

SUPPLEMENTARY MATERIAL FOR:

The genomic architecture of a rapid island radiation: recombination rate variation, chromosome structure, and genome assembly of the Hawaiian cricket *Laupala*.

GENETICS/2018/300894

Table S1. Geographic locations of sampled populations

Table S2. Segregation distortion (count of heterozygotes per genotype) statistics.

Table S3. Summary statistics for anchored assembly

Table S4. Integrated AFLP and SNP map for the *L. kohalensis* x *L. paranigra* cross

Figure S1. Comprehensive linkage maps.

Figure S2. ALLMAPS output

Figure S3. Coverage per cross per linkage group

TABLES

Table S1. Geographic locations of sampled populations

Species	Locality Name	Latitude (N)	Longitude (W)
<i>L. kona</i>	Manuka	19 deg 12'	155 deg 81'
<i>L. paranigra</i>	Kaiwika	19 deg 46'	155 deg 10'
<i>L. kohalensis</i>	Pololu Valley	20 deg 10'	155 deg 46'
<i>L. pruna</i>	Kaiholena	19 deg 10'	155 deg 35'

Table S2. Segregation distortion statistics. Tukey Honest Significant Differences between expected and observed frequencies of heterozygotes (a) across linkage groups (b) across species, (c) and across species nested in linkage groups

contrast	difference	lower bound	upper bound	P-adjusted
(a)				

1--3	0.017921	0.009122	0.026719	0.0000
2--3	0.008175	-0.00072	0.017069	0.0954
4--3	-0.00601	-0.01562	0.003601	0.5168
5--3	0.008896	-0.00102	0.018812	0.1125
7--3	-0.02664	-0.03742	-0.01586	0.0000
6--3	-0.01786	-0.02932	-0.0064	0.0001
2--1	-0.00975	-0.01874	-0.00075	0.0237
4--1	-0.02393	-0.03364	-0.01423	0.0000
5--1	-0.00902	-0.01903	0.000982	0.1086
7--1	-0.04456	-0.05543	-0.0337	0.0000
6--1	-0.03578	-0.04732	-0.02425	0.0000
4--2	-0.01419	-0.02398	-0.0044	0.0004
5--2	0.00072	-0.00937	0.01081	1.0000
7--2	-0.03482	-0.04576	-0.02388	0.0000
6--2	-0.02604	-0.03764	-0.01443	0.0000
5--4	0.014907	0.004178	0.025637	0.0009
7--4	-0.02063	-0.03216	-0.0091	0.0000
6--4	-0.01185	-0.02402	0.000318	0.0622
7--5	-0.03554	-0.04732	-0.02375	0.0000
6--5	-0.02676	-0.03917	-0.01435	0.0000
6--7	0.008781	-0.00433	0.021891	0.4295
(b)				
konpar-parkoh	-0.0155	-0.02039	-0.01062	0.0000
prukoh-parkoh	-0.02437	-0.03058	-0.01816	0.0000
prukoh-konpar	-0.00886	-0.01475	-0.00297	0.0012
(c)				
1:parkoh-3:parkoh	-0.00225	-0.01967	1.52E-02	1.0000
2:parkoh-3:parkoh	0.008894	-0.00981	2.76E-02	0.9835
4:parkoh-3:parkoh	-0.02438	-0.0469	-1.87E-03	0.0178
5:parkoh-3:parkoh	0.003542	-0.01602	2.31E-02	1.0000
7:parkoh-3:parkoh	-0.05123	-0.07443	-2.80E-02	0.0000
6:parkoh-3:parkoh	-0.03392	-0.05676	-1.11E-02	0.0000
3:konpar-3:parkoh	-0.03299	-0.04963	-1.63E-02	0.0000
1:konpar-3:parkoh	-0.0081	-0.02516	8.96E-03	0.9839
2:konpar-3:parkoh	-0.01921	-0.03615	-2.27E-03	0.0089
4:konpar-3:parkoh	-0.01981	-0.03754	-2.07E-03	0.0113
5:konpar-3:parkoh	-0.0266	-0.04561	-7.60E-03	0.0001
7:konpar-3:parkoh	-0.05016	-0.06964	-3.07E-02	0.0000
6:konpar-3:parkoh	-0.03407	-0.05469	-1.35E-02	0.0000
3:prukoh-3:parkoh	-0.03762	-0.05901	-1.62E-02	0.0000
1:prukoh-3:parkoh	0.000708	-0.02165	2.31E-02	1.0000

2:prukoh-3:parkoh	-0.0359	-0.05673	-1.51E-02	0.0000
4:prukoh-3:parkoh	-0.04794	-0.06946	-2.64E-02	0.0000
5:prukoh-3:parkoh	-0.01828	-0.04429	7.73E-03	0.5987
7:prukoh-3:parkoh	-0.04113	-0.06927	-1.30E-02	0.0000
6:prukoh-3:parkoh	-0.0881	-0.12526	-5.09E-02	0.0000
2:parkoh-1:parkoh	0.011142	-0.00727	2.96E-02	0.8411
4:parkoh-1:parkoh	-0.02214	-0.04441	1.39E-04	0.0537
5:parkoh-1:parkoh	0.00579	-0.0135	2.51E-02	1.0000
7:parkoh-1:parkoh	-0.04899	-0.07195	-2.60E-02	0.0000
6:parkoh-1:parkoh	-0.03167	-0.05428	-9.06E-03	0.0001
3:konpar-1:parkoh	-0.03074	-0.04706	-1.44E-02	0.0000
1:konpar-1:parkoh	-0.00585	-0.02259	1.09E-02	0.9997
2:konpar-1:parkoh	-0.01696	-0.03359	-3.44E-04	0.0391
4:konpar-1:parkoh	-0.01756	-0.03498	-1.32E-04	0.0457
5:konpar-1:parkoh	-0.02436	-0.04308	-5.64E-03	0.0007
7:konpar-1:parkoh	-0.04791	-0.06712	-2.87E-02	0.0000
6:konpar-1:parkoh	-0.03183	-0.05218	-1.15E-02	0.0000
3:prukoh-1:parkoh	-0.03537	-0.05651	-1.42E-02	0.0000
1:prukoh-1:parkoh	0.002956	-0.01916	2.51E-02	1.0000
2:prukoh-1:parkoh	-0.03366	-0.05422	-1.31E-02	0.0000
4:prukoh-1:parkoh	-0.04569	-0.06696	-2.44E-02	0.0000
5:prukoh-1:parkoh	-0.01603	-0.04183	9.77E-03	0.8077
7:prukoh-1:parkoh	-0.03888	-0.06683	-1.09E-02	0.0001
6:prukoh-1:parkoh	-0.08585	-0.12287	-4.88E-02	0.0000
4:parkoh-2:parkoh	-0.03328	-0.05656	-9.99E-03	0.0001
5:parkoh-2:parkoh	-0.00535	-0.0258	1.51E-02	1.0000
7:parkoh-2:parkoh	-0.06013	-0.08407	-3.62E-02	0.0000
6:parkoh-2:parkoh	-0.04281	-0.06642	-1.92E-02	0.0000
3:konpar-2:parkoh	-0.04188	-0.05956	-2.42E-02	0.0000
1:konpar-2:parkoh	-0.01699	-0.03506	1.08E-03	0.0965
2:konpar-2:parkoh	-0.02811	-0.04606	-1.02E-02	0.0000
4:konpar-2:parkoh	-0.0287	-0.0474	-1.00E-02	0.0000
5:konpar-2:parkoh	-0.0355	-0.05541	-1.56E-02	0.0000
7:konpar-2:parkoh	-0.05905	-0.07942	-3.87E-02	0.0000
6:konpar-2:parkoh	-0.04297	-0.06442	-2.15E-02	0.0000
3:prukoh-2:parkoh	-0.04651	-0.06872	-2.43E-02	0.0000
1:prukoh-2:parkoh	-0.00819	-0.03132	1.49E-02	0.9997
2:prukoh-2:parkoh	-0.0448	-0.06645	-2.31E-02	0.0000
4:prukoh-2:parkoh	-0.05684	-0.07916	-3.45E-02	0.0000
5:prukoh-2:parkoh	-0.02717	-0.05385	-4.95E-04	0.0402
7:prukoh-2:parkoh	-0.05003	-0.07879	-2.13E-02	0.0000

