

Table S4A Scattered repetitive sequences in CKX

ID	Repeat Start 1	Type	Size(bp)	Repeat Start 2	Mismatch(bp)	E-value	Gene	Region
1	78817	P	46	78817	0	1.39E-18	<i>petD(intron)</i>	LSC
2	100578	F	42	122415	0	3.56E-16	<i>trnA-UGC(intron)</i>	IRA
3	122415	P	42	142192	0	3.56E-16	<i>ndhA(intron)</i>	SSC
4	93540	F	38	93558	0	9.12E-14	<i>ycf2</i>	IRA
5	93540	P	38	149216	0	9.12E-14	<i>ycf2</i>	IRA
6	93558	P	38	149234	0	9.12E-14	<i>ycf2</i>	IRA
7	149216	F	38	149234	0	9.12E-14	<i>ycf2</i>	IRB
8	9039	P	30	46915	0	5.98E-09		LSC
9	89882	P	26	89882	0	1.53E-06	<i>ycf2</i>	IRA
10	89882	F	26	152904	0	1.53E-06	<i>ycf2</i>	IRA
11	127120	P	26	127120	0	1.53E-06	<i>ycf1</i>	SSC
12	152904	P	26	152904	0	1.53E-06	<i>ycf2</i>	IRB
13	10606	P	23	10637	0	9.80E-05		LSC
14	31975	P	22	31975	0	3.92E-04		LSC
15	95965	P	22	95991	0	3.92E-04		IRA
16	95965	F	22	146799	0	3.92E-04		IRA
17	95991	F	22	146825	0	3.92E-04		IRA
18	127179	P	22	127179	0	3.92E-04	<i>ycf1</i>	SSC
19	146799	P	22	146825	0	3.92E-04		IRB
20	9045	F	21	36988	0	1.57E-03	<i>trnS-GCU</i>	LSC
21	36988	P	21	46918	0	1.57E-03	<i>trnS-UGA</i>	LSC
22	38128	F	21	68728	0	1.57E-03	<i>trnfm-CAU</i>	LSC
23	82702	R	21	82702	0	1.57E-03		LSC
24	32195	P	20	114911	0	6.27E-03		LSC
25	32828	F	20	72890	0	6.27E-03		LSC
26	48510	C	20	68911	0	6.27E-03		LSC
27	48612	P	20	60839	0	6.27E-03		LSC
28	52432	R	20	52432	0	6.27E-03	<i>ndhC</i>	LSC
29	93540	F	20	93576	0	6.27E-03	<i>ycf2</i>	IRA
30	93540	P	20	149216	0	6.27E-03	<i>ycf2</i>	IRA
31	93576	P	20	149252	0	6.27E-03	<i>ycf2</i>	IRA
32	128082	F	20	128587	0	6.27E-03	<i>ycf1</i>	SSC
33	149216	F	20	149252	0	6.27E-03	<i>ycf2</i>	IRB
34	10542	F	19	37935	0	2.51E-02	<i>trnG-UCC(exon)</i>	LSC
35	30973	P	19	73420	0	2.51E-02		LSC
36	31419	F	19	129838	0	2.51E-02		LSC
37	31423	F	19	65496	0	2.51E-02		LSC
38	32192	R	19	32192	0	2.51E-02		LSC
39	32835	F	19	129730	0	2.51E-02		LSC
40	33620	R	19	33620	0	2.51E-02		LSC
41	37233	P	19	60378	0	2.51E-02		LSC

42	46379	R	19	46379	0	2.51E-02		LSC
43	68972	C	19	100926	0	2.51E-02		LSC
44	68972	R	19	141867	0	2.51E-02		LSC
45	71795	R	19	71795	0	2.51E-02		LSC
46	122623	R	19	122623	0	2.51E-02		SSC
47	8087	F	18	127135	0	1.00E-01		LSC
48	9248	C	18	88163	0	1.00E-01		LSC
49	9248	R	18	154631	0	1.00E-01		LSC

Table S4B Scattered repetitive sequences in XG

ID	Repeat Start 1	Type	Size(bp)	Repeat Start 2	Mismatch(bp)	E-value	Gene	Region
1	78778	P	46	78778	0	1.39E-18	<i>petD(intron)</i>	LSC
2	100539	F	42	122376	0	3.56E-16		IRA
3	122376	P	42	142155	0	3.56E-16	<i>ndhA(intron)</i>	SSC
4	93501	F	38	93519	0	9.12E-14	<i>ycf2</i>	IRA
5	93501	P	38	149179	0	9.12E-14	<i>ycf2</i>	IRA
6	93519	P	38	149197	0	9.12E-14	<i>ycf2</i>	IRA
7	149179	F	38	149197	0	9.12E-14	<i>ycf2</i>	IRB
8	9002	P	30	46876	0	5.98E-09		LSC
9	89843	P	26	89843	0	1.53E-06	<i>ycf2</i>	IRA
10	89843	F	26	152867	0	1.53E-06	<i>ycf2</i>	IRA
11	152867	P	26	152867	0	1.53E-06	<i>ycf2</i>	IRB
12	10569	P	23	10600	0	9.79E-05		LSC
13	31938	P	22	31938	0	3.92E-04		LSC
14	95926	P	22	95952	0	3.92E-04		IRA
15	95926	F	22	146762	0	3.92E-04		IRA
16	95952	F	22	146788	0	3.92E-04		IRA
17	127142	P	22	127142	0	3.92E-04	<i>ycf1</i>	SSC
18	146762	P	22	146788	0	3.92E-04		IRB
19	9008	F	21	36949	0	1.57E-03	<i>trnS-GCU</i>	LSC
20	32156	P	21	114872	0	1.57E-03		LSC
21	36949	P	21	46879	0	1.57E-03	<i>trnS-UGA</i>	LSC
22	38089	F	21	68688	0	1.57E-03	<i>trnFM-CAU</i>	LSC
23	82663	R	21	82663	0	1.57E-03		LSC
24	32790	F	20	72850	0	6.27E-03		LSC
25	48471	C	20	68871	0	6.27E-03		LSC
26	48573	P	20	60798	0	6.27E-03		LSC
27	52392	R	20	52392	0	6.27E-03	<i>ndhC</i>	LSC
28	93501	F	20	93537	0	6.27E-03	<i>ycf2</i>	IRA
29	93501	P	20	149179	0	6.27E-03	<i>ycf2</i>	IRA
30	93537	P	20	149215	0	6.27E-03	<i>ycf2</i>	IRA
31	128045	F	20	128550	0	6.27E-03	<i>ycf1</i>	SSC
32	149179	F	20	149215	0	6.27E-03	<i>ycf2</i>	IRB

33	10505	F	19	37896	0	2.51E-02	<i>trnG-GCC(intron)</i>	LSC
34	30936	P	19	73381	0	2.51E-02		LSC
35	31382	F	19	129801	0	2.51E-02		LSC
36	31386	F	19	65456	0	2.51E-02		LSC
37	33581	R	19	33581	0	2.51E-02		LSC
38	37194	P	19	60337	0	2.51E-02		LSC
39	46340	R	19	46340	0	2.51E-02		LSC
40	68932	C	19	100887	0	2.51E-02		LSC
41	68932	R	19	141830	0	2.51E-02		LSC
42	71755	R	19	71755	0	2.51E-02		LSC
43	122584	R	19	122584	0	2.51E-02		SSC
44	8050	F	18	127098	0	1.00E-01		LSC
45	9211	C	18	88124	0	1.00E-01		LSC
46	9211	R	18	154594	0	1.00E-01		LSC
47	19039	C	18	83192	0	1.00E-01	<i>rpoC2</i>	LSC
48	26030	P	18	26030	0	1.00E-01	<i>rpoB</i>	LSC
49	26741	R	18	116398	0	1.00E-01	<i>rpoB</i>	LSC

