

# Supplementary:

XM_044936650.2	CCGGCTTGGACAGCCTCTCTTGTACCTTCCGCCGGCCGGCCAGGCAGGGGCGGGACCTGA	60
H	CCGGCTTGGACAGCCTCTCTTGTACCTTCCGCCGGCCGGCCAGGCAGGGGCGGGACCTGA	60
RD	CCGGCTTGGACAGCCTCTCTTGTACCTTCCGCCGGCCGGCCAGGCAGGGGCGGGACCTGA	60
*****	*****	*****
XM_044936650.2	GCGTTTTACTTCCGGATCCACAGCTTAGACACCGGAAGCCGGATGTGAGAAGTTGGCAG	120
H	GCGTTTTACTTCCGGATCCACAGCTTAGACACCGGAAGCCGGATGTGAGAAGTTGGCAG	120
RD	GCGTTTTACTTCCGGATCCACAGCTTAGACACCGGAAGCCGGATGTGAGAAGTTGGCAG	120
*****	*****	*****
XM_044936650.2	CGGGAGAAGGGAAGGGCGGCAGCGGGAGAAGGGAAGGGCTACAGCGGAACCTCGGACTTTC	180
H	CGGGAGAAGGGAAGGGCGGCAGCGGGAGAAGGGAAGGGCTACAGCGGAACCTCGGACTTTC	180
RD	CGGGAGAAGGGAAGGGCGGCAGCGGGAGAAGGGAAGGGCTACAGCGGAACCTCGGACTTTC	180
*****	*****	*****
XM_044936650.2	TCGGAGCGCCGGGGGTCCGAGGAACGCTCGGGGCCCGCGTTCCCGCCCTTCTCACGTGC	240
H	TCGGAGCGCCGGGGGTCCGAGGAACGCTCGGGGCCCGCGTTCCCGCCCTTCTCACGTGC	240
RD	TCGGAGCGCCGGGGGTCCGAGGAACGCTCGGGGCCCGCGTTCCCGCCCTTCTCACGTGC	240
*****	*****	*****
XM_044936650.2	GACCGACTCAGCTGACAGGCCCTGACGTGTTGGATGAGCAGGCCCCCTGGAAGAGTCCA	300
H	GACCGACTCAGCTGACAGGCCCTGACGTGTTGGATGAGCAGGCCCCCTGGAAGAGTCCA	300
RD	GACCGACTCAGCTGACAGGCCCTGACGTGTTGGATGAGCAGGCCCCCTGGAAGAGTCCA	300
*****	*****	*****
XM_044936650.2	CTGTGTGAGATGGTGACAGCCGAGTGGCGGTCCGGCAGGGGACCAGGACATGCTGGGTGAA	360
H	CTGTGTGAGATGGTGACAGCCGAGTGGCGGTCCGGCAGGGGACCAGGACATGCTGGGTGAA	360
RD	CTGTGTGAGATGGTGACAGCCGAGTGGCGGTCCGGCAGGGGACCAGGACATGCTGGGTGAA	360
*****	*****	*****
XM_044936650.2	GAGTCTTCTCTGGGGAAGCCAGCCATGCTCCATGTGCCTTCAGAGCAGGGCA	412
H	GAGTCTTCTCTGGGGAAGCCAGCCATGCTCCATGTGCCTTCAGAGCAGGGCA	412
RD	GAGTCTTCTCTGGGGAAGCCAGCCATGCTCCATGTGCCTTCAGAGCAGGGCA	412
*****	*****	*****

**Figure S1.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|XM\_044936650.2| and *IKBKG* marker (412-bp) sequences.

