

Table S1. Details of g-SSR primers used for characterization 28 *Tinospora* accessions

S. N.	Primer	Forward Primer Sequence (5'-3')	Reverse Primer Sequence (5'-3')	Repeat Motif	Ta (°C)	Expected Product Size in (bp)	NCBI Accession numbers
1	Tcgssr1	CTTCGCTCTACCGCCTCAT	AGCTTCGGATCCACGTTACA	(GTT)2	52	103bp	-
2	Tcgssr2*	TTCTGCGCACAGAGAGAGA	TTCAGTGAACGACTCCAACG	(GA)10..(AG)8	52	241bp	KT384120
3	Tcgssr3*	TTGCTGGTGTGTGTGAGAGA	TTCATTGCTTTGTGCAGTCC	(AG)21	52	205bp	KT384121
4	Tcgssr4*	TGGAGCACTTTGACAGAGCA	AGATGTCAATCATGCCACCA	(GTG)2CA(GTG)2	51.6	211bp	-
5	Tcgssr5	CCAGCTTCTCCACTTCTTCG	TATGGGTGCGTCAAAACAGA	(CA)4AAC(CA)2	53	153bp	KT384122
6	Tcgssr6*	CCCAAGCTTCGCATCCTAT	ATCGGAACGACAAGTTCGAC	(TTTT)6	50	216bp	-
7	Tcgssr7*	CAAGCTTCGGATCGTTTGAT	CGCAAAGGAAGAAGAGGAAA	(CAG)2..(CAG)3	50.3	163bp	-
8	Tcgssr8	GAGCTGCACCCAAACAATTT	GCATAGGAATTCGGGGGTAT	(AG)3..(AG)2	51.6	182bp	-
9	Tcgssr9*	AGATGTCAATCATGCCACCA	TGGAGCACTTTGACAGAGCA	(ACAAC)2	52	211bp	-
10	Tcgssr10*	AGAAAAGTAGGCCGCGAGTA	CTTCGGATCGGTGGATTCT	(AC)3	50	182bp	-
11	Tcgssr11	GCTTCGAATCAAGGCATGAA	CCCAAGCTTCGCATCTTTA	(GT)4	50	150bp	-
12	Tcgssr12*	CTCAATGAGAGGGGGTTCAA	AGGTATATTTGGCGCTTGGA	(CCTA)3	50	220bp	-
13	Tcgssr13*	CCAAGCTTCGCATCAATTCT	GGATGAGCTTTTGACGAAGG	(CTT)3	50	174bp	-
14	Tcgssr14*	TATGGGTGCGTCAAAACAGA	CCAGCTTCTCCACTTCTTCG	(GAA)3(CTA)3(GAA)2	52	153bp	-
15	Tcgssr15*	TTGGGGATTTTGAGAGATTTG	CCGCATAATACTAATGAGCAAGG	(TGA)2G(TGA)2G(TGA) 2	52	150bp	KT384123
16	Tcgssr16	GAACAGGGGATTCGAAACAG	GGATGCGCTCTCCTTTGTTA	(TTC)3	50	155bp	-
17	Tcgssr17*	AATTGGGAGAGAGAGAGAGAG	TTCTGCGTCCCTCCCTCT	(GA)25	53	239bp	KT384124
18	Tcgssr18*	CGTGACACGAGAGAGAGAGAG	GCAACTCCGACGCTTTTTTC	(GA)26	53	228bp	KT384125
19	Tcgssr19	TCCTCCAAAATCATCGGAAG	GAGAGAGCTCACGTTTTGG	(AAC)2AAT(AAC)2	52	194bp	-
20	Tcgssr20*	TTCTACTCCTTCGCCTCCA	CACCAATCCACCATTTTTTC	(CT)18	52	171bp	KT384126
21	Tcgssr21*	TCAGACGAGAAACGAGCGTA	TCTTCACATTCGACGCAGAC	(AG)24	51.6	193bp	KT384128
22	Tcgssr22*	GAGGTTGTCCACCACTTA	TTGATCCACTATGCGACCTG	(AAAA)4	52	234bp	-
23	Tcgssr23*	ACCCAAGCTTCGCTAATTT	ACGTGTGTCGCTCAATCAAC	(GAGGT)3	52	151bp	-
24	Tcgssr24*	GCTTCGGACCTATTCCTCT	CAGCTTAACCTGCAACACCA	(CTCT)4	50	183bp	-
25	Tcgssr25	GCGCAAGAAGACGGTAACA	GCTGCTGAGACGAGTTGTTG	(AAC)9(AAC)4AG (CAA)9(CAG)5	53	154bp	KT384129
26	Tcgssr26	AGCGATCGTGTTGCACTTA	ATCAGCCACCACATTCACCT	(TATA)2	52	199bp	-
27	Tcgssr27*	GCTGTTGGGCAGTTCTTAGC	ACGAAATGGAAATGGGAATG	(CT)4..(CTCT)4	52	177bp	-
28	Tcgssr28*	CCATCTCACTGTGCGTGTCT	GCACGAGTGTGTGTGTGTA	(TC)16	53	215bp	KT384130
29	Tcgssr29	GACCCAAGCTTCGCTAAAT	ATGCAAAAACGCAGATAGGG	(GAA)3..(GAA)2	53	215bp	-

