

Figure S1. Genotyping of rs1714766362 SNP in *KIAA1462* gene by AS-PCR.

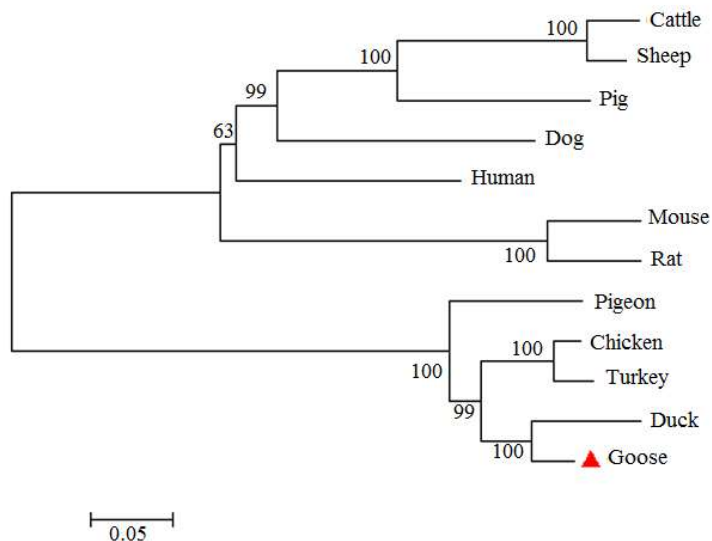


Figure S2. The phylogenetic tree of *KIAA1462* protein was constructed with the neighbour-joining method by using MEGA5. A 1000 bootstrap replication was chosen to test the reliability of each branch. Bootstrap values are indicated as numbers at the branch nodes. Aminoacid sequences of *KIAA1462* for these species were downloaded from protein database of NCBI. Their corresponding accession numbers are same as given in Table 4.

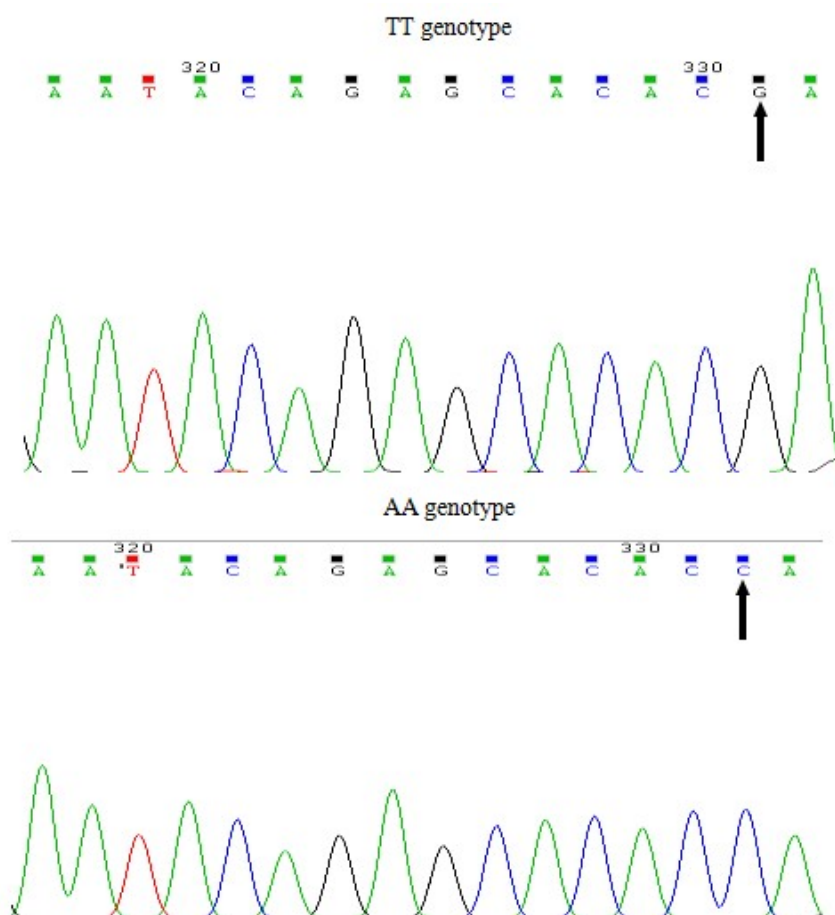


Figure S3. Direct DNA sequencing of the 3-kb promoter region using DNA from AA genotype individuals and TT genotype individuals of SNP rs1714766362. A mutation (c.-413C>G) 413-bp upstream of the start codon point of *KIAA1462* gene was completely linked with SNP rs1714766362: it was C in AA genotype individuals and G in TT genotype individuals.

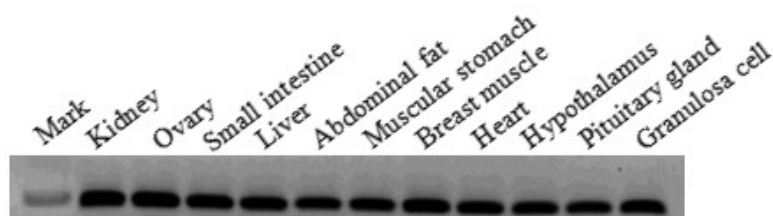


Figure S4. mRNA expression levels of goose GAPDH gene in different tissues was detected by Semi-quantitative RT-PCR.

Table S1. The sequences of each oligo used in the EMSA.

| | | Forward | Reverse |
|------|-----------------|-------------------------------------|-------------------------------------|
| EMSA | SNP(g.413C>G)-C | AAACAGCTTTCCTCTGGTGTG CTCTGTATTC | GAATACAGAGCACACCAGAGGAAAG CTGTTT |
| | SNP(g.413C>G)-G | AAACAGCTTTCCTCTCGTGTG CTCTGTATTC | GAATACAGAGCACACGAGAGGAAAG CTGTTT |
| | GR (GRE) | TCGACTGTACAGGATGTTGCT ACT | AGCTGACATGTCCTACAACGATGA |