

## Supplementary Materials

### Regulatory Effects of 198-bp Structural Variants in the *GSTA2* Promoter Region on Adipogenesis in Chickens

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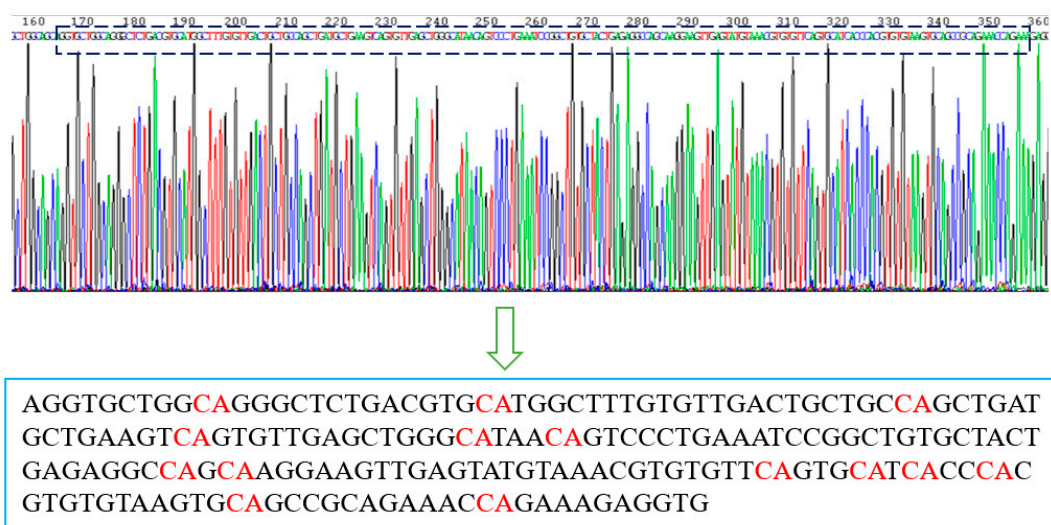
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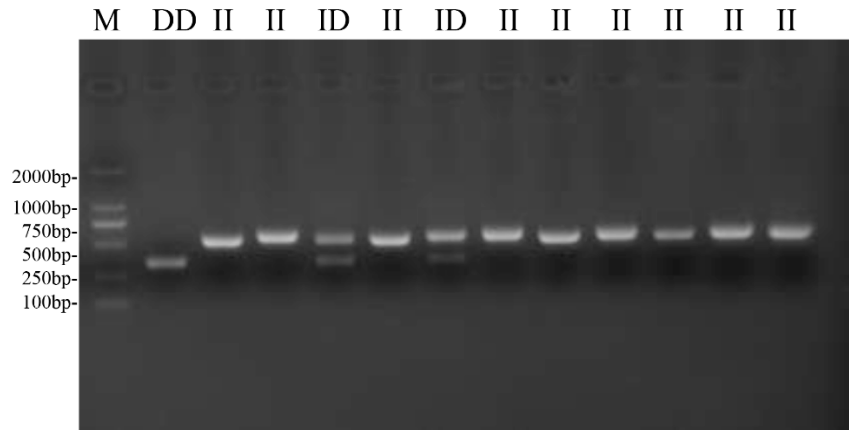
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**Figure S1.** Insertion sequence of the II genotype. The sequence of the inserted fragment of the II genotype in the *GSTA2* gene is 200-bp in length. Interestingly, compared to the II genotype, the DD genotype is missing only the 198-bp segment and has an additional 2-bp (bases CA). However, unfortunately, our current technological means cannot determine whether the CA bases in the DD genotype are a replacement for the II genotype insertion fragment or if the DD genotype is missing the 200-bp segment and retains the CA bases. Therefore, we named this mutation a 198-bp SV. The CA bases in the 200-bp insertion sequence are highlighted in red.



