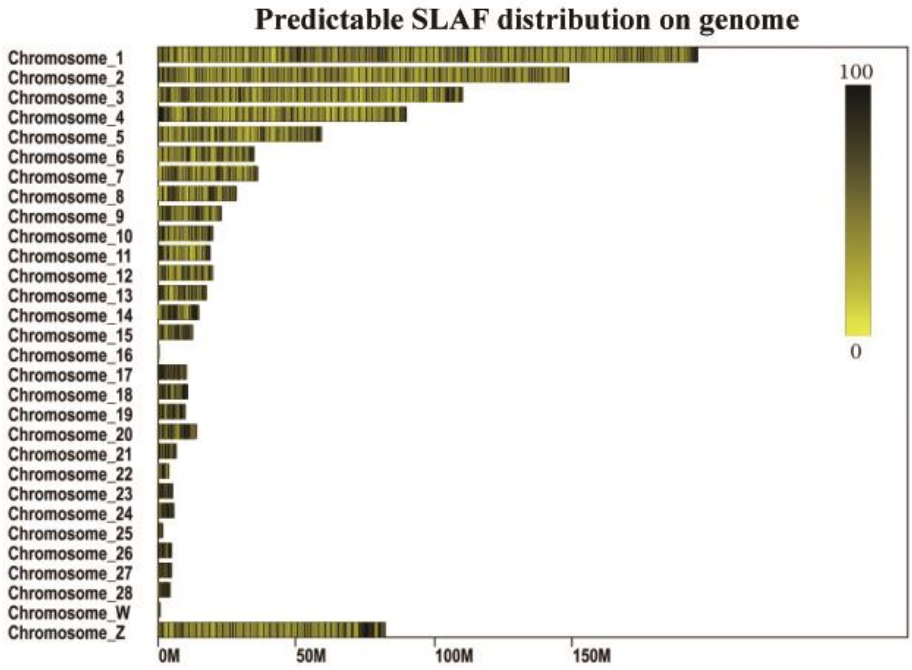


Figure S1. Predictable SLAF distribution on genome. Reference Gallus_gallus-4.0 is digested by restriction enzyme HaeIII in silico. The SLAF density across each genome is indicated by the color gradient of yellow to black, from low to high.

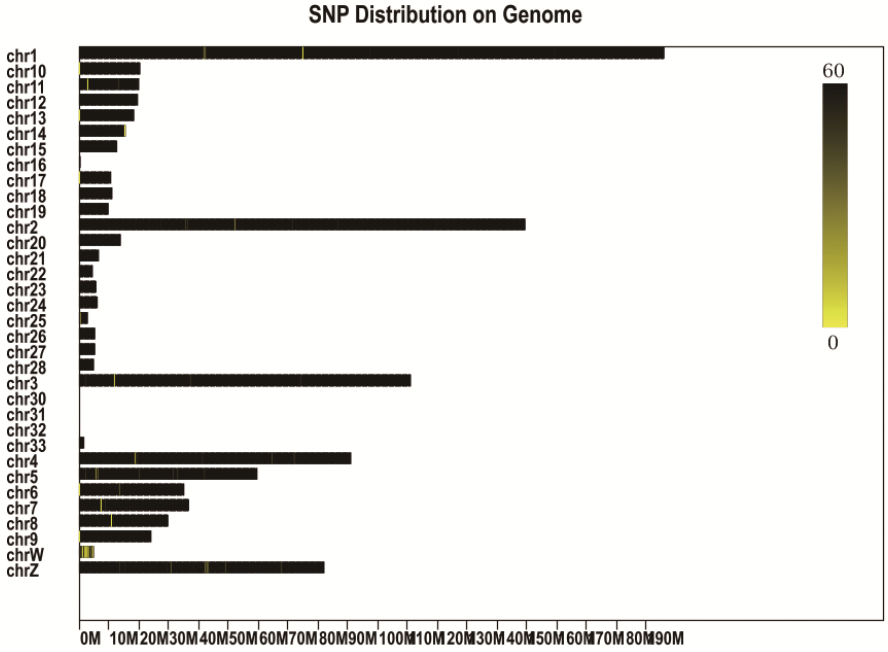


Figure S2. SNP distribution on genome. Each SNP of each genome is projected to its position, along with the SNP density indicated by the color gradient of yellow to black, from low to high.

