Plant Breed. Biotech. 2021 (March) 9(1):45~54
https://doi.org/10.9787/PBB.2021.9.1.45

Online ISSN: 2287-9366
Print ISSN: 2287-9358

Supplementary Table S1. Summary of 45 major candidate selective sweep genes in kohlrabi detected by multiple statistics analysis

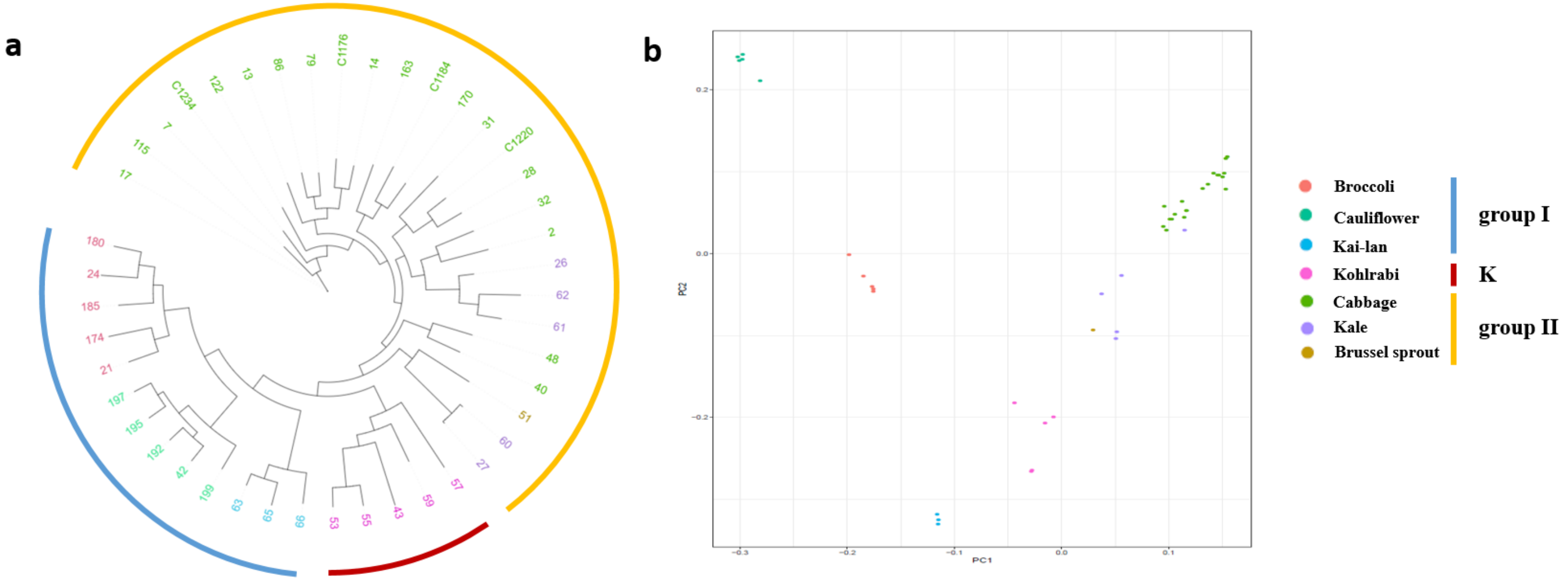
Symbol	Description	CHR *	Window (Mb)	XP-CLR (K-G1)	Max XP-EHH (K-G1)	XP-EHH P-value (K-G1)	XP-CLR (K-G2)	Max XP-EHH (K-G2)	XP-EHH P-value (K-G2)	Tajima D
LOC106317615	serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' gamma isoform	1	16.75-16.76	-	4.152	4.51E-05	-	2.458	2.07E-03	-1.805
LOC106311930	BAHD acyltransferase	1	16.87-16.88	22.505	-	-	24.843	-	-	-1.331
LOC106341591	choline-phosphate cytidylyltransferase 2-like	1	17.04-17.05	21.047	2.915	1.73E-03	-	2.556	1.42E-03	-0.800
LOC106322623	36.4 kDa proline-rich protein-like	1	17-17.01	-	2.673	3.47E-03	-	2.155	5.95E-03	-1.433
LOC106310518	protein TIC 62	1	20.89-20.9	24.030	-	-	25.276	-	-	-1.387
LOC106316308	nitrile-specifier protein 2-like	1	36.89-36.9	26.680	-	-	36.161	-	-	-0.636
LOC106327257	callose synthase 9-like	1	41.73-41.74	22.948	-	-	37.053	-	-	-1.335
LOC106324739	uncharacterized	2	12.46-12.47	-	3.008	1.35E-03	-	2.752	3.60E-04	-1.401
LOC106323475	late embryogenesis abundant protein D-34-like	2	12.48-12.49	-	2.572	4.75E-03	23.702	2.098	7.70E-03	-1.112
LOC106325709	sulfate transporter 1.1	2	12.73-12.74	-	2.424	7.19E-03	-	2.135	6.51E-03	-0.032
LOC106320417	ras-related protein RABA1c	2	39.47-39.48	21.399	-	-	29.377	-	-	-0.575
LOC106321573	GDSL esterase/lipase	2	39.72-39.73	-	3.111	9.69E-04	-	2.269	4.19E-03	-1.112
LOC106324352	Dihomo methionine N-hydroxylase-like	2	44.99-45	-	2.668	3.54E-03	-	2.504	1.80E-03	-0.018
LOC106326111	uncharacterized	2	46.3-46.31	-	2.972	1.60E-03	-	2.814	3.15E-04	-0.643
LOC106328431	tuberculostearic acid methyltransferase UfaA1-like	3	27-27.01	-	2.533	5.27E-03	-	2.255	4.35E-03	-1.534
LOC106332868	two-component response regulator ARR1-like	3	27-27.01	-	2.533	5.27E-03	-	2.255	4.35E-03	-1.534
LOC106333135	uncharacterized	3	37.64-37.65	-	2.808	2.34E-03	-	2.241	4.55E-03	-0.318
LOC106334682	uncharacterized	3	51.03-51.04	-	2.512	5.59E-03	-	2.121	6.87E-03	-0.438
LOC106330891	uncharacterized	3	52.24-52.25	-	2.460	6.46E-03	-	2.384	2.75E-03	-1.194
LOC106333915	polyribonucleotide nucleotidyl transferase 2	3	61.15-61.16	-	2.576	4.62E-03	-	2.160	5.81E-03	-0.100
LOC106336680	omega-3 fatty acid desaturase	4	13.44-13.45	28.267	-	-	23.754	-	-	-0.493
LOC106340721	CASP-like protein 4D2	4	4.93-4.94	-	3.545	3.60E-04	-	2.721	5.41E-04	-1.048
LOC106341264	uncharacterized	4	9.49-9.5	29.810	2.531	5.29E-03	21.353	-	-	-0.195