XM_025282898.3	CTCATTTCCTCTGCAGAGTCTTCAGACAGCTGGTGCCGAAGTTTCAGGAACATCCTCCTC	60
H	CTCATTTCCTCTGCAGAGTCTTCAGACAGCTGGTGCCGAAGTTTCAGGAACATCCTCCTC	60
RD	CTCATTTCCTCTGCAGAGTCTTCAGACAGCTGGTGCCGAAGTTTCAGGAACATCCTCCTC	60
*****	*****	*****
XM_025282898.3	TCTTCAATCATGGCTTGTGGTCTGGTCCGACCAACCTGAATCTCAAACCTGGGGAGTGC	120
H	TCTTCAATCATGGCTTGTGGTCTGGTCCGACCAACCTGAATCTCAAACCTGGGGAGTGC	120
RD	TCTTCAATCATGGCTTGTGGTCTGGTCCGACCAACCTGAATCTCAAACCTGGGGAGTGC	120
*****	*****	*****
XM_025282898.3	CTCAGAGTGCGGGGCGAGGTGGCCGACAGCCCAAGAGCTTCTTGCTGAACCTGGGCAAA	180
H	CTCAGAGTGCGGGGCGAGGTGGCCGACAGCCCAAGAGCTTCTTGCTGAACCTGGGCAAA	180
RD	CTCAGAGTGCGGGGCGAGGTGGCCGACAGCCCAAGAGCTTCTTGCTGAACCTGGGCAAA	180
*****	*****	*****
XM_025282898.3	GATGACAACAATCTGTGCCTCCACTTCAACCCTCGTTTCAACGCGCATGGGGACATCAAC	240
H	GATGACAACAATCTGTGCCTCCACTTCAACCCTCGTTTCAACGCGCATGGGGACATCAAC	240
RD	GATGACAACAATCTGTGCCTCCACTTCAACCCTCGTTTCAACGCGCATGGGGACATCAAC	240
*****	*****	*****
XM_025282898.3	ACCATTGTGTGTAAACAGCAAGGACGCTGGGGCCTGGGGGACCGAGCAGAGGGAATCTGCC	300
H	ACCATTGTGTGTAAACAGCAAGGACGCTGGGGCCTGGGGGACCGAGCAGAGGGAATCTGCC	300
RD	ACCATTGTGTGTAAACAGCAAGGACGCTGGGGCCTGGGGGACCGAGCAGAGGGAATCTGCC	300
*****	*****	*****
XM_025282898.3	TTCCCCCTCCAGCCTGGAAGTGTCTGGAGGTATGCATCTCCTTCGACCAGACAGACCTA	360
H	TTCCCCCTCCAGCCTGGAAGTGTCTGGAGGTATGCATCTCCTTCGACCAGACAGACCTA	360
RD	TTCCCCCTCCAGCCTGGAAGTGTCTGGAGGTATGCATCTCCTTCGACCAGACAGACCTA	360
*****	*****	*****
XM_025282898.3	ACCATCAAGCTGCCTGATGGATAACGAATTCAGTT	395
H	ACCATCAAGCTGCCTGATGGATAACGAATTCAGTT	395
RD	ACCATCAAGCTGCCTGATGGATAACGAATTCAGTT	395
*****	*****	*****

**Figure S2.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|XM\_025282898.3| and *LGALS* marker (395-bp) sequences.