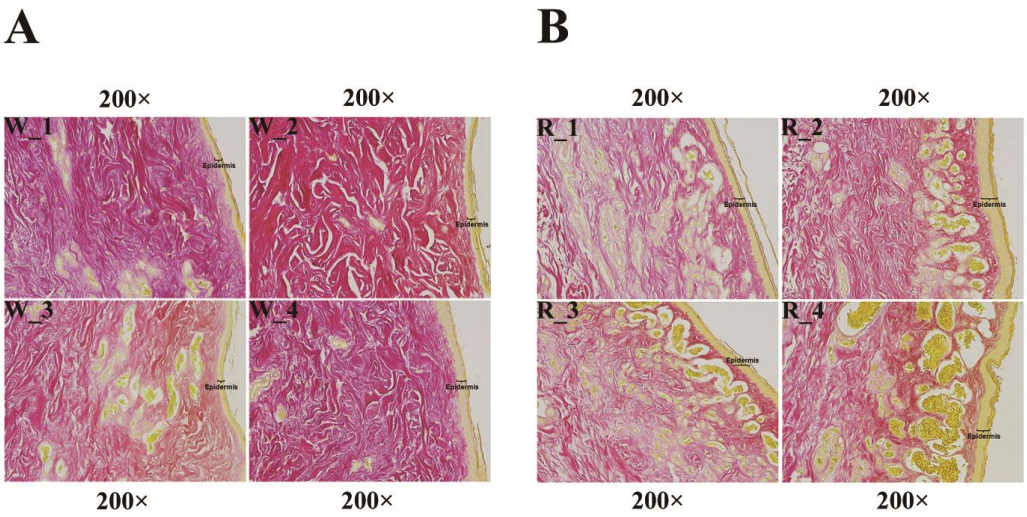


Figure S3. Masson-Fontana staining on white earlobe tissues (A) and red earlobe tissues (B). White earlobes and red earlobes separately include four indivisuals, including W_1, W_2, W_3, W_4, R_1, R_2, R_3 and R_4, respectively. Melanin and cytoplasm granules of argentaffin cells are both stained to black, collagenous fiber is stained to red, and muscle fiber and erythrocyte are both stained to yellow. All sections above are image-captured under 200× lens.

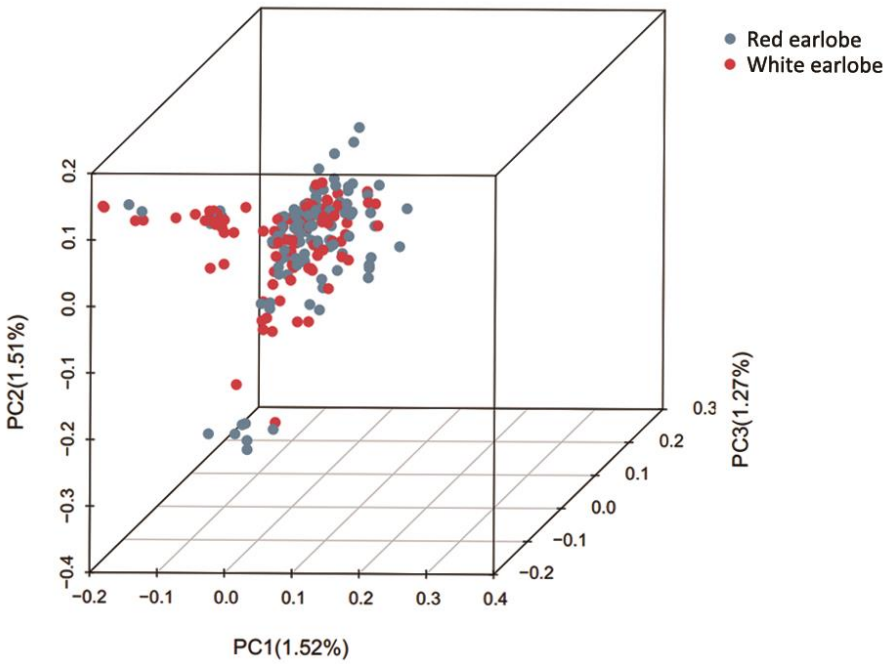


Figure S4. Principal Component Analysis (PCA) on GWAS population. The red dot in plot represents the white earlobes and the blue dot represents the red earlobes. PC1, PC2 and PC3 indicate the first principal component, the second principal component and the third component, respectively.

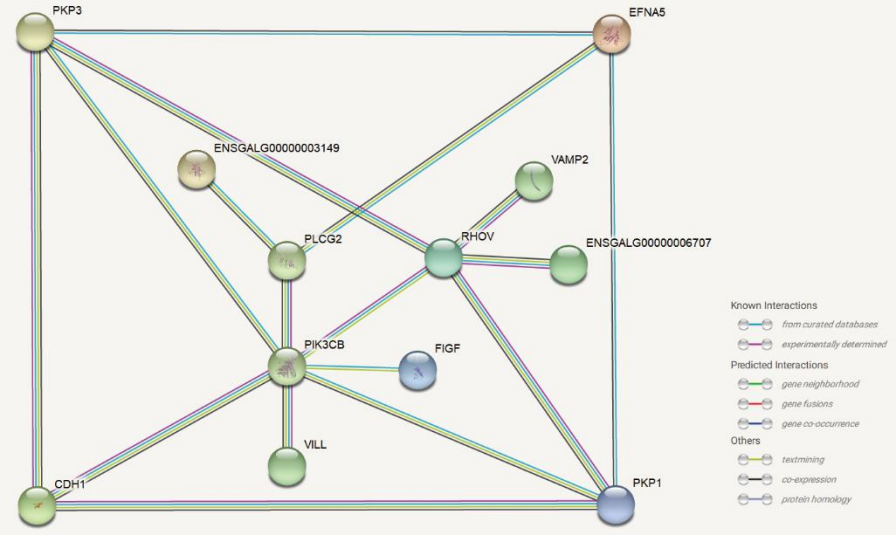


Figure S5. Protein-Protein Interaction network analysis on DEGs and significantly associated genes identified in this study. Known interactions include light blue and purple lines, separately supported by the curated databases and the experimentally determined. Predicted interactions include green and red lines, separately supported by the gene neighborhood and gene fusions. Other interactions include textmining (light green line), co-expression (black line) and protein homology (grey line).

