

***HIGH CROSSOVER RATE1* encodes PROTEIN PHOSPHATASE X1 and restricts meiotic crossovers in Arabidopsis**

Divyashree C. Nageswaran^{1§}, Jaeil Kim^{2§}, Christophe Lambing¹, Juhyun Kim², Jihye Park², Eun-Jung Kim², Hyun Seob Cho², Heejin Kim², Dohwan Byun², Yeong Mi Park², Pallas Kuo¹, Seungchul Lee², Andrew J. Tock¹, Xiaohui Zhao¹, Ildoo Hwang², Kyuha Choi^{1,2,*} and Ian R. Henderson^{1,*}

¹ Department of Plant Sciences, Downing Street, University of Cambridge, Cambridge, CB2 3EA, United Kingdom

² Department of Life Sciences, Pohang University of Science and Technology, Pohang, Gyeongbuk, Republic of Korea

§ Equal contribution

* Correspondence: kyuha@postech.ac.kr and irh25@cam.ac.uk

Supplementary Tables 1 - 24

Supplementary Table 1. 420 crossover frequency in wild type, *fancm*, *hcr* and *lcr* mutants. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $cM = 100 \times (1 - [1 - 2(N_{Green} + N_{Red})/N_{Total}]^{1/2})^{3,4}$. To test for significant differences between wild type and mutants, *P* values were calculated using one-sided Welch's t-tests. G/nG shows the ratio of green color seed number (G) to non-green seed number (nG). R/nR indicates the ratio of red color seed number to non-red seed number.

CTL	Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
420	Wild type	174	183	1432	381	2170	18.09	2.85	2.91	20.19	1.43	
420	Wild type	214	229	1475	348	2266	21.96	2.93	3.03			
420	Wild type	227	217	1513	359	2316	21.48	3.02	2.95			
420	Wild type	141	156	1168	280	1745	18.78	3	3.14			
420	Wild type	174	205	1398	362	2139	19.65	2.77	2.99			
420	Wild type	204	197	1393	330	2124	21.11	3.03	2.98			
420	Wild type	214	179	1438	329	2160	20.24	3.25	2.98			
420	<i>lcr1 (taf4b-3)</i>	177	182	1834	499	2692	14.37	2.95	2.98	15.97	1.14	2.93×10^{-5}
420	<i>lcr1 (taf4b-3)</i>	27	32	318	85	462	13.71	2.95	3.13			
420	<i>lcr1 (taf4b-3)</i>	176	187	1584	400	2347	16.89	3	3.07			
420	<i>lcr1 (taf4b-3)</i>	191	193	1631	422	2437	17.24	2.96	2.98			
420	<i>lcr1 (taf4b-3)</i>	157	155	1477	373	2162	15.66	3.09	3.08			
420	<i>lcr1 (taf4b-3)</i>	155	185	1613	433	2386	15.44	2.86	3.06			
420	<i>lcr1 (taf4b-3)</i>	169	183	1550	411	2313	16.6	2.89	2.99			
420	<i>lcr1 (taf4b-3)</i>	127	144	1217	328	1816	16.24	2.85	2.99			
420	<i>lcr1 (taf4b-3)</i>	181	179	1497	429	2286	17.23	2.76	2.75			
420	<i>lcr1 (taf4b-3)</i>	161	166	1618	410	2355	15.01	3.09	3.12			
420	<i>lcr1 (taf4b-3)</i>	140	142	1213	330	1825	16.88	2.87	2.88			
420	<i>lcr1 (taf4b-3)</i>	158	172	1543	464	2337	15.29	2.67	2.76			
420	<i>lcr1 (taf4b-3)</i>	95	109	811	247	1262	17.74	2.54	2.69			
420	<i>lcr1 (taf4b-3)</i>	198	177	1659	382	2416	16.96	3.32	3.17			
420	<i>lcr1 (taf4b-3)</i>	182	166	1537	445	2330	16.26	2.81	2.72			
420	<i>lcr1 (taf4b-3)</i>	150	159	1491	392	2192	15.26	2.98	3.04			
420	<i>lcr1 (taf4b-3)</i>	154	171	1568	479	2372	14.8	2.65	2.75			
420	<i>fancm-1</i>	285	259	1140	212	1896	34.72	3.03	2.81	34.55	1.31	1.02×10^{-10}
420	<i>fancm-1</i>	271	275	1110	229	1885	35.14	2.74	2.77			
420	<i>fancm-1</i>	229	222	1038	190	1679	31.97	3.08	3.01			
420	<i>fancm-1</i>	221	221	883	181	1506	35.73	2.75	2.75			
420	<i>fancm-1</i>	239	239	1025	186	1689	34.12	2.97	2.97			
420	<i>fancm-1</i>	253	220	1020	171	1664	34.31	3.26	2.92			
420	<i>fancm-1</i>	209	190	821	137	1357	35.82	3.15	2.92			
420	<i>hcr4 (fancm-11)</i>	273	273	1140	199	1885	35.14	2.99	2.99	34.37	2.59	1.86×10^{-6}
420	<i>hcr4 (fancm-11)</i>	290	284	1340	263	2177	31.25	2.98	2.94			
420	<i>hcr4 (fancm-11)</i>	216	234	991	190	1631	33.05	2.85	3.02			
420	<i>hcr4 (fancm-11)</i>	239	250	1076	187	1752	33.53	3.01	3.11			
420	<i>hcr4 (fancm-11)</i>	260	255	1134	163	1812	34.31	3.33	3.28			

420	<i>hcr4 (fancm-11)</i>	292	321	1150	192	1955	38.94	2.81	3.04			
420	<i>hcr1</i>	310	309	1576	330	2525	28.61	2.95	2.95	27.84	0.44	1.20×10^{-6}
420	<i>hcr1</i>	246	278	1394	282	2200	27.64	2.93	3.17			
420	<i>hcr1</i>	242	250	1274	275	2041	28.04	2.89	2.95			
420	<i>hcr1</i>	257	267	1387	275	2186	27.85	3.03	3.11			
420	<i>hcr1</i>	281	278	1470	291	2320	28.02	3.08	3.06			
420	<i>hcr1</i>	261	270	1418	290	2239	27.5	3	3.06			
420	<i>hcr1</i>	265	241	1383	262	2151	27.23	3.28	3.08			
420	<i>hcr2</i>	536	507	2228	380	3651	34.53	3.12	2.99	35.35	2.05	3.84×10^{-9}
420	<i>hcr2</i>	538	523	2174	395	3630	35.55	2.95	2.89			
420	<i>hcr2</i>	502	565	2252	413	3732	34.56	2.82	3.08			
420	<i>hcr2</i>	488	486	1915	345	3234	36.94	2.89	2.88			
420	<i>hcr2</i>	538	567	2145	415	3665	36.99	2.73	2.85			
420	<i>hcr2</i>	520	573	2139	366	3598	37.35	2.83	3.06			
420	<i>hcr2</i>	453	451	2146	355	3405	31.52	3.22	3.21			
420	<i>hcr3</i>	290	284	1340	263	2177	31.25	2.98	2.94	31.47	1.32	1.69×10^{-9}
420	<i>hcr3</i>	258	265	1281	230	2034	30.3	3.11	3.17			
420	<i>hcr3</i>	281	293	1268	229	2071	33.24	2.97	3.06			
420	<i>hcr3</i>	253	257	1168	269	1947	31	2.7	2.73			
420	<i>hcr3</i>	288	258	1270	241	2057	31.51	3.12	2.89			
420	<i>hcr3</i>	278	282	1374	274	2208	29.8	2.97	3			
420	<i>hcr3</i>	299	265	1244	229	2037	33.2	3.12	2.86			
420	<i>hcr4/fancm-1 F₁</i>	215	159	768	185	1327	33.95	2.86	2.32	34.24	0.91	2.39×10^{-9} Between <i>fancm-1</i> and $F_1 = 0.68$ Between <i>fancm-11</i> and $F_1 = 0.55$
420	<i>hcr4/fancm-1 F₁</i>	331	292	1341	197	2161	34.93	3.42	3.09			
420	<i>hcr4/fancm-1 F₁</i>	212	232	927	171	1542	34.88	2.83	3.03			
420	<i>hcr4/fancm-1 F₁</i>	287	295	1309	235	2126	32.73	3.01	3.07			
420	<i>hcr4/fancm-1 F₁</i>	130	128	524	112	894	34.98	2.73	2.69			
420	<i>hcr4/fancm-1 F₁</i>	212	232	927	171	1542	34.88	2.83	3.03			
420	<i>hcr4/fancm-1 F₁</i>	333	311	1435	237	2316	33.38	3.23	3.06			

Supplementary Table 2. 420 crossover frequency in wild type, *taf4b-1*, *lcr1* and *taf4b-1/lcr1* hybrid plants. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $\text{cM} = 100 \times (1 - [1 - 2(N_{\text{Green}} + N_{\text{Red}})/N_{\text{Total}}]^{1/2})^{3,4}$. To test for significant differences between genotypes, *P* values were calculated using one-sided Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Wild type	211	220	1819	446	2696	17.52	3.05	3.1	18.33	1.14	
Wild type	224	203	1729	471	2627	17.85	2.9	2.78			
Wild type	215	218	1646	450	2529	18.91	2.79	2.8			
Wild type	219	228	1658	490	2595	19.04	2.61	2.66			
Wild type	209	188	1648	453	2498	17.41	2.9	2.77			
Wild type	190	183	1591	406	2370	17.22	3.02	2.98			
Wild type	239	189	1643	388	2459	19.26	3.26	2.92			
Wild type	128	101	976	273	1478	16.93	2.95	2.69			
Wild type	190	206	1465	370	2231	19.69	2.87	2.98			
Wild type	145	136	1160	319	1760	17.5	2.87	2.79			
Wild type	242	202	1588	402	2434	20.3	3.03	2.78			
<i>taf4b-1/taf4b-1</i>	188	166	1584	410	2348	16.43	3.08	2.93	14.32	0.98	1.66×10^{-7}
<i>taf4b-1/taf4b-1</i>	129	168	1534	419	2250	14.21	2.83	3.11			
<i>taf4b-1/taf4b-1</i>	138	161	1551	447	2297	14	2.78	2.93			
<i>taf4b-1/taf4b-1</i>	156	165	1585	462	2368	14.63	2.78	2.83			
<i>taf4b-1/taf4b-1</i>	162	127	1457	410	2156	14.45	3.01	2.77			
<i>taf4b-1/taf4b-1</i>	142	131	1536	437	2246	13	2.95	2.88			
<i>taf4b-1/taf4b-1</i>	126	161	1532	405	2224	13.87	2.93	3.19			
<i>taf4b-1/taf4b-1</i>	158	126	1445	452	2181	14	2.77	2.58			
<i>lcr1lcr1</i>	153	178	1682	410	2423	14.75	3.12	3.3	16.13	0.94	2.44×10^{-4}
<i>lcr1lcr1</i>	167	169	1432	405	2173	16.89	2.79	2.8			
<i>lcr1lcr1</i>	79	78	722	217	1096	15.53	2.72	2.7			
<i>lcr1lcr1</i>	152	163	1440	371	2126	16.12	2.98	3.07			
<i>lcr1lcr1</i>	153	170	1420	366	2109	16.71	2.93	3.06			
<i>lcr1lcr1</i>	187	198	1599	436	2420	17.43	2.82	2.88			
<i>lcr1lcr1</i>	77	97	783	262	1219	15.47	2.4	2.6			
<i>lcr1/taf4b-1</i>	143	152	1809	473	2577	12.19	3.12	3.18	13.11	0.66	4.03×10^{-10}
<i>lcr1/taf4b-1</i>	145	132	1647	465	2389	12.36	3	2.92			
<i>lcr1/taf4b-1</i>	149	147	1630	509	2435	13	2.71	2.7			
<i>lcr1/taf4b-1</i>	151	132	1614	424	2321	13.04	3.17	3.04			
<i>lcr1/taf4b-1</i>	133	154	1642	420	2349	13.07	3.09	3.25			
<i>lcr1/taf4b-1</i>	171	164	1857	523	2715	13.21	2.95	2.91			
<i>lcr1/taf4b-1</i>	171	173	1780	541	2665	13.87	2.73	2.74			
<i>lcr1/taf4b-1</i>	168	129	1535	433	2265	14.11	3.03	2.77			

Supplementary Table 3. 420 crossover frequency in wild type (Col), *hcr1*, *hcr1/+* and high recombination *hcr1* BC₁F₂ individuals. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $cM = 100 \times (1 - [1 - 2(N_{Green} + N_{Red})/N_{Total}]^{1/2})^{3,4}$. To test for significant differences between genotypes, *P* values were calculated using one-sided Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Wild type	158	130	998	278	1564	20.52	2.83	2.59	20.72	0.84	
Wild type	167	184	1335	316	2002	19.42	3	3.14			
Wild type	182	172	1310	322	1986	19.78	3.02	2.94			
Wild type	245	232	1619	396	2492	21.44	2.97	2.89			
Wild type	148	180	1133	306	1767	20.71	2.64	2.89			
Wild type	179	171	1176	309	1835	21.35	2.82	2.76			
Wild type	217	166	1364	357	2104	20.25	3.02	2.67			
Wild type	164	207	1321	358	2050	20.12	2.63	2.93			
Wild type	215	219	1478	333	2245	21.68	3.07	3.1			
Wild type	226	266	1624	409	2525	21.88	2.74	2.98			
<i>hcr1-1/+</i>	209	208	1436	352	2205	21.15	2.94	2.93	20.99	0.7	0.241
<i>hcr1-1/+</i>	203	215	1473	351	2242	20.81	2.96	3.05			
<i>hcr1-1/+</i>	231	211	1548	388	2378	20.74	2.97	2.84			
<i>hcr1-1/+</i>	217	243	1600	392	2452	20.96	2.86	3.03			
<i>hcr1-1/+</i>	211	248	1596	405	2460	20.83	2.77	2.99			
<i>hcr1-1/+</i>	241	241	1546	399	2427	22.36	2.79	2.79			
<i>hcr1-1/+</i>	101	120	817	187	1225	20.05	2.99	3.25			
<i>hcr1-1</i>	181	191	1027	229	1628	26.31	2.88	2.97	27.32	1.22	8.64×10 ⁻¹⁰
<i>hcr1-1</i>	232	191	1136	258	1817	26.9	3.05	2.71			
<i>hcr1-1</i>	208	204	1195	245	1852	25.5	3.12	3.09			
<i>hcr1-1</i>	429	446	962	37	1874	25.8	2.88	3.02			
<i>hcr1-1</i>	245	279	1362	271	2157	28.3	2.92	3.18			
<i>hcr1-1</i>	224	238	1187	254	1903	28.27	2.87	2.98			
<i>hcr1-1</i>	283	322	1565	337	2507	28.07	2.8	3.04			
<i>hcr1-1</i>	276	281	1430	330	2317	27.94	2.79	2.82			
<i>hcr1-1</i>	242	208	1133	242	1825	28.81	3.06	2.77			
<i>hcr1</i> BC ₁ F ₂	180	213	976	185	1554	29.7	2.9	3.26	28.79	0.85	3.22×10 ⁻¹³
<i>hcr1</i> BC ₁ F ₂	266	253	1294	272	2085	29.14	2.97	2.88			
<i>hcr1</i> BC ₁ F ₂	248	263	1293	292	2096	28.42	2.78	2.88			
<i>hcr1</i> BC ₁ F ₂	270	290	1466	276	2302	28.34	3.07	3.22			
<i>hcr1</i> BC ₁ F ₂	272	298	1475	300	2345	28.32	2.92	3.1			
<i>hcr1</i> BC ₁ F ₂	157	190	916	201	1464	27.48	2.74	3.09			
<i>hcr1</i> BC ₁ F ₂	162	159	750	191	1262	29.91	2.61	2.58			
<i>hcr1</i> BC ₁ F ₂	223	213	1093	203	1732	29.53	3.16	3.07			
<i>hcr1</i> BC ₁ F ₂	307	306	1518	340	2471	29.02	2.83	2.82			
<i>hcr1</i> BC ₁ F ₂	276	295	1427	314	2312	28.86	2.8	2.92			
<i>hcr1</i> BC ₁ F ₂	265	306	1469	323	2363	28.12	2.76	3.02			

