

TH	GAAAGAAAGTAAGCCTTTCTGGGGACAGTGAGTGCAGTCTCCCTGCACACCCAGCCTTGG	60
NM_174182.1	GAAAGAAAGTAAGCCTTTCTGGGGACAGTGAGTGCAGTCTCCCTGCACACCCAGCCTTGG	60
MH	GAAAGAAAGTAAGCCTTTCTGGGGACAGTGAGTGCAGTCTCCCTGCACACCCAGCCTTGG	60
TB	GAAAGAAAGTAAGCCTTTCTGGGGACAGTGAGTGCAGTCTCCCTGCACACCCAGCCTTGG	60
MB	GAAAGAAAGTAAGCCTTTCTGGGGACAGTGAGTGCAGTCTCCCTGCACACCCAGCCTTGG	60

TH	GCAAGGATCCAGAGACCTGTGGTGCTGAGCTGAGAGGCTGAAGGGCTACGAAAGGACGGA	120
NM_174182.1	GCAAGGATCCAGAGACCTGTGGTGCTGAGCTGAGAGGCTGAAGGGCTACGAAAGGACGGA	120
MH	GCAAGGATCCAGAGACCTGTGGTGCTGAGCTGAGAGGCTGAAGGGCTACGAAAGGACGGA	120
TB	GCAAGGATCCAGAGACCTGTGGTGCTGAGCTGAGAGGCTGAAGGGCTACGAAAGGACGGA	120
MB	GCAAGGATCCAGAGACCTGTGGTGCTGAGCTGAGAGGCTGAAGGGCTACGAAAGGACGGA	120

TH	GCAAAGCCATGCTATGTCCATGGAATGTCAAATGCTCAGAGGGGCTTATGGAATGTCT	180
NM_174182.1	GCAAAGCCATGCTATGTCCATGGAATGTCAAATGCTCAGAGGGGCTTATGGAATGTCT	180
MH	GCAAAGCCATGCTATGTCCATGGAATGTCAAATGCTCAGAGGGGCTTATGGAATGTCT	180
TB	GCAAAGCCATGCTATGTCCATGGAATGTCAAATGCTCAGAGGGGCTTATGGAATGTCT	180
MB	GCAAAGCCATGCTATGTCCATGGAATGTCAAATGCTCAGAGGGGCTTATGGAATGTCT	180

TH	TTAAACTGTGGGTCTGGATTATGCTCTGTTGTGATTCTTTGCTCATCGTGGCACCATT	240
NM_174182.1	TTAAACTGTGGGTCTGGATTATGCTCTGTTGTGATTCTTTGCTCATCGTGGCACCATT	240
MH	TTAAACTGTGGGTCTGGATTATGCTCTGTTGTGATTCTTTGCTCATCGTGGCACCATT	240
TB	TTAAACTGTGGGTCTGGATTATGCTCTGTTGTGATTCTTTGCTCATCGTGGCACCATT	240
MB	TTAAACTGTGGGTCTGGATTATGCTCTGTTGTGATTCTTTGCTCATCGTGGCACCATT	240

TH	GCTGGACTTACCATTATTCTAAAAGACCCATGCCCTGGGAAAAGGCTAGAGCGTTCTGCA	300
NM_174182.1	GCTGGACTTACCATTATTCTAAAAGACCCATGCCCTGGGAAAAGGCTAGAGCGTTCTGCA	300
MH	GCTGGACTTACCATTATTCTAAAAGACCCATGCCCTGGGAAAAGGCTAGAGCGTTCTGCA	300
TB	GCTGGACTTACCATTATTCTAAAAGACCCATGCCCTGGGAAAAGGCTAGAGCGTTCTGCA	300
MB	GCTGGACTTACCATTATTCTAAAAGACCCATGCCCTGGGAAAAGGCTAGAGCGTTCTGCA	300

TH	GGGAAAATTACACAGATTTAGTTGCCATACAAAACAAGGGAGAGATCGAATACCTGAATA	360
NM_174182.1	GGGAAAATTACACAGATTTAGTTGCCATACAAAACAAGGGAGAGATCGAATACCTGAATA	360
MH	GGGAAAATTACACAGATTTAGTTGCCATACAAAACAAGGGAGAGATCGAATACCTGAATA	360
TB	GGGAAAATTACACAGATTTAGTTGCCATACAAAACAAGGGAGAGATCGAATACCTGAATA	360
MB	GGGAAAATTACACAGATTTAGTTGCCATACAAAACAAGGGAGAGATCGAATACCTGAATA	360

TH	AGACACTTCCCTTCAGCCGTACTTACTACTGGATTGGAATCCGGAAAGTAGAAGGGGTGT	420
NM_174182.1	AGACACTTCCCTTCAGCCGTACTTACTACTGGATTGGAATCCGGAAAGTAGAAGGGGTGT	420
MH	AGACACTTCCCTTCAGCCGTACTTACTACTGGATTGGAATCCGGAAAGTAGAAGGGGTGT	420
TB	AGACACTTCCCTTCAGCCGTACTTACTACTGGATTGGAATCCGGAAAGTAGAAGGGGTGT	420
MB	AGACACTTCCCTTCAGCCGTACTTACTACTGGATTGGAATCCGGAAAGTAGAAGGGGTGT	420

TH	GGACTTGGGTGGGAACCAACAAATCTCTCACTGAAGAAGCAAAGAACTGGGGTGCAGGGG	480
NM_174182.1	GGACTTGGGTGGGAACCAACAAATCTCTCACTGAAGAAGCAAAGAACTGGGGTGCAGGGG	480
MH	GGACTTGGGTGGGAACCAACAAATCTCTCACTGAAGAAGCAAAGAACTGGGGTGCAGGGG	480
TB	GGACTTGGGTGGGAACCAACAAATCTCTCACTGAAGAAGCAAAGAACTGGGGTGCAGGGG	480
MB	GGACTTGGGTGGGAACCAACAAATCTCTCACTGAAGAAGCAAAGAACTGGGGTGCAGGGG	480

TH	AGCCCAACAACAGGAAGAGTAAGGAGGACTGTGTGGAATCTATATCAAGAGGAACAAAG	540
NM_174182.1	AGCCCAACAACAGGAAGAGTAAGGAGGACTGTGTGGAATCTATATCAAGAGGAACAAAG	540
MH	AGCCCAACAACAGGAAGAGTAAGGAGGACTGTGTGGAATCTATATCAAGAGGAACAAAG	540
TB	AGCCCAACAACAGGAAGAGTAAGGAGGACTGTGTGGAATCTATATCAAGAGGAACAAAG	540
MB	AGCCCAACAACAGGAAGAGTAAGGAGGACTGTGTGGAATCTATATCAAGAGGAACAAAG	540