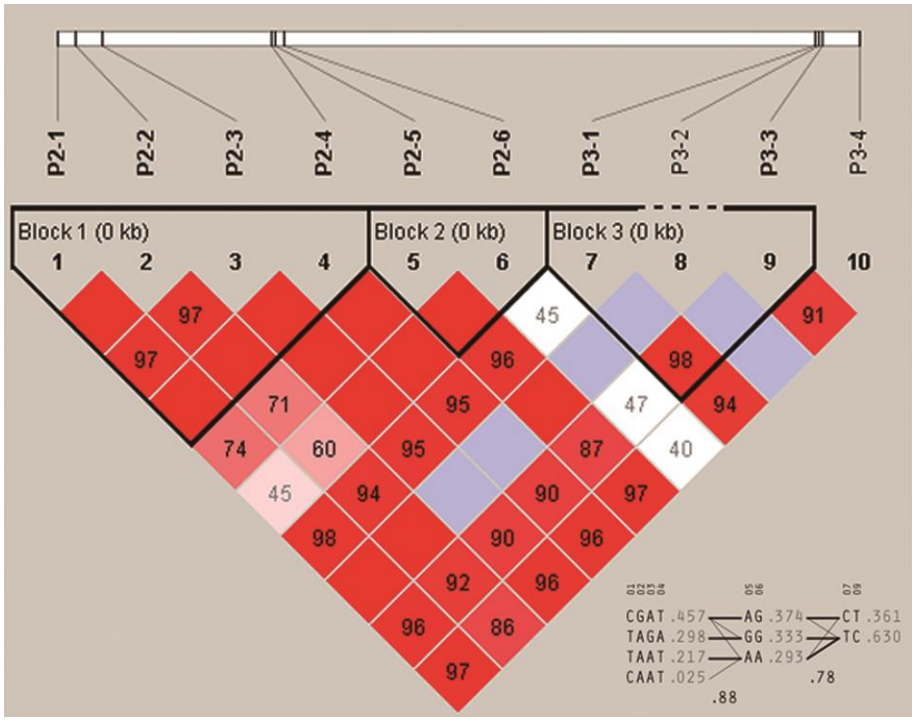


Figure S6. Linkage disequilibrium analysis on the proximal 5` flanking region (Chr.9_14,189,720 to 265 Chr.9_ 14,191,557) of *TP63*. Block 1 consists of 4 SNP sites (P2-1, P2-2, P2-3 and P2-4), including haplotypes C-G-A-T, T-A-G-A, T-A-A-T and C-A-A-T. Block 2 consists of 2 SNP sites (P2-5 and P2-6), including haplotypes A-G, G-G and A-A. Block 3 consists of 2 SNP sites (P3-1 and P3-3), including haplotypes C-T and T-C.

Table S1. Distribution of predictable SLAF on each chromosome (Gallus_gallus-4.0).

Chromosome ID	Chromosome length	Expected SLAF number	Average SLAF distance
Chromosome_1	238,100,707	20,163	11,809
Chromosome_2	181,443,565	14,813	12,249
Chromosome_3	134,668,872	11,276	11,943
Chromosome_4	110,001,279	8,931	12,317
Chromosome_5	72,646,263	6,485	11,202
Chromosome_6	42,616,510	4,026	10,585
Chromosome_7	44,193,534	4,077	10,840
Chromosome_8	35,075,866	3,452	10,161
Chromosome_9	28,582,412	2,954	9,676
Chromosome_10	24,277,567	2,571	9,443
Chromosome_11	23,655,712	2,214	10,685
Chromosome_12	24,260,402	2,446	9,918
Chromosome_13	21,654,789	2,439	8,879
Chromosome_14	18,486,771	2,276	8,122
Chromosome_15	15,432,425	1,918	8,046
Chromosome_16	652,654	76	8,588
Chromosome_17	12,746,733	1,896	6,723
Chromosome_18	13,680,380	1,866	7,331
Chromosome_19	12,172,740	1,680	7,246
Chromosome_20	17,439,144	2,266	7,696
Chromosome_21	8,294,619	1,166	7,114
Chromosome_22	4,976,077	617	8,065
Chromosome_23	6,978,338	1,073	6,504
Chromosome_24	7,709,969	1,177	6,551
Chromosome_25	2,671,653	440	6,072
Chromosome_26	6,498,844	1,028	6,322
Chromosome_27	6,351,675	952	6,672
Chromosome_28	5,782,679	855	6,763
Chromosome_W	1,521,897	208	7,317
Chromosome_Z	100,425,924	9,234	10,876
Total	1,223,000,000	114,575	10,674

Table S2. Statistics of developed SLAF markers from each chromosome.

Chromosome ID	SLAF number	Polymorphic SLAF
Chr_1	101,322	74,358
Chr_2	73,012	53,035
Chr_3	54,848	40,419
Chr_4	43,829	32,358
Chr_5	31,812	23,344
Chr_6	19,677	14,922
Chr_7	19,273	14,312
Chr_8	16,633	12,324
Chr_9	14,411	11,121
Chr_10	12,299	9,445
Chr_11	11,208	8,015
Chr_12	12,250	9,423
Chr_13	11,700	9,050
Chr_14	10,712	8,426
Chr_15	9,146	6,970
Chr16	497	282
Chr_17	8,883	7,004
Chr_18	8,729	6,896
Chr_19	8,012	6,253
Chr_20	10,502	7,967
Chr_21	5,476	4,326
Chr_22	2,935	1,765
Chr_23	5,242	4,209
Chr_24	5,364	4,372
Chr_25	2,093	1,622
Chr_26	4,846	3,883
Chr_27	5,115	3,699
Chr_28	4,664	3,667
Chr_30	13	10
Chr_31	54	13
Chr_32	80	64
Chr_33	1,378	1,070
Chr_W	3,668	359
Chr_Z	40,324	22,785
Total	622,443	424,810
Other	62,436	17,042

Table S3. Statistics of SLAF sequencing.

