGACGTGCGGCTACTGTGGCCTGCAGTTCAGACAGCACCACCA	300

XM_031442846.1	CTA	303
H	CTA	303
M	CTA	303

Figure S12. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_031442846.1| and *NDUFS6* marker (303-bp) sequences.

XM_031466025.1	TCCTGAATCAGAGCCGACCTGCCGCTGAAACTTTTCATCCATACTTCTCTAAGGCCGCAAG	60
H	TCCTGAATCAGAGCCGACCTGCCGCTGAAACTTTTCATCCATACTTCTCTAAGGCCGCAAG	60
M	TCCTGAATCAGAGCCGACCTGCCGCTGAAACTTTTCATCCATACTTCTCTAAGGCCGCAAG	60

XM_031466025.1	AAGAGAAATATCCTGTGGGACCGTGGCTGCTGGCCCTCTTTGTTTTGTTGCTGTGGCT	120
H	AAGAGAAATATCCTGTGGGACCGTGGCTGCTGGCCCTCTTTGTTTTGTTGCTGTGGCT	120
M	AAGAGAAATATCCTGTGGGACCGTGGCTGCTGGCCCTCTTTGTTTTGTTGCTGTGGCT	120

XM_031466025.1	CAGGTCGACCGCATAAAACACTGGCCTTTCTGGAGAAACCCCTTCTGTTTCACCACGAAGG	180
H	CAGGTCGACCGCATAAAACACTGGCCTTTCTGGAGAAACCCCTTCTGTTTCACCACGAAGG	180
M	CAGGTCGACCGCATAAAACACTGGCCTTTCTGGAGAAACCCCTTCTGTTTCACCACGAAGG	180

XM_031466025.1	AAAGACTGAGGACATGCCTCTGCTCTGGAACCTCCTGCCCTCAGGATCTGAGATGGACAATC	240
H	AAAGACTGAGGACATGCCTCTGCTCTGGAACCTCCTGCCCTCAGGATCTGAGATGGACAATC	240
M	AAAGACTGAGGACATGCCTCTGCTCTGGAACCTCCTGCCCTCAGGATCTGAGATGGACAATC	240

XM_031466025.1	TGGAAGATGTCTCATCAGCCGTTGGCTCCCTCAAGCTATCTTCCAGATCATTGAGGC	300
H	TGGAAGATGTCTCATCAGCCGTTGGCTCCCTCAAGCTATCTTCCAGATCATTGAGGC	300
M	TGGAAGATGTCTCATCAGCCATTTGGCTCCCTCAAGCTATCTTCCAGATCATTGAGGC	300

XM_031466025.1	ATAAGGATGGGCATGTGAGCAGGTTTGACACGCCCCCTCCCGCTGGAGGGTGGAGGACC	360
H	ATAAGGATGGGCATGTGAGCAGGTTTGACACGCCCCCTCCCGCTGGAGGGTGGAGGACC	360
M	ATAAGGATGGGCATGTGAGCAGGTTTGACACGCCCCCTCCCGCTGGAGGGTGGAGGACC	360

XM_031466025.1	ACTTCAGCTCTTA	373
H	ACTTCAGCTCTTA	373
M	ACTTCAGCTCTTA	373

Figure S13. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_031466025.1| and *SERP2* marker (373-bp) sequences.

XM_010994738.2	AGCCCTGAGTGCTGGCAACATCGACGACGCGTTACAGTGCTACTCAGAAGCCATTAAAGTT	60
H	AGCCCTGAGTGCTGGCAACATCGACGACGCGTTACAGTGCTACTCAGAAGCCATTAAAGTT	60
M	AGCCCTGAGTGCTGGCAACATCGACGACGCGTTACAGTGCTACTCAGAAGCCATTAAAGTT	60

XM_010994738.2	AGACCCCTCAGAACCATGTGCTCTACAGTAATCGCTCAGCTGCCTATGCCAAGAAAGGAGA	120
H	AGACCCCTCAGAACCATGTGCTCTACAGTAATCGCTCAGCTGCCTATGCCAAGAAAGGAGA	120
M	AGACCCCTCAGAACCATGTGCTCTACAGTAATCGCTCAGCTGCCTATGCCAAGAAAGGAGA	120