6:prukoh-2:parkoh	-0.09699	-0.13463	-5.94E-02	0.0000
5:parkoh-4:parkoh	0.027926	0.003943	5.19E-02	0.0058
7:parkoh-4:parkoh	-0.02685	-0.05388	1.77E-04	0.0539
6:parkoh-4:parkoh	-0.00953	-0.03626	1.72E-02	0.9996
3:konpar-4:parkoh	-0.0086	-0.03027	1.31E-02	0.9982
1:konpar-4:parkoh	0.016287	-0.0057	3.83E-02	0.4920
2:konpar-4:parkoh	0.005171	-0.01673	2.71E-02	1.0000
4:konpar-4:parkoh	0.004578	-0.01794	2.71E-02	1.0000
5:konpar-4:parkoh	-0.00222	-0.02575	2.13E-02	1.0000
7:konpar-4:parkoh	-0.02577	-0.04969	-1.85E-03	0.0192
6:konpar-4:parkoh	-0.00969	-0.03454	1.52E-02	0.9986
3:prukoh-4:parkoh	-0.01323	-0.03873	1.23E-02	0.9584
1:prukoh-4:parkoh	0.025092	-0.00122	5.14E-02	0.0841
2:prukoh-4:parkoh	-0.01152	-0.03654	1.35E-02	0.9886
4:prukoh-4:parkoh	-0.02356	-0.04916	2.05E-03	0.1190
5:prukoh-4:parkoh	0.006104	-0.02337	3.56E-02	1.0000
7:prukoh-4:parkoh	-0.01675	-0.04812	1.46E-02	0.9452
6:prukoh-4:parkoh	-0.06372	-0.10339	-2.40E-02	0.0000
7:parkoh-5:parkoh	-0.05478	-0.0794	-3.02E-02	0.0000
6:parkoh-5:parkoh	-0.03746	-0.06175	-1.32E-02	0.0000
3:konpar-5:parkoh	-0.03653	-0.05511	-1.79E-02	0.0000
1:konpar-5:parkoh	-0.01164	-0.03059	7.32E-03	0.8233
2:konpar-5:parkoh	-0.02275	-0.0416	-3.91E-03	0.0031
4:konpar-5:parkoh	-0.02335	-0.04291	-3.79E-03	0.0038
5:konpar-5:parkoh	-0.03015	-0.05087	-9.42E-03	0.0000
7:konpar-5:parkoh	-0.0537	-0.07486	-3.25E-02	0.0000
6:konpar-5:parkoh	-0.03761	-0.05982	-1.54E-02	0.0000
3:prukoh-5:parkoh	-0.04116	-0.0641	-1.82E-02	0.0000
1:prukoh-5:parkoh	-0.00283	-0.02667	2.10E-02	1.0000
2:prukoh-5:parkoh	-0.03944	-0.06185	-1.70E-02	0.0000
4:prukoh-5:parkoh	-0.05148	-0.07454	-2.84E-02	0.0000
5:prukoh-5:parkoh	-0.02182	-0.04911	5.47E-03	0.3364
7:prukoh-5:parkoh	-0.04467	-0.074	-1.53E-02	0.0000
6:prukoh-5:parkoh	-0.09164	-0.12971	-5.36E-02	0.0000
6:parkoh-7:parkoh	0.017315	-0.00999	4.46E-02	0.7787
3:konpar-7:parkoh	0.018246	-0.00413	4.06E-02	0.2992
1:konpar-7:parkoh	0.043137	0.020451	6.58E-02	0.0000
2:konpar-7:parkoh	0.032021	0.009425	5.46E-02	0.0001
4:konpar-7:parkoh	0.031428	0.008233	5.46E-02	0.0003
5:konpar-7:parkoh	0.02463	0.000448	4.88E-02	0.0402
7:konpar-7:parkoh	0.001077	-0.02349	2.56E-02	1.0000

