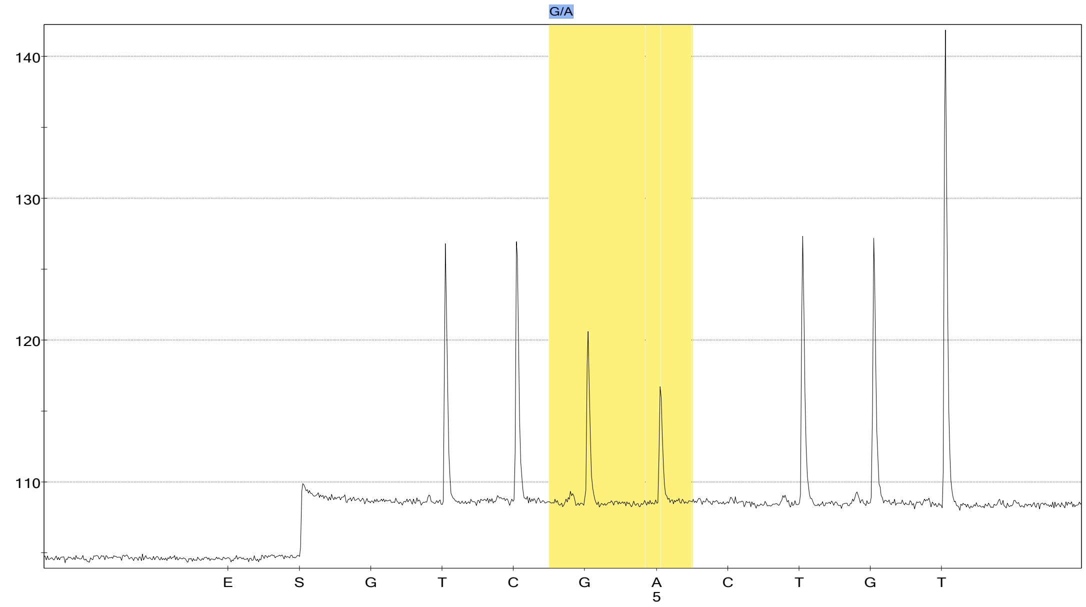
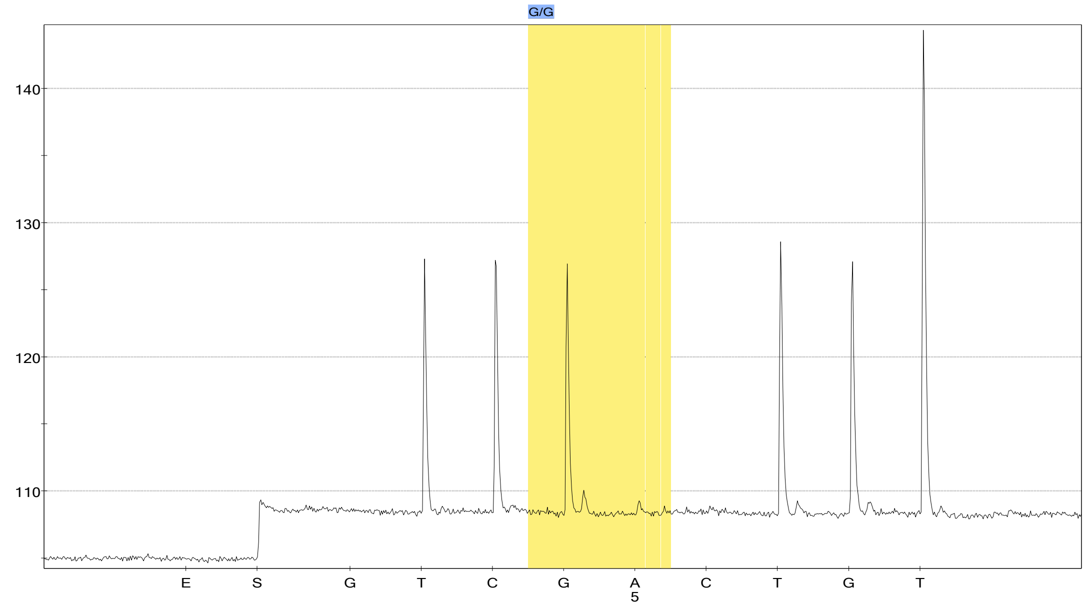
Appendix C