NM_001290898.1	CCATGGCAACCGTACCTGAACCCATCAATGAAATGATGGCCTACTACAGTGACGAGAATG	60
H	CCATGGCAACCGTACCTGAACCCATCAATGAAATGATGGCCTACTACAGTGATGAGAATG	60
RD	CCATGGCAACCGTACCTGAACCCATCAATGAAATGATGGCCTACTACAGTGACGAGAATG	60
	*****	
NM_001290898.1	AGCTGTTATTTGAGGCTGATGGCCCCAAACAGATGAAGAGCTGCATCCACACCTGGACC	120
H	AGCTGTTATTTGAGGCTGATGGCCCCAAACAGATGAAGAGCTGCATCCACACCTGGACC	120
RD	AGCTGTTATTTGAGGCTGATGGCCCCAAACAGATGAAGAGCTGCATCCACACCTGGACC	120
	*****	
NM_001290898.1	TCGGTTCCATGGGAGATGGAACATCCAGCTGCAGATTCTCACCAGCTCTACAACAAAA	180
H	TCGGTTCCATGGGAGATGGAACATCCAGCTGCAGATTCTCACCAGCTCTACAACAAAA	180
RD	TCGGTTCCATGGGAGATGGAACATCCAGCTGCAGATTCTCACCAGCTCTACAACAAAA	180
	**** *****	
NM_001290898.1	GCTTCAGGCAGGTGGTGTGGTTCATTGTGGCCATGGAGAAGCTGAGGAACAGTGCCTACG	240
H	GCTTCAGGCAGGTGGTGTGGTTCATTGTGGCCATGGAGAAGCTGAGGAACAGTGCCTACG	240
RD	GCTTCAGGCAGGTGGTGTGGTTCATTGTGGCCATGGAGAAGCTGAGGAACAGTGCCTACG	240
	*****	
NM_001290898.1	CACATGTCTTCCATGATGATGACCTGAGGAGCATCCTTTTCATTTCATCTTTGAAGAAGAGC	300
H	CACATGTCTTCCATGATGATGACCTGAGGAGCATCCTTTTCATTTCATCTTTGAAGAAGAGC	300
RD	CACATGTCTTCCATGATGATGACCTGAGGAGCATCCTTTTCATTTCATCTTTGAAGAAGAGC	300
	*****	
NM_001290898.1	CTGTTCATCTTCGAAACGTCCTCCGACGAGTTTCTGTGTGACGCACCCGTGCAGTCAGT	358
H	CTGTTCATCTTCGAAACGTCCTCCGACGAGTTTCTGTGTGACGCACCCGTGCAGTCAGT	358
RD	CTGTTCATCTTCGAAACGTCCTCCGACGAGTTTCTGTGTGACGCACCCGTGCAGTCAGT	358
	*****	

**Figure S3.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|NM\_001290898.1| and *IL1B* marker (358-bp) sequences.

HQ889748.1	CTTGAATCCTCTCGCTGCAACATGAAGGTCTCCGCTGCCCTCCTGTGCCTGCTACTCACA	60
H	CTTGAATCCTCTCGCTGCAACATGAAGGTCTCCGCTGCCCTCCTGTGCCTGCTACTCACA	60
RD	CTTGAATCCTCTCGCTGCAACATGAAGGTCTCCGCTGCCCTCCTGTGCCTGCTACTCACA	60
	*****	
HQ889748.1	GTAGCTGCCTTCAGCACCGAGGTGCTCGCTCAGCCAGATGCAATTAACATCCCAAGTCGCC	120
H	GTAGCTGCCTTCAGCACCGAGGTGCTCGCTCAGCCAGATGCAATTAACATCCCAAGTCGCC	120
RD	GTAGCTGCCTTCAGCACCGAGGTGCTCGCTCAGCCAGATGCAATTAACATCCCAAGTCGCC	120
	*****	
HQ889748.1	TGCTGCTATACATTCAACAGTAAGAAGATCTCCATGCAGAGGCTGATGAACTACAGAAGA	180
H	TGCTGCTATACATTCAACAGTAAGAAGATCTCCATGCAGAGGCTGATGAACTACAGAAGA	180
RD	TGCTGCTATACATTCAACAGTAAGAAGATCTCCATGCAGAGGCTGATGAACTACAGAAGA	180
	*****	
HQ889748.1	GTCACCAGCAGCAAGTGTCCCAAAGAGGCTGTGATTTTCAAGACCGTCCTGGGCAAGGAG	240
H	GTCACCAGCAGCAAGTGTCCCAAAGAGGCTGTGATTTTCAAGACCGTCCTGGGCAAGGAG	240
R	GTCACCAGCAGCAAGTGTCTTAAAGAGGCTGTGATTTTCAAGACCGTCCTGGGCAAGGAG	240
	*****	
HQ889748.1	TTATGTGCAGACCCCAAGCAGAAATGGGTCCAGGACTCCATAAACTATCTCAACAAGAAA	300
H	TTATGTGCAGACCCCAAGCAGAAATGGGTCCAGGACTCCATAAACTATCTCAACAAGAAA	300
RD	TTATGTGCAGACCCCAAGCAGAAATGGGTCCAGGACTCCATAAACTATCTCAACAAGAAA	300
	*****	
HQ889748.1	AACCAAATCCGAAGCCTTGAGCACTCACTCCACAACCCAAGATCT	347
H	AACCAAATCCGAAGCCTTGAGCACTCACTCCACAACCCAAGATCT	347
RD	AACCAAATCCGAAGCCTTGAGCACTCACTCCACAACCCAAGATCT	347
	*****	