XM_010994738.2	CTACCAGAAGGCCTACGAGGATGCCTGTAAAACCGTTGACCTGAAGCCTGACTGGGGCAA	180
H	CTACCAGAAGGCCTACGAGGATGCCTGTAAAACCGTTGACCTGAAGCCTGACTGGGGCAA	180
M	CTACCAGAAGGCCTACGAGGATGCCTGTAAAACCGTTGACCTGAAGCCTGACTGGGGCAA	180

XM_010994738.2	GGGCTATTTCGCGAAAAGCAGCAGCTCTTGAGTTCTTAAACCGATTGAAGAAGCCAAGAG	240
H	GGGCTATTTCGCGAAAAGCAGCAGCTCTTGAGTTCTTAAACCGATTGAAGAAGCCAAGAG	240
M	GGGCTATTTCGCGAAAAGCAGCAGCTCTTGAGTTCTTAAACCGATTGAAGAAGCCAAGAG	240

XM_010994738.2	AACCTATGAGGAGGGTTTTAAACATGAAGCAAACAACCCCTCAGCTCAAAGAGGGTTTACA	300
H	AACCTATGAGGAGGGTTTTAAACATGAAGCAAACAACCCCTCAGCTCAAAGAGGGTTTACA	300
M	AACCTATGAGGAGGGTTTTAAACATGAAGCAAACAACCCCTCAGCTCAAAGAGGGTTTACA	300

XM_010994738.2	GAATATGGAGACCCGGTTGGCAGAGAGGAAATTCATGAACCCTTTCAACATGCCTAATCT	360
H	GAATATGGAGACCCGGTTGGCAGAGAGGAAATTCATGAACCCTTTCAACATGCCTAATCT	360
M	GAATATGGAGACCCGGTTGGCAGAGAGGAAATTCATGAACCCTTTCAACATGCCTAATCT	360

XM_010994738.2	GTATCAGAAGTTGGAGAGTGATCCCAGGACAAAGACTCTGCTCGCTGACCCTACCTACCG	420
H	GTATCAGAAGTTGGAGAGTGATCCCAGGACAAAGACTCTGCTCGCTGACCCTACCTACCG	420
M	GTATCAGAAGTTGGAGAGTGATCCCAGGACAAAGACTCTGCTCGCTGACCCTACCTACCG	420

XM_010994738.2	GGAGCTGATAGAGCAACTGCGA	442
H	GGAGCTGATAGAGCAACTGCGA	442
M	GGAGCTGATAGAGCAACTGCGA	442

Figure S14. Analysis of nitrogenous bases matching for DNA in healthy and mastitis affected camels using GenBank gb|XM_010994738.2| and *ST1P1* marker (442-bp) sequences.

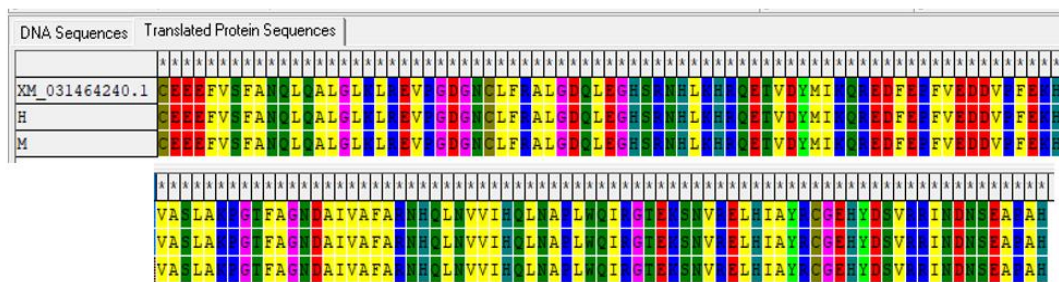


Figure S15. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_031464240.1| and *OTUD3* marker (452-bp).

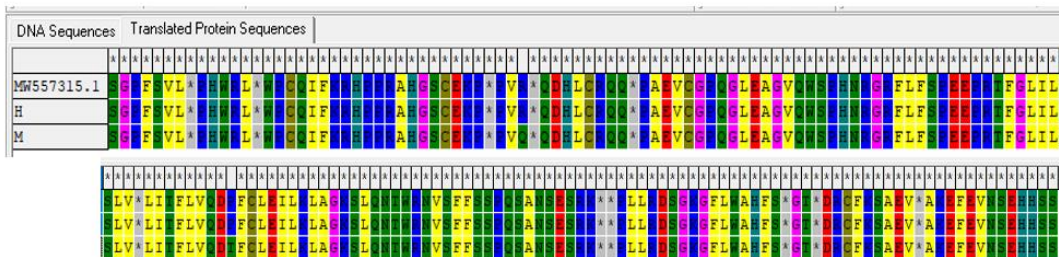


Figure S16. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|MW557315.1| and *TLR2* marker (540-bp).

