

Table S1. Statistically suggestive independent signals within each QTL identified as nominally significant ($p < 0.05$) in the forward-selection procedure. For each QTL, Model 1 was first fitted for all markers and the most significant marker was selected and added as a covariate before refitting model 1 again. This procedure, selecting the most significant marker as a covariate and refitting Model 1, was repeated until no markers within the QTL reached the nominal significance threshold. QTL that were selected at 20% FDR in the following backward-elimination procedure (Table 2 in main manuscript) are highlighted in bold italics.

GGA ^a	QTL ^b	Position ^c (bp)	Marker ^d	$a \pm SE^e$	Sign ^f	p_{HWS}^g	p_{LWS}^h	MAF ⁱ F_2-F_8
1	Growth1	173 709 608	rs14916997	-36.6 ± 5.5	3.6×10^{-11}	0.11	0.82	0.48
		179 613 655	rs313927704	41.6 ± 12.2	6.5×10^{-4}	0.30	0.04	0.05
		170 637 618	rs13968052	19.1 ± 6.6	3.8×10^{-3}	0.35	0.07	0.21
		176 383 356	rs13975251	19.7 ± 7.7	1.1×10^{-2}	0.43	0.09	0.12
		178 029 363	rs317567034	-31.6 ± 11.6	6.4×10^{-3}	0.20	0.02	0.05
		179 806 129	rs314200699	28.8 ± 12.2	1.8×10^{-2}	0.04	0.14	0.05
		169 810 898	rs15487296	161.7 ± 78.5	4.0×10^{-2}	0.00	0.34	0.00
2	Growth2	64 317 336	rs14194723	-101.5 ± 15.9	1.5×10^{-10}	0.04	0.04	0.03
		62 837 662	rs14192893	458.6 ± 138.1	9.0×10^{-4}	0.02	0.00	0.00
		59 778 572	rs316345242	-28.7 ± 9.2	1.8×10^{-3}	0.20	0.02	0.09
		56 720 515	rs14185295	15.3 ± 5.5	5.2×10^{-3}	0.46	0.14	0.39
		54 865 875	rs14183473	57.4 ± 20.3	4.7×10^{-3}	0.00	0.30	0.02
		57 198 629	rs14185836	-14.1 ± 5.4	9.7×10^{-3}	0.41	0.25	0.39
		65 460 002	rs14196021	14.4 ± 6.0	1.7×10^{-2}	0.43	0.11	0.25
2	Growth3	55 330 630	rs15100427	13.7 ± 6.4	3.2×10^{-2}	0.37	0.34	0.21
		62 639 245	rs15107150	-74.8 ± 36.2	3.9×10^{-2}	0.11	0.00	0.00
		130 133 780	rs14248248	20.2 ± 6.5	1.9×10^{-3}	0.07	0.57	0.21
2	Growth3	130 592 117	rs16133110	-62.2 ± 25.4	1.4×10^{-2}	0.00	0.11	0.01
		126 000 254	rs16120360	13.8 ± 6.1	2.3×10^{-2}	0.54	0.18	0.28
3	Growth4	37 287 334	rs316425755	-32.6 ± 6.4	2.9×10^{-7}	0.26	0.38	0.23
		26 215 175	rs14328509	-21.8 ± 5.4	5.1×10^{-5}	0.26	0.79	0.45
		28 981 759	rs313368484	92.5 ± 24.7	1.8×10^{-4}	0.02	0.16	0.01
		36 103 180	rs13723817	26.3 ± 6.8	1.0×10^{-4}	0.02	0.55	0.18
		57 624 596	rs14363139	-18.0 ± 5.2	5.7×10^{-4}	0.13	0.77	0.50