**Figure S4.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|HQ889748.1| and *CCL2* marker (347-bp) sequences.

XM_006056212.4	CAGCCGGAGCTGCAGAGGATCAGCACGCGGATCGCCAGCCTCTGCCACAGCTACCATG	60
H	CAGCCGGAGCTGCAGAGGATCAGCACGCGGATCGCCAGCCTCTGCCACAGCTACCATG	60
RD	CAGCCGGAGCTGCAGAGGATCAGCACGCGGATCGCCAGCCTCTGCCACAGCTACCATG	60
	*****	
XM_006056212.4	AAGGTCTCCGCCGCTGCCCTCGCTGTCTCTGACGGTGGCCGCCCTCTGCGCTCCTGCG	120
H	AAGGTCTCCGCCGCTGCCCTCGCTGTCTCTGACGGTGGCCGCCCTCTGCGCTCCTGCG	120
RD	AAGGTCTCCGCCGCTGCCCTCGCTGTCTCTGACGGTGGCCGCCCTCTGCGCTCCTGCG	120
	*****	
XM_006056212.4	TCTGCTCCCATATGCCTCAGACACACGCCCTGCTGCTTTGCCTACATCTCCCGCCCG	180
H	TCTGCTCCCATATGCCTCAGACACACGCCCTGCTGCTTTGCCTACATCTCCCGCCCG	180
RD	TCTGCTCCCATATGCCTCAGACACACGCCCTGCTGCTTTGCCTACATCTCCCGCCCG	180
	*****	
XM_006056212.4	CTGCCCCGCACCCACGCTCCAGGAGTATTTCTACACCAGCAGCAAGTGCTCCATGGCAGCA	240
H	CTGCCCCGCACCCACGCTCCAGGAGTATTTCTACACCAGCAGCAAGTGCTCCATGGCAGCA	240
RD	CTGCCCCGCACCCACGCTCCAGGAGTATTTCTACACCAGCAGCAAGTGCTCCATGGCAGCA	240
	*****	
XM_006056212.4	GTTGTCTTTATCACCAGGAAGAACCAGGAGTGTGCGCCAACCCAGAGAAGAAGTGGGTG	300
H	GTTGTCTTTATCACCAGGAAGAACCAGGAGTGTGCGCCAACCCAGAGAAGAAGTGGGTG	300
RD	GTTGTCTTTATCACCAGGAAGAACCAGGAGTGTGCGCCAACCCAGAGAAGAAGTGGGTG	300
	*****	
XM_006056212.4	CGAGAGTACATCAACGCTTTGGAGTTGAGCTAGGGTGGAGGACGCCTTGAACCTGAACCT	360
H	CGAGAGTACATCAACGCTTTGGAGTTGAGCTAGGGTGGAGGACGCCTTGAACCTGAACCT	360
RD	CGAGAGTACATCAACGCTTTGGAGTTGAGCTAGGGTGGAGGACGCCTTGAACCTGAACCT	360
	*****	
XM_006056212.4	GCGCCAACCTCTGCTTCTCGCTCTTGTCTTAAGCAGCTTG	399
H	GCGCCAACCTCTGCTTCTCGCTCTTGTCTTAAGCAGCTTG	399
RD	GCGCCAACCTCTGCTTCTCGCTCTTGTCTTAAGCAGCTTG	399
	*****	

**Figure S5.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|XM\_006056212.4| and *RANTES* marker (399-bp) sequences.

