

Table S6 the pi values in XG, CKX and HZP

#No.	Region	Pi	Total Number of mutations	Region length
1	IR.gene1.trnN-GUU	0	0	72
2	IR.gene10.rps7	0	0	468
3	IR.gene11.ndhB	0.00012	1	1533
4	IR.gene12.trnL-CAA	0	0	81
5	IR.gene13.ycf15	0	0	249
6	IR.gene14.ycf2	0.00032	10	6897
7	IR.gene15.trnI-CAU	0	0	74
8	IR.gene16.rpl23	0	0	282
9	IR.gene17.rpl2	0.00022	1	825
10	IR.gene2.trnR-ACG	0	0	74
11	IR.gene3.rrn5	0	0	121
12	IR.gene4.rrn4.5	0	0	103
13	IR.gene5.rrn23	0.00026	4	2810
14	IR.gene6.trnA-UGC	0	0	73
15	IR.gene7.trnI-GAU	0	0	77
16	IR.gene8.rrn16	0.00012	1	1490
17	IR.gene9.trnV-GAC	0	0	72
18	LSC.gene1.trnH-GUG	0	0	75
19	LSC.gene10.trnG-GCC	0	0	60
20	LSC.gene11.trnR-UCU	0	0	72
21	LSC.gene12.atpA	0.00084	7	1524
22	LSC.gene13.atpF	0.00111	2	555
23	LSC.gene14.atpH	0	0	246
24	LSC.gene15.atpI	0	0	744
25	LSC.gene16.rps2	0.00153	6	711
26	LSC.gene17.rpoC2	0.00141	27	4131
27	LSC.gene18.rpoC1	0.0008	9	2052
28	LSC.gene19.rpoB	0.00086	12	3213
29	LSC.gene2.psbA	0.00017	1	1062
30	LSC.gene20.trnC-GCA	0	0	81
31	LSC.gene21.petN	0	0	90
32	LSC.gene22.psbM	0.00485	2	105
33	LSC.gene23.trnD-GUC	0	0	74
34	LSC.gene24.trnY-GUA	0	0	84
35	LSC.gene25.trnE-UUC	0.00249	1	73
36	LSC.gene26.trnT-GGU	0	0	72
37	LSC.gene27.psbD	0.00017	1	1062
38	LSC.gene28.psbC	0.0009	5	1422
39	LSC.gene29.trnS-UGA	0	0	92
40	LSC.gene3.trnK-UUU	0	0	72
41	LSC.gene30.psbZ	0.00096	1	189
42	LSC.gene31.trnG-UCC	0	0	71

43	LSC.gene32.trnfM-CAU	0	0	74
44	LSC.gene33.rps14	0.0006	1	303
45	LSC.gene34.psaB	0.00053	5	2205
46	LSC.gene35.psaA	0.00065	6	2253
47	LSC.gene36.ycf3	0	0	507
48	LSC.gene37.trnS-GGA	0	0	87
49	LSC.gene38.rps4	0.0003	1	606
50	LSC.gene39.trnT-UGU	0	0	73
51	LSC.gene4.matK	0.00279	18	1500
52	LSC.gene40.trnL-UAA	0	0	87
53	LSC.gene41.trnF-GAA	0	0	73
54	LSC.gene42.ndhJ	0.00114	3	477
55	LSC.gene43.ndhK	0.0008	3	678
56	LSC.gene44.ndhC	0.0009	1	363
57	LSC.gene45.trnV-UAC	0	0	76
58	LSC.gene46.trnM-CAU	0	0	72
59	LSC.gene47.atpE	0.00136	3	402
60	LSC.gene48.atpB	0.00182	9	1497
61	LSC.gene49.rbcL	0.00115	7	1428
62	LSC.gene5.rps16	0.00068	1	267
63	LSC.gene50.accD	0.00218	16	1497
64	LSC.gene51.psaI	0	0	111
65	LSC.gene52.ycf4	0.00164	3	555
66	LSC.gene53.cemA	0.00052	2	696
67	LSC.gene54.petA	0.00038	2	963
68	LSC.gene55.psbJ	0.00148	1	123
69	LSC.gene56.psbL	0.00155	1	117
70	LSC.gene57.psbF	0	0	120
71	LSC.gene58.psbE	0	0	252
72	LSC.gene59.petL	0	0	96
73	LSC.gene6.trnQ-UUG	0	0	72
74	LSC.gene60.petG	0	0	114
75	LSC.gene61.trnW-CCA	0	0	74
76	LSC.gene62.trnP-UGG	0	0	74
77	LSC.gene63.psaJ	0.00404	1	135
78	LSC.gene64.rpl33	0.00362	2	201
79	LSC.gene65.rps18	0	0	327
80	LSC.gene66.rpl20	0.00103	2	354
81	LSC.gene67.rps12	0.00098	2	372
82	LSC.gene68.clpP	0.00062	2	588
83	LSC.gene69.psbB	0.00048	4	1527
84	LSC.gene7.psbK	0.00371	2	186
85	LSC.gene70.psbT	0	0	108
86	LSC.gene71.psbN	0	0	132

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87	LSC.gene72.psbH	0.00164	2	222
88	LSC.gene73.petB	0.00028	1	648
89	LSC.gene74.petD	0.00113	3	483
90	LSC.gene75.rpoA	0.0018	8	1008
91	LSC.gene76.rps11	0.00087	2	417
92	LSC.gene77.rpl36	0	0	114
93	LSC.gene78.infA	0.00264	2	234
94	LSC.gene79.rps8	0.00299	5	408
95	LSC.gene8.psbI	0	0	111
96	LSC.gene80.rpl14	0.00187	3	369
97	LSC.gene81.rpl16	0.00223	3	408
98	LSC.gene82.rps3	0.00194	7	657
99	LSC.gene83.rpl22	0.00078	2	468
100	LSC.gene9.trnS-GCU	0	0	88
101	SSC.gene1.ycf1	0.00174	5	1074
102	SSC.gene10.ndhI	0.00159	3	504
103	SSC.gene11.ndhA	0.001	6	1092
104	SSC.gene12.ndhH	0.00148	6	1182
105	SSC.gene13.rps15	0.00253	3	273
106	SSC.gene14.ycf1	0.00294	72	5622
107	SSC.gene2.ndhF	0.00214	19	2247
108	SSC.gene3.rpl32	0.00415	2	162
109	SSC.gene4.trnL-UAG	0	0	80
110	SSC.gene5.ccsA	0.00139	6	966
111	SSC.gene6.ndhD	0.00142	10	1533
112	SSC.gene7.psaC	0	0	246
113	SSC.gene8.ndhE	0	0	306
114	SSC.gene9.ndhG	0.00103	3	531

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