		61 227 711	rs16284878	-34.6 ± 11.0	1.6×10^{-3}	0.59	0.09	0.06
		47 729 342	rs316384373	21.9 ± 6.9	1.6×10^{-3}	0.04	0.34	0.16
		53 589 855	rs14359071	34.7 ± 11.9	3.5×10^{-3}	0.37	0.27	0.05
		60 099 912	rs14364587	-33.2 ± 11.2	3.0×10^{-3}	0.57	0.00	0.06
		39 139 081	rs15468467	-16.6 ± 6.4	9.2×10^{-3}	0.15	0.38	0.21
		33 743 569	rs314044798	15.6 ± 5.0	1.9×10^{-3}	0.09	0.55	0.38
		40 789 962	rs16256006	-53.8 ± 20.0	7.2×10^{-3}	0.04	0.00	0.01
		38 049 506	rs14341458	72.7 ± 26.2	5.6×10^{-3}	0.09	0.00	0.01
		36 036 392	rs14339632	29.3 ± 10.7	6.1×10^{-3}	0.00	0.11	0.05
		53 236 895	rs13570951	-17.9 ± 7.1	1.2×10^{-2}	0.52	0.05	0.10
		49 677 389	rs15350215	55.0 ± 21.0	8.9×10^{-3}	0.17	0.00	0.01
		24 558 483	rs14326932	-180.3 ± 75.5	1.7×10^{-2}	0.00	0.20	0.00
52 685 153	rs13570803	14.0 ± 5.8	1.7×10^{-2}	0.33	0.68	0.20		
61 496 004	rs315203852	24.7 ± 10.3	1.6×10^{-2}	0.57	0.00	0.06		
25 074 560	rs14327473	41.5 ± 19.5	3.3×10^{-2}	0.22	0.11	0.02		
50 259 236	rs14356142	-46.7 ± 22.5	3.8×10^{-2}	0.00	0.16	0.01		
4	Growth6	13 511 203	rs15500313	25.4 ± 5.5	3.3×10^{-6}	0.91	0.13	0.46
		10 914 312	rs14428120	17.3 ± 5.3	1.1×10^{-3}	0.07	0.84	0.43

		2 392 397	rs14419462	23.4 ± 8.1	3.8 × 10⁻³	0.35	0.05	0.13
		1 379 849	rs314301286	-42.3 ± 13.3	1.5 × 10 ⁻³	0.04	0.07	0.04
		3 589 044	rs10732133	-36.6 ± 11.1	9.4 × 10 ⁻⁴	0.28	0.04	0.06
		4 908 910	rs14422558	-151.2 ± 55.9	6.9 × 10 ⁻³	0.00	0.11	0.00
		11 693 052	rs314301286	37.0 ± 14.8	1.3 × 10 ⁻²	0.07	0.18	0.03
		11 345 880	rs14428501	-22.5 ± 9.2	1.4 × 10 ⁻²	0.02	0.34	0.09
		2 850 506	rs14420072	49.5 ± 22.0	2.5 × 10 ⁻²	0.00	0.09	0.01
4	Growth7	88 325 118	rs15639000	-21.0 ± 5.4	9.9 × 10⁻⁵	0.46	0.52	0.47
		86 755 267	rs14499758	-28.0 ± 6.3	7.9 × 10⁻⁶	0.11	0.43	0.26
		87 755 983	rs318052788	21.0 ± 8.9	1.8 × 10 ⁻²	0.04	0.18	0.09
				-286.6 ± 138.1				
5	Growth8	36 291 277	rs13585490	-32.9 ± 5.3	4.5 × 10⁻¹⁰	0.39	0.54	0.40
		38 774 986	rs315605733	-29.6 ± 6.5	5.8 × 10⁻⁶	0.04	0.27	0.19
		35 299 978	rs16487933	-19.9 ± 6.2	1.2 × 10⁻³	0.65	0.25	0.24
		36 426 195	rs15697504	-49.3 ± 16.0	2.0 × 10 ⁻³	0.22	0.46	0.03
		38 867 279	rs314075508	-12.6 ± 4.9	1.1 × 10⁻²	0.09	0.46	0.48
		36 575 445	rs16489220	-43.4 ± 17.5	1.3 × 10 ⁻²	0.15	0.48	0.02
		34 772 650	rs16487762	14.0 ± 7.0	4.6 × 10⁻²	0.67	0.14	0.17
		33 713 055	rs14530756	11.5 ± 5.3	3.2 × 10⁻²	0.22	0.68	0.35
7	Growth9	23 959 214	rs16596357	-38.9 ± 5.4	7.1 × 10⁻¹³	0.33	0.50	0.34
		26 021 398	rs14618036	80.8 ± 22.6	3.6 × 10 ⁻⁴	0.11	0.00	0.01
		18 544 622	rs14611566	18.3 ± 5.3	5.8 × 10⁻⁴	0.50	0.50	0.46
		33 699 148	rs16610251	67.0 ± 23.0	3.5 × 10 ⁻³	0.24	0.04	0.01
		32 262 733	rs317586448	-15.1 ± 5.2	3.4 × 10⁻³	0.74	0.41	0.44
		27 518 867	rs14619679	32.7 ± 12.1	6.8 × 10 ⁻³	0.09	0.09	0.05
		29 631 963	rs10727581	17.2 ± 6.2	5.4 × 10⁻³	0.39	0.07	0.22
		29 999 307	rs14622731	-30.3 ± 10.6	4.3 × 10 ⁻³	0.26	0.00	0.06
		23 134 876	rs312633887	-30.8 ± 12.0	1.0 × 10 ⁻²	0.41	0.18	0.05
		35 390 789	rs317022486	-25.2 ± 10.0	1.2 × 10 ⁻²	0.15	0.30	0.07
		14 071 039	rs16088281	34.6 ± 15.8	2.9 × 10 ⁻²	0.02	0.09	0.03
		25 726 731	rs317769956	-22.5 ± 9.0	1.2 × 10 ⁻²	0.00	0.34	0.09
		24 549 929	rs14616465	-101.8 ± 50.3	4.3 × 10 ⁻²	0.00	0.11	0.00
20	Growth12	10 667 729	rs16172598	26.3 ± 5.4	1.1 × 10⁻⁶	0.67	0.11	0.33
		10 965 403	rs16173231	346.1 ± 139.1	1.3 × 10 ⁻²	0.04	0.00	0.00
		8 814 245	rs314843162	21.9 ± 8.8	1.3 × 10 ⁻²	0.24	0.11	0.09
		13 427 530	rs16176151	-13.9 ± 5.2	7.0 × 10⁻³	0.35	0.48	0.48
		7 881 700	rs312541071	-73.1 ± 29.7	1.4 × 10 ⁻²	0.20	0.07	0.01
		11 389 861	rs13634923	19.2 ± 8.3	2.1 × 10 ⁻²	0.24	0.20	0.11
		10 165 171	rs14278292	-12.7 ± 5.8	2.9 × 10⁻²	0.50	0.13	0.26
		9 302 754	rs14277526	14.1 ± 6.1	2.0 × 10⁻²	0.39	0.05	0.23

^aGallus Gallus Autosome; ^bQTL name as in (Jacobsson et al. 2005); ^cBase pair position according to *Chicken* genome assembly (galGal3) of May 2006; ^dSNP name as in NCBI dbSNP; ^eAdditive effect ± Standard Error calculated within each QTL as described in model 1; ^fSignificance of the estimated additive genetic effect from fitting model 1 where the allelicoding is based on the major/minor allele-frequencies and not the line origin of the alleles as in Table 2; ^gFrequency of the allele corresponding to the estimated effect, calculated from all founder birds which originates from the high-weight selection line; ^hFrequency of the allele corresponding to the estimated effect, calculated from all founder birds which originates from the low-weight selection line; ⁱMinor allele frequency calculated from all 1348 birds, AIL generation F₂-F₈, included in the study.