**Figure S2.** Agarose gel electrophoresis (1.5%) pattern for the *GSTA2* SVs polymorphism. DD (344-bp), ID (542 and 344-bp) and II (542-bp) are the three different genotypes, and M represents DL2000.

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seq( 0.. 59)      aggtgctggcagggtctgacgtgcatggcttgtgtgactgctgccagctgatgctga
Segments:
1.1.3.0      12   21      =C/EBPαp=
1.1.2.0      13   22      =====CREB=====
0.5.1.0      14   23      =E1A 12S =
1.1.1.6      14   23      ==CRE-BP1=
2.1.2.1      14   23      =RAR-αph=
2.3.3.0      14   23      =CPE bind=
1.3.1.2      15   24      =====USF=====
9.9.539      38   47      =====NF-1=====
1.2.1.0      46   55      =====E1=====
1.2.2.0      46   55      ===Myf-3===
1.1.3.0      48   57      =C/EBPαp=
9.9.29       48   57      =====AP-1=====
1.1.1.6      55   64      =ATF=
2.1.1.4      59   68      =
=====
seq( 60.. 119)    agtcagtgttgagctgggcataacagtcacctgaaatccggctgtgctactgagaggccag
Segments:
1.1.1.6      55   64      3del=
2.1.1.4      59   68      =====ER=====
2.4.1.0      64   73      =====p40x=====
2.3.1.0      69   78      =====Sp1=====
1.2.8.0      81   90      =====Olf-1=====
2.3.1.0      96  105      =====Sp1=====
2.3.1.0     111  120      =====Sp1=====
=====
seq( 120.. 179)   caaggaagttgagtatgtaaactgtgttcagtgcacccacgtgtgtaagtgcagcc
Segments:
2.3.1.0     111  120      =
1.1.3.0     124  133      =C/EBPαp=
3.1.2.2     131  140      ===Oct-1===
1.3.1.2     159  168      =====USF=====
3.5.1.2     174  183      ===Adf
=====
seq( 180.. 239)   gcagaaaccagaaagaggtg
Segments:
3.5.1.2     174  183      -1=
3.5.2.0     191  200      ===E1k-1===
2.3.1.0     192  201      =====Sp1=====

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**Figure S3.** The predicted results of transcription factor-binding sites in the insertion sequence of the II genotype. The parameters employed in the Alibaba 2.1 online tool are as follows: cons = 75% and classification level K = 4.

**Table S1.** Pairwise fixation indices (F<sub>st</sub>s) of the GSTA2 gene in different chickens.

Breeds	F2	N409	ND	GS	GX	WC	QY	ISA
N409	0.059							
ND	0.009	0.046						
GS	0.002	0.011	0.047					
GX	0.078	0.002	0.179	0.061				
WC	0.000	0.018	0.023	0.005	0.089			
QY	0.013	0.005	0.081	0.007	0.03	0.022		
ISA	0.000	0.023	0.023	0.004	0.097	0.000	0.022	
RW	0.013	0.043	0.009	0.073	0.191	0.049	0.102	0.042

