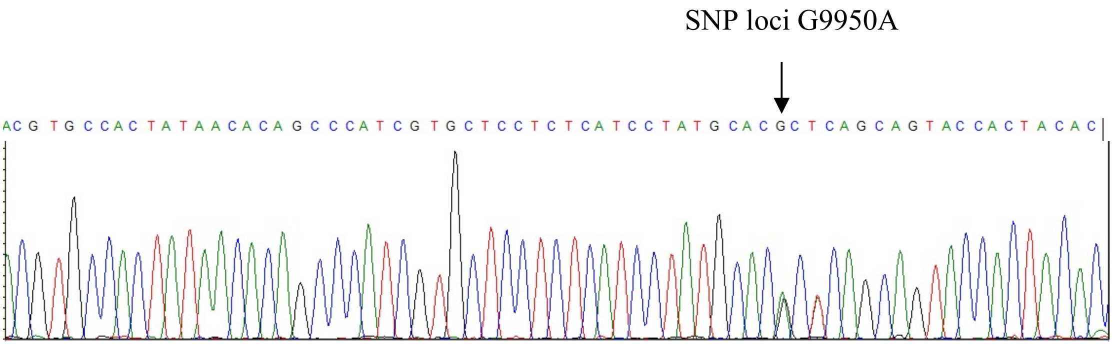
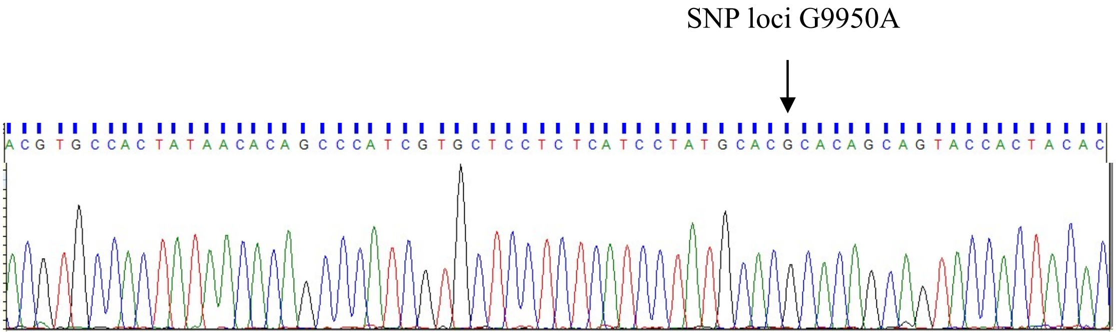
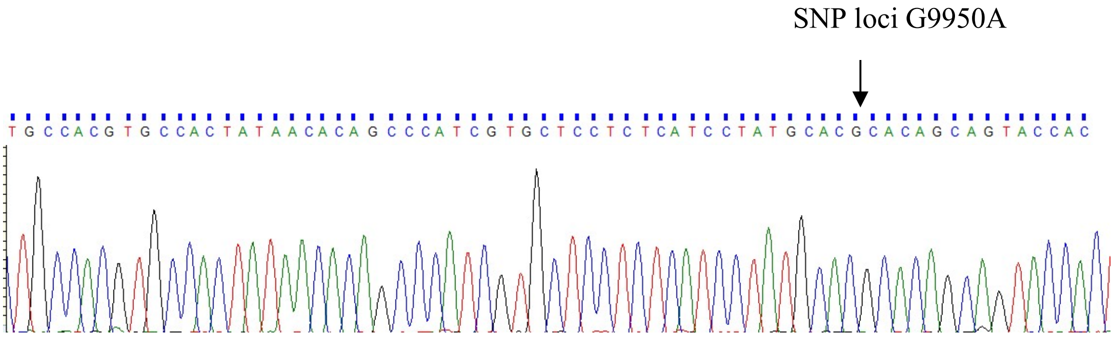
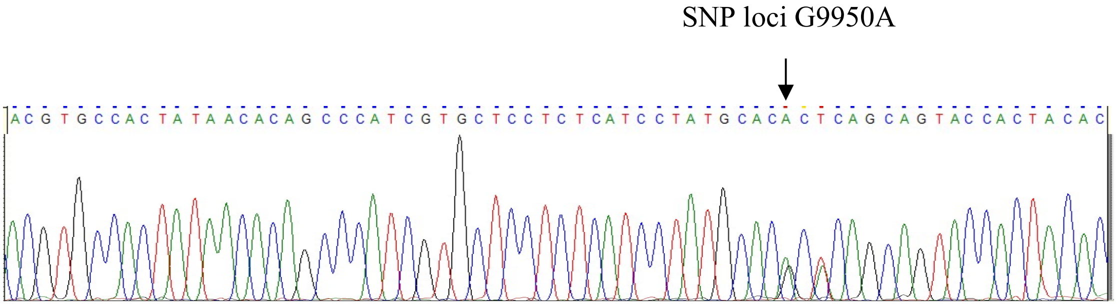
APPENDICES

