

TABLE III (supp.) Highly Polymorphic Rice-Sorghum Loci

CDS Model ID ^a	TIGR Common Name ^b	Chr.	CDS Start	CDS End	E-value	Sorghum		Rice	
						SNP/kb (SNP#)		SNP/kb (SNP#)	
8350.m00187	putative Integral membrane protein	1	1007164	1008937	6.00E-140	8.88 (6)		6.2 (11)	
8350.m00328	sterol-C5(6)-desaturase	1	1885412	1888722	0	3.93 (5)		3.93 (13)	
8350.m00722	putative Ubiquitin isopeptidase T	1	3983573	3991800	0	8.88 (14)		7.54 (62)	
8350.m00802	unknown protein	1	4506027	4509900	1.20E-25	7.65 (11)		3.61 (14)	
8350.m01155	hypothetical protein	1	6860103	6860529	1.00E-25	3.13 (4)		4.69 (2)	
8350.m02867	putative oxalyl-CoA decarboxylase	1	17371294	17374956	5.00E-126	3.65 (4)		4.92 (18)	
8350.m04547	guanine nucleotide-binding protein beta subunit-like protein	1	28115825	28117991	0	3.8 (5)		7.39 (16)	
8350.m04740	hypothetical protein	1	29208674	29212561	3.00E-116	3.21 (5)		3.09 (12)	
8350.m04751	putative WD-repeat protein RBAP1	1	29286218	29291567	7.00E-117	6.78 (12)		12.15 (65)	
8350.m05583	proteasome subunit alpha type 3	1	34256593	34260218	4.00E-152	3.35 (5)		5.52 (20)	
8350.m06968	cell cycle switch protein	1	42584409	42591212	9.50E-88	5.23 (7)		4.12 (28)	
8351.m00758	Similar to DNA-binding protein	2	4499317	4499857	8.20E-24	3.72 (6)		3.7 (2)	
8351.m01005	conserved hypothetical protein	2	6063138	6072320	7.00E-104	3.02 (4)		6.86 (63)	
8351.m01670	protein serine/threonine kinase-like protein	2	10466385	10472188	3.30E-68	3.17 (3)		5.51 (32)	
8351.m01795	Similar to AF133840 heat shock protein HSP101	2	11195288	11197635	8.30E-24	5.5 (9)		3.83 (9)	
8351.m02126	conserved hypothetical protein protein	2	13331124	13333197	1.70E-93	6.72 (15)		3.86 (8)	
8351.m02694	putative Ribosomal protein S8e	2	16783550	16785771	2.00E-134	3.05 (3)		5.4 (12)	
8351.m02822	putative ribosomal protein L29	2	17596760	17598085	5.00E-110	3.39 (3)		3.02 (4)	
8351.m02837	N97201 come from this gene	2	17684513	17689587	0	3.67 (4)		7.88 (40)	
8351.m02852	polyprotein	2	17793812	17804038	0	4.14 (7)		3.72 (38)	
8351.m03082	hydrolase, carbon-nitrogen family	2	19403820	19407488	0	4.23 (5)		4.63 (17)	
8351.m04452	putative endoxylglucan transferase	2	28245881	28247772	2.00E-141	3.56 (5)		6.35 (12)	
8351.m04643	rho protein GDP-dissociation inhibitor homolog	2	29456196	29458260	2.00E-150	6.95 (9)		3.39 (7)	
8351.m04759	conserved hypothetical protein	2	30094399	30095176	3.30E-37	6.86 (6)		5.15 (4)	
8351.m05393	AL035527 putative NADPH quinone oxidoreductase	2	33946898	33948866	1.00E-151	4.54 (6)		4.07 (8)	
8360.m00226	Similar to receptor-protein kinase-like protein	3	1389759	1391159	5.00E-151	3.63 (5)		3.57 (5)	
8360.m01221	hypothetical protein	3	7437311	7439718	1.30E-39	6.82 (6)		9.97 (24)	
8360.m01398	T23J18.7	3	8527947	8530788	7.00E-113	4.62 (5)		3.17 (9)	
8360.m02934	putative dioxygenase	3	18038186	18040910	5.10E-40	3.81 (5)		4.04 (11)	
8360.m04370	Similar to AY085198	3	26729046	26733144	2.40E-97	6.8 (8)		4.88 (20)	
8360.m04396	EST AU032834, C26211, AU065338, AU100680	3	26884169	26886418	1.00E-170	3.35 (4)		3.56 (8)	
8360.m05228	putative heat shock transcription factor	3	31731069	31733341	1.30E-67	5.12 (5)		3.08 (7)	
8352.m01835	conserved hypothetical protein	4	11056859	11059602	1.60E-21	5.32 (7)		5.1 (14)	
8352.m03569	AY061912 At1g24020/T23E23_22	4	22268016	22268632	1.00E-135	4.58 (4)		6.49 (4)	
8352.m04346	hypothetical protein	4	26778681	26783647	0	4.2 (5)		3.62 (18)	
8352.m05211	Similar to nuclease I	4	32235301	32237568	7.70E-79	4.15 (5)		7.94 (18)	
8352.m05487	protein c20orf13. [human	4	33822242	33825851	4.80E-79	3.93 (3)		3.05 (11)	
8353.m02199	putative superoxide dismutase (Mn/Fe family)	5	13954249	13958666	1.50E-95	3.25 (4)		4.98 (22)	
8353.m02449	Similar to DNA-binding protein GBP16	5	15434599	15437716	0	5.15 (8)		4.49 (14)	
8353.m03261	hypothetical protein	5	20556413	20557972	7.00E-151	4.19 (7)		7.7 (12)	
8353.m03958	At2g5740/F3N11.19	5	24622896	24627929	3.40E-80	3.55 (3)		10.13 (51)	
8353.m04060	hypothetical protein	5	25115972	25118565	1.70E-77	4.16 (7)		3.86 (10)	
8353.m04380	iron-sulfur cluster assembly protein IscU	5	26910146	26913131	4.10E-83	7.12 (7)		4.02 (12)	
8354.m00456	Proline-rich protein APG isolog	6	2493641	2495306	3.00E-165	3.26 (5)		3.6 (6)	
8354.m01454	UV excision repair protein Rad23	6	8686442	8692098	4.30E-84	4.4 (7)		9.55 (54)	
8354.m02346	hypothetical protein	6	14286129	14291001	0	3.02 (6)		4.52 (22)	
8354.m04440	putative Glycosyltransferase family 43	6	27649457	27652685	1.00E-174	3.39 (7)		23.23 (75)	
8354.m04490	conserved hypothetical protein	6	27918972	27919925	3.10E-31	4.52 (4)		6.3 (6)	
8355.m01338	calreticulin precursor	7	8036756	8040706	0	5.19 (10)		3.04 (12)	
8355.m04087	AC021044 FH protein interacting protein FIP1	7	25350213	25351870	9.40E-72	5.83 (6)		4.83 (8)	
8355.m04093	putative Ribosomal protein S6e	7	25395276	25397471	0	3.55 (4)		4.1 (9)	
8355.m04103	putative arginine/serine-rich splicing factor	7	25462813	25468572	4.90E-86	5.41 (6)		3.13 (18)	
8356.m00705	hypothetical protein	8	4421989	4424965	3.90E-47	3.49 (5)		9.07 (27)	
8356.m00873	starch synthase III	8	5441415	5455534	2.50E-47	14.15 (13)		5.24 (74)	
8356.m01014	At1g31070/F17F8_1	8	6326697	6330885	4.10E-62	3.95 (5)		3.82 (16)	
8356.m01593	BT000265 putative protein	8	9873218	9883512	0	3.61 (4)		3.3 (34)	
8356.m04440	predicted protein	8	15975410	15980723	3.00E-23	3.96 (6)		3.39 (18)	
8356.m03279	hypothetical protein	8	20688407	20702292	0	3.64 (7)		3.24 (45)	
8357.m00510	putative Ferredoxin thioredoxin reductase variable alpha chain	9	3097121	3100692	8.00E-72	3.41 (3)		3.08 (11)	
8357.m02408	putative disulfide isomerase-related protein	9	15502060	15506607	0	6.23 (10)		7.04 (32)	
8362.m01545	Hypothetical ORF82 from chr10 chloroplast insertion	10	10199774	10200022	6.50E-30	4.21 (5)		12.1 (3)	
8362.m01686	Putative Myo-inositol-1-phosphate synthase (MI-1-P synthase)	10	11017610	11022199	0	5.84 (11)		3.05 (14)	
8362.m02670	unknown protein	10	17574401	17581688	3.00E-178	4.54 (11)		3.02 (22)	
8362.m02778	similar to phytochelatin synthetase	10	18202973	18205735	4.40E-29	5.41 (11)		3.62 (10)	
8362.m03133	similar to receptor lectin kinase 3	10	19990400	19992424	2.00E-103	3.76 (3)		7.91 (16)	
8362.m03215	putative WD-repeat containing protein	10	20479906	20480876	3.40E-49	5.07 (4)		3.09 (3)	
8358.m01213	putative Kelch motif	11	7359862	7361013	7.00E-129	7.93 (11)		10.43 (12)	
8358.m01304	putative uracil phosphoribosyltransferase	11	8037883	8047109	0	3.24 (6)		5.42 (50)	
8358.m02276	putative HSPC140	11	14133707	14139537	7.00E-157	4.24 (7)		4.12 (24)	
8358.m02597	repressor protein	11	16335027	16338255	5.00E-160	8.07 (9)		3.72 (12)	
8358.m03049	65476-64429	11	19204171	19207997	1.20E-33	3.58 (3)		3.14 (12)	
8359.m03290	phenylalanyl-tRNA synthetase	12	20631798	20636314	2.00E-121	7.46 (6)		3.1 (14)	
8359.m03973	conserved hypothetical protein protein	12	25131451	25136990	4.50E-99	6.58 (9)		10.47 (58)	

^aCDS (protein-coding nucleotide sequence) model ID from TIGR pseudomolecule assembly v1.0; ^bCommon name from TIGR annotations