**Table S2.** Details of the primer pairs used in this study.

Gene name	Primer sequences (5'-3')	Annealing temperature (°C)
GSTA2	F: ATTGCCTTAATCACTGAAC R: TGCCAACAAGATAATCCT	60
CCNB2	F: CAGTAAAGGCTACGAAAG R: ACATCCATAGGGACAGG	58
CDKN1B	GCTGTGCTGGGCTGAA GGACGAAAGGATGTGGG	58
CCNG2	F: TGCCAACAATACCAGAGG R: TACAGAATACCACAATCCC	58
CCND2	F: AACTTGCTCTACGACGACC R: TTCACAGACCTCCAACATC	58
PPAR $\gamma$	F: TCCTTCCCGCTGACCAAA R: TCCTGCACTGCCTCCACA	60
C/EBP $\alpha$	F: GACAAGAACAGCAACGAGTACCGC R: CCTGAAGATGCCCCGCAGAGT	60
C/EBP $\beta$	F: GCGGACTGTTTGGCTGCTCT R: CGGGTGAGGCTGATGTAGGTGT	60
ADIPOR1	F: GACAAGAACAGCAACGAGTACCGC R: CCTGAAGATGCCCCGCAGAGT	60
FABP4	F: ATGTGCGACCAGTTTGTG R: TTTGCCATCCCACCTTCTG	60
FAS	F: CGCAGGCATAGCAGGAAA R: CCAAAGAAGGAGGCATCAA	60
LEPR	F: CCAACCCTTCCTTGCTAA R: GCCTTCAACCCAACATTC	60
ATGL	F: TGTCCAAAGAAGCACGAAA R: GAGGTATCAGCCCACAGTAGA	60
$\beta$ -actin	F: CAGGATGCAGAAGGAGATC R: CTGGAAGGTGGACAGGGAG	60
GSTA2-Genotyping	F: GCTTCAACTTAGATGTTCTGCT R: CAGCGTCACCGTGCTATCAA	60

Note: The primers used for *GSTA2* genotyping were used for SV genotyping.

**Table S3.** The sequence information of the dual-luciferase reporter plasmids used in this study.

Plasmid name	S
PGL3-II	AGCTGTTACAGTTGGAGGAAGGAGGACTCTGGCTGGCAGCAGGTGCTGGCAGGGCTCTGACGT GCATGGCTTTGTGTTGACTGCTGCCAGCTGATGCTGAAGTCAGTGTTGAGCTGGGCATAACAGT CCCTGAAATCCGGCTGTGCTACTGAGAGGCCAGCAAGGAAGTTGAGTATGTAAACGTGTGTTT AGTGCATCACCCACGTGTGTAAGTGCAGCCGCAGAAACCAGAAAGAGGTGGATGTTGCAGCA CTCCCAGCACGAAGCTGGGCCACCTCCA
PGL3-DD	AGCTGTTACAGTTGGAGGAAGGAGGACTCTGGCTGGCAGCCAGATGTTGCAGCACTCCCAGCA CGAAGCTGGGCCACCTCCA
PGL3-SP1	AGCTGTTACAGTTGGAGGAAGGAGGACTCTGGCTGGCAGCAGGTGCTGGCAGGGCTCTGACGT GCATGGCTTTGTGTTGACTGCTGCCAGCTGATGCTGAAGTCAGTGATAACAGTCCCTGAAATT ACTGAAGGAAGTTGAGTATGTAAACGTGTGTTTCAAGTGCATCACCCACGTGTGTAAGTGCAGCC GCAGAAACCAGGATGTTGCAGCACTCCCAGCACGAAGCTGGGCCACCTCCA
PGL3- C/EBPa	AGCTGTTACAGTTGGAGGAAGGAGGACTCTGGCTGGCAGCAGGTGCTGGCAGTGCATGGCTTT GTGTTGACTGCTGCCGAAGTCAGTGTTGAGCTGGGCATAACAGTCCCTGAAATCCGGCTGTGC TACTGAGAGGCCAGCAAGATGTAAACGTGTGTTTCAAGTGCATCACCCACGTGTGTAAGTGCAGC CGCAGAAACCAGAAAGAGGTGGATGTTGCAGCACTCCCAGCACGAAGCTGGGCCACCTCCA
PGL3-OCT-1	AGCTGTTACAGTTGGAGGAAGGAGGACTCTGGCTGGCAGCAGGTGCTGGCAGGGCTCTGACGT GCATGGCTTTGTGTTGACTGCTGCCAGCTGATGCTGAAGTCAGTGTTGAGCTGGGCATAACAGT CCCTGAAATCCGGCTGTGCTACTGAGAGGCCAGCAAGGAAGTTGCGTGTGTTTCAAGTGCATCACCCACGT