<i>hcr1 BC₁ F₂</i>	186	168	934	180	1468	28.05	3.22	3.01
<i>hcr1 BC₁ F₂</i>	324	298	1554	316	2492	29.23	3.06	2.89
<i>hcr1 BC₁ F₂</i>	293	288	1448	321	2350	28.9	2.86	2.83
<i>hcr1 BC₁ F₂</i>	147	146	754	147	1194	28.64	3.08	3.06
<i>hcr1 BC₁ F₂</i>	290	310	1555	346	2501	27.88	2.81	2.93
<i>hcr1 BC₁ F₂</i>	298	288	1555	312	2453	27.74	3.09	3.02
<i>hcr1 BC₁ F₂</i>	244	268	1257	279	2048	29.29	2.74	2.92
<i>hcr1 BC₁ F₂</i>	544	554	1263	37	2398	29.02	3.06	3.13
<i>hcr1 BC₁ F₂</i>	274	297	1431	308	2310	28.89	2.82	2.97
<i>hcr1 BC₁ F₂</i>	141	152	731	175	1199	28.5	2.67	2.79
<i>hcr1 BC₁ F₂</i>	211	188	1050	208	1657	28.0	3.18	2.95
<i>hcr1 BC₁ F₂</i>	274	274	1422	307	2277	27.98	2.92	2.92
<i>hcr1 BC₁ F₂</i>	164	166	879	170	1379	27.79	3.1	3.13
<i>hcr1 BC₁ F₂</i>	294	278	1395	354	2321	28.79	2.67	2.58
<i>hcr1 BC₁ F₂</i>	220	210	1096	223	1749	28.71	3.04	2.95
<i>hcr1 BC₁ F₂</i>	300	284	1426	375	2385	28.57	2.62	2.53
<i>hcr1 BC₁ F₂</i>	300	282	1532	323	2437	27.73	3.03	2.91
<i>hcr1 BC₁ F₂</i>	270	267	1411	318	2266	27.47	2.87	2.85
<i>hcr1 BC₁ F₂</i>	314	282	1569	365	2530	27.28	2.91	2.73
<i>hcr1 BC₁ F₂</i>	263	296	1507	311	2377	27.22	2.92	3.14
<i>hcr1 BC₁ F₂</i>	285	265	1258	278	2086	31.25	2.84	2.71
<i>hcr1 BC₁ F₂</i>	274	262	1281	293	2110	29.86	2.8	2.72
<i>hcr1 BC₁ F₂</i>	236	236	1165	223	1860	29.82	3.05	3.05
<i>hcr1 BC₁ F₂</i>	194	228	1058	238	1718	28.67	2.69	2.98
<i>hcr1 BC₁ F₂</i>	292	291	1469	322	2374	28.67	2.87	2.87
<i>hcr1 BC₁ F₂</i>	302	265	1428	323	2318	28.53	2.94	2.71
<i>hcr1 BC₁ F₂</i>	295	310	1539	331	2475	28.51	2.86	2.95
<i>hcr1 BC₁ F₂</i>	297	309	1573	315	2494	28.3	3	3.08
<i>hcr1 BC₁ F₂</i>	177	189	868	183	1417	30.47	2.81	2.94
<i>hcr1 BC₁ F₂</i>	321	325	1524	344	2514	30.28	2.76	2.78
<i>hcr1 BC₁ F₂</i>	306	303	1468	295	2372	30.25	2.97	2.95
<i>hcr1 BC₁ F₂</i>	217	246	1135	243	1841	29.5	2.76	3
<i>hcr1 BC₁ F₂</i>	154	172	822	166	1314	29.02	2.89	3.11
<i>hcr1 BC₁ F₂</i>	274	268	1338	320	2200	28.78	2.74	2.7
<i>hcr1 BC₁ F₂</i>	276	296	1429	322	2323	28.76	2.76	2.88
<i>hcr1 BC₁ F₂</i>	311	303	1511	324	2449	29.39	2.91	2.86
<i>hcr1 BC₁ F₂</i>	203	207	1007	220	1637	29.35	2.83	2.87
<i>hcr1 BC₁ F₂</i>	278	298	1445	309	2330	28.9	2.84	2.97
<i>hcr1 BC₁ F₂</i>	133	119	648	124	1024	28.74	3.21	2.98

Supplementary Table 4. High frequency EMS mutations identified from sequencing high 420 recombination *hcr1* BC₁F₂ plants. EMS mutations were analyzed using SHORE^{5,6}. Sequencing quality score (Qual score) measure the probability that a base is called incorrectly and is defined by the equation: $Q = -10\log_{10}(P)$, where P is the estimated probability of the base call being incorrect. A Qual score of 40 indicates an error rate of 1 in 10,000, with a corresponding call accuracy of 99.99%. Mutation (Mut) allele indicates EMS-driven base substitutions, compared to reference (Ref) alleles. The support column shows read depth of sequencing at the position in chromosome (Chr). Frequency (Freq) represents the ratio of mutation alleles to reference allele reads.

Chr	Position	Ref allele	Mut allele	Support	Freq	Qual score	Gene ID	Type of Change	Ref amino acid	Mutation-induced amino acid
1	14592362	C	T	68	0.38	40				
1	16026725	G	A	32	0.39	40				
1	8849288	C	T	34	0.41	40				
1	15931420	G	A	37	0.41	40	AT1G42470.1	Nonsyn	A	T
1	20697206	C	T	35	0.41	40				
1	11371412	C	T	14	0.42	40	AT1G31750.1			
1	3493292	G	A	62	0.46	40	AT1G10580.1	Nonsyn	P	L
1	20820201	G	A	19	0.47	40				
1	24478713	C	T	52	0.48	40	AT1G65810.1			
1	24478713	C	T	52	0.48	40	AT1G65810.2			
1	12255550	C	T	41	0.49	40				
1	21529618	C	T	23	0.56	40				
1	12592042	C	T	42	0.68	40	AT1G34440.1	Syn	Q	Q
2	17189098	C	T	21	0.36	40				
2	2680417	G	A	42	0.38	40				
2	2561293	C	T	75	0.45	40				
2	6851201	C	T	52	0.5	40	AT2G15730.1	Syn	N	N
2	9351668	C	T	48	0.5	40	AT2G21940.1			
2	9351668	C	T	48	0.5	40	AT2G21940.2			
2	9351668	C	T	48	0.5	40	AT2G21940.3			
2	9351668	C	T	48	0.5	40	AT2G21940.4			
2	9351668	C	T	48	0.5	40	AT2G21940.5			
2	2646255	C	T	63	0.53	40				
2	4489446	C	T	70	0.55	40				
3	4426808	G	A	65	0.45	40	AT3G13560.1	Nonsyn	A	V
3	4426808	G	A	65	0.45	40	AT3G13560.2	Nonsyn	A	V
3	4426808	G	A	65	0.45	40	AT3G13560.3	Nonsyn	A	V
3	13801565	C	T	14	0.47	40				
3	8901306	G	A	20	0.49	40	AT3G24480.1	Nonsyn	P	S
3	2968465	C	T	62	0.5	40	AT3G09670.1	Nonsyn	T	I
3	2968465	C	T	62	0.5	40	AT3G09670.2	Nonsyn	T	I
3	8598244	G	A	37	0.51	40				
3	12217216	C	T	72	0.51	40				
3	2350190	G	A	28	0.58	40				
4	15277823	C	T	56	0.86	40				

4	15484080	G	A	101	0.89	40	AT4G32010.1			
4	12032472	C	T	88	0.96	40	AT4G22960.1			
4	13471378	C	T	119	0.98	40	AT4G26720.1/PPX1, HCR1			
5	17848364	C	T	28	0.36	40	AT5G44310.1	Syn	K	K
5	17848364	C	T	28	0.36	40	AT5G44310.2	Syn	K	K
5	4046904	C	T	58	0.42	40	AT5G12470.1	Syn	A	A
5	10075739	G	A	40	0.43	40				
5	10336128	G	A	56	0.43	40				
5	10994278	C	T	34	0.43	40				
5	12769404	G	A	57	0.43	40				
5	13313698	C	T	29	0.43	40				
5	22166578	C	T	30	0.43	40				
5	5153800	G	A	35	0.45	40	AT5G15800.1			
5	5153800	G	A	35	0.45	40	AT5G15800.2			
5	17848369	C	T	33	0.45	40	AT5G44310.1	Nonsyn	V	M
5	17848369	C	T	33	0.45	40	AT5G44310.2	Nonsyn	V	M
5	10214637	G	A	36	0.47	40				
5	18666017	G	A	27	0.47	40				
5	10459490	G	A	10	0.48	40				
5	13664914	C	T	62	0.48	40	AT5G35430.1	Nonsyn	R	W
5	21318563	G	A	135	0.48	40	AT5G52530.1	Nonsyn	V	M
5	21318563	G	A	135	0.48	40	AT5G52530.2	Nonsyn	V	M
5	21318563	G	A	135	0.48	40	AT5G52530.3	Nonsyn	V	M
5	4004534	G	A	97	0.51	40	AT5G12370.1			
5	4004534	G	A	97	0.51	40	AT5G12370.2			
5	4004534	G	A	97	0.51	40	AT5G12370.3			
5	25962334	C	T	73	0.51	40	AT5G64980.1	Nonsyn	G	E
5	13299008	C	T	44	0.55	40				
5	1999606	G	A	67	0.56	40	AT5G06540.1	Nonsyn	L	F
5	1999606	G	A	67	0.56	40	AT5G06540.1	Nonsyn	L	F

Supplementary Table 5. 420 crossover frequency in wild type and *hcr1-1* transformed with *PPX1* transgenes or empty vector. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $\text{cM} = 100 \times (1 - [1 - 2(N_{\text{Green}} + N_{\text{Red}})/N_{\text{Total}}]^{1/2})^{3,4}$. To test for significant differences between genotypes, *P* values were calculated using one-sided Welch's t-tests.

Genotype	Transgene	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Wild type	None	215	174	1427	379	2195	19.65	2.97	2.7	19.12	0.75	
Wild type	None	151	147	1168	308	1774	18.51	2.9	2.86			
Wild type	None	180	182	1453	350	2165	18.42	3.07	3.08			
Wild type	None	199	191	1503	357	2250	19.17	3.11	3.05			
Wild type	None	170	216	1560	362	2308	18.42	2.99	3.34			
Wild type	None	200	185	1404	324	2113	20.28	3.15	3.03			
Wild type	None	196	180	1388	350	2114	19.73	2.99	2.87			
Wild type	None	195	159	1328	310	1992	19.71	3.25	2.94			
Wild type	None	177	197	1508	377	2259	18.21	2.94	3.08			
<i>hcr1-1</i>	None	175	145	922	183	1425	25.78	3.34	2.98			
<i>hcr1-1</i>	None	188	202	1158	269	1817	24.45	2.86	2.98			
<i>hcr1-1</i>	None	190	201	1204	237	1832	24.29	3.18	3.29			
<i>hcr1-1</i>	None	144	136	778	145	1203	26.89	3.28	3.16			
<i>hcr1-1</i>	None	236	234	1462	267	2199	24.33	3.39	3.37			
<i>hcr1-1</i>	None	232	240	1419	305	2196	24.49	3.03	3.09			
<i>hcr1-1</i>	None	286	238	1443	306	2273	26.59	3.18	2.84			
<i>hcr1-1</i>	None	252	246	1397	282	2177	26.35	3.12	3.08			
<i>hcr1-1</i>	None	208	239	1328	333	2108	24.11	2.69	2.9			
<i>hcr1-1</i>	None	253	238	1394	306	2191	25.72	3.03	2.92			
<i>hcr1-1</i>	None	286	238	1443	306	2273	26.59	3.18	2.84	19.59	1.33	0.141 Between wild type and <i>hcr1-1</i> +Empty = 3.17×10 ⁻⁹
Wild type	Empty	131	107	859	202	1299	20.4	3.2	2.9			
Wild type	Empty	130	102	881	222	1335	19.23	3.12	2.79			
Wild type	Empty	78	66	476	119	739	21.88	2.99	2.75			
Wild type	Empty	127	158	1120	296	1701	18.46	2.75	3.02			
Wild type	Empty	167	118	990	236	1511	21.08	3.27	2.75			
Wild type	Empty	146	110	986	253	1495	18.91	3.12	2.75			
Wild type	Empty	53	62	457	101	673	18.87	3.13	3.37			
Wild type	Empty	88	94	731	173	1086	18.46	3.07	3.16			
Wild type	Empty	108	129	921	221	1379	18.99	2.94	3.19			
Wild type	Empty	227	254	1655	462	2598	20.65	2.63	2.77			
Wild type	Empty	187	174	1549	393	2303	17.14	3.06	2.97			
Wild type	Empty	267	200	1564	396	2427	21.57	3.07	2.66			
Wild type	Empty	204	170	1440	413	2227	18.51	2.82	2.61			
Wild type	Empty	250	221	1688	439	2598	20.16	2.94	2.77			
Wild type	Empty	229	223	1685	426	2563	19.55	2.95	2.91			
<i>hcr1-1</i>	Empty	213	188	1131	225	1757	26.27	3.25	3.01	25.01	1.50	3.45×10 ⁻⁹
<i>hcr1-1</i>	Empty	173	195	1171	245	1784	23.36	3.05	3.27			

<i>hcr1-1</i>	Empty	142	135	699	180	1156	27.84	2.67	2.59			Between <i>hcr1-1</i> +Empty and <i>hcr1-1</i> + <i>PPX1</i> = 1.94×10^{-8}
<i>hcr1-1</i>	Empty	213	218	1183	234	1848	26.96	3.09	3.13			
<i>hcr1-1</i>	Empty	141	92	678	157	1068	24.92	3.29	2.58			
<i>hcr1-1</i>	Empty	204	164	1123	226	1717	24.41	3.4	2.99			
<i>hcr1-1</i>	Empty	175	187	1143	259	1764	23.22	2.96	3.06			
<i>hcr1-1</i>	Empty	162	142	963	200	1467	23.48	3.29	3.05			
<i>hcr1-1</i>	Empty	72	80	461	93	706	24.54	3.08	3.28			
<i>hcr1-1</i>	Empty	157	187	1002	237	1583	24.81	2.73	3.02			
<i>hcr1-1</i>	Empty	169	168	949	239	1525	25.3	2.75	2.74			
<i>hcr1-1</i>	<i>PPX1</i>	157	185	1178	284	1804	21.21	2.85	3.09	19.29	0.98	0.357
<i>hcr1-1</i>	<i>PPX1</i>	159	181	1329	327	1996	18.8	2.93	3.11			
<i>hcr1-1</i>	<i>PPX1</i>	171	181	1318	295	1965	19.89	3.13	3.22			
<i>hcr1-1</i>	<i>PPX1</i>	172	230	1612	415	2429	18.21	2.77	3.14			
<i>hcr1-1</i>	<i>PPX1</i>	210	205	1567	410	2392	19.19	2.89	2.86			
<i>hcr1-1</i>	<i>PPX1</i>	243	205	1715	462	2625	18.84	2.94	2.72			
<i>hcr1-1</i>	<i>PPX1</i>	142	137	1064	287	1630	18.9	2.84	2.8			

Supplementary Table 6. 420 crossover frequency in wild type (Col), *hcr1-1*, *hcr1-2*, and *hcr1-1/hcr1-2* hybrid plants. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $\text{cM} = 100 \times (1 - [1 - 2(N_{\text{Green}} + N_{\text{Red}})/N_{\text{Total}}]^{1/2})^{3,4}$. To test for significant differences between wild type and genotypes, *P* values were calculated using one-sided Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Wild type	175	173	1314	295	1957	19.73	3.18	3.16	19.87	1.45	
Wild type	158	152	1208	310	1828	18.71	2.96	2.91			
Wild type	178	147	1230	317	1872	19.21	3.03	2.78			
Wild type	180	169	1323	317	1989	19.44	3.09	3			
Wild type	181	166	1392	311	2050	18.67	3.3	3.17			
Wild type	154	167	1264	342	1927	18.34	2.79	2.89			
Wild type	200	160	1406	334	2100	18.94	3.25	2.93			
Wild type	148	169	1258	274	1849	18.94	3.17	3.38			
Wild type	222	175	1196	333	1926	23.34	2.79	2.47			
Wild type	154	151	1137	293	1735	19.48	2.91	2.88			
Wild type	162	186	1205	284	1837	21.19	2.91	3.12			
Wild type	162	156	1168	294	1780	19.83	2.96	2.9			
Wild type	160	159	1048	259	1626	22.05	2.89	2.88			
Wild type	198	154	1230	345	1927	20.33	2.86	2.55			
Wild type	191	151	1107	296	1745	22.02	2.9	2.58			
Wild type	127	106	972	231	1436	17.81	3.26	3.01			
Wild type	172	179	1379	325	2055	18.86	3.08	3.13			
Wild type	184	166	1282	292	1924	20.24	3.2	3.04			
Wild type	167	159	1265	328	1919	18.74	2.94	2.88			
Wild type	188	196	1304	317	2005	21.45	2.91	2.97			
<i>hcr1-1</i>	145	129	930	166	1370	22.54	3.64	3.41	25.01	2.15	1.62×10^{-10}
<i>hcr1-1</i>	169	183	965	186	1503	27.09	3.07	3.23			
<i>hcr1-1</i>	184	175	1108	243	1710	23.83	3.09	3			
<i>hcr1-1</i>	195	176	1090	232	1693	25.05	3.15	2.96			
<i>hcr1-1</i>	204	155	1042	205	1606	25.64	3.46	2.93			
<i>hcr1-1</i>	155	176	1118	228	1677	22.2	3.15	3.38			
<i>hcr1-1</i>	150	143	1001	218	1512	21.74	3.19	3.11			
<i>hcr1-1</i>	185	198	1216	236	1835	23.67	3.23	3.36			
<i>hcr1-1</i>	191	153	996	195	1535	25.72	3.41	2.98			
<i>hcr1-1</i>	210	209	1102	216	1737	28.06	3.09	3.08			
<i>hcr1-1</i>	155	117	724	194	1190	26.32	2.83	2.41			
<i>hcr1-1</i>	207	176	1110	226	1719	25.54	3.28	2.97			
<i>hcr1-1</i>	201	157	922	190	1470	28.38	3.24	2.76			
<i>hcr1-1</i>	179	184	1156	246	1765	23.28	3.1	3.15			
<i>hcr1-1</i>	144	171	1146	239	1700	20.66	3.15	3.44			
<i>hcr1-1</i>	180	218	1179	286	1863	24.32	2.7	3			
<i>hcr1-1</i>	165	141	881	164	1351	26.04	3.43	3.11			

