Additional analyses:

Table S1 shows the results from QTL Express at the best position of a full parent-of-origin model [2] or that of a reduced model [4] (Table 2 of manuscript). Significance of the parent-of-origin effect was tested in two ways: an *F*-test of full versus Mendelian as described in Section 2 of the article; a *t*-test on the significance of *i* [2] using the estimate of *i* and its standard error. For both tests we used tabulated *P* values.

For five of the seven parent-of-origin specific QTL, the best position using the full model [2] of QTL Express is within 10 cM of our best QTL position using reduced models with uni-parental expression [4] (Table 1). It shows furthermore that at all QTL positions from Table 2 of the article, the test for imprinting, based on either variance or size of *i*, is significant. The lower part of Table S2 illustrates that inclusion of the grand-dam effect does not affect the significance of the imprinting effects (compare with Table 3 of article).

We subsequently re-analysed our best QTL positions using GENSTAT, as described under Section 2.vii (Additional simulations and analyses). This way we could evaluate the effect of fitting fixed effects

Table S1. *Results for a full imprinting model in QTL Express*

Trait	Chr.	Best QTL from full model [2]			Best QTL from Table 2		
		Position	F_{imp}[a]	t_i[b]	Position	F_{imp}[a]	t_i[b]
AFE	1	1	0·47	−0·69	204	4·74*	−2·18*
BW40	1	294	5·08*	2·25*	239	6·32*	2·51*
HU40	1	117	6·68*	−2·58*	121	6·52*	−2·55*
FI40	1	332	8·83**	2·96**	338	8·07**	2·85**
FI40	36	8	4·27*	2·07*	13	5·19*	2·28*
EWb	3	230	6·02*	2·45**	233	5·77*	2·40*
ENa	30	1	10·19**	−3·2**	1	10·19**	−3·2**
Including grand-dam effect							
AFE	1	1	0·47	−0·68	204	3·83*	−1·95*
HU40	1	121	6·02*	−2·45*	121	6·02*	−2·45*
EWb	3	229	4·32*	2·08*	233	3·97*	1·99*

Hatch fitted as fixed effect in all analyses.
[a] *F*-test of full [2] versus Mendelian [1] model at the position of the QTL.
[b] *t*-test whether *i* [2] is significantly different from zero.
*, ** indicate tabulated $P < 0.05$ and 0.01, respectively.

Table S2. *Results of full and reduced imprinting models using GENSTAT and QTL Express derived line-origin probabilities*

Trait	GGA	Position	*F* ratios from full model[a]			Uni-parental model[b]		
			Mat	Pat	d	*F*	Effect	SE
AFE	1	204	0·18	**12·61**	0·86	12·7	−2·15	0·6
BW40	1	239	**13·82**	0·06	0·20	13·9	−67	18
HU40	1	121	**11·7**	0·01	0·05	10·35	1·6	0·5
FI40	1	338	**11·78**	0·05	0·45	11·84	−4·1	1·2
FI40	36	13	**11·54**	0·05	0·45	11·6	−3·05	0·90
EWb	3	233	0·0	**10·39**	0·23	10·38	1·41	0·43
ENa	30	1	0·1	**17·16**	0·2	17·15	−5·3	1·28
Including grand-dam effect								
AFE	1	204	0·07	**9·23**	2·32	9·83	−1·87	0·6
HU40	1	121	**10·25**	0·02	0·05	10·32	16·2	5·05
EWb	3	230	0·22	**9·24**	0·2	9·50	1·34	0·43

[a] Partial *F* ratio for adding an effect to the model, which already contains the other two effects. Mat, maternal; Pat, paternal; d, dominance. The inferred genetic models following parent-of-origin tests are in bold.
[b] Estimates from a model fitting only the inferred uni-parental effect.

simultaneously as well as corroborating the results obtained with custom-written software.

Table S2 is very similar to Table 2 of the article, indicating that we can verify the uni-parentally expressed QTL independently from our custom-written software. Table S2 also shows that, for the present results, there is little effect of estimating the fixed effect jointly with the QTL compared with pre-adjusting phenotypes.

Additional simulations:

Table S3 shows the results of 1000 replicates for seven scenarios where an imprinted QTL was simulated. For details on the simulation study see de Koning *et al.* (2002). For smaller QTL effects, the difference in power between the reduced model [4] and the Mendelian and full model, respectively is substantial (Table S3).

Table S3. *Proportion of imprinted QTL detected using a Mendelian model, a full imprinting model, or the correct reduced model*

QTL effect	QTL frequency[a]	Mendelian [1] a + d	Maternal [4] Mat	Full [3] or [2] Mat + Pat + d (a + d + i)
1	Fixed	1·00	1·00	1·00
0·5	Fixed	0·99	1·00	1·00
0·25	Fixed	0·50	0·90	0·78
0·15	Fixed	0·20	0·46	0·30
0·5	0·80/0·20	0·62	0·93	0·85
0·25	0·80/0·20	0·20	0·46	0·31
0·15	0·80/0·20	0·10	0·20	0·12

Detection is defined as proportion of analyses where the test statistic exceeded an empirical chromosome-wide 5% threshold.
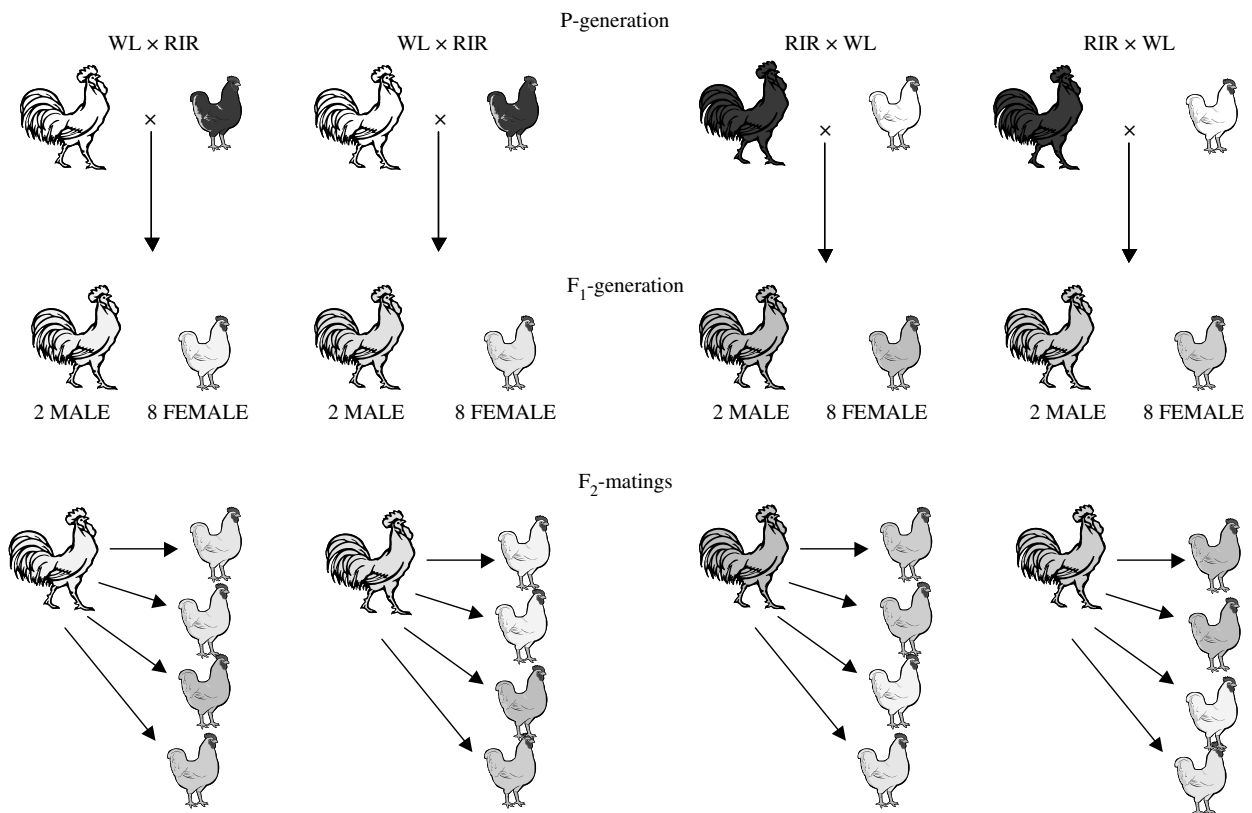[a] QTL allele frequency in founder lines.

Fig. S1. Mating design of experimental chicken cross. Parental lines are Rhode Island Red (RIR) and White Leghorn (WL).