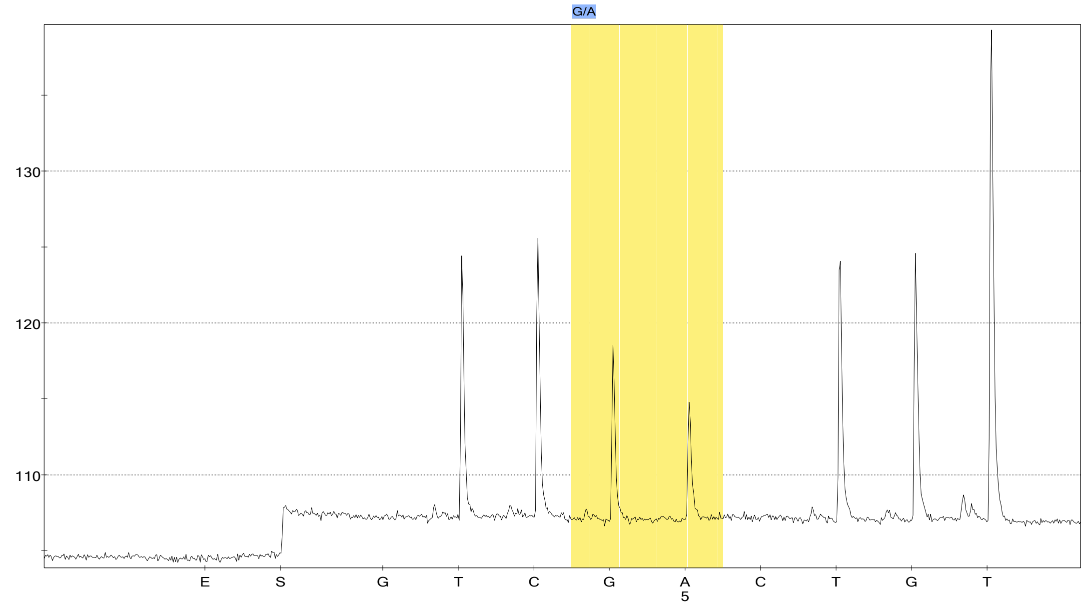
(a)



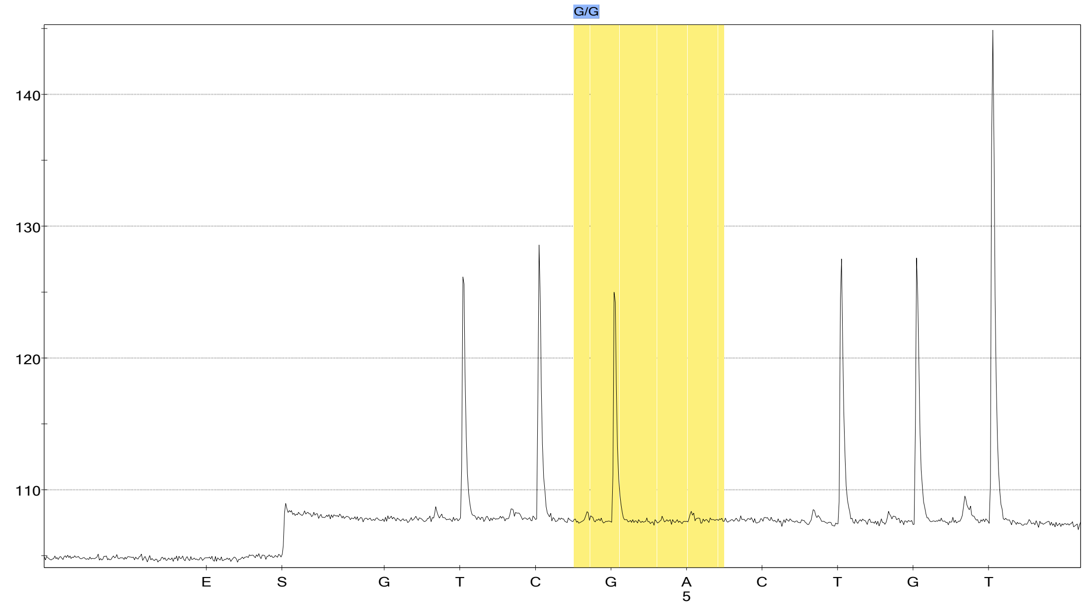
(b)