<i>hcr1-1</i>	143	132	774	128	1177	27.01	3.53	3.34			
<i>hcr1-1</i>	172	182	981	208	1543	26.44	2.96	3.06			
<i>hcr1-1</i>	133	157	801	162	1253	26.71	2.93	3.25			
<i>hcr1-2</i>	180	147	1042	247	1616	22.84	3.1	2.78			
<i>hcr1-2</i>	115	124	816	205	1260	21.22	2.83	2.94			
<i>hcr1-2</i>	183	192	1127	265	1767	24.13	2.87	2.94			
<i>hcr1-2</i>	173	138	1050	247	1608	21.69	3.18	2.83			
<i>hcr1-2</i>	111	150	843	195	1299	22.66	2.77	3.25			
<i>hcr1-2</i>	186	167	1107	238	1698	23.57	3.19	3			
<i>hcr1-2</i>	139	144	882	206	1371	23.37	2.92	2.97			
<i>hcr1-2</i>	148	164	928	219	1459	24.35	2.81	2.98			
<i>hcr1-2</i>	175	170	1055	274	1674	23.33	2.77	2.73			
<i>hcr1-2</i>	166	176	1053	208	1603	24.28	3.17	3.29	22.98	1.5	5.43×10^{-8}
<i>hcr1-2</i>	75	78	500	121	774	22.24	2.89	2.95			
<i>hcr1-2</i>	204	167	1093	267	1731	24.41	2.99	2.68			
<i>hcr1-2</i>	126	82	729	160	1097	21.21	3.53	2.84			
<i>hcr1-2</i>	168	156	1111	252	1687	21.52	3.13	3.02			
<i>hcr1-2</i>	171	212	1035	271	1689	26.08	2.5	2.82			
<i>hcr1-2</i>	184	140	1155	273	1752	20.62	3.24	2.83			
<i>hcr1-2</i>	206	208	1209	254	1877	25.24	3.06	3.08			
<i>hcr1-2</i>	135	134	915	205	1389	21.73	3.1	3.09			
<i>hcr1-2</i>	191	166	1187	265	1809	22.2	3.2	2.97			
<i>hcr1-1/hcr1-2</i>	227	195	1153	256	1831	26.58	3.06	2.79			
<i>hcr1-1/hcr1-2</i>	256	172	1175	256	1859	26.55	3.34	2.63			
<i>hcr1-1/hcr1-2</i>	194	171	1139	273	1777	23.24	3	2.81			
<i>hcr1-1/hcr1-2</i>	225	221	1192	316	1954	26.28	2.64	2.61			
<i>hcr1-1/hcr1-2</i>	163	192	961	246	1562	26.15	2.57	2.82			
<i>hcr1-1/hcr1-2</i>	204	185	1174	221	1784	24.91	3.39	3.2			
<i>hcr1-1/hcr1-2</i>	203	164	1191	250	1808	22.93	3.37	2.99			
<i>hcr1-1/hcr1-2</i>	159	148	1040	200	1547	22.34	3.45	3.31			
<i>hcr1-1/hcr1-2</i>	232	155	1158	243	1788	24.69	3.49	2.76			4.91×10^{-10}
<i>hcr1-1/hcr1-2</i>	175	160	1181	287	1803	20.73	3.03	2.9	24.17	1.71	Between <i>hcr1-1</i> and <i>hcr1-1/hcr1-2</i> = 0.0591
<i>hcr1-1/hcr1-2</i>	188	149	1177	239	1753	21.55	3.52	3.11			
<i>hcr1-1/hcr1-2</i>	141	192	995	237	1565	24.21	2.65	3.14			
<i>hcr1-1/hcr1-2</i>	187	174	1038	218	1617	25.6	3.13	2.99			
<i>hcr1-1/hcr1-2</i>	126	109	738	182	1155	22.99	2.97	2.75			
<i>hcr1-1/hcr1-2</i>	177	212	1154	262	1805	24.57	2.81	3.11			
<i>hcr1-1/hcr1-2</i>	203	185	1314	273	1975	22.08	3.31	3.15			
<i>hcr1-1/hcr1-2</i>	216	174	1188	234	1812	24.53	3.44	3.03			
<i>hcr1-1/hcr1-2</i>	185	162	1070	269	1686	23.29	2.91	2.71			
<i>hcr1-1/hcr1-2</i>	229	232	1332	298	2091	25.23	2.95	2.97			
<i>hcr1-1/hcr1-2</i>	228	202	1241	300	1971	24.92	2.93	2.73			

Supplementary Table 7. 420 crossover frequency in wild type, *ppx1*, *ppx2* and *pp4r2* mutants. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $\text{cM} = 100 \times (1 - [1 - 2(N_{\text{Green}} + N_{\text{Red}})/N_{\text{Total}}]^{1/2})^{3,4}$. To test for significant differences between genotypes, *P* values were calculated using one-sided Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Wild type	240	201	1544	382	2367	20.79	3.06	2.81	18.58	1.82	
Wild type	199	193	1703	443	2538	16.87	2.99	2.95			
Wild type	252	199	1795	521	2767	17.9	2.84	2.58			
Wild type	241	233	1707	411	2592	20.36	3.02	2.98			
Wild type	218	205	1723	452	2598	17.88	2.95	2.88			
Wild type	194	119	1337	332	1982	17.29	3.39	2.77			
Wild type	195	203	1854	432	2684	16.13	3.23	3.28			
Wild type	172	107	955	237	1471	21.22	3.28	2.6			
Wild type	238	196	1683	433	2550	18.78	3.05	2.8			
<i>hcr1-2</i>	238	259	1525	376	2398	23.48	2.78	2.91			
<i>hcr1-2</i>	312	258	1620	400	2590	25.18	2.94	2.64			
<i>hcr1-2</i>	193	173	1203	285	1854	22.21	3.05	2.88			
<i>hcr1-2</i>	309	267	1619	365	2560	25.84	3.05	2.8			
<i>hcr1-2</i>	308	240	1728	334	2610	23.84	3.55	3.07			
<i>hcr1-2</i>	263	228	1488	370	2349	23.71	2.93	2.71			
<i>hcr1-2</i>	267	277	1643	374	2561	24.16	2.93	3			
<i>hcr1-2</i>	276	179	1426	281	2162	23.9	3.7	2.88			
<i>ppx2-1</i>	176	178	1399	308	2061	18.98	3.24	3.26	19.4	0.68	0.119
<i>ppx2-1</i>	190	157	1276	315	1938	19.88	3.11	2.84			
<i>ppx2-1</i>	165	162	1231	284	1842	19.69	3.13	3.1			
<i>ppx2-1</i>	148	159	1126	289	1722	19.79	2.84	2.94			
<i>ppx2-1</i>	66	64	495	108	733	19.67	3.26	3.21			
<i>ppx2-1</i>	136	132	1096	270	1634	18.03	3.06	3.02			
<i>ppx2-1</i>	167	160	1225	281	1833	19.8	3.16	3.09			
<i>hcr1-2 ppx2-1</i>	229	226	1205	257	1917	27.52	2.97	2.94	26.90	1.38	1.46×10 ⁻⁸
<i>hcr1-2 ppx2-1</i>	289	249	1368	320	2226	28.12	2.91	2.66			
<i>hcr1-2 ppx2-1</i>	310	265	1613	381	2569	25.68	2.98	2.72			
<i>hcr1-2 ppx2-1</i>	205	199	1191	241	1836	25.17	3.17	3.12			
<i>hcr1-2 ppx2-1</i>	207	258	1143	230	1838	29.71	2.77	3.21			
<i>hcr1-2 ppx2-1</i>	192	206	1169	259	1826	24.90	2.93	3.05			
<i>hcr1-2 ppx2-1</i>	197	182	1012	217	1608	27.29	3.03	2.88			
<i>hcr1-2 ppx2-1</i>	197	213	1137	233	1780	26.56	2.99	3.14			
<i>hcr1-2 ppx2-1</i>	210	198	1075	227	1710	27.69	3.02	2.91			
<i>hcr1-2 ppx2-1</i>	227	231	1271	271	2000	26.38	2.98	3.02			
<i>hcr1-2 ppx2-1</i>	201	216	1156	223	1796	26.81	3.09	3.24			
<i>hcr1-2 ppx2-1</i>	170	162	943	229	1504	25.27	2.85	2.77			
<i>pp4r2</i>	162	152	969	204	1487	24	3.18	3.06	24.3	3.52	4.24×10 ⁻⁵

<i>pp4r2</i>	230	179	1372	318	2099	21.88	3.22	2.83			
<i>pp4r2</i>	128	143	608	130	1009	31.97	2.7	2.91			
<i>pp4r2</i>	219	198	1252	293	1962	24.18	3	2.83			
<i>pp4r2</i>	190	165	1055	227	1637	24.75	3.18	2.93			
<i>pp4r2</i>	131	140	841	177	1289	23.87	3.07	3.19			
<i>pp4r2</i>	101	84	567	120	872	24.13	3.27	2.95			
<i>pp4r2</i>	86	87	601	145	919	21.04	2.96	2.98			
<i>pp4r2</i>	171	166	1063	207	1607	23.8	3.31	3.25			
<i>pp4r2</i>	215	177	913	177	1482	31.37	3.19	2.78			
<i>pp4r2</i>	156	169	1146	273	1744	20.8	2.95	3.07			
<i>pp4r2</i>	220	191	1289	355	2055	22.54	2.76	2.57			
<i>pp4r2</i>	119	101	754	166	1140	21.64	3.27	3			

Supplementary Table 8. 420 crossover frequency in wild type and *meiMIGS-PPX1*, *meiMIGS-PPX2* and *meiMIGS-PPX1-PPX2* T₁ and T₂ transgenic lines. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $cM=100 \times (1 - [1-2(N_{Green}+N_{Red})/N_{Total}]^{1/2})^{3,4}$. To test for significant differences between wild type and genotypes, *P* values were calculated using one-sided Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Wild type	193	188	1386	337	2104	20.14	3.01	2.97	18.89	1.09	
Wild type	215	214	1628	360	2417	19.69	3.21	3.2			
Wild type	123	130	1038	235	1526	18.24	3.18	3.26			
Wild type	141	142	1179	278	1740	17.86	3.14	3.15			
Wild type	189	182	1467	356	2194	18.65	3.08	3.03			
Wild type	217	222	1662	406	2507	19.39	2.99	3.02			
Wild type	213	188	1628	378	2407	18.34	3.25	3.07			
Wild type	193	181	1626	378	2378	17.21	3.25	3.16			
Wild type	214	211	1522	367	2314	20.46	3	2.98			
<i>hcr1-1</i>	214	243	1472	286	2215	23.36	3.19	3.43	24.87	1.38	4.13×10 ⁻⁹
<i>hcr1-1</i>	230	189	1173	261	1853	25.99	3.12	2.77			
<i>hcr1-1</i>	189	167	1097	281	1734	23.23	2.87	2.69			
<i>hcr1-1</i>	207	201	1072	248	1728	27.35	2.85	2.8			
<i>hcr1-1</i>	167	138	862	169	1336	26.28	3.35	2.98			
<i>hcr1-1</i>	204	229	1248	269	1950	25.44	2.92	3.12			
<i>hcr1-1</i>	182	174	1095	242	1693	23.88	3.07	2.99			
<i>hcr1-1</i>	178	177	1116	229	1700	23.69	3.19	3.18			
<i>hcr1-1</i>	185	148	983	223	1539	24.68	3.15	2.77			
<i>hcr1-1</i>	193	184	1118	238	1733	24.84	3.11	3.02			
<i>meiMIGS-PPX1</i> T ₁	208	207	1103	214	1732	27.83	3.11	3.1	26.13	1.51	4.88×10 ⁻¹¹ Between <i>hcr1</i> and <i>meiMIGS-PPX1</i> T ₁ = 0.0279
<i>meiMIGS-PPX1</i> T ₁	183	128	878	159	1348	26.61	3.7	2.94			
<i>meiMIGS-PPX1</i> T ₁	210	206	1097	223	1736	27.84	3.05	3.01			
<i>meiMIGS-PPX1</i> T ₁	249	247	1335	285	2116	27.12	2.98	2.96			
<i>meiMIGS-PPX1</i> T ₁	216	248	1212	278	1954	27.54	2.71	2.96			
<i>meiMIGS-PPX1</i> T ₁	183	171	979	210	1543	26.44	3.05	2.93			
<i>meiMIGS-PPX1</i> T ₁	240	274	1365	309	2188	27.19	2.75	2.99			
<i>meiMIGS-PPX1</i> T ₁	253	241	1425	315	2234	25.32	3.02	2.93			
<i>meiMIGS-PPX1</i> T ₁	161	154	915	192	1422	25.37	3.11	3.03			
<i>meiMIGS-PPX1</i> T ₁	131	110	761	154	1156	23.64	3.38	3.06			
<i>meiMIGS-PPX1</i> T ₁	206	207	1290	281	1984	23.6	3.07	3.07			
<i>meiMIGS-PPX1</i> T ₁	245	281	1539	336	2401	25.04	2.89	3.13			
<i>meiMIGS-PPX1</i> T ₁	132	128	670	128	1058	28.69	3.13	3.07			
<i>meiMIGS-PPX1</i> T ₁	243	237	1439	315	2234	24.48	3.05	3	23.99	2.07	4.11×10 ⁻⁵ Between <i>hcr1</i> and <i>meiMIGS-PPX2</i> T ₁ = 0.159
<i>meiMIGS-PPX1</i> T ₁	192	206	1190	264	1852	24.49	2.94	3.06			
<i>meiMIGS-PPX1</i> T ₁	246	205	1477	311	2239	22.73	3.34	3.02			
<i>meiMIGS-PPX1</i> T ₁	241	211	1428	297	2177	23.53	3.29	3.05			
<i>meiMIGS-PPX1</i> T ₁	238	201	1450	323	2212	22.34	3.22	2.94			