30	Tcgssr30*	TCTGATGTGTGTTGCGTGAA	GCTCCTTCCTTCATCATTCG	(TGC)2(TG)3(TGC)3(TG) 3	53	161bp	KT384131
31	Tcgssr31*	TTGCTGTGCATCAATACCAAC	TGCAAAACACAACCACAACA	(GTGT)5	52	185bp	KT384132
32	Tcgssr32*	AGCTCCCTCTCTCACGAAT	GTGCGAGATAAAGAGAGAAACTG	(TC)14	52	190bp	KT384133
33	Tcgssr33*	CGTGGTTTCTCGCAGCTCT	CAAGCTTCGCTACGAGAGAGA	(CT)8...(CT)7; (TC)7	52	348bp	-
34	Tcgssr34*	TGCAGTCTCTCGTCGCTCT	GCAAGAGAGAGCTTGCCAAA	(CT)6	52	241bp	-
35	Tcgssr35*	GCCTATCGGCGTAACAACAT	AAGGCAGACACGGTCTTAGA	(CTGCTG)4...(TC)4	52	234bp	KT384135
36	Tcgssr36*	CGATCCGAAGGCTGTGATTA	TGTGCTGAAATCTTGCCAAA	(AAAA)N	52	194bp	KT384136
37	Tcgssr37	TGTTGCATGTTTGAGGCATT	GCCCTGGTTCTTTCTTCCTT	(AAAA)N	52	227	KT384137
38	Tcgssr38*	AATGAACGCCAGCAACCTAC	GCATAGCAAGGCAGGGTAAG	(AAAA)N	52	154bp	KT384138
39	Tcgssr39*	ACCGCAGTCACACTCACAAC	GACAGGCATAGGGCAATGAT	(AGAG)N	52	237bp	KT384139
40	Tcgssr40*	GATGCGATCGAGGTTTATCC	GAAATTGGCTTGAATTGGA	(AAAA)N	51.6	152bp	KT384140
41	Tcgssr41	CAACCCCAGTAGTCAAGGA	TTCAGCGAAATAGGCTTGCT	(AAAA)N	52	235bp	KT384141
42	Tcgssr42*	GAGAGTTGCTGCCCTAGCTG	CCTTTCCTTAGGCGCAAAAT	(CTT)4...(CTT)2	52	178bp	KT384142
43	Tcgssr43*	CAACGTGTTCTACCACACA	GGGTCACGATATCGGAAGAA	(TCTC)N...(TCTCTC)N	52	176bp	KT384143
44	Tcgssr44	TATTCGCCCTTTCATTTTT	GCATATTGGGCACTGCTTCT	(A)10...(A)8...(A)4	52	208bp	KT384144
45	Tcgssr45	AAACAAAAGGTCACAAATCATCA	ATGACGCACAGCCTAATTGA	(AAT)5	52	152bp	KT384145
46	Tcgssr46*	TCAATGAAGAACAGGGGAGA	CACACCAGCAGCTGCATAAC	(GT)5	52	153bp	KT384147
47	Tcgssr47*	AAGTTCAGGGAGGAGGTGT	TTTGGGACGCAAAGTTTTCT	(CA)13A(AC)13A(AC)14	50.3	177bp	KT384148
48	Tcgssr48*	AGAACCCAGCAGTGATTTGC	TGCCTACGGGCTAGATCAAC	(AAAA)4	51.6	203bp	KT384149
49	Tcgssr49*	GATGAAATCCCAGGACGAT	CCCCAAGCATAGGAAATTAGC	(AAAA)n(A)7	52	163bp	KT384150
50	Tcgssr50*	TTCGGGCAAAGATGAATAGG	GCAGCTGCATAACCCAGAAT	(GT)5	51.6	209bp	KT384151
51	Tcgssr51*	GGACATATGGCCAAGGACTG	TCAATGGCAAACACTCTTGC	(AAC)11GA(CAA)10	52	236bp	KT384091
52	Tcgssr52*	TAGGGACACCAGAGGCCAAAT	ACCTTTGACAGCCGAAGTTG	(AAC)22	52	248bp	KT384092
53	Tcgssr53*	ACCGTCTCCATGCTTTTT GA	AAC ACA TAG CTT ATG CAA CA	(GT)16	49	206bp	KT384168
54	Tcgssr54*	CATGTGCTCGTGTGTGTGTG	CGCGTGCTTCTCTCTCTCT	(GT)9...(AG)31	51.6	100bp	KT384084
55	Tcgssr55*	TCTCTCTCTCTCTGTGAGAT GTAAA	TCTTCGGTCTCTCCCTCTCC	(CT)12CA(CT)15	53	167bp	KT384087
56	Tcgssr56*	AATCTCTCTCTCTCTCTCT	GTCCTCCCTCTTTCTCTGC	(CT)12CA(CT)15	53	147bp	KT384087
57	Tcgssr57*	GGTTGGATCGTCTTGATTCC	AACCATTGCAAGTTCTTCAAAA	(CT)23	53	151bp	KT384088
58	Tcgssr58*	AGAGAGAGAGAGAGAGAGAGA	CCA GTA CAC CCA CGT CAC TG	(GA)29	50.3	175bp	KT384099
59	Tcgssr59	TAGTCCCTTCGCCAATTGAT	CCC TCT CTC TCA GCC CTC TA	(GA)5...(GA)7...(GA)5	50.3	168bp	KT384110
60	Tcgssr60*	ATTCTCGTCGACCGATTCTG	TTTTGACACACAGCACACACA	(GA)15	51.6	195bp	KT384114