Sample ID	SLAF number	Total depth	Average depth
1	253377	2823388	11.14
2	271912	2517240	9.26
3	239122	1729342	7.23
4	234386	2055342	8.77
5	268804	1861163	6.92
6	252420	2366495	9.38
7	266502	1592509	5.98
8	250500	1510844	6.03
9	218423	1376019	6.3
10	250396	1961428	7.83
11	224475	1482684	6.61
12	242395	1473277	6.08
13	241170	1561066	6.47
14	202341	1213235	6
15	256940	1971090	7.67
16	255134	1644299	6.44
17	264421	1974474	7.47
18	203875	1543865	7.57
19	233158	1856147	7.96
20	245035	1604896	6.55
21	277167	1782698	6.43
22	259146	1963463	7.58
23	237244	1481467	6.24
24	274726	2182205	7.94
25	264852	2081915	7.86
26	249066	1653007	6.64
27	261482	2246654	8.59
28	260882	1811803	6.94
29	264528	1886823	7.13
30	256832	1257702	4.9
31	256768	1574815	6.13
32	231865	2256448	9.73
33	271961	2346263	8.63
34	268834	2371933	8.82
35	229490	2625952	11.44
36	238532	1710507	7.17
37	209283	1193583	5.7
38	248153	2128417	8.58
39	242724	1853361	7.64
40	248798	1777362	7.14
41	227035	1940419	8.55
42	212434	1713698	8.07

43	200617	1515470	7.55
44	202668	2291372	11.31
45	203808	1873562	9.19
46	223361	3233383	14.48
47	221596	1994994	9
48	213740	2530935	11.84
49	205432	1634316	7.96
50	230191	1819382	7.9
51	226983	2303549	10.15
52	195686	1654274	8.45
53	215953	1849368	8.56
54	239025	1836758	7.68
55	210601	1538716	7.31
56	184820	1515244	8.2
57	223443	2094751	9.37
58	213784	1625655	7.6
59	218233	2301811	10.55
60	214687	1759452	8.2
61	229470	1992739	8.68
62	224925	1977777	8.79
63	232341	2130476	9.17
64	236956	1970935	8.32
65	241772	2158951	8.93
66	231878	2017236	8.7
67	248475	2388286	9.61
68	244043	1899465	7.78
69	238780	2734603	11.45
70	210169	2123703	10.1
71	212266	1637791	7.72
72	221496	2034059	9.18
73	224181	2006626	8.95
74	231811	2151010	9.28
75	242899	2061302	8.49
76	254131	2364459	9.3
77	237268	2137168	9.01
78	241149	2374650	9.85
79	240981	2151920	8.93
80	234492	2039742	8.7
81	224374	2085451	9.29
82	175920	2300496	13.08
83	185319	2740368	14.79
84	173739	2477006	14.26
85	157987	1805629	11.43
86	173653	2276602	13.11
87	156031	1991045	12.76

88	205789	2965135	14.41
89	179457	2249783	12.54
90	171240	2077887	12.13
91	177720	2338505	13.16
92	175254	2302212	13.14
93	186550	2283537	12.24
94	162250	1892460	11.66
95	177384	2219542	12.51
96	176563	2356365	13.35
97	172280	2050609	11.9
98	163803	1910688	11.66
99	198228	3267025	16.48
100	185463	2725598	14.7
101	269991	2055497	7.61
102	252253	1767934	7.01
103	259314	2362559	9.11
104	258553	1691349	6.54
105	223182	1545421	6.92
106	243915	1654219	6.78
107	235220	1384576	5.89
108	236935	1831296	7.73
109	247264	1861718	7.53
110	273957	2424506	8.85
111	249899	1937145	7.75
112	271894	1837944	6.76
113	265352	1521918	5.74
114	259419	1754383	6.76
115	266031	1824072	6.86
116	262576	2200489	8.38
117	260396	1667761	6.4
118	261326	1948517	7.46
119	261218	1570563	6.01
120	260591	1388105	5.33
121	235399	2068414	8.79
122	267085	1765247	6.61
123	275283	2104125	7.64
124	277655	2053471	7.4
125	282369	2035871	7.21
126	272770	2010667	7.37
127	282220	2623629	9.3
128	251136	1941862	7.73
129	258246	2490934	9.65
130	193650	3063018	15.82
131	185908	2497369	13.43
132	186105	2914762	15.66