<i>meiMIGS-PPX1 T₁</i>	177	185	1159	266	1787	22.87	2.96	3.03			
<i>meiMIGS-PPX1 T₁</i>	94	107	650	146	997	22.75	2.94	3.15			
<i>meiMIGS-PPX1-PPX2 T₁</i>	189	223	952	163	1527	32.15	2.96	3.34	28.06	2.1	9.45×10 ⁻¹⁴ Between <i>hcr1</i> and <i>meiMIGS-PPX1-PPX2 T₁</i> = 3.75×10 ⁻⁵
<i>meiMIGS-PPX1-PPX2 T₁</i>	211	220	1120	252	1803	27.76	2.82	2.89			
<i>meiMIGS-PPX1-PPX2 T₁</i>	160	182	954	146	1442	27.5	3.4	3.71			
<i>meiMIGS-PPX1-PPX2 T₁</i>	206	302	1399	318	2225	26.29	2.59	3.25			
<i>meiMIGS-PPX1-PPX2 T₁</i>	108	100	495	105	808	30.35	2.94	2.79			
<i>meiMIGS-PPX1-PPX2 T₁</i>	205	185	1017	226	1633	27.73	2.97	2.79			
<i>meiMIGS-PPX1-PPX2 T₁</i>	162	155	852	190	1359	26.96	2.94	2.86			
<i>meiMIGS-PPX1-PPX2 T₁</i>	181	168	969	189	1507	26.73	3.22	3.07			
<i>meiMIGS-PPX1-PPX2 T₁</i>	113	117	582	136	948	28.25	2.75	2.81			
<i>meiMIGS-PPX1-PPX2 T₁</i>	127	117	629	128	1001	28.41	3.09	2.93			
<i>meiMIGS-PPX1-PPX2 T₁</i>	127	116	637	140	1020	27.64	2.98	2.82			
<i>meiMIGS-PPX1-PPX2 T₁</i>	136	173	791	175	1275	28.22	2.66	3.1			
<i>meiMIGS-PPX1-PPX2 T₁</i>	176	170	951	192	1489	26.84	3.11	3.05			
<i>meiMIGS-PPX1-PPX2 T₁</i>	164	196	953	246	1559	26.64	2.53	2.8			
<i>meiMIGS-PPX1-PPX2 T₁</i>	122	110	489	112	833	33.44	2.75	2.56			
<i>meiMIGS-PPX1-PPX2 T₁</i>	157	147	814	192	1310	26.8	2.86	2.75			
<i>meiMIGS-PPX1-PPX2 T₁</i>	187	181	1059	240	1667	25.27	2.96	2.9			
<i>meiMIGS-PPX1 T₂ #1</i>	297	292	1517	307	2413	28.46	3.03	3	27.43	1.81	8.12×10 ⁻⁹
<i>meiMIGS-PPX1 T₂ #1</i>	296	261	1406	299	2262	28.76	3.04	2.8			
<i>meiMIGS-PPX1 T₂ #1</i>	306	290	1454	287	2337	30	3.05	2.94			
<i>meiMIGS-PPX1 T₂ #1</i>	274	285	1563	339	2461	26.13	2.94	3.01			
<i>meiMIGS-PPX1 T₂ #1</i>	263	272	1488	329	2352	26.17	2.91	2.97			
<i>meiMIGS-PPX1 T₂ #1</i>	265	255	1426	311	2257	26.57	2.99	2.92			
<i>meiMIGS-PPX1 T₂ #1</i>	298	296	1488	286	2368	29.41	3.07	3.05			
<i>meiMIGS-PPX1 T₂ #1</i>	295	274	1697	378	2644	24.53	3.06	2.93			
<i>meiMIGS-PPX1 T₂ #1</i>	262	263	1420	317	2262	26.8	2.9	2.91			
<i>meiMIGS-PPX1 T₂ #1</i>	299	280	1707	369	2655	24.91	3.09	2.97			
<i>meiMIGS-PPX1 T₂ #1</i>	230	224	1529	372	2355	21.61	2.95	2.91	25.07	2.17	3.41×10 ⁻⁶
<i>meiMIGS-PPX1 T₂ #1</i>	272	254	1501	335	2362	25.53	3.01	2.89			
<i>meiMIGS-PPX1 T₂ #1</i>	297	285	1435	304	2321	29.4	2.94	2.86			
<i>meiMIGS-PPX1 T₂ #1</i>	247	232	1438	335	2252	24.2	2.97	2.87			
<i>meiMIGS-PPX1 T₂ #1</i>	221	184	1269	265	1939	23.69	3.32	2.99			
<i>meiMIGS-PPX1 T₂ #1</i>	250	250	1493	337	2330	24.45	2.97	2.97			
<i>meiMIGS-PPX1 T₂ #1</i>	283	261	1596	361	2501	24.84	3.02	2.88			
<i>meiMIGS-PPX1 T₂ #1</i>	274	285	1515	317	2391	27.03	2.97	3.05			
<i>meiMIGS-PPX2 T₂ #1</i>	274	261	1752	402	2689	22.41	3.06	2.98			
<i>meiMIGS-PPX2 T₂ #1</i>	250	246	1759	494	2749	20.05	2.71	2.69			
<i>meiMIGS-PPX2 T₂ #1</i>	282	273	1734	430	2719	23.07	2.87	2.82			
<i>meiMIGS-PPX2 T₂ #1</i>	256	224	1780	457	2717	19.58	2.99	2.81			

<i>meiMIGS-PPX2 T₂ #1</i>	281	282	1735	500	2798	22.7	2.58	2.58			
<i>meiMIGS-PPX2 T₂ #1</i>	272	268	1692	387	2619	23.34	3	2.97			
<i>meiMIGS-PPX2 T₂ #1</i>	258	272	1645	388	2563	23.42	2.88	2.97			
<i>meiMIGS-PPX2 T₂ #1</i>	287	247	1732	381	2647	22.77	3.21	2.96			
<i>meiMIGS-PPX2 T₂ #1</i>	304	317	1705	429	2755	25.89	2.69	2.76			
<i>meiMIGS-PPX2 T₂ #1</i>	231	218	1424	333	2206	23	3	2.91			
<i>meiMIGS-PPX2 T₂ #1</i>	309	359	1637	491	2796	27.74	2.29	2.5			
<i>meiMIGS-PPX2 T₂ #1</i>	275	259	1730	523	2787	21.46	2.56	2.49			
<i>meiMIGS-PPX2 T₂ #1</i>	292	281	1720	438	2731	23.82	2.8	2.74			
<i>meiMIGS-PPX2 T₂ #1</i>	210	211	1326	323	2070	22.98	2.88	2.88	25.33	2.91	4.49×10 ⁻⁵
<i>meiMIGS-PPX2 T₂ #1</i>	296	282	1463	283	2324	29.11	3.11	3.01			
<i>meiMIGS-PPX2 T₂ #1</i>	278	311	1440	311	2340	29.53	2.76	2.97			
<i>meiMIGS-PPX2 T₂ #1</i>	271	288	1574	331	2464	26.09	2.98	3.09			
<i>meiMIGS-PPX2 T₂ #1</i>	296	306	1707	516	2825	24.25	2.44	2.48			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	324	300	1234	203	2061	37.19	3.1	2.91			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	291	296	1274	211	2072	34.17	3.09	3.13			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	263	277	1098	189	1827	36.06	2.92	3.04			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	344	326	1305	196	2171	38.13	3.16	3.02			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	287	288	1250	217	2042	33.91	3.04	3.05			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	270	259	1056	152	1737	37.48	3.23	3.12	36.71	1.47	2.2×10 ⁻¹⁶
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	211	213	814	137	1375	38.09	2.93	2.95			Between <i>hcr1</i> and <i>meiMIGS-PPX1-PPX2 T₂ #1</i> = 3.96×10 ⁻¹⁴
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	262	231	994	138	1625	37.29	3.4	3.06			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	212	220	840	139	1411	37.74	2.93	3.02			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	259	253	1043	168	1723	36.31	3.09	3.04			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	167	150	632	92	1041	37.47	3.3	3.02			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	224	234	1180	244	1882	28.36	2.94	3.02			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	455	446	1018	33	1952	27.72	3.08	3			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	194	217	1166	267	1844	25.55	2.81	3			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	232	215	1190	238	1875	27.67	3.14	2.99			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	212	201	959	174	1546	31.76	3.12	3.01			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	221	217	1239	267	1944	25.88	3.02	2.98	26.88	2.09	4.93×10 ⁻⁹
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	117	111	712	155	1095	23.61	3.12	3.03			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	216	198	1140	227	1781	26.85	3.19	3.02			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	125	145	777	180	1227	25.17	2.78	3.02			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	194	173	1042	184	1593	26.57	3.46	3.21			
<i>meiMIGS-PPX1-PPX2 T₂ #1</i>	155	170	889	198	1412	26.54	2.84	3			

Supplementary Table 9. Seed based FTL crossover frequency in wild type and *hcr1*. FTL crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized FTL hemizygote plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $cM = 100 \times (1 - [1 - 2(N_{Green} + N_{Red})/N_{Total}]^{1/2})^{3,4}$. *P* values were calculated using one-sided Welch's t-test, which assessed significant differences between wild type and *hcr1-1* in each seed based FTL line⁷.

CTL	Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
1.17	Wild type	225	214	1492	324	2255	21.86	3.19	3.11	22.83	1.73	
1.17	Wild type	213	241	1527	355	2336	21.81	2.92	3.11			
1.17	Wild type	257	230	1520	328	2335	23.65	3.18	2.99			
1.17	Wild type	269	254	1499	330	2352	25.48	3.03	2.93			
1.17	Wild type	211	202	1407	346	2166	21.35	2.95	2.89			
1.17	<i>hcr1-1</i>	96	107	456	72	731	33.32	3.08	3.35	32.23	3.09	1.08×10^{-4}
1.17	<i>hcr1-1</i>	299	319	1338	291	2247	32.92	2.68	2.81			
1.17	<i>hcr1-1</i>	221	230	1188	230	1869	28.07	3.06	3.14			
1.17	<i>hcr1-1</i>	242	295	1056	181	1774	37.18	2.73	3.19			
1.17	<i>hcr1-1</i>	171	152	783	152	1258	30.25	3.14	2.89			
1.17	<i>hcr1-1</i>	323	301	1488	233	2345	31.6	3.39	3.22			
1.26	Wild type	24	37	1849	659	2569	2.4	2.69	2.76	2.76	0.43	
1.26	Wild type	31	34	1951	671	2687	2.45	2.81	2.83			
1.26	Wild type	40	40	1954	674	2708	3	2.79	2.79			
1.26	Wild type	33	38	1389	527	1987	3.64	2.52	2.55			
1.26	Wild type	42	26	1966	609	2643	2.61	3.16	3.06			
1.26	Wild type	34	33	1851	666	2584	2.63	2.7	2.69			
1.26	Wild type	36	36	2053	673	2798	2.61	2.95	2.95			
1.26	<i>hcr1-1</i>	83	67	2280	738	3168	4.85	2.94	2.86	4.25	0.29	7.21×10^{-6}
1.26	<i>hcr1-1</i>	80	60	2543	811	3494	4.09	3.01	2.92			
1.26	<i>hcr1-1</i>	66	83	2590	833	3572	4.26	2.9	2.97			
1.26	<i>hcr1-1</i>	75	64	2565	809	3513	4.04	3.02	2.97			
1.26	<i>hcr1-1</i>	57	72	2392	788	3309	3.98	2.85	2.92			
1.26	<i>hcr1-1</i>	71	62	2347	741	3221	4.22	3.01	2.97			
1.26	<i>hcr1-1</i>	69	65	2304	730	3168	4.32	2.98	2.96			
3.15	Wild type	68	76	488	117	749	21.55	2.88	3.05	23.46	2.15	
3.15	Wild type	217	196	1113	250	1776	26.86	2.98	2.8			
3.15	Wild type	268	283	1646	381	2578	24.33	2.88	2.97			
3.15	Wild type	167	193	1235	259	1854	21.79	3.1	3.35			
3.15	Wild type	204	152	1175	235	1766	22.75	3.56	3.02			
3.15	Wild type	182	204	1023	264	1673	26.61	2.57	2.75			
3.15	Wild type	146	170	1002	215	1533	23.34	2.98	3.25			
3.15	Wild type	102	97	661	114	974	23.1	3.62	3.51			
3.15	Wild type	169	175	1051	224	1619	24.17	3.06	3.12			
3.15	Wild type	158	144	1129	242	1673	20.06	3.33	3.18			
3.15	<i>hcr1-1</i>	221	191	936	181	1529	32.1	3.11	2.8	29.29	1.6	1.08×10^{-6}
3.15	<i>hcr1-1</i>	174	207	968	180	1529	29.17	2.95	3.32			

3.15	<i>hcr1-1</i>	221	216	1175	219	1831	27.7	3.21	3.16			
3.15	<i>hcr1-1</i>	224	243	1258	227	1952	27.78	3.15	3.33			
3.15	<i>hcr1-1</i>	121	119	639	132	1011	27.53	3.03	3			
3.15	<i>hcr1-1</i>	234	246	1154	220	1854	30.56	2.98	3.08			
3.15	<i>hcr1-1</i>	246	253	1225	215	1939	30.34	3.14	3.21			
3.15	<i>hcr1-1</i>	90	136	588	109	923	28.57	2.77	3.64			
3.15	<i>hcr1-1</i>	50	49	256	51	406	28.42	3.06	3.02			
3.15	<i>hcr1-1</i>	151	161	857	146	1315	27.51	3.28	3.43			
3.15	<i>hcr1-1</i>	203	223	1030	187	1643	30.61	3.01	3.21			
3.15	<i>hcr1-1</i>	253	239	1154	224	1870	31.17	3.04	2.92			
5.11	Wild type	298	245	1518	408	2469	25.16	2.78	2.5			
5.11	Wild type	192	272	1719	407	2590	19.89	2.81	3.32			
5.11	Wild type	287	235	1539	417	2478	23.93	2.8	2.52			
5.11	Wild type	238	180	1346	342	2106	22.34	3.03	2.63			
5.11	Wild type	221	258	1409	363	2251	24.21	2.62	2.85			
5.11	Wild type	175	170	1099	270	1714	22.71	2.9	2.85	22.22	1.8	
5.11	Wild type	232	198	1489	343	2262	21.27	3.18	2.93			
5.11	Wild type	163	113	924	273	1473	20.93	2.82	2.38			
5.11	Wild type	204	180	1427	332	2143	19.9	3.19	3			
5.11	Wild type	258	189	1456	397	2300	21.81	2.92	2.51			
5.11	<i>hcr1-1</i>	240	204	1375	405	2224	22.49	2.65	2.45			
5.11	<i>hcr1-1</i>	244	204	1587	411	2446	20.4	2.98	2.73			
5.11	<i>hcr1-1</i>	228	213	1383	302	2126	23.51	3.13	3.01			
5.11	<i>hcr1-1</i>	206	265	1602	325	2398	22.08	3.06	3.52			
5.11	<i>hcr1-1</i>	157	147	980	257	1541	22.19	2.81	2.72	21.95	1.02	0.652
5.11	<i>hcr1-1</i>	205	193	1454	323	2175	20.37	3.22	3.12			
5.11	<i>hcr1-1</i>	236	223	1439	387	2285	22.65	2.75	2.67			
5.11	<i>hcr1-1</i>	232	234	1556	345	2367	22.14	3.09	3.1			
5.11	<i>hcr1-1</i>	256	188	1481	367	2292	21.73	3.13	2.68			
5.14	Wild type	97	75	1299	503	1974	9.13	2.42	2.29			
5.14	Wild type	112	82	1208	523	1925	10.64	2.18	2.03			
5.14	Wild type	64	91	1236	529	1920	8.43	2.1	2.24			
5.14	Wild type	91	74	1267	536	1968	8.77	2.23	2.14			
5.14	Wild type	65	49	902	355	1371	8.69	2.39	2.26			
5.14	Wild type	80	80	1229	464	1853	9.04	2.41	2.41	9.23	0.64	
5.14	Wild type	77	51	920	340	1388	9.69	2.55	2.33			
5.14	Wild type	82	72	1164	479	1797	8.97	2.26	2.2			
5.14	Wild type	84	103	1346	501	2034	9.66	2.37	2.48			
5.14	Wild type	85	90	1338	574	2087	8.77	2.14	2.17			
5.14	Wild type	69	99	1141	510	1819	9.71	1.99	2.14			
5.14	<i>hcr1-1</i>	91	84	1147	470	1792	10.3	2.23	2.19			
5.14	<i>hcr1-1</i>	88	101	1127	432	1748	11.47	2.28	2.36			
5.14	<i>hcr1-1</i>	82	94	1099	480	1755	10.59	2.06	2.12			
5.14	<i>hcr1-1</i>	94	82	1167	498	1841	10.07	2.17	2.11	11.92	1.31	8.33×10 ⁻⁷
5.14	<i>hcr1-1</i>	104	110	1284	510	2008	11.3	2.24	2.27			
5.14	<i>hcr1-1</i>	104	108	1335	492	2039	11	2.4	2.42			

5.14	<i>hcr1-1</i>	120	110	1330	511	2071	11.8	2.33	2.28			
5.14	<i>hcr1-1</i>	122	119	1186	468	1895	13.65	2.23	2.21			
5.14	<i>hcr1-1</i>	111	129	1112	470	1822	14.18	2.04	2.14			
5.14	<i>hcr1-1</i>	102	93	1161	486	1842	11.22	2.18	2.13			
5.14	<i>hcr1-1</i>	114	112	1243	464	1933	12.47	2.36	2.34			
5.14	<i>hcr1-1</i>	101	109	1172	453	1835	12.19	2.27	2.31			
5.14	<i>hcr1-1</i>	113	111	1136	498	1858	12.89	2.05	2.04			
5.14	<i>hcr1-1</i>	95	102	970	375	1542	13.72	2.23	2.28			

Supplementary Table 10. Seed-based FTL crossover frequency in wild type and *meiMIGS-PPX1-PPX2*. FTL crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from *FTL*/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized *FTL* hemizygote plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $cM=100 \times (1 - [1 - 2(N_{\text{Green}} + N_{\text{Red}}) / N_{\text{Total}}]^{1/2})^{3,4}$. *P* values were calculated using one-sided Welch's t-tests, which assessed significant differences between wild type and *meiMIGS-PPX1-PPX2*, in each seed based FTL line⁷.