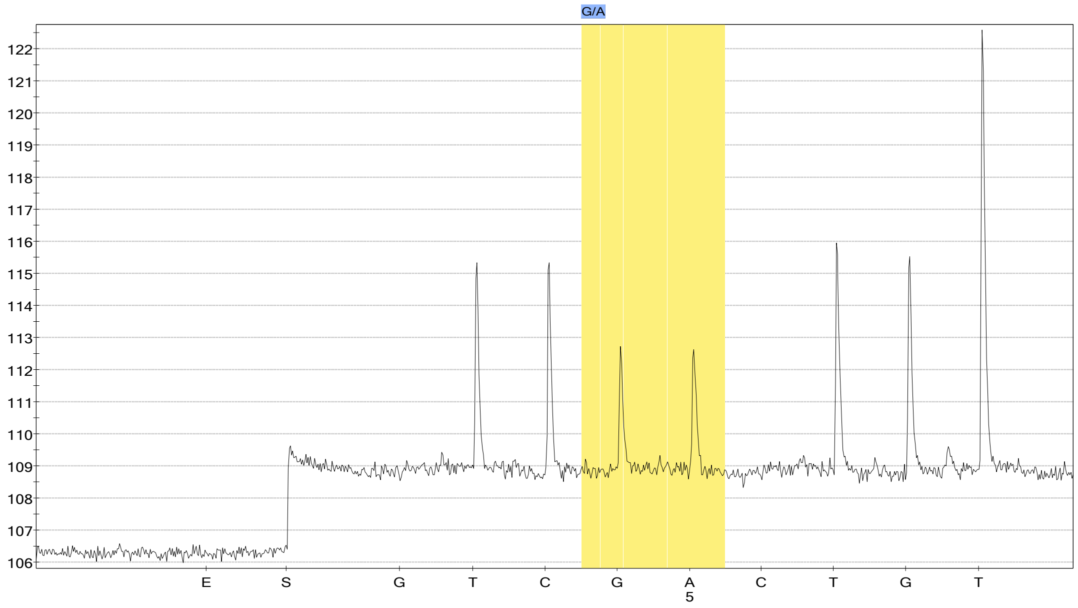
(c)



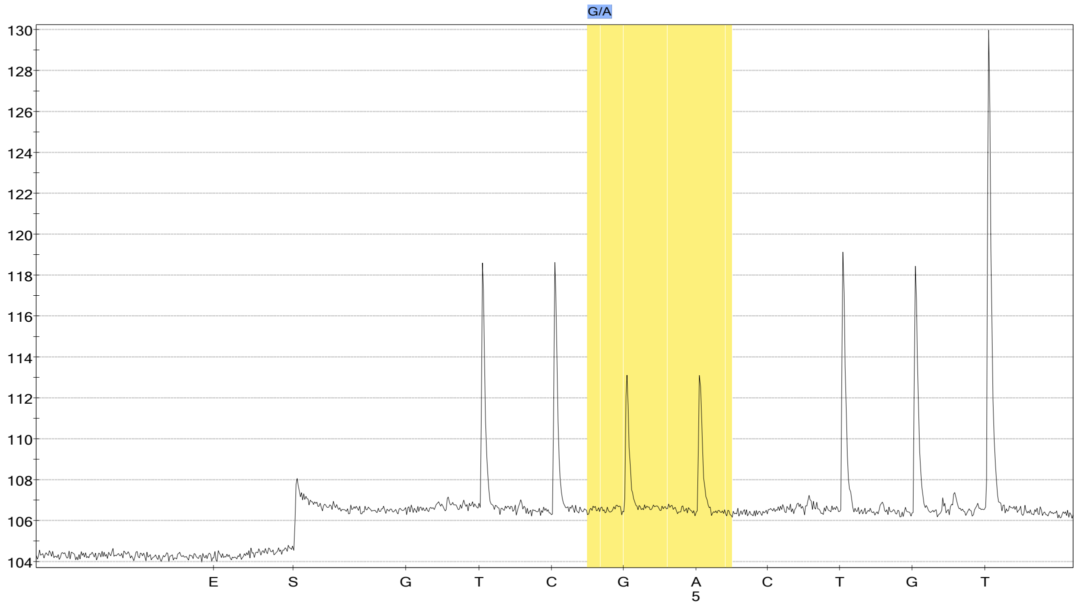
(d)



