

Supplementary Material

1 Supplementary Tables

Supplementary Table S1. Information of ten re-sequenced varieties used in the study. R: low temperature resistant. S: low temperature sensitive.

Individual code ^a	Individual code ^b	Accession Name	Accession Number ^c	Geographical origin	Low temperature phenotype	Low temperature injury index(LTII)
CG104(P ₁)	CG3087	Sekino No. 2 (Ochiai No.2)	SRX174877	Osaka, Japan	R	5.7±1.2
CG29	CG3010	Sagami Hanpaku Fushinari Kyuri	SRX174872	Japan	R	4.3±0.8
CG56	CG4358	K2148	SRX174887	Southern China	R	5.4±1.1
CG61	CG3147	185	-	Japan	R	6.3±1.0
CG90	CG1077	Qing Pi Ba Cha	SRX174857	China, Jilin	R	4.2±0.3
CG37(P ₂)	CG5479	Muromskij	SRX174897	Russian Federation	S	57.8±2.9
CG10	CG7023	Rasht	SRX174917	Iran	S	63.3±1.9
CG21	CG8160	Poona Kheera	SRX174930	India, Madhya Pradesh	S	62.8±2.1
CG43	CG6562	SC 53-B (6)	SRX174908	United States	S	59.7±0.8
CG109	CG5232	Nemet Kigyo	SRX174892	Hungary	S	60.2±3.6

^aCG # in this study; ^bCG # in Qi et al. (2013); ^cAccession number in NCBI database.

Supplementary Table S2. Environment used for evaluating low temperature tolerance of F_{2:3} populations and core germplasms.

Population	Treatment	Seedling age	Duration of low temperature	Average temperature	Site
F _{2:3}	March 2017	Three-week-old	11 days	15.6°C	Greenhouse
	April 2017	Three-week-old	14 days	16.6°C	Plastic greenhouse
Core germplasms	February 2016	Three-week-old	14 days	12.0°C	Greenhouse
	March 2016	Three-week-old	11 days	19.3°C	Greenhouse

Supplementary Table S3. 214 non-synonymous SNPs in the 42-kb region among 10 CG lines.

rs#	position	CG10	CG21	CG37	CG43	CG109	CG29	CG56	CG61	CG90	CG104
SNP3031244	20779616	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031247	20779823	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031251	20779851	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031257	20780091	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031258	20780095	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031261	20780229	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031264	20780245	AA	AA	AA	AA	AA	GG	GG	GG	GG	GG
SNP3031265	20780286	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031272	20780688	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031274	20780750	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031280	20780921	AA	AA	NN	AA	AA	TT	TT	TT	TT	TT
SNP3031281	20780926	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC

SNP3031282	20780947	CC	NN	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031283	20780962	AA	NN	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031284	20780974	CC	CC	CC	CC	CC	TT	NN	TT	TT	TT
SNP3031285	20781002	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031287	20781044	TT	TT	TT	TT	TT	CC	CC	CC	CC	CC
SNP3031290	20781161	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031291	20781182	GG	GG	GG	NN	GG	AA	AA	AA	AA	AA
SNP3031327	20782412	TT	TT	TT	NN	TT	GG	GG	GG	GG	GG
SNP3031355	20784113	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031356	20784184	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031364	20784298	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031366	20784321	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031368	20784367	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031369	20784380	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031372	20784406	AA	AA	NN	AA	AA	TT	TT	TT	TT	TT
SNP3031375	20784475	AA	AA	GA	AA	AA	CC	CC	CC	CC	CC
SNP3031376	20784500	GG	GG	GC	GG	GG	CC	CC	CC	CC	CC
SNP3031377	20784510	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031382	20784694	GC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031383	20784700	GC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031384	20784793	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031385	20784805	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031386	20784866	TT	TT	TC	TT	TT	GG	GG	GG	GG	GG
SNP3031393	20785203	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031394	20785226	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031396	20785258	TT	TT	NN	TT	TT	AA	AA	AA	AA	AA
SNP3031403	20785465	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031406	20785675	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031411	20786082	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031412	20786264	GG	GG	GG	GG	GG	CC	CC	CC	CC	CC
SNP3031422	20787866	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031423	20787899	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031424	20788611	CC	CC	GT	CC	CC	TT	TT	TT	TT	TT
SNP3031425	20788645	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031427	20788941	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031441	20789893	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031453	20790302	AA	AA	AA	NN	AA	CC	CC	CC	CC	CC
SNP3031454	20790362	TT	TT	TT	NN	TT	AA	AA	AA	AA	AA
SNP3031455	20790377	AA	AA	AA	NN	AA	CC	CC	CC	CC	CC
SNP3031458	20790634	TT	TT	TT	TT	TT	AA	NN	AA	AA	AA
SNP3031467	20790930	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031468	20790965	GG	NN	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031469	20790967	TT	NN	TT	TT	TT	GG	GG	TC	GG	GG
SNP3031471	20791187	GG	GG	GG	GG	GG	AA	AA	AA	AA	AA
SNP3031472	20791323	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031473	20791339	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031491	20791602	CC	CC	NN	CC	CC	AA	AA	AA	AA	AA
SNP3031492	20791626	TT	TT	NN	TT	TT	AA	AA	NN	AA	AA

SNP3031493	20791650	CC	CC	CC	CC	CC	AA	NN	AA	AA	AA
SNP3031494	20791665	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031495	20791675	GG	GG	GG	GG	GG	AA	AA	AA	AA	AA
SNP3031496	20791688	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031499	20791804	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031500	20791943	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031503	20792076	AA	AA	NN	AA	AA	CC	CC	CC	CC	CC
SNP3031504	20792099	AA	AA	AA	AA	AA	GG	GG	GG	GG	GG
SNP3031512	20792491	GG	GG	GG	GG	GG	AA	AA	NN	AA	AA
SNP3031528	20793291	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031529	20793303	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031531	20793355	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031534	20793407	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031535	20793451	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031536	20793468	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031538	20793507	GG	GG	GG	GG	GG	CC	CC	CC	CC	CC
SNP3031540	20793568	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031550	20793963	TT	TT	TT	TT	TT	TT	TT	NN	TT	TT
SNP3031556	20794115	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031560	20794168	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031564	20794262	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031571	20794941	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031572	20795196	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031575	20795310	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031576	20795315	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031580	20795444	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031584	20795680	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031585	20795739	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031588	20795768	CC	CC	NN	CC	CC	AA	AA	AA	AA	AA
SNP3031589	20795883	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031592	20796005	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031593	20796066	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031598	20796164	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031599	20796183	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031605	20796885	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031606	20796914	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031607	20796931	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031612	20797272	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031614	20797331	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031615	20797363	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031616	20797378	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031621	20797492	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031633	20798249	GG	GG	GG	GG	GG	CC	CC	CC	CC	CC
SNP3031642	20798572	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031644	20798602	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031645	20798656	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031648	20798687	TT	TT	TT	TT	TT	CC	CC	CC	CC	CC
SNP3031650	20798707	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG

SNP3031653	20798807	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031654	20798822	AA	AA	AA	AA	NN	TT	TT	TT	TT	TT
SNP3031655	20798858	CC	CC	NN	CC	CC	GG	GG	GG	GG	GG
SNP3031658	20799027	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031661	20799180	AA	AA	NN	AA	AA	GG	GG	GG	GG	GG
SNP3031669	20799304	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031671	20799384	GG	GG	NN	GG	GG	TT	TT	TT	TT	TT
SNP3031676	20799480	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031679	20799523	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031680	20799526	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031683	20799665	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031688	20799905	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031696	20800166	AA	NN	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031697	20800218	AA	AA	AA	AA	AA	GG	GG	GG	GG	GG
SNP3031698	20800382	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031701	20800729	TT	TT	NN	TT	TT	CC	CC	CC	CC	CC
SNP3031702	20800816	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031703	20800818	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031715	20801363	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031716	20801446	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031722	20801801	TT	TT	TT	TT	TT	CC	CC	CC	CC	CC
SNP3031726	20802633	TT	TT	TT	TT	TT	AA	AA	NN	AA	AA
SNP3031732	20802778	TT	TT	NN	TT	TT	GG	GG	NN	GG	GG
SNP3031747	20803301	NN	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031749	20803317	GG	GG	NN	GG	GG	TT	TT	TT	TT	TT
SNP3031750	20803342	TT	TT	NN	TT	TT	AA	AA	AA	AA	AA
SNP3031751	20803350	GG	GG	NN	GG	GG	TT	TT	TT	TT	TT
SNP3031753	20803390	CC	CC	NN	CC	CC	GG	GG	GG	GG	GG
SNP3031754	20803400	TT	TT	NN	TT	NN	AA	AA	AA	AA	AA
SNP3031761	20803738	CC	CC	CC	CC	CC	TT	TT	NN	TT	TT
SNP3031762	20803742	TT	TT	TT	TT	TT	GG	GG	NN	GG	GG
SNP3031765	20803920	AA	AA	AA	AA	AA	TT	TT	TT	TT	TT
SNP3031766	20804002	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031767	20804007	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031775	20804618	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031776	20804704	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031779	20805032	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031780	20805053	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031781	20805066	NN	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031783	20805084	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031785	20805138	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031791	20805585	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031797	20805881	GG	GG	GG	GG	GG	CC	CC	CC	CC	CC
SNP3031798	20805917	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031799	20805922	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031802	20805991	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031808	20806215	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031809	20806332	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT

SNP3031813	20806430	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031818	20807378	CC	CC	CC	CC	CC	AA	NN	AA	AA	AA
SNP3031819	20807440	AA	AA	AA	AA	AA	TT	TT	TT	TT	TT
SNP3031820	20807664	GG	GG	GG	GG	GG	AA	AA	NN	AA	AA
SNP3031823	20807859	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031824	20807902	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031832	20808197	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031833	20808218	AA	AA	AA	AA	AA	TT	TT	TT	TT	TT
SNP3031837	20808492	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031839	20808631	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031840	20808730	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031843	20808767	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031844	20808769	GG	GG	GG	GG	GG	CC	CC	CC	CC	CC
SNP3031846	20809016	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031851	20809513	AA	AA	AA	AA	AA	TT	TT	TT	TT	TT
SNP3031853	20809530	AA	AA	AA	AA	AA	GG	GG	GG	GG	GG
SNP3031856	20809681	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031857	20809688	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031858	20809752	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031861	20810087	CC	CC	CC	CC	CC	AA	NN	AA	AA	AA
SNP3031864	20810465	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031867	20811160	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3031874	20812261	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031879	20812926	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031881	20813136	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031883	20813632	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031884	20813718	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031885	20814033	CC	CC	CC	CC	CC	TT	TT	TT	TT	TT
SNP3031888	20814218	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031890	20814314	GG	GG	GG	GG	GG	AA	AA	AA	AA	AA
SNP3031891	20814904	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031892	20815099	CC	CC	CC	CC	CC	AA	AA	AA	AA	AA
SNP3031896	20815615	AA	AA	AA	AA	AA	TT	TT	TT	TT	TT
SNP3031906	20816191	CC	NN	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031907	20816195	CC	NN	CC	CC	CC	GG	GG	GG	GG	GG
SNP3031910	20816305	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3031911	20816348	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3031917	20816402	TT	TT	TT	TT	TT	GG	GG	GG	GG	GG
SNP3031918	20816412	TT	TT	TT	TT	NN	GG	GG	GG	GG	GG
SNP3031938	20816802	CC	CC	NN	CC	CC	TT	NN	TT	TT	TT
SNP3031939	20816906	TT	TT	TT	TT	TT	NN	AA	AA	AA	AA
SNP3032015	20820005	GG	GG	NN	GG	GG	AA	AA	NN	AA	AA
SNP3032021	20820284	AA	AA	AA	AA	AA	CC	CC	CC	CC	CC
SNP3032022	20820290	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3032023	20820350	TT	TT	TT	TT	TT	GG	GG	NN	GG	GG
SNP3032024	20820381	GG	GG	NN	GG	GG	TT	TT	TT	TT	TT
SNP3032025	20820397	AA	AA	NN	AA	AA	CC	CC	CC	CC	CC
SNP3032031	20820481	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT

SNP3032032	20820534	CC	CC	NN	CC	CC	AA	AA	AA	AA	AA
SNP3032033	20820621	GG	GG	GG	GG	GG	TT	TT	TT	TT	TT
SNP3032035	20820719	AA	AA	AA	AA	AA	TT	TT	TT	TT	TT
SNP3032040	20820994	TT	TT	TT	TT	TT	CC	CC	CC	CC	CC
SNP3032043	20821125	TT	TT	TT	TT	TT	AA	AA	AA	AA	AA
SNP3032044	20821153	CC	CC	CC	CC	CC	GG	GG	GG	GG	GG
SNP3032047	20821287	GG	GG	GG	GG	GG	AA	AA	AA	AA	AA
SNP3032052	20821448	CC	CC	NN	CC	CC	GG	GG	GG	GG	GG
SNP3032054	20821614	CC	CC	NN	CC	CC	AA	AA	AA	AA	AA
SNP3032055	20821620	AA	AA	NN	AA	AA	TT	TT	TT	TT	TT

Supplementary Table S4. The primers used for gene cloning and gene expression analysis.