XR_006551148.1	AGAGCACAGACACAGAGCGGGCGCCTGGCAACGACACCTTCTACTCACCGGGCTCCAGCC	60
H	AGAGCACAGACACAGAGCGGGCGCCTGGCAACGACACCTTCTACTCACCGGGCTCCAGCC	60
RD	AGAGCACAGACACAGAGCGGGCGCCTGGCAACGACACCTTCTACTCACCGGGCTCCAGCC	60
	*****	
XR_006551148.1	TGGATGTACCTTCCGCTCCGACTACTCCAACGAGAAGCAGTTACAGGCTTCGAGGCCT	120
H	TGGATGTACCTTCCGCTCCGACTACTCCAACGAGAAGCAGTTACAGGCTTCGAGGCCT	120
RD	TGGATGTACCTTCCGCTCCGACTACTCCAACGAGAAGCAGTTACAGGCTTCGAGGCCT	120
	*****	
XR_006551148.1	TCTACTCTGCAGAGGACATTGACGAGTGCCAGGTGCCCCAGGAGAGGCCCCACCTGCG	180
H	TCTACTCTGCAGAGGACATTGACGAGTGCCAGGTGCCCCAGGAGAGGCCCCACCTGCG	180
RD	TCTACTCTGCAGAGGACATTGACGAGTGCCAGGTGCCCCAGGAGAGGCCCCACCTGCG	180
	*****	
XR_006551148.1	ACCACCACTGCCACAACCACCTGGGCGGCTTCTACTGCTCCTGCCGTGTGGGCTATGTTT	240
H	ACCACCACTGCCACAACCACCTGGGCGGCTTCTACTGCTCCTGCCGTGTGGGCTATGTTT	240
RD	ACCACCACTGCCACAACCACCTGGGCGGCTTCTACTGCTCCTGCCGTGTGGGCTATGTTT	240
	*****	
XR_006551148.1	TCCACAGGAACAGCGCACCTGCTCAGATTCAAACAGACAGGCGGAATACGGCCCGTTT	300
H	TCCACAGGAACAGCGCACCTGCTCAGATTCAAACAGACAGGCGGAATACGGCCCGTTT	300
RD	TCCACAGGAACAGCGCACCTGCTCAGATTCAAACAGACAGGCGGAATACGGCCCGTTT	300
	*****	
XR_006551148.1	TGTGGGAAGACATTGCCAGCAGGATTGAAACCAAGAGCAATACCGTGACCATCACCTTT	360
H	TGTGGGAAGACATTGCCAGCAGGATTGAAACCAAGAGCAATACCGTGACCATCACCTTT	360
RD	TGTGGGAAGACATTGCCAGCAGGATTGAAACCAAGAGCAATACCGTGACCATCACCTTT	360
	*****	
XR_006551148.1	ACCACCGATCAGTCGGGGGACCATGCGCTGGAAGGTCCGATACACAGCACAGACTTG	420
H	ACCACCGATCAGTCGGGGGACCATGCGCTGGAAGGTCCGATACACAGCACAGACTTG	420
RD	ACCACCGATCAGTCGGGGGACCATGCGCTGGAAGGTCCGATACACAGCACAGACTTG	420
	*****	
XR_006551148.1	CCTGCTGTAGACCACAGCCAAACCCATACGTCTCATTTCTTGCTCAGCTGAGCCTTGCC	480
H	CCTGCTGTAGACCACAGCCAAACCCATACGTCTCATTTCTTGCTCAGCTGAGCCTTGCC	480
RD	CCTGCTGTAGACCACAGCCAAACCCATACGTCTCATTTCTTGCTCAGCTGAGCCTTGCC	480
	*****	
XR_006551148.1	CTGATCCATTGGCGCCACCTAATGGCCGCATCT	513
H	CTGATCCATTGGCGCCACCTAATGGCCGCATCT	513
RD	CTGATCCATTGGCGCCACCTAATGGCCGCATCT	513
	*****	

**Figure S6.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|XR\_006551148.1| and *MASP2* marker (513-bp) sequences.

XM_006078587.2	CGCTGGCTGGAGAGTAATGTTACAGAGCGGAGAGAGTGAGGAGGCTGCGTCTGGCTCCCG	60
H	CGCTGGCTGGAGAGTAATGTTACAGAGCGGAGAGAGTGAGGAGGCTGCGTCTGGCTCCCG	60
RD	CGCTGGCTGGAGAGTAATGTTACAGAGCGGAGAGAGTGAGGAGGCTGCGTCTGGCTCCCG	60
	*****	
XM_006078587.2	CTCTCACAGCCATTGCAGTACATTGAGCTCCATAGAGACAGCGCCGGGCAAGTGAGAGC	120
H	CTCTCACAGCCATTGCAGTACATTGAGCTCCATAGAGACAGCGCCGGGCAAGTGAGAGC	120
RD	CTCTCACAGCCATTGCAGTACATTGAGCTCCATAGAGACAGCGCCGGGCAAGTGAGAGC	120
	*****	
XM_006078587.2	CGGACGGGCACTGGGCGACTCTGTGCCTCGCGGAGGAAAAATAATTAACATGGGCAAG	180
H	CGGACGGGCACTGGGCGACTCTGTGCCTCGCGGAGGAAAAATAATTAACATGGGCAAG	180
RD	CGGACGGGCACTGGGCGACTCTGTGCCTCGCGGAGGAAAAATAATTAACATGGGCAAG	180
	*****	
XM_006078587.2	GAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTCTTCGTGCAAACTTGCC	240
H	GAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTCTTCGTGCAAACTTGCC	240
RD	GAGATCCTAAGAAGCCGAGAGGCAAAATGTCATCATATGCATTCTTCGTGCAAACTTGCC	240
	*****	
XM_006078587.2	GGGAGGAGCACAAGAAGAAGCACC CGGATGCTTCCGTCAACTTCTCAGAGTTTTCTAAGA	300
H	GGGAGGAGCACAAGAAGAAGCACC CGGATGCTTCCGTCAACTTCTCAGAGTTTTCTAAGA	300
RD	GGGAGGAGCACAAGAAGAAGCACC CGGATGCTTCCGTCAACTTCTCAGAGTTTTCTAAGA	300
	*****	
XM_006078587.2	AGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAATTTGAAGACATGG	360
H	AGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAATTTGAAGACATGG	360
RD	AGTGCTCAGAGAGGTGGAAGACCATGTCTGCTAAAGAGAAAGGAAAATTTGAAGACATGG	360
	*****	
XM_006078587.2	CAAAGGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATTCCTCCTAAAGGGG	420
H	CAAAGGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATTCCTCCTAAAGGGG	420
RD	CAAAGGCGGACAAGGCCCGTTATGAAAGAGAAATGAAAACCTATATTCCTCCTAAAGGGG	420
	*****	
XM_006078587.2	AAACAAAAAAGAGTTCAAGGATCCCAATGCACCCAGAGGCGCTCCTTCGGCCTTTTTCT	480
H	AAACAAAAAAGAGTTCAAGGATCCCAATGCACCCAGAGGCGCTCCTTCGGCCTTTTTCT	480
RD	AAACAAAAAAGAGTTCAAGGATCCCAATGCACCCAGAGGCGCTCCTTCGGCCTTTTTCT	480
	*****	
XM_006078587.2	TGTTTTGTTCTGAGTATCGTCCAAAAATCAAAGGCGAACATCCTGGCCTGTCTATTGGTG	540
H	TGTTTTGTTCTGAGTATCGTCCAAAAATCAAAGGCGAACATCCTGGCCTGTCTATTGGTG	540
RD	TGTTTTGTTCTGAGTATCGTCCAAAAATCAAAGGCGAACATCCTGGCCTGTCTATTGGTG	540
	*****	

**Figure S7.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|XM\_006078587.2| and *HMBG1* marker (540-bp) sequences.