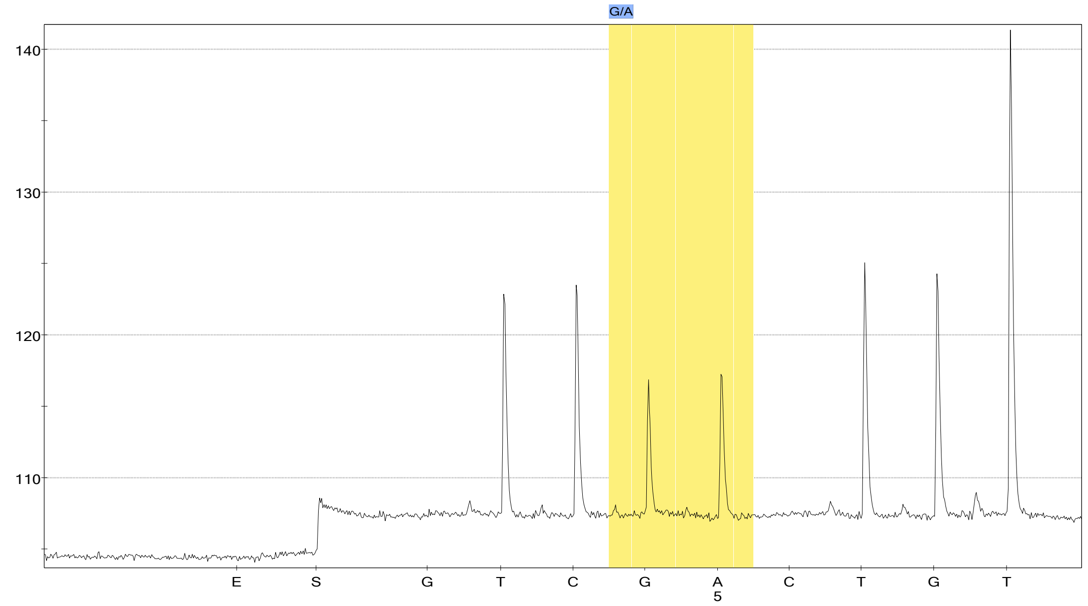
(e)


G/A
122
121
120
119
118
117
116
115
114
113
112
111
110
109
108
107
106
E
S
G
T
C
G
A
5
C
T
G
T

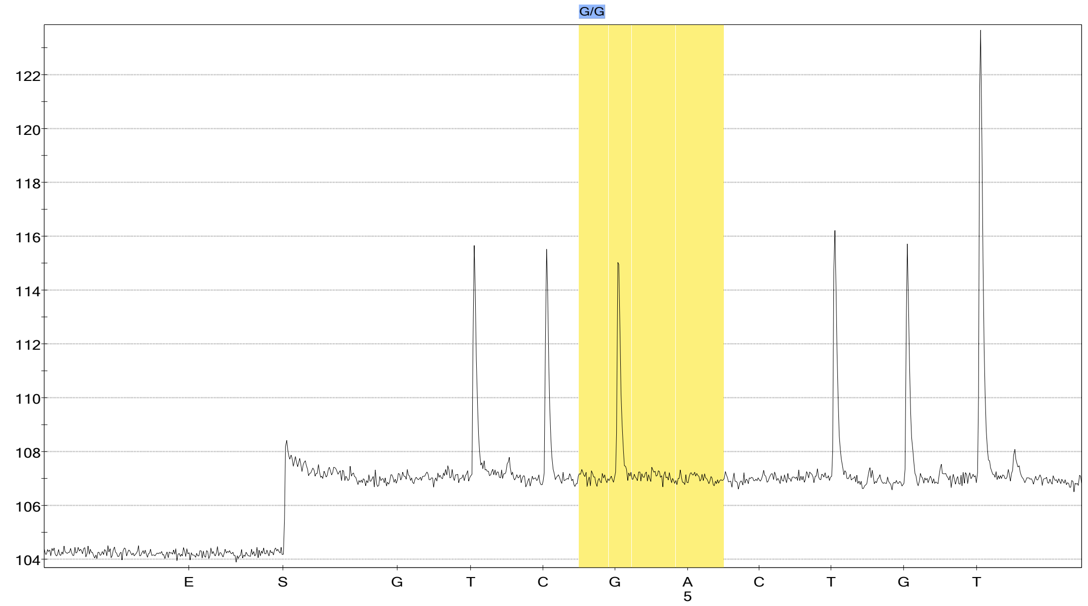
(f)