APPENDIX I: Mutation in nucleotide sequence of CAPN1 G9950A SNP.









APPENDIX II: CLUSTAL multiple sequence alignment for G3535A

```
CLUSTAL multiple sequence alignment by MUSCLE (3.8)


_1_COMM__F       -CCCATA--TGCTTTGATATGGAGCAGTGACCTTC-AGAAGCTGGTGAAGGGCCATGCCT
_2_COMM__F       --CCATAATGCCTTTGATATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_3_COMM__F       -CCATTAATGCCTTTGA-ATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_4_COMM__F       -CCCCTAG-TGCTTTGA-ATGGAGCAGTGACCTTC-AGAAGCTGGTGAAAGGCCATGCCT
_5_COMM__F       CCCCAAAATTGCTTTGATATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_6_COMM__F       -CCCCTAATTGCTTTGA-ATGGAGCAGTGACCTTC-AGAAGCTGGTGAAGGGCCATGCCT
_7_COMM__F       --CCCTAT-GGCTTTGATATGGAGCAGTGACCTTC-AGAAGCTGGTGAAAGGCCATGCCT
_8_COMM__F       -CCCATA--TGCTTTGATATGGAGCAGTGACCTTCAAGAAGCTGGTGAAGGGCCATGCCT
_9_COMM__F       -CCCATAA-TGCTTTGATATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_10_COMM__F      -CCCAAA--TGCTTTGAATGGAAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
1_org__F         -CCCAAAA-TGCTTTGA-ATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
2_org__F         -CCCATTATGCCTTTGATATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_3_org__F        -CCCATAA-TGCTTTGATATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_4_org__F        --CCTAATGGCCTTTGATATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_5_org__F        -CCAAAAGTGCCTTTGA-ATGGAGCAGTGACCTTC-AGAAGCTGGTGAAGGGCCATGCCT
_6_org__F        -CCAAAA--TGCTTTGA-ATGGAGCAGTGACCTTC-AGAAGCTGGTGAAAGGCCATGCCT
_7_org__F        -NNNNANNNNNCTTTGA-ATGGAGCAGTGACCTTC-AGAAGCTGGTGAAGGGCCATGCCT
_8__org__F       --CCCTA--TGCTTTGA-ATGGAGCAGTGACCTTC-AGAAGCTGGTGAAAGGCCATGCCT
_9_org__F        --CCATTATGCCTTTGA-ATGGAGCAGTGACCTTCAAGAAGCTGGTGAAAGGCCATGCCT
_10__org__F      -CGGACA--GGTCTTGA-ATGGAGCAGTGACCTTC-AGAAGCTGGTGAAGGGCCATGCCT
                              ****   * ************* ************* **********

_1_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_2_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_3_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_4_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_5_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_6_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_7_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_8_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_9_COMM__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_10_COMM__F      ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
1_org__F         ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
2_org__F         ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_3_org__F        ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_4_org__F        ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_5_org__F        ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_6_org__F        ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_7_org__F        ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_8__org__F       ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_9_org__F        ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
_10__org__F      ATTCTGTCACCGCCTTCAAAGATGTGAGTTGGGTACATAAGACTGTAATAGAGCTAAAAT
                 ************************************************************
_1_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_2_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_3_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_4_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_5_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_6_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_7_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_8_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_9_COMM__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_10_COMM__F      GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
1_org__F         GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
2_org__F         GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_3_org__F        GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_4_org__F        GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_5_org__F        GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_6_org__F        GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_7_org__F        GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGC--
_8__org__F       GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_9_org__F        GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
_10__org__F      GCCGTGGCCTGTGGTGTGGGTTTGACTTCCTGCATTTGATGGCTA
```