CTL	Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
1.13	Wild type	316	299	2019	502	3136	22.04	2.92	2.83	23.11	0.96	
1.13	Wild type	321	363	2324	503	3511	21.87	3.05	3.26			
1.13	Wild type	305	374	2225	488	3392	22.56	2.94	3.28			
1.13	Wild type	361	366	2211	494	3432	24.08	2.99	3.01			
1.13	Wild type	275	338	1891	461	2965	23.42	2.71	3.03			
1.13	Wild type	385	353	2208	516	3462	24.26	2.98	2.84			
1.13	Wild type	394	290	2136	471	3291	23.56	3.32	2.8			
1.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	192	186	1093	257	1728	25	2.9	2.85	27.47	2.93	6.72×10^{-3}
1.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	176	166	834	186	1362	29.45	2.87	2.76			
1.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	217	197	1078	227	1719	28.01	3.05	2.87			
1.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	223	186	944	167	1520	32.04	3.31	2.9			
1.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	147	178	973	220	1518	24.38	2.81	3.14			
1.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	189	198	1083	244	1714	25.94	2.88	2.96			
1.22	Wild type	275	276	2057	502	3110	19.65	3	3	20.07	0.8	
1.22	Wild type	280	297	2075	524	3176	20.21	2.87	2.95			
1.22	Wild type	254	272	1835	461	2822	20.8	2.85	2.95			
1.22	Wild type	266	294	2011	523	3094	20.12	2.79	2.92			
1.22	Wild type	291	293	2016	483	3083	21.19	2.97	2.98			
1.22	Wild type	249	299	2011	521	3080	19.74	2.76	3			
1.22	Wild type	241	263	1960	500	2964	18.76	2.88	3			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	225	204	1275	282	1986	24.64	3.09	2.92	24.45	1.02	8.42×10^{-9}
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	215	208	1237	291	1951	24.74	2.91	2.86			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	209	189	1274	257	1929	23.36	3.33	3.14			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	173	185	1087	263	1708	23.79	2.81	2.92			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	203	206	1200	281	1890	24.69	2.88	2.9			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	202	204	1183	264	1853	25.05	2.96	2.98			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	266	265	1660	373	2564	23.46	3.02	3.01			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	257	247	1657	381	2542	22.32	3.05	2.98			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	261	268	1521	347	2397	25.26	2.9	2.94			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	256	240	1511	327	2334	24.17	3.12	3			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	280	261	1620	372	2533	24.31	3	2.88			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	269	260	1454	303	2286	26.71	3.06	3			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	260	268	1567	353	2448	24.59	2.94	2.99			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	239	259	1548	337	2383	23.71	3	3.14			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	242	267	1499	370	2378	24.38	2.73	2.89			
1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	289	262	1547	337	2435	26.01	3.07	2.89			

1.22	<i>meiMIGS-PPX1-PPX2 F₁</i>	239	278	1498	399	2414	24.39	2.57	2.78			
2.2	Wild type	221	227	1599	364	2411	20.73	3.08	3.12	21.66	0.52	
2.2	Wild type	197	199	1373	327	2096	21.12	2.98	3			
2.2	Wild type	220	225	1522	356	2323	21.46	3	3.03			
2.2	Wild type	239	235	1565	375	2414	22.07	2.96	2.93			
2.2	Wild type	249	248	1671	400	2568	21.71	2.96	2.96			
2.2	Wild type	244	249	1633	378	2504	22.14	2.99	3.03			
2.2	Wild type	231	219	1490	346	2286	22.13	3.05	2.96			
2.2	Wild type	208	211	1394	337	2150	21.88	2.92	2.94			
2.2	<i>meiMIGS-PPX1-PPX2 F₁</i>	210	222	1074	233	1739	29.07	2.82	2.93	26.89	1.98	1.71×10 ⁻³
2.2	<i>meiMIGS-PPX1-PPX2 F₁</i>	187	178	1096	230	1691	24.61	3.14	3.06			
2.2	<i>meiMIGS-PPX1-PPX2 F₁</i>	233	235	1317	293	2078	25.87	2.94	2.95			
2.2	<i>meiMIGS-PPX1-PPX2 F₁</i>	181	173	900	179	1433	28.87	3.07	2.98			
2.2	<i>meiMIGS-PPX1-PPX2 F₁</i>	171	164	944	201	1480	26.02	3.05	2.98			
2.7	Wild type	248	228	1767	500	2743	19.2	2.77	2.67	20.85	1	
2.7	Wild type	247	236	1784	488	2755	19.42	2.81	2.75			
2.7	Wild type	234	219	1546	365	2364	21.47	3.05	2.95			
2.7	Wild type	234	250	1662	396	2542	21.31	2.93	3.03			
2.7	Wild type	264	259	1759	437	2719	21.56	2.91	2.88			
2.7	Wild type	256	269	1756	414	2695	21.87	2.95	3.02			
2.7	Wild type	264	257	1749	501	2771	21.01	2.66	2.62			
2.7	Wild type	268	252	1745	506	2771	20.96	2.66	2.58			
2.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	208	203	1255	290	1956	23.86	2.97	2.93	24.6	0.85	3.75×10 ⁻⁶
2.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	192	196	1141	257	1786	24.8	2.94	2.98			
2.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	159	169	997	233	1558	23.91	2.88	2.97			
2.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	173	173	1048	252	1646	23.87	2.87	2.87			
2.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	166	176	982	221	1545	25.35	2.89	2.99			
2.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	194	189	1080	241	1704	25.81	2.96	2.92			
4.7	Wild type	301	270	2133	545	3249	19.47	2.99	2.84	18.67	0.88	
4.7	Wild type	308	307	2329	557	3501	19.46	3.05	3.05			
4.7	Wild type	268	301	2166	510	3245	19.42	3	3.17			
4.7	Wild type	278	311	2227	564	3380	19.29	2.86	3.01			
4.7	Wild type	270	279	2115	563	3227	18.78	2.83	2.87			
4.7	Wild type	188	241	1746	470	2645	17.8	2.72	3.02			
4.7	Wild type	258	282	2245	564	3349	17.69	2.96	3.07			
4.7	Wild type	267	272	2215	633	3387	17.43	2.74	2.76			
4.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	175	166	1075	335	1751	21.86	2.5	2.43	22.33	1.85	1.58×10 ⁻³
4.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	178	124	954	275	1531	22.19	2.84	2.38			
4.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	151	142	1035	290	1618	20.14	2.75	2.67			
4.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	185	133	1046	284	1648	21.64	2.95	2.51			
4.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	195	187	1032	290	1704	25.73	2.57	2.51			
4.7	<i>meiMIGS-PPX1-PPX2 F₁</i>	195	143	1070	291	1699	22.4	2.91	2.5			
5.1	Wild type	305	358	2320	615	3598	20.54	2.7	2.91	21.07	1.23	
5.1	Wild type	301	320	2074	483	3178	21.95	2.96	3.05			
5.1	Wild type	336	398	2563	623	3920	20.91	2.84	3.09			
5.1	Wild type	342	274	2133	544	3293	20.89	3.03	2.72			

5.1	Wild type	368	411	2517	548	3844	22.88	3.01	3.2			
5.1	Wild type	329	347	2578	627	3881	19.28	2.98	3.06			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	216	188	1191	281	1876	24.55	3	2.77	26.03	1.19	9.06×10 ⁻⁶
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	223	223	1272	280	1998	25.6	2.97	2.97			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	209	228	1251	282	1970	25.41	2.86	3.01			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	225	232	1234	277	1968	26.82	2.87	2.92			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	268	218	1164	297	1947	29.23	2.78	2.45			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	240	235	1326	295	2096	26.06	2.95	2.92			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	287	295	1669	360	2611	25.56	2.99	3.04			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	289	286	1609	330	2514	26.34	3.08	3.06			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	278	288	1692	396	2654	24.27	2.88	2.94			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	299	295	1608	331	2533	27.13	3.05	3.02			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	295	292	1682	389	2658	25.28	2.9	2.89			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	293	286	1640	353	2572	25.85	3.03	2.98			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	305	303	1655	357	2620	26.8	2.97	2.96			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	278	281	1586	344	2489	25.78	2.98	3			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	277	297	1672	369	2615	25.1	2.93	3.05			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	313	290	1728	392	2723	25.36	2.99	2.86			
5.1	<i>meiMIGS-PPX1-PPX2 F₁</i>	315	319	1684	365	2683	27.38	2.92	2.95			
5.5	Wild type	379	407	1842	374	3002	30.98	2.84	2.99	28.8	1.84	
5.5	Wild type	402	430	2078	439	3349	29.07	2.85	2.98			
5.5	Wild type	366	363	2040	443	3212	26.1	2.99	2.97			
5.5	Wild type	413	412	2124	433	3382	28.44	3	3			
5.5	Wild type	408	423	1922	376	3129	31.53	2.92	2.99			
5.5	Wild type	409	419	2079	428	3335	29.05	2.94	2.98			
5.5	Wild type	406	414	2230	480	3530	26.83	2.95	2.98			
5.5	Wild type	401	408	2077	431	3317	28.43	2.95	2.99	28.52	2.39	0.625
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	210	211	1101	266	1788	27.26	2.75	2.76			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	181	195	1167	304	1847	23	2.7	2.81			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	219	248	1070	257	1794	30.76	2.55	2.77			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	221	204	1146	249	1820	27	3.02	2.87			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	183	180	1034	232	1629	25.55	2.95	2.93			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	228	251	1136	283	1898	29.63	2.55	2.71			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	329	373	1576	307	2585	32.41	2.8	3.06			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	575	595	1316	72	2558	29.19	2.84	2.95			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	533	526	1214	34	2307	28.62	3.12	3.07			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	233	215	1180	224	1852	28.15	3.22	3.05			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	338	327	1576	300	2541	30.96	3.05	2.98			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	308	322	1612	338	2580	28.47	2.91	2.99			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	309	329	1454	291	2383	31.84	2.84	2.97			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	318	330	1662	305	2615	28.98	3.12	3.2			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	302	289	1622	319	2532	26.98	3.16	3.08			
5.5	<i>meiMIGS-PPX1-PPX2 F₁</i>	318	292	1644	319	2573	27.48	3.21	3.04			
5.13	Wild type	427	424	2169	431	3451	28.81	3.04	3.02	29.33	0.9	
5.13	Wild type	380	395	2055	436	3266	27.51	2.93	3			
5.13	Wild type	421	437	2135	433	3426	29.35	2.94	3.01			

5.13	Wild type	401	411	2040	419	3271	29.04	2.94	2.99			
5.13	Wild type	419	432	2054	423	3328	30.1	2.89	2.95			
5.13	Wild type	438	435	2111	410	3394	30.32	3.02	3			
5.13	Wild type	403	412	2019	411	3245	29.45	2.94	2.99			
5.13	Wild type	441	448	2166	430	3485	30.01	2.97	3			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	213	204	1001	198	1616	30.44	3.02	2.93			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	276	235	1083	177	1771	34.97	3.3	2.91			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	241	215	1086	187	1729	31.26	3.3	3.04			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	216	230	979	184	1609	33.25	2.89	3.02			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	274	281	1131	208	1894	35.66	2.87	2.93			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	241	232	1047	203	1723	32.85	2.96	2.88			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	283	288	1298	249	2118	32.12	2.94	2.98			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	237	242	1186	238	1903	29.53	2.96	3.01	32.33	1.76	1.87×10 ⁻⁵
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	237	222	1089	212	1760	30.83	3.06	2.92			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	276	275	1182	233	1966	33.71	2.87	2.86			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	458	476	1066	60	2060	30.53	2.84	2.98			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	252	261	1166	225	1904	32.09	2.92	2.99			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	247	262	1110	211	1830	33.39	2.87	3			
5.13	<i>meiMIGS-PPX1-PPX2 F₁</i>	237	307	1197	285	2026	31.96	2.42	2.88			

Supplementary Table 11. Pollen-based FTL crossover frequency in wild type and *meiMIGS-PPX1-PPX2*. Pollen-based FTL crossover frequency was measured by DeepTetrad using two or three-color FTL intervals that have two intervals (*i1* and *i2*) with four chromatids (1–4). The 12-tetrad possible classes are no recombination (A), single crossover interval 1 (B; SCO-*i1*), single crossover interval 2 (C; SCO-*i2*), two-strand double crossover (D; 2stDCO), three-strand double crossover a (E; 3st DCOa), three-strand double crossover b (F; 3st DCOb), four-strand double crossover (G; 4st DCO), non-parental ditype interval 1, non-crossover interval 2 (H; NPD-*i1* NCO-*i2*), non-crossover interval 1, non-parental ditype interval 2 (I; NCO-*i1* NPD-*i2*), non-parental ditype interval 1, single crossover interval 2 (J; NPD-*i1* SCO-*i2*), single crossover interval 1, non-parental ditype interval 2 (K; SCO-*i1* NPD-*i2*) and non-parental ditype interval 1, non-parental ditype interval 2 (L; NPD-*i1* NPD-*i2*)⁸. Fluorescent tetrad states were identified using DeepTetrad and crossover frequency (cM) was calculated using the Perkin's equations^{9,10}. *P* values were calculated using one-sided Welch's t-tests, which assessed significant differences between wild type and *meiMIGS-PPX1-PPX2* in each pollen-based FTL line⁸.

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	<i>l1b</i> cM	<i>l1c</i> cM	<i>l1bc</i> cM
Wild type	502	142	334	10	3	4	5	0	12	1	1	0	1014	8.43	21.45	28.94
Wild type	662	150	411	11	10	9	6	3	12	0	1	0	1275	8.04	20.59	27.73
Wild type	511	149	341	6	7	5	4	0	11	1	0	0	1035	8.55	20.77	28.65
Wild type	856	205	624	15	8	14	11	3	10	0	0	0	1746	7.76	20.96	28.49
Wild type	683	174	450	7	4	6	14	0	4	0	0	0	1342	7.64	18.82	27.65
Wild type	564	126	369	3	7	6	5	0	3	0	1	0	1084	6.83	19.1	25.69
Wild type	556	168	335	7	1	4	8	3	7	0	3	0	1092	9.57	19	28.34
Wild type	348	80	234	5	2	3	4	2	3	1	0	0	682	8.21	19.57	27.42
Mean														8.13	20.03	27.86
SD														0.8	1.03	1.03
<i>meiMIGS-PPX1-PPX2</i>	580	188	463	12	15	12	10	1	11	0	1	0	1293	9.44	22.58	31.36
<i>meiMIGS-PPX1-PPX2</i>	319	98	301	8	6	10	6	0	8	0	0	0	756	8.47	25.07	33
<i>meiMIGS-PPX1-PPX2</i>	710	215	570	16	18	9	15	2	11	0	2	0	1568	9.15	22.51	31.31
<i>meiMIGS-PPX1-PPX2</i>	311	114	266	19	9	16	8	0	7	1	0	0	751	11.45	24.03	33.02
<i>meiMIGS-PPX1-PPX2</i>	266	99	191	19	7	10	6	0	3	1	0	0	602	12.21	20.93	30.07
<i>meiMIGS-PPX1-PPX2</i>	486	151	397	18	16	17	9	1	15	2	2	0	1114	10.37	25.18	32.99
<i>meiMIGS-PPX1-PPX2</i>	301	113	238	12	14	14	13	1	10	0	2	1	719	12.52	25.66	36.51
Mean														10.51	23.71	32.61
SD														1.58	1.75	2.06
<i>P</i> value														3.03×10 ⁻³	3.85×10 ⁻⁴	2.19×10 ⁻⁴
Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	<i>l1f</i> cM	<i>l1g</i> cM	<i>l1fg</i> cM
Wild type	1060	138	45	1	0	0	1	1	0	0	1	0	1247	5.89	2.13	7.86
Wild type	1128	174	53	1	0	0	0	1	0	0	0	0	1357	6.67	1.99	8.59
Wild type	556	73	21	1	0	0	0	1	0	0	0	0	652	6.13	1.69	7.67
Wild type	772	103	38	1	0	0	0	0	0	0	0	0	914	5.69	2.13	7.71
Wild type	868	124	34	1	0	0	1	2	0	0	0	0	1030	6.7	1.75	8.54
Wild type	1027	163	47	0	0	1	0	0	0	0	0	0	1238	6.62	1.94	8.52
Wild type	900	121	34	3	0	0	0	1	0	0	0	0	1059	6.14	1.75	7.6
Wild type	775	110	31	1	1	0	0	0	0	0	0	0	918	6.1	1.8	7.73