G/A
130
128
126
124
122
120
118
116
114
112
110
108
106
104
E
S
G
T
C
G
A
5
C
T
G
T

(g)


G/A
140
130
120
110
E
S
G
T
C
G
A
5
C
T
G
T

(h)


G/G
122
120
118
116
114
112
110
108
106
104
E
S
G
T
C
G
A
5
C
T
G
T

(i)

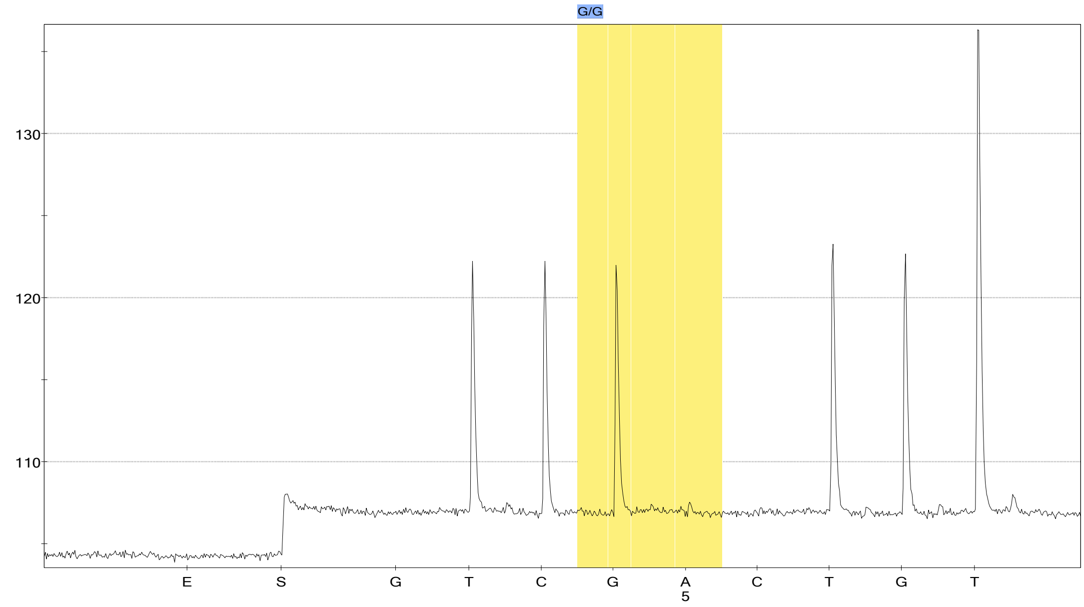


Fig. S1 Results of Gga_rs16172722 pyrosequencing in different breeds. (a) Crossed population, F1 generation -♂-D328, black skin [G/A]; (b) crossed population, F1 generation -♀-D310 (Youxima), white skin [G/G]; (c) crossed population, F2 generation -B00793, black skin [G/A]; (d) crossed population, F2 generation -B00791, white skin [G/G]; (e) Silkie, black skin [G/A]; (f) Jinhu Silkie, black skin [G/A]; (g) Kuaida Silkie, black skin [G/A]; (h) Anak chicken, white skin [G/G]; (i) White Recessive chicken, white skin [G/G]. The SNP Gga_rs16172722 was examined in diverse breeds. The individuals with Gga_rs16172722 (G/A) were hyperpigmented and the individuals with Gga_rs16172722 (G/G) were pigmented normally.