6:konpar-7:parkoh	0.017161	-0.00831	4.26E-02	0.6787
3:prukoh-7:parkoh	0.013617	-0.01249	3.97E-02	0.9562
1:prukoh-7:parkoh	0.051942	0.025044	7.88E-02	0.0000
2:prukoh-7:parkoh	0.015331	-0.0103	4.10E-02	0.8547
4:prukoh-7:parkoh	0.003292	-0.02291	2.95E-02	1.0000
5:prukoh-7:parkoh	0.032954	0.002954	6.30E-02	0.0145
7:prukoh-7:parkoh	0.010102	-0.02176	4.20E-02	0.9999
6:prukoh-7:parkoh	-0.03687	-0.07693	3.19E-03	0.1187
3:konpar-6:parkoh	0.000931	-0.02108	2.29E-02	1.0000
1:konpar-6:parkoh	0.025822	0.003496	4.81E-02	0.0065
2:konpar-6:parkoh	0.014706	-0.00753	3.69E-02	0.7117
4:konpar-6:parkoh	0.014113	-0.00873	3.70E-02	0.8152
5:konpar-6:parkoh	0.007315	-0.01653	3.12E-02	1.0000
7:konpar-6:parkoh	-0.01624	-0.04047	7.99E-03	0.6886
6:konpar-6:parkoh	-0.00015	-0.0253	2.50E-02	1.0000
3:prukoh-6:parkoh	-0.0037	-0.02949	2.21E-02	1.0000
1:prukoh-6:parkoh	0.034627	0.008032	6.12E-02	0.0007
2:prukoh-6:parkoh	-0.00198	-0.0273	2.33E-02	1.0000
4:prukoh-6:parkoh	-0.01402	-0.03992	1.19E-02	0.9374
5:prukoh-6:parkoh	0.015639	-0.01409	4.54E-02	0.9525
7:prukoh-6:parkoh	-0.00721	-0.03882	2.44E-02	1.0000
6:prukoh-6:parkoh	-0.05418	-0.09404	-1.43E-02	0.0003
1:konpar-3:konpar	0.024891	0.008963	4.08E-02	0.0000
2:konpar-3:konpar	0.013775	-0.00202	2.96E-02	0.1878
4:konpar-3:konpar	0.013182	-0.00346	2.98E-02	0.3552
5:konpar-3:konpar	0.006384	-0.01161	2.44E-02	0.9996
7:konpar-3:konpar	-0.01717	-0.03567	1.33E-03	0.1099
6:konpar-3:konpar	-0.00109	-0.02077	1.86E-02	1.0000
3:prukoh-3:konpar	-0.00463	-0.02513	1.59E-02	1.0000
1:prukoh-3:konpar	0.033696	0.012189	5.52E-02	0.0000
2:prukoh-3:konpar	-0.00291	-0.02282	1.70E-02	1.0000
4:prukoh-3:konpar	-0.01495	-0.03559	5.68E-03	0.5369
5:prukoh-3:konpar	0.014708	-0.01057	4.00E-02	0.8830
7:prukoh-3:konpar	-0.00814	-0.03561	1.93E-02	1.0000
6:prukoh-3:konpar	-0.05511	-0.09177	-1.85E-02	0.0000
2:konpar-1:konpar	-0.01112	-0.02735	5.12E-03	0.6496
4:konpar-1:konpar	-0.01171	-0.02877	5.35E-03	0.6448
5:konpar-1:konpar	-0.01851	-0.03689	-1.26E-04	0.0461
7:konpar-1:konpar	-0.04206	-0.06094	-2.32E-02	0.0000
6:konpar-1:konpar	-0.02598	-0.04602	-5.94E-03	0.0007
3:prukoh-1:konpar	-0.02952	-0.05036	-8.68E-03	0.0001

1:prukoh-1:konpar	0.008805	-0.01303	3.06E-02	0.9978
2:prukoh-1:konpar	-0.02781	-0.04806	-7.55E-03	0.0002
4:prukoh-1:konpar	-0.03984	-0.06082	-1.89E-02	0.0000
5:prukoh-1:konpar	-0.01018	-0.03574	1.54E-02	0.9982
7:prukoh-1:konpar	-0.03304	-0.06076	-5.31E-03	0.0039
6:prukoh-1:konpar	-0.08	-0.11685	-4.32E-02	0.0000
4:konpar-2:konpar	-0.00059	-0.01753	1.63E-02	1.0000
5:konpar-2:konpar	-0.00739	-0.02566	1.09E-02	0.9977
7:konpar-2:konpar	-0.03094	-0.04972	-1.22E-02	0.0000
6:konpar-2:konpar	-0.01486	-0.0348	5.08E-03	0.4790
3:prukoh-2:konpar	-0.0184	-0.03915	2.34E-03	0.1635
1:prukoh-2:konpar	0.019921	-0.00182	4.17E-02	0.1233
2:prukoh-2:konpar	-0.01669	-0.03684	3.46E-03	0.2713
4:prukoh-2:konpar	-0.02873	-0.0496	-7.85E-03	0.0002
5:prukoh-2:konpar	0.000933	-0.02454	2.64E-02	1.0000
7:prukoh-2:konpar	-0.02192	-0.04957	5.73E-03	0.3532
6:prukoh-2:konpar	-0.06889	-0.10568	-3.21E-02	0.0000
5:konpar-4:konpar	-0.0068	-0.0258	1.22E-02	0.9996
7:konpar-4:konpar	-0.03035	-0.04984	-1.09E-02	0.0000
6:konpar-4:konpar	-0.01427	-0.03488	6.35E-03	0.6288
3:prukoh-4:konpar	-0.01781	-0.03921	3.59E-03	0.2622
1:prukoh-4:konpar	0.020514	-0.00184	4.29E-02	0.1220
2:prukoh-4:konpar	-0.0161	-0.03692	4.73E-03	0.4037
4:prukoh-4:konpar	-0.02814	-0.04966	-6.61E-03	0.0006
5:prukoh-4:konpar	0.001526	-0.02448	2.75E-02	1.0000
7:prukoh-4:konpar	-0.02133	-0.04947	6.81E-03	0.4444
6:prukoh-4:konpar	-0.06829	-0.10546	-3.11E-02	0.0000
7:konpar-5:konpar	-0.02355	-0.04421	-2.90E-03	0.0081
6:konpar-5:konpar	-0.00747	-0.02919	1.43E-02	0.9998
3:prukoh-5:konpar	-0.01101	-0.03348	1.15E-02	0.9769
1:prukoh-5:konpar	0.027312	0.00393	5.07E-02	0.0055
2:prukoh-5:konpar	-0.0093	-0.03122	1.26E-02	0.9958
4:prukoh-5:konpar	-0.02134	-0.04392	1.24E-03	0.0922
5:prukoh-5:konpar	0.008324	-0.01857	3.52E-02	1.0000
7:prukoh-5:konpar	-0.01453	-0.04349	1.44E-02	0.9705
6:prukoh-5:konpar	-0.0615	-0.09928	-2.37E-02	0.0000
6:konpar-7:konpar	0.016084	-0.00606	3.82E-02	0.5321
3:prukoh-7:konpar	0.01254	-0.01033	3.54E-02	0.9299
1:prukoh-7:konpar	0.050865	0.02709	7.46E-02	0.0000
2:prukoh-7:konpar	0.014254	-0.00808	3.66E-02	0.7695
4:prukoh-7:konpar	0.002215	-0.02077	2.52E-02	1.0000