TH	ACTCGGGGAAATGGAATGATGATGCCTGCCACAAAGCAAAGACAGCCCTCTGCTACACAG	600
NM_174182.1	ACTCGGGGAAATGGAATGATGATGCCTGCCACAAAGCAAAGACAGCCCTCTGCTACACAG	600
MH	ACTCGGGGAAATGGAATGATGATGCCTGCCACAAAGCAAAGACAGCCCTCTGCTACACAG	600
TB	ACTCGGGGAAATGGAATGATGATGCCTGCCACAAAGCAAAGACAGCCCTCTGCTACACAG	600
MB	ACTCGGGGAAATGGAATGATGATGCCTGCCACAAAGCAAAGACAGCCCTCTGCTACACAG	600

TH	CTTCTTGTAACCCTGGTCATGCAGCGGCCATGGACAATGTGTGGAAGTCATCAATAATT	660
NM_174182.1	CTTCTTGTAACCCTGGTCATGCAGCGGCCATGGACAATGTGTGGAAGTCATCAATAATT	660
MH	CTTCTTGTAACCCTGGTCATGCAGCGGCCATGGACAATGTGTGGAAGTCATCAATAATT	660
TB	CTTCTTGTAACCCTGGTCATGCAGCGGCCATGGACAATGTGTGGAAGTCATCAATAATT	660
MB	CTTCTTGTAACCCTGGTCATGCAGCGGCCATGGACAATGTGTGGAAGTCATCAATAATT	660

TH	ACACCTGCAACTGTGATTGGGGTACTACGGGCCTGAGTGTGAGTTCGTGACTCAATGTG	720
NM_174182.1	ACACCTGCAACTGTGATTGGGGTACTACGGGCCTGAGTGTGAGTTCGTGACTCAATGTG	720
MH	ACACCTGCAACTGTGATTGGGGTACTACGGGCCTGAGTGTGAGTTCGTGACTCAATGTG	720
TB	ACACCTGCAACTGTGATTGGGGTACTACGGGCCTGAGTGTGAGTTCGTGACTCAATGTG	720
MB	ACACCTGCAACTGTGATTGGGGTACTACGGGCCTGAGTGTGAGTTCGTGACTCAATGTG	720

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TH      TGCCTTTGGAGGCCCCAAAGCTGGGTACCATGGCCTGCACTCACCCCTTTGGGGAACTTCA      780
NM_174182.1 TGCCTTTGGAGGCCCCAAAGCTGGGTACCATGGCCTGCACTCACCCCTTTGGGGAACTTCA      780
MH      TGCCTTTGGAGGCCCCAAAGCTGGGTACCATGGCCTGCACTCACCCCTTTGGGGAACTTCA      780
TB      TGCCTTTGGAGGCCCCAAAGCTGGGTACCATGGCCTGCACTCACCCCTTTGGGGAACTTCA      780
MB      TGCCTTTGGAGGCCCCAAAGCTGGGTACCATGGCCTGCACTCACCCCTTTGGGGAACTTCA      780
*****

TH      GCTTCATGTCGCAGTGTGCCTTCAACTGC      809
NM_174182.1 GCTTCATGTCGCAGTGTGCCTTCAACTGC      809
MH      GCTTCATGTCGCAGTGTGCCTTCAACTGC      809
TB      GCTTCATGTCGCAGTGTGCCTTCAACTGC      809
MB      GCTTCATGTCGCAGTGTGCCTTCAACTGC      809
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Fig. S1. Representative DNA sequence alignment of *SELL* gene (809-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|NM_174182.1|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.

EU570105.1 AAAGCTTGCGAAGTGAGGCTGAAGTCGGTGCTGCCTGCGCTCGCTCGTCGGCCCTCGACC 48
 TH AAAGCTTGCGAAGTGAGGCTGAAGTCGGTGCTGCCTGCGCTCGCTCGTCGGCCCTCGACC 48
 MH AAAGCTTGCGAAGTGAGGCTGAAGTCGGTGCTGCCTGCGCTCGCTCGTCGGCCCTCGACC 48
 TB AAAGCTTGCGAAGTGAGGCTGAAGTCGGTGCTGCCTGCGCTCGCTCGTCGGCCCTCGACC 60
 MB AAAGCTTGCGAAGTGAGGCTGAAGTCGGTGCTGCCTGCGCTCGCTCGTCGGCCCTCGACC 60

 EU570105.1 GCCGGCTCGCCGCCCGCTCTCTCCGACGTGACGGTAACCCGGGGCCATTGCCTTCCCAGG 120
 TH GCCGGCTCGCCGCCCGCTCTCTCCGACGTGACGGTAACCCGGGGCCATTGCCTTCCCAGG 120
 MH GCCGGCTCGCCGCCCGCTCTCTCCGACGTGACGGTAACCCGGGGCCAGTGCCTTCCCAGG 120
 TB GCCGGCTCGCCGCCCGCTCTCTCCGACGTGACGGTAACCCGGGGCCATTGCCTTCCCAGG 120
 MB GCCGGCTCGCCGCCCGCTCTCTCCGACGTGGCGGTAACCCGGGGCCATTGCCTTCCCAGG 120

 EU570105.1 TCAGCCGCTGCGCCGGAAGGCGGAAATGCTCAAAATGTCTTCCAATAGTTACGAGGTTTC 180
 TH TCAGCCGCTGCGCCGGAAGGCGGAAATGCTCAAAATGTCTTCCAATAGTTACGAGGTTTC 180
 MH TCAGCCGCTGCGCCGGAAGGCGGAAATGCTCAAAATGTCTTCCAATAGTTACGAGGTTTC 180
 TB TCAGCCGCTGCGCCGGAAGGCGGAAATGCTCAAAATGTCTTCCAATAGTTACGAGGTTTC 180
 MB TCAGCCGCTGCGCCGGAAGGCGGAAATGCTCAAAATGTCTTCCAATAGTTACGAGGTTTC 180

 EU570105.1 TATCCCAATGTCAAAAAAATCAACGGCATTCCAGAGACAACCTCTAAGGACCTGCAGAC 240
 TH TATCCCAATGTCAAAAAAATCAACGGCATTCCAGAGACAACCTCTAAGGACCTGCAGAC 240
 MH TATCCCAATGTCAAAAAAATCAACGGCATTCCAGAGACAACCTCTAAGGACCTGCAGAC 240
 TB TATCCCAATGTCAAAAAAATCAACGGCATTCCAGAGACAACCTCTAAGGACCTGCAGAC 240
 MB TATCCCAATGTCAAAAAAATCAACGGCATTCCAGAGACAACCTCTAAGGACCTGCAGAC 240