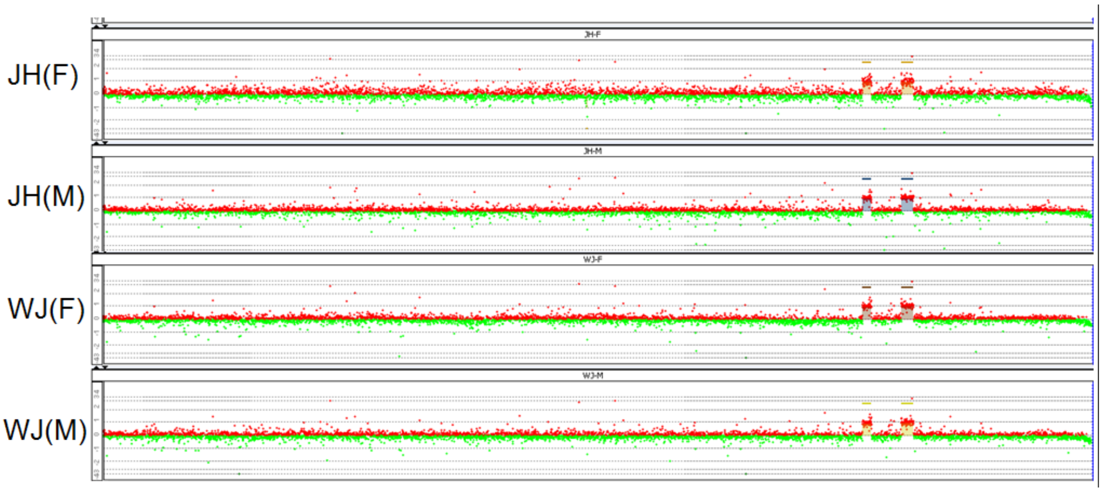


Fig. S2 CNV distribution on chr20 in Silkie and Jinhu chickens. Two CNV regions are uniquely present on chr20 in Silkie (WJ) and Jinhu chickens (JH). Dup-CNV-1 was on chr20: 10718139–10844289 bp (126.15 kb); Dup-CNV-2 was on chr20: 11263937–11435137 bp (171.2 kb).

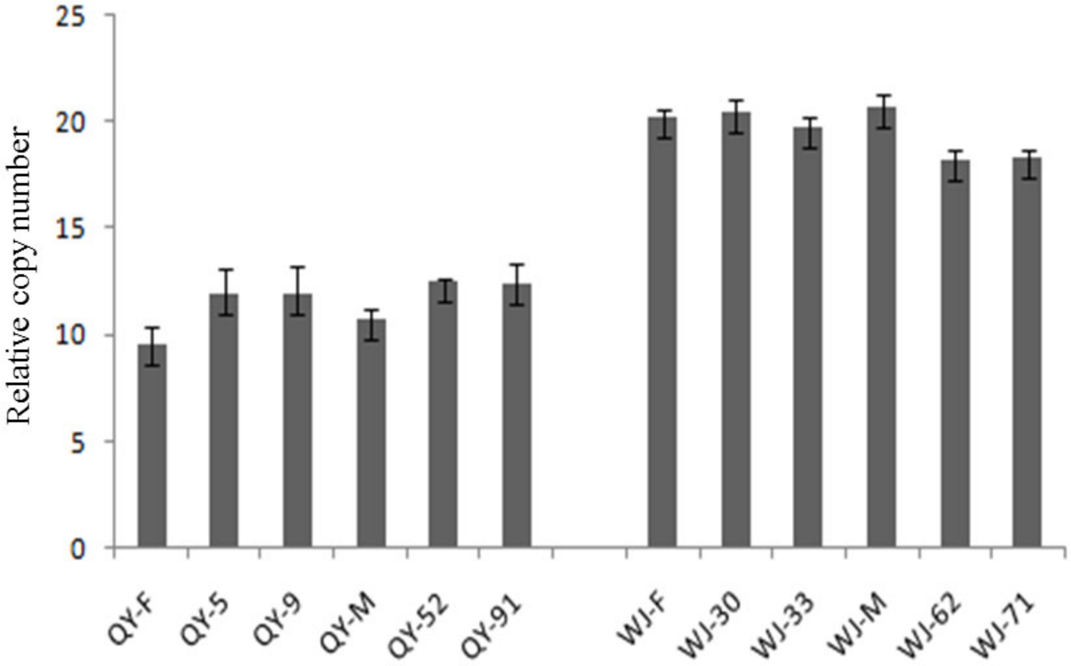


Fig. S3 Results of qPCR analysis of fragments for Dup-CNV-2 detection. Genomic copy number was determined with qPCR in Silkie (WJ) and Qingyuan ma (QY) chickens. Silkie chickens show an estimated copy number of approximately 2 × compared with wild-type individuals. The numbers after the hyphen mean the label when feeding.