61	Tcgssr61	CAAATCTTGAGCGCAAACACT	TTGTAAGTGGTAATTAAGTGGGTTT T	(AG)28	50.3	163bp	KT384116
62	Tcgssr62*	TTGCCTAATAATGGCTGCAA	CTCTTGCTTACGCGTGGACT	(CA)3CC(CA)2A(CA)16	49	100bp	-
63	Tcgssr63*	TCCCATGTATCCTCCCCTTC	GACACGAACCAAGGATATAAGC	(GT)5..(GT)8	53	152bp	KT384160
64	Tcgssr64*	GAAAAACCAGTTGAGAGAG AGAGA	TGTCCATTCTTTAAGCGTCA	(GA)25	51.6	152bp	KT384107
65	Tcgssr65	TGGGAAGTGTTCATCAAATG	TTCAAAAAGAAGACTTAGTTGTCTC G	(CT)27 CC (CT)9	49	214bp	KT384083

---

\*Polymorphic markers

**Table S2.** Major allele frequency, Allele number, Gene diversity, Heterozygosity and PIC generated by 49 g-SSR in 28 *Tinospora* accessions

Marker	Major Allele Frequency	Allele No	Gene Diversity	Heterozygosity	PIC
Tcgssr17	0.463	4	0.6173	0.8519	0.5399
Tcgssr23	0.4783	3	0.6115	0.913	0.5321
Tcgssr14	0.5357	3	0.574	0.9286	0.4913
Tcgssr56	0.4821	3	0.5759	0.9643	0.4839
Tcgssr20	0.5357	3	0.5644	0.8571	0.4769
Tcgssr57	0.5192	3	0.5614	0.9615	0.4683
Tcgssr39	0.5179	3	0.5453	0.9643	0.4442
Tcgssr15	0.5556	4	0.5384	0.8889	0.4435
Tcgssr40	0.5577	3	0.5377	0.8846	0.4426
Tcgssr62	0.6071	3	0.523	0.6786	0.442
Tcgssr13	0.6087	3	0.5189	0.5217	0.4361
Tcgssr64	0.5000	3	0.5397	0.913	0.4338
Tcgssr55	0.5000	3	0.5368	1.000	0.4295
Tcgssr4	0.4815	3	0.535	0.963	0.4262
Tcgssr31	0.5893	3	0.5108	0.8214	0.4119
Tcgssr54	0.5217	3	0.5189	0.8696	0.405
Tcgssr2	0.5000	3	0.5185	0.9615	0.4026
Tcgssr10	0.5000	3	0.5185	0.9231	0.4026
Tcgssr49	0.5000	3	0.5172	1.000	0.4007
Tcgssr6	0.5179	3	0.5159	0.9643	0.4000
Tcgssr33	0.5192	2	0.4993	0.8846	0.3746
Tcgssr58	0.5217	2	0.4991	0.6957	0.3745
Tcgssr60	0.5217	2	0.4991	0.8696	0.3745
Tcgssr52	0.5370	2	0.4973	0.9259	0.3736
Tcgssr28	0.5577	2	0.4933	0.8846	0.3716
Tcgssr51	0.5714	2	0.4898	0.8571	0.3698
Tcgssr9	0.5741	2	0.489	0.8519	0.3695
Tcgssr44	0.6607	3	0.4598	0.6786	0.3693
Tcgssr34	0.5893	2	0.4841	0.8214	0.3669
Tcgssr47	0.6042	2	0.4783	0.7083	0.3639
Tcgssr35	0.6071	2	0.477	0.7857	0.3633
Tcgssr42	0.6071	2	0.477	0.7857	0.3633
Tcgssr63	0.6346	2	0.4638	0.7308	0.3562
Tcgssr27	0.6429	2	0.4592	0.7143	0.3538