 EU570105.1 ATTAAGTGAAGGAGCTGTGTTAAGTTTTTCATAACATCTGCTATCGAGTAAAAGTGAAGAC 300
 TH ATTAAGTGAAGGAGCTGTGTTAAGTTTTTCATAACATCTGCTATCGAGTAAAAGTGAAGAC 300
 MH ATTAAGTGAAGGAGCTGTGTTAAGTTTTTCATAACATCTGCTATCGAGTAAAAGTGAAGAC 300
 TB ATTAAGTGAAGGAGCTGTGTTAAGTTTTTCATAACATCTGCTATCGAGTAAAAGTGAAGAC 300
 MB ATTAAGTGAAGGAGCTGTGTTAAGTTTTTCATAACATCTGCTATCGAGTAAAAGTGAAGAC 300

 EU570105.1 TGGCTTTCTACTTTGTTCGGAAGAACAAATGAGAAAGAAATACTAGCAAATATCAATGGAGT 360
 TH TGGCTTTCTACTTTGTTCGGAAGAACAAATGAGAAAGAAATACTAGCAAATATCAATGGAGT 360
 MH TGGCTTTCTACTTTGTTCGGAAGAACAAATGAGAAAGAAATACTAGCAAATATCAATGGAGT 360
 TB TGGCTTTCTACTTTGTTCGGAAGAACAAATGAGAAAGAAATACTAGCAAATATCAATGGAGT 360
 MB TGGCTTTCTACTTTGTTCGGAAGAACAAATGAGAAAGAAATACTAGCAAATATCAATGGAGT 360

 EU570105.1 CATGAAACCTGGCCTCAATGCCATTCTGGGACCCACAGGTGGAGGCAAATCTTCGTTGTT 420
 TH CATGAAACCTGGCCTCAATGCCATTCTGGGACCCACAGGTGGAGGCAAATCTTCGTTGTT 420
 MH CATGAAACCTGGCCTCAATGCCATTCTGGGACCCACAGGTGGAGGCAAATCTTCGTTGTT 420
 TB CATGAAACCTGGCCTCAATGCCATTCTGGGACCCACAGGTGGAGGCAAATCTTCGTTGTT 420
 MB CATGAAACCTGGCCTCAATGCCATTCTGGGACCCACAGGTGGAGGCAAATCTTCGTTGTT 420

 EU570105.1 AGATATCTTAGCTGCAAGGAAGGATCCACATGGATTATCTGGAGATGTTTTGATCAATGG 480
 TH AGATATCTTAGCTGCAAGGAAGGATCCACATGGATTATCTGGAGATGTTTTGATCAATGG 480
 MH AGATATCTTAGCTGCAAGGAAGGATCCACATGGATTATCTGGAGATGTTTTGATCAATGG 480
 TB AGATATCTTAGCTGCAAGGAAGGATCCACATGGATTATCTGGAGATGTTTTGATCAATGG 480
 MB AGATATCTTAGCTGCAAGGAAGGATCCACATGGATTATCTGGAGATGTTTTGATCAATGG 480

 EU570105.1 AGCACCTCGACCTGCCAATTTTAAATGTAACCTCAGGTTATGTGGTACAAGATGATGTTGT 540
 TH AGCACCTCGACCTGCCAATTTTAAATGTAACCTCAGGTTATGTGGTACAAGATGATGTTGT 540
 MH AGCACCTCGACCTGCCAATTTTAAATGTAACCTCAGGTTATGTGGTACAAGATGATGTTGT 540
 TB AGCACCTCGACCTGCCAATTTTAAATGTAACCTCAGGTTATGTGGTACAAGATGATGTTGT 540
 MB AGCACCTCGACCTGCCAATTTTAAATGTAACCTCAGGTTATGTGGTACAAGATGATGTTGT 540

 EU570105.1 GATGGGAACCTCTGACAGTGAGAGAAAACCTTACAGTTCTCAGCAGCCCTTCGGCTTCCAAC 600
 TH GATGGGAACCTCTGACAGTGAGAGAAAACCTTACAGTTCTCAGCAGCCCTTCGGCTTCCAAC 600
 MH GATGGGAACCTCTGACAGTGAGAGAAAACCTTACAGTTCTCAGCAGCCCTTCGGCTTCCAAC 600
 TB GATGGGAACCTCTGACAGTGAGAGAAAACCTTACAGTTCTCAGCAGCCCTTCGGCTTCCAAC 600
 MB GATGGGAACCTCTGACAGTGAGAGAAAACCTTACAGTTCTCAGCAGCCCTTCGGCTTCCAAC 600

 EU570105.1 AACTATGACAAGTTACGAAAAAATGAACGGATTAACAAGGTTATTCAAGAGTTAGGTCT 660
 TH AACTATGACAAGTTACGAAAAAATGAACGGATTAACAAGGTTATTCAAGAGTTAGGTCT 660
 MH AACTATGACAAGTTACGAAAAAATGAACGGATTAACAAGGTTATTCAAGAGTTAGGTCT 660

TB	AACTATGACAAGTTACGAAAAAATGAACAGATTAACAAGGTTATTCAAGAGTTAGGTCT	660
MB	AACTATGACAAGTTACGAAAAAATGAACGATTAAACAAGGTTATTCAAGAGTTAGGTCT	660

EU570105.1	GGATAAAGTGGCAGATTCCAAGGTTGGAACCTCAGTTTATCCGTGGTGTGTCTGGAGGAGA	720
TH	GGATAAAGTGGCAGATTCCAAGGTTGGAACCTCAGTTTATCCGTGGTGTGTCTGGAGGAGA	720
MH	GGATAAAGTGGCAGATTCCAAGGTTGGAACCTCAGTTTATCCGTGGTGTGTCTGGAGGAGA	720
TB	GGATAAAGTGGCAGATTCCAAGGTTGGAACCTCAGTTTATCCGTGGTGTGTCTGGAGGAGA	720
MB	GGATAAAGTGGCAGATTCCAAGGTTGGAACCTCAGTTTATCCGTGGTGTGTCTGGAGGAGA	720

EU570105.1	AAGAAAAAGGACTAGTATTGCAATGGAGCTTATTAC	756
TH	AAGAAAAAGGACTAGTATTGCAATGGAGCTTATTAC	756
MH	AAGAAAAAGGACTAGTATTGCAATGGAGCTTATTAC	756
TB	AAGAAAAAGGACTAGTATTGCAATGGAGCTTATTAC	756
MB	AAGAAAAAGGACTAGTATTGCAATGGAGCTTATTAC	756

Fig. S2. Representative DNA sequence alignment of *ABCG2* gene (756-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|EU570105.1|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.

