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Combined QTL and selective sweep mappings with coding SNP annotation and *cis*-eQTL analysis revealed *PARK2* and *JAG2* as new candidate genes for adiposity regulation

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All types of SNP	SNP		Genes
	N	%	N
Intergenic	4513004	48.68	-
Regulatory regions	776080	8.37	17352
Intronic	3873604	41.78	14087
Coding - Synonymous	65276	0.70	11905
Coding - Non Synonymous	43410	0.47	10676

Coding SNP	SNP		Genes
	N	%	N
Synonymous	65276	59.45	11905
Missense	27711	25.24	8214
Initiator or stop codon	495	0.45	461
Splicing site	16286	14.83	7155
Mature mi-RNA	34	0.03	30

Figure S1 Annotation of the 9.4 million SNPs identified in the two lines using whole-genome re-sequencing.

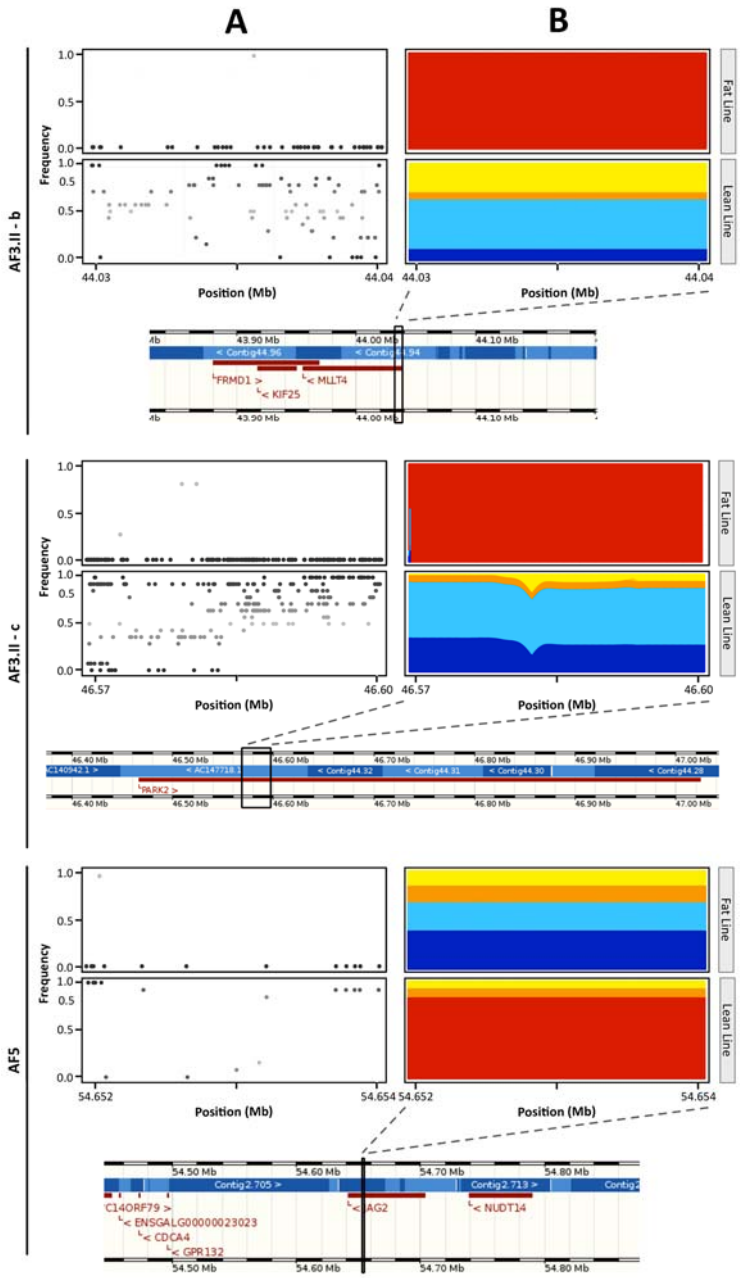

Figure S2 Allelic and haplotypic cluster frequencies in each sweep underlying QTLs.