5:prukoh-7:konpar	0.031877	0.004642	5.91E-02	0.0053
7:prukoh-7:konpar	0.009024	-0.02025	3.83E-02	1.0000
6:prukoh-7:konpar	-0.03794	-0.07598	8.89E-05	0.0514
3:prukoh-6:konpar	-0.00354	-0.02738	2.03E-02	1.0000
1:prukoh-6:konpar	0.034781	0.010074	5.95E-02	0.0001
2:prukoh-6:konpar	-0.00183	-0.02516	2.15E-02	1.0000
4:prukoh-6:konpar	-0.01387	-0.03782	1.01E-02	0.8876
5:prukoh-6:konpar	0.015793	-0.01226	4.38E-02	0.9112
7:prukoh-6:konpar	-0.00706	-0.0371	2.30E-02	1.0000
6:prukoh-6:konpar	-0.05403	-0.09265	-1.54E-02	0.0001
1:prukoh-3:prukoh	0.038325	0.012961	6.37E-02	0.0000
2:prukoh-3:prukoh	0.001714	-0.02231	2.57E-02	1.0000
4:prukoh-3:prukoh	-0.01032	-0.03495	1.43E-02	0.9964
5:prukoh-3:prukoh	0.019338	-0.0093	4.80E-02	0.6747
7:prukoh-3:prukoh	-0.00352	-0.0341	2.71E-02	1.0000
6:prukoh-3:prukoh	-0.05048	-0.08953	-1.14E-02	0.0008
2:prukoh-1:prukoh	-0.03661	-0.06149	-1.17E-02	0.0000
4:prukoh-1:prukoh	-0.04865	-0.07412	-2.32E-02	0.0000
5:prukoh-1:prukoh	-0.01899	-0.04835	1.04E-02	0.7487
7:prukoh-1:prukoh	-0.04184	-0.0731	-1.06E-02	0.0004
6:prukoh-1:prukoh	-0.08881	-0.12839	-4.92E-02	0.0000
4:prukoh-2:prukoh	-0.01204	-0.03617	1.21E-02	0.9722
5:prukoh-2:prukoh	0.017623	-0.01058	4.58E-02	0.8001
7:prukoh-2:prukoh	-0.00523	-0.03541	2.50E-02	1.0000
6:prukoh-2:prukoh	-0.0522	-0.09093	-1.35E-02	0.0003
5:prukoh-4:prukoh	0.029662	0.000935	5.84E-02	0.0339
7:prukoh-4:prukoh	0.006809	-0.02386	3.75E-02	1.0000
6:prukoh-4:prukoh	-0.04016	-0.07927	-1.04E-03	0.0364
7:prukoh-5:prukoh	-0.02285	-0.05682	1.11E-02	0.6817
6:prukoh-5:prukoh	-0.06982	-0.11157	-2.81E-02	0.0000
6:prukoh-7:prukoh	-0.04697	-0.09008	-3.86E-03	0.0164

Table S3. Summary statistics for the anchored assembly. For each cross and for the combined pseudomolecule assembly the number of scaffolds, those with at least 2 markers, those with at least two markers that are > 0.1 cM apart, the combined size of the anchored scaffolds, the N50, and the average coverage are shown per LG.

LG	# scaffolds	# scaffolds >= 2 markers	# scaffolds >=2 well-spaced markers	Size (bp)	N50 (bp)	coverage
ParKoh						
1	117	21	14	106312036	1301586	52.89792
2	89	8	4	59124686	886001	54.757

3	109	14	12	98715872	1184645	51.15361
4	49	1	1	39589978	1093907	54.17022
5	76	18	16	62735740	1197186	66.5671
6	47	7	6	19057194	730017	57.78891
7	45	6	5	38543039	1485176	60.40972
X	76	4	2	84017840	1519936	29.56227
Sum/median	608	79	60	508096385	1190916	53.41334375
KonPar						
1	128	17	13	103734776	1143465	37.22859
2	132	17	10	95158272	1019600	40.18552
3	143	22	19	134318749	1355019	34.98008
4	109	24	12	110192983	1660236	40.38131
5	84	13	9	67417874	1136159	44.86084
6	64	7	6	23922075	733389	46.43391
7	77	17	13	58701654	1180700	38.07606
X	86	14	3	98541466	1540389	25.64274
Sum/median	823	131	85	691987849	1162083	38.47363125
PruKoh						
1	50	5	3	46785714	1325001	41.55226
2	62	4	3	45819772	1106261	47.8152
3	57	2	2	54629290	1375220	40.13577
4	56	11	5	60827800	2025849	45.12183
5	33	3	2	20743600	725518	51.94363
6	14	0	0	7779385	859092	45.60227
7	27	4	2	17783624	1224531	49.36982
X	84	9	0	82253003	1268875	28.72471
Sum/median	383	38	17	336622188	1246703	43.78318625
Combined						
1	167	43	30	117180395	1089296	
2	170	29	17	101876544	816734	
3	175	38	33	137279277	1044733	
4	118	36	18	89703238	957048	
5	102	34	27	62192538	880080	
6	80	14	12	25387579	569059	
7	88	27	20	52742540	916807	
X	154	27	5	133989488	1249941	
Sum/median	1054	248	162	720351599	936928	

Table S4. Integrated AFLP and SNP map for the *L. kohalensis* x *L. paranigra* cross. The highlighted AFLP markers are located under a QTL peak in the Shaw & Lesnick 2009 study. The highlighted AFLP markers on linkage group 1 indicate the location where a male song and female preference QTL peak co-localize.