Tcgssr53	0.7037	3	0.4273	0.5185	0.3505
Tcgssr50	0.7143	2	0.4082	0.5714	0.3249
Tcgssr3	0.8036	3	0.3221	0.3929	0.2805
Tcgssr24	0.8036	2	0.3157	0.3929	0.2659
Tcgssr12	0.8393	2	0.2698	0.3214	0.2334
Tcgssr21	0.8929	3	0.1964	0.2143	0.1862

<b>Tcgssr22</b>	0.9107	3	0.1652	0.1429	0.1562
<b>Tcgssr18</b>	0.9286	3	0.1352	0.1429	0.1308
<b>Tcgssr36</b>	0.9286	2	0.1327	0.1429	0.1239
<b>Tcgssr48</b>	0.9423	2	0.1087	0.1154	0.1028
<b>Tcgssr32</b>	0.9643	2	0.0689	0.0714	0.0665
<b>Tcgssr7</b>	0.9792	2	0.0408	0.0417	0.0400
<b>Tcgssr30</b>	0.9821	2	0.0351	0.0357	0.0345
<b>Tcgssr38</b>	0.9821	2	0.0351	0.0357	0.0345
<b>Tcgssr43</b>	1.0000	1	0.0000	0.0000	0.0000
<b>Mean</b>	<b>0.653</b>	<b>2.551</b>	<b>0.4144</b>	<b>0.6564</b>	<b>0.3345</b>

**Table S3.** Major allele frequency, Allele number, Gene diversity, Heterozygosity and PIC generated by 80 EST-SSR in 28 *Tinospora* accessions

Marker	Major Allele Frequency	Allele No	Gene Diversity	Heterozygosity	PIC
Tcestssr-3	0.5714	2.0000	0.4898	0.8571	0.3698
Tcestssr-4	0.9286	2.0000	0.1327	0.0000	0.1239
Tcestssr-5	0.5769	2.0000	0.4882	0.8462	0.3690
Tcestssr-6	0.9464	2.0000	0.1014	0.0357	0.0963
Tcestssr-7	0.9643	2.0000	0.0689	0.0714	0.0665
Tcestssr-8	0.9444	2.0000	0.1049	0.1111	0.0994
Tcestssr-9	0.7679	2.0000	0.3565	0.4643	0.2930
Tcestssr-11	0.7143	2.0000	0.4082	0.5714	0.3249
Tcestssr-12	0.5179	2.0000	0.4994	0.9643	0.3747
Tcestssr-13	0.9600	2.0000	0.0768	0.0000	0.0739
Tcestssr-14	0.5357	2.0000	0.4974	0.9286	0.3737
Tcestssr-15	0.7200	2.0000	0.4032	0.5600	0.3219
Tcestssr-16	0.8600	2.0000	0.2408	0.0400	0.2118
Tcestssr-17	0.5357	2.0000	0.4974	0.7857	0.3737
Tcestssr-18	0.9200	2.0000	0.1472	0.1600	0.1364
Tcestssr-19	0.9000	2.0000	0.1800	0.2000	0.1638
Tcestssr-20	0.7143	3.0000	0.4177	0.5714	0.3441
Tcestssr-21	0.9107	2.0000	0.1626	0.1071	0.1494
Tcestssr-22	0.9286	2.0000	0.1327	0.0476	0.1239
Tcestssr-23	0.6875	2.0000	0.4297	0.6250	0.3374
Tcestssr-26	0.9643	2.0000	0.0689	0.0000	0.0665
Tcestssr-29	0.5536	3.0000	0.5364	0.8929	0.4391