(A) Allelic and (B) haplotypic cluster frequencies for both chicken lines in each selective sweep underlying QTL for abdominal fat weight (AF3.I, AF3.II, AF5). In A, the reference allele used for the SNP frequency calculation is arbitrary. In B, the difference in color along the Y-axis gives the frequencies of each haplotype cluster. The difference in color along the X-axis has no meaning. Almost fixed clusters are colored red. Under each graph, a genomic map gives the position of the sweep (in a black box) along the genome, and highlights genes inside or around the sweep (red).

Table S1 Description of primers used for SNP validations by Sanger re-sequencing.

ID	Sequence	Targeted strand	Start Position[1]	Length	Tm (°C)
JAG2-Fwd1	ACCAGCAGATTCCAGTGCCAC	+	1	20	64
JAG2-Fwd2	TCAGTATCTCATGTCAAGTGAC	+	411	22	58
JAG2-Fwd3	AGTACAAGAAATGCATGGTTCC	+	844	22	59
JAG2-Fwd4	ACAGTTCTTCTGGTTGTTAAGG	+	1271	22	59
JAG2-Fwd5	TGCTTCTCAGTCTTTCTTTCAC	+	1735	22	59
JAG2-Rev1	GCCCCACTAAAACATGAGGG	-	1	20	59
JAG2-Rev2	AAGCTAACTCCTTAACAACCAG	-	517	22	58
JAG2-Rev3	TGGCTTACTGTAAAGCATCAACTG	-	930	24	62
JAG2-Rev4	AATGTCTGGTCATAAGTAGCAG	-	1333	22	58
JAG2-Rev5	CAATCAAGCAATTGATCGTG	-	1759	20	56

[1] Relatively to the 3' end of the targeted PCR amplicon.

Tables S2 Description of primers used for RT-qPCR.

ID	Species	Sequence (5' -> 3')	Length	Tm (°C)
GG-JAG2-F	*Gallus gallus*	AAATGCAATCACCAAGCGGC	20	65
GG-JAG2-R	*Gallus gallus*	ACCGCACAAAGAATTGGAACC	21	65
GG-PARK2-F	*Gallus gallus*	AGCACACCCAACAACTGACA	20	60
GG-PARK2-R	*Gallus gallus*	GAGTCTGGACAGCCAGCTAC	20	58
GG-MLLT4-F	*Gallus gallus*	ACTGCCACAACTCAGGATGT	20	58
GG-MLLT4-R	*Gallus gallus*	TTCAGGGCCATTACTCTGAGC	21	60
GG-GAPDH-F	*Gallus gallus*	GCTAAGGCTGTGGGGAAAGT	20	61
GG-GAPDH-R	*Gallus gallus*	TCAGCAGCAGCCTTCACTAC	20	60
MM-PARK2-F	*Mus musculus*	ATGAATCACAGCCTGCATTGTG	22	62
MM-PARK2-R	*Mus musculus*	TACCACCACACACACAGACTTC	22	60
MM-HPRT-F	*Mus musculus*	TGGCCATCTGCCTAGTAAAGC	21	62
MM-HPRT-R	*Mus musculus*	GGACGCAGCAACTGACATTTC	21	63

Table S3 Description of primers used for pyro-sequencing-based allelic imbalance analyses.

Chromosome	SNP position	Forward primer	Reverse primer	Sequencing primer
3	46581638	[BTN]--GTGCAGCTAGTTACAACAG	CCTTGCCAAAGTGAGTGTT	TTACATTCATTGCATCG
3	46581695	[BTN]--GTGCAGCTAGTTACAACAG	CCTTGCCAAAGTGAGTGTT	ATTCTTGCAAAAAACATAAA

[BTN]-- Biotinylated on 5' end.