LOC106293902	sulfate transporter 1.3	5	11.75-11.76	49.598	2.640	3.87E-03	26.312	-	-	-1.112
LOC106300762	uncharacterized	6	1.78-1.79	-	2.865	2.05E-03	-	2.424	2.37E-03	-0.697
LOC106302167	replication protein A 70 kDa DNA-binding subunit B-like	7	21.38-21.39	-	2.573	4.69E-03	-	2.667	7.43E-04	-0.115
LOC106305289	probable serine/threonine-protein kinase	7	40.79-40.8	-	2.900	1.85E-03	-	2.396	2.61E-03	-1.562
LOC106303849	MATE efflux family protein DTX1-like	7	42.52-42.53	19.476	3.237	6.98E-04	35.440	2.824	2.93E-04	
LOC106301507	probable sodium/metabolite cotransporter BASS6	7	42.55-42.56	32.822	2.908	1.80E-03	21.885	-	-	-0.015
LOC106312087	TMV resistance protein N-like	8	24.32-24.33	18.658	-	-	34.024	-	-	-1.330
LOC106311965	Phosphoribosyl formyl glycinamidine cyclo-ligase	8	29.52-29.53	24.525	-	-	20.456	-	-	-0.227
LOC106308097	OTU domain-containing protein	8	31.41-31.42	40.369	-	-	35.103	-	-	-0.015
LOC106307523	ankyrin repeat and zinc finger domain-containing protein 1	8	41.63-41.64	20.794	-	-	27.254	-	-	-0.043
LOC106311968	flap endonuclease GEN-like 1	8	41.63-41.64	20.794	-	-	27.254	-	-	-0.043
LOC106312955	actin-related protein 2/3 complex subunit 3	9	14.57-14.58	19.673	-	-	23.420	-	-	-0.299
LOC106315835	uncharacterized	9	14.57-14.58	19.673	-	-	23.420	-	-	-0.299
LOC106315634	WAT1-related protein	9	18.62-18.63	-	2.684	3.38E-03	-	2.124	6.76E-03	-0.223
LOC106313386	AP-2 complex subunit mu-like	9	19.55-19.56	-	3.075	1.10E-03	-	2.116	7.14E-03	-0.782
LOC106314511	uncharacterized	9	19.61-19.62	-	2.873	1.98E-03	-	2.238	4.62E-03	-0.279
LOC106316601	uncharacterized	9	19.6-19.61	-	2.793	2.52E-03	-	2.331	3.27E-03	-0.362
LOC106314527	uncharacterized	9	20.41-20.42	23.804	3.244	6.53E-04	20.347	-	-	-1.557
LOC106314549	uncharacterized	9	21.12-21.13	18.863	-	-	25.201	-	-	-0.507
LOC106317031	putative auxin efflux carrier component 5	9	48.69-48.7	18.723	-	-	24.285	-	-	-1.270
LOC106318866	serine/threonine-protein kinase BLUS1	9	48.91-48.92	22.839	2.660	3.58E-03	22.082	-	-	-0.468
LOC106313855	transcription factor TGA1-like	9	5.77-5.78	-	2.631	3.92E-03	-	2.606	1.06E-03	-0.657