	Primer name	Forward primer	Reverse primer
Gene cloning for sequencing	<i>Csa6G445210-1</i>	TCTCTTCGCTTCTCTTCTG	TTAATTCCTCTGCCAACCA
	<i>Csa6G445210-2</i>	TTGCTGTTGTTAGATGGTC	GGCGTCCCTCTATAAATGT
	<i>Csa6G445210-3</i>	AGTCTGATGCTAACAATGGT	GTGGTAAGGTCAACTACTACA
	<i>Csa6G445210-4</i>	GCTTCTTCAGGTAATCACTGT	AGGAGTCTTCACGCCATC
	<i>Csa6G445210-5</i>	CGTATCTTGCTTGCTAACC	GAAGGACCTGATATTGACCA
	<i>Csa6G445210-6</i>	CATCAAGACAGCAAGAAGAT	TCCAAATACACCCATAGACT
	<i>Csa6G445220-1</i>	GCGAATCTTCTTCCTTACAC	TTACAAGACCTCAGCGATAG
	<i>Csa6G445220-2</i>	CGTTACAGAGTCAATGAAC	CAACAGCAGCAACAAGATA
	<i>Csa6G445220-3</i>	GCTGTTGGCTAATGTTACTC	ACACTTGTAAAGGTCATTGC
	<i>Csa6G445220-4</i>	AATAAGGAGTCGTGTTGTC	AAAGAAATCGCGACTGGAGTG
	<i>Csa6G445230-1</i>	AGCAGTCTATCACTCTCATC	CCTTACCTTACCGCCTATT
	<i>Csa6G445230-2</i>	TTTGGGTTCTGGGTTCTG	TGTGGTTATCTTCCTTAGCA
	<i>Csa6G445230-3</i>	TCCTTCTCTGATGCTAATGG	GCTGCTTGATAGACACAAC
	<i>Csa6G445230-4</i>	TGGTCACTGGAAGAGGTC	TGGCTGGAAGTCTGGAAT
	<i>Csa6G445230-5</i>	CAACGAGGAGTATGATAAGTG	CAACCGCCTAGAATGACA
	<i>Csa6G445230-6</i>	AATCTCATGCCGACAAGG	TGACCACCAAGACTCCAT
	<i>Csa6G445230-7</i>	TGGAGTCTTGGTGGTCAA	TATAGGCTCGCGACTGTAT
	<i>Csa6G445230-8</i>	GGATATGGCAGAGGTTAGAC	CAATAGGTGATGAGTGAGGAA
	<i>Csa6G445230-9</i>	GAGAAGGATGATTATGAGGTTG	CTGGATACTGTGATGTTGGA
	<i>Csa6G445230-10</i>	TTCCAACATCACAGTATCCA	ACAGCCTTCTCCACAATG
qRT-PCR	<i>Csa6G445230-11</i>	GCTTCTCCAGTCCCTTCAG	TTGCCATTAGAGTTCACAAG
	<i>Csa6G445230-12</i>	GTGCTTACTGGCTCCATT	GTCCATTGAGTCACATCCTA
	<i>Csa6G445230-13</i>	CCACTCACGAAGTATCATCT	ACGATCATATCATGGAGCAA
	<i>Actin1</i>	CACCAAGCCCCAAGAAGATC	TAAACCTAATCACCACCAGC
	<i>Csa6G445210</i>	TGTCTTGATACCGTGATGTT	GCTCCTACATTGTTACTTCC
	<i>Csa6G445220</i>	TATCTTGTTGCTGCTGTTG	GTAAGGGTGGACGTAACA
	<i>Csa6G445230</i>	AACATGATCTTGGGCATTTC	CCATCTTCCAGAAGGTCAG

Supplementary Table S5. Specific SNP markers used for amplifying mutation sites from F₂ individuals.

Gene name	Primer name	Primer sequence	Restriction endonuclease	Restriction site	Mutation site	Phenotype
Csa445210	SNP_10-F	AAACCTCTCCGATGGCTCTG	MfeI	5'...C▼AATTG...3' 3'...GTTAA▲C...5'	...CAATTGC C...	R
	SNP_10-R	TGTTTCGTCACCGACATGTT			...CAATCGC C...	S
Csa445230	SNP_30-F	GGTTTGTTCATGGGTATAGGT	BbvI	5'...GCAGC(N) ₈ ...3' 3'...CGTCG▲(N) ₁₂ ...5'	...GCAACG... ▼	R
	SNP_30-R	ACACATGTGAAGAGGTCCTCA			...GCAGCG... ▲	S

Supplementary Table S6. Low temperature injury index of F₁ and F₁' showed that the LT

tolerance is controlled by nuclear genes.

Parental Lines		F ₁	F ₁ '
CG104	CG37	CG104 x CG37	CG37 x CG104
(Mean ± S.E)		(Mean ± S.E)	(Mean ± S.E)
4.1 ± 1.7		27 ± 7.8	30.0 ± 3.4

Three replicates were conducted in the experiment, and eight plants were phenotyped for each replicate.

Supplementary Table S7. Distribution of markers on the linkage map.

Chromosome	Number of markers	Length (cM)	Average distance (cM/marker)
Chr1	27	119.1	4.4
Chr2	47	160.4	3.4
Chr3	29	160.9	5.5
Chr4	18	144.7	8.0
Chr5	35	152.8	4.4
Chr6	44	163.3	3.8
Chr7	25	89.4	3.6
Total	190	990.8	5.2

Supplementary Table S8. Transmembrane helix position of protein encoded by *Csa6G445230*.

Name	CG104		CG37	
	Start	End	Start	End
transmembrane region	13	32	13	32
transmembrane region	52	74	52	74
transmembrane region	95	117	120	142
transmembrane region	122	144	157	176
transmembrane region	156	178	197	219
transmembrane region	238	255	234	256
transmembrane region	288	310	288	310
transmembrane region	325	347	325	347
transmembrane region	354	376	354	376
transmembrane region	396	418	396	418
transmembrane region	439	461	439	461
low complexity	554	569	554	569
low complexity	635	666	635	666

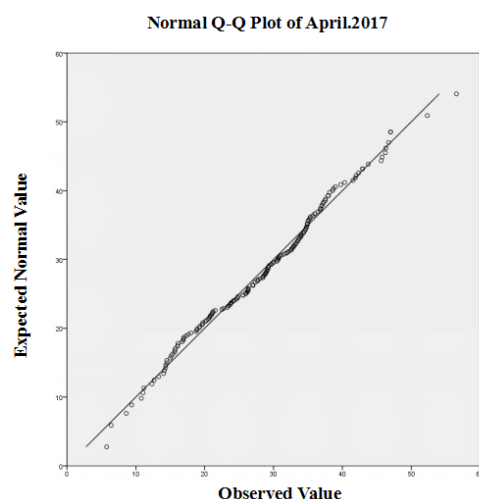
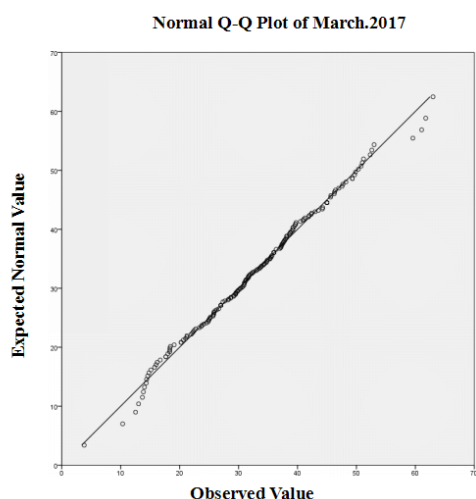
Supplementary Table S9. Correlation between phenotype and the non-synonymous SNP site of *Csa6G445210* (SNP_10) and *Csa6G445230* (SNP_30) in 158 F₂ individuals. The individuals that produced the same digestion products as CG104, CG37, and F₁ were defined as type a, b, and ab, respectively.

Code	Mar-17	April 2017	SNP_10	SNP_30	Code	Mar-17	April 2017	SNP_10	SNP_30
2	47.7	33.7	b	b	108	22	18.9	a	a
3	40.5	37.5	ab	ab	109	27	20.1	a	a
4	63	-	ab	ab	110	34.8	34.5	ab	ab
5	15.7	27	ab	ab	113	31.5	33.9	ab	ab
6	14.6	14.3	a	a	114	34.9	30.7	b	b
7	27	23.5	ab	ab	115	34.7	31.2	ab	ab
8	47	37.6	-	b	116	21	17.6	a	a
9	39.2	37.2	ab	ab	117	35.3	20.7	a	a

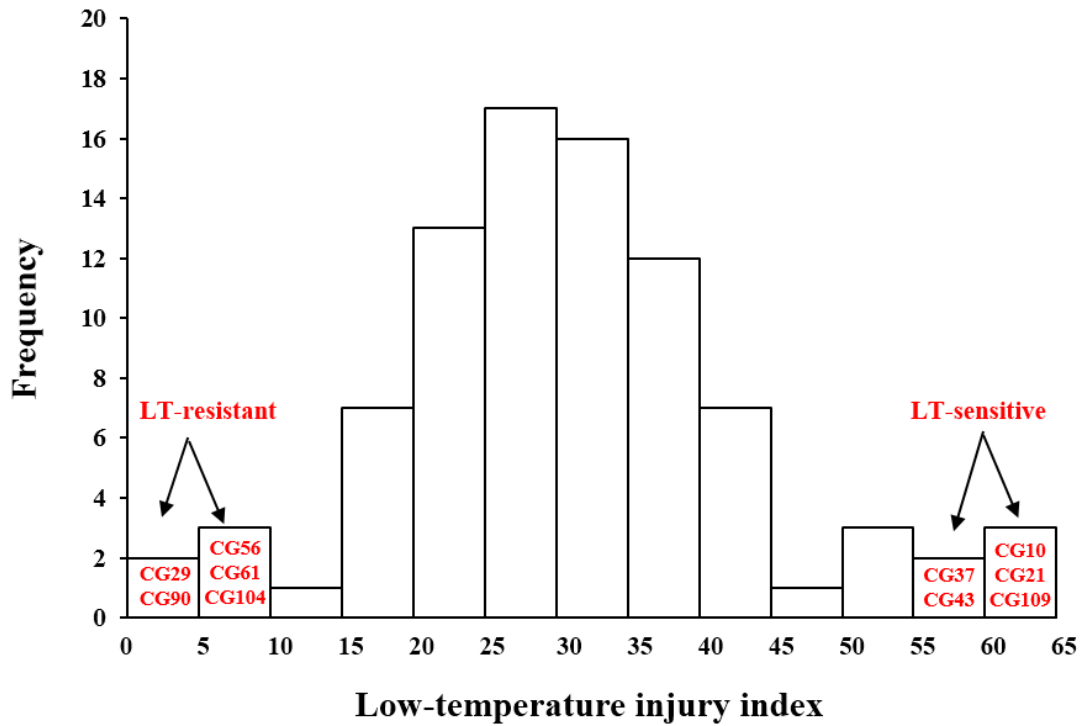
10	45	38.7	ab	ab	118	37.8	33.5	ab	ab
12	44.2	29.3	ab	ab	119	61.1	56.6	b	b
13	39.7	36.8	b	b	120	17.7	17	a	a
15	20.3	14.5	ab	ab	121	34.3	30.9	ab	ab
16	21.2	15.3	a	a	122	44.3	42.3	ab	ab
18	18.3	8.6	a	a	123	27	27.8	ab	ab
22	12.5	6.4	a	a	125	36	24.6	ab	ab
23	32.3	30	ab	ab	126	17.6	18.9	a	a
24	30.9	28.5	ab	ab	127	32	28.9	b	b
26	27	14.3	a	a	129	31	29	ab	ab
27	31	28.8	-	ab	133	35.7	35.7	b	b
28	33.9	32	ab	ab	136	38.8	37	ab	ab
29	24.1	16.7	ab	ab	139	26.3	28.5	ab	ab
30	50.3	37	b	b	140	24.8	24.8	ab	ab
31	42.3	29.7	ab	ab	145	38	34	b	b
33	61.7	46.2	b	b	146	30.3	30.7	ab	ab
34	41.9	32.7	ab	ab	147	29.8	24.2	a	a
35	25.8	19.6	ab	ab	148	38.2	29.7	ab	ab
36	25.8	21	a	a	149	45	42.9	b	b
37	14.8	5.7	ab	ab	152	49.7	45.8	b	b
39	49.3	36.8	ab	ab	153	13	15.7	a	a
40	48.2	33.9	b	b	156	33.8	27.6	ab	ab
42	13.8	11.2	a	a	157	37.6	33.2	ab	-
48	52.3	36	b	b	158	28.3	23.3	ab	ab
49	35.6	32.6	b	b	159	37.4	31.5	ab	ab
50	36	32.2	ab	ab	162	28.2	20.8	a	a
51	16.7	16.1	a	a	163	38.2	33.5	ab	ab
52	29.2	32.9	ab	ab	164	34.2	19.6	ab	ab
53	25.1	28.6	ab	ab	165	31	23.5	ab	ab
54	45	34.3	ab	ab	166	45.7	46.3	b	b
55	51	47	b	b	169	30.6	31.9	ab	ab
56	22.7	15.6	a	a	172	17.6	35.2	a	a
58	35.5	37	b	b	174	15.1	13.3	a	a
60	21.2	18.7	a	a	175	34.8	34.6	ab	ab
61	19.1	12.7	a	a	176	41.3	38.6	ab	ab
62	18.3	16.1	a	a	178	28.7	26	ab	ab
63	45	36.8	ab	ab	179	42.4	34.7	ab	ab
65	42	39	b	b	180	39	34.1	ab	ab
66	46.4	33	b	b	181	29.3	16.9	ab	ab
67	39.8	34.9	ab	ab	182	3.8	9.4	-	a
69	49.3	37.3	ab	ab	183	45.6	43.8	ab	ab
70	49.9	34.9	ab	ab	184	35.7	35.3	ab	ab
71	11.7	27	a	a	185	31.3	27.4	ab	ab
72	38.8	26.3	ab	-	186	33.6	18	ab	ab
74	18.4	14.1	a	a	187	36.4	33.6	ab	ab
77	46.2	42	b	b	188	39.2	37.9	ab	ab
80	39.2	28.9	ab	ab	189	16.2	20.3	a	a
81	28.7	30.5	ab	ab	190	19.5	12.5	a	a

82	45	34.3	ab	ab	191	33	27.8	ab	ab
83	29.5	30.6	ab	ab	192	51.2	52.3	b	b
84	23.3	23.7	a	a	193	43	24.8	ab	ab
85	24.6	24.8	ab	ab	194	13.7	16.1	a	a
86	20.3	15	a	a	195	25.8	19.2	ab	ab
87	29.8	22.8	ab	ab	197	41.1	38.1	b	b
89	33.7	28	ab	ab	198	27	25.6	ab	ab
90	53	41.9	b	b	199	27	26.2	a	a
91	31.7	29.4	ab	ab	200	31.7	37.9	ab	ab
92	37.8	34.6	ab	ab	202	38.2	37.9	b	b
93	29.6	26.3	a	a	203	35.4	35.4	b	b
94	39.2	29.3	ab	ab	205	43.6	34.8	ab	ab
95	36	33.5	ab	ab	206	25.2	19.3	ab	ab
96	25.7	21.2	a	-	209	30.2	10.5	a	a
98	14.4	21.1	a	a	210	37.2	35.7	ab	ab
99	23.7	19.7	a	a	211	30.7	23.8	a	a
101	37.4	39.8	ab	ab	212	32.3	29.9	ab	ab
102	26	26	a	a	213	27.4	25.6	ab	ab
103	18	20.5	a	a	215	31.2	30.6	ab	ab
104	22.2	23.9	a	a	217	14	15.1	a	a
105	22.3	16.9	a	a	218	46.3	33	ab	ab
106	45	45.6	ab	ab	219	16	12.3	a	a
107	30.9	27	a	a	222	23.8	27	ab	ab

2 Supplementary Figures



Supplementary Figure S1. The Normal Q-Q plot of phenotypic data generated in March 2017 and April 2017.



Supplementary Figure S2. The frequency distribution of the low temperature injury index of 87 core germplasm. The ten CG lines in red were selected to generate LT-resistant and LT-sensitive bulks.

Csa6G445210

CG104	1	CTTCTTCCTTCTTCTCCTCTCTAGGATTCTCTTTTCCCTTCCTTCCATCAATTCCCACT	60
CG37	1	CTTCTTCCTTCTTCTCCTCTCTAGGATTCTCTTTTCCCTTCCTTCCATCAATTCCCACT	60
CG104	61	TGGCTTTCTTCCCTTCTCTTGATCGACCTCACTCTACCCTCCATCTCGATTTTGTTC	120
CG37	61	TGGCTTTCTTCCCTTCTCTTGATCGACCTCACTCTACCCTCCATCTCGATTTTGTTC	120
CG104	121	AACTCTGTTACAGTTGCAACCCCTTTCTTCTTCCTTTTAACTCTATTTTATCCAATTT	180
CG37	121	AACTCTGTTACAGTTGCAACCCCTTTCTTCTTCCTTTTAACTCTATTTTATCCAATTT	180
CG104	181	TTGTTTCATGGGTTTTCGCTCTGGTGGTATATGAAGTGGTCAAAGCACGGTGAAGAAGCTC	240
CG37	181	TTGTTTCATGGGTTTTCGCTCTGGTGGTATATGAAGTGGTCAAAGCACGGTGAAGAAGCTC	240
CG104	241	CTAGAGAACCCTTTGAATTTGGTGAATGGTAGGTTCTGGAGCTGTGGAATTTGTTC	300
CG37	241	CTAGAGAACCCTTTGAATTTGGTGAATGGTAGGTTCTGGAGCTGTGGAATTTGTTC	300
CG104	301	CATTTATAAGGGGCGAATTCCCGAGAACGGAAGGGTTGTTGGGAAATTTTGATATGGGT	360
CG37	301	CATTTATAAGGGGCGAATTCCCGAGAACGGAAGGGTTGTTGGGAAATTTTGATATGGGT	360
CG104	361	ATGGAGATTTTGGAGACGTATTTCGTCTCTTACCTTCTGCAATGTTCTGTTCTGAGAA	420
CG37	361	ATGGAGATTTTGGAGACGTATTTCGTCTCTTACCTTCTGCAATGTTCTGTTCTGAGAA	420
CG104	421	TTTGGAAATCAATTTCTGGATTTTGCTGTTGTTAGATGGTCGACGGGAAGGAGTTATTT	480
CG37	421	TTTGGAAATCAATTTCTGGATTTTGCTGTTGTTAGATGGTCGACGGGAAGGAGTTATTT	480

CG104	481	ATGTTCTACAAGGTAAGAATCTTTAGGGTTGGGTTGGGTTGTGAATACACTTGATATTC	540
CG37	481	ATGTTCTACAAGGTAAGAATCTTTAGGGTTGGCTTGGGTTGTGAATACACTTGATATTC	540
CG104	541	AGttttttttttttttttttGAAATGTTAGTTTTTCGTGGTTGGCAGAGGAATTAATTGG	600
CG37	541	AGTTTTTTTTTTTTTTTTTGAATGTTAGTTTTTCGTGGTTGGCAGAGGAATTAATTGG	600
CG104	601	CTTTGATTGAGATGATTACGTTTATGGATTTCGAAAGAGAACTGAAAGAGGTGGAGAAAT	660
CG37	601	CTTTGATTGAGATGATTACGTTTATGGATTTCGAAAGAGAACTGAAAGAGGTGGAGAAAT	660
CG104	661	GTTTAGATCCTCAGTTATGGCATGCCTGTGCTGGAGGAATGGTTCAAATGCCGCCGGTGA	720
CG37	661	GTTTAGATCCTCAGTTATGGCATGCCTGTGCTGGAGGAATGGTTCAAATGCCGCCGGTGA	720
CG104	721	ACGCCAGAGTTTTCTATTTTCCACAAGGTCATGCTGAGCATTCTTGTGCGCCAGTTGATT	780
CG37	721	ACGCCAGAGTTTTCTATTTTCCACAAGGTCATGCTGAGCATTCTTGTGCGCCAGTTGATT	780
CG104	781	TCAGGAACTGTCCTAAGGTTCTTCATATACCCTTTGCAGAGTTTCTGCCATCAAGTTCC	840
CG37	781	TCAGGAACTGTCCTAAGGTTCTTCATATACCCTTTGCAGAGTTTCTGCCATCAAGTTCC	840
CG104	841	TTGCAGATCCTGACACTGATGAGGTATTGCCAAACTTAGGTTGATTCCCATAAATGGAA	900
CG37	841	TTGCAGATCCTGACACTGATGAGGTATTGCCAAACTTAGGTTGATTCCCATAAATGGAA	900
CG104	901	GCGAACTAGATTTTGAAGATGATGGAATTGGAAGGCTTAATGGGTCCGAACAGGATAAAC	960
CG37	901	GCGAACTAGATTTTGAAGATGATGGAATTGGAAGGCTTAATGGGTCCGAACAGGATAAAC	960
CG104	961	CAACCTCATTGCAAAGACACTGACTCAGTCTGATGCTAACAATGGTGGGGTTTCTCTG	1020
CG37	961	CAACCTCATTGCAAAGACACTGACTCAGTCTGATGCTAACAATGGTGGGGTTTCTCTG	1020
CG104	1021	TTCCAAGGTATTGTGCAGAAACTATCTTCCCTCGGTTGGATTATTCTGCTGATCCACCCG	1080
CG37	1021	TTCCAAGGTATTGTGCAGAAACTATCTTCCCTCGGTTGGATTATTCTGCTGATCCACCCG	1080
CG104	1081	TTCAAACCATTTCTGCTAAGGATGTTTCATGGGGAGACATGGAATTCAGGCACATTATA	1140
CG37	1081	TTCAAACCATTTCTGCTAAGGATGTTTCATGGGGAGACATGGAATTCAGGCACATTATA	1140
CG104	1141	GAGGGACGCCTCGCCGGCATCTTTGACTACTGGCTGGAGTACTTTTGTTAACCATAAGA	1200
CG37	1141	GAGGGACGCCTCGCCGGCATCTTTGACTACTGGCTGGAGTACTTTTGTTAACCATAAGA	1200
CG104	1201	AGCTCGTTGCAGGTGATTCCATTGTTTTCTAAGGGCAGAAAACGGAGATCTCTGCGTTG	1260
CG37	1201	AGCTCGTTGCAGGTGATTCCATTGTTTTCTAAGGGCAGAAAACGGAGATCTCTGCGTTG	1260
CG104	1261	GGATTAGACGGGCCAAGAGAGGAATTGGGGATGGACCGGAGTCATCCTGTGGCTGGAATC	1320
CG37	1261	GGATTAGACGGGCCAAGAGAGGAATTGGGGATGGACCGGAGTCATCCTGTGGCTGGAATC	1320
CG104	1321	CAGCAGGTGGTAACTGTGCTGTTTCGTATGGGGCATTCTCTGCGTTTTTGAGGGAAGATG	1380
CG37	1321	CAGCAGGTGGTAACTGTGCTGTTTCGTATGGGGCATTCTCTGCGTTTTTGAGGGAAGATG	1380
CG104	1381	ACAACAGATTGACGAGGTCTGCTAATGGCATGAATGGAAATGGAAGTCTTATGGGAAAGG	1440
CG37	1381	ACAACAGATTGACGAGGTCTGCTAATGGCATGAATGGAAATGGAAGTCTTATGGGAAAGG	1440
CG104	1441	GGAAAGTGAAGCCTGAATCAGTTACTGAAGCTGCTAAACTTGCTTCAAATGGACAACCCCT	1500
CG37	1441	GGAAAGTGAAGCCTGAATCAGTTACTGAAGCTGCTAAACTTGCTTCAAATGGACAACCCCT	1500

CG104	1501	TTGAAATAATATTCTATCCAAGAGCTAGTACTCCTGAATTCTGTGTCAAGGCAGCACTGG	1560
CG37	1501	TTGAAATAATATTCTATCCAAGAGCTAGTACTCCTGAATTCTGTGTCAAGGCAGCACTGG	1560
CG104	1561	TGAAAGCAGCATTACAGATCCGGTGGTGCTCAGGTATGAGGTTCAAGATGGCCTTTGAAA	1620
CG37	1561	TGAAAGCAGCATTACAGATCCGGTGGTGCTCAGGTATGAGGTTCAAGATGGCCTTTGAAA	1620
CG104	1621	CCGAGGACTCTTCACGAATTAGTTGGTTCATGGGTACCATCAATTCGGTTCAGGTTTCGG	1680
CG37	1621	CCGAGGACTCTTCACGAATTAGTTGGTTCATGGGTACCATCAATTCGGTTCAGGTTTCGG	1680
CG104	1681	ACCCACTGCGCTGGCCTGAATCACCATGGAGGCTTCTTCAGGTAATCACTGtttttttCT	1740
CG37	1681	ACCCACTGCGCTGGCCTGAATCACCATGGAGGCTTCTTCAGGTAATCACTGTTTTTTTCT	1740
CG104	1741	CCCTGCCTGAATTCATTGCCAATAATCAATGTATTCTGAACATGGTGATTCAGGACCGAA	1800
CG37	1741	CCCTGCCTGAATTCATTGCCAATAATCAATGTATTCTGAACATGGTGATTCAGGACCGAA	1800
CG104	1801	TATATCACGTCTGCAGAAACATAGAAGTTTGAAGTTCAGTGATTGTCGGGATGATTTGT	1860
CG37	1801	TATATCACGTCTGCAGAAACATAGAAGTTTGAAGTTCAGTGATTGTCGGGATGATTTGT	1860
CG104	1861	AGTAGTTGACCTTACCACAACATTTCACTTTCAGTTTGTGCACTATTGATGGTCTATGGAT	1920
CG37	1861	AGTAGTTGACCTTACCACAACATTTCACTTTCAGTTTGTGCACTATTGATGGTCTATGGAT	1920
CG104	1921	TCATGGAAGGTCGTTTCGTTGCCTTATCACTTGCTAATAACATATTTTGTGCAGGTTACTT	1980
CG37	1921	TCACGGAAGGTCGTTTCGTTGCCTTATCACTTGCTAATAACATATTTTGTGCAGGTTACTT	1980
CG104	1981	GGGATGAACCAGATTTACTTCAGAATGTGAAACGCGTTAGCCCATGGTTGGTTGAATTGG	2040
CG37	1981	GGGATGAACCAGATTTACTTCAGAATGTGAAACGCGTTAGCCCATGGTTGGTTGAATTGG	2040
CG104	2041	TATCAAGCATGTCTCCAATTCACCTTGCCCCCTTCTCACCACCAAGGAAAAAGTTCAGAT	2100
CG37	2041	TATCAAGCATGTCTCCAATTCACCTTGCCCCCTTCTCACCACCAAGGAAAAAGTTCAGAT	2100
CG104	2101	ATCCACAACACCCTGATTTCCCCCTTGATAATCAACCTCCTGTGCCATCGTTTCTAGTT	2160
CG37	2101	ATCCACAACACCCTGATTTCCCCCTTGATAATCAACCTCCTGTGCCATCGTTTCTAGTT	2160
CG104	2161	ATCTCCATGGGACTGGCAGCCCCCTTCGGTTGTCTCCCGACAACAACCCTGCTGGCATGC	2220
CG37	2161	ATCTCCATGGGACTGGCAGCCCCCTTCGGTTGTCTCCCGACAACAACCCTGCTGGCATGC	2220
CG104	2221	AGGGAGCCAGGCATGCTCATTTTGGTCTATCCTTGTGAGATTTTCATGTCAGTAAACTGC	2280
CG37	2221	AGGGAGCCAGGCATGCTCATTTTGGTCTATCCTTGTGAGATTTTCATGTCAGTAAACTGC	2280
CG104	2281	AGTCAGGTCTGTTTTCGATTGGTTATCGATCACTGGATCCAGCTGCTGGATCAACTAGAC	2340
CG37	2281	AGTCAGGTCTGTTTTCGATTGGTTATCGATCACTGGATCCAGCTGCTGGATCAACTAGAC	2340
CG104	2341	TTTCTGGTAATGTAATGACTGAAAAACCAAGTATGAGTGAAAACGTATCTTGCTTGCTAA	2400
CG37	2341	TTTCTGGTAATGTAATGACTGAAAAACCAAGTATGAGTGAAAACGTATCTTGCTTGCTAA	2400
CG104	2401	CCATGGCACATTCTACTCAAGCTTCAAAGAAATTTGATGGCGTGAAGACTCCTCAGCTAA	2460
CG37	2401	CCATGGCACATTCTACTCAAGCTTCAAAGAAATTTGATGGCGTGAAGACTCCTCAGCTAA	2460
CG104	2461	TACTTTTGGCCGACCCATACTTACAGAATTGCAGATGTCTCAAAGCTTCTTGCGGATA	2520

CG37	2461	TACTTTTGGCCGACCCATACTTACAGAATTGCAGATGTCTCAAAGCTTCTCTGGCGATA	2520
CG104	2521	CCGTTTCTCCAGTAGGTACTGGAATAGTTTCGTGAGATGGAAATGGAGACAAAATGACAA	2580
CG37	2521	CCGTTTCTCCAGTAGGTACTGGAATAGTTTCGTGAGATGGAAATGGAGACAAAATGACAA	2580
CG104	2581	ACCTCTCCGATGGCTCTGGATCTGCTTTACATCAACAAGGTCTACCAGAAGGCTCTGCTG	2640
CG37	2581	ACCTCTCCGATGGCTCTGGATCTGCTTTACATCAACAAGGTCTACCAGAAGGCTCGGCTG	2640
CG104	2641	GCGAAAATTTCCAGTGGTACAAGGACAATTGCCAAGAAATCGACCCAAACTTGGATATCG	2700
CG37	2641	GCGAAAATTTCCAGTGGTACAAGGACAATCGCCAAGAAATCGACCCAAACTTGGATATCG	2700
CG104	2701	GCCACTGTAAAGTCTTTATGGAATCAGAAGATGTAGGACGCACTCTCGATCTTTCTTCAC	2760
CG37	2701	GCCACTGTAAAGTCTTTATGGAATCAGAAGATGTAGGACGCACTCTCGATCTTTCTTCAC	2760
CG104	2761	TTGGGTCTTATGAAGAATTGTACAGAAAACCTGGAAATATGTTTGGTATAGATAATTGAG	2820
CG37	2761	TTGGGTCTTATGAAGAATTGTACAGAAAACCTGGAAATATGTTTGGTATAGATAATTGAG	2820
CG104	2821	AGACATTGAACCATGTCTTGTACCGTGATGTTCCGGTGCTGTCAAACATGTCGGTGACG	2880
CG37	2821	AGACATTGAACCATGTCTTGTACCGTGATGTTCCGGTGCTGTCAAACATGTCGGTGACG	2880
CG104	2881	AACAATTCAGGTATATTTCTTCTCTCTTTGGCAACGTTGAGACATCGTCTTACATTCTGT	2940
CG37	2881	AACAATTCAGGTATATTTCTTCTCTCTTTGGCAACGTTGAGACATCGTCTTACATTCTGT	2940
CG104	2941	CATTTCCAATACATATCACGTCTGATTAACGCTCCTCGTTTCTGTTTCAGTGACTTCAT	3000
CG37	2941	CATTTCCAATACATATCACGTCTGATTAACGCTCCTCGTTTCTGTTTCAGTGACTTCAT	3000
CG104	3001	CAAGACAGCAAGAAGATTGACAATTCTAACAGATTGAGGAAGTAACAATGTAGGAGCTTA	3060
CG37	3001	CAAGACAGCAAGAAGATTGACAATTCTAACAGATTGAGGAAGTAACAATGTAGGAGCTTA	3060
CG104	3061	GAAGGAAGAATAAGAGTTGATTTCAACTGTACAGCTGGTCAATATCAGGTCCTTCATTC	3120
CG37	3061	GAAGGAAGAATAAGAGTTGATTTCAACTGTACAGCTGGTCAATATCAGGTCCTTCATTC	3120
CG104	3121	CTTGCTGACCGTTCTCTGTTTCAAATCTGGGAGCTGCTGCTAAGATTCAAGCtttttttA	3180
CG37	3121	CTTGCTGACCGTTCTCTGTTTCAAATCTGGGAGCTGCTGCTAAGATTCAAGCTTTTTTTA	3180
CG104	3181	ACTATGAAAAAGCTGATATTTTCTTTTCTTATAATTAAttttttttttCCCAATC	3240
CG37	3181	ACTATGAAAAAGCTGATATTTTCTTTTCTTATAATTAATTTTTTTTTTCCCAATC	3240
CG104	3241	CAACTTCTGGAGGGAATGTTTGAATTTTGGAACTTGCTTACATCCCCATGTTCTGTGATG	3300
CG37	3241	CAACTTCTGGAGGGAATGTTTGAATTTTGGAACTTGCTTACATCCCCATGTTCTGTGATG	3300
CG104	3301	AACTTTGAGGGGGtttctttttGGGGGtttttttCTTCTTTCCATTTAGGTGGTTAGT	3360
CG37	3301	AACTTTGAGGGGGTTTCTTTTGGGGGTTTTTTTCTTCTTTCCATTTAGGTGGTTAGT	3360
CG104	3361	TCTTATTATATAAGTGGAAGTGATTGAGAGAGTATTGGGAATGTGTTTGAAGAGAAGC	3420
CG37	3361	TCTTATTATATAAGTGGAAGTGATTGAGAGAGTATTGGGAATGTGTTTGAAGAGAAGC	3420
CG104	3421	ATTGTGAAATATAATGAGTTAAAGTGGAGTTGTTTCTAAAGGTTTGTGGTCAAAGTAAGT	3480
CG37	3421	ATTGTGAAATATAATGAGTTAAAGTGGAGTTGTTTCTAAAGGTTTGTGGTCAAAGTAAGT	3480
CG104	3481	CATAAAAGAAAGGCATTTTGAAGAAGAAAAGCAAAAAGGGCTTACCTTGAAACTTGAGT	3540

CG37	3481	CATAAAAGAAAGGCATTTTGAAGAAGAAAAGACAAAAGGGCTTACCTTGAAACTTGAGT	3540
CG104	3541	TTCATTTGTAAAAGTTCAATGTTAATGATGTAGTGAGTTGTGAGTTTGTGAAATTAATGC	3600
CG37	3541	TTCATTTGTAAAAGTTCAATGTTAATGATGTAGTGAGTTGTGAGTTTGTGAAATTAATGC	3600
CG104	3601	CATTCCCCAAAAGATGGGGAATTCAAAAGTTTCATAAAAAAGAAAGTGGTTTTCATTTCAT	3660
CG37	3601	CATTCCCCAAAAGATGGGGAATTCAAAAGTTTCATAAAAAAGAAAGTGGTTTTCATTTCAT	3660
CG104	3661	TGTATGACCAAAATGAATGATGTAAATTTGTTTGGTTGGAAATCTACTCTACTATTAGTC	3720
CG37	3661	TGTATGACCAAAATGAATGATGTAAATTTGTTTGGTTGGAAATCTACTCTACTATTAGTC	3720
CG104	3721	T 3721	
CG37	3721	T 3721	

