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Supplemental Information

Massive genome inversion drives coexistence of divergent morphs in common quails

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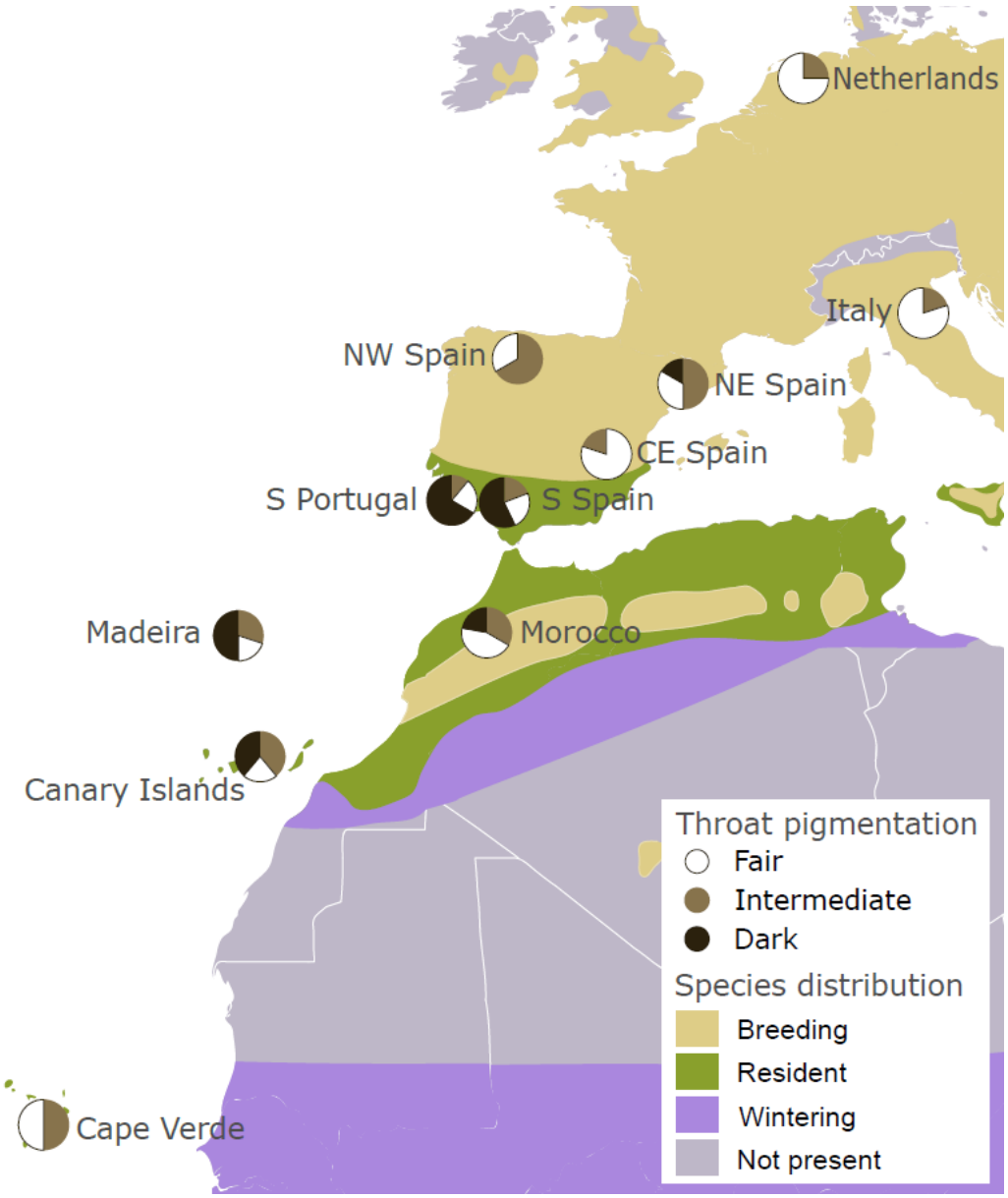

Figure S1. Distribution of the throat pigmentation of 95 quail males. Related to Figure 1E and Data S1A.