APPENDIX III: CLUSTAL multiple sequence alignment for C7198A

```
1_COMM_F          -GTCGAT----GCCCGTCTCATCTACTCAGACAAGATCTGAAGACG-GTATGGCTTCAGT
2_COMM_F          -GCGGATTTT-CCGTC-TC-AT-CTCTCAGACAAGATCTG-AGACGG--ATGGCTTCAGT
3_COMM_F          ---GCCGGGATCCC-GGCTCATCTCCTCAGACAAGATCTG-AGA-C-GGATGGCTTCAGT
4_COMM_F.         --GACCGTTGCCAGTTCTCAC-CTACTCGACAAAGATCTGAAGACGG-TATGGCTTCAGT
5_COMM_F          -GACCGTGGACCAGTCGTCACCCTACTCAGACAAGATCTG-AGACTG-TATGGCTTCAGT
6_COMM_F          -----GAGCTTGCA-GTCTCACCTACTCAGACAAGATCTCGAGACT-GTATGGCTTCAGT
7_COMM_F          ---GCGGGATTCAG-TCCTCATCTACTCAGACAAGATCTG-AGAC--GGATGGCTTCAGT
8_COMM_F          ------ACATTGAA-GTCTCATCTACTCAGACAAGATCTCGAGACGGTATGGCATTCAGT
9_COMM_F          -GGACGTATTCCGG-TCTCTCCCTACTCAGACAAGATCTG-AGACG-GTATGGCTTCAGT
9_ORG_F           --GCGAA----TCCAGTCTCTTCTACTCAGACAAGATCTGAAGACG-GTATGGCTTCAGT
10_COMM_F         -----GGAGAGGCC-GTCTCATCTACTCAGACAAGATCTG-AAGACGGTATGGCTTCAGT
2_ORG_F           --GACAT----TCCAGTCTCATCTACTCAGACAAGATCTGAAGACG-G-ATGGCTTCAGT
1_ORG_F           ---GAGGAATGGCC-GTCTCATCTACTCAGACAAGATCTG-AG-ACGGTATGGCTTCAGT
5_ORG_F           --GACCGAAGCCC--TCTC-ATCTACTCAGACAAGATCTGAAGACGG--ATGGCTTCAGT
10_ORG_F          ---GCGATTGCGG--TCTC-ATCTACTCAGACAAGATCTGAAGACGG-TATGGCTTCAGT
3_ORG_F           --GCCGTATACC-G-TCTCACTCTACTCAGACAAGATCTG-AGACGG-TATGGCTTCAGT
7_ORG_F           --GACGATTG-CCGTCCTC-AT-TTCTCAGACAAGATCTG-AAGACG-GATGGATTCAGT
6_ORG_F           -GACCGATTG-CCGT-CTC-ATCTACTCAGACAAGATCTG-AGACGG--ATGGCTTCAGT
4_ORG_F           ---GCGATTG-CCGTC-TC--TTCTCTCAGACAAGATCTG-AGACGG--ATGGCTTCAGT
8_ORG_F           TGAGGATTTT-CAGTCCTC-ATCTACTCAGACAAGATCTG-AGACGG-TATGGCTTCAGT
                                           ***....*******  *.      : * .******

9_ORG_F           CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
1_COMM_F          CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
2_ORG_F           CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
6_COMM_F          CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
8_COMM_F          CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
9_COMM_F          CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
7_COMM_F          CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
1_ORG_F           CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
3_COMM_F          CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
10_COMM_F         CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
5_ORG_F           CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
10_ORG_F          CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
4_COMM_F.ab1      CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
3_ORG_F           CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
5_COMM_F          CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
7_ORG_F           CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
6_ORG_F           CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
4_ORG_F           CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
2_COMM_F          CTGGACTCCT-GCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
8_ORG_F           CTGGACTCCTAGCCGCAACATGGTCAACCTGATGGATGTATCCTCTTGGCATTGTGGGCA
                  ********** *************************************************

9_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
1_COMM_F          GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
2_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
6_COMM_F          GGGGCTGGCGTTCCTGGCGCTCAGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
8_COMM_F          GGGGCTGGCGTTCCTGGCGCTCAGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
9_COMM_F          GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
7_COMM_F          GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
1_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
3_COMM_F          GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
10_COMM_F         GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
5_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
10_ORG_F          GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
4_COMM_F.ab1      GGGGCTGGCGTTCCTGGCGCTCAGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
3_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
5_COMM_F          GGGGCTGGCGTTCCTGGCGCTCAGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
7_ORG_F           GGGGCTGGCGTTCCTGGCGCTCAGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
6_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
4_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
2_COMM_F          GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
8_ORG_F           GGGGCTGGCGTTCCTGGCGCTCGGCCTGGCAGCCAGCACACTTCTCCGTGGGAACTAGGG
                  **********************.*************************************
```