scaffold	locus	LG	position (cM)	AFLP	scaffold midpoint position (bp)
S002761	S002761_729410	1	0	NA	106423286
	as030	1	1.821	PaggcA53	NA
	as074	1	3.282	PggacA54	NA
	ac007	1	6.09	PagacA52B55	NA
	ac013	1	7.301	PcgacA51B51	NA
	ac017	1	8.604	PgcacA07B54	NA
S000817	S000817_120415	1	9.734	NA	114208815
S002077	S002077_311803	1	11.288	NA	109788919
S007909	S007909_155126	1	13.752	NA	104812030
	as087	1	23.642	PgtgcA54	NA
	as081	1	25.658	PgtacA56	NA
	as085_x	1	30.736	PgtgcA3	NA
	as080	1	36.928	PgtacA55	NA
	as023	1	38.868	PaaacA63	NA
S001330	S001330_135948	1	42.507	NA	100949675
S001771	S001771_116507	1	46.906	NA	105601414
S000392	S000392_74030	1	51.737	NA	NA
S001680	S001680_315523	1	52.615	NA	88172650
S000409	S000409_474112	1	53.517	NA	84174036
S001489	S001489_769426	1	56.166	NA	41585373
S004205	S004205_29098	1	57.827	NA	50498860
S000949	S000949_205067	1	58.259	NA	42520204
S008139	S008139_68543	1	58.542	NA	NA
S000696	S000696_137337	1	58.549	NA	NA
S002946	S002946_738803	1	58.707	NA	67349798
C120306	C120306_385	1	58.847	NA	NA
S006572	S006572_95801	1	58.928	NA	46181571
S001914	S001914_404347	1	59.118	NA	66160290
S009296	S009296_110864	1	59.329	NA	65039174
S000663	S000663_611964	1	59.641	NA	53947499
S004747	S004747_292840	1	59.784	NA	49933664
S000671	S000671_1033505	1	61.079	NA	NA
S001489	S001489_639186	1	61.694	NA	41585373
S004313	S004313_69835	1	61.699	NA	40812282
S002548	S002548_423714	1	62.493	NA	45749393
S000105	S000105_348801	1	63.591	NA	36945493

S004771	S004771_628132	1	64.917	NA	31081394
S004771	S004771_1175996	1	65.21	NA	31081394
S002151	S002151_1377807	1	66.292	NA	22870317
	as034	1	68.191	PatgcA52	NA
	as012	1	70.107	PccacA55	NA
	ac014	2	0	PgaacA10B60	NA
S001206	S001206_1546586	2	2.303	NA	1821533
S000518	S000518_766492	2	6.245	NA	6192438
	as077	2	26.628	PgggcA52	NA
S003191	S003191_528616	2	31.612	NA	16874625
S001838	S001838_6021	2	42.989	NA	23233385
S000416	S000416_552586	2	47.133	NA	24694735
S004218	S004218_23553	2	51.627	NA	31927917
S001550	S001550_214202	2	52.41	NA	33996652
S003798	S003798_463488	2	53.5	NA	36725738
S002376	S002376_431585	2	54.951	NA	38303813
	as052	2	57.787	PgggcA53	NA
S005289	S005289_526503	2	58.474	NA	45049140
S000230	S000230_200879	2	58.756	NA	46073354
S002156	S002156_413885	2	61.643	NA	90147661
S003079	S003079_192141	2	61.705	NA	56392065
S004728	S004728_52289	2	61.99	NA	77439224
S001050	S001050_43796	2	62.025	NA	71210412
S001881	S001881_642832	2	62.193	NA	60129008
S003118	S003118_235274	2	62.379	NA	56724422
S003735	S003735_82587	2	62.896	NA	NA
	ac006	2	63.793	PacacA56B69	NA
	as040_x	2	64.823	PcagcA08	NA
S003067	S003067_20757	2	67.28	NA	80842581
S000199	S000199_193260	2	74.457	NA	83353553
S001797	S001797_1827615	2	75.671	NA	85052994
S001855	S001855_342231	2	82.018	NA	89412353
S004792	S004792_152639	2	85.245	NA	NA
S001901	S001901_315332	2	87.985	NA	94264609
S001602	S001602_266912	2	109.791	NA	99970919
S000793	S000793_627068	2	116.258	NA	NA
	as115	3	0	PttacA54	NA
	as083	3	3.848	PgtacA58	NA
S001338	S001338_29965	3	5.698	NA	168668
	as037	3	9.753	PcaacA57	NA
S000075	S000075_156551	3	11.248	NA	1642392

S002528	S002528_794391	3	19.911	NA	18001031
S009989	S009989_70944	3	21.779	NA	6045815
S002528	S002528_794393	3	23.255	NA	18001031
S005403	S005403_7134	3	27.914	NA	18662141
	ac009_a	3	48.316	PaggcA07B19	NA
	as063	3	49.481	PgaacA60	NA
	as064	3	51.877	PgaacA61	NA
	as025	3	53.754	PaagcA57	NA
S000558	S000558_1959639	3	59.995	NA	40534699
S000558	S000558_1232157	3	60.337	NA	40534699
	as088	3	63.867	PgtgcA55	NA
	as069	3	64.465	PgcacA51	NA
	ad100.as079	3	65.149	NA	NA
S004777	S004777_221108	3	66.442	NA	36430961
S000558	S000558_748836	3	66.865	NA	40534699
S007419	S007419_788393	3	67.162	NA	42061284
S002934	S002934_242739	3	68.016	NA	56760880
S003072	S003072_393178	3	68.244	NA	63064570
S001785	S001785_133632	3	68.301	NA	60906412
S000726	S000726_1782089	3	68.399	NA	48678466
S000529	S000529_530363	3	68.572	NA	72186930
	as108_a	3	68.59	PtgacA03	NA
S002665	S002665_282741	3	68.951	NA	NA
S005483	S005483_46807	3	69.079	NA	62650842
S013086	S013086_40139	3	69.12	NA	NA
S002194	S002194_96231	3	69.157	NA	66669112
S006750	S006750_274965	3	69.245	NA	NA
S004654	S004654_237626	3	69.303	NA	NA
S002002	S002002_376411	3	69.412	NA	44975632
S003472	S003472_9538	3	70.555	NA	82404642
S002613	S002613_31096	3	71.526	NA	NA
S001060	S001060_728231	3	72.259	NA	89191537
S002297	S002297_775779	3	72.322	NA	91133138
S001060	S001060_1929755	3	72.461	NA	89191537
S006865	S006865_338439	3	72.867	NA	101275163
	as101	3	73.62	PtcgcA09	NA
S001265	S001265_211884	3	74.555	NA	106649134
S000385	S000385_1480834	3	75.848	NA	108764126
S001106	S001106_481878	3	82.071	NA	114989880
	as114_ax	3	86.713	PttacA02	NA
S001275	S001275_1127865	3	88.98	NA	122746700