<b>Tcestssr-30</b>	0.6481	2.0000	0.4561	0.7037	0.3521
<b>Tcestssr-32</b>	0.8929	3.0000	0.1971	0.2143	0.1879
<b>Tcestssr-33</b>	0.6111	2.0000	0.4753	0.7778	0.3623
<b>Tcestssr-34</b>	0.8929	2.0000	0.1913	0.2143	0.1730
<b>Tcestssr-36</b>	0.5000	3.0000	0.5800	1.0000	0.4918
<b>Tcestssr-37</b>	0.5556	2.0000	0.4938	0.8148	0.3719
<b>Tcestssr-38</b>	0.9423	2.0000	0.1087	0.1154	0.1028
<b>Tcestssr-39</b>	0.9800	2.0000	0.0392	0.0400	0.0384
<b>Tcestssr-41</b>	0.6481	2.0000	0.4561	0.7037	0.3521
<b>Tcestssr-42</b>	0.9815	2.0000	0.0364	0.0370	0.0357
<b>Tcestssr-44</b>	0.5536	4.0000	0.5886	0.6071	0.5220
<b>Tcestssr-45</b>	0.8750	2.0000	0.2188	0.0357	0.1948
<b>Tcestssr-46</b>	0.5000	2.0000	0.5000	0.6667	0.3750
<b>Tcestssr-47</b>	0.5714	2.0000	0.4898	0.8571	0.3698
<b>Tcestssr-48</b>	0.5179	2.0000	0.4994	0.9643	0.3747
<b>Tcestssr-49</b>	0.6786	3.0000	0.4471	0.6429	0.3618
<b>Tcestssr-50</b>	0.6875	4.0000	0.4627	0.4583	0.4013
<b>Tcestssr-51</b>	0.9231	2.0000	0.1420	0.1538	0.1319
<b>Tcestssr-52</b>	0.5000	3.0000	0.5343	1.0000	0.4259
<b>Tcestssr-53</b>	0.5741	2.0000	0.4890	0.7037	0.3695
<b>Tcestssr-54</b>	0.8696	2.0000	0.2268	0.1739	0.2011
<b>Tcestssr-55</b>	0.5536	3.0000	0.5096	0.8929	0.3967
<b>Tcestssr-56</b>	0.6296	2.0000	0.4664	0.7407	0.3576
<b>Tcestssr-57</b>	0.8214	2.0000	0.2934	0.0000	0.2503
<b>Tcestssr-58</b>	0.5185	2.0000	0.4993	0.9630	0.3747

