

Table 1 Major allele frequency, number of alleles, gene diversity, heterozygosity and polymorphism information content of 60 SSR markers in 52 soybean landraces from Jilin Province

Marker	LG	MAF	Allele No.	Gene Diversity	Heterozygosity	PIC
Satt002	D2	0.4 904	7	0.6 877	0.0 192	0.6 509
Satt005	D1a	0.1 765	15	0.8 956	0.0 196	0.8 865
Satt012	G	0.5 288	11	0.6 940	0.0 192	0.6 787
Satt022	N	0.2 788	8	0.8 138	0.0 192	0.7 890
Sat_099	L	0.2 500	8	0.8 358	0.0 000	0.8 150
Sat_112	E	0.4 082	13	0.7 888	0.0 000	0.7 725
Sat_130	C2	0.5 096	5	0.6 477	0.0 192	0.5 966
Satt146	F	0.3 269	11	0.8 055	0.0 000	0.7 818
satt157	D1b	0.1 000	14	0.9 206	0.0 333	0.9 149
Satt168	B2	0.2 157	7	0.8 314	0.0 392	0.8 092
Satt173	O	0.3 922	13	0.8 035	0.0 000	0.7 889
Satt180	C1	0.2 308	11	0.8 314	0.0 000	0.8 100
Satt184	D1a	0.2 788	8	0.8 068	0.0 192	0.7 793
Satt187	A2	0.3 529	8	0.7 682	0.0 000	0.7 346
Satt194	C1	0.3 529	6	0.7 559	0.0 000	0.7 185
Satt197	B1	0.2 353	9	0.8 322	0.0 196	0.8 112
Satt216	D1b	0.5 769	5	0.5 969	0.0 000	0.5 482
Satt226	D2	0.1 731	12	0.8 719	0.0 192	0.8 583
Satt230	E	0.5 577	4	0.5 518	0.0 000	0.4 654
Satt236	A1	0.2 900	7	0.7 790	0.0 200	0.7 445
Satt239	I	0.2 500	10	0.8 597	0.0 192	0.8 450
Satt242	K	0.2 353	13	0.8 387	0.0980	0.8 193
Satt243	O	0.3 462	11	0.8 082	0.0 577	0.7 874
Satt267	D1a	0.6 923	6	0.4 926	0.0 385	0.4 652
Satt268	E	0.5 588	10	0.6 476	0.0 196	0.6 217
Satt279	H	0.6 078	6	0.5 844	0.0 000	0.5 492
Satt281	C2	0.3 654	16	0.8 238	0.0 192	0.8 109
Satt286	C2	0.3 462	8	0.8 018	0.0 000	0.7 786
Satt307	C2	0.3 173	7	0.7 616	0.0 192	0.7 247
Satt308	M	0.2 745	11	0.8 235	0.0 000	0.8 026
Satt309	G	0.5 686	4	0.5 890	0.0 000	0.5 304
Satt334	F	0.2 959	8	0.7 782	0.0 204	0.7 440
Satt339	N	0.3 333	8	0.7 782	0.0 000	0.7 464
Satt429	A2	0.3 654	10	0.7 803	0.0 000	0.7 527
Satt345	O	0.2 115	10	0.8 565	0.0 000	0.8 402
Satt346	M	0.5 098	5	0.6 259	0.0 000	0.5 634
Satt352	G	0.3 462	6	0.7 653	0.0 577	0.7 301
Satt373	L	0.2 941	13	0.8 412	0.0 000	0.8 249
Satt386	D2	0.3 824	5	0.7 265	0.0 196	0.6 807
Satt387	N	0.6 863	4	0.4 529	0.0 000	0.3 811
Satt390	A2	0.2 889	7	0.8 116	0.0 222	0.7 862
Satt453	B1	0.5 481	12	0.6 694	0.1 154	0.6 506
Satt434	H	0.1 569	17	0.9 064	0.0 196	0.8 990
Satt442	H	0.2 549	12	0.8 566	0.0 588	0.8 417
Satt300	A1	0.5 385	9	0.6 688	0.0 385	0.6 438

Continuing Table 1

Marker	LG	MAF	Allele No.	Gene Diversity	Heterozygosity	PIC
Satt462	L	0.1 346	18	0.9 210	0.0 192	0.9 157
Satt487	O	0.3 429	6	0.7 882	0.0 286	0.7 596
Satt530	N	0.3 627	9	0.7 997	0.0 784	0.7 780
Satt556	B2	0.5 385	7	0.6 389	0.0 577	0.5 955
Satt565	C1	0.4 216	9	0.7 518	0.0 196	0.7 236
satt571	I	0.5 769	9	0.6 429	0.0 385	0.6 263
Satt577	B2	0.3 269	6	0.7 626	0.0 000	0.7 250
Satt586	F	0.3 235	10	0.8 085	0.0 588	0.7 866
Satt588	K	0.4 200	10	0.7 496	0.0 000	0.7 206
Satt590	M	0.2 692	14	0.8504	0.0 192	0.8 355
Satt596	J	0.3 269	8	0.7 722	0.0 000	0.7 384
Sct_188	F	0.6 346	2	0.4 638	0.0 385	0.3 562
Sct_189	I	0.2 212	10	0.8 452	0.0 192	0.8 264
Satt431	J	0.2 157	10	0.8 664	0.0 392	0.8 524
Satt414	J	0.3 922	7	0.7 482	0.0 000	0.7 131
Mean		0.3 668	9.08	0.7 579	0.0 215	0.7 288