List of samples per population and level of pigmentation in Data S1A.

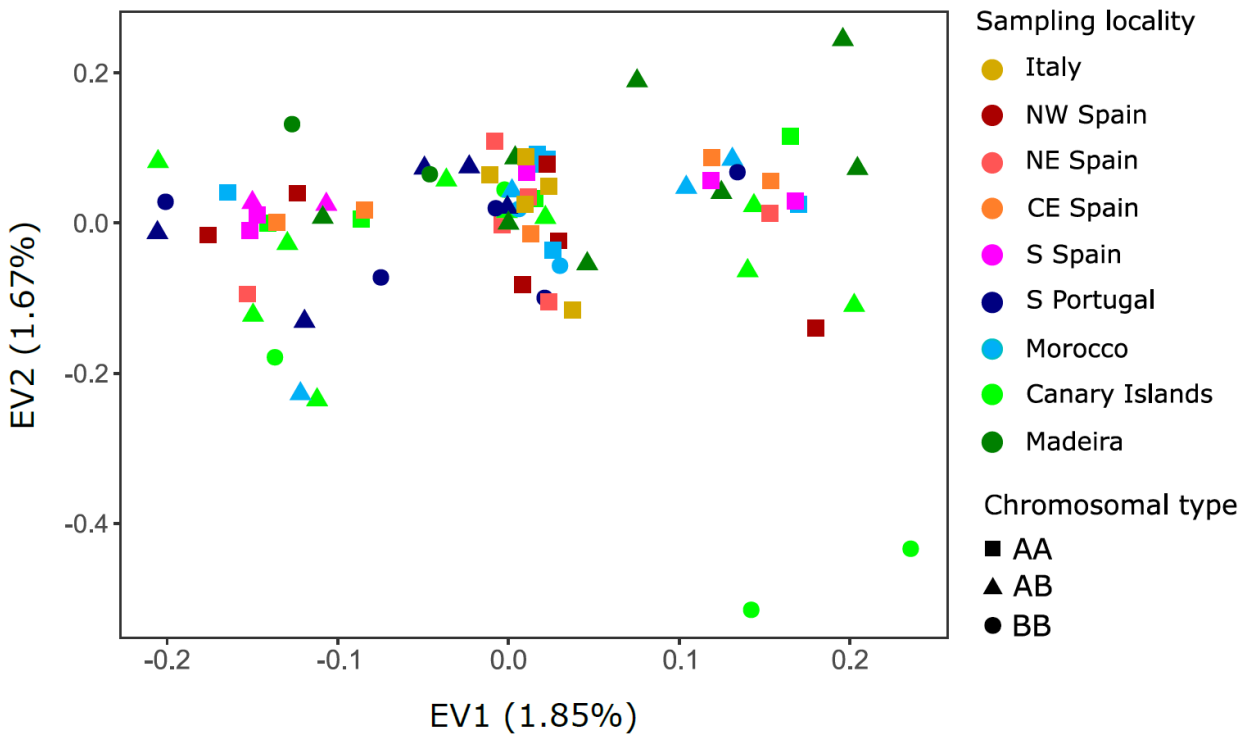

Figure S2. PCA of 80 common quails from 9 populations genotyped at 43,351 SNPs outside the inversion. Related to Figure 1D and Data S1A.

Samples do not form groups according to chromosomal types or localities.