133	171925	2172692	12.64
134	167789	1990677	11.86
135	163785	1979213	12.08
136	165202	1861672	11.27
137	178332	2502328	14.03
138	166755	1857892	11.14
139	162807	2185443	13.42
140	155140	1529838	9.86
141	166447	1855951	11.15
142	172734	1879098	10.88
143	166966	2007730	12.02
144	180106	2055508	11.41
145	171108	1733159	10.13
146	145465	1522393	10.47
147	159221	1731768	10.88
148	157972	1715844	10.86
149	162029	1611425	9.95
150	170300	2288364	13.44
151	158093	1573097	9.95
152	157401	1746163	11.09
153	161350	1860961	11.53
154	183112	2123525	11.6
155	188370	2992366	15.89
156	163209	1982251	12.15
157	180470	2443493	13.54
158	151850	1799771	11.85
159	163462	2075038	12.69
160	155445	1673760	10.77
161	168424	1852902	11
162	163142	1542399	9.45
163	162590	1906513	11.73
164	157333	1816868	11.55
165	171462	2108525	12.3
166	166722	2037189	12.22
167	164944	2109818	12.79
168	159945	2010059	12.57
169	170601	1945579	11.4
170	175362	2166686	12.36
171	184700	2120441	11.48
172	167433	2168199	12.95
173	150670	1776010	11.79
174	167630	2323839	13.86
175	166506	2524138	15.16
176	220130	2155128	9.79
177	178139	2323204	13.04

178	180146	2696737	14.97
179	158816	2070427	13.04
180	242156	2640074	10.9
181	203522	3165945	15.56
182	191018	2502954	13.1
183	151398	2309913	15.26
184	177757	2266156	12.75
185	222136	2124658	9.56
186	181192	3211731	17.73
187	165871	1803671	10.87
188	176137	2452918	13.93
189	171340	2233347	13.03
190	162990	2122928	13.02
191	203320	2572395	12.65
192	179965	2446558	13.59
193	184657	1842732	9.98
194	132117	1491835	11.29
195	182766	2629720	14.39
196	142278	1218742	8.57
197	181402	2539929	14
198	201718	2914390	14.45
199	164943	2015460	12.22
200	152862	1452982	9.51

Samples from 1 to 100 are the chickens with white earlobe color, and 101 to 200 are the chickens with red earlobe color. Besides, Samples from 1 to 30 and 101 to 129 are the male chickens, and the left are the females.

Table S4. Statistics of SNPs identified from 59 samples.

Sample ID	SNP number	Integrity	Heter ratio
1	1,011,916	0.4658	0.1054
2	1,130,673	0.5205	0.1071
3	985,062	0.4534	0.0969
4	918,743	0.4229	0.099
5	1,133,150	0.5216	0.1048
6	1,049,727	0.4832	0.1071
7	1,102,909	0.5077	0.1013
8	1,062,694	0.4892	0.1019
9	907,076	0.4175	0.0967
10	1,041,279	0.4793	0.1044
11	919,866	0.4234	0.0933
12	1,013,703	0.4666	0.1018
13	1,005,444	0.4628	0.0966
14	859,441	0.3956	0.1032
15	1,052,634	0.4845	0.1007
16	1,065,444	0.4904	0.1046
17	1,106,964	0.5095	0.1086
18	848,283	0.3905	0.1011
19	964,815	0.4441	0.1037
20	1,053,768	0.4851	0.106
21	1,148,753	0.5288	0.1022
22	1,054,426	0.4854	0.1006
23	959,517	0.4417	0.0939
24	1,139,655	0.5246	0.1077
25	1,108,465	0.5102	0.1073
26	1,018,794	0.469	0.1015
27	1,066,997	0.4911	0.1027
28	1,070,327	0.4927	0.1006
29	1,088,354	0.501	0.1044
30	1,065,210	0.4903	0.1011
31	990,033	0.4557	0.0955
32	862,602	0.3971	0.1035
33	1,056,656	0.4864	0.1021
34	1,037,445	0.4775	0.1005
35	855,105	0.3936	0.1022
36	902,623	0.4155	0.0968
37	792,039	0.3646	0.0896
38	947,920	0.4363	0.0994
39	924,868	0.4257	0.0972
40	946,488	0.4357	0.0994
41	882,922	0.4064	0.0963
42	819,695	0.3773	0.0931

43	769,139	0.354	0.0897
44	769,884	0.3544	0.0977
45	777,825	0.358	0.0964
46	843,154	0.3881	0.1025
47	850,260	0.3914	0.0955
48	804,093	0.3701	0.0999
49	663,110	0.3052	0.1063
50	896,051	0.4125	0.0912
51	871,878	0.4013	0.0985
52	747,675	0.3442	0.0904
53	830,650	0.3824	0.0945
54	931,857	0.4289	0.0955
55	814,555	0.3749	0.0882
56	704,854	0.3244	0.0906
57	862,831	0.3972	0.0973
58	816,324	0.3758	0.0936
59	841,447	0.3873	0.0963
60	827,584	0.3809	0.0927
61	891,019	0.4101	0.0964
62	862,698	0.3971	0.0973
63	886,795	0.4082	0.0978
64	916,261	0.4218	0.0978
65	940,992	0.4331	0.0974
66	896,183	0.4125	0.097
67	964,246	0.4438	0.0976
68	953,192	0.4388	0.0969
69	901,348	0.4149	0.1043
70	796,591	0.3667	0.0985
71	815,133	0.3752	0.0929
72	847,552	0.3901	0.0955
73	862,511	0.397	0.0959
74	895,027	0.412	0.0969
75	935,787	0.4307	0.1054
76	985,206	0.4535	0.0983
77	917,699	0.4224	0.0952
78	923,717	0.4252	0.1345
79	929,174	0.4277	0.1003
80	902,770	0.4155	0.0983
81	859,553	0.3957	0.0983
82	639,222	0.2942	0.1046
83	679,584	0.3128	0.1181
84	625,985	0.2881	0.1172
85	571,498	0.2631	0.1035
86	628,238	0.2892	0.1085
87	553,532	0.2548	0.1116

