

Table 3.1 Annotated genes within the B5M12 locus and flanking regions (highlighted in grey) and polymorphisms identified in these genes with regard to HB3 and Dd2.

STS	Gene	Location	Annotated function	Length	Domains	Codon polymorphisms	Length polymorphisms
SM17	MAL7P1.17	235411-246090	conserved membrane protein, unknown function	3592	-	N1389I, N1390D, D1391K, I1393K, D1403N	1395-1398 (del), 1417-1421(del), 1444-1452(del)
SM15	PF07_0015	246684-250265	putative methyltransferase	1193	S-adenosyl-methionine-dependent methyltransferase NOP1/NOP2/sun families	Q104E, H1060D	405 (del), 714-719 (ins)
	PF07_0016	253048-258627	conserved membrane protein, unknown function	1859	Family A G-protein coupled receptor-like pentapeptide MxKDx repeat protein	K1474I	1016-1017 (ins)
	PF07_0017	260097-263129	putative phosphoinositide binding protein	1010	Px domain, WD40 repeat like	-	-
LT103	MAL7P1.18	264069-268880	putative serine/threonine protein kinase	1603	PKC, catalytic domain of protein kinases	D808H, V815G, V823G	309-311 (del), 784-807 (ins), 1351-1352 (ins)
	MAL7P1.19	271404-284452	putative ubiquitin transferase	3893	HECT domain, C-terminal catalytic domain of a E3 ubiquitin ligase	E199K, E249D, E309Q, P535L, T589S, Y1233C, N1376S, Y1388F, E1406D, G1409C, E1410D, K1578E, K1614E, E1632K, V1692L, M1707L, P1740H, K1780N, D1905N	174-175 (del), 1960-1967 (ins), 3118-3122 (ins), 3189-3192(del)
	PF07_0018	288781-292794	conserved membrane protein, unknown function	1337	P-loop containing nucleoside triphosphate hydrolase, nucleotidyl transferase	R1039S	751-755 (del)
SM19	PF07_0019	293539-297432	conserved protein, unknown function	1297	ST/phosphatase 2C, pentapeptide repeats, HR1 repeats	P397S	435-439 (del), 455-459 (del)
	MAL7P1.20	299278-300336	putative peptide chain release factor	352	PCRF domain, RF-1 domain	-	-
SM20	PF07_0020	301639-305532	putative methyltransferase	1213	methyltransferase domain	-	712-751 (del)
SM21a/b	PF07_0021	307662-310631	conserved protein, unknown function	989	-	I29M, K232E, V376L, I468T, D500G, N503K, N519K, F542Y, R595S, R657S	51-53 (del), 568-629 (del)
SM22a/b	PF07_0022	311466-316064	conserved protein, unknown function	1532	-	L264S, D417E, A546S, L550Y, Y551Q, I552Y, M553I, P554Y, L555P, N604S, F1208L	1168-1170 (del)
	MAL7P1.21	317358-319835	putative origin recognition complex subunit 2	825	ODC2 origin recognition complex subunit 2	A101T	-
	PF07_0023	320354-322819	putative DNA replication licensing factor mcm7 homologue	821	minichromosome maintenance protein, P-loop containing nucleoside triphosphate hydrolase	-	-
SM24a/b/c	PF07_0024	325403-334087	putative inositol phosphatase	2814	phosphoinositol polyphosphatase (sac family), SacI homology domain, endonuclease/exonuclease/phosphatase family	M443I, Y1738E, H2592Y, G2744D	598-600 (del), 1006 (del), 1212-1213 (ins), 1742-1745 (del)

Results

STS	Gene	Location	Annotated function	Length	Domains	Codon polymorphisms	Length polymorphisms
	MAL7P1.201	336416-339814	putative RNA helicase	1132	P-loop containing nucleoside triphosphate hydrolase, Helicase conserved C-terminal domain	-	126 (del)
	MAL7P1.300	340853-341547	putative 40S ribosomal S29 protein	54	S14 ribosomal protein	n.d.	n.d.
	MAL7P1.339	343138-344469	putative Ca ²⁺ chelating serine protease	165	PR-1 like	n.d.	n.d.
	MAL7P1.340	345481-346601	putative ATP synthase subunit c	166	F ₁ F ₀ ATP synthase subunit C	n.d.	n.d.
	MAL7P1.202	348781-352470	conserved protein, unkown function	1229	ARM repeat	-	-
	MAL7P1.203	352977-358440	conserved protein, unkown function	1526	PAH2 domain	E638D, S1334R	-
	MAL7P1.203b	359885-360136	conserved protein, unkown function	52	CHCH domain	n.d.	n.d.
B5M12	MAL7P1.203a	360944-361413	conserved protein, unkown function	118	-	-	-
	MAL7P1.320	362236-362514	putative ribosomal L37e protein	92	L37e ribosomal protein	-	-
	MAL7P1.204	365281-370401	conserved protein, unkown function	1706	winged helix DNA binding domain	N1344D, N1353D, N1371K	300 (del), 819-820 (ins), 1054-1055 (del), 1228-1229 (ins), 1345-1348 (del), 1360 (del)
SM205	MAL7P1.205	375627-377660	conserved protein, unkown function	677	-	-	190-193 (ins)
	MAL7P1.206	378286-380907	putative DNA mismatch repair enzyme	873	MutS DNA repair protein	-	-
	MAL7_tRNA_Thr1	381451-381523	tRNA				
	MAL7_tRNA_His1	382105-382176	tRNA				
	MAL7_tRNA_Lys1	393244-383316	tRNA				
	MAL7_tRNA_Lys2	384391-384463	tRNA				
SM207	MAL7P1.207	385315-391704	conserved protein, unkown function	2129	-	F928L, I942M, C981S, H982D, D984G	1038-1049 (ins), 1387 (del), 2009-2015 (del)
SM208	MAL7P1.208	394264-397462	RAMA (rophty associated membrane antigen)	861	nucleic acid binding protein	T196A, K272E, I286M, V315Q, D318Y, M321F, D328N, Q330E, M331F, Y333N, Q394E, M623I	381-382 (ins)
	MAL7P1.209	399291-401282	putative ATPase	663	AAA ATPase	N516T	348 (ins), 409 (ins)
SM22	MAL7P1.22	403656-408461	conserved protein, unkown function	1601	BAG domain, phospholipase A2	V1420I	286-287 (del)
	PF07_0025	409365-410099	conserved protein, unknown function	244	-	-	-
	PF07_0026	413079-415964	putative ubiquitin ligase E3	961	fibronectin type III, TRPlike domain, RING/U box	N547S, S553G, S555N, G561S, S562N, N565T	548-572(del)
	PF07_0029	436970-439992	heat shock protein 90	745	heat shock protein 90		Intron length polymorphism

n.d., not detected; -, no polymorphism; ins, insertion; del, deletion