APPENDIX IV: CLUSTAL multiple sequence alignment for G9950A SNP marker

```
3_org__F        ---GAACGTGGACTCTTTCTGCGTGGCTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
5_COMM__F       -----CCGTCTACTCTTTCTGCGTGGCTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
5_org__F        ATTTACGT--CACTCATTCTGGTGGCCTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
2_org__F        ---CA----CGTCACTCTTCTCGTGGCTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
6_COMM__F       ----ACCTGCACCTCTTTCT-GGTGGCTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
10_COMM__F      ---AAATTCGACGTCTATCT-GGTGGCTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
10_org__F       ---CACGGTC-ACTCTTTCTGCGTGGCTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
8_org__F        --CAACGGCGACGTCTTTCTGCGTGGCTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
1_COMM__F       ----AACGTCACGTCTTTCTGCGTGGCTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
4_org__F        ---AAAAGTCGACTCTTTCTGCGTGGCTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
6_org__F        -AACG----TCACTCTTTCTCGTGG-CTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
4_COMM__F       -AACTTGGTACGTCTTTCTGCGTGG-CTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
2_COMM__F       -CCCG--TGACGTCGTTCTGCGTGGCCTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
3_COMM__F       ---CAATGTA-CTCTTTCTGCGTGG-CTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
9_org__F        ----GCGGTCTACTCTTTCTCGTGG-CTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
7_org__F        ---CACCGTGGACTCTTTCTGGTGG-CTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
9_COMM__F       ----CACGTGGTCTCTTTCTGGTGG-CTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
7_COMM__F       -CAAGTCGTACGTCTTTCTGCGTGG-CTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
8_COMM__F       --CCGTCAA---CTCTTTCTGGTGG-CTTCAGCTCTCCCTCACACCCCTTACTCTCTGCC
1_org__F        -CACGTTGT---ACTCTTCTGGTGG-CTTCAGCTCTC-CTCACACCCCTTACTCTCTGCC
                                        * *********** **********************

3_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
5_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
5_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
2_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
6_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
10_COMM__F      CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
10_org__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
8_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
1_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
4_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
6_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
4_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
2_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
3_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
9_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
7_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
9_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
7_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
8_COMM__F       CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
1_org__F        CCCCTCTGTCCCACCATAGGGCCAAAGCCTATCATTTAAGCACTCCCCTGCCACGTGCCA
                ************************************************************

3_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCACAGCAGTACCACTACACC
5_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCACAGCAGTACCACTACACC
5_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
2_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACACTCAGCAGTACCACTACACC
6_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
10_COMM__F      CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
10_org__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
8_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
1_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
4_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
6_org__F        CTATAACACAGCCCATCTTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
4_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCACAGCAGTACCACTACACC
2_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
3_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCACAGCAGTACCACTACACC
9_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACACTCAGCAGTACCACTACACC
7_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
9_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
7_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCACAGCAGTACCACTACACC
8_COMM__F       CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
1_org__F        CTATAACACAGCCCATCGTGCTCCTCTCATCCTATGCACGCTCAGCAGTACCACTACACC
```

APPENDIX V:

Statistical Analysis to evaluate the association between SNP and meat quality traits.