S002311	S002311 254807	3	89.321	NA	123571440
	as076 a	4	0	PgggcA01	NA
	as073 a	4	1.753	PggacA01	NA
S005844	S005844 224400	4	18.591	NA	4097279
	as117 a	4	41.053	PttacA06	NA
	as099	4	41.551	PtcacA54	NA
S001783	S001783 279356	4	43.04	NA	63112104
S000590	S000590 1997032	4	43.249	NA	29331168
S014891	S014891 36875	4	43.589	NA	NA
S003206	S003206 599818	4	43.711	NA	NA
S000836	S000836 228275	4	43.801	NA	NA
S000679	S000679 623688	4	43.895	NA	57825201
	as075 a	4	44.445	PggacA13	NA
S002196	S002196 584574	4	44.674	NA	42514727
S001005	S001005 1065597	4	44.857	NA	39878575
S003635	S003635 7993	4	45.443	NA	63978342
S009873	S009873 154713	4	49.074	NA	71866807
S002058	S002058 706797	4	49.408	NA	72523035
S000455	S000455 692625	4	52.283	NA	73544308
	as029 a	4	61.5	PagacA5	NA
S001486	S001486 61579	4	64.17	NA	77623428
	as028 x	4	65.829	PagacA1	NA
S001279	S001279 277406	4	67.269	NA	78135382
S001608	S001608 399358	4	83.462	NA	89198891
	as021	5	0	PaaacA54	NA
S005326	S005326 57790	5	1.807	NA	466530
	ac016	5	2.394	PgagcA56B62	NA
	ac011	5	4.24	PcagcA52B53	NA
	ac015	5	5.865	PgaacA62B66	NA
	as116 a	5	7.016	PttacA05	NA
S002190	S002190 273188	5	13.671	NA	3452268
	as100	5	15.717	PtcgcA54	NA
S000809	S000809 365747	5	19.221	NA	6005121
	as066 a	5	21.423	PgagcA08	NA
	as027 a	5	25.245	PacacA06	NA
	ad082.as062	5	26.337	NA	NA
	as045	5	27.055	PccacA53	NA
S004462	S004462 54127	5	28.207	NA	13078451
S005610	S005610 84211	5	28.338	NA	13179099
S000366	S000366 42046	5	28.803	NA	17964325
S000745	S000745 339612	5	30.425	NA	21039003

S002565	S002565_116928	5	33.166	NA	22902902
S004683	S004683_48328	5	34.768	NA	24389284
S006506	S006506_7146	5	35.301	NA	27839633
S005519	S005519_111372	5	37.975	NA	32385211
S000305	S000305_70577	5	40.26	NA	33073185
S000979	S000979_164421	5	41.485	NA	35633669
S005459	S005459_70152	5	42.698	NA	37847956
S000180	S000180_656202	5	44.503	NA	40272446
S021890	S021890_296	5	45.368	NA	42534517
	as068	5	46.655	PgagcA51	NA
S005334	S005334_732385	5	48.033	NA	43080568
S005064	S005064_175253	5	49.954	NA	45035858
	as091	5	52.052	PtaacA51	NA
S003838	S003838_738497	5	54.849	NA	46738481
S001560	S001560_398299	5	59.376	NA	50508185
S004681	S004681_23198	5	61.431	NA	53592894
	as057	5	62.937	PctacA55	NA
	as058	5	63.812	PctacA56	NA
	as059	5	65.211	PctacA57	NA
	as043	5	71.183	PcagcA51	NA
	as118_x	5	72.676	PttacA13	NA
	as041	5	73.969	PcagcA56	NA
S007270	S007270_308120	5	76.332	NA	58235091
S002503	S002503_741242	5	77.495	NA	58956874
	as110	6	0	PtggcA52	NA
	as047_x	6	1.51	PcgacA02	NA
S001034	S001034_78522	6	2.72	NA	24400658
S022584	S022584_1139	6	5.895	NA	23964288
	as105	6	6.664	PtgacA58	NA
S005236	S005236_14409	6	7.404	NA	16442306
S001507	S001507_262717	6	8.078	NA	13978219
S002799	S002799_37080	6	10.159	NA	22063251
	ac003	6	11.251	PaagcA61B63	NA
	ac019	6	13.745	PtgacA57B60	NA
S001904	S001904_134885	6	15.337	NA	16620760
	as109	6	17.735	PtgacA56	NA
	as039	6	20.554	PcagcA54	NA
S000218	S000218_4280	6	21.865	NA	10002544
S001761	S001761_1745572	6	27.303	NA	6635712
S005439	S005439_103276	6	35.966	NA	4315651
S011721	S011721_76537	6	47.364	NA	849742

S003103	S003103_949190	7	0	NA	1904957
S008107	S008107_29859	7	3.613	NA	2842152
S003103	S003103_1019194	7	3.994	NA	1904957
S000557	S000557_589404	7	7.085	NA	3829489
S002304	S002304_728504	7	9.873	NA	4666925
S002736	S002736_346176	7	10.997	NA	5494164
S002736	S002736_115345	7	12.279	NA	5494164
S014172	S014172_53634	7	13.346	NA	5971292
S000628	S000628_1159720	7	17.535	NA	8386281
S000628	S000628_169050	7	18.732	NA	8386281
	as033	7	21.278	PatacA55	NA
	as071_a	7	22.74	PgcgcA11	NA
S000677	S000677_527760	7	24.152	NA	12625625
	as070_a	7	26.358	PgcacA10	NA
S002087	S002087_530732	7	44.525	NA	31673319
S004909	S004909_906373	7	50.728	NA	39335421
S010292	S010292_145463	7	53.418	NA	40115847
S004220	S004220_129736	7	53.983	NA	43031005
S001469	S001469_584893	7	65.118	NA	50836753
S002493	S002493_175861	7	67.129	NA	48491131
	xs032_x	X	0	PttacA04	NA
S000571	S000571_30159	X	2.403	NA	4915702
	xd024	X	11.115	PtagcB55	NA
S001780	S001780_509180	X	24.446	NA	10902308
	xd004	X	25.132	PatacB52	NA
	xs020	X	29.168	PatgcA56	NA
S000766	S000766_827724	X	30.52	NA	11869181
S000360	S000360_70566	X	32.459	NA	17072014
S003455	S003455_1122569	X	35.526	NA	19186595
S004887	S004887_81621	X	42.013	NA	NA
	xs024_x	X	43.011	PcggcA10	NA
S000604	S000604_43741	X	43.459	NA	NA
S000648	S000648_2315784	X	44.883	NA	34819414
S000219	S000219_2024096	X	45.729	NA	26925418
S000777	S000777_1339236	X	46.733	NA	30344332
S000777	S000777_461461	X	46.887	NA	30344332
S000648	S000648_2255296	X	47.453	NA	34819414
S001873	S001873_641123	X	49.384	NA	36757980
	xd016_x	X	49.672	PatgcB02	NA
S001241	S001241_171252	X	53.266	NA	44632865
S003053	S003053_264327	X	55.937	NA	56937852