Wild type	556	73	21	1	0	0	0	1	0	0	0	0	652	6.13	1.69	7.67
Mean														6.23	1.87	7.99
SD														0.36	0.18	0.43
<i>meiMIGS-PPX1-PPX2</i>	1079	159	52	1	4	1	1	3	0	0	0	0	1300	7.08	2.27	9.23
<i>meiMIGS-PPX1-PPX2</i>	516	107	22	1	0	0	0	0	0	0	0	0	646	8.36	1.78	9.98
<i>meiMIGS-PPX1-PPX2</i>	1382	236	53	4	0	2	1	0	0	0	0	0	1678	7.24	1.79	8.85
<i>meiMIGS-PPX1-PPX2</i>	1145	173	58	0	2	1	1	0	0	0	0	0	1381	6.41	2.24	8.69
<i>meiMIGS-PPX1-PPX2</i>	574	80	29	0	1	1	0	1	0	0	0	0	686	6.41	2.26	8.53
<i>meiMIGS-PPX1-PPX2</i>	458	72	19	2	0	0	0	2	0	0	0	0	553	7.78	1.9	9.31
<i>meiMIGS-PPX1-PPX2</i>	942	150	43	1	3	0	1	2	0	0	0	0	1142	7.31	2.1	9.37
<i>meiMIGS-PPX1-PPX2</i>	929	150	37	0	0	1	0	0	0	0	0	0	1117	6.76	1.7	8.42
Mean														7.17	2.01	9.05
SD														0.67	0.24	0.52
<i>P</i> value														2.52×10 ⁻³	0.114	2.45×10 ⁻⁴
Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	<i>I3b</i> cM	<i>I3c</i> cM	<i>I3bc</i> cM
Wild type	750	431	113	3	6	5	5	8	0	0	0	0	1321	18.85	5	23.96
Wild type	626	316	82	2	2	3	3	3	0	0	0	0	1037	16.59	4.44	21.17
Wild type	409	207	49	2	1	0	2	4	2	0	0	0	676	17.46	4.88	22.56
Wild type	1136	624	157	5	7	4	12	6	1	0	0	0	1952	17.62	4.89	23.21
Wild type	501	271	54	7	1	1	5	3	0	0	0	0	843	17.97	4.03	22.24
Wild type	504	264	57	6	1	5	1	5	0	1	0	0	844	18.54	4.21	21.56
Wild type	1042	559	132	3	4	7	6	10	1	0	0	0	1764	18.11	4.48	22.79
Wild type	378	184	39	1	3	3	0	5	1	0	0	0	614	18	4.23	21.58
Mean														17.89	4.52	22.38
SD														0.69	0.36	0.94
<i>meiMIGS-PPX1-PPX2</i>	516	338	101	19	9	7	6	9	2	0	0	0	1007	21.5	7.65	27.66
<i>meiMIGS-PPX1-PPX2</i>	478	366	88	16	7	7	5	5	0	0	0	0	972	22.17	6.33	27.16
<i>meiMIGS-PPX1-PPX2</i>	448	342	108	11	6	9	3	7	2	1	1	0	938	22.39	8.32	28.73
<i>meiMIGS-PPX1-PPX2</i>	701	580	167	12	9	10	6	18	2	2	1	0	1508	24.47	7.43	30.67
<i>meiMIGS-PPX1-PPX2</i>	472	309	77	9	6	9	6	6	2	1	2	0	899	21.3	7.34	27.14
<i>meiMIGS-PPX1-PPX2</i>	471	322	94	12	5	8	5	5	1	1	1	0	925	21.03	7.41	26.86
<i>meiMIGS-PPX1-PPX2</i>	548	384	139	11	6	10	5	6	2	1	2	0	1114	20.65	8.8	27.83
Mean														21.93	7.61	28.01
SD														1.28	0.79	1.33
<i>P</i> value														1.92×10 ⁻⁵	4.99×10 ⁻⁶	9.08×10 ⁻⁷
Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	<i>I5a</i> cM	<i>I5b</i> cM	<i>I5ab</i> cM
Wild type	256	213	108	8	8	13	8	6	1	0	0	0	621	23.03	12.16	34.78
Wild type	235	220	137	9	12	6	9	4	0	0	1	0	633	22.2	14.14	35.86
Wild type	320	303	159	13	6	8	10	4	3	0	1	0	827	22.07	13.3	35.01
Wild type	273	240	133	6	15	6	11	2	1	3	0	0	690	22.32	13.04	34.86
Wild type	254	214	109	8	8	13	8	6	1	0	0	0	621	23.11	12.24	34.94
Wild type	249	234	164	11	3	5	6	5	1	2	0	0	680	22.13	14.49	35.29

Wild type	470	434	250	16	15	16	12	11	2	1	2	0	1229	23.07	13.59	35.31
Wild type	202	205	119	5	4	6	4	7	0	0	0	0	552	24.09	12.5	36.23
Wild type	339	345	202	8	11	11	9	5	2	1	1	0	934	22.54	13.92	35.71
Mean														22.73	13.26	35.33
SD														0.66	0.84	0.5
<i>meiMIGS-PPX1-PPX2</i>	366	369	224	40	36	32	23	12	7	4	4	0	1117	26.86	19.02	41.23
<i>meiMIGS-PPX1-PPX2</i>	287	289	159	19	25	27	27	10	3	3	3	0	852	27.46	17.37	43.78
<i>meiMIGS-PPX1-PPX2</i>	260	246	118	24	25	20	20	12	0	6	0	0	731	30.3	14.57	41.52
<i>meiMIGS-PPX1-PPX2</i>	312	243	150	22	21	22	29	5	4	2	0	0	810	23.4	16.67	41.11
<i>meiMIGS-PPX1-PPX2</i>	307	363	224	25	38	46	37	13	2	4	1	0	1060	28.87	18.49	46.6
<i>meiMIGS-PPX1-PPX2</i>	368	484	267	69	41	43	35	22	6	10	2	0	1347	32.15	19.04	45.47
<i>meiMIGS-PPX1-PPX2</i>	280	290	166	33	22	27	23	19	4	8	0	0	872	31.94	17.37	45.24
Mean														28.71	17.51	43.56
SD														3.11	1.58	2.29
<i>P</i> value														1.00×10^{-3}	7.28×10^{-5}	2.75×10^{-5}

Supplementary Table 12. *CEN3* crossover frequency in wild type and *meiMIGS-PPX1-PPX2*. Pollen-based FTL *CEN3* crossover frequency is measured by DeepTetrad using two FTL intervals. Two color-FTL interval (*CEN3*) produces parental ditype (PD), tetra type (T), and non-parental ditype (NPD) tetrads. Fluorescent tetrad states were identified using DeepTetrad and crossover frequency (cM) was calculated using the Perkin's equations^{9,10}. The *P* value was calculated using a one-sided Welch's t-test, which assessed significant differences between wild type and *meiMIGS-PPX1-PPX2*⁸.

Genotype	NPD	T	Total	<i>CEN3</i> cM
Wild type	2	326	1282	13.18
Wild type	6	287	1297	12.45
Wild type	5	173	782	12.98
Wild type	2	157	741	11.40
Wild type	4	317	1340	12.72
Wild type	1	185	754	12.67
Wild type	4	355	1465	12.94
Wild type	0	276	1056	13.07
Wild type	2	198	875	12.00
Mean				12.60
SD				0.58
<i>meiMIGS-PPX1-PPX2</i>	9	488	2202	12.31
<i>meiMIGS-PPX1-PPX2</i>	6	298	1995	8.37
<i>meiMIGS-PPX1-PPX2</i>	10	513	2306	12.42
<i>meiMIGS-PPX1-PPX2</i>	7	446	2261	10.79
<i>meiMIGS-PPX1-PPX2</i>	9	456	2203	11.58
<i>meiMIGS-PPX1-PPX2</i>	7	495	2316	11.59
<i>meiMIGS-PPX1-PPX2</i>	4	223	1183	10.44
<i>meiMIGS-PPX1-PPX2</i>	7	339	1829	10.42
Mean				10.99
SD				1.31
<i>P</i> value				4.53×10^{-3}

Supplementary Table 13. 420 crossover frequency of male and female meiosis in wild type, *hcr1-1* and *meiMIGS-PPX1-PPX2*. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. Genetic distances of 420 male and female meiosis were separately measured by reciprocally crossing wild type, *hcr1-1* and *meiMIGS-PPX1-PPX2* of 420 hemizygote plants with wild type plants. CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $\text{cM} = 100 \times (N_{\text{Green}} + N_{\text{Red}}) / N_{\text{Total}}$. *P* values were calculated using one-sided Welch's t-tests, which assessed significant differences between wild type, *hcr1-1* and *meiMIGS-PPX1-PPX2*⁷.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Col male	93	89	278	329	789	23.07	0.89	0.87	24.23	1.68	
Col male	76	60	201	236	573	23.73	0.94	0.84			
Col male	51	50	143	142	386	26.17	1.01	1.00			
Col male	122	125	348	362	957	25.81	0.98	0.97			
Col male	71	82	265	266	684	22.37	0.97	1.03			
<i>hcr1-1</i> male	94	110	73	64	341	40.18	0.96	1.16	41.69	2.20	6.25×10^{-7}
<i>hcr1-1</i> male	207	209	124	140	680	38.82	0.95	0.96			
<i>hcr1-1</i> male	138	181	185	214	718	44.43	0.82	1.04			
<i>hcr1-1</i> male	281	287	375	391	1334	42.58	0.99	0.97			
<i>hcr1-1</i> male	215	218	279	308	1020	42.45	0.94	0.95			
<i>meiMIGS-PPX1-PPX2</i> male	126	152	247	274	799	34.79	0.88	1.00	36.93	1.66	2.15×10^{-7}
<i>meiMIGS-PPX1-PPX2</i> male	216	213	374	348	1151	37.27	1.05	1.04			
<i>meiMIGS-PPX1-PPX2</i> male	210	242	377	318	1147	39.41	1.05	1.17			
<i>meiMIGS-PPX1-PPX2</i> male	183	181	301	330	995	36.58	0.94	0.95			
<i>meiMIGS-PPX1-PPX2</i> male	167	194	297	329	987	36.58	0.89	0.99			
Col female	32	38	304	334	708	9.89	0.93	0.90	10.98	1.94	
Col female	35	41	315	276	667	11.39	1.14	1.10			
Col female	56	30	329	281	696	12.36	1.07	1.24			
Col female	37	31	391	367	826	8.23	1.04	1.08			
Col female	69	58	420	426	973	13.05	0.97	1.01			
<i>hcr1-1</i> female	50	39	231	253	573	15.53	0.89	0.96	15.79	1.29	2.81×10^{-3}
<i>hcr1-1</i> female	50	65	285	276	676	17.01	1.07	0.98			
<i>hcr1-1</i> female	36	47	250	274	607	13.67	0.96	0.89			
<i>hcr1-1</i> female	72	67	358	351	848	16.39	1.00	1.03			
<i>hcr1-1</i> female	80	71	392	381	924	16.34	1.00	1.04			
<i>meiMIGS-PPX1-PPX2</i> female	29	42	169	170	410	17.32	1.06	0.93	17.22	2.65	1.75×10^{-3}
<i>meiMIGS-PPX1-PPX2</i> female	54	47	306	262	669	15.10	1.12	1.17			
<i>meiMIGS-PPX1-PPX2</i> female	46	55	307	303	711	14.21	1.04	0.99			
<i>meiMIGS-PPX1-PPX2</i> female	45	54	234	193	526	18.82	1.21	1.13			
<i>meiMIGS-PPX1-PPX2</i> female	56	59	243	198	556	20.68	1.19	1.16			

Supplementary Table 14. Crossover interference measurements in wild type, *meiMIGS-PPX1-PPX2* and *hcr1* mutants. DeepTetrad, a deep learning based tetrad analyzer, was used with three-color FTL interval pollen (*I1bc*, *Ifg*, *I3bc*, *I5ab*) to measure crossover frequency (cM) and interference ratio (IFR) in two linked intervals^{8,9}. Crossover interference ratio (IFR) is the ratio of the map distance with adjacent crossover (*w_adj_CO*) to the map distance without adjacent crossover (*w/o_adj_CO*). *P* values were calculated using Welch's t-tests, to assess significance between wild type and genotypes.

Genotype	Col	Col	Col	Col	Mean	SD	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	Mean	SD	<i>P</i>															
A	1013	1204	1218	1247			846	620	1021	486			3.05 ×10 ⁻³															
B	291	285	318	300			287	211	329	151				3.05 ×10 ⁻³														
C	675	858	746	819			654	539	836	397					3.05 ×10 ⁻³													
D	16	20	18	10			31	20	35	18						3.05 ×10 ⁻³												
E	10	10	11	11			22	20	27	16							3.05 ×10 ⁻³											
F	9	17	13	12			22	24	25	17								3.05 ×10 ⁻³										
G	9	15	14	19			16	19	23	9									3.05 ×10 ⁻³									
H	0	5	6	0			1	1	2	1										3.05 ×10 ⁻³								
I	23	13	19	7			14	18	18	15											3.05 ×10 ⁻³							
J	2	1	0	0			1	0	1	2												3.05 ×10 ⁻³						
K	1	0	4	1			1	2	2	2													3.05 ×10 ⁻³					
L	0	0	0	0			0	1	0	0														3.05 ×10 ⁻³				
Total	2049	2428	2367	2426			1895	1475	2319	1114															3.05 ×10 ⁻³			
<i>I1b</i> (cM)	8.49	7.89	8.75	7.28	8.10	0.66	10.32	10.44	9.90	10.37	10.26	0.24														3.05 ×10 ⁻³		
<i>I1c</i> (cM)	21.11	20.57	19.86	18.94	20.12	0.94	22.06	25.36	23.01	25.18	23.90	1.63															3.05 ×10 ⁻³	
<i>I1bc</i> (cM)	28.79	28.19	28.01	26.77	27.94	0.85	30.95	34.71	31.87	32.99	32.63	1.62																3.05 ×10 ⁻³
<i>w/o_adj_CO</i>	0.11	0.11	0.11	0.10	0.11	0.01	0.13	0.13	0.13	0.12	0.13	0.00																
<i>w_adj_CO</i>	0.04	0.04	0.04	0.03	0.04	0.00	0.06	0.07	0.06	0.08	0.07	0.01	3.05 ×10 ⁻³															
IFR	0.34	0.35	0.32	0.31	0.33	0.02	0.50	0.54	0.48	0.63	0.54	0.07		3.05 ×10 ⁻³														
Genotype	Col	Col	Col	Col	Mean	SD	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	Mean	SD			<i>P</i>													
A	2188	1672	1980	1802			1595	2311	1032	2087					1.1 ×10 ⁻³													
B	312	224	270	273			266	386	152	323						1.1 ×10 ⁻³												
C	98	72	76	78			74	90	48	101							1.1 ×10 ⁻³											
D	2	4	3	1			2	4	2	1								1.1 ×10 ⁻³										
E	0	0	0	1			4	0	1	5									1.1 ×10 ⁻³									
F	0	0	0	1			1	3	1	1										1.1 ×10 ⁻³								
G	1	0	1	0			1	1	0	2											1.1 ×10 ⁻³							
H	2	1	4	0			3	0	3	2												1.1 ×10 ⁻³						
I	0	0	0	0			0	0	0	0													1.1 ×10 ⁻³					
J	0	0	0	0			0	0	0	0														1.1 ×10 ⁻³				
K	1	0	0	0			0	0	0	0															1.1 ×10 ⁻³			
L	0	0	0	0			0	0	0	0																1.1 ×10 ⁻³		
Total	2604	1973	2334	2156			1946	2795	1239	2523																	1.1 ×10 ⁻³	
<i>I1f</i> (cM)	6.3	5.93	6.38	6.4	6.25	0.22	7.5	7.05	7.02	6.82	7.1	0.29																1.1 ×10 ⁻³
<i>I1g</i> (cM)	2.05	1.93	1.71	1.88	1.89	0.14	2.11	1.75	2.1	2.18	2.03	0.19	1.1 ×10 ⁻³															
<i>I1fg</i> (cM)	8.24	7.65	8.05	8.19	8.03	0.27	9.48	8.68	8.88	9	9.01	0.34		1.1 ×10 ⁻³														
<i>w/o_adj_CO</i>	0.06	0.06	0.07	0.07	0.07	0.01	0.08	0.07	0.07	0.07	0.07	0.01																
<i>w_adj_CO</i>	0.02	0.03	0.03	0.02	0.03	0.01	0.05	0.04	0.04	0.04	0.04	0			1.1 ×10 ⁻³													
IFR	0.3	0.43	0.38	0.28	0.35	0.07	0.64	0.57	0.54	0.59	0.58	0.04				1.1 ×10 ⁻³												
Genotype	Col	Col	Col	Col	Mean	SD	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	Mean	SD					<i>P</i>											
A	1545	1254	1127	1420			964	1173	1019	478																		
B	831	695	587	743			680	889	706	366																		