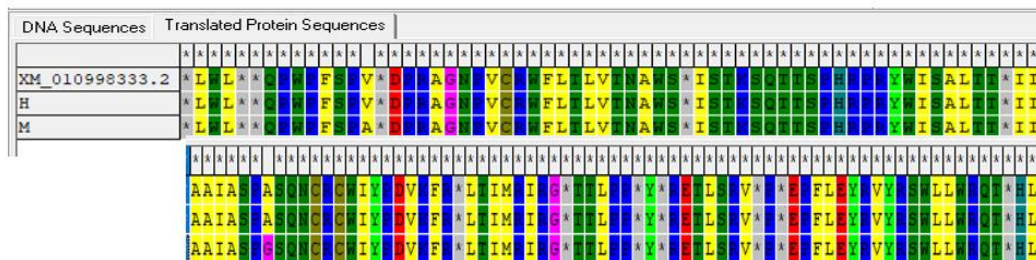


Figure S17. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_010998333.2| and *TLR4* marker (405-bp).

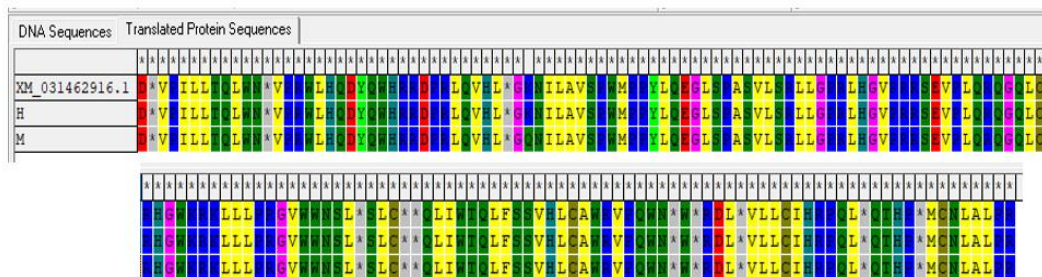


Figure S18. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_031462916.1| and *STAB2* marker (498-bp).

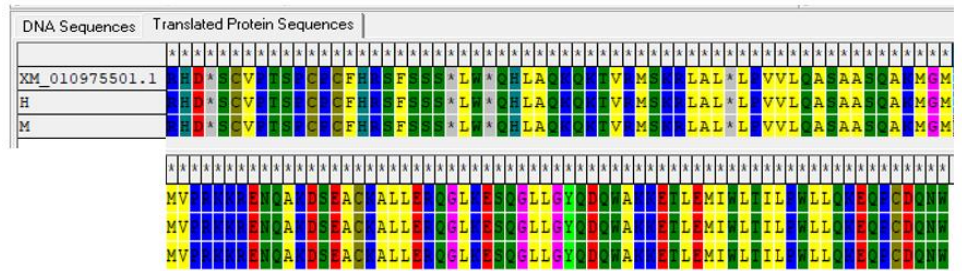


Figure S19. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_010975501.1| and *MBL2* marker (389-bp).

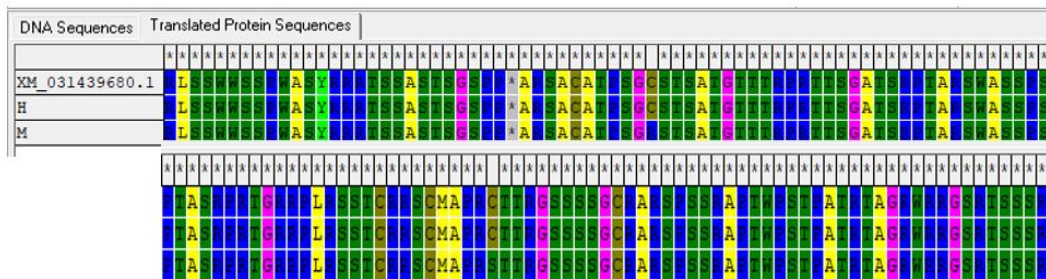


Figure S20. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_031439680.1| and *TRAPPC9* marker (423-bp).

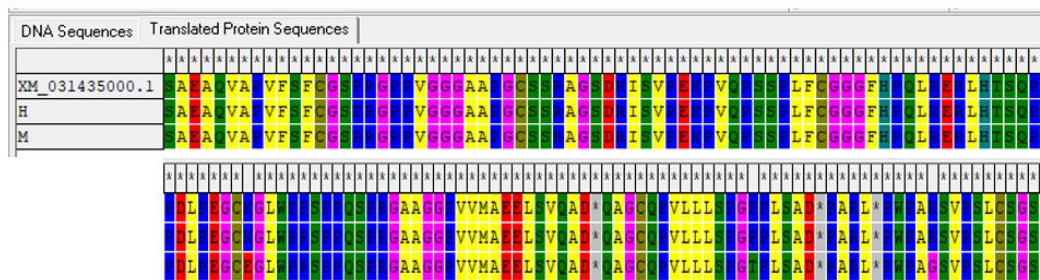


Figure S21. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_031435000.1| and *C4A* marker (444-bp).

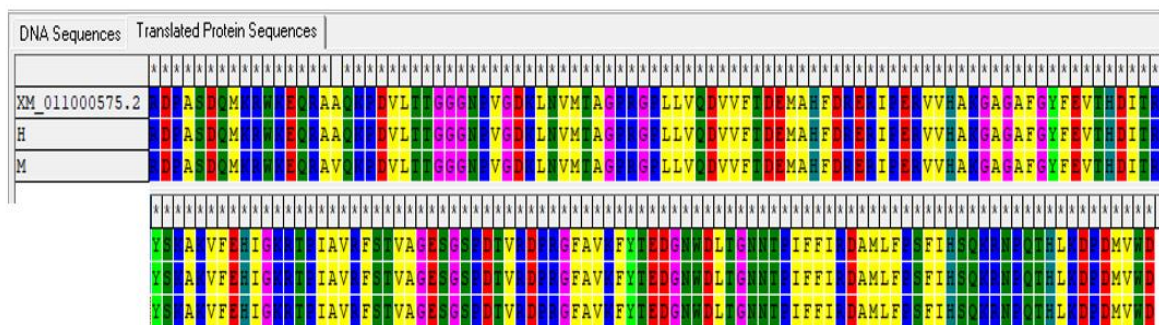


Figure S22. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_011000575.2| and *CAT* marker (540-bp).

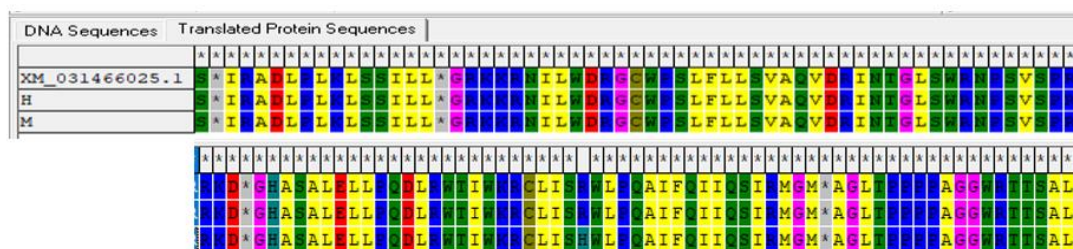


Figure S27. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_031466025.1| and *SERP2* marker (373-bp).

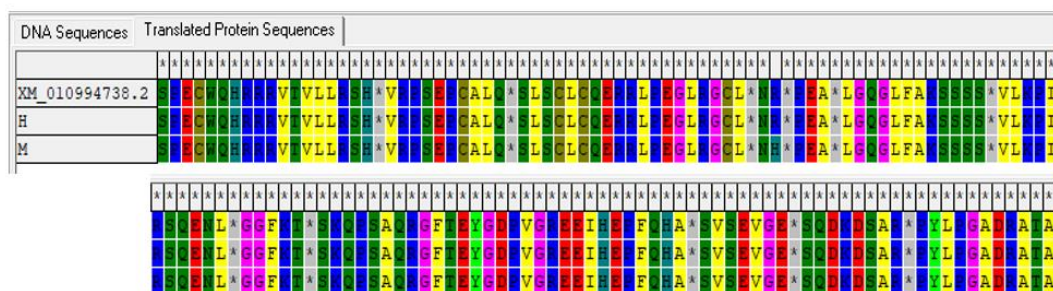


Figure S28. Analysis of amino acid matching in healthy and mastitis affected camels using GenBank gb|XM_010994738.2| and *ST1P1* marker (442-bp).