

Region	CHR	position	\log_{10} pval -	\log_{10} pval +	Significant line
1:a	1	7422723	5.21077455	4.6074471	both
1:b	1	20580348	5.47044894	3.5682896	pHu-
1:b	1	23041817	1.75932274	5.0142726	pHu+
1:b	1	23252056	2.45288017	4.5683206	pHu+
1:b	1	23272229	2.83719381	5.9396324	pHu+
1:b	1	23320089	1.68565070	4.6247660	pHu+
1:b	1	24859232	4.60007599	4.3567040	pHu+
1:b	1	25657556	2.35853939	4.5047457	pHu+
1:b	1	25685185	3.44890614	5.0023590	pHu+
1:b	1	25810165	2.48970129	5.2272238	pHu+
1:b	1	26057879	3.56103427	6.4782438	pHu+
1:b	1	26172004	2.18477907	5.3908145	pHu+
1:b	1	26417615	2.96563878	4.5251675	pHu+
1:b	1	26484802	4.44639584	5.4721635	pHu+
1:b	1	26535744	2.56158176	4.9235733	pHu+
1:b	1	26549337	4.44639584	5.4721635	pHu+
1:b	1	26585179	4.44639584	5.4721635	pHu+
1:b	1	26664752	3.94536868	6.4587606	pHu+
1:b	1	26719501	2.92295423	4.3987421	pHu+
1:b	1	26895425	5.36602115	4.1493245	pHu-
1:b	1	26915492	5.53265616	3.3652977	pHu-
1:b	1	27053505	4.95463188	1.2118964	pHu-
2:a	2	24035796	0.05527689	4.5356497	pHu+
2:a	2	28483504	5.33780455	0.7743481	pHu-
2:a	2	28502208	5.14240939	0.7091620	pHu-
2:a	2	31975586	5.65490823	0.5064980	pHu-
3:a	3	16910143	0.51844889	5.1225303	pHu+
3:a	3	17256775	0.34720312	4.9183282	pHu+
3:a	3	18221565	0.46198157	4.3883626	pHu+
3:a	3	18348456	0.07279455	5.2099823	pHu+
3:a	3	18598504	0.15273550	5.5729773	pHu+
3:b	3	104194096	0.66134818	5.3095180	pHu+
4:a	4	63446574	5.64460484	0.9894550	pHu-
6:a	6	6356771	0.44110600	4.7090271	pHu+
13:a	13	14544320	1.23371366	5.4294493	pHu+
14:a	14	1718020	0.21743406	4.7147736	pHu+
17:a	17	8225007	0.16401880	4.5066901	pHu+
21:a	21	4259090	0.32265976	4.5090274	pHu+
22:a	22	4635167	0.83432065	5.3513924	pHu+

Table S1: All Significant SNPs found with HMM approach in the chicken data. CHR column indicates the chromosome where the significant SNP is found, position indicates at which position in this chromosome, \log_{10} pval - is the pvalue found at this locus in the pHu- line, \log_{10} pval + is the pvalue found at this locus in the pHu+ line and the column Significant line indicates the line for which this locus is significant