C	206	170	136	171			209	244	233	88				
D	7	9	9	4			30	21	23	16				
E	8	7	3	7			15	15	11	7				
F	4	10	4	10			16	19	18	7				
G	14	6	8	6			9	12	10	5				
H	10	13	6	15			16	24	11	5				
I	3	0	0	2			4	4	3	0				
J	0	1	0	0			1	3	2	0				
K	0	0	0	0			1	3	3	0				
L	0	0	0	0			0	0	0	0				
Total	2628	2165	1880	2378			1945	2407	2039	972				
<i>I3b</i> (cM)	17.58	18.73	17.21	18.08	17.9	0.66	21.93	23.29	20.82	22.17	22.05	1.01		
<i>I3c</i> (cM)	4.89	4.69	4.26	4.42	4.57	0.28	7.97	7.4	8.17	6.33	7.47	0.82		
<i>I3bc</i> (cM)	23.04	23.03	21.65	22.48	22.55	0.65	28.17	29.35	27.39	27.16	28.02	0.99		
w/o_adj_CO	0.19	0.2	0.18	0.19	0.19	0.01	0.23	0.25	0.22	0.23	0.23	0.01		
w_adj_CO	0.07	0.09	0.08	0.07	0.08	0.01	0.14	0.14	0.13	0.14	0.14	0.01		
IFR	0.37	0.48	0.41	0.35	0.4	0.06	0.58	0.55	0.57	0.61	0.58	0.02		
2.3 ×10 ⁻³														
Genotype	Col	Col	Col	Col	Mean	SD	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	<i>meiMIGS-PPX1-PPX2</i>	Mean	SD		<i>P</i>
A	576	593	484	945			599	567	648	366				
B	516	559	454	879			532	609	774	369				
C	267	311	301	502			309	342	433	224				
D	21	16	20	27			41	49	102	40				
E	14	19	15	34			46	63	63	36				
F	21	24	11	28			49	66	70	32				
G	18	17	15	27			56	57	58	23				
H	10	11	9	20			15	25	41	12				
I	4	3	1	3			7	2	10	7				
J	0	1	2	4			5	10	18	4				
K	1	1	1	2			3	1	2	4				
L	0	0	0	0			0	0	0	0				
Total	1448	1555	1313	2471			1662	1791	2219	1117				
<i>I5a</i> (cM)	22.48	22.77	22.16	23.09	22.62	0.4	25.48	29.45	32.06	26.86	28.46	2.91		
<i>I5b</i> (cM)	12.81	13.25	14.32	13.19	13.39	0.65	17.03	16.89	18.39	19.02	17.83	1.04		
<i>I5ab</i> (cM)	34.91	35.4	35.57	35.39	35.32	0.28	42.48	44.53	45.38	41.23	43.4	1.89		
w/o_adj_CO	0.26	0.27	0.27	0.27	0.27	0.01	0.27	0.32	0.35	0.3	0.31	0.03		
w_adj_CO	0.11	0.11	0.1	0.11	0.11	0.01	0.22	0.25	0.27	0.21	0.24	0.03		
IFR	0.41	0.39	0.38	0.42	0.4	0.02	0.8	0.79	0.76	0.73	0.77	0.03		
3.9 ×10 ⁻⁶														
Genotype	Col	Col	Col	Col	Mean	SD	<i>hcr1-1</i>	<i>hcr1-1</i>	<i>hcr1-1</i>	<i>hcr1-1</i>	Mean	SD		<i>P</i>
A	731	570	528	893			441	435	392	521				
B	180	138	115	258			154	152	134	171				
C	439	364	356	615			338	411	314	404				
D	17	5	7	13			16	11	18	27				
E	4	6	7	16			16	22	12	15				
F	11	7	10	14			12	12	13	16				
G	3	6	2	11			9	9	11	13				
H	5	0	2	1			3	0	3	4				
I	9	6	9	9			10	12	10	12				
J	1	0	0	0			1	0	0	0				
K	1	0	0	2			1	2	0	0				
L	0	0	0	0			0	0	0	0				
Total	1401	1102	1036	1832			1001	1066	907	1183				
<i>I1b</i> (cM)	8.99	7.35	7.38	8.73	7.91	0.94	11.59	9.76	11.36	11.24	10.99	0.83		
<i>I1c</i> (cM)	19.09	19.24	21.04	20.06	19.79	1.09	22.88	25.75	23.59	23.12	23.84	1.31		
<i>I1bc</i> (cM)	26.34	26.63	27.32	28.14	26.76	0.5	32.67	34.01	34.01	32.97	33.41	0.7		
0.27 ×10 ⁻³														

w/o_adj_C O	0.11	0.1	0.1	0.11	0.1	0.01	0.14	0.13	0.14	0.14	0.14	0.01	
w_adj_CO	0.04	0.03	0.03	0.04	0.04	0.01	0.07	0.06	0.07	0.07	0.07	0.07	0.01
IFR	0.38	0.31	0.34	0.36	0.34	0.03	0.52	0.45	0.5	0.52	0.5	0.03	
Genotype	Col	Col	Col	Col	Mean	SD	<i>hcr1-1</i>	<i>hcr1-1</i>	<i>hcr1-1</i>	<i>hcr1-1</i>	Mean	SD	<i>P</i>
A	879	670	766	815			479	614	396	560			8.1 ×10 ⁻³
B	458	332	353	366			391	480	349	515			
C	111	74	94	87			127	175	86	146			
D	5	3	4	5			8	17	7	17			
E	6	5	4	1			11	15	8	14			
F	3	4	1	4			8	11	9	15			
G	2	2	4	1			5	14	11	13			
H	7	3	4	5			10	17	11	21			
I	2	2	1	1			3	2	1	1			
J	1	0	0	0			1	1	1	1			
K	0	0	0	0			2	3	0	0			
L	0	0	0	0			0	0	0	0			
Total	1474	1095	1231	1285			1045	1349	879	1303			
<i>I3b</i> (cM)	17.71	16.62	15.84	15.84	16.5	0.88	23.49	24.02	25.94	27.09	25.14	1.68	
<i>I3c</i> (cM)	4.75	4.57	4.59	4.05	4.49	0.31	9.09	9.75	7.28	8.14	8.56	1.08	
<i>I3bc</i> (cM)	21.88	20.87	20.55	19.46	20.69	1	31	32.73	33.62	34.57	32.98	1.52	
w/o_adj_C O	0.19	0.17	0.17	0.17	0.17	0.01	0.26	0.26	0.27	0.29	0.27	0.02	
w_adj_CO	0.08	0.08	0.06	0.06	0.07	0.01	0.12	0.14	0.17	0.16	0.15	0.02	
IFR	0.45	0.45	0.36	0.33	0.4	0.06	0.47	0.53	0.61	0.54	0.54	0.06	

Supplementary Table 15. 420 crossover frequency in wild type and *meiMIGS-PPX1-PPX2* Col/Ler F₁ hybrids. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $cM = 100 \times (1 - [1 - 2(N_{Green} + N_{Red})/N_{Total}]^{1/2})^{3,4}$. To test for significant differences between wild type and *meiMIGS-PPX1-PPX2*, a *P* value was calculated using a one-sided Welch's t-test.

Genotype	Green	Red	Both	None	Total	cM	G/Ng	R/nR	Mean	SD	<i>P</i> value
Wild type Col/Ler	143	146	1471	387	2147	14.51	3.03	3.05	13.45	0.9	
Wild type Col/Ler	134	106	1358	358	1956	13.13	3.22	2.98			
Wild type Col/Ler	116	94	1295	356	1861	12	3.14	2.94			
Wild type Col/Ler	157	122	1461	398	2138	14.03	3.11	2.85			
Wild type Col/Ler	110	150	1353	385	1998	13.99	2.73	3.04			
Wild type Col/Ler	148	121	1453	360	2082	13.88	3.33	3.1			
Wild type Col/Ler	82	89	998	282	1451	12.58	2.91	2.99			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	207	169	1345	296	2017	20.81	3.34	3.01	21.17	1.56	6.55×10 ⁻¹¹
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	204	219	1319	316	2058	23.26	2.85	2.96			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	194	172	1286	326	1978	20.63	2.97	2.8			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	200	201	1307	308	2016	22.4	2.96	2.97			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	147	150	1212	310	1819	17.94	2.95	2.98			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	178	185	1299	318	1980	20.42	2.94	2.99			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	175	169	1257	300	1901	20.12	3.05	3			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	165	181	1076	254	1676	23.38	2.85	3			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	137	144	1030	257	1568	19.9	2.91	2.98			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	150	154	984	242	1530	22.37	2.86	2.9			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	152	149	1011	245	1557	21.68	2.95	2.92			
<i>meiMIGS-PPX1-PPX2</i> Col/Ler F ₁	138	158	1011	258	1565	21.15	2.76	2.95			

Supplementary Table 16. Crossover numbers identified by sequencing wild type and *meiMIGS-PPX1-PPX2* Col/Ler F₂ populations.

	Wild type	<i>meiMIGS-PPX1-PPX2</i>
Total crossovers	1,132	1,645
Chr1 crossovers	271	395
Chr2 crossovers	193	281
Chr3 crossovers	220	323
Chr4 crossovers	187	262
Chr5 crossovers	261	384
Individuals	144	192
Crossovers width (bp)	962	936
Crossovers/F ₂	7.86	8.57

Supplementary Table 17. Pollen viability in wild type, *hcr1-1*, *hcr1-2*, *ppx2-1* and *pp4r2* mutants measured using Alexander staining. Alexander staining of pollen was performed to measure pollen viability. Significance between wild type and mutant measurements were assessed by one-sided Welch's t-tests.

Genotype	Plant	Viable	Inviabile	Total	% Viable	% Inviabile	<i>P</i> value
Wild type	1	1180	7	1187	99.41	0.59	
Wild type	2	1130	6	1136	99.47	0.53	
Wild type	3	1204	6	1210	99.50	0.50	
Wild type	4	1002	6	1008	99.40	0.60	
Wild type	5	1191	56	1247	95.51	4.49	
Wild type	6	1121	0	1121	100.00	0.00	
<i>hcr1-1</i>	1	1109	0	1109	100.00	0.00	0.126
<i>hcr1-1</i>	2	1152	0	1152	100.00	0.00	
<i>hcr1-1</i>	3	1288	1	1289	99.92	0.08	
<i>hcr1-1</i>	4	1147	6	1153	99.48	0.52	
<i>hcr1-1</i>	5	1153	9	1162	99.23	0.77	
<i>hcr1-1</i>	6	1068	0	1068	100.00	0.00	
<i>hcr1-2</i>	1	1092	2	1094	99.82	0.18	0.121
<i>hcr1-2</i>	2	1081	4	1085	99.63	0.37	
<i>hcr1-2</i>	3	1012	4	1016	99.61	0.39	
<i>hcr1-2</i>	4	1348	0	1348	100.00	0.00	
<i>hcr1-2</i>	5	1407	1	1408	99.93	0.07	
<i>hcr1-2</i>	6	1093	3	1096	99.73	0.27	
<i>ppx2-1</i>	1	1085	0	1085	100.00	0.00	0.140
<i>ppx2-1</i>	2	1106	11	1117	99.02	0.98	
<i>ppx2-1</i>	3	955	0	955	100.00	0.00	
<i>ppx2-1</i>	4	1336	0	1336	100.00	0.00	
<i>ppx2-1</i>	5	1194	0	1194	100.00	0.00	
<i>ppx2-1</i>	6	1015	7	1022	99.32	0.68	
<i>pp4r2</i>	1	1068	0	1068	100.00	0.00	0.094
<i>pp4r2</i>	2	1067	5	1072	99.53	0.47	
<i>pp4r2</i>	3	1022	0	1022	100.00	0.00	
<i>pp4r2</i>	4	1141	0	1141	100.00	0.00	
<i>pp4r2</i>	5	1258	0	1258	100.00	0.00	
<i>pp4r2</i>	6	1023	0	1023	100.00	0.00	

Supplementary Table 18. RAD51 foci number per cell in wild type and *hcr1*. To test for significant differences in RAD51 foci number between wild type and *hcr1-1*, *P* values were calculated using a Wilcoxon test.

	Wild type	<i>hcr1-1</i>
	193	193
	140	140
	153	153
	139	139
	167	167
	164	164
	155	155
	129	129
	177	177
	129	129
	136	136
	143	143
	142	142
	149	149
Mean	151 (n=14)	145 (n=14)
SD	18.5	21.4
<i>P</i> value		0.32

Supplementary Table 19. MLH1 foci number per cell in wild type and *hcr1*. To test for significant differences in MLH1 foci numbers between wild type and *hcr1-1*, *P* values were calculated using a Wilcoxon test.

Total MLH1 foci in wild type	Total MLH1 foci in <i>hcr1-1</i>
12	14
11	10
12	14
9	11
10	13
9	12
10	13
9	12
11	14
11	12
9	12
12	14
11	10
12	12
8	15
10	12
9	9
11	13
12	11
12	12
10	11
10	9
11	11
9	14
10	11
11	12
9	9
13	12
10	10
9	14
9	12
11	13
10	10
9	12
10	13

	9	11
	10	14
	10	14
	8	9
	11	14
	10	11
	10	12
	12	11
	11	11
	13	12
	12	14
	12	14
	12	15
	11	13
	10	13
	9	
Mean	10.4 (n=51)	12.1 (n=50)
SD	1.3	1.6
<i>P</i> value		5.3×10^{-7}

Supplementary Table 20. MLH1 foci at diakinesis cells in Col and *meiMIGS-PPX1-PPX2*.
 To test for significant differences in MLH1 foci numbers between wild type and *meiMIGS-PPX1-PPX2*, *P* values were calculated using a Wilcoxon test.

	Wild type (Col)	<i>meiMIGS-PPX1-PPX2</i>
	11	15
	12	12
	9	14
	12	12
	11	12
	11	16
	11	13
	12	16
	12	13
	11	12
	10	13
	11	15
	11	11
	13	10
	12	13
	10	12
	11	13
	12	14
	9	13
	13	13
	10	14
	9	13
	8	11
	10	14
	9	11
	9	11
	9	12
		13
		12
		12
Mean	10.7	12.8
SD	1.4	1.5
<i>P</i>		2.5×10^{-6}

Supplementary Table 21. Chiasma, univalent and bivalent counts from meiotic chromosome spreads in wild type (Col), *zip4* and *zip4 hcr1*. To test for significant differences in bivalent counts between wild type, *zip4* and *zip4 hcr1*, *P* values were calculated using a Wilcoxon test.