88	756,586	0.3483	0.1228
89	649,939	0.2992	0.1057
90	622,399	0.2865	0.1137
91	645,776	0.2973	0.1114
92	633,999	0.2918	0.11
93	679,934	0.313	0.1044
94	586,547	0.27	0.1047
95	648,013	0.2983	0.1056
96	642,012	0.2955	0.1034
97	625,130	0.2877	0.1069
98	586,328	0.2699	0.1094
99	722,601	0.3326	0.1113
100	670,580	0.3087	0.1081
101	1,077,496	0.496	0.1106
102	1,016,654	0.468	0.1021
103	1,052,018	0.4842	0.1045
104	1,054,861	0.4856	0.1
105	932,148	0.4291	0.1014
106	985,788	0.4538	0.097
107	975,941	0.4492	0.0966
108	950,616	0.4376	0.0988
109	1,005,738	0.4629	0.1006
110	1,119,582	0.5153	0.1085
111	1,033,889	0.4759	0.1026
112	1,120,644	0.5158	0.1053
113	1,128,456	0.5194	0.1006
114	1,062,335	0.489	0.1028
115	1,099,107	0.5059	0.1047
116	1,073,213	0.494	0.1061
117	1,072,186	0.4935	0.1
118	1,066,028	0.4907	0.1004
119	1,089,622	0.5016	0.1036
120	1,118,657	0.5149	0.1058
121	989,356	0.4554	0.1084
122	1,111,033	0.5114	0.1035
123	1,131,976	0.5211	0.1045
124	1,157,649	0.5329	0.0993
125	1,163,154	0.5354	0.1072
126	1,121,177	0.5161	0.1019
127	1,164,632	0.5361	0.108
128	1,020,936	0.4699	0.0992
129	1,044,992	0.481	0.1027
130	698,029	0.3213	0.1123
131	673,557	0.31	0.1098
132	675,162	0.3108	0.1108

133	612,165	0.2818	0.1173
134	604,096	0.2781	0.1107
135	592,695	0.2728	0.1047
136	594,692	0.2737	0.11
137	646,700	0.2977	0.1033
138	602,319	0.2772	0.1038
139	584,896	0.2692	0.1084
140	554,542	0.2553	0.1063
141	603,084	0.2776	0.1042
142	619,800	0.2853	0.1126
143	599,504	0.276	0.1095
144	653,744	0.3009	0.1052
145	616,853	0.2839	0.1075
146	522,568	0.2405	0.1047
147	566,797	0.2609	0.1135
148	566,252	0.2606	0.1038
149	580,122	0.267	0.1091
150	612,260	0.2818	0.1114
151	566,551	0.2608	0.1092
152	559,488	0.2575	0.1146
153	574,736	0.2646	0.1115
154	657,317	0.3026	0.1129
155	677,401	0.3118	0.1118
156	586,498	0.27	0.1089
157	656,143	0.302	0.1116
158	544,089	0.2504	0.1074
159	581,691	0.2678	0.1093
160	556,852	0.2563	0.1039
161	598,562	0.2755	0.1154
162	582,313	0.268	0.109
163	581,917	0.2679	0.1107
164	559,684	0.2576	0.1096
165	610,379	0.281	0.1131
166	593,159	0.273	0.1166
167	584,564	0.2691	0.1189
168	567,393	0.2612	0.1102
169	609,142	0.2804	0.112
170	625,714	0.288	0.1157
171	673,697	0.3101	0.1017
172	599,582	0.276	0.1082
173	537,324	0.2473	0.1059
174	601,901	0.2771	0.1119
175	595,144	0.2739	0.1091
176	836,296	0.3849	0.0989
177	645,652	0.2972	0.1065

178	654,141	0.3011	0.1091
179	565,543	0.2603	0.1098
180	943,129	0.4341	0.103
181	737,156	0.3393	0.1108
182	700,544	0.3225	0.1056
183	540,841	0.249	0.1078
184	641,161	0.2951	0.1072
185	852,002	0.3922	0.0999
186	650,194	0.2993	0.1117
187	585,596	0.2696	0.1075
188	637,154	0.2933	0.1086
189	612,742	0.282	0.1068
190	582,596	0.2682	0.109
191	757,515	0.3487	0.1012
192	644,153	0.2965	0.1088
193	664,302	0.3058	0.1041
194	465,174	0.2141	0.1006
195	651,784	0.3	0.1037
196	503,081	0.2316	0.1142
197	652,975	0.3006	0.1107
198	739,149	0.3402	0.1097
199	589,835	0.2715	0.1073
200	548,589	0.2525	0.0961

Samples from 1 to 100 are the chickens with white earlobe color, and 101 to 200 are the chickens with red earlobe color. Besides, samples from 1 to 30 and 101 to 129 are the male chickens, and the left are the females.

Table S5. Statistics of RNA-seq data and its quality control.