NM_174652.2	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
TH	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
MH	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
TB	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
MB	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60

NM_174652.2	GCCTGCGGTCTCATGTCTCAGGTGACACGGGGCCCCCAAAGCAGGGAGGGACCAGATATGG	120
TH	GCCTGCGGTCTCATGTCTCAGGTGACACGGGGCCCCCAAAGCAGGGAGGGACCAGATATGG	120
MH	GCCTGCGGTCTCATGTCTCAGGTGACACGGGGCCCCCAAAGCAGGGAGGGACCAGATATGG	120
TB	GCCTGCGGTCTCATGTCTCAGGTGACACGGGGCCCCCAAAGCAGGGAGGGACCAGATATGG	120
MB	GCCTGCGGTCTCATGTCTCAGGTGACACGGGGCCCCCAAAGCAGGGAGGGACCAGATATGG	120

NM_174652.2	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCACCTCCCGGAGGGACCTACCT	180
TH	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCACCTCCCGGAGGGACCTACCT	180
MH	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCACCTCCCGGAGGGACCTACCT	180
TB	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCGCCTCCCGGAGGGACCTACCT	180
MB	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCACCTCCCGGAGGGACCTACCT	180

NM_174652.2	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGAGGAAGCTGTG	240
TH	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGAGGAAGCTGTG	240
MH	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGCGGAAGCTGTG	240
TB	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTGCATTACGCCTGAGGAAGCTGTG	240
MB	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGAGGAAGCTGTG	240

NM_174652.2	GGCCTTCACGGGGCCTGGATTCTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
TH	GGCCTTCACGGGGCCTGGATTCTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
MH	GGCCTTCACGGGGCCTGGATTCTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
TB	GGCCTTCACGGGGCCTGGATTCTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
MB	GGCCTTCACGGGGCCTGGATTCTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300

NM_174652.2	GTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACCTGCTCTGGGTGCTGCTGTGGGC	360
TH	GTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACCTGCTCTGGGTGCTGCTGTGGGC	360
MH	GTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACCTGCTCTGGGTGCTGCTGTGGGC	360
TB	GTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACCTGCTCTGGGTGCTGCTGTGGGC	360
MB	GTCGGATCTTCAGGCTGGGGCTGTGGCTGGATTCAAACCTGCTCTGGGTGCTGCTGTGGGC	360

NM_174652.2	CACAGTGTGGGCTTGCTTTGCCAGCGACTGGCTGCCCCGGCTGGGCGTGGTGACAGGCCAA	420
TH	CACAGTGTGGGCTTGCTTTGCCAGCGACTGGCTGCCCCGGCTGGGCGTGGTGACAGGCCAA	420
MH	CACAGTGTGGGCTTGCTTTGCCAGCGACTGGCTGCCCCGGCTGGGCGTGGTGACAGGCCAA	420
TB	CACAGTGTGGGCTTGCTTTGCCAGCGACTGGCTGCCCCGGCTGGGCGTGGTGACAGGCCAA	420
MB	CACAGTGTGGGCTTGCTTTGCCAGCGACTGGCTGCCCCGGCTGGGCGTGGTGACAGGCCAA	420

NM_174652.2	GGACTTGGGCGAGGTCTGCCATCTCTACTA 450	
TH	GGACTTGGGCGAGGTCTGCCATCTCTACTA 450	
MH	GGACTTGGGCGAGGTCTGCCATCTCTACTA 450	
TB	GGACTTGGGCGAGGTCTGCCATCTCTACTA 450	
MB	GGACTTGGGCGAGGTCTGCCATCTCTACTA 450	

Fig. S3. Representative DNA sequence alignment of *SLC11A1* gene (450-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|NM_174652.2|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.

NM_001038198.2	GATTGGACCGTCTCAATTATACAAACATGACTTCATGTGATGTCAGCTGAATGTAAAAGA	60
TH	GATTGGACCGTCTCAATTATACAAACATGACTTCATGTGATGTCAGCTGAATGTAAAAGA	60
MH	GATTGGACCGTCTCAATTATACAAACATGACTTCATGTGATGTCAGCTGAATGTAAAAGA	60
TB	GATTGGACCGTCTCAATTATACAAACATGACTTCATGTGATGTCAGCTGAATGTAAAAGA	60
MB	GATTGGACCGTCTCAATTATACAAACATGACTTCATGTGATGTCAGCTGAATGTAAAAGA	60

NM_001038198.2	CAGTGATCTCACGCGGAGGGGAAGATGTTTGCCATCAAATGTGACAGAGGAGACAGGCT	120
TH	CAGTGATCTCACGCGGAGGGGAAGATGTTTGCCATCAAATGTGACAGAGGAGACAGGCT	120
MH	CAGTGATCTCACGCGGAGGGGAAGATGTTTGCCATCAAATGTGACAGAGGAGACAGGCT	120
TB	CAGTGATCTCACGCGGAGGGGAAGATGTTTGCCATCAAATGTGACAGAGGAGACAGGCT	120
MB	CAGTGATCTCACGCGGAGGGGAAGATGTTTGCCATCAAATGTGACAGAGGAGACAGGCT	120

NM_001038198.2	GCATGGCTCGGACCGCATCTCCTTGCGGTTGGGGGAAAGAGACTTAGAGGAGAGAGGCTG	180
TH	GCATGGCTCGGACCGCATCTCCTTGCGGTTGGGGGAAAGAGACTTAGAGGAGAGAGGCTG	180
MH	GCATGGCTCGGACCGCATCTCCTTGCGGTTGGGGGAAAGAGACTTAGAGGAGAGAGGCTG	180
TB	GCATGGCTCGGACCGCATCTCCTTGCGGTTGGGGGAAAGAGACTTAGAGGAGAGAGGCTG	180
MB	GCATGGCTCGGACCGCATCTCCTTGCGGTTGGGGGAAAGAGACTTAGAGGAGAGAGGCTG	180

NM_001038198.2	CGCCCTGGCCCAGTCCGGTACGACTCGGCTCGGCGGCCATGGCAAGCTCGGCTTCCCTG	240
TH	CGCCCTGGCCCAGTCCGGTACGACTCGGCTCGGCGGCCATGGCAAGCTCGGCTTCCCTG	240
MH	CGCCCTGGCCCAGTCCGGTACGACTCGGCTCGGCGGCCATGGCAAGCTCGGCTTCCCTG	240
TB	CGCCCTGGCCCAGTCCGGTACGACTCGGCTCGGCGGCCATGGCAAGCTCGGCTTCCCTG	240
MB	CGCCCTGGCCCAGTCCGGTACGACTCGGCTCGGCGGCCATGGCAAGCTCGGCTTCCCTG	240