S000327	S000327_278424	X	56.293	NA	55828014
S000470	S000470_76715	X	56.911	NA	59714238
	xd008_x	X	57.404	PgggcB22	NA
S003307	S003307_279141	X	57.747	NA	63486064
S001912	S001912_587919	X	58.069	NA	62108629
S000965	S000965_1228070	X	59.663	NA	73444967
S000808	S000808_1583160	X	59.672	NA	69248171
S006304	S006304_697561	X	59.908	NA	NA
S013985	S013985_11114	X	60.241	NA	82920002
	xd020	X	63.263	PcggcB53	NA
S007907	S007907_144642	X	64.648	NA	94604867
	xs011	X	67.511	PaaacA60	NA
S001930	S001930_1745657	X	68.641	NA	88122926
S001930	S001930_2410442	X	69.247	NA	88122926
S004832	S004832_609791	X	70.344	NA	91521965
S001247	S001247_68215	X	71.108	NA	92776928
	xs012	X	75.227	PaagcA53	NA
S000238	S000238_1169086	X	90.242	NA	113789231
S003071	S003071_613045	X	95.05	NA	116953618
S002737	S002737_694631	X	117.43	NA	NA
S000176	S000176_35913	X	126.585	NA	132559092
S001187	S001187_211572	X	130.879	NA	127829472
S003230	S003230_1425064	X	131.437	NA	129558233
S002008	S002008_1089204	X	131.468	NA	126707516

FIGURES

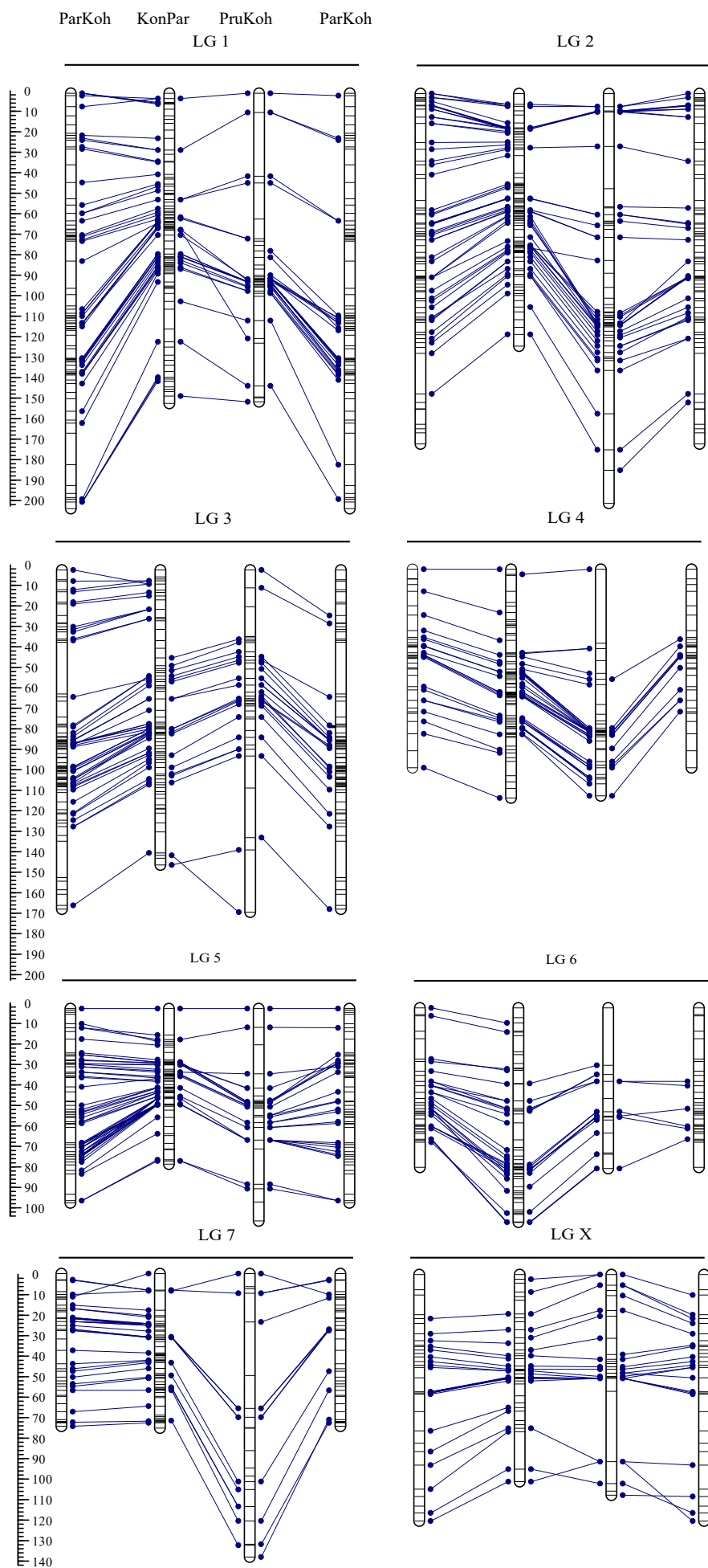


Figure S1. Comprehensive linkage maps. Bars represent linkage groups (LG) for ParKoh, KonPar, and PruKoh. Lines within the bars indicate marker positions. The scale on the left measures marker spacing in cM. Blue lines connect markers on the same scaffold between the different maps. The map for ParKoh is shown twice to facilitate comparison across all three maps.