Sample name	Raw reads	Clean reads	Clean bases	Error rate (%)	Q20 (%)	Q30 (%)	GC content (%)
white_1	46,208,932	44,563,410	6.68G	0.01	96.71	92.93	50.98
white_2	44,992,438	43,160,422	6.47G	0.01	97.29	94.12	53.02
white_3	43,529,604	41,701,672	6.26G	0.01	97.39	94.35	52.33
red_1	50,294,718	48,163,640	7.22G	0.01	97.46	94.48	52.34
red_2	48,577,764	46,760,152	7.01G	0.01	97.07	93.44	52.44
red_3	47,756,246	45,959,096	6.89G	0.01	96.52	92.53	52.45

White earlobe color group includes white_1, white_2 and white_3. Red earlobe color group includes red_1, red_2 and red_3.

Table S6. Statistics of the differentially expressed genes between white earlobes and red earlobes.

Ensembl Gene_id	Read Count_W	Read Count_R	Log2_Fold Change	Padj	Official Gene Symbol
ENSGALG00000029452	0	68.84	#NAME?	4.78E-03	*Novel gene*
ENSGALG00000035738	0	19.97	#NAME?	5.36E-04	*Novel gene*
ENSGALG00000038970	5.12	63.54	-3.63	4.26E-08	*Novel gene*
ENSGALG00000014858	55.93	471.84	-3.08	3.33E-31	*PACAP*
ENSGALG00000022827	11.29	58.45	-2.37	1.10E-03	*SDR16C5*
ENSGALG00000004261	99.09	398.94	-2.01	2.41E-03	*AQP9*
ENSGALG00000033116	163.97	512.17	-1.64	6.55E-07	*Novel gene*
ENSGALG00000024296	119.09	301.29	-1.34	9.77E-03	*Novel gene*
ENSGALG00000019552	200.93	493.58	-1.30	2.34E-02	*SERPINB2*
ENSGALG00000006707	59.69	135.74	-1.19	3.13E-02	*NOX1*
ENSGALG00000042386	195.80	444.63	-1.18	1.98E-04	*Novel gene*
ENSGALG00000013762	151.13	342.40	-1.18	3.03E-02	*Novel gene*
ENSGALG00000005763	107.98	238.55	-1.14	4.45E-03	*VILL*
ENSGALG00000000452	87.84	189.39	-1.11	1.99E-02	*Novel gene*
ENSGALG00000011355	182.41	392.06	-1.10	1.39E-03	*WNT10A*
ENSGALG00000015151	167.09	356.52	-1.09	1.93E-02	*B4GALT6*
ENSGALG00000034285	1343.23	2850.31	-1.09	4.79E-02	*Novel gene*
ENSGALG00000028047	98.64	201.04	-1.03	3.03E-02	*RHOV*
ENSGALG00000026426	508.34	1024.54	-1.01	3.85E-02	*OTUD1*
ENSGALG00000031003	802.29	1581.55	-0.98	2.20E-04	*Novel gene*
ENSGALG00000002121	218.83	428.89	-0.97	6.80E-03	*PLEKHN1*
ENSGALG00000	281.48	546.57	-0.96	4.45E-	*KIAA1522*

003539				03	
ENSGALG00000036616	304.70	591.40	-0.96	2.86E-03	*NUAK2*
ENSGALG00000000299	2246.04	4347.78	-0.95	2.20E-04	*PKP1*
ENSGALG00000028424	265.39	503.82	-0.92	9.33E-03	*GJB3*
ENSGALG00000039634	366.11	694.23	-0.92	4.45E-03	*KRT80*
ENSGALG00000033251	306.73	579.40	-0.92	6.80E-03	*Novel gene*
ENSGALG00000004747	1071.95	1990.49	-0.89	3.03E-02	*Novel gene*
ENSGALG00000023279	262.36	486.37	-0.89	1.13E-02	*EPN3*
ENSGALG00000001343	372.32	689.68	-0.89	8.04E-03	*LAMB3*
ENSGALG00000029382	428.58	782.30	-0.87	9.11E-03	*BARX2B*
ENSGALG00000035636	4422.01	8024.68	-0.86	6.12E-03	*PHYH*
ENSGALG00000039687	210.37	380.94	-0.86	4.11E-02	*NIPAL4*
ENSGALG00000003149	1347.16	2415.17	-0.84	2.86E-03	*Novel gene*
ENSGALG00000005087	236.26	420.10	-0.83	3.74E-02	*FAM83G*
ENSGALG00000032672	33637.11	59276.37	-0.82	2.12E-03	*KRT5*
ENSGALG00000038631	312.11	548.68	-0.81	2.47E-02	*Novel gene*
ENSGALG00000000309	440.26	773.06	-0.81	2.04E-02	*Novel gene*
ENSGALG00000002283	326.37	567.27	-0.80	3.13E-02	*MAPKAPK3*
ENSGALG00000003527	320.96	554.37	-0.79	3.03E-02	*ARRDC2*
ENSGALG00000036846	9292.96	16050.68	-0.79	4.96E-03	*Novel gene*
ENSGALG00000007324	**681.77**	**1171.59**	**-0.78**	**1.71E-02**	***TP63***
ENSGALG00000000608	2585.02	4440.83	-0.78	6.80E-03	*CDH1*
ENSGALG00000017398	3018.78	5162.40	-0.77	2.34E-02	*Novel gene*
ENSGALG00000036460	420.25	707.00	-0.75	3.97E-02	*Novel gene*
ENSGALG00000002260	2941.69	4933.85	-0.75	1.16E-02	*CISH*