NM_001038198.2	GAGACCATGGTGCCCCCGGCCTGCCCGCGCGCAGGAGCGTCGCCGGCCACTTCCAAGACT	300
TH	GAGACCATGGTGCCCCCGGCCTGCCCGCGCGCAGGAGCGTCGCCGGCCACTTCCAAGACT	300
MH	GAGACCATGGTGCCCCCGGCCTGCCCGCGCGCAGGAGCGTCGCCGGCCACTTCCAAGACT	300
TB	GAGACCATGGTGCCCCCGGCCTGCCCGCGCGCAGGAGCGTCGCCGGCCACTTCCAAGACT	300
MB	GAGACCATGGTGCCCCCGGCCTGCCCGCGCGCAGGAGCGTCGCCGGCCACTTCCAAGACT	300

NM_001038198.2	CTGGCCTTTTCCATCGAGCGCATCATGGCTAAGACGTCGGAGCCCCGCGCGCCCTTTGAG	360
TH	CTGGCCTTTTCCATCGAGCGCATCATGGCTAAGACGTCGGAGCCCCGCGCGCCCTTTGAG	360
MH	CTGGCCTTTTCCATCGAGCGCATCATGGCTAAGACGTCGGAGCCCCGCGCGCCCTTTGAG	360
TB	CTGGCCTTTTCCATCGAGCGCATCATGGCTAAGACGTCGGAGCCCCGCGCGCCCTTTGAG	360
MB	CTGGCCTTTTCCATCGAGCGCATCATGGCTAAGACGTCGGAGCCCCGCGCGCCCTTTGAG	360

NM_001038198.2	CCCCGGCCGGGGGCACCTGGAGGCGGATAGCGGCCAGGGCAAGAAATTGCTCAACCTCTGC	420
TH	CCCCGGCCGGGGGCACCTGGAGGCGGATAGCGGCCAGGGCAAGAAATTGCTCAACCTCTGC	420
MH	CCCCGGCCGGGGGCACCTGGAGGCGGATAGCGGCCAGGGCAAGAAATTGCTCAACCTCTGC	420
TB	CCCCGGCCGGGGGCACCTGGAGGCGGATAGCGGCCAGGGCAAGAAATTGCTCAACCTCTGC	420
MB	CCCCGGCCGGGGGCACCTGGAGGCGGATAGCGGCCAGGGCAAGAAATTGCTCAACCTCTGC	420

NM_001038198.2	TCGCCGCTGCCCTGTATGATCCCCCTCCAGCCCCTAGGCTACGAGATGCCGTCCAAGACG	480
TH	TCGCCGCTGCCCTGTATGATCCCCCTCCAGCCCCTAGGCTACGAGATGCCGTCCAAGACG	480
MH	TCGCCGCTGCCCTGTATGATCCCCCTCCAGCCCCTAGGCTACGAGATGCCGTCCAAGACG	480
TB	TCGCCGCTGCCCTGTATGATCCCCCTCCAGCCCCTAGGCTACGAGATGCCGTCCAAGACG	480
MB	TCGCCGCTGCCCTGTATGATCCCCCTCCAGCCCCTAGGCTACGAGATGCCGTCCAAGACG	480

NM_001038198.2	CTGCTCAGTTACTCTGAGCTCTGGAAAAGCAGCCTCCGGGCGGGCGGCAGCGCGCGGGA	540
TH	CTGCTCAGTTACTCTGAGCTCTGGAAAAGCAGCCTCCGGGCGGGCGGCAGCGCGCGGGA	540
MH	CTGCTCAGTTACTCTGAGCTCTGGAAAAGCAGCCTCCGGGCGGGCGGCAGCGCGCGGGA	540
TB	CTGCTCAGTTACTCTGAGCTCTGGAAAAGCAGCCTCCGGGCGGGCGGCAGCGCGCGGGA	540
MB	CTGCTCAGTTACTCTGAGCTCTGGAAAAGCAGCCTCCGGGCGGGCGGCAGCGCGCGGGA	540

NM_001038198.2	GGAGGAGGTGGAGGCGGCGGTGGGGGGGCCCGGTGTGCGGCGCCAGCGGCTTGTGCAAA	600
TH	GGAGGAGGTGGAGGCGGCGGTGGGGGGGCCCGGTGTGCGGCGCCAGCGGCTTGTGCAAA	600
MH	GGAGGAGGTGGAGGCGGCGGTGGGGGGGCCCGGTGTGCGGCGCCAGCGGCTTGTGCAAA	600
TB	GGAGGAGGTGGAGGCGGCGGTGGGGGGGCCCGGTGTGCGGCGCCAGCGGCTTGTGCAAA	600
MB	GGAGGAGGTGGAGGCGGCGGTGGGGGGGCCCGGTGTGCGGCGCCAGCGGCTTGTGCAAA	600

NM_001038198.2	ACCAACTGTGGCGTGTGCTGCAAGGCCGAGCTGGGCCTGGTACCGTCGGCGCTGCCCGCG	660
TH	ACCAACTGTGGCGTGTGCTGCAAGGCCGAGCTGGGCCTGGTACCGTCGGCGCTGCCCGCG	660
MH	ACCAACTGTGGCGTGTGCTGCAAGGCCGAGCTGGGCCTGGTACCGTCGGCGCTGCCCGCG	660
TB	ACCAACTGTGGCGTGTGCTGCAAGGCCGAGCTGGGCCTGGTACCGTCGGCGCTGCCCGCG	660
MB	ACCAACTGTGGCGTGTGCTGCAAGGCCGAGCTGGGCCTGGTACCGTCGGCGCTGCCCGCG	660

NM_001038198.2	GGCAGGGTCATCAAGCCCGAGGTCATCAACCAGGCTGTGGGGCTTCCGGCCAGCGGTTTCG	720
TH	GGCAGGGTCATCAAGCCCGAGGTCATCAACCAGGCTGTGGGGCTTCCGGCCAGCGGTTTCG	720
MH	GGCAGGGTCATCAAGCCCGAGGTCATCAACCAGGCTGTGGGGCTTCCGGCCAGCGGTTTCG	720
TB	GGCAGGGTCATCAAGCCCGAGGTCATCAACCAGGCTGTGGGGCTTCCGGCCAGCGGTTTCG	720
MB	GGCAGGGTCATCAAGCCCGAGGTCATCAACCAGGCTGTGGGGCTTCCGGCCAGCGGTTTCG	720

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NM_001038198.2 CTCTACTACTTCAACTACCTGGACTCCGCCACTTACCCGTCGTCTGAGCTCCTCGGCGGC 780
TH CTCTACTACTTCAACTACCTGGACTCCGCCACTTACCCGTCGTCTGAGCTCCTCGGCGGC 780
MH CTCTACTACTTCAACTACCTGGACTCCGCCACTTACCCGTCGTCTGAGCTCCTCGGCGGC 780
TB CTCTACTACTTCAACTACCTGGACTCCGCCACTTACCCGTCGTCTGAGCTCCTCGGCGGC 780
MB CTCTACTACTTCAACTACCTGGACTCCGCCACTTACCCGTCGTCTGAGCTCCTCGGCGGC 780
*****
NM_001038198.2 CACCTCTTCCCGTCCGGTCTCCTCAACACACAG 813
TH CACCTCTTCCCGTCCGGTCTCCTCAACACACAG 813
MH CACCTCTTCCCGTCCGGTCTCCTCAACACACAG 813
TB CACCTCTTCCCGTCCGGTCTCCTCAACACACAG 813
MB CACCTCTTCCCGTCCGGTCTCCTCAACACACAG 813
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Fig. S4. Representative DNA sequence alignment of *FEZL* gene (813-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|NM_001038198.2|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.