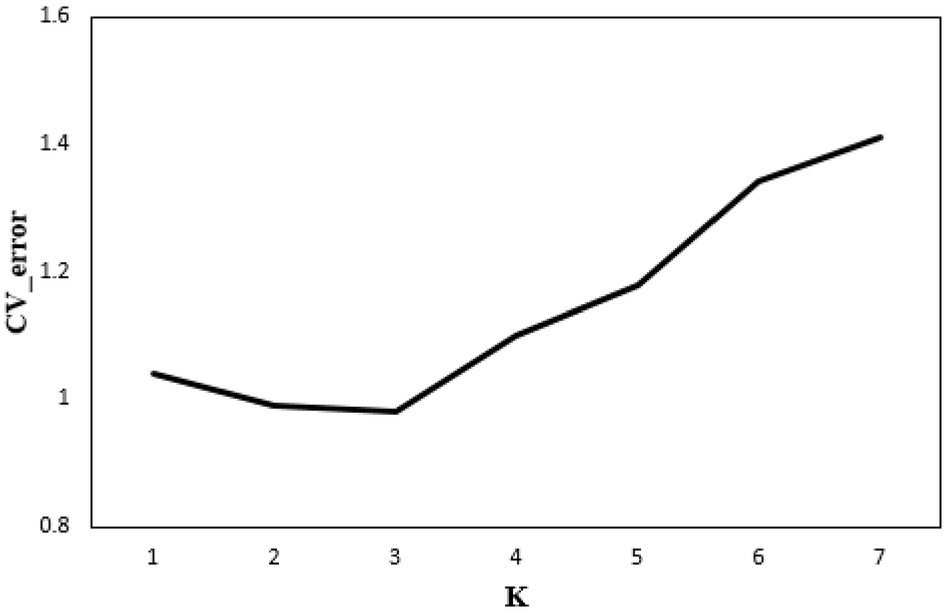
*chromosome.

XP-CLR: cross-population composite likelihood ratio; XP-EHH: cross-population extended haplotype homozygosity

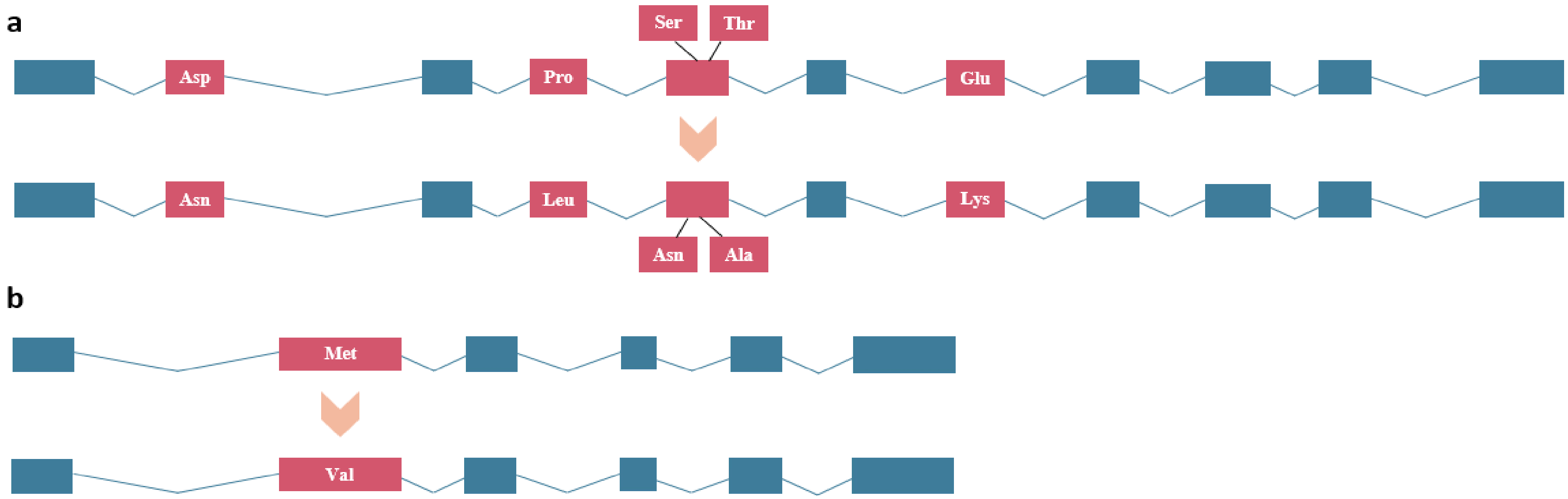
Dash (-) indicates non-significant.



Supplementary Fig S1. (a) The phylogenetic tree based on the whole genomic SNPs of different *B. oleracea* **(b)** Results of principal component analysis (PCA) of *B. oleracea* cultivar



Supplementary Fig S2. Cross Validation (CV) error of population structure analysis



Supplementary Fig S3. Structure of amino acid change in kohlrabi specific genes, (a) LOC106333915 **(b)** LOC106308097.