

Appendix A – Sequencing Data Information

The total output of data on the sequencer: Raw data 321.8 G.

The detail statistics for the quality of sequencing data are shown in **Table 1**.

Table 1 Data Quality Summary

Sample	Library	Flowcell/Lane	Raw reads	Raw data(G)	Effective(%)	Error(%)	Q20(%)	Q30(%)	GC(%)
Pool_1	DSW66575-V	HTGLMCCXY_L3	45588845		99.64	0.02	96.64	92.33	37.62
Pool_1	DSW66575-V	HTGLMCCXY_L2	44994742	54.1	99.66	0.02	96.60	92.19	37.59
Pool_1	DSW66575-V	HTGLMCCXY_L1	45323762		99.54	0.02	96.69	92.46	37.65
Pool_1	DSW66575-V	HTGLMCCXY_L4	44453097		99.66	0.02	96.63	92.33	37.61
Pool_2	DSW66576-V	HTGLMCCXY_L1	44941502		99.35	0.02	96.66	92.39	39.02
Pool_2	DSW66576-V	HTGLMCCXY_L2	44540806	53.5	99.49	0.02	96.59	92.15	38.96
Pool_2	DSW66576-V	HTGLMCCXY_L3	45042986		99.48	0.02	96.62	92.28	39.01
Pool_2	DSW66576-V	HTGLMCCXY_L4	43941019		99.49	0.02	96.62	92.29	38.99
Pool_3	DSW66577-V	HTGLMCCXY_L2	47609474		99.62	0.02	96.44	91.87	38.02
Pool_3	DSW66577-V	HTGLMCCXY_L1	48289716	57.2	99.50	0.02	96.51	92.10	38.08
Pool_3	DSW66577-V	HTGLMCCXY_L4	46914992		99.62	0.02	96.49	92.04	38.05
Pool_3	DSW66577-V	HTGLMCCXY_L3	47987705		99.61	0.02	96.49	92.02	38.06
Pool_4	DSW66578-V	HTGLMCCXY_L3	42831806		99.57	0.02	96.54	92.18	37.96
Pool_4	DSW66578-V	HTGLMCCXY_L4	41786651	50.6	99.58	0.02	96.54	92.18	37.94
Pool_4	DSW66578-V	HTGLMCCXY_L1	41911893		99.45	0.02	96.58	92.28	38.03
Pool_4	DSW66578-V	HTGLMCCXY_L2	42122352		99.58	0.02	96.50	92.04	37.93
Ning_1	DSW66579-V	HTGLMCCXY_L4	43685111		99.68	0.02	96.64	92.32	37.56
Ning_1	DSW66579-V	HTGLMCCXY_L3	44863004	53.2	99.66	0.02	96.64	92.31	37.57
Ning_1	DSW66579-V	HTGLMCCXY_L2	44238108		99.67	0.02	96.60	92.18	37.54
Ning_1	DSW66579-V	HTGLMCCXY_L1	44677205		99.56	0.02	96.67	92.41	37.63
Ning_7	DSW66580-V	HTFL3CCXY_L1	43867679		99.60	0.02	95.98	90.78	37.42
Ning_7	DSW66580-V	HTFL3CCXY_L6	43264862	53.2	99.67	0.02	96.11	91.11	37.41
Ning_7	DSW66580-V	HTFL3CCXY_L4	45479151		99.66	0.02	96.13	91.16	37.43
Ning_7	DSW66580-V	HTFL3CCXY_L5	44745323		99.68	0.02	95.99	90.87	37.42

Sample: sample name

Raw reads: four rows are taken as a unit to calculate the total amount of read1 and read2 in raw data files

Raw bases: (total raw reads) * (sequence length), calculating in G

Error rate: base error rate

Q20, Q30: (Base count of Phred value > 20 or 30) / (Total base count)

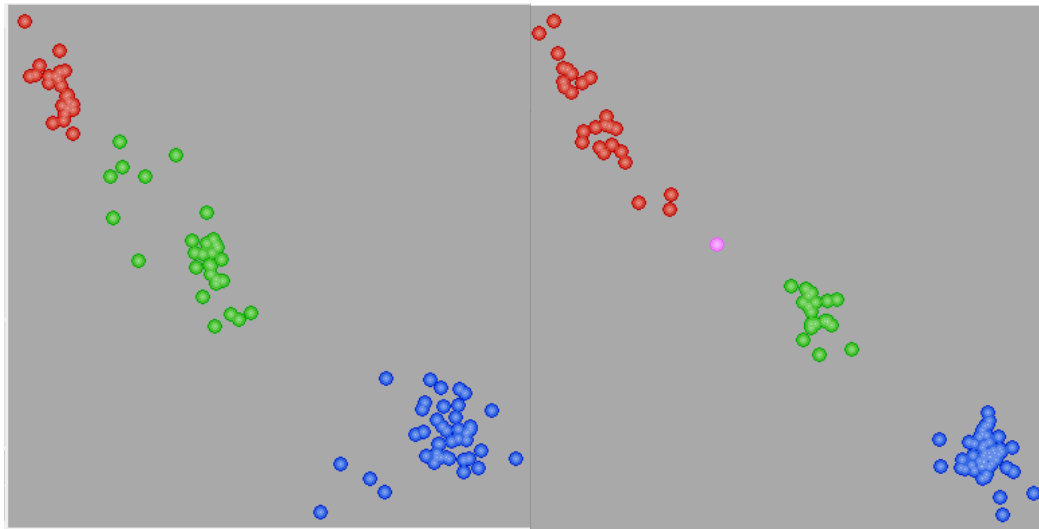
GC content: (G & C base count) / (Total base count)

Appendix B – Genotyping results of KASP markers

Table Appendix - B: Annotation and Effect prediction of SNPs used to design the KASP markers, with corresponded locations on Darmor-bzh genome with data regards to their usage in this PhD study to map the interested region.

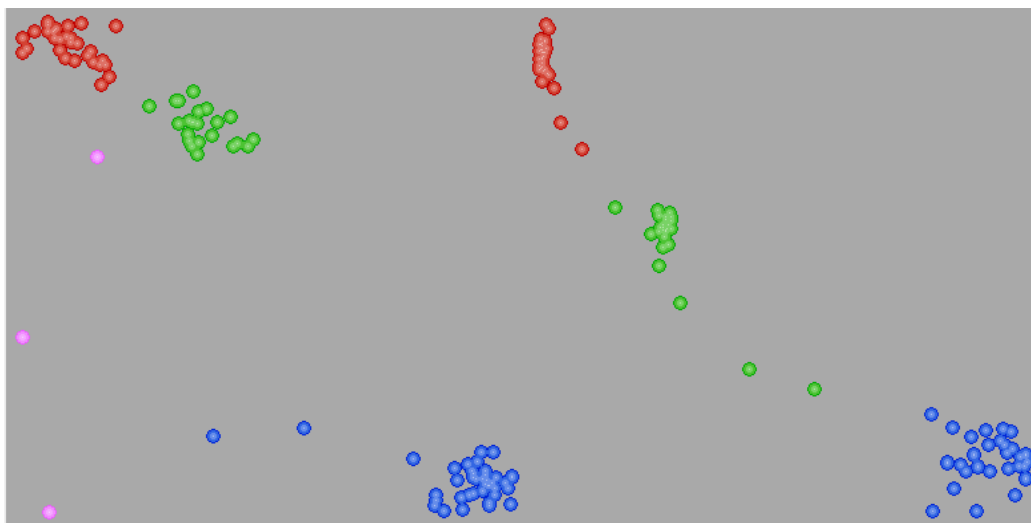
Marker	Chromosome	Position	REF	ALT	Quality	RO	AO	DP	Predicted Effect	Impact	Annotated Gene	BFR_AO_Res_Nonres	BFR_RO_Res_Nonres	Used
Nlp_1	chrA04	9,431,578	T	A	3287.84	121	107	228	stop_lost	HIGH	BnaA04g10830D	3.38	0.42	N
Nlp_2	chrA04	9,485,795	T	A	2990.3	6	90	96	stop_lost	HIGH	BnaA04g10900D	1.44	0.00	N
Nlp_3	chrA04	9,869,554	C	A	3207.83	124	107	232	stop_gained	HIGH	BnaA04g11350D	4.18	0.35	Y
Nlp_4	chrA04	9,981,183	A	G	2635.33	96	89	185	stop_lost	HIGH	BnaA04g11530D	4.63	0.37	N
Nlp_5	chrA04	12,590,399	G	T	2935.91	142	91	233	intergenic_region	MODIFIER	GENE_CDS_A04_12587236_12587357- GENE_EXON_A04_12592938_12593229	57.65	0.26	Y
Nlp_6	chrA04	12,920,723	G	A	3257.27	116	103	219	stop_gained	HIGH	BnaA04g15640D	#DIV/0!	0.23	Y
Nlp_7	chrA04	12,920,864	A	C	3494.2	86	105	191	stop_lost	HIGH	BnaA04g15640D	0.18	#DIV/0!	Y
Nlp_8	chrA04	12,935,023	A	G	3587.58	129	110	239	upstream_gene_variant	MODIFIER	BnaA04g15670D	70.30	0.12	Y
Nlp_9	chrA04	12,998,985	G	T	2730.3	122	87	209	synonymous_variant	LOW	BnaA04g15740D	50.58	0.29	Y
Nlp_10	chrA04	13,113,304	C	T	3518.67	113	110	223	synonymous_variant	LOW	BnaA04g15940D	60.49	0.14	N
Nlp_11	chrA04	13,248,612	C	T	2737.32	104	91	195	synonymous_variant	LOW	BnaA04g16190D	52.81	0.14	Y
Nlp_12	chrA04	13,262,249	A	G	2489.86	131	79	211	synonymous_variant	LOW	BnaA04g16230D	44.11	0.36	Y
Nlp_13	chrA04	13,306,300	G	A	3308.52	101	105	206	splice_acceptor_variant&intron_variant	HIGH	BnaA04g16310D	0.22	35.19	N
Nlp_14	chrA04	13,328,318	G	A	3021.55	122	95	217	downstream_gene_variant	MODIFIER	BnaA04g16340D	40.45	0.31	N
Nlp_15	chrA04	13,373,588	T	C	3326.32	116	103	219	upstream_gene_variant	MODIFIER	BnaA04g16380D	67.94	0.12	Y
Nlp_16	chrA04	13,376,311	T	G	3861.2	87	122	209	splice_donor_variant&intron_variant	HIGH	BnaA04g16390D	0.30	13.65	Y
Nlp_17	chrA04	13,454,192	T	C	5363.25	117	166	283	synonymous_variant	LOW	BnaA04g16450D	#DIV/0!	0.14	Y
Nlp_18	chrA04	13,550,948	A	T	4344.13	122	138	261	stop_gained	HIGH	BnaA04g16580D	22.51	0.25	Y
Nlp_19	chrA04	13,555,045	T	A	2869.37	155	92	247	upstream_gene_variant	MODIFIER	BnaA04g16580D	66.11	0.22	Y
Nlp_20	chrA04	13,586,747	G	A	3799.3	138	119	257	downstream_gene_variant	MODIFIER	BnaA04g16610D	59.30	0.21	N
Nlp_21	chrA04	13,736,357	C	A	3921.55	125	120	245	intron_variant	MODIFIER	BnaA04g16790D	#DIV/0!	0.19	N
Nlp_22	chrA04	13,739,289	A	T	4591.04	97	140	237	stop_gained	HIGH	BnaA04g16790D	0.33	51.60	N
Nlp_23	chrA04	13,740,102	A	C	2535.33	85	81	166	stop_lost	HIGH	BnaA04g16790D	0.10	43.10	Y
Nlp_24	chrA04	13,864,444	G	A	3497.4	118	112	230	upstream_gene_variant	MODIFIER	BnaA04g17010D	50.38	0.23	N
Nlp_25	chrA04	13,971,209	A	T	2320.12	94	80	174	stop_gained	HIGH	BnaA04g17140D	0.17	11.26	N
Nlp_26	chrA04	13,973,124	G	C	3491.15	99	109	208	stop_lost	HIGH	BnaA04g17140D	0.27	44.95	N
Nlp_27	chrA04	14,208,010	A	T	4003.66	94	122	216	stop_lost	HIGH	BnaA04g17480D	0.29	41.23	Y
Nlp_28	chrA04	14,242,994	C	A	3361.48	68	106	174	stop_gained	HIGH	BnaA04g17540D	0.35	33.71	Y
Nlp_29	chrA04	14,349,111	T	C	2148.08	114	71	186	missense_variant	MODERATE	BnaA04g17800D	42.14	0.29	Y
Nlp_30	chrA04	14,355,700	G	A	3009.07	127	96	223	splice_region_variant&intron_variant	LOW	BnaA04g17810D	49.93	0.28	N
Nlp_31	chrA04	14,372,201	G	T	3285.25	139	106	245	splice_region_variant&intron_variant	LOW	BnaA04g17830D	66.96	0.18	Y
Nlp_32	chrA04	14,715,600	C	G	3585.34	63	112	175	stop_lost	HIGH	BnaA04g18380D	0.40	16.81	Y
Nlp_33	chrA04	14,760,609	T	A	3808.65	126	121	247	stop_gained	HIGH	BnaA04g18500D	20.27	0.30	N
Nlp_34	chrA04	14,773,177	A	G	3697.65	103	117	220	synonymous_variant	LOW	BnaA04g18530D	0.15	20.05	Y
Nlp_35	chrA04	15,010,155	A	C	3426.09	151	114	265	stop_lost	HIGH	BnaA04g18890D	6.78	0.34	Y
Nlp_36	chrA04	16,507,816	A	G	2543.71	102	83	185	stop_lost	HIGH	BnaA04g21720D	11.16	0.31	N
Nlp_37	chrA04	16,957,051	A	C	3359.72	113	108	221	stop_gained&splice_region_variant	HIGH	BnaA04g22510D	8.55	0.21	N
Nlp_38	chrA04	16,967,745	T	A	2469.45	117	84	201	stop_lost	HIGH	BnaA04g22540D	5.58	0.38	N
Nlp_39	chrA04	17,007,520	T	G	2066.65	132	79	211	stop_lost	HIGH	BnaA04g22650D	4.86	0.43	N
Nlp_40	chrA04	17,479,568	C	T	2216.21	83	75	158	stop_gained	HIGH	BnaA04g23580D	0.37	4.17	N
Nlp_41	chrA04	18,322,024	G	T	2065.71	122	74	196	splice_donor_variant&intron_variant	HIGH	BnaA04g2530D	5.12	0.46	N

Appendix B – Genotyping results of KASP markers



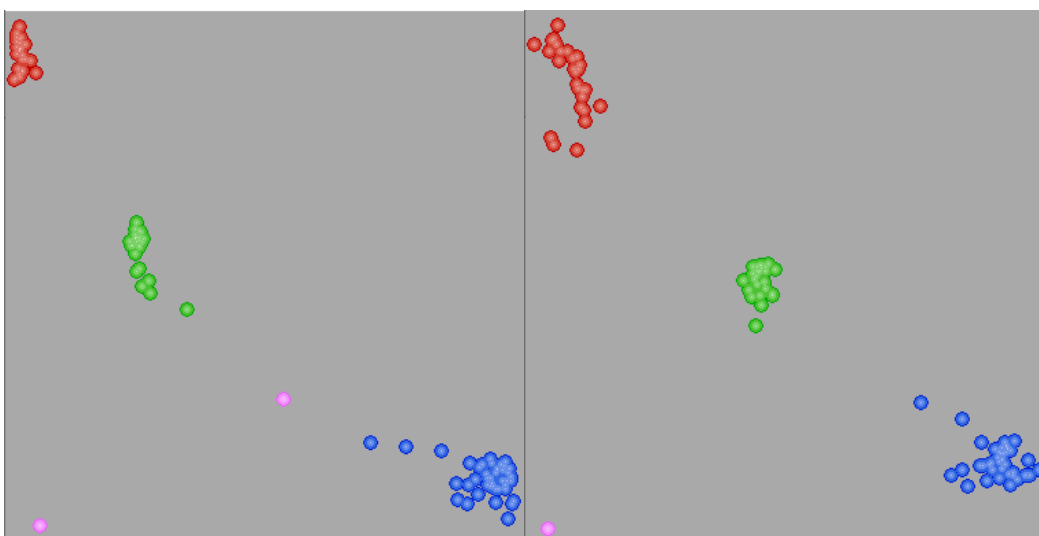
Nlp_3

Nlp_5



Nlp_6

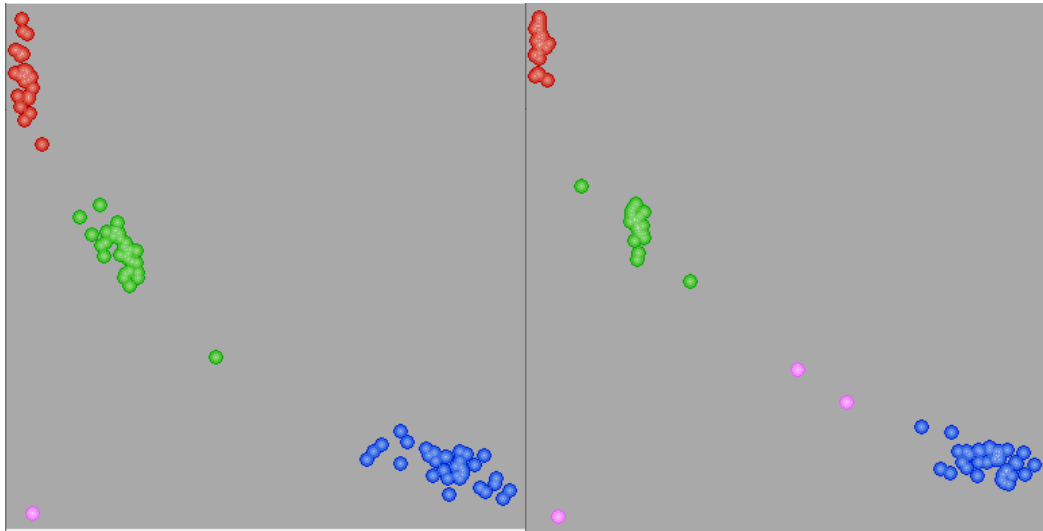
Nlp_7



Nlp_8

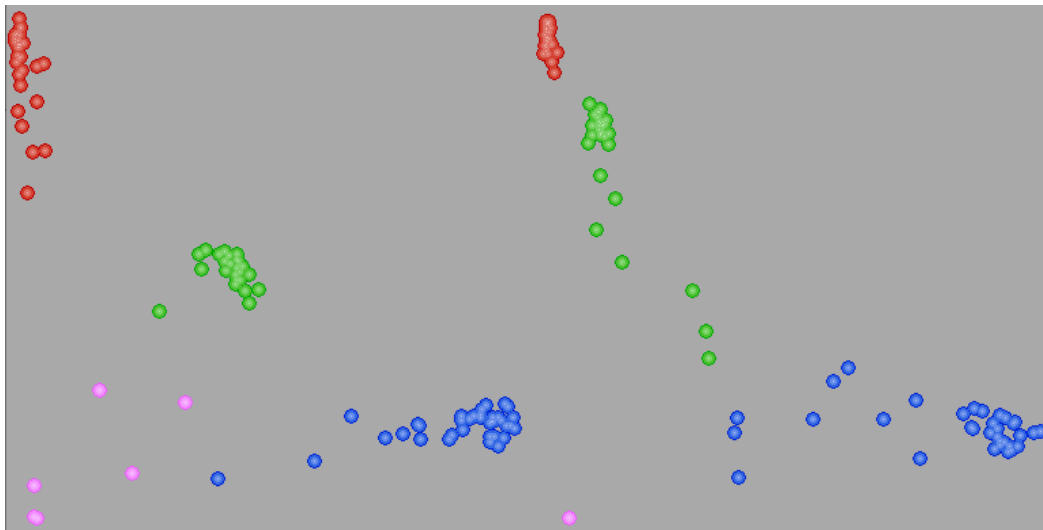
Nlp_9

Appendix B – Genotyping results of KASP markers



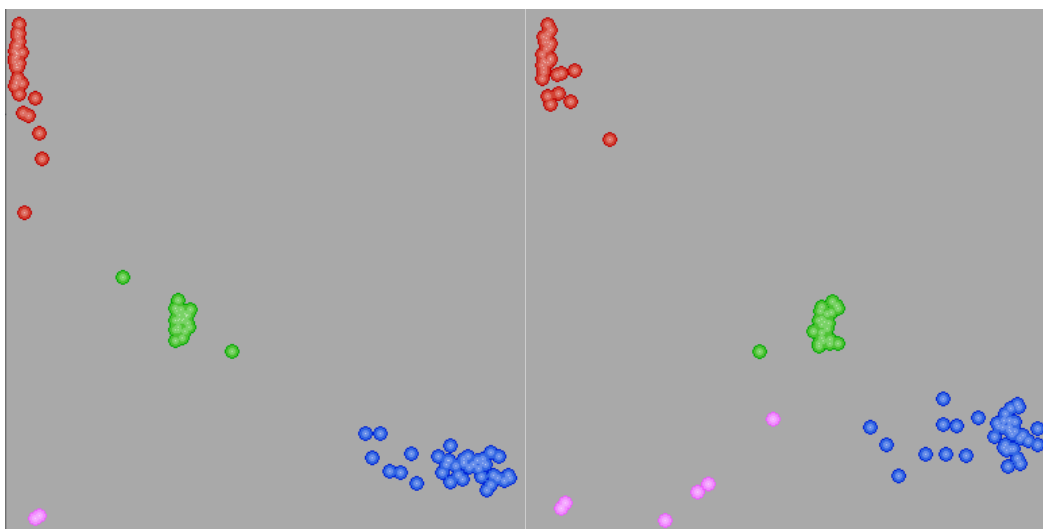
Nlp_11

Nlp_12



Nlp_15

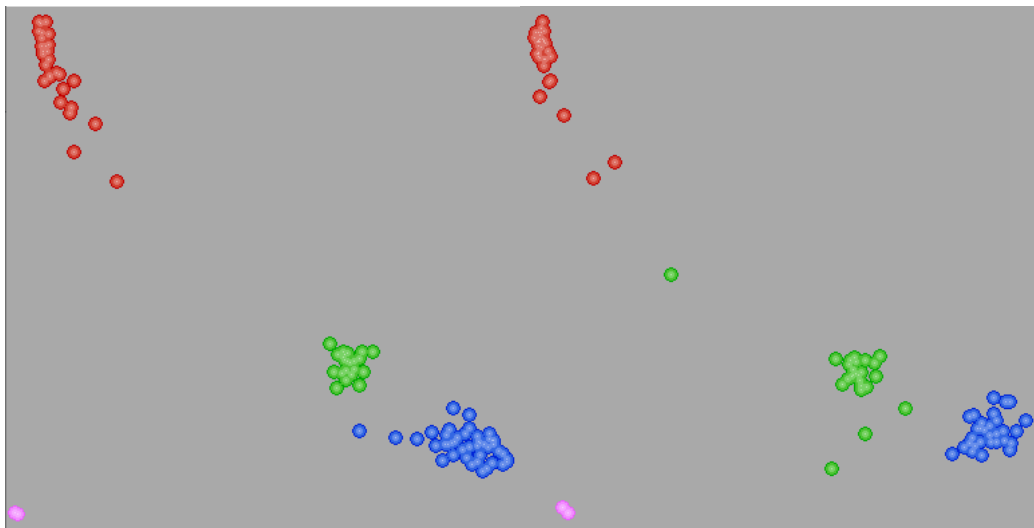
Nlp_16



Nlp_17

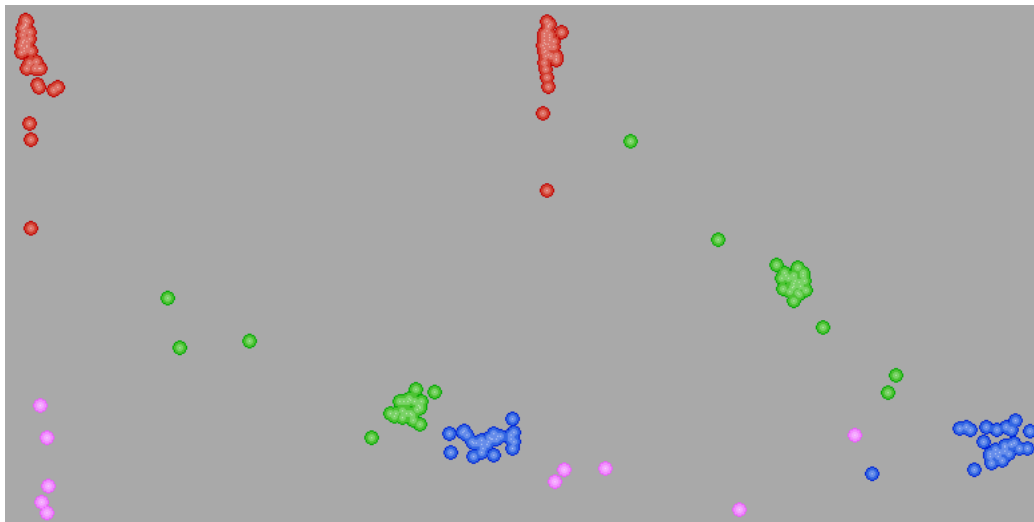
Nlp_18

Appendix B – Genotyping results of KASP markers



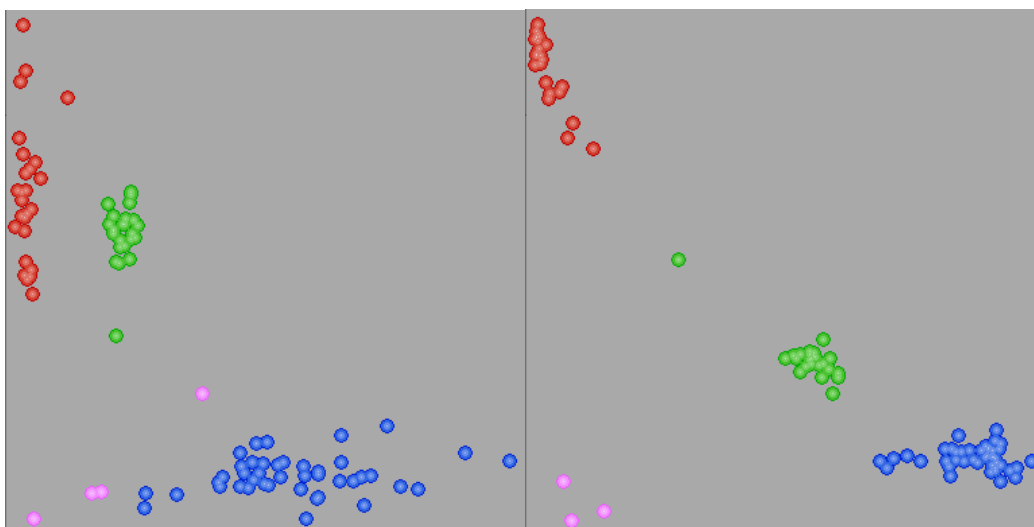
Nlp_19

Nlp_23



Nlp_27

Nlp_28



Nlp_29

Nlp_31

Appendix C – Variations have effect on BnaA01g02190D with computed BFR values

Table C – Annotation and Effect prediction of 106 variations on ChrA01 have predicted effect on BnaA01g02190D with their corresponding locations on Darmor-*bzh* genome and computed bulk frequency ratio (BFR AO & BFR RO) values for High NLP and High flg22 phenotype (AO: counts of Alternative (Alt) variation, RO: counts of Reference (Ref) variation).

Chrom	Position	Ref	Alt	Type	Qual	Depth	Predicted Effect	Effect Impact	Annotated Gene	BFR AO High NLP	BFR RO High NLP	BFR AO High flg22	BFR RO High flg22
chrA01	1,082,609	CTTT TTTT TG	CTTTTT TTTG	del	2070.97	140	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.44	3.33	1.10	1.14
chrA01	1,082,922	T	G	snp	3222.51	236	upstream_gene_variant	MODIFIER	BnaA01g02190D	2.16	0.64	1.38	0.79
chrA01	1,082,948	T	C	snp	3134.4	242	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.96	0.75	1.42	0.75
chrA01	1,082,996	CG	CGACGA TG	ins	2223.86	217	upstream_gene_variant	MODIFIER	BnaA01g02190D	4.59	0.64	1.70	0.67
chrA01	1,083,002	C	A	snp	3400.47	246	upstream_gene_variant	MODIFIER	BnaA01g02190D	2.50	0.65	1.60	0.61
chrA01	1,083,038	G	A	snp	3286.9	246	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.55	0.77	1.94	0.57
chrA01	1,083,092	CCTAC AAC	CC	del	2778.12	105	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.84	*	0.98	1.14
chrA01	1,083,187	T	C	snp	8563.13	243	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*
chrA01	1,083,242	T	G	snp	3506.26	224	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.68	0.69	1.46	0.69
chrA01	1,083,293	ATCTT CTTCT TCTT	ATCTTC TTCTTCT TCTT,TT CTTCTT CTTCTT	ins,snp	5977.42	187	upstream_gene_variant	MODIFIER	BnaA01g02190D	*	*	*	*
chrA01	1,083,293	ATCTT CTTCT TCTT	ATCTTC TTCTTCT TCTT,TT CTTCTT CTTCTT	ins,snp	5977.42	187	upstream_gene_variant	MODIFIER	BnaA01g02190D	*	*	*	*
chrA01	1,083,326	TAATT CGT	TT	del	2102.66	189	upstream_gene_variant	MODIFIER	BnaA01g02190D	2.17	0.48	1.77	0.68

Appendix C – Variations have effect on BnaA01g02190D with computed BFR values

chrA01	1,083,368	A	T	snp	2577.46	203	upstream_gene_variant	MODIFIER	BnaA01g02190D	2.52	0.38	2.36	0.60
chrA01	1,083,613	CCGC	GCGG	complex	3007.1	188	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.67	1.55	0.93	1.12
chrA01	1,083,622	T	G	snp	6973.97	197	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*
chrA01	1,083,635	T	C	snp	3184.26	188	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.80	1.41	0.84	1.32
chrA01	1,083,659	T	C	snp	6185.4	176	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*
chrA01	1,083,671	A	G	snp	3135.42	181	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.75	1.59	0.68	1.68
chrA01	1,083,695	G	T	snp	2992.06	187	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.80	1.64	0.59	1.60
chrA01	1,083,759	AGT	TCC	complex	2596.4	156	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.87	1.36	0.54	1.87
chrA01	1,083,815	T	A	snp	2823.83	154	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.01	0.97	0.55	1.71
chrA01	1,083,869	C	T	snp	2538.84	78	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*
chrA01	1,083,944	A	G	snp	3091.47	97	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.05	0.00	1.00	*
chrA01	1,084,135	TGCTC C	GGCTAG	complex	2814.99	207	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.13	0.93	2.64	0.32
chrA01	1,084,183	A	G	snp	3332.42	243	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.58	0.73	3.09	0.35
chrA01	1,084,189	G	A	snp	3281.89	244	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.27	0.84	2.65	0.39
chrA01	1,084,219	C	T	snp	4203.47	251	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.74	1.51	0.32	3.98
chrA01	1,084,222	A	G	snp	3374.09	245	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.41	0.76	4.13	0.34
chrA01	1,084,261	T	C	snp	3834.62	257	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.59	1.70	0.41	2.45
chrA01	1,084,267	G	A	snp	3841.56	262	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.52	1.88	0.45	2.30
chrA01	1,084,280	G	T	snp	4009.41	252	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.86	0.50	1.96	0.51
chrA01	1,084,288	ATTTT TTG	ATTG,A ATTTT G	del,snp	7113.31	223	upstream_gene_variant	MODIFIER	BnaA01g02190D	*	*	*	*
chrA01	1,084,288	ATTTT TTG	ATTG,A ATTTT G	del,snp	7113.31	223	upstream_gene_variant	MODIFIER	BnaA01g02190D	*	*	*	*
chrA01	1,084,300	GTTC	GTTTT	complex	3409.81	258	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.57	2.16	0.43	2.14

Appendix C – Variations have effect on BnaA01g02190D with computed BFR values

chrA01	1,084,329	G	C	snp	4005.02	261	upstream_gene_variant	MODIFIER	BnaA01g02190D	2.07	0.62	1.66	0.50
chrA01	1,084,356	T	C	snp	3810.07	238	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.61	0.73	1.33	0.65
chrA01	1,084,383	A	G	snp	9239.91	261	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*
chrA01	1,084,401	T	C	snp	3582.12	256	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.61	2.10	0.83	1.14
chrA01	1,084,593	T	C	snp	3303.71	256	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.77	1.37	0.95	1.03
chrA01	1,084,632	C	G	snp	2764.1	221	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.94	1.07	1.22	0.88
chrA01	1,084,669	G	A	snp	2773.31	219	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.84	1.20	1.32	0.84
chrA01	1,084,681	C	T	snp	2636.75	221	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.81	1.27	1.20	0.91
chrA01	1,084,693	A	T	snp	3869.67	217	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.28	0.81	0.91	1.20
chrA01	1,084,702	TCCC	CCCT	complex	3809.62	218	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.18	0.88	0.88	1.24
chrA01	1,084,735	G	A	snp	3748.34	218	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.26	0.82	0.89	1.20
chrA01	1,084,750	T	G	snp	3706.59	210	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.06	0.95	0.83	1.41
chrA01	1,084,774	T	C	snp	3238.98	188	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.26	0.83	0.93	1.14
chrA01	1,084,797	A	G	snp	3346.46	191	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.69	0.59	0.93	1.11
chrA01	1,084,819	C	T	snp	3015.87	168	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.34	0.72	1.02	0.96
chrA01	1,084,825	G	C	snp	2728.81	160	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.28	0.77	1.06	0.91
chrA01	1,085,227	C	T	snp	7306.57	208	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*
chrA01	1,085,599	T	A	snp	8516.91	240	upstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*
chrA01	1,085,734	T	C	snp	2664.66	171	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.84	1.32	0.95	1.08
chrA01	1,085,901	C	T	snp	4265.74	272	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.98	1.03	1.17	0.84
chrA01	1,086,195	A	G	snp	3434.59	239	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.44	1.99	0.59	1.99
chrA01	1,086,292	T	C	snp	3374.44	245	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.47	2.06	0.59	1.62
chrA01	1,086,325	TGT	TGGT	ins	3562.44	259	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.43	2.46	0.64	1.59
chrA01	1,086,369	A	C	snp	3890.51	276	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.35	2.80	0.67	1.51

Appendix C – Variations have effect on BnaA01g02190D with computed BFR values

chrA01	1,086,427	TATTC AA	TATTCA ATTCAA	ins	2865.36	259	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.43	1.96	0.79	1.25
chrA01	1,086,616	C	G	snp	4047.41	253	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.64	1.78	0.72	1.48
chrA01	1,086,622	G	T	snp	3862.59	242	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.49	2.61	0.65	1.54
chrA01	1,086,762	A	G	snp	2101.79	206	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.57	1.45	0.63	1.25
chrA01	1,086,901	CAAA AAAA AAAT	CAAAAA AAAAAT	del	3469.97	233	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.42	2.45	0.73	1.46
chrA01	1,087,168	A	G	snp	2046.72	177	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.62	1.49	1.28	0.84
chrA01	1,087,174	G	T	snp	2357.68	189	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.62	1.52	1.24	0.83
chrA01	1,087,194	A	C	snp	2620.15	193	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.56	1.80	0.97	1.03
chrA01	1,087,199	A	T	snp	2914.53	205	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.63	1.64	1.03	0.97
chrA01	1,087,244	G	A	snp	3467.51	225	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.83	1.17	1.27	0.76
chrA01	1,087,374	TAA	TA	del	2242.99	185	upstream_gene_variant	MODIFIER	BnaA01g02190D	0.79	1.22	1.18	0.88
chrA01	1,087,494	GAAA AAAA AAAAG	GAAAA AAAAAA AG,GAA AAAAAA AAAAG	ins,ins	3963.14	161	5_prime_UTR_variant	MODIFIER	BnaA01g02190D	*	2.67	*	*
chrA01	1,087,494	GAAA AAAA AAAAG	GAAAA AAAAAA AG,GAA AAAAAA AAAAG	ins,ins	3963.14	161	5_prime_UTR_variant	MODIFIER	BnaA01g02190D	*	2.67	*	*
chrA01	1,087,886	ATT	AT	del	2402.47	237	intron_variant	MODIFIER	BnaA01g02190D	0.56	1.47	0.72	1.22
chrA01	1,087,898	GTC	ATC,TTT	snp,com plex	3311.13	244	intron_variant	MODIFIER	BnaA01g02190D	*	1.62	*	1.25
chrA01	1,087,898	GTC	ATC,TTT	snp,com plex	3311.13	244	intron_variant	MODIFIER	BnaA01g02190D	*	1.62	*	1.25

Appendix C – Variations have effect on BnaA01g02190D with computed BFR values

chrA01	1,088,090	ACTCT CTCTC TCTA	ACTCTC TCTCTC TCTA	ins	3724.56	131	intron_variant	MODIFIER	BnaA01g02190D	0.92	0.00	0.91	*
chrA01	1,088,165	GTT	GTTT	ins	2413.35	196	intron_variant	MODIFIER	BnaA01g02190D	0.73	1.78	0.94	1.06
chrA01	1,088,236	T	C	snp	2924.76	204	intron_variant	MODIFIER	BnaA01g02190D	0.63	1.86	0.82	1.23
chrA01	1,088,247	CATGT	TATGC	complex	2738.59	197	intron_variant	MODIFIER	BnaA01g02190D	0.65	1.75	0.75	1.29
chrA01	1,088,416	A	T	snp	3669.07	237	splice_region_variant&int ron_variant	LOW	BnaA01g02190D	0.73	1.57	1.09	0.92
chrA01	1,088,440	C	T	snp	3625.57	232	intron_variant	MODIFIER	BnaA01g02190D	0.72	1.71	1.04	0.97
chrA01	1,088,448	T	G	snp	3398.51	226	intron_variant	MODIFIER	BnaA01g02190D	0.76	1.53	1.09	0.94
chrA01	1,088,465	CAA	CC	complex	2531.3	205	intron_variant	MODIFIER	BnaA01g02190D	0.67	1.60	1.08	0.95
chrA01	1,088,474	T	G	snp	2481.45	197	intron_variant	MODIFIER	BnaA01g02190D	0.61	1.75	1.18	0.90
chrA01	1,088,484	G	T	snp	2430.56	203	splice_region_variant&int ron_variant	LOW	BnaA01g02190D	0.61	1.70	1.03	0.99
chrA01	1,088,510	C	G	snp	2210.67	202	synonymous_variant	LOW	BnaA01g02190D	0.58	1.81	0.69	1.24
chrA01	1,088,519	CTTG	TTTA	complex	2614.65	203	synonymous_variant	LOW	BnaA01g02190D	0.56	1.88	0.76	1.20
chrA01	1,088,579	T	G	snp	2619.82	214	synonymous_variant	LOW	BnaA01g02190D	0.62	1.64	0.54	1.79
chrA01	1,088,585	TCTG	CCTA	complex	2726.13	210	synonymous_variant	LOW	BnaA01g02190D	0.70	1.59	0.53	1.90
chrA01	1,088,601	TC	CA	mnp	3312.82	242	splice_region_variant&int ron_variant	LOW	BnaA01g02190D	0.60	1.91	0.60	1.74
chrA01	1,088,614	CTCTT	ATCTCT	complex	3596.69	253	intron_variant	MODIFIER	BnaA01g02190D	0.70	1.63	0.61	1.88
chrA01	1,088,637	T	G	snp	4411.31	271	intron_variant	MODIFIER	BnaA01g02190D	0.71	1.66	0.69	1.69
chrA01	1,088,658	T	A	snp	4513.19	275	intron_variant	MODIFIER	BnaA01g02190D	0.74	1.71	0.73	1.53
chrA01	1,088,665	ATT	ATTT	ins	3864.45	266	intron_variant	MODIFIER	BnaA01g02190D	0.70	1.60	0.70	1.54
chrA01	1,088,679	TT	TATAAT	ins	3320.09	247	intron_variant	MODIFIER	BnaA01g02190D	0.65	1.73	0.73	1.39
chrA01	1,088,689	A	G	snp	3910.43	266	intron_variant	MODIFIER	BnaA01g02190D	0.78	1.41	0.85	1.19
chrA01	1,088,719	G	C	snp	3944.9	276	splice_region_variant&int ron_variant	LOW	BnaA01g02190D	0.81	1.35	0.96	1.04

Appendix C – Variations have effect on BnaA01g02190D with computed BFR values

chrA01	1,088,769	T	C	snp	3703.15	273	synonymous_variant	LOW	BnaA01g02190D	0.95	1.08	0.99	1.01
chrA01	1,088,784	CGGA	TGGT	complex	3493.91	253	synonymous_variant	LOW	BnaA01g02190D	1.03	0.95	0.93	1.06
chrA01	1,090,078	G	A	snp	2238.24	215	intron_variant	MODIFIER	BnaA01g02190D	0.61	1.48	0.43	1.43
chrA01	1,090,084	C	G	snp	2393.04	220	intron_variant	MODIFIER	BnaA01g02190D	0.74	1.31	0.43	1.48
chrA01	1,090,139	C	T	snp	3211.25	230	synonymous_variant	LOW	BnaA01g02190D	0.70	1.45	0.61	1.49
chrA01	1,090,172	A	T	snp	3312.06	249	synonymous_variant	LOW	BnaA01g02190D	0.59	1.69	0.81	1.19
chrA01	1,090,557	GCAA TAC	GC	del	3027.69	202	3_prime_UTR_variant	MODIFIER	BnaA01g02190D	0.67	1.43	0.85	1.24
chrA01	1,090,827	CTTTT TTTTT C	CTTTTTT TTTTTC	ins	5491.44	180	downstream_gene_variant	MODIFIER	BnaA01g02190D	1.09	0.00	1.00	0.00
chrA01	1,092,263	G	A	snp	7291.01	209	downstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.02	*
chrA01	1,092,420	CAATT TGGT A	CA	del	6170.81	187	downstream_gene_variant	MODIFIER	BnaA01g02190D	1.00	*	1.00	*

Appendix D – QTLs obtained with Multiple-QTL Mapping (MQM) analysis that significantly associated with interested traits on *B. oleracea* genome

Table D QTLs associated with ROS responses against various concentrations of flg22 & elf18 PAMP molecules in control and drought conditions and QTLs associated with the induced traits – Fold Change (FC) in ROS response and difference between the lesion sizes of *B. cinerea* infection (delta) in comparison to control with genome-wide $\alpha \leq 0.05$. The locations of the QTLs with increased genotype and linked amplified fragment length polymorphism (AFLP) and restriction fragment length polymorphism (RFLP) markers are represented. LOD scores are coloured in Green – Yellow -Red colour scale according to their decreasing values from Green to Red. (Tables are generated by Dr. Peter Walley from Liverpool University with data generated in this PhD study).

a. QTL with genome-wide $\alpha \leq 0.05$

Trait	QTL name	Chr	pos	LOD	CI (cM)				P-value	% var	Increasing genotype	Linked markers		
					1.5-LOD	1-LOD	1-LOD	1.5-LOD				m1	m2	m3
FC_10nM_elf18	FC_10nM_elf18_2.0	C2	43.556	1.81	36.947	37.947	57.832	57.832	0.017	9.5	A12DHd	pN121E1	pN13E2	pN102E2
FC_50nM_flg22	FC_50nM_flg22_3.1	C3	94.233	4.68	80.864	81.665	97.725	99.854	0.001	11.8	GDDH33	94472_1074996	pW148E1	pR85E2
D_10nM_flg22	D_10nM_flg22_4.1	C4	23.191	4.79	17.624	18.624	37.016	37.016	0.001	11.4	GDDH33	94428_325673	94375_3337211	94371_1107050
D_10nM_flg22	D_10nM_flg22_4.2	C4	42.787	5.25	40.331	41.331	43.741	45.251	0.001	11	A12DHd	94482_3605744	pN120J1	pW137J2
D_10nM_flg22	D_10nM_flg22_4.0	C4	5.007	3.40	0.000	0.000	15.970	15.970	0.024	10.1	GDDH33	94354_516884	94348_2235919	94447_1805515
FC_50nM_flg22	FC_50nM_flg22_4.1	C4	119.493	3.31	114.654	115.654	122.493	123.493	0.018	8.2	GDDH33	94446_3246610	94366_1451853	pR113E3
delta_ALL_lesion	delta_ALL_lesion_4.0	C4	100.324	3.21	86.398	92.483	104.105	105.105	0.03	15.2	A12DHd	pW139E1	94350_1506853	94363_1064357
C_10nM_elf18	C_10nM_elf18_5.0	C5	107.317	4.00	96.289	97.289	114.935	115.935	0.01	25.6	A12DHd	94464_2234677	94453_3319744	94425_876921
C_10nM_flg22	C_10nM_flg22_5.0	C5	87.395	2.75	72.128	72.128	90.395	111.029	0.049	19.4	A12DHd	pN91E3	pO123J1	sORA21b
C_2nM_elf18	C_2nM_elf18_5.0	C5	113.935	3.32	97.985	102.317	117.935	118.935	0.029	22.1	A12DHd	94425_876921	94470_4529825	pW172E1
C_50nM_flg22	C_50nM_flg22_5.0	C5	85.656	3.22	71.291	77.836	90.395	91.395	0.033	15.3	A12DHd	pN91E3	pO123J1	sORA21b
D_10nM_elf18	D_10nM_elf18_5.0	C5	109.130	3.50	95.416	96.289	112.029	112.374	0.01	17.5	A12DHd	AA-CATE16	94453_3319744	94425_876921
D_10nM_flg22	D_10nM_flg22_5.0	C5	87.395	4.68	79.656	80.656	89.395	89.395	0.002	12	A12DHd	pN91E3	pO123J1	sORA21b
D_2nM_flg22	D_2nM_flg22_5.0	C5	87.395	3.51	77.836	80.656	89.395	90.395	0.006	12.7	A12DHd	pN91E3	pO123J1	sORA21b

Appendix D – QTLs obtained with Multiple-QTL Mapping (MQM) analysis that significantly associated with interested traits on *B. oleracea* genome

C_2nM_flg22	C_2nM_flg22_6.0	C6	32.296	3.48	24.636	26.130	36.046	36.983	0.008	8.5	A12DHd	mNGA111J1	83844_4952	pS29
D_10nM_flg22	D_10nM_flg22_6.0	C6	95.557	5.02	87.300	90.300	100.799	101.631	0.001	14	GDDH33	94362_1297271	pO10E2	mCa72
FC_10nM_flg22	FC_10nM_flg22_6.0	C6	31.060	5.23	28.983	28.983	31.945	31.945	0.001	17	GDDH33	78180_1904	94451_1163113	BoAP1-a
FC_10nM_flg22	FC_10nM_flg22_6.1	C6	24.636	7.57	24.238	24.238	25.130	25.130	0.001	39.7	A12DHd	86928_632	94427_394042	pR94E1
C_10nM_elf18	C_10nM_elf18_7.0	C7	77.512	4.94	66.317	74.884	78.713	80.934	0.002	30.6	GDDH33	93197_4673	94482_2037427	94209_69490
C_10nM_flg22	C_10nM_flg22_7.0	C7	84.645	4.54	83.230	83.230	87.645	88.645	0.001	29.9	GDDH33	mBN72AJ1	pO43J1	94028_20947
C_2nM_flg22	C_2nM_flg22_7.0	C7	59.998	4.27	48.462	50.517	65.317	67.527	0.003	10.2	GDDH33	94440_692264	pN97J2	pN97J2
C_50nM_flg22	C_50nM_flg22_7.0g	C7	52.334	4.05	51.780	51.780	65.317	66.317	0.005	22.4	GDDH33	94365_1394512	BoFUL-bcDNA-PCR-1	AtFULcDNA-PCR-b-5
C_50nM_flg22	C_50nM_flg22_7.1g	C7	86.645	5.01	80.934	83.230	88.893	88.893	0.001	26.7	GDDH33	mBN72AJ1	pO43J1	94028_20947
C_50nM_flg22	C_50nM_flg22_7.0	C7	61.352	3.72	51.780	51.780	65.317	88.893	0.01	20.8	GDDH33	pO29E1	pO59E1	pW104E1
D_10nM_elf18	D_10nM_elf18_7.0	C7	57.286	4.02	59.998	48.462	59.326	47.135	0.003	19.8	GDDH33	AC-CAGE10	94441_1093200	94441_1225613
D_10nM_elf18	D_10nM_elf18_7.1	C7	70.769	4.29	48.462	64.317	77.713	77.713	0.002	20.9	GDDH33	94364_1330402	94349_826956	pR36E4NM
D_10nM_flg22	D_10nM_flg22_7.0	C7	84.230	10.45	83.230	83.230	86.645	87.645	0.001	41.5	GDDH33	94457_1074300	mBN72AJ1	pO43J1
D_2nM_elf18	D_2nM_elf18_7.0	C7	55.294	4.50	46.600	48.462	59.326	59.998	0.003	20.8	GDDH33	94428_846176	94450_50360	AC-CAGE10
D_2nM_elf18	D_2nM_elf18_7.1	C7	69.992	4.51	64.317	64.317	77.512	77.713	0.003	20.8	GDDH33	94375_2724613	94364_1330402	94349_826956
D_2nM_flg22	D_2nM_flg22_7.0	C7	83.230	3.46	80.205	80.205	87.645	88.645	0.007	12.2	GDDH33	94457_1074300	mBN72AJ1	pO43J1
D_50nM_flg22	D_50nM_flg22_7.0	C7	83.230	7.16	80.934	81.259	84.645	88.893	0.001	37.5	GDDH33	94457_1074300	mBN72AJ1	pO43J1
D_10nM_elf18	D_10nM_elf18_8.0	C8	42.605	4.40	36.893	37.893	43.393	43.393	0.001	21.5	GDDH33	pW205E1	pR97J1	94168_25325
D_10nM_flg22	D_10nM_flg22_8.0	C8	80.472	3.63	70.699	74.700	86.893	89.461	0.016	7.9	GDDH33	pW123E2	AC-CATE20	pN123J1
D_2nM_elf18	D_2nM_elf18_8.0	C8	38.923	5.60	36.893	36.893	41.923	42.605	0.001	22.6	GDDH33	pW188J1	pW205E1	pR97J1
FC_10nM_elf18	FC_10nM_elf18_8.0	C8	25.016	2.74	13.183	13.183	35.662	35.662	0.032	13.7	GDDH33	94371_3564048	94333_2004801	94454_765755
FC_10nM_flg22	FC_10nM_flg22_8.0	C8	34.662	3.67	27.156	30.375	35.662	36.662	0.001	23.5	GDDH33	94468_4348829	94352_318418	pW188J1
FC_2nM_flg22	FC_2nM_flg22_8.1	C8	80.472	3.18	68.699	68.699	86.893	87.893	0.014	22.3	GDDH33	pW123E2	AC-CATE20	pN123J1
FC_2nM_flg22	FC_2nM_flg22_8.0	C8	40.923	3.08	31.375	36.662	43.393	43.393	0.018	18.9	GDDH33	pW205E1	pR97J1	94168_25325
FC_50nM_flg22	FC_50nM_flg22_8.0	C8	2.120	4.62	0.000	0.000	2.865	2.865	0.001	23	GDDH33	pO159J1	pW104E2	pR86E2

Appendix D – QTLs obtained with Multiple-QTL Mapping (MQM) analysis that significantly associated with interested traits on *B. oleracea* genome

FC_50nM_flg22	FC_50nM_flg22_8.1	C8	37.893	4.23	34.228	34.662	40.923	42.605	0.003	21.3	GDDH33	94352_318418	pW188J1	pW205E1
FC_50nM_flg22	FC_50nM_flg22_8.2	C8	80.472	3.97	68.699	69.699	84.893	86.893	0.003	18.2	GDDH33	pW123E2	AC-CATE20	pN123J1
delta_ALL_lesion	delta_ALL_lesion_8.0	C8	99.952	4.46	95.171	96.171	101.95 2	102.59 3	0.002	22.3	A12DHd	pN23J1	pN21E1	94329_1712555
delta_All_over_Control	delta_All_over_Control_8.0	C8	99.952	4.00	94.171	96.171	101.95 2	102.59 3	0.005	20.3	A12DHd	pN23J1	pN21E1	94329_1712555
C_10nM_flg22	C_10nM_flg22_9.0	C9	70.623	4.54	63.908	65.941	74.503	75.095	0.001	30	GDDH33	pR34E1	pO127E1	JCVI_29779_442
C_2nM_flg22	C_2nM_flg22_9.0	C9	70.623	11.33	69.380	69.380	70.980	71.304	0.001	36.2	GDDH33	pR34E1	pO127E1	pN181E1
D_10nM_flg22	D_10nM_flg22_9.0	C9	77.164	4.49	68.838	69.380	82.478	83.196	0.004	15.5	GDDH33	JCVI_35058_102	77711_5972	94454_2506581
D_2nM_flg22	D_2nM_flg22_9.0	C9	67.650	3.24	52.793	56.634	81.717	84.196	0.013	22.7	GDDH33	94426_2065534	pW233J1	77411_686
FC_10nM_flg22	FC_10nM_flg22_9.1	C9	121.814	3.50	118.437	119.437	125.81 4	124.81 4	0.02	22.6	GDDH33	BoFLC-BAC-PCR-2	94432_302792	77174_3414
FC_10nM_flg22	FC_10nM_flg22_9.0	C9	100.377	3.60	98.461	98.461	102.96 7	103.96 7	0.016	12	A12DHd	94473_318848	pO118J1	pO7E1
FC_50nM_flg22	FC_50nM_flg22_9.0	C9	26.289	3.90	19.289	21.289	36.582	36.582	0.003	16.9	A12DHd	pN52E2	pW137J1	pW167E2