NM_174615.2	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
TH	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
MH	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
TB	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60
MB	GCTTGCCATGCCCCTGAGGGGCTGCCCGGCACGCCAGCCACTCGCACAGAGAGTGCCCGA	60

NM_174615.2	GCCTGCGGTCCTCATGTCAAGTGACACGGGCCCCCAAAGCAGGGAGGGAGCCAGATATGG	120
TH	GCCTGCGGTCCTCATGTCAAGTGACACGGGCCCCCAAAGCAGGGAGGGAGCCAGATATGG	120
MH	GCCTGCGGTCCTCATGTCAAGTGACACGGGCCCCCAAAGCAGGGAGGGAGCCAGATATGG	120
TB	GCCTGCGGTCCTCATGTCAAGTGACACGGGCCCCCAAAGCAGGGAGGGAGCCAGATATGG	120
MB	GCCTGCGGTCCTCATGTCAAGTGACACGGGCCCCCAAAGCAGGGAGGGAGCCAGATATGG	120

NM_174615.2	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCACCTCCCGGAGGGACCTACCT	180
TH	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCGCCTCCCGGAGGGACCTACCT	180
MH	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCACCTCCCGGAGGGACCTACCT	180
TB	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCGCCTCCCGGAGGGACCTACCT	180
MB	CTCCATCTCCAGCCCACCCAGTCCAGAGCCACAGCAAGCACCTCCCGGAGGGACCTACCT	180

NM_174615.2	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGAGGAAGCTGTG	240
TH	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGAGGAAGCTGTG	240
MH	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGAGGAAGCTGTG	240
TB	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTGCATTACGCCTGCGGAAGCTGTG	240
MB	AAGTGAGAAGATCCCCATTCCGGATACAGAATCGGGTACATTACGCCTGAGGAAGCTGTG	240

NM_174615.2	GGCCTTCACGGGGCCTGGATTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
TH	GGCCTTCACGGGGCCTGGATTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
MH	GGCCTTCACGGGGCCTGGATTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
TB	GGCCTTCACGGGGCCTGGATTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300
MB	GGCCTTCACGGGGCCTGGATTCTCATGAGCATCGCATTCTGGACCCAGGAAACATTGA	300

NM_174615.2	GTCCGATCTTCAGGCTGGGGCTGTGGCTGGATTC	334
TH	GTCCGATCTTCAGGCTGGGGCTGTGGCTGGATTC	334
MH	GTCCGATCTTCAGGCTGGGGCTGTGGCTGGATTC	334
TB	GTCCGATCTTCAGGCTGGGGCTGTGGCTGGATTC	334
MB	GTCCGATCTTCAGGCTGGGGCTGTGGCTGGATTC	334

Fig. S5. Representative DNA sequence alignment of *SOD1* gene (334-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|NM_174615.2|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.


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MK423993.1      CTATCCTGACACTCACCGCCACCGCCTGGGACCCAACCTATCTCCAGATACCTGTGAACTG 60
TH              CTATCCTGACACTCACCGCCACCGCCTGGGACCCAACCTATCTCCAGATACCTGTGAACTG 60
MH              CTATCCTGACACTCACCGCCACCGCCTGGGACCCAACCTATCTCCAGATACCTGTGAACTG 60
TB              CTATCCTGACACTCACCGCCACCGCCTGGGACCCAACCTATCTCCAGATACCTGTGAACTG 60
MB              CTATCCTGACACTCACCGCCACCGCCTGGGACCCAACCTATCTCCAGATACCTGTGAACTG 60
                *****

MK423993.1      TCCCTACCGTGCTCGAGTGGCCAACTACCAGCGTGACGGCCCCATGTGCATGATGGACAA 120
TH              TCCCTACCGTGCTCGAGTGGCCAACTACCAGCGTGACGGCCCCATGTGCATGATGGACAA 120
MB              TCCCTACCGTGCTCGAGTGGCCAACTACCAGCGTGACGGCCCCATGTGCATGATGGACAA 120
TB              TCCCTACCGTGCTCGAGTGGCCAACTACCAGCGTGACGGCCCCATGTGCATGATGGACAA 120
MB              TCCCTACCGTGCTCGAGTGGCCAACTACCAGCGTGACGGCCCCATGTGCATGATGGACAA 120
                *****

MK423993.1      TCAGGGTGGGGCTCCAAATTACTACCCCAATAGCTTTAGTGCTCCCGAGCATCAGCCTTC 180
TH              TCAGGGTGGGGCTCCAAATTACTACCCCAATAGCTTTAGTGCTCCCGAGCATCAGCCTTC 180
MH              TCAGGGTGGGGCTCCAAATTACTACCCCAATAGCTTTAGTGCTCCCGAGCATCAGCCTTC 180
TB              TCAGGGTGGGGCTCCAAATTACTACCCCAATAGCTTTAGTGCTCCCGAGCATCAGCCTTC 180
MB              TCAGGGTGGGGCTCCAAATTACTACCCCAATAGCTTTAGTGCTCCCGAGCATCAGCCTTC 180
                *****

MK423993.1      TGCCCTGGAACACAGGACCCACTTCTCTGGGGATGTACAGCGCTTCAACAGTGCCAACGA 240
TH              TGCCCTGGAACACAGGACCCACTTCTCTGGGGATGTACAGCGCTTCAACAGTGCCAACGA 240
MH              TGCCCTGGAACACAGGACCCACTTCTCTGGGGATGTACAGCGCTTCAACAGTGCCAACGA 240
TB              TGCCCTGGAACACAGGACCCACTTCTCTGGGGATGTACAGCGCTTCAACAGTGCCAACGA 240
MB              TGCCCTGGAACACAGGACCCACTTCTCTGGGGATGTACAGCGCTTCAACAGTGCCAACGA 240
                *****

MK423993.1      TGACAATGTCACTCAGGTGCGGACTTTC                268
TH              TGACAATGTCACTCAGGTGCGGACTTTC                268
MH              TGACAATGTCACTCAGGTGCGGACTTTC                268
TB              TGACAATGTCACTCAGGTGCGGACTTTC                268
MB              TGACAATGTCACTCAGGTGCGGACTTTC                268
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Fig. S6. Representative DNA sequence alignment of *CAT* gene (268-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|MK423993.1|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.

