

Table S5 Genetic changes revealed by sequence comparison between CAU5 and 14 non-inducers in the *qhir11* and *qhir12* region.

ID	Region	Genetic changes ^a	Reference allele/sequence	CAU5 allele/sequence	Gene
<i>qhir11</i> region					
1	68113989	1	C	T	GRMZM2G382717
2	68133550- 68133553	2	TTTA	-	GRMZM2G120587
3	68237718	1	C	T	GRMZM2G703616
4	68241406- 68241413	2	GCATGCAT	-	GRMZM2G471240
5	68437173- 68437174	3	-	AACCCC	GRMZM2G003530
6	68444236	1	G	T	GRMZM2G301743
7	68561973	1	C	A	GRMZM2G077897
8	68563560	1	G	T	GRMZM2G077897
9	68563604	1	C	G	GRMZM2G077897
<i>qhir12</i> region					
10	71794984- 71794985	3	-	CCGCCTCCGCCTCC GCCT	GRMZM2G035557
11	72012420	1	G	C	GRMZM5G835433
12	72012529	1	G	A	GRMZM2G313009
13	72041330- 72041331	3	-	TCCATTTCCATC	GRMZM2G313104
14	72192659	1	C	T	AC210719.3
15	72234480- 72234481	3	-	TGCTCTCCCATCCC CATCC	GRMZM2G135834
16	72235167- 72235168	3	-	GGCGGCGGC	GRMZM2G135834
17	72402957	1	C	G	GRMZM5G837210
18	72411336	1	T	A	GRMZM2G060617
19	72618114- 72618115	3	-	ACGGTGGTC	GRMZM2G137502
20	72703124- 72703136	4	CAAATATTGTTG	GAAATGTTTGCCA	GRMZM2G096682
21	72796140	1	T	C	AC177908.3
22	72796440	1	G	A	AC177908.3
23	72883524	1	C	T	GRMZM2G351259
25	72884024	1	A	T	GRMZM2G351259
26	72884346	1	A	G	GRMZM2G351259
24	72884006- 72884024	4	CGCGCCTGCGCCGCCG CCA	TGCGCCT	GRMZM2G351259, GRMZM2G051224
27	72938407	1	A	T	GRMZM2G568442
28	73101227- 73101228	3	-	CTTTGTA	AC212231.3_FG003
29	73102017-	2	GGAATATATACTGTTA	-	AC212231.3_FG003

ID	Region	Genetic changes ^a	Reference allele/sequence	CAU5 allele/sequence	Gene
	73102071		TATATATTACGACGTA CGTACGTGTAATATAT ACTGTAC		
30	73232428- 73232433	2	ACAGTG	-	GRMZM2G117930
31	73233044	1	G	T	GRMZM2G552697
32	73344674	1	A	T	GRMZM2G496269
33	73379506- 73379507	3	-	GTGGT	GRMZM2G172244
34	73512009- 73512012	2	TCTC	-	GRMZM2G067371
35	73967088- 73967089	3	-	ACGACAGG	GRMZM2G125241
36	73967552- 73967553	3	-	ACGCCG	GRMZM2G125241
37	74264018- 74264022	2	ACAGA	-	GRMZM2G036629
38	74274773- 74274775	2	TGG	-	GRMZM2G036543
39	74279629	1	A	G	GRMZM2G036484
40	74279670	1	G	C	GRMZM2G036484
41	74279675	1	C	T	GRMZM2G036484
42	74279690	1	C	T	GRMZM2G036484
43	74279701	1	C	T	GRMZM2G036484
44	74280722	1	T	G	AC217311.3
45	74280928	1	C	T	AC217311.3
46	74280937	1	T	A	AC217311.3
47	74280984	1	A	C	AC217311.3
48	74280988- 74280989	1	TG	CC	AC217311.3
49	74281033	1	C	T	AC217311.3
50	74281051	1	C	T	AC217311.3
51	74281453	1	G	A	AC217311.3
52	74281455- 74281456	1	AG	GA	AC217311.3
53	74281466- 74281467	1	GG	AT	AC217311.3
54	74281480	1	T	G	AC217311.3
55	74281489	1	G	A	AC217311.3
56	74491394	1	T	G	GRMZM2G464580
57	74606411- 74606418	4	CGATACAG	AGATACAT	GRMZM2G086992
58	74608550	1	T	C	GRMZM2G181218
59	74608805	1	G	C	GRMZM2G481691
60	74630494	1	C	G	GRMZM2G130121

ID	Region	Genetic changes ^a	Reference allele/sequence	CAU5 allele/sequence	Gene
61	74769786- 74769830	2	GTAAACAGTTTTGTT TCAGAAAACAGTTGTC ACTACCCCCCACT	-	GRMZM2G030955
62	74770969	1	G	A	GRMZM2G030955
63	74785214	1	A	G	AC208123.3
64	74785457	1	A	G	AC208123.3
65	74800417	1	T	C	AC208123.3
66	74800422	1	T	C	AC208123.3
67	75143942- 75143951	2	ATATTGCAGG	-	GRMZM2G042881
68	75145218	1	T	C	AC200879.4
69	75145236	1, 5	A	C	AC200879.4
70	75149675	1	A	G	GRMZM2G043141
71	75319146	1	T	A	GRMZM2G583289
72	75405727- 75405728	3	-	TCAAATAGTGT	GRMZM2G032821

^aGenetic changes: 1=AAC; 2=Deletion; 3=Insertion; 4=Replacement; 5=Possible splice site disruption