Genotype	Chiasma	Bivalents	Univalents
Col	11	5	0
Col	9	5	0
Col	10	5	0
Col	9	5	0
Col	9	5	0
Col	10	5	0
Col	10	5	0
Col	10	5	0
Col	10	5	0
Col	10	5	0
Col	10	5	0
Col	9	5	0
Col	11	5	0
Col	11	5	0
Col	10	5	0
Col	11	5	0
Col	10	5	0
Col	10	5	0
Col	10	5	0
Col	11	5	0
Col	10	5	0
Col	10	5	0
Col	9	5	0
Col	11	5	0
Col	11	5	0
Col	9	5	0
Col	11	5	0
Col	9	5	0
Mean	10.04	5	0
<i>zip4</i>	2	2	6
<i>zip4</i>	1	1	8
<i>zip4</i>	2	1	8
<i>zip4</i>	1	1	8
<i>zip4</i>	0	0	10
<i>zip4</i>	2	1	8
<i>zip4</i>	2	1	8
<i>zip4</i>	2	2	6
<i>zip4</i>	0	0	10

<i>zip4</i>	1	1	8
<i>zip4</i>	3	2	6
<i>zip4</i>	1	1	8
<i>zip4</i>	1	1	8
<i>zip4</i>	0	0	10
<i>zip4</i>	0	0	10
<i>zip4</i>	2	2	6
<i>zip4</i>	0	0	10
<i>zip4</i>	1	1	8
<i>zip4</i>	2	2	6
<i>zip4</i>	0	0	10
<i>zip4</i>	0	0	10
<i>zip4</i>	0	0	10
<i>zip4</i>	1	1	8
<i>zip4</i>	0	0	10
<i>zip4</i>	1	1	8
<i>zip4</i>	1	0	10
<i>zip4</i>	2	1	8
<i>zip4</i>	0	0	10
<i>zip4</i>	1	0	10
<i>zip4</i>	2	2	6
<i>zip4</i>	1	1	8
<i>zip4</i>	0	0	10
Mean	1.00	0.8	8.44
<i>P</i> value (Col vs <i>zip4</i>)		5.22×10^{-12}	
<i>zip4 hcr1</i>	2	2	6
<i>zip4 hcr1</i>	2	2	6
<i>zip4 hcr1</i>	0	0	10
<i>zip4 hcr1</i>	2	2	6
<i>zip4 hcr1</i>	0	0	10
<i>zip4 hcr1</i>	0	0	10
<i>zip4 hcr1</i>	2	2	6
<i>zip4 hcr1</i>	0	0	10
<i>zip4 hcr1</i>	1	0	10
<i>zip4 hcr1</i>	1	0	10
<i>zip4 hcr1</i>	2	2	6
<i>zip4 hcr1</i>	3	3	4
<i>zip4 hcr1</i>	2	1	8
<i>zip4 hcr1</i>	1	1	8
<i>zip4 hcr1</i>	2	1	8
<i>zip4 hcr1</i>	1	1	8

<i>zip4 hcr1</i>	3	2	6
<i>zip4 hcr1</i>	3	2	6
<i>zip4 hcr1</i>	1	0	10
<i>zip4 hcr1</i>	4	3	4
<i>zip4 hcr1</i>	0	0	10
<i>zip4 hcr1</i>	0	0	10
<i>zip4 hcr1</i>	4	3	4
<i>zip4 hcr1</i>	2	2	6
<i>zip4 hcr1</i>	1	1	8
<i>zip4 hcr1</i>	1	1	8
<i>zip4 hcr1</i>	5	4	2
<i>zip4 hcr1</i>	0	0	10
<i>zip4 hcr1</i>	2	2	6
Mean	1.62	1.3	7.45
<i>P</i> value (Col vs <i>zip4 hcr1</i>)		1.43×10^{-11}	
<i>P</i> value (<i>zip4</i> vs <i>zip4 hcr1</i>)	0.075	0.11	

Supplementary Table 22. 420 crossover frequency (cM) in wild type, *hcr1*, *fancm*, *fancm zip4*, *hcr1 fancm* and *hcr1 fancm zip4* mutants. 420 crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from 420/++ hemizygote plants, using CellProfiler^{1,2}. In the seeds from self-fertilized 420/++ plants, CellProfiler determines the numbers of green-alone fluorescent seeds (N_{Green}), red-alone fluorescent seeds (N_{Red}) and total seeds (N_{Total}). Crossover frequency (cM) is calculated using the formula: $\text{cM} = 100 \times (1 - [1 - 2(N_{\text{Green}} + N_{\text{Red}}) / N_{\text{Total}}]^{1/2})^{3,4}$. To test for significant differences between genotypes, *P* values were calculated using one-sided Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	<i>P</i> value
Wild type	196	176	1463	367	2202	18.63	3.06	2.91	19.01	1.2	
Wild type	160	174	1457	363	2154	16.94	3.01	3.12			
Wild type	184	190	1536	369	2279	18.04	3.08	3.12			
Wild type	164	169	1320	313	1966	18.68	3.08	3.12			
Wild type	223	190	1435	344	2192	21.06	3.1	2.87			
Wild type	178	190	1443	249	2060	19.83	3.69	3.82			
Wild type	193	151	1384	317	2045	18.54	3.37	3.01			
Wild type	145	146	1067	263	1621	19.94	2.96	2.97			
Wild type	191	165	1344	333	2033	19.39	3.08	2.88			
<i>hcr1</i>	219	167	1120	266	1772	24.88	3.09	2.65	24.48	0.87	Between wild type and <i>hcr1</i> = 1.24×10^{-8}
<i>hcr1</i>	188	176	1016	241	1621	25.78	2.89	2.78			
<i>hcr1</i>	164	133	897	204	1398	24.16	3.15	2.8			
<i>hcr1</i>	201	202	1306	271	1980	23	3.19	3.19			
<i>hcr1</i>	255	202	1332	287	2076	25.18	3.25	2.83			
<i>hcr1</i>	189	155	1036	224	1604	24.43	3.23	2.88			
<i>hcr1</i>	186	190	1143	279	1798	23.73	2.83	2.87			
<i>hcr1</i>	164	194	1046	251	1655	24.68	2.72	2.99			
<i>fancm</i>	174	155	710	146	1185	33.31	2.94	2.7	34.52	1.92	Between wild type and <i>fancm</i> = 1.54×10^{-10}
<i>fancm</i>	173	152	738	156	1219	31.68	2.96	2.71			
<i>fancm</i>	206	209	800	165	1380	36.87	2.69	2.72			
<i>fancm</i>	218	190	830	152	1390	35.74	3.06	2.76			
<i>fancm</i>	134	150	537	135	956	36.29	2.35	2.55			
<i>fancm</i>	212	215	961	179	1567	32.55	2.98	3.01			
<i>fancm</i>	319	277	1218	213	2027	35.82	3.14	2.81			
<i>fancm</i>	224	250	979	232	1685	33.86	2.5	2.7			
<i>hcr1 fancm</i>	189	183	672	109	1153	40.44	2.95	2.87	40.32	1.56	Between <i>hcr1</i> and <i>hcr1 fancm</i> = 2.7×10^{-11} Between <i>fancm</i> and <i>hcr1 fancm</i> = 6.77×10^{-6}
<i>hcr1 fancm</i>	232	209	814	121	1376	40.08	3.17	2.9			
<i>hcr1 fancm</i>	276	270	1048	161	1755	38.54	3.07	3.02			
<i>hcr1 fancm</i>	246	250	932	131	1559	39.69	3.09	3.14			
<i>hcr1 fancm</i>	263	269	892	138	1562	43.54	2.84	2.9			
<i>hcr1 fancm</i>	309	257	1077	156	1799	39.11	3.36	2.87			
<i>hcr1 fancm</i>	316	297	1141	172	1926	39.71	3.11	2.95			
<i>hcr1 fancm</i>	267	245	897	149	1558	41.46	2.95	2.75			
<i>fancm zip4</i>	269	290	1187	227	1973	34.17	2.82	2.98	35	1.77	Between <i>fancm</i> and <i>fancm zip4</i> = 0.292
<i>fancm zip4</i>	252	295	1131	187	1865	35.7	2.87	3.25			
<i>fancm zip4</i>	354	301	1274	246	2175	36.94	2.98	2.63			
<i>fancm zip4</i>	278	327	1316	202	2123	34.42	3.01	3.42			

<i>fanm zip4</i>	160	148	688	110	1106	33.44	3.29	3.1			
<i>fanm zip4</i>	200	172	708	116	1196	38.52	3.15	2.78			
<i>fanm zip4</i>	264	216	1061	179	1720	33.53	3.35	2.88			
<i>fanm zip4</i>	272	327	1247	208	2054	35.44	2.84	3.28			
<i>fanm zip4</i>	298	293	1269	262	2122	33.44	2.82	2.79			
<i>fanm zip4</i>	336	329	1334	232	2231	36.45	2.98	2.93			
<i>fanm zip4</i>	256	251	1143	193	1843	32.93	3.15	3.1			
<i>hcr1 fanm zip4</i>	260	282	1074	184	1800	36.93	2.86	3.05			
<i>hcr1 fanm zip4</i>	232	273	959	145	1609	38.99	2.85	3.27			
<i>hcr1 fanm zip4</i>	306	292	1201	169	1968	37.37	3.27	3.14			
<i>hcr1 fanm zip4</i>	250	252	1105	142	1749	34.73	3.44	3.46			
<i>hcr1 fanm zip4</i>	258	237	987	179	1661	36.44	2.99	2.8			
<i>hcr1 fanm zip4</i>	251	251	1026	150	1678	36.62	3.18	3.18			
<i>hcr1 fanm zip4</i>	308	288	1176	225	1997	36.51	2.89	2.75			
<i>hcr1 fanm zip4</i>	339	312	1230	218	2099	38.38	2.96	2.77	37.47	1.79	Between <i>fanm</i> <i>zip4</i> and <i>hcr1</i> <i>fanm</i> <i>zip4</i> = 9.93×10^{-4}
<i>hcr1 fanm zip4</i>	260	293	1003	166	1722	40.19	2.75	3.04			
<i>hcr1 fanm zip4</i>	290	357	1245	217	2109	37.84	2.67	3.16			Between <i>hcr1</i> <i>fanm</i> and <i>hcr1</i> <i>fanm</i> <i>zip4</i> = 5.60×10^{-4}
<i>hcr1 fanm zip4</i>	322	308	1274	210	2114	36.44	3.08	2.97			
<i>hcr1 fanm zip4</i>	300	332	1235	209	2076	37.46	2.84	3.08			
<i>hcr1 fanm zip4</i>	381	351	1297	189	2218	41.7	3.11	2.89			
<i>hcr1 fanm zip4</i>	278	268	1074	184	1804	37.18	2.99	2.9			
<i>hcr1 fanm zip4</i>	322	291	1271	223	2107	35.34	3.1	2.87			

Supplementary Table 23. Yeast two hybrid analysis of interactions between PPX1/HCR1 with meiotic proteins. ++ indicates a strong interaction between PPX1 and meiotic proteins, meaning that yeast cells grew on synthetic dropout medium lacking leucine, tryptophan, histidine and adenine in 3 days. + indicates a weak interaction and that yeast cells grew in 5-7 days. - displays no yeast cell growth and non-interaction. In this yeast two hybrid (Y2H) assay, PPX1 interacts with PTD, HEI10, MSH5, MER3, ZIP4, SHOC1, MLH1, ZYP1a, RPA1A, DMC1, RAD51, PRD1, PRD2, SPO11-1, MTOPVIB, ASY1, REC8, CDKA;1 and PP4R2L in at least one of Y2H combinations. PPX1 does not interact with SWI1, ASY3, PRD3, and HEIP1. PRD1-N indicates 1-821 of 1,330 amino acids, SHOC1-C indicates 850-1209 of 1594 amino acids. Asterisk (*) shows auto-activity when a protein is fused to BD. n.d indicates not determined. The number in parentheses indicates the number of FxxP motifs. Kinase-specific phosphorylation sites for CDK, CDC7/DDK, ATM and ATR were predicted using GPS 5.0 (group based prediction system) (<http://gps.biocuckoo.cn/online.php>)¹¹.

Y2H components	Y2H combination			Y2H combination			FxxP motif number	CDK CDC7/DDK ATM/ATR
	AD-protein	BD alone	BD-PPX1	BD-protein	AD alone	AD-PPX1		
ZMMs	AD-PTD	-	++	BD-PTD	-	++	2	2/0/1
	AD-MSH5	-	++	BD-MSH5	-	++	1	0/1/1
	AD-HEI10	-	-	BD-HEI10	-	++	2	4/2/0
	AD-HEIP1	-	-	BD-HEIP1*	n.d.	n.d.	3	6/3/0
	AD-SHOC1-C	-	+	BD-SHOC1-C*	n.d.	n.d.	0 (5)	10/13/2
	AD-MER3	-	+	BD-MER3	-	-	2	9/5/1
	AD-ZIP4	-	+	BD-ZIP4	-	+	1	3/4/2
	AD-MLH1	-	+	BD-MLH1*	n.d.	n.d.	2	2/2/2
SC component	AD-ZYP1a	-	+	BD-ZYP1A	-	-	1	1/4/2
DSB Repair	AD-RPA1A	-	++	BD-RPA1A	n.d.	n.d.	1	1/1/2
	AD-DMC1	-	+	BD-DMC1	-	-	0	0/0/2
	AD-RAD51	-	+	BD-RAD51	-	-	1	4/1/1
DSB formation	AD-PRD1-N	-	++	BD-PRD1-N	n.d.	n.d.	0 (2)	2/3/6
	AD-PRD2	-	-	BD-PRD2	-	+	1	0/2/0
	AD-PRD3	-	-	BD-PRD3	-	-	1	0/0/4
	AD-SPO11-1	-	++	BD-SPO11-1	-	-	0	2/0/1
	AD-MTOPVIB	n.d.	n.d.	BD-MTOPVIB	-	++	0	1/2/2
Axis element	AD-ASY1	-	-	BD-ASY1	-	+	0	2/1/7
	AD-ASY3	-	-	BD-ASY3	-	-	1	7/5/4
	AD-REC8	-	++	BD-REC8	-	-	1	5/2/1
	AD-SWI1	-	-	BD-SWI1	-	-	1	6/3/2
CDK	AD-CDKA;1	-	+	BD-CDKA;1	-	-	1	1/0/0
PP4 complex	AD-PP4R2L	-	++	BD-PP4R2L	n.d.	n.d.	0	0/1/1
	AD-PP4R3A	-	+	AD-PP4R3A	n.d.	n.d.	1	1/2/3

Supplementary Table 24. List of oligonucleotides used in this study.

Primer	Nucleotide sequence (5' to 3')
ppx-1-F	CCATTTGATACAACATTACGAATCC
ppx-1-R	CTTAAGAACACGACTGAA
GABI_LB	ATAATAACGCTGCGGACATCTACATTTT
ppx-2-F	ATTTTGTGGACCGAGGTTTTTATT
ppx-2-R	TGATCTGCCACAAGATATGTATGA
pp4r2-F	TGAAAAACCTTCTCTTTGGGG
pp4r2-R	TGTTCAACAGATCCTTTTGGC
LBb1.3	ATTTTGCCGATTCGGAAC
zip4-2-F	TTGCTACCTTGGGCTCTCTC
zip4-2-R	ATTCTGTTCTCGCTTTCCAG
hcr1-F	CATGAAAGCAGGCAAATCACACGG
hcr1-R	GAGCCATATTTACGCAAACACTC
fancm-F	ACAATATATGTTTCGTGCAGGTAAGACATTGGAAG
fancm-R	CACCAATAGATGTTGCGACAAT
QRT-F	GATGATGGTAATGTTTATGTTTGAGG
QRT-R	CAAACACGGTTTATGTCTTAAATC
PPX1-F	AAAACCTGCAGGCTGTTATCAACCTGACCCTTAGC
PPX1-R	TCCCCGGGGTCCTAATGCTTCCCTGTGAATC
PPX1-mid-F1	GCTGTATCAACCTGACCCTTAGC
PPX1-mid-R1	GCAAGTACAACAGTCCCCACTCT
PPX1-mid-F2	ATGTATGTATTAGGATCGCAGGC
PPX1-mid-R2	GTATGAGGTTTCGATGGAGCTTCT
PPX1-mid-F3	GTGATTATGATTCTCCAGACGCC
PPX1-mid-R3	GTCCTTTTAGAGTCTTGAAGTTTG
PPX1-mid-F4	CCAAGATCGTTGATGTTGCTAATG
PPX1-mid-R4	CTGTGCAATGTATTAAGCTCGT
PPX1-mid-F5	AGCTAATTCTCTCTCCTTGGGAAG
PPX1-mid-R5	CATAGAACTGCCCATGGATGTC
PPX1-mid-F6	TCCATTGGGATAGTTATGTGGT
PPX1-mid-F7	GACTTGTCTTTGGAATATCCGCAC
PPX1-mid-F8	ACTCCTATTTCACTTATGCTCCAG
pGreen-kan-NosT-F	ATCGCCTTCTTGACGAGTT
pGreen-kan-NosT-R	CGATCCCCGGAATTAGAT
pGreen-PPX1-LB-F	CCATGCTTTGACTTGTGTATGT
pGreen-PPX1-LB-R	CTGACGTATGTGCTTAGCTCAT
pGreen-PPX1-RB-F	AGCTCGGAATTAACCCTCACT
pGreen-PPX1-RB-R	CTTCAATTCTAGAGCTTGACG
FANCM-1F	CTAAGGGTTTCTTCCAAAGAACG
FANCM-1R	CAGTAAGAGCCAGTATTCTCAGCT
FANCM-2F	GTGTTTGGACTTTTAAGTATCTTTC
FANCM-2R	GACTGGCCTTTCAATGTCTTACC
FANCM-3F	TGAGTTTATTGGTCAAAGTTCAGG
FANCM-3R	ACCATGATTGATGCAAGAACACTC
FANCM-4F	CTAGAGTAACCACTACGAGAACAGG
FANCM-4R	GCACTGTACTTCAATAGGATATAC
FANCM-3F-1	CAATCAAGCAATTCGTTCCACGTG
FANCM-4F-1	GTGGTