

**Supplemental file 8** The characteristics of the 19 studied SSR- loci for subset of 297 (235 cultivated and 62 wild) species accessions

Locus	Complete genotypic data <sup>1</sup>	Number of gaps <sup>2</sup>	% missing data	Minimal fragment size	Maximum fragment size	Number of alleles	PIC	% of zeroes	% of homozygote	% heterozygote	Heterozygote, %			
											% di-	% tri-	% tetra-	% penta-
STM 1104	286	11	3,7	163	196	8	0.74	0.0	49.8	50.2	43.6	4.2	2.4	0.0
STM 5127	290	7	2,4	230	272	13	0.86	0.0	22.9	77.1	53.2	20.5	0.7	2.7
STM 5114	291	6	2,0	280	316	10	0.77	0.0	25.9	74.1	55.8	15.0	3.4	0.0
STI 012	279	18	6,1	164	215	11	0.80	0.0	44.8	55.2	47.3	7.1	0.7	0.0
STI 032	295	2	0,7	102	126	8	0.79	0.0	38.3	61.7	41.6	15.1	5.0	0.0
STI 004	296	1	0,3	64	103	11	0.70	0.0	53.8	46.2	33.1	11.0	2.0	0.0
STI 033	286	11	3,7	112	142	10	0.70	0.0	50.9	49.1	39.8	6.2	3.1	0.0
STM 1106	268	29	9,8	127	199	24	0.85	0.0	56.8	43.2	31.0	9.2	3.0	0.0
STG 0025	294	3	1,0	190	210	5	0.51	0.0	56.2	43.8	43.4	0.3	0.0	0.0
STM 5121	281	16	5,4	280	289	4	0.74	0.0	72.9	27.1	26.8	0.4	0.0	0.0
STI 001	294	3	1,0	161	202	12	0.81	0.0	39.1	60.9	43.1	15.8	2.0	0.0
STM 0031	257	40	13,5	161	202	10	0.70	23.3	27.1	49.6	44.2	5.0	0.4	0.0
STM 0037	287	10	3,4	70	108	19	0.82	0.0	31.4	68.6	48.6	14.8	5.2	0.0
STI 014	292	5	1,7	115	139	9	0.75	0.0	41.7	58.3	48.5	8.1	1.7	0.0
STG 0016	295	2	0,7	112	157	15	0.81	0.0	26.2	73.8	49.0	14.4	10.4	0.0
STM 1064	269	28	9,4	179	195	9	0.68	0.0	52.0	48.0	33.1	13.8	1.1	0.0
STG 0001	220	77	25,9	118	194	15	0.79	0.0	35.9	64.1	50.0	11.4	2.3	0.5
STM1052	206	91	30,6	196	260	17	0.82	0.0	52.2	47.8	30.4	15.9	1.4	0.0
STI 030	291	6	2,0	82	121	13	0.81	0.0	23.8	76.2	61.2	13.6	1.4	0.0
In total	5643	366	6.5			223								

<sup>1</sup>The number of genotypes for which SSR analysis results for this locus are available

<sup>2</sup>Genotypes which lack data on this locus, no. of genotypes with missing data for concrete