NM_174076.3	GGTCGCCCCGCTTTTAAAGCAGGCGCTTCCGACCCCTTGTTCTTCAAGTCCGCGGCG	60
TH	GGTCGCCCCGCTTTTAAAGCAGGCGCTTCCGACCCCTTGTTCTTCAAGTCCGCGGCG	60
MH	GGTCGCCCCGCTTTTAAAGCAGGCGCTTCCCAACCCCTTGTTCTTCAAGTCCGCGGCG	60
TB	GGTCGCCCCGCTTTTAAAGCAGGCGCTTCCGACCCCTTGTTCTTCAAGTCCGCGGCG	60
MB	GGTCGCCCCGCTTTTAAAGCAGGCGCTTCCGACCCCTTGTTCTTCAAGTCCGCGGCG	60

NM_174076.3	CTCTGCTCTGGATTTCGAAACGGATACCATGTGCGCCGCTCAGCGCTCGGCGGCCGCCCT	120
TH	CTCTGCTCTGGATTTCGAAACGGATACCATGTGCGCCGCTCAGCGCTCGGCGGCCGCCCT	120
MH	CTCTGCTCTGGATTTCGAAACGGATACCATGTGCGCCGCTCAGCGCTCGGCGGCCGCCCT	120
TB	CTCTGCTCTGGATTTCGAAACGGATACCATGTGCGCCGCTCAGCGCTCGGCGGCCGCCCT	120
MB	CTCTGCTCTGGATTTCGAAACGGATACCATGTGCGCCGCTCAGCGCTCGGCGGCCGCCCT	120

NM_174076.3	GGCGGGCGCAGCCCCGCGCACAGTGTACGCCTTCTCCGCGGCCCTCTGGCCGGCGGGGA	180
TH	GGCGGGCGCAGCCCCGCGCACAGTGTACGCCTTCTCCGCGGCCCTCTGGCCGGCGGGGA	180
MH	GGCGGGCGCAGCCCCGCGCACAGTGTACGCCTTCTCCGCGGCCCTCTGGCCGGCGGGGA	180
TB	GGCGGGCGCAGCCCCGCGCACAGTGTACGCCTTCTCCGCGGCCCTCTGGCCGGCGGGGA	180
MB	GGCGGGCGCAGCCCCGCGCACAGTGTACGCCTTCTCCGCGGCCCTCTGGCCGGCGGGGA	180

NM_174076.3	GCCCTTCAACCTGTCTCCCTGCGGGGCAAGGTGCTGCTCATTGAGAACGTAGCATCGCT	240
TH	GCCCTTCAACCTGTCTCCCTGCGGGGCAAGGTGCTGCTCATTGAGAACGTAGCATCGCT	240
MH	GCCCTTCAACCTGTCTCCCTGCGGGGCAAGGTGCTGCTCATTGAGAACGTAGCATCGCT	240
TB	GCCCTTCAACCTGTCTCCCTGCGGGGCAAGGTGCTGCTCATTGAGAACGTAGCATCGCT	240
MB	GCCCTTCAACCTGTCTCCCTGCGGGGCAAGGTGCTGCTCATTGAGAACGTAGCATCGCT	240

NM_174076.3	CTGAGGCACAACGGTGCGGGACTACACCCAGATGAATGACCTGCAGCGGCGCCTTGGAAC	300
TH	CTGAGGCACAACGGTGCGGGACTACACCCAGATGAATGACCTGCAGCGGCGCCTTGGAAC	300
MH	CTGAGGCACAACGGTGCGGGACTACACCCAGATGAATGACCTGCAGCGGCGCCTTGGAAC	300
TB	CTGAGGCACAACGGTGCGGGACTACACCCAGATGAATGACCTGCAGCGGCGCCTTGGAAC	300
MB	CTGAGGCACAACGGTGCGGGACTACACCCAGATGAATGACCTGCAGCGGCGCCTTGGAAC	300

NM_174076.3	CCGGGGCCTGGTCGTGCTCGGCTTCCCCTGCAACCAGTTTGGGCATCAGGAAAACGCCAA	360
TH	CCGGGGCCTGGTCGTGCTCGGCTTCCCCTGCAACCAGTTTGGGCATCAGGAAAACGCCAA	360
MH	CCGGGGCCTGGTCGTGCTCGGCTTCCCCTGCAACCAGTTTGGGCATCAGGAAAACGCCAA	360
TB	CCGGGGCCTGGTCGTGCTCGGCTTCCCCTGCAACCAGTTTGGGCATCAGGAAAACGCCAA	360
MB	CCGGGGCCTGGTCGTGCTCGGCTTCCCCTGCAACCAGTTTGGGCATCAGGAAAACGCCAA	360

NM_174076.3	GAACGAGGAGATCCTGAATTGCCTGAAGTACGTCCGACCAGGCGGCGGGTTCGAGCCCAA	420
TH	GAACGAGGAGATCCTGAATTGCCTGAAGTACGTCCGACCAGGCGGCGGGTTCGAGCCCAA	420
MH	GAACGAGGAGATCCTGAATTGCCTGAAGTACGTCCGACCAGGCGGCGGGTTCGAGCCCAA	420
TB	GAACGAGGAGATCCTGAATTGCCTGAAGTACGTCCGACCAGGCGGCGGGTTCGAGCCCAA	420
MB	GAACGAGGAGATCCTGAATTGCCTGAAGTACGTCCGACCAGGCGGCGGGTTCGAGCCCAA	420

NM_174076.3	CTTTATGCTCTTCGAAAAGTGCAGAGTGAATGGCGAGAAGGCGCATCCGCTCTTCGCCTT	480
TH	CTTTATGCTCTTCGAAAAGTGCAGAGTGAATGGCGAGAAGGCGCATCCGCTCTTCGCCTT	480
MH	CTTTATGCTCTTCGAAAAGTGCAGAGTGAATGGCGAGAAGGCGCATCCGCTCTTCGCCTT	480
TB	CTTTATGCTCTTCGAAAAGTGCAGAGTGAATGGCGAGAAGGCGCATCCGCTCTTCGCCTT	480
MB	CTTTATGCTCTTCGAAAAGTGCAGAGTGAATGGCGAGAAGGCGCATCCGCTCTTCGCCTT	480

NM_174076.3	CCTTCGGGAGGTTCTGCCCACGCCAAGTGACGACGCCACTGCTCTCATGACCGA	534
TH	CCTTCGGGAGGTTCTGCCCACGCCAAGTGACGACGCCACTGCTCTCATGACCGA	534
MH	CCTTCGGGAGGTTCTGCCCACGCCAAGTGACGACGCCACTGCTCTCATGACCGA	534
TB	CCTTCGGGAGGTTCTGCCCACGCCAAGTGACGACGCCACTGCTCTCATGACCGA	534
MB	CCTTCGGGAGGTTCTGCCCACGCCAAGTGACGACGCCACTGCTCTCATGACCGA	534

Fig. S7. Representative DNA sequence alignment of *GPXI* gene (534-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|NM_174076.3|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.