Table S4C Scattered repetitive sequences in HZP

ID	Repeat Start 1	Type	Size(bp)	Repeat Start 1	Mismatch(bp)	E-value	Gene	Region
1	9038	P	30	47304	0	6.01E-09		LSC
2	9044	F	21	37369	0	1.58E-03	<i>trnS-GCU</i>	LSC
3	10533	F	19	38318	0	2.52E-02	<i>trnG-GCC(exon)</i>	LSC
4	10597	P	23	10628	0	9.85E-05		LSC
5	12542	R	19	32583	0	2.52E-02		LSC
6	15269	F	19	101325	0	2.52E-02		LSC
7	15269	P	19	142302	0	2.52E-02		LSC
8	31366	P	19	73789	0	2.52E-02		LSC
9	32368	P	22	32368	0	3.94E-04		LSC
10	32584	C	20	83075	0	6.31E-03		LSC
11	32585	R	19	32585	0	2.52E-02		LSC
12	32585	P	19	83076	0	2.52E-02		LSC
13	32587	P	20	53343	0	6.31E-03		LSC
14	32589	P	19	115380	0	2.52E-02		LSC
15	34001	R	19	34001	0	2.52E-02		LSC
16	37369	P	21	47307	0	1.58E-03	<i>trnS-UGA</i>	LSC
17	38512	F	21	69078	0	1.58E-03	<i>trnfM-CAU</i>	LSC
18	46483	P	19	121393	0	2.52E-02		LSC
19	46768	R	19	46768	0	2.52E-02		LSC
20	48873	C	20	69261	0	6.31E-03		LSC
21	48975	P	20	61193	0	6.31E-03		LSC
22	52788	R	20	52788	0	6.31E-03	<i>ndhC</i>	LSC
23	53346	R	23	53346	0	9.85E-05	<i>trnV-UAC(intron)</i>	LSC

24	69322	C	19	101305	0	2.52E-02		LSC
25	69322	R	19	142322	0	2.52E-02		LSC
26	70507	F	33	70528	0	9.40E-11		LSC
27	79191	P	46	79191	0	1.40E-18	<i>petD(intron)</i>	LSC
28	83076	R	19	83076	0	2.52E-02		LSC
29	83603	R	22	83603	0	3.94E-04		LSC
30	90256	P	26	90256	0	1.54E-06	<i>ycf2</i>	IRA
31	90256	F	26	153364	0	1.54E-06	<i>ycf2</i>	IRA
32	93914	F	38	93932	0	9.18E-14	<i>ycf2</i>	IRA
33	93914	P	38	149676	0	9.18E-14	<i>ycf2</i>	IRA
34	93914	F	20	93950	0	6.31E-03	<i>ycf2</i>	IRA
35	93914	P	20	149676	0	6.31E-03	<i>ycf2</i>	IRA
36	93932	P	38	149694	0	9.18E-14	<i>ycf2</i>	IRA
37	93950	P	20	149712	0	6.31E-03	<i>ycf2</i>	IRA
38	96344	P	22	96370	0	3.94E-04		IRA
39	96344	F	22	147254	0	3.94E-04		IRA
40	96370	F	22	147280	0	3.94E-04		IRA
41	100957	F	42	122886	0	3.58E-16		IRA
42	110752	F	19	127330	0	2.52E-02		IRA
43	122886	P	42	142647	0	3.58E-16	<i>ndhA(intron)</i>	SSC
44	127641	P	22	127641	0	3.94E-04	<i>ycf1</i>	SSC
45	128544	F	20	129055	0	6.31E-03	<i>ycf2</i>	SSC
46	147254	P	22	147280	0	3.94E-04		IRB
47	149676	F	38	149694	0	9.18E-14	<i>ycf2</i>	IRB
48	149676	F	20	149712	0	6.31E-03	<i>ycf2</i>	IRB
49	153364	P	26	153364	0	1.54E-06	<i>ycf2</i>	IRB