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EF535848.1      TCTGGACATTGACTTCTCAGTCAACATGAAGGCTCTCATTATTCTGGGGTTTCTCTTCC 60
H              TCTGGACATTGACTTCTCAGTCAACATGAAGACTCTCATTATTCTGGGGTTTCTCTTCC 60
RD            TCTGGACATTGACTTCTCAGTCAACATGAAGGCTCTCATTATTCTGGGGTTTCTCTTCC 60
*****

EF535848.1      TTTCTGTTGCTGTCCAAGGCAAGGTCCTTGAGAGATGTGAGCTTGCCAGAACGCTGAAGA 120
H              TTTCTGTTGCTGTCCAAGGCAAGGTCCTTGAGAGATGTGAGCTTGCCAGAACGCTGAAGA 120
RD            TTTCTGTTGCTGTCCAAGGCAAGGTCCTTGAGAGATGTGAGCTTGCCAGAACGCTGAAGA 120
*****

EF535848.1      AACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCGAACTGGTTGTGTTTGACCAAAT 180
H              AACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCGAACTGGTTGTGTTTGACCAAAT 180
RD            AACTTGGACTGGACGGCTATAAGGGAGTCAGCCTGGCGAACTGGTTGTGTTTGACCAAAT 180
*****

EF535848.1      GGGAAAGCAGTTATAACACAAAAGCTACAACTACAATCCTAGCAGTGAAGCACTGATT 240
H              GGGAAAGCAGTTATAACACAAAAGCTACAACTACAATCCTAGCAGTGAAGCACTGATT 240
RD            GGGAAAGCAGTTATAACACAAAAGCTACAACTACAATCCTGGCAGTGAAGCACTGATT 240
*****

EF535848.1      ATGGGATATTCAGATCAACAGCAAATGGTGGTGTAAATGATGGCAAACCCCTAACGCAG 300
H              ATGGGATATTCAGATCAACAGCAAATGGTGGTGTAAATGATGGCAAACCCCTAACGCAG 300
RD            ATGGGATATTCAAATCAACAGCAAATGGTGGTGTAAATGATGGCAAACCCCTAACGCAG 300
*****

EF535848.1      TTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAG 360
H              TTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAG 360
RD            TTGACGGCTGTCATGTATCCTGCAGCGAATTAATGGAAAATGACATCGCTAAAGCTGTAG 360
*****

EF535848.1      CCTGTGCAAAGCAGATCGTCAGTGAGCAAGGCATTACAGCATGGGTGGCATGGAAAAGTC 420
H              CCTGTGCAAAGCAGATCGTCAGTGAGCAAGGCATTACAGCATGGGTGGCATGGAAAAGTC 420
RD            CCTGTGCAAAGCAGATCGTCAGTGAGCAAGGCATTACAGCATGGGTGGCATGGAAAAGTC 420
*****

EF535848.1      ATTGTCGAGACCATGACGTCAGCAGTTACATTGAG          455
H              ATTGTCGAGACCATGACGTCAGCAGTTACATTGAG          455
RD            ATTGTCGAGACCATGACGTCAGCAGTTACATTGAG          455
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**Figure S8.** Analysis of nitrogenous bases matching for DNA in healthy and reproductive disorders affected buffaloes using GenBank gb|EF535848.1| and S-LZ marker (455-bp) sequences.