XM_005210409.4	TAAGAATTGTTTAACTGAAAAATAAGAAATTTTGTAAATTTAAATGTACACTATGATTT	60
TH	TAAGAATTGTTTAACTGAAAAATAAGAAATTTTGTAAATTTAAATGTACACTATGATTT	60
MH	TAAGAATTGTTTAACTGAAAAATAAGAAATTTTGTAAATTTAAATGTACACTATGATTT	60
TB	TAAGAATTGTTTAACTGAAAAATAAGAAATTTTGTAAATTTAAATGTACACTATGATTT	60
MB	TAAGAATTGTTTAACTGAAAAATAAGAAATTTTGTAAATTTAAATGTACACTATGATTT	60

XM_005210409.4	GGTGTATACTCTCAAACAGCTTCTACTTCCCACCCCAAGTTGCTTTTATTTAGTGAAC	120
TH	GGTGTATACTCTCAAACAGCTTCTACTTCCCACCCCAAGTTGCTTTTATTTAGTGAAC	120
MH	GGTGTATACTCTCAAACAGCTTCTACTTCCCACCCCAAGTTGCTTTTATTTAGTGAAC	120
TB	GGTGTATACTCTCAAACAGCTTCTACTTCCCACCCCAAGTTGCTTTTATTTAGTGAAC	120
MB	GGTGTATACTCTCAAACAGCTTCTACTTCCCACCCCAAGTTGCTTTTATTTAGTGAAC	120

XM_005210409.4	AATTGTCGTCTTTTATTTTCTTGAGTCTTAATATCTTTAGTGGGAAGTGCTCCTAGGAAT	180
TH	AATTGTCGTCTTTTATTTTCTTGAGTCTTAATATCTTTAGTGGGAAGTGCTCCTAGGAAT	180
MH	AATTGTCGTCTTTTATTTTCTTGAGTCTTAATATCTTTAGTGGGAAGTGCTCCTAGGAAT	180
TB	AATTGTCGTCTTTTATTTTCTTGAGTCTTAATATCTTTAGTGGGAAGTGCTCCTAGGAAT	180
MB	AATTGTCGTCTTTTATTTTCTTGAGTCTTAATATCTTTAGTGGGAAGTGCTCCTAGGAAT	180

XM_005210409.4	TCTGATGAAAAGTACAGCAAGATTAAAAATTGATAATTATTAGCAAGTATAATACTGCT	240
TH	TCTGATGAAAAGTACAGCAAGATTAAAAATTGATAATTATTAGCAAGTATAATACTGCT	240
MH	TCTGATGAAAAGTACAGCAAGATTAAAAATTGATAATTATTAGCAAGTATAATACTGCT	240
TB	TCTGATGAAAAGTACAGCAAGATTAAAAATTGATAATTATTAGCAAGTATAATACTGCT	240
MB	TCTGATGAAAAGTACAGCAAGATTAAAAATTGATAATTATTAGCAAGTATAATACTGCT	240

XM_005210409.4	TTGAACCTAAAAATACGTTTATAACAAGCATATAAAGGTCATACACAAAATATACTTTAAA	300
TH	TTGAACCTAAAAATACGTTTATAACAAGCATATAAAGGTCATACACAAAATATACTTTAAA	300
MH	TTGAACCTAAAAATACGTTTATAACAAGCATATAAAGGTCATACACAAAATATACTTTAAA	300
TB	TTGAACCTAAAAATACGTTTATAACAAGCATATAAAGGTCATACACAAAATATACTTTGAA	300
MB	TTGAACCTAAAAATACGTTTATAACAAGCATATAAAGGTCATACACAAAATATACTTTAAA	300

XM_005210409.4	GTGTCCAAAAATCTGAATCTATTTTCATGTGTATACAGACAGAAATCATGTTTTTAATAA	360
TH	GTGTCCAAAAATCTGAATCTATTTTCATGTGTATACAGACAGAAATCATGTTTTTAATAA	360
MH	GTGTCCAAAAATCTGAATCTATTTTCATGTGTATACAGACAGAAATCATGTTTTTAATAA	360
TB	GTGTCCAAAAATCTGAATCTATTTTCATGTGTATACAGACAGAAATCATGTTTTTAATAA	360
MB	GTGTCCAAAAATCTGAATCTATTTTCATGTGTATACAGACAGAAATCATGTTTTTAATAA	360

XM_005210409.4	TGGAAATGGGATAGCTCATAAAAAATTAAAAATTAAGGTGTTTTGGACTATTTTATTAAGTA	420
TH	TGGAAATGGGATAGCTCATAAAAAATTAAAAATTAAGGTGTTTTGGACTATTTTATTAAGTA	420
MH	TGGAAATGGGATAGCTCATAAAAAATTAAAAATTAAGGTGTTTTGGACTATTTTATTAAGTA	420
TB	TGGAAATGGGATAGCTCATAAAAAATTAAAAATTAAGGTGTTTTGGACTATTTTATTAAGTA	420
MB	TGGAAATGGGATAGCTCATAAAAAATTAAAAATTAAGGTGTTTTGGACTATTTTATTAAGTA	420

XM_005210409.4	AGGAAACATTGGTGGCCACATCCCTTTATTAACCTTTAGACTTAAACTGCTGAATCATA	480
TH	AGGAAACATTGGTGGCCACATCCCTTTATTAACCTTTAGACTTAAACTGCTGAATCATA	480
MH	AGGAAACATTGGTGGCCACATCCCTTTATTAACCTTTAGACTTAAACTGCTGAATCATA	480
TB	AGGAAACATTGGTGGCCACATCCCTTTATTAACCTTTAGACTTAAACTGCTGAATCATA	480
MB	AGGAAACATTGGTGGCCACATCCCTTTATTAACCTTTAGACTTAAACTGCTGAATCATA	480

Fig. S8. Representative DNA sequence alignment of *AhpC/TSA* gene (480-bp) among tolerant and mastitis affected Holstein and Brown Swiss dairy cows and reference sequence available in the GenBank gb|XM_005210409.4|. TH= Tolerant Holstein; MH= Mastitic Holstein; TB= Tolerant Brown Swiss and MB= Mastitic Brown Swiss. The asterisks represent the similarity.