ENSGALG00000005886	955.49	1597.33	-0.74	2.43E-02	*WSCD1*
ENSGALG00000002108	1369.55	2288.28	-0.74	1.99E-02	*EVPL*
ENSGALG00000041347	1424.54	2361.02	-0.73	2.03E-02	*PROM2*
ENSGALG00000042360	1830.83	3015.72	-0.72	2.03E-02	*TRIM29*
ENSGALG00000004260	1146.74	1887.95	-0.72	2.80E-02	*PKP3*
ENSGALG00000034986	682.69	1123.70	-0.72	3.85E-02	*Novel gene*
ENSGALG00000005842	820.11	1347.62	-0.72	3.74E-02	*GDPD2*
ENSGALG00000028924	2405.53	3901.95	-0.70	3.42E-02	*S100A16*
ENSGALG00000002553	1614.25	2614.77	-0.70	3.74E-02	*PCDH1*
ENSGALG00000006919	3246.28	5203.62	-0.68	3.74E-02	*POF1B*
ENSGALG00000012420	13957.43	8662.07	0.69	2.29E-02	*LGALS1*
ENSGALG00000014096	1017.06	616.24	0.72	3.85E-02	*ARNTL2*
ENSGALG00000014999	1156.09	680.94	0.76	2.03E-02	*Novel gene*
ENSGALG00000037863	1194.05	698.39	0.77	1.99E-02	*SEC61G*
ENSGALG00000004438	778.88	453.96	0.78	2.76E-02	*ARSB*
ENSGALG00000041330	1282.94	745.31	0.78	1.71E-02	*Novel gene*
ENSGALG00000016558	492.35	267.35	0.88	1.54E-02	*VEGFD*
ENSGALG00000007334	229.62	120.38	0.93	4.64E-02	*ABAT*
ENSGALG00000001768	947.07	492.06	0.94	1.10E-03	*TENM2*
ENSGALG00000034236	2036.76	1050.47	0.96	4.96E-03	*Novel gene*
ENSGALG00000005408	748.15	385.21	0.96	2.41E-03	*BCO1*
ENSGALG00000011274	49837.33	25152.29	0.99	6.40E-05	*DCN*
ENSGALG00000032262	204.20	101.16	1.01	3.07E-02	*Novel gene*
ENSGALG00000004290	534.17	257.20	1.05	1.28E-02	*ANGPTL1*
ENSGALG00000	501.30	236.03	1.09	6.40E-	*MFAP2*

030647				04	
ENSGALG00000016945	456.07	188.13	1.28	1.34E-02	*LECT1*
ENSGALG00000009730	106.74	40.98	1.38	3.98E-02	*SLC38A4*
ENSGALG00000003283	1726.90	658.83	1.39	9.87E-10	*COMP*
ENSGALG00000013940	144.55	53.41	1.44	3.85E-02	*LNX1*
ENSGALG00000004393	95.36	34.21	1.48	1.34E-02	*Novel gene*
ENSGALG00000006877	67.70	20.99	1.69	1.71E-02	*KLHL4*
ENSGALG00000032371	78.68	18.96	2.05	5.46E-04	*Novel gene*
ENSGALG00000038587	33.89	6.21	2.45	2.15E-02	*Novel gene*
ENSGALG00000039379	19.32	1.56	3.63	3.03E-02	*Novel gene*
ENSGALG00000034976	32.66	2.56	3.68	4.70E-04	*Novel gene*

Table S7. Primers used in this study.

Gnen ID	Primer sequences (5'-3')	Tm
β-actin	F: 5`-CGGACTGTTACCAACACCCA-3` R: 5`-TCCTGAGTCAAGCGCCAAAA-3`	60 ℃
TP63	F: 5`-AACGCATCAAGGAGGAAGGG-3` R: 5`-AGGGCATAAGTAGCGTGAGC-3`	60 ℃
AQP9	F: 5`-CGGTGGGCCCATGACAATA-3` R: 5`-TGGCTAATGAAACGGCAGGG-3`	60 ℃
SLC38A4	F: 5`-ACACAGAGCTGATTGACTCGG-3` R: 5`-ATGATGGCGTTGCTGAGGTT-3`	60 ℃
KRT5	F: 5`-CCAGCCTCTCTCAGGGTACT-3` R: 5`-GCCCCATTGGTGACTTGCTA-3`	60 ℃
LECT1	F: 5`-CATGGCATAGCGGTTGTTCG-3` R: 5`-GAGTTTGCCTGGGCAACAAG-3`	60 ℃
NOX1	F: 5`-TAACACTTCTTCCCCACGCC-3` R: 5`-GTGGAGTGCTGCATTGTTGG-3`	60 ℃
VILL	F: 5`-GGATGGCAGATGGTGACACA-3` R: 5`-GTCCCATAGGCTTTTTCAGGT-3`	60 ℃
P2	F: 5`-TTTTCTTTGCTGCCTGTGCC-3` R: 5`-ACTGGCTGCCTCATCTTGAC-3`	60 ℃
P3	F: 5`-AACACAGCACAGCAGCAATG-3` R: 5`-ACTGGCAGTAAGCACCCATC-3`	60 ℃