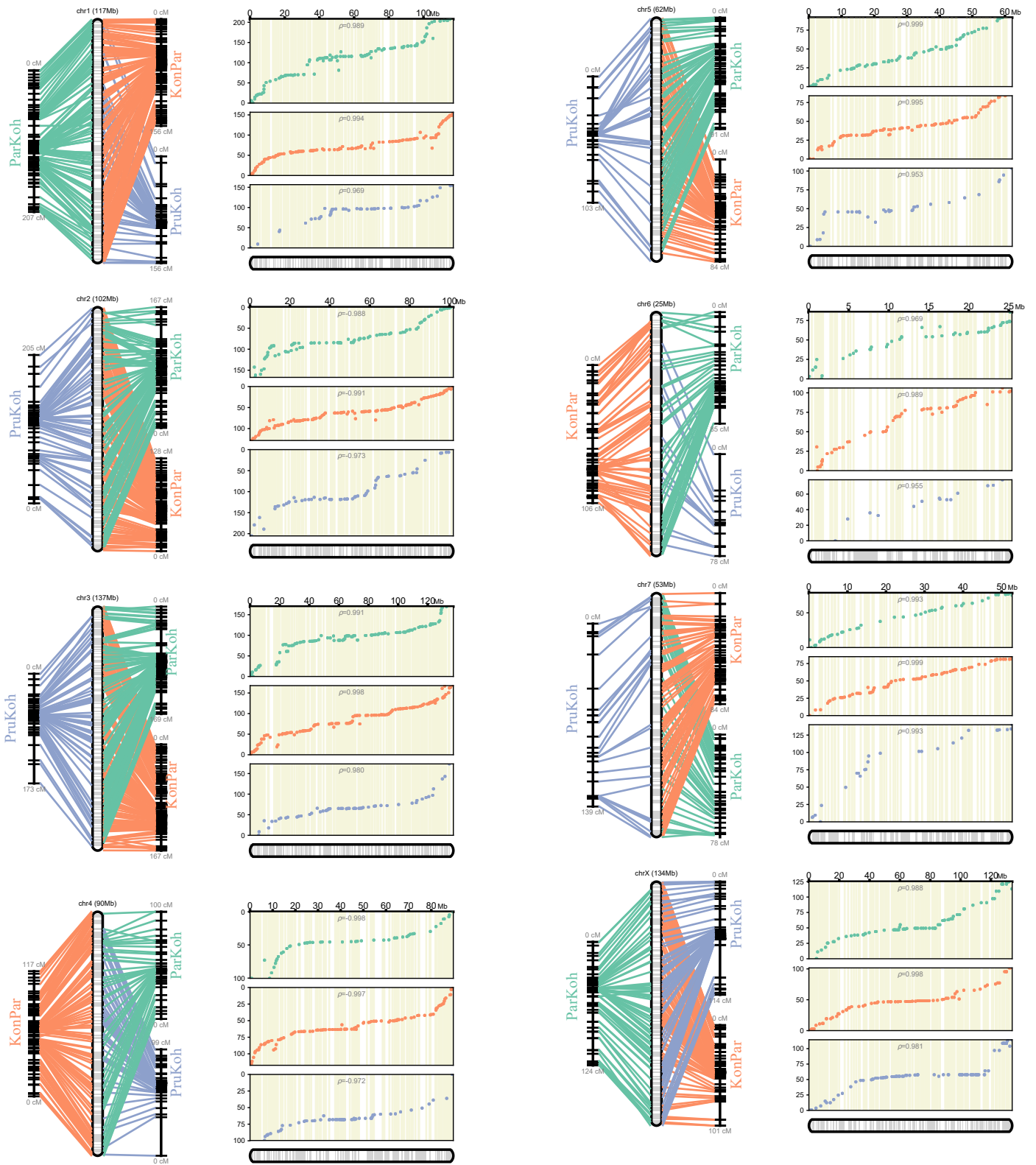


Figure S2. ALLMAPS output. For each of the linkage groups (chr) the relative order with respect to the shared map (i.e. the pseudomolecule assembly) is shown as well as Spearman's rho (ρ) for the strength of correlation between marker orders.

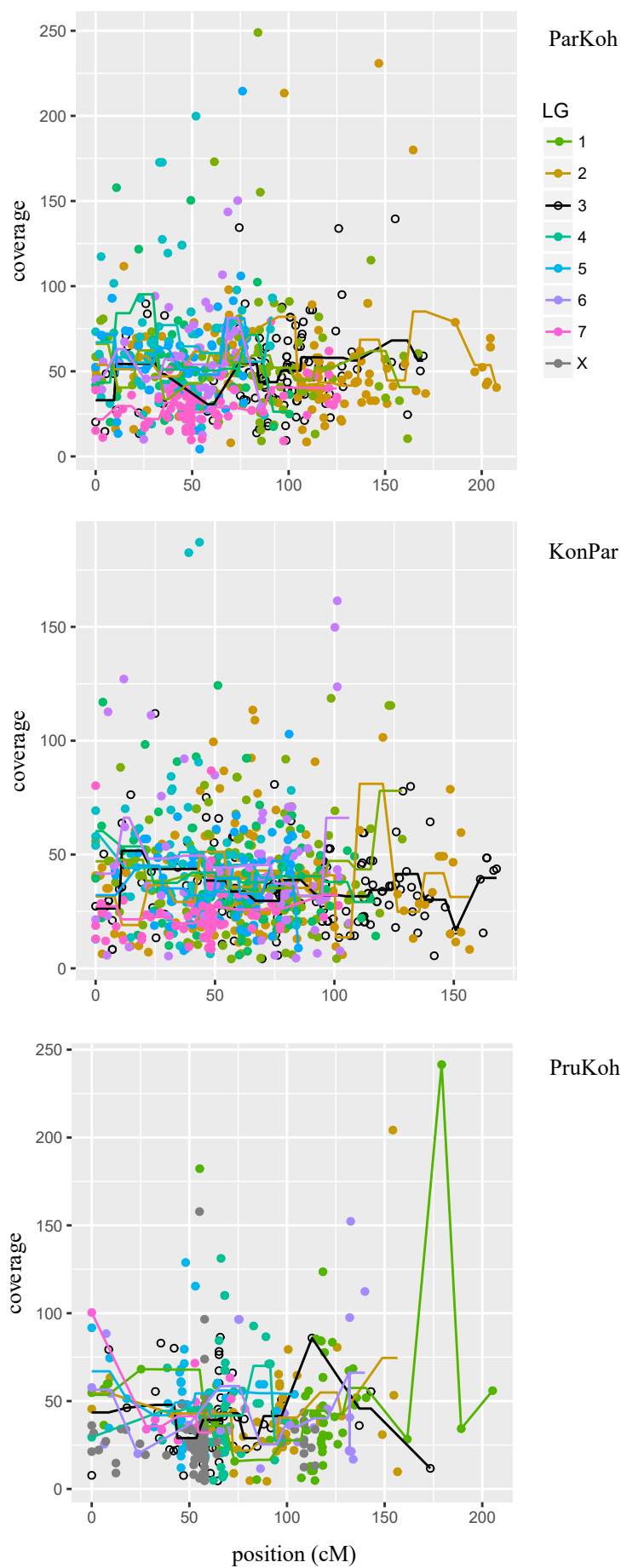


Figure S3. Coverage per cross per linkage group. For each of the three linkage maps (ParKoh, KonPar, PruKoh) the variation in coverage across the 8 linkage groups is shown. Coverage is calculated as the average (across individuals) read count per marker (points). Solid lines show 10-cM non-sliding window averages.