2/14/2016 6:24:06 PM

General Linear Model: Tenderness versus Allele, Chickens

```
Factor coding  (-1, 0, +1)

Factor Information

Factor  Type   Levels  Values
Allele  Fixed       2  A, G


Analysis of Variance

Source    DF  Adj SS  Adj MS  F-Value  P-Value
  Allele   1   3.492   3.492     2.39    0.140
Error     18  26.307   1.462
Total     19  29.799


Model Summary

      S    R-sq  R-sq(adj)  R-sq(pred)
1.20893  11.72%      6.81%       0.83%


Coefficients

Term        Coef  SE Coef  T-Value  P-Value   VIF
Constant  3.704    0.451     8.22    0.000
Allele
  A       0.696    0.451     1.55    0.140  1.00


Regression Equation

Tenderness = 3.704 + 0.696 Allele_A - 0.696 Allele_G


Fits and Diagnostics for Unusual Observations

Obs  Tenderness    Fit   Resid  Std Resid
 12       4.500  4.400   0.100       0.12  X
 17       4.300  4.400  -0.100      -0.12  X

X  Unusual X
```

General Linear Model: Thawing loss versus Allele, Chickens

```
The following terms cannot be estimated and were removed:
   Chickens


Method

Factor coding  (-1, 0, +1)


Factor Information

Factor  Type   Levels  Values
Allele  Fixed       2  A, G
```

```
Analysis of Variance

Source    DF   Adj SS  Adj MS  F-Value  P-Value
  Allele   1    5.984   5.984     1.01    0.328
Error     18  106.489   5.916
Total     19  112.473


Model Summary

      S   R-sq  R-sq(adj)  R-sq(pred)
2.43229  5.32%      0.06%       0.00%


Coefficients

Term        Coef  SE Coef  T-Value  P-Value   VIF
Constant  4.943    0.906     5.45    0.000
Allele
  A       0.912    0.906     1.01    0.328  1.00


Regression Equation

Thawing loss = 4.943 + 0.912 Allele_A - 0.912 Allele_G


Fits and Diagnostics for Unusual Observations

     Thawing
Obs     loss   Fit  Resid  Std Resid
 11     9.06  4.03   5.03       2.13  R
 12     4.55  5.86  -1.31      -0.76     X
 17     7.16  5.86   1.30       0.76     X

R  Large residual
X  Unusual X
```

General Linear Model: Cooking loss versus Allele, Chickens

```
The following terms cannot be estimated and were removed:
   Chickens


Method

Factor coding  (-1, 0, +1)


Factor Information

Factor  Type   Levels  Values
Allele  Fixed       2  A, G


Analysis of Variance

Source    DF   Adj SS  Adj MS  F-Value  P-Value
  Allele   1   0.3538  0.3538     0.15    0.703
Error     18  42.4439  2.3580
Total     19  42.7977


Model Summary

      S   R-sq  R-sq(adj)  R-sq(pred)
1.53558  0.83%      0.00%       0.00%


Coefficients

Term        Coef  SE Coef  T-Value  P-Value   VIF
Constant  22.163    0.572    38.73    0.000
```

```
Allele
  A        0.222    0.572     0.39    0.703  1.00


Regression Equation

Cooking loss = 22.163 + 0.222 Allele_A - 0.222 Allele_G


Fits and Diagnostics for Unusual Observations

     Cooking
Obs     loss     Fit   Resid  Std Resid
  7   18.950  21.942  -2.992      -2.00  R
 12   21.790  22.385  -0.595      -0.55     X
 17   22.980  22.385   0.595       0.55     X

R  Large residual
X  Unusual X
```