<b>Tcestssr-59</b>	0.5536	3.0000	0.5236	0.8214	0.4190
<b>Tcestssr-60</b>	0.5179	2.0000	0.4994	0.8929	0.3747
<b>Tcestssr-61</b>	0.7105	2.0000	0.4114	0.5789	0.3267
<b>Tcestssr-62</b>	0.5893	2.0000	0.4841	0.8214	0.3669
<b>Tcestssr-63</b>	0.5000	4.0000	0.5658	0.7778	0.4728
<b>Tcestssr-65</b>	0.5714	2.0000	0.4898	0.8571	0.3698
<b>Tcestssr-66</b>	0.5536	2.0000	0.4943	0.8929	0.3721
<b>Tcestssr-68</b>	0.6200	2.0000	0.4712	0.6800	0.3602
<b>Tcestssr-70</b>	0.4630	3.0000	0.5919	0.8519	0.5044
<b>Tcestssr-71</b>	0.5357	2.0000	0.4974	0.8571	0.3737
<b>Tcestssr-72</b>	0.5370	2.0000	0.4973	0.9259	0.3736
<b>Tcestssr-73</b>	0.8333	2.0000	0.2778	0.0370	0.2392
<b>Tcestssr-74</b>	0.9464	2.0000	0.1014	0.1071	0.0963
<b>Tcestssr-75</b>	0.5000	3.0000	0.5733	0.8571	0.4823
<b>Tcestssr-76</b>	0.5893	3.0000	0.4981	0.8214	0.3906
<b>Tcestssr-77</b>	0.9815	2.0000	0.0364	0.0370	0.0357
<b>Tcestssr-78</b>	0.5000	3.0000	0.5478	1.0000	0.4456
<b>Tcestssr-79</b>	0.5357	2.0000	0.4974	0.9286	0.3737
<b>Tcestssr-80</b>	0.9821	2.0000	0.0351	0.0357	0.0345
<b>Tcestssr-81</b>	0.6964	2.0000	0.4228	0.6071	0.3334
<b>Tcestssr-82</b>	0.5714	3.0000	0.5045	0.8571	0.3940
<b>Tcestssr-83</b>	0.5000	3.0000	0.5178	1.0000	0.4016
<b>Tcestssr-84</b>	0.6071	2.0000	0.4770	0.7857	0.3633
<b>Tcestssr-85</b>	0.4815	4.0000	0.5521	0.8148	0.4512
<b>Tcestssr-86</b>	0.9815	2.0000	0.0364	0.0370	0.0357



<b>Tcestssr-87</b>	0.5357	3.0000	0.5644	0.8214	0.4769
<b>Tcestssr-89</b>	0.5000	2.0000	0.5000	1.0000	0.3750
<b>Tcestssr-90</b>	0.5185	2.0000	0.4993	0.8889	0.3747
<b>Tcestssr-91</b>	0.7407	2.0000	0.3841	0.5185	0.3103
<b>Tcestssr-92</b>	0.9821	2.0000	0.0351	0.0357	0.0345
<b>Tcestssr-94</b>	0.5000	3.0000	0.5478	0.9286	0.4456
<b>Tcestssr-95</b>	0.9821	2.0000	0.0351	0.0357	0.0345
<b>Tcestssr-96</b>	0.6071	2.0000	0.4770	0.7857	0.3633
<b>Mean</b>	<b>0.6972</b>	<b>2.3000</b>	<b>0.3686</b>	<b>0.5527</b>	<b>0.2952</b>

**Table S4.** Major allele frequency, Allele number, Gene diversity, Heterozygosity and PIC generated by 19 SCoT markers in 28 *Tinospora* accessions

Marker	Major Allele Frequency	Allele No	Gene Diversity	Heterozygosity	PIC
SCoT1	0.9643	6	0.0655	0	0.0606
SCoT2	0.7531	6	0.3182	0	0.2517
SCoT3	0.756	7	0.2902	0	0.2316
SCoT4	0.9	6	0.1778	0	0.1607
SCoT5	0.8571	6	0.2041	0	0.1686
SCoT6	0.7143	5	0.3327	0	0.2567
SCoT7	0.7407	6	0.3356	0	0.2673
SCoT8	0.8741	5	0.1679	0	0.1392
SCoT9	0.801	7	0.2992	0	0.2465
SCoT10	0.7884	7	0.2986	0	0.2446
SCoT11	0.9364	5	0.1033	0	0.0882
SCoT12	0.8365	4	0.1901	0	0.1504
SCoT13	0.9792	6	0.0399	0	0.0383
SCoT14	0.821	5	0.2725	0	0.2276
SCoT15	0.6646	7	0.39	0	0.2988
SCoT16	0.8636	7	0.2037	0	0.1726
SCoT17	0.8299	6	0.2643	0	0.2212
SCoT18	0.8571	7	0.2279	0	0.1931
SCoT19	0.74	6	0.3381	0	0.2675
Mean	0.8251	6	0.2379	0	0.1939

**Table S5.** Percentage of variation explained by the first 3 axes among the *Tinospora* accessions by g-SSR, EST-SSR and SCoT markers

Marker	Axis	%	Cum %
g-SSR	1	16.97	16.97
	2	10.95	27.93
	3	9.44	37.37
EST-SSR	1	26.84	26.84
	2	15.51	42.34
	3	8.79	51.13
SCoT	1	26.65	26.65
	2	15.09	41.74
	3	10.88	52.62