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CG104	1	TTCTCTTTCTCTTTCTCTTTCTATATATAAAGCTTATGCAATTAACCTCTCTGGCGTTACT	60
CG37	1	TTCTCTTTCTCTTTCTCTTTCTATATATAAAGCTTATGCAATTAACCTCTCTGGCGTTACT	60
CG104	61	GAAGCATCTATGAGATCTACTGTCCACACTGAATTCATGGATTCAATGAGATTTCTCTACG	120
CG37	61	GAAGCATCTATGAGATCTACTGTCCACACTGAATTCATGGATTCAATGAGATTTCTCTACG	120
CG104	121	AATTAAGCCAGTACGGAACCCAGGTGAATATCAAAAGAAGTAGAACAGCAATGAAATC	180
		.	
CG37	121	AATTAAGCCAAATACGGAACCCAGGTGAATATCAAAAGAAGTAGAACAGCAACGAAATC	180
CG104	181	AACAAACAATTTTACAACCCTATCTCCTTTTTTTTCTTTTCTTTTGTTCAGCTTCAT	240
CG37	181	AACAAACAATTTTACAACCCTATCTCCTTTTTTTTCTTTTCTTTTGTTCAGCTTCAT	240
CG104	241	GTGGGTTTCTTTTGTTTATCCATAACCTCTCTTAAATCTGTGTTTTGAAGCTTGGGTT	300
CG37	241	GTGGGTTTCTTTTGTTTATCCATAACCTCTCTTAAATCTGTGTTTTGAAGCTTGGGTT	300
CG104	301	TTAATTCCTTTTCTTTTCTTCACCTTTAGCTTGCATCGGATCCGTGGTTTTTTATTCTGA	360
CG37	301	TTAATTCCTTTTCTTTTCTTCACCTTTAGCTTGCATCGGATCCGTGGTTTTTTATTCTGA	360
CG104	361	TCTTCATTTCTCGTGGCCAATTTCTTTTGGGAGAGTAGGTTTTGGGTTCTGGGTTCTGGG	420
CG37	361	TCTTCATTTCTCGTGGCCAATTTCTTTTGGGAGAGTAGGTTTTGGGTTCTGGGTTCTGGG	420
CG104	421	TTGGGCTTTATTTTAGGTGTATGTCCCAATTTGAGATACCCTTTGTGTTTCGATGAAAG	480
CG37	421	TTGGGCTTTATTTTAGGTGTATGTCCCAATTTGAGATACCCTTTGTGTTTCGATGAAAG	480
CG104	481	TCCCCGGTATTTTTTTATTTTTTATTTTTTTTTTTTATAATTTGAGCTGTTTTCTGG	540
CG37	481	TCCCCGGTATTTTTTTATTTTTTATTTTTTTTTTTTATAATTTGAGCTGTTTTCTGG	540
CG104	541	ATTTTGACTGTCTAGGGTTTGAATTGTAATGGGGCTCTATTAATTTGAACTATAGGTAT	600
CG37	541	ATTTTGACTGTCTAGGGTTTGAATTGTAATGGGGCTCTATTAATTTGAACTATAGGTAT	600
CG104	601	GCATTTAGGTTGTTGACTTTCTATAAGGAGAAATAAAAAATAGGCGGTAAGGTAAGGCCG	660
CG37	601	GCATTTAGGTTGTTGACTTTCTATAAGGAGAAATAAAAAATAGGCGGTAAGGTAAGGCCG	660
CG104	661	AACCAGGATTATTTATTATTAGAATTACTCATGGTAGTTAACATGTAGAATTCTTGTACC	720
CG37	661	AACCAGGATTATTTATTATTAGAATTACTCATGGTAGTTAACATGTAGAATTCTTGTACC	720

CG104	721	TCCCTAAATCGAGTTTCTTAATTGCTAAACTGATTTCGTGGGGAATTAGCTGCTTTTC	780
CG37	721	TCCCTAAATCGAGTTTCTTAATTGCTAAACTGATTTCGTGGGAAATTAGCTGCTTTTC	780
CG104	781	AGTTTGTTTAGTCAACATCTGATTTTGATTCTCTAAAAATTATCCTATGCATGATTTCAC	840
CG37	781	AGTTTGTTTAGTCAACATCTGATTTTGATTCTCTAAAAATTATCCTATGCATGATTTCAC	840
CG104	841	AATTTTGTGTCTTTATAGTAAAGTTTGATTCTGGACTTTCGGTTTCTACTTTATTATT	900
CG37	841	AATTTTGTGTCTTTATAGTAAAGTTTGATTCTGGACTTTCGGTTTCTACTTTATTATT	900
CG104	901	GTAATTTTGAGATCCTATCATCACCTATTGTTTCTCATAGATTTCCTTTACCAAAAATCT	960
CG37	901	GTGATTTTGAGATCCTATCATCACCTATTGTTTCTCATAGATTTCCTTTACCAAAAATCT	960
CG104	961	ATTATTTCTTTGAATGTATTGCATAAACAACTATTTGTTCTGCATTACCGTTGTCCTCT	1020
CG37	961	ATTATTTCTTTGAATGTATTGCATAAACAACTATTTGTTCCGCATTACCGTTGTCCTCT	1020
CG104	1021	TCTCTGATGCTAATGGATATGCTTTCATTGATTTAGGCGAGGGGTGGCACAGAATATTCT	1080
CG37	1021	TCTCTGATGCTAATGGATGTCTTTCATTGATTTAGGCGAGGGGTGGCACAGAATATTCT	1080
CG104	1081	TTTCGGAGCAGGCACTAAATTAATAAGTTATCAAGATCACTCTAGAGTGCCATTCAATTG	1140
CG37	1081	TTTCGGAGCAGGCACTAAATTAATAAGTTATCAAGATCACTCTAGAGTGCCATTCAATTG	1140
CG104	1141	GCATTCATTCTAAGAATGCTAAGGAAGATAACCACAGCTATCGTTCGAGGATTTTCGTGG	1200
CG37	1141	GCATTCATTCTAAGAATGCTAAGGAAGATAACCACAGCTATCGTTCGAGGATTTTCGTGG	1200
CG104	1201	CGTTAGGACTGAGGGATTGAGCACATATAATGTGCTAGAAGGATATTTGTTGAAGCAAGG	1260
CG37	1201	CGTTAGGACTGAGGGATTGAGCACATATAATGTGCTAGAAGGATATTTGTTGAAGCAAGG	1260
CG104	1261	ATGGATGTTTATGTTATATTGTCACAATATAATGGAACAGGGGTATTTACAATGGATGA	1320
CG37	1261	ATGGATGTTTATGTTATATTGTCACAATATAATGGAACAGGGGTATTTACAATGGATGA	1320
CG104	1321	TTTTTGTCTTTTTCTTTTTCTTCGGTTGTAGAAATTTTACTTTCTAGTTAGTAAA	1380
CG37	1321	TTTTTGTCTTTTTCTTTTTCTTCGGTTGTAGAAATTTTACTTTCTAGTTAGTAAA	1380
CG104	1381	AGAGTGGTAGTTGCAGAGAACACAAACACCTGATGTAAATTGTTTATCTCGATGCTTATT	1440
CG37	1381	AGAGTGGTAGTTGCAGAGAACACAAACACCTGATGTAAATTGTTTATCTCGATGCTTATT	1440
CG104	1441	AGGAAGTTGTAGTTTCTGGACTTGTTAGCCACGCTTTACACACTGCTCCATTCCGACT	1500
CG37	1441	AGGAAGTTGTAGTTTCTGGACTTGTTAGCCACGCTTTACACACTGCTCCATTCCGACT	1500
CG104	1501	ATTTTGTGGAATACTCCATTTATACCATGGAATCTACGACATTGCATACAACCTCATCAG	1560
CG37	1501	ATTTTGTGGAATACTCCATTTATACCATGGAATCTACGACATTGCATACAACCTCATCAG	1560
CG104	1561	TCGGGTGCTATTTCATAGGTTTATACCTTTTCATTGCACCTGCACCTCTAGTTTCAATTAGT	1620
CG37	1561	TCGGGTGCTATTTCATAGGTTTATACCTTTTCATTGCACCTGCACCTCTAGTTTCAATTAGT	1620
CG104	1621	TATGTTGACCCTGGAAGTGGGCTGCAACTGTTGAAGGAGGTGCTCGGTTTGGCTTTGAT	1680
CG37	1621	TATGTTGACCCTGGAAGTGGGCTGCAACTGTTGAAGGAGGTGCTCGGTTTGGCTTTGAT	1680
CG104	1681	TTGTTTGTGTTAGTGCTTCTTTCAATCTTGCTGCTATTTATGCCAGTATCTCTCAGCT	1740

CG37	1681	TTGTTTGTGTTAGTGCTTCTTTTCAATCTTGCTGCTATTTTATGCCAGTATCTCTCAGCT	1740
CG104	1741	AGCATTGGTGTGGTCACTGGAAGAGGTCTTGCCCAGGTAATTTATTTGTTTTCAAGGCTT	1800
CG37	1741	AGCATTGGTGTGGTCACTGGAAGAGGTCTTGCCCAGGTAATTTAATTGTTTTCAAGGCTT	1800
CG104	1801	TCGCATTTTTACTTATGTTGTGTCTATCAAGCAGCTTTTATCTGAAAATCAGTCAATTGA	1860
CG37	1801	TAGCATTTTTACTTATGTTGTGTCTATCAAGCAGCTTTTATCTGAAAATCAGTCAATTGA	1860
CG104	1861	CCGATGTTGATTTTTCCCTTTATTAGTTTGAATTTTTTTTTATGGGAGAATTCATGT	1920
CG37	1861	CCGATGTTGATTTTTCCCTTTATTAGTTTGAATTTTTTTTTATGGGAGAATTCATGT	1920
CG104	1921	GTTGGTTGTATCTTGATTCTCCTATGTGGTTCGTTTGCATCTTCTCATTAGTCTTCAA	1980
CG37	1921	GTTGGTTGTATCTTGATTCTCCTATGTGGTTGTTGCGTCTTCTCATTAGTCTTCAA	1980
CG104	1981	TTTCGAGGACTTTTTGTAATTATCTTTTAGACACGAATCTCTATGGTTGAATTCCTTC	2040
CG37	1981	TTTCGAGGACTTTTTGTAATTATCTTTTAGACACGAATCTCTGTGGTTGAATTCCTTC	2040
CG104	2041	TTGTAGAAGGGGTCCCCTGTTTTTTTGTGGCTTTG-TTTTTTATGCCCGTTATTCTT	2099
CG37	2041	TTGTAGAAGGGGTCCCCTGTTTTTTTGTGGCTTTGTTTTTTTATGCCCGTTATTCTT	2100
CG104	2100	TCATTTATTCTCAATGAAAGTTGTTCTTATAAATAAATAAATGTGTGTGGACGTGTCTCT	2159
CG37	2101	TCATTTATTCTCAATGAAAGTTGTTCTTATAAATAAATAAATGTGTGTGGACGTGTCTCT	2160
CG104	2160	GTTTCCAGTTTGGGTGATGTTTGATATGTTAGCTTGTAACCTTCACTTTCACTTTATGC	2219
CG37	2161	GTTTCCAGTTTGGGTGATGTTTGATATGTTAGCTTGTAACCTTCACTTTCACTTTATGC	2220
CG104	2220	CTCTTCCATTTTGGTTTGTTCATGGGTATAGGTTGATTTTGTATTTTTTAAATTACT	2279
CG37	2221	CTCTTCCATTTTGGTTTGTTCATGGGTATAGGTTGATTTTGTATTTTTTAAATTACT	2280
CG104	2280	TGACTGCTAGTTGTTAAATGTTACTGGAGGTTGACATATTACCCTATTTGTTTGTG	2339
CG37	2281	TGACTGCTAGTTGTTAAATGTTACTGGAGGTTGACATATTACCCTATTTGTTTGTG	2340
CG104	2340	ATTATACCAAAGATATGCAACGAGGAGTATGATAAGTGATACATGTTTCTTCTGGGAATC	2399
CG37	2341	ATTATACCAAAGATATGCAACGAGGAGTATGATAAGTGATACATGTTTCTTCTGGGAATC	2400
CG104	2400	CAAGCAGAGGCTTCTGTGATTCTGTTAGACCTTAACATGGTATTTATTTTGTCTGCT	2459
CG37	2401	CAAGCAGAGGCTTCTGTGATTCTGTTAGACCTTAACATGGTATTTATTTTGTCTGCT	2460
CG104	2460	AAGTTATTCCAGACTTCCAGCCAAACCTGTGATTGAGTTTGTAAAGATTTTTTTAGTG	2519
CG37	2461	AAGTTATTCCAGACTTCCAGCCAAACCTGTGATTGAGTTTGTAAAGATTTTTTTAGTG	2520
CG104	2520	AAGCATGGTCTAATTTGACCATAATTTAATCTTCATTTTCATTATAAAGCTAACATGTC	2579
CG37	2521	AAGCATGGTCTAATTTGACCATAATTTAATCTTCATTTTCATTATAAAGCTAACATGTC	2580
CG104	2580	ATTTAAAAACATACTAGATCTTGGGCATTTCAAATGGACTTAATCTTCTACTTGGGTGG	2639
CG37	2581	ATTTAAAAACATACTAGATCTTGGGCATTTCAAATGGACTTAATCTTCTACTTGGGTGG	2640
CG104	2640	GACCTCTTCACATGTGTCCTTTTGACGGGTGTGCTGCTGCTTTATTTCTCCTTTTGCT	2699
CG37	2641	GACCTCTTCACATGTGTCCTTTTGACGGGTGTGCTGCTGCTTTATTTCTCCTTTTGCT	2700
CG104	2700	GACCTTCTGGTAAATAGAACTTTTAATCAATCATGCATAACTTTCTCTTTGATGTAATTC	2759

CG37	2701	GACCTTCTG	GTAATAAGAACTTTTAATCAATCATGCACAACCTTCTCTTTGATGTAATTC	2760
CG104	2760	ATTATCTCAAGGGTTTCTATTTTCTAG	GAAGATGGCAGGGCAAAGTTCCTCTATATATGT	2819
CG37	2761	ATTATCTCAAGGGTTTCTATTTTCTAG	GAAGATGGCAGGGCAAAGTTCCTCTATATATGT	2820
CG104	2820	ATGGCGGGATTTGTACTGCTCTCTTTGGTTCTTGGAGTATTAATCAGTCAACCTGAAATC		2879
CG37	2821	ATGGCGGGATTTGTACTGCTCTCTTTGGTTCTTGGAGTATTAATCAGTCAACCTGAAATC		2880
CG104	2880	CCACTTTCCATGAATCTCATGCCGACAAGGTTAAATGGGGAAAGTGCCTTTACTCTTATG		2939
CG37	2881	CCACTTTCCATGAATCTCATGCCGACAAGGTTAAATGGGGAAAGTGCCTTTACTCTTATG		2940
CG104	2940	AGTCTTCTTGGAGCAAGTGTCTATGCCACACAATTTTATGTGCATTCTTCTATTGTGCAG		2999
CG37	2941	AGTCTTCTTGGAGCAAGTGTCTATGCCACACAATTTTATGTGCATTCTTCTATTGTGCAG		3000
CG104	3000	GTACTTCTCGTTTCTTCTATCGCCATTGTATTGTATTGAGCATAAACTGCAAAATGTTT		3059
CG37	3001	GTACTTCTCGTTTCTTCTATCGCCATTGTATTGTATTGAGCATAAACTGCAAAATGTTT		3060
CG104	3060	TACTTTTCTTAGTCAATGTGTATGTGCAGACAAGGAAAGTCCAATGAGATGATTTTGCC		3119
CG37	3061	TACTTTTCTTAGTCAATGTGTATGTGCAGACAAGGAAAGTCCAATGAGATGATTTTGCC		3120
CG104	3120	TACCAATATCTTAAGATTAGGATGTCATTCTAGGCGGTTGATCAAGTTCAAAACTTCTGG		3179
CG37	3121	TACCAATATCTTAAGATTAGGATGTCATTCTAGGCGGTTGATCAAGTTCAAAACTTCTGG		3180
CG104	3180	GATTCAAATGTTTTAATCATTTAGATTCTTCATAGTATAAAATTGGATATCCTTATGTG		3239
CG37	3181	GATTCAAATGTTTTAATCATTTAGATTCTTCATAGTATAAAATTGGATATCCTTATGTG		3240
CG104	3240	CTTTATAATGATTTTCTTTCTTCTTTTTCGAG	CAGCACCAGAGTCCACCAAAATTTTCC	3299
CG37	3241	CTTTATAATGATTTTCTTTCTTCTTTTTCGAG	CAGCACCAGAGTCCACCAAAATTTTCC	3300
CG104	3300	AAAGAAGTTTCGTGTTATAATCATTTGTTTGCTATTTTCTGCATATTCAGTGAATTTAT		3359
CG37	3301	AAAGAAGTTTCGTGTTATAATCATTTGTTTGCTATTTTCTGCATATTCAGTGAATTTAT		3360
CG104	3360	GTGGTGAATAACGTTCTCATGAACTCAGCTGCAAATGTATTCTATAGCAGTGGTCTTGCT		3419
CG37	3361	GTGGTGAATAACGTTCTCATGAACTCAGCTGCAAATGTATTCTATAGCAGTGGTCTTGCT		3420
CG104	3420	TTGCACACCTTTACAGATGCATTGTCTTTAATGGAGCAG	GTGTTCTAGAGTCCCCCCTC	3479
CG37	3421	TTGCACACCTTTTACAGATGCATTGTCTTTAATGGAGCAG	GTGTTCTAGAGTCCCCCCTC	3480
CG104	3480	CCTTTTAAATTTATTTATTTTGTGTTACTTGCTCCTTAACACAGTTTTACTGTAATAAGT		3539
CG37	3481	CCTTTTAAATTTATTTATTTTGTGTTACTTGCTCCTTAACACAGTTTTACTGTAATAAGT		3540
CG104	3540	ATTGATTTTATTTCCATTTCCTCCAAACTATGCAG	GTATTGGGAGCTCAGTGGTATA	3599
CG37	3541	ATTGATTTTATTTCCATTTCCTCCAAACTATGCAG	GTATTGGGAGCTCAGTGGTATA	3600
CG104	3600	TGTTCCTCTTACTTGTTTTGTTTCTATCAAATCAAATCACAGCTCTCACATGGAGTCT		3659
CG37	3601	TGTTCCTCTTACTTGTTTTGTTTCTATCAAATCAAATCACAGCTCTCACATGGAGTCT		3660
CG104	3660	TGGTGGTCAACTGGTTCTGACCAATTTCTTAAAAATAGATATTCCTGGTTGGCTCCATTG		3719
CG37	3661	TGGTGGTCAACTGGTTCTGACCAATTTCTTAAAAATAGATATTCCTGGTTGGCTCCATTG		3720

CG104	3720	TGCTACAATTAGGATTATTGCCATTATTCCAGCACTATGCTGTGTCTGGAGTTCGGGTGC	3779
CG37	3721	TGCTACAATTAGGATTATTGCCATTATTCCAGCACTATGCTGTGTCTGGAGTTCGGGTGC	3780
CG104	3780	TGAAGGGATGTATCAACTTCTTATATTTTCTCAGGTATGGTAGCTCTATTGCTTCCATC	3839
CG37	3781	TGAAGGGATGTATCAACTTCTTATATTTTCTCAGGTATGGTAGCTCTATTGCTTCCATC	3840
CG104	3840	TTCTGTGATTCCCCTCTATCGTGTGCTTCATCAAGAACAATAATGGGTGCCCTCAAAAT	3899
CG37	3841	TTCTGTGATTCCCCTCTATCGTGTGCTTCATCAAGAACAATAATGGGTGCCCTCAAAAT	3900
CG104	3900	ATCGCAGCTTGTGGAATTTATAGCAATTGGTATCTTTATTGGAATATTAGGACTGAAAAAT	3959
CG37	3901	ATCGCAGCTTGTGGAATTTATAGCAATTGGTATCTTTATTGGAATATTAGGACTGAAAAAT	3960
CG104	3960	TATATTTGTTGTAGAGATGATTTTGGTAACAGTGATTGGGTAGTTAACTTGAGGTGGAA	4019
CG37	3961	TATATTTGTTGTAGAGATGATTTTGGTAACAGTGATTGGGTAGTTAACTTGAGGTGGAA	4020
CG104	4020	CATGGGGAGTGGTATGTCAATCCCATTTGTGGTTCTTCTTATTACTGCTTGTTTCATCGTT	4079
CG37	4021	CATGGGGAGTGGTATGTCAATCCCATTTGTGGTTCTTCTTATTACTGCTTGTTTCATCGTT	4080
CG104	4080	TTGTCTGATGCTATGGTTGGCAGCTACCCCATTAATACTGCTACTACTATTGCCCAATT	4139
CG37	4081	TTGTCTGATGCTATGGTTGGCAGCTACCCCATTAATACTGCTACTACTATTGCCCAATT	4140
CG104	4140	AGATGCTCAAGTATTGAACTGGGATATGGCAGAGGTTAGACCCGATTCATCTGAAGAGAG	4199
CG37	4141	AGATGCTCAAGTATTGAACTGGGATATGGCAGAGGTTAGACCCGATTCATCTGAAGAGAG	4200
CG104	4200	GGAAAAACATAGATTTGGGGAAAAAGTTCATACAGTGCCGAGCCTATAGAAAGTCATTCTGA	4259
CG37	4201	GGAAAAACATAGATTTGGGGAAAAAGTTCATACAGTGCCGAGCCTATAGAAAGTCATTCTGA	4260
CG104	4260	CCTATCTTCAACAAAGTTTGATTTTAATTTGCCTGAAAAATATTATGGAACCTGATCAGGT	4319
CG37	4261	CCTATCTTCAACAAAGTTTGATTTTAATTTGCCTGAAAAATATTATGGAACCTGATCAGGT	4320
CG104	4320	TCTTGGTTCAGTTAATCAAAACGAGAATCGATCTAGTACTGTAGTTCCAAGCTCCCCAAA	4379
CG37	4321	TCTTGGTTCAGTTAATCAAAACGAGAATCGATCTAGTACTGTAGTTCCAAGCTCCCCAAA	4380
CG104	4380	ATATGTACAAGAGGAACTTGAATCCACTGAGGAGTTAGTCTCATCCTCAATTGTGACTCA	4439
CG37	4381	ATATGTACAAGAGGAACTTGAATCCACTGAGGAGTTAGTCTCATCCTCAATTGTGACTCA	4440
CG104	4440	CGATGTTCTGATTCAACATTGGCTGACAAAAAGGTCTTAAAAATAGAGTCAGTGGAGGC	4499
CG37	4441	CGATGTTCTGATTCAACATTGGCTGACAAAAAGGTCTTAAAAATAGAGTCAGTGGAGGC	4500
CG104	4500	CGTTGAAAAGACTGTTGGACTCGATGGTGATTTCGCTTCTGAGAAGGATGATTATGAGGT	4559
CG37	4501	CGTTGAAAAGACTGTTGGACTCGATGGTGATTTCGCTTCTGAGAAGGATGATTATGAGGT	4560
CG104	4560	TGATAACTGGGAGGCTGAAGAGTCACTGAAAGAGATCTCTGGGAATATACCATCCTCAAC	4619
CG37	4561	TGATAACTGGGAGGCTGAAGAGTCACTGAAAGAGATCTCTGGGAATATACCATCCTCAAC	4620
CG104	4620	ATCTGAGGGTCCTGGTTCTTTTAGAAGTATTGGTGGGAGAAGTGAAGAAGGTGGGAATGG	4679
CG37	4621	ATCTGAGGGTCCTGGTTCTTTTAGAAGTATTGGTGGGAGAAGTGAAGAAGGTGGGAATGG	4680
CG104	4680	AACTGGTAGTCTTTCAAGGTTAGCTGGCCTCGGGCGTGCTGCAAGGCCCAACTTACTGG	4739
CG37	4681	AACTGGTAGTCTTTCAAGGTTAGCTGGCCTCGGGCGTGCTGCAAGGCCCAACTTACTGG	4740

CG104	4740	AAATCTTGATGAATTTGGGGACAATTGTATGATTCCATGGGGTGCCTACTCAAGATGC	4799
CG37	4741	AAATCTTGATGAATTTGGGGACAATTGTATGATTCCATGGGGTGCCTACTCAAGATGC	4800
CG104	4800	AAAGGTTAAGAACTAGATTGTACTGGGTTTACCTCTCTGAAATTGGATGCTGTTGG	4859
CG37	4801	AAAGGTTAAGAACTAGATTGTACTGGGTTTACCTCTCTGAAATTGGATGCTGTTGG	4860
CG104	4860	TAAAGATTTTCCTCACTCATCACCTATTGGATGCAAAACATCCGATCCAATTTCTTCTAG	4919
CG37	4861	TAAAGATTTTCCTCACTCATCACCTATTGGATGCAAAACATCCGATCCAATTTCTTCTAG	4920
CG104	4920	TTTGTACGACTCCCCAAGAGTCAGAGGGTACAAAGTGGGTAGAACACCCTATGGGAT	4979
CG37	4921	TTTGTACGACTCCCCAAGAGTCAGAGGGTACAAAGTGGGTAGAACACCCTATGGGAT	4980
CG104	4980	ACAAAAGGGGCACCAGCCATTGTGGTCTAACCACATGCAGCATTGGGATGCATATGTGAA	5039
CG37	4981	ACAAAAGGGGCACCAGCCATTGTGGTCTAACCACATGCAGCATTGGGATGCATATGTGAA	5040
CG104	5040	TAATTCTAGCCATAATGCTCTGGACTCTGGAGTGAAGCGATATTCTAGTTTGCGCAGTTT	5099
CG37	5041	TAATTCTAGCCATAATGCTCTGGACTCTGGAGTGAAGCGATATTCTAGTTTGCGCAGTTT	5100
CG104	5100	GCCTTCTACTGAGAGTTGGGATTATCAGCCTGCCACAGTCCATGGCTATCAGTTAACTTA	5159
CG37	5101	GCCTTCTACTGAGAGTTGGGATTATCAGCCTGCCACAGTCCATGGCTATCAGTTAACTTA	5160
CG104	5160	TCTGAGTAGAATGGCAAAGGACAGAAGTTCTGGTAATTCGAACGGTCAGTTGGATTTCATC	5219
CG37	5161	TCTGAGTAGAATGGCAAAGGACAGAAGTTCTGGTAATTCGAACGGTCAGTTGGATTTCATC	5220
CG104	5220	AGGCTCTAAATATCATACCTTGGGTGGTGGTGGTGCAGGCTTGCAGAGCTCAGTTGCATT	5279
CG37	5221	AGGCTCTAAATATCATACCTTGGGTGGTGGTGGTGCAGGCTTGCAGAGCTCAGTTGCATT	5280
CG104	5280	TGCAATGGGGCAAAAGTTGCAAAATGGCTTGGGTGCTTGTACAGAGGCGGCTCCCCCAGG	5339
CG37	5281	TGCAATGGGGCAAAAGTTGCAAAATGGCTTGGGTGCTTGTACAGAGGCGGCTCCCCCAGG	5340
CG104	5340	TTTTTCCAACATCACAGTATCCAGGAAACCTTCTTCCGAATCTGAAAGGAAATATTATGA	5399
CG37	5341	TTTTTCCAACATCACAGTATCCAGGAAACCTTCTTCCGAATCTGAAAGGAAATATTATGA	5400
CG104	5400	TCATTCTCTTTCTGGAACGTGGTGAGAATTTAGTGAGTGTATCTAACACAAAGAAATACCA	5459
CG37	5401	TCATTCTCTTTCTGGAACGTGGTGAGAATTTAGTGAGTGTATCTAACACAAAGAAATACCA	5460
CG104	5460	TAGCTTACCGGATATTACCGTGATCAGCACACATCAGATAAGAGTTCTCAGTGGGATAA	5519
CG37	5461	TAGCTTACCGGATATTACCGTGATCAGCACACATCAGATAAGAGTTCTCAGTGGGATAA	5520
CG104	5520	TGTGAGTGGTTATGGAACATCTATTGGTAGAATAACAGCTCGTGGAGTGTCCACAAATTC	5579
CG37	5521	TGTGAGTGGTTATGGAACATCTATTGGTAGAATAACAGCTCGTGGAGTGTCCACAAATTC	5580
CG104	5580	TGGATCAAGATTAGTTTCTCCTTTAGCATTTGATGAACTATCTCCTGCAATGTCTACAG	5639
CG37	5581	TGGATCAAGATTAGTTTCTCCTTTAGCATTTGATGAACTATCTCCTGCAATGTCTACAG	5640
CG104	5640	TGGTGCATTATCACCACAAATGAATCCTCATCTGGATTCTGGATCTTTCTGGCATAGACA	5699
CG37	5641	TGGTGCATTATCACCACAAATGAATCCTCATCTGGATTCTGGATCTTTCTGGCATAGACA	5700
CG104	5700	GCCTTCTGAGCAATTTGGCTTGGACAAAAATAGCAACTCCGAGAGTAAAGGAATTGGGAG	5759

CG37	5701	GCCTTCTGAGCAATTGGCTTGGACAAAAATAGCAACTCCGAGAGTAAAGGAATTGGGAG	5760
CG104	5760	GCTGCATTCAATTAGTCACGAAGCTTCTTTTGTGTTAATTCAGAGGCCAGGCTTCTCCA	5819
CG37	5761	GCTGCATTCAATTAGTCACGAAGCTTCTTTTGTGTTAATTCAGAGGCCAGGCTTCTCCA	5820
CG104	5820	GTCCTTCAGAGACTGCATTGTCAAACCTCTGAAATTAGAAGGATCAGACTGGTTATTTGG	5879
CG37	5821	GTCCTTCAGAGACTGCATTGTCAAACCTCTGAAATTAGAAGGATCAGACTGGTTATTTGG	5880
CG104	5880	GCAAAGTGATGGTGTGCTGACGAGGAGCTAATTGATTGTGTAGCTGCCAGGGAGAAATTTCT	5939
CG37	5881	GCAAAGTGATGGTGTGCTGACGAGGAACTAATTGATTGTGTAGCTGCCAGGGAGAAATTTCT	5940
CG104	5940	TTATGAAGCTGAGGCAAGGAGATGGGTGCGGTGGTCCGCATGAAAGAATCTCCTTCATT	5999
CG37	5941	TTATGAAGCTGAGGCAAGGAGATGGGTGCGGTGGTCCGCATGAAAGAATGTCCTTCATT	6000
CG104	6000	TTCTCCTGATAGGAGACCAGGTTCTGGAATGAAGAATGATACAAATTTCTCCAATGTTTC	6059
CG37	6001	TTCTCCTGATAGGAGACCAGGTTCTGGAATGAAGAATGATACAAATTTCTCCAATGTTTC	6060
CG104	6060	TATTTCTCTGTACCTCATTGTGGAGAAGGCTGTATTTGGAGATCAGATTTGATTGTAAG	6119
CG37	6061	TATTTCTCTGTACCTCATTGTGGAGAAGGCTGTATTTGGAGATCAGATTTGATTGTAAG	6120
CG104	6120	TTTTGGTGATGGTGCATTACCGTATTCTAGATCTCTCACTTATGAAAAGTCGGCCTGA	6179
CG37	6121	TTTTGGTGATGGTGCATTACCGTATTCTAGATCTCTCACTTATGAAAAGTCGGCCTGA	6180
CG104	6180	ACTATGGGGAAAAATATACCTATGTACTCAATCGTCTTCAG	6239
CG37	6181	ACTATGGGGAAAAATATACCTATGTACTCAATCGTCTTCAG	6240
CG104	6240	TTTGTATCATTAGCATATAACCTAGTGTATCAGGTAAAAGTCTCTTACTGAAAATACCAT	6299
CG37	6241	TTTGTATCATTAGCATATAACCTAGTGTATCAGGTAAAAGTCTCTTACTGAAAATACCAT	6300
CG104	6300	TGGTCTTTGTTGAGATCACATCCATTTACATAAGTTGAGAGTTCGATCAGTTGCAGGGCT	6359
CG37	6301	TGGTCGTTGTTGAGATCACATCCATTTACATAAGTTGAGAGTTCGATCAGTTGCAGGGCT	6360
CG104	6360	GACATATTTTGAGTCAAAATGGCT---AGTAGTTTGGATTATATGAATTACAGATATT	6416
CG37	6361	GACATATTTTGAGTCAAAATGGCTAGAGTAGTTTGGATTATATGAATTACAGATATT	6420
CG104	6417	CTAATGGGATCAATTGTTTTATGCATCCGACCTAAGTGTTGGGTTGAGAGTTGTATTG	6476
CG37	6421	CTAATGGGATCAATTGTTTTATGCATCCGACCTAAGTGTTGGGTTGAGAGTTGTATTG	6480
CG104	6477	TTTGCATACGGATATTTTCAGAATATGTTGATTTTAATCTCTTCTGCCCTGAGTGTGTTGG	6536
CG37	6481	TTTGCATACGGATATTTTCAGAATATGTTGATTTTAATCTCTTCTGCCCTGAGTGTGTTGG	6540
CG104	6537	GTGGTTTTGATAATGTGCTTACTGGCTCCATTTAGAGTCAATATGAAAGATACAAATAGT	6596
CG37	6541	GTGGTTTTGATAATGTGCTTACTGGCTCCATTTAGAGTCAATATGAAAGCTACAAATAGT	6600
CG104	6597	AAGGAACATGCTTTTCCATCTTAAGATAAATATGCACAACCTGTATGTGCATGTCGTAGGA	6656
CG37	6601	AAGGAACATGCTTTTCCATCTTAAGATAAATATGCACAACCTGTATGTGCATGTCGTAGGA	6660
CG104	6657	ATTGTAATCAAATTTTCCTTTTAGATCGTCATGGAAGATTGTGAAATGAGGGTGTACTGT	6716
CG37	6661	ATTGTAATCAAATTTTCCTTTTAGATCGTCATGGAAGATTGTGAAATGAGGGTGTACTGT	6720
CG104	6717	CCACTGATTTGCTTTTACTCCTTGTGAACTCTAATGGCAAACATTCTTTCAGGGTATTAT	6776

CG37	6721	 CCACTGATTTGCTTTTACTCCTGTGAACTCTAATGGCAAACATTCTTTCAGGGTATTAT	6780
CG104	6777	CGATCCTGCATTTTCGAAGCCTCGTATACCGATGCCACCATGCTTCTGCCTCCAAATTCC	6836
CG37	6781	CGATCCTGCATTTTCGAAGCCTCGTATACCGATGCCACCATGCTTCTGCCTCCAAATTCC	6840
CG104	6837	CCAAGCATTCCAGCAGAGGTCAAGCCCACAAATTGCAAAATGGAATGTTGCCTCCTGCTGC	6896
CG37	6841	CCAAGCATTCCAGCAGAGGTCAAGCCCACAAATTGCAAAATGGAATGTTGCCTCCTGCTGC	6900
CG104	6897	AAAACCTGGCAAGGGAAAATGCACCACTGCTGCAATGCTTCTGGATATGGTCAAGGATGT	6956
CG37	6901	AAAACCTGGCAAGGGAAAATGCACCACTGCTGCAATGCTTCTGGATATGGTCAAGGATGT	6960
CG104	6957	GGAGATAGCCATCTCTTGCCGAAAAGGTGCAACTGGTACAGCAGCCGGCGACGTAGCTTT	7016
CG37	6961	GGAGATAGCCATCTCTTGCCGAAAAGGTGCAACTGGTACAGCAGCCGGCGACGTAGCTTT	7020
CG104	7017	CCCAAAGGGGAAGGAGAACTTGGCTTCAGTCTCAAACGCTACAAGCGCCGATTATCCAA	7076
CG37	7021	CCCAAAGGGGAAGGAGAACTTGGCTTCAGTCTCAAACGCTACAAGCGCCGATTATCCAA	7080
CG104	7077	TAAACCAGTTGCCACTCACGAAGTATCATCTATTTACGCAAGATTTTCAGCAACATCCGT	7136
CG37	7081	TAAACCAGTTGCCACTCACGAAGTATCATCTATTTACGCAAGATTTTCAGCAACATCCGT	7140
CG104	7137	TCCTTATAGCTCATAGTATTTACCCAAAAATGGTGATCAAATCACCCAGCTGTTTAATTT	7196
CG37	7141	TCCTTATAGCTCATAGTATTTACCCAAAAATGGTGATCAGATCACCCAGCTGTTTAATTT	7200
CG104	7197	TGGAAGCAGCTCATGGTTTGGAACGAGATGCCCTCGTCTTGGTCTTTACTCTCTCTCAA	7256
CG37	7201	TGGAAGCAGCTCATGGTTTGGAACGAGATGCCCTCGTCTTGGTCTTTACTCTCTCTCAA	7260
CG104	7257	AACATGTATCAAGGCTCTTTGCTGCGAATTTTCTTCTCACATGTAAAAATATGATTAGGA	7316
CG37	7261	AACATGTATCAAGGCTCTTTGCTGCGAATTTTCTTCTCACATGTAAAAATATGATTAGGA	7320
CG104	7317	TGTGACTCAATGGACCCTTAGTTGCAGCAAACTCAGGAACTGGTGAAACACACATGG	7376
CG37	7321	TGTGACTCAATGGACCCTTAGTTGCAGCAAACTCAGGAACTGGTGAAACACACATGG	7380
CG104	7377	AAAGTTGATTGTTATGATGGTTGCACTACTTACTTGATCAAAGTAATTGCTGGAGGAGA	7436
CG37	7381	AAAGTTGATTGTTATGATGGTTGCACTACTTACTTGATCAAAGTAATTGCTGGAGGAGA	7440
CG104	7437	GATCACAAGGTGACTTTGAAAAGTTGAAAAAAAATGTTAGTATATAGCAGACAGAGCTA	7496
CG37	7441	GATCACAAGGTGACTTTGAAAAGTTGAAAAAAAATGTTAGTATATAGCAGACAGAGCTA	7500
CG104	7497	ATGTGCTGTATATATTGTCTGTGCAAACTTTCTGAAACATTTCAAATCTCTTTCCACAA	7556
CG37	7501	ATGTGCTGTATATATTGTCTGTGCAAACTTTCTGAAACATTTCAAATCTCTTTCCACAA	7560
CG104	7557	AAGCTATTCTAGATCTTGCTGTTTGTGTTAGATCATGCAGAACTTTCTTCTGTTGCC	7616
CG37	7561	AAGCTATTCTAGATCTTGCTGTTTGTGTTAGATCATGCAGAACTTTCTTCTGTTGCC	7620
CG104	7617	GTTTCGGTGAGTCAAAAGATAACTACATACTCTAGGG	7653
CG37	7621	GTTTCGGTGAGTCAAAAGATAACTACATACTCTAGGG	7657

Supplementary Figure S3. DNA sequence alignments of the candidate gene, *Csa6G445210* and *Csa6G445230*, between CG104 and CG37 (the highlight indicates the exons)

Csa6G445210

CG104	1	MITFMDSKEKLKEVEKCLDPQLWHACAGGMVQMPPVNARVFYFPQGHAHSCAPVDFRNC	60
CG37	1	MITFMDSKEKLKEVEKCLDPQLWHACAGGMVQMPPVNARVFYFPQGHAHSCAPVDFRNC	60
CG104	61	PKVPSYTLCRVSAIKFLADPDTDEVFAKLRLIPINGSELDGEDGIGRLNGSEQDKPTSF	120
CG37	61	PKVPSYTLCRVSAIKFLADPDTDEVFAKLRLIPINGSELDGEDGIGRLNGSEQDKPTSF	120
CG104	121	AKTLTQSDANNGGFSVPRYCAETIFPRLDYSADPPVQTIKADVHGETWKFRHIYRGTP	180
CG37	121	AKTLTQSDANNGGFSVPRYCAETIFPRLDYSADPPVQTIKADVHGETWKFRHIYRGTP	180
CG104	181	RRHLLTTGWSTFVNHKKL VAGDSIVFLRAENGDL CVGIRRAKRGIGDGPESSCGWNPAGG	240
CG37	181	RRHLLTTGWSTFVNHKKL VAGDSIVFLRAENGDL CVGIRRAKRGIGDGPESSCGWNPAGG	240
CG104	241	NCAVSYGAFSAFLREDDNRLTRSANGMNGNSLMGKGKVKPESVTEAAKLASNGQPFEII	300
CG37	241	NCAVSYGAFSAFLREDDNRLTRSANGMNGNSLMGKGKVKPESVTEAAKLASNGQPFEII	300
CG104	301	FYPRASTPEFCVKAALVKAALQIRWCSGMRFKMAFETEDSSRISWFMGTINSVQVSDPLR	360
CG37	301	FYPRASTPEFCVKAALVKAALQIRWCSGMRFKMAFETEDSSRISWFMGTINSVQVSDPLR	360
CG104	361	WPESPWRLQLQVTWDEPDLLQNVKRVSPWLVELVSSMSPIHLAPFSPPRKKFRYPQHPDFP	420
CG37	361	WPESPWRLQLQVTWDEPDLLQNVKRVSPWLVELVSSMSPIHLAPFSPPRKKFRYPQHPDFP	420
CG104	421	LDNQPPVPFSFSSYLHGTGSPFGCPPDNNPAGMQGARHAHFGLSLSDFHVS KLQSGLFSIG	480
CG37	421	LDNQPPVPFSFSSYLHGTGSPFGCPPDNNPAGMQGARHAHFGLSLSDFHVS KLQSGLFSIG	480
CG104	481	YRSLDPAAGSTRLSGNVMTEKPSMSENVSCLLTMAHSTQASKKFDGVKTPQLILFGRPIL	540
CG37	481	YRSLDPAAGSTRLSGNVMTEKPSMSENVSCLLTMAHSTQASKKFDGVKTPQLILFGRPIL	540
CG104	541	TELQMSQSFSGDTVSPVGTGNSSSDGNGDKMTNLSDGSGSALHQQGLPEGSAGENFQWYK	600
CG37	541	TELQMSQSFSGDTVSPVGTGNSSSDGNGDKMTNLSDGSGSALHQQGLPEGSAGENFQWYK	600
CG104	601	DNCQEIDPNLDIGHCKVFMESEDVGRTLDLSSLGSYEELYRKLGNMFGIDNSETLNHVLY	660
CG37	601	DNRQEIDPNLDIGHCKVFMESEDVGRTLDLSSLGSYEELYRKLGNMFGIDNSETLNHVLY	660
CG104	661	RDVSGAVKHVGDEQFSDFIKTARRLTILTDSGSNNVGA	698
CG37	661	RDVSGAVKHVGDEQFSDFIKTARRLTILTDSGSNNVGA	698

Csa6G445230

CG104	1	MESTTLHTTHQSGAIHRFIPFIAPALLVSI SYVDPGKWAATVEGGARFGFDLFVLVLLFN	60
CG37	1	MESTTLHTTHQSGAIHRFIPFIAPALLVSI SYVDPGKWAATVEGGARFGFDLFVLVLLFN	60
CG104	61	LAAILCQYLSASIGVVTGRGLAQICNEEYDKCTCFFLGIAEASVILLDLNMILGISNGL	120
CG37	61	LAAILCQYLSASIGVVTGRGLAQICSEEDYDKCTCFFLGIAEASVILLDLNMILGISNGL	120
CG104	121	NLLLGWDLFTCVLLTGVAALFPFPADLLEDGRAKFLYICMAGFVLLSLVLGVLISQPEI	180
CG37	121	NLLLGWDLFTCVLLTGVAALFPFPADLLEDGRAKFLYICMAGFVLLSLVLGVLISQPEI	180
CG104	181	PLSMNLMPTRLNGESAFTLMSLLGASVMPHNFYVHSSIVQQHQSPPNISKEVSCYNHLFA	240
CG37	181	PLSMNLMPTRLNGESAFTLMSLLGASVMPHNFYVHSSIVQQHQSPPNISKEVSCYNHLFA	240

CG104	241	IFCIFSGLIYVNNVLMNSAANVFYSSGLALHTFTDALSLMEQVFGSSVYVFLFLVLFLS	300
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CG37	241	IFCIFSGLIYVNNVLMNSAANVFYSSGLALHTFSDALSLMEQVFGSSVYVFLFLVLFLS	300
CG104	301	NQITALTWSLGGQLVTNFKLDIPGWLHCATIRIIAIIPALCCVWSSGAEGMYQLLIFS	360
CG37	301	NQITALTWSLGGQLVTNFKLDIPGWLHCATIRIIAIIPALCCVWSSGAEGMYQLLIFS	360
CG104	361	QVMVALLPSSVIPLYRVASSRTIMGALKISQLVEFIAIGIFIGILGLKIIFFVEMIFGN	420
CG37	361	QVMVALLPSSVIPLYRVASSRTIMGALKISQLVEFIAIGIFIGILGLKIIFFVEMIFGN	420
CG104	421	SDWVVNLRWNMGSGMSIPFVLLITACSSFCLMLWLAATPLKSATTIAQLDAQVLNWDMA	480
CG37	421	SDWVVNLRWNMGSGMSIPFVLLITACSSFCLMLWLAATPLKSATTIAQLDAQVLNWDMA	480
CG104	481	EVRPDSSEERENIDLKSSSYSAEPIESHSDLSSTKFDNLPENIMEPDQVLGSVNQENR	540
CG37	481	EVRPDSSEERENIDLKSSSYSAEPIESHSDLSSTKFDNLPENIMEPDQVLGSVNQENR	540
CG104	541	SSTVVPSSPKYVQEELESTEELVSSSIVTHDVPDSTLADKKVLKIESVEAVEKTVGLDGD	600
CG37	541	SSTVVPSSPKYVQEELESTEELVSSSIVTHDVPDSTLADKKVLKIESVEAVEKTVGLDGD	600
CG104	601	LRSEKDDYEVDNWEAEESLKEISGNIPSSTSEGPSFRSIGGRSEEGNGTGSLSRLAGL	660
CG37	601	LRSEKDDYEVDNWEAEESLKEISGNIPSSTSEGPSFRSIGGRSEEGNGTGSLSRLAGL	660
CG104	661	GRAARRQLTGILDEFWGQLYDFHGVPTQDAKVKKLDLLLGFTSLKLDVAGKDFPHSSPIG	720
CG37	661	GRAARRQLTGILDEFWGQLYDFHGVPTQDAKVKKLDLLLGFTSLKLDVAGKDFPHSSPIG	720
CG104	721	CKTSDPISSSLYDSPKSQRVQSGLEPPYGIQKGHQPLWSNHMQHWDAYVNNSSHNLDSG	780
CG37	721	CKTSDPISSSLYDSPKSQRVQSGLEPPYGIQKGHQPLWSNHMQHWDAYVNNSSHNLDSG	780
CG104	781	VKRYSSLRSLPSTESWDYQPATVHGYQLTYLSRMAKDRSSGNSNGQLDSSGSKYHTLGGG	840
CG37	781	VKRYSSLRSLPSTESWDYQPATVHGYQLTYLSRMAKDRSSGNSNGQLDSSGSKYHTLGGG	840
CG104	841	GAGLRDSVAFAMGQKLQNLGACQQAAPPGFNSNITVSRKPSSERKYYDHSLSGTGENL	900
CG37	841	GAGLRDSVAFAMGQKLQNLGACQQAAPPGFNSNITVSRKPSSERKYYDHSPSGTGENL	900
CG104	901	VSVSNTKKYHSLPDIHRDQHTSDKSSQWQDNVSGYGTSIGRITARGVSTNSGSRVLSPLAF	960
CG37	901	VSVSNTKKYHSLPDIHRDQHTSDKSSQWQDNVSGYGTSIGRITARGVSTNSGSRVLSPLAF	960
CG104	961	DELSPANVYSGALSPQMNPDLDSGSFWHRQPSEQFLDKNSNSESKEIGRLHSISHEASF	1020
CG37	961	DELSPANVYSGALSPQMNPDLDSGSFWHRQPSEQFLDKNSNSESKEIGRLHSISHEASF	1020
CG104	1021	VVNSEARLLQSFRDCIVKLLKLEGSDFWFGQSDGADEELIDCVAAREKFLYEAEAREMGR	1080
CG37	1021	VVNSEARLLQSFRDCIVKLLKLEGSDFWFGQSDGADEELIDCVAAREKFLYEAEAREMGR	1080
CG104	1081	VVRMKESPSFSPDRRPGSGMKNDTNFSNVSISSVPHCGEGCIWRSDLIVSFGVWC IHRIL	1140
		.	
CG37	1081	VVRMKESPSFSPDRRPGSGMKNDTNFSNVSISSVPHCGEGCIWRSDLIVSFGVWC IHRIL	1140
CG104	1141	DLSLMESRPELWGKYTYVLNRLQGIIDPAFSKPRIPMPPCFCLQIPQAFQQRSSPQIANG	1200
CG37	1141	DLSLMESRPELWGKYTYVLNRLQGIIDPAFSKPRIPMPPCFCLQIPQAFQQRSSPQIANG	1200
CG104	1201	MLPPAAKPGKGKCTTAAMLLDMVKDVEIAISCRKGRTGTAAGDVAFPKGKENLASVLKRY	1260
CG37	1201	MLPPAAKPGKGKCTTAAMLLDMVKDVEIAISCRKGRTGTAAGDVAFPKGKENLASVLKRY	1260

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CG104 1261 KRRLSNKPVATHEVSSISRKISATSVPYSS 1290
          ||||||||||||||||||||||||||||
CG37   1261 KRRLSNKPVATHEVSSISRKISATSVPYSS 1290
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Supplementary Figure S4. Amino acid sequence alignments of the candidate genes, *Csa6G445210* and *Csa6G445230*, between CG104 and CG37