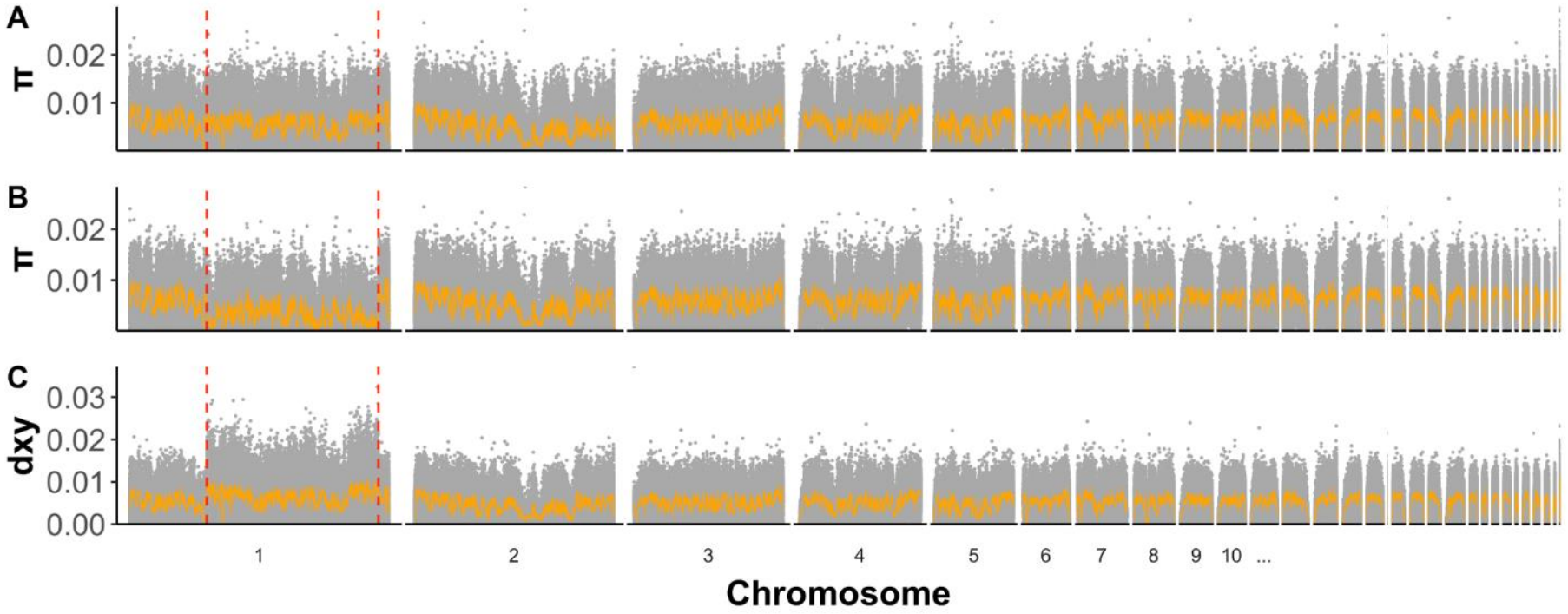

Figure S3. Genomic comparison of common quails with and without a large inversion in chromosome 1. Related to Figure 3.

(**A**) Nucleotide diversity π in 1 Kbp windows in 6 homokaryotype AA common quails. (B) Nucleotide diversity π in 1 Kbp windows in 10 homokaryotype BB common quails. In BB quails, nucleotide diversity is lower within the inversion than elsewhere in the genome and compared to the same region in AA quails. (**C**) Divergence between AA and BB quails measured as d_{xy}. The divergence is elevated across the inversion region compared to elsewhere in the genome. Grey dots represent average values over 1 Kbp windows. Orange lines are 100 Kbp window averages. Red dotted vertical lines indicate location of the inversion.

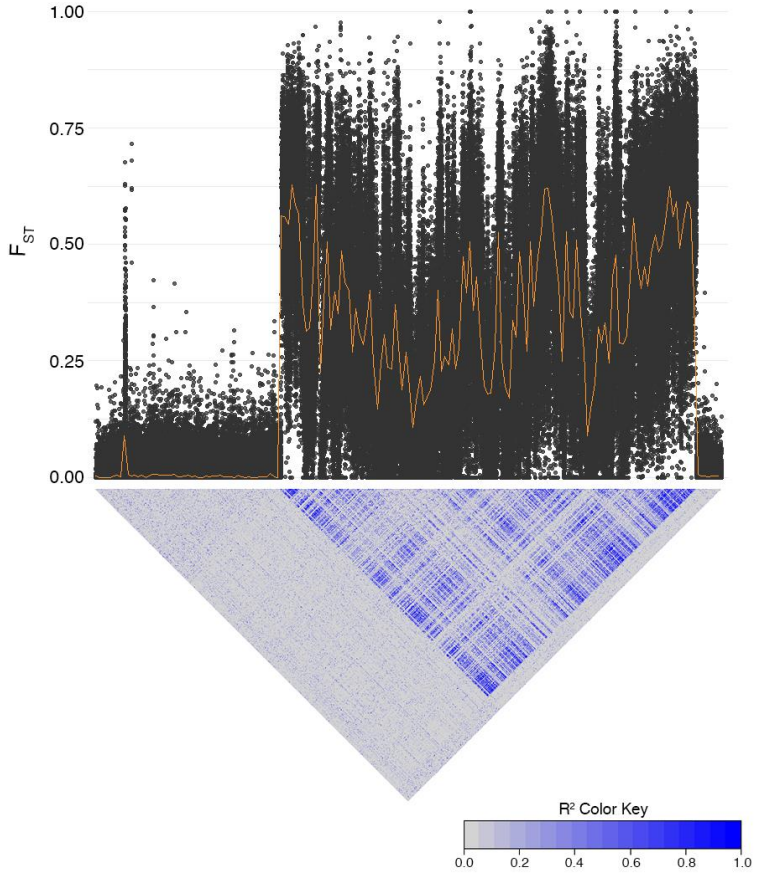

Figure S4. Linkage disequilibrium within chromosome 1. Related to Figure 3.
Weir and Cockerham's F_{ST} along chromosome 1 in 1Kbp windows comparing homokaryotype AA (N= 6) and BB (N= 10) quails. A 115 Mbp region of chromosome 1 shows very high levels of genetic differentiation due to an inversion. The orange line represents F_{ST} values in 1 Mbp windows. Below, linkage disequilibrium (LD) heatmap. Blue regions indicate higher LD, corresponding with the inverted region.

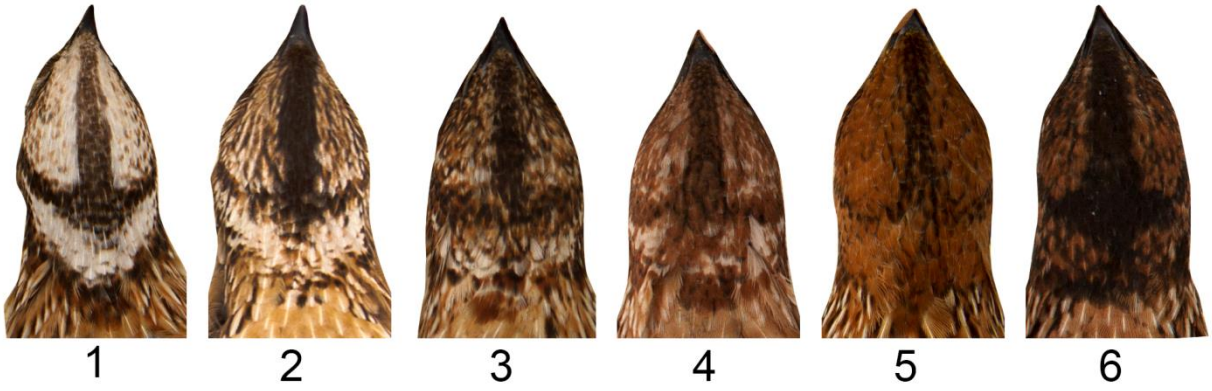

Figure S5. Variability of throat pigmentation. Related to STAR Methods and Data S1A.

Throat pigmentation was categorized into six levels, from pale (level 1) to completely pigmented (level 6), by visual examination of throat pictures and comparing them to a predefined scale.

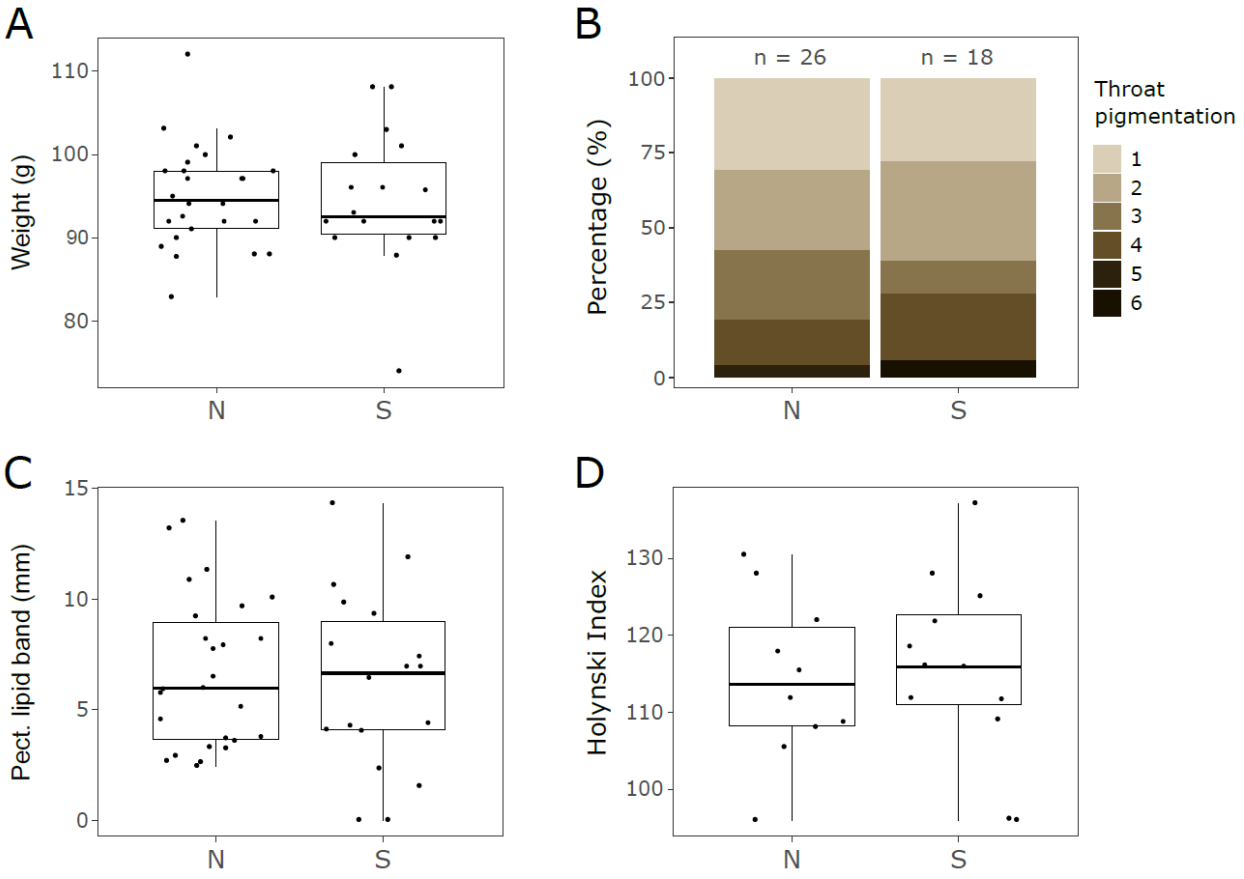

Figure S6. Morphology of AA common quail males in relation to their sampling locality. Related to Figure 4 and Data S1A.

Northern localities (N): Netherlands, Italy, NW Spain, NE Spain and CE Spain. Southern localities (S): S Spain, Morocco, Canary Islands and Cape Verde. (**A**) Body weight. (**B**) Proportion of individuals with different degrees of throat pigmentation. (**C**) Width of the pectoral lipid band. (**D**) Variation in the Holynski index, which measures wing pointedness and is related to flight efficiency.

Sample ID	Sampling locality 1	Sampling locality 2	Karyotype	Average distance (K19-J23), µm
17061401	NE Spain	St. Boi de Lluçanès	AA	24.79
17061402	NE Spain	St. Boi de Lluçanès	AA	20.11
17061600	NE Spain	Alp	AA	20.03
17061609	NE Spain	Alp	AA	22.55
17061614	NE Spain	Alp	AA	31.54
17061615	NE Spain	Alp	AA	23.67
17062601	S Portugal	Aljezur	BB	11.43
17062602	S Portugal	Tavira	BB	13.50
17062603	S Portugal	Tavira	BB	13.53
17062609	S Portugal	Aljezur	BB	10.53
17062613	S Portugal	Aljezur	BB	10.85
17062604	S Portugal	Tavira	AB	28.37
17062606	S Portugal	Aljezur	AB	20.71
17062607	S Portugal	Aljezur	AB	31.02
17062610	S Portugal	Aljezur	AB	20.95

Table S1. Immunofluorescence essays on spermatocytes in meiotic prophase. Related to Figure 2A and STAR Methods.

Average distance between two fluorochromes (K19 and J23) along chromosome 1 of quail spermatocytes. Karyotype composition indicates individuals identified as homokaryotypes without inversion (AA), heterokaryotypes (AB) or homokaryotypes with the inversion (BB) as represented in Figure 2A.

Individual	ID in Fig. 3	Sampling locality 1	Sampling locality 2	Karyotype	Number of mapped reads	Coverage
09051003	Italy	Italy	Monte Brisighella	AA	82,693,872	9.6
08030502	Morocco 1	Morocco	El Gara	AA	70,519,520	8.5
08030503	Morocco 2	Morocco	El Gara	BB	67,394,401	8.2
080410XX	Morocco 3	Morocco	Beni Mellal	BB	90,962,857	10.6
14052112	S Portugal 1	S Portugal	Tavira	BB	85,400,857	10.1
14052312	S Portugal 2	S Portugal	Odiaxere	BB	92,760,611	10.7
14042507	NE Spain	NE Spain	Figuerola	AA	78,214,047	9.6
12052702	NW Spain	NW Spain	Valdesogo	AA	97,266,382	11.6
15051702	S Spain	S Spain	Coronil	AA	114,679,132	13.5
14041210	El Hierro 1	Canary islands	El Hierro	BB	94,729,231	11.4
14041313	El Hierro 2	Canary islands	El Hierro	AA	79,754,285	9.4
15041807	Gran Canaria	Canary islands	Gran Canaria	BB	75,682,609	8.7
14040907	Tenerife 1	Canary islands	Tenerife	BB	77,717,165	9.3
14040910	Tenerife 2	Canary islands	Tenerife	BB	91,084,220	10.6
15061003	Madeira 1	Madeira	Madeira	BB	76,739,862	9.3
15061103	Madeira 2	Madeira	Madeira	BB	87,358,186	10.0

Table S2. Whole genome resequencing of common quails. Related to Figure 3 and STAR Methods.

Homokaryotype AA and BB quails, as identified by genotyping-by-sequencing, resequenced.

		RAB-38	TYR					
Individual	**Kar.**	**168386797**	**168000480**	**168000490**	**168023081**	**168032000**	**168043879**	**168044032**
9051003	AA	Glu	Val	Leu/Phe	Gly	Arg	Thr	Leu
14042507	AA	Glu	Val	Leu/Phe	Gly	Arg	Thr	Leu
12052702	AA	Glu	Val	Leu	Gly	Arg	Thr	Leu
15051702	AA	Glu	Val/Leu	Leu	Gly	Arg	Thr	Leu
14041313	AA	Glu	Val/Leu	Leu	Gly	Arg	Thr	Leu
8030502	AA	Glu	Val	Leu	Gly	Arg	Thr	Leu
15061103	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
15061003	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
14052112	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
14041210	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
080410XX	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
14040910	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
8030503	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
14040907	BB	Lys	Leu	Leu	Ser	Gln	Ile	Gln
15041807	BB	Lys	Leu	Leu	Ser	-	Ile	Gln
14052312	BB	Lys	Leu	Leu	Ser	Gln	Ile	Leu/Gln

Table S3. Nonsynonymous differences in RAB-38 and TYR. Related to STAR Methods.

Nonsynonymous changes in RAB-38 and TYR genes in homokaryotype common quails. The position along the reference genome of a Japanese quail is indicated for each nonsynonymous change, and the corresponding aminoacid is indicated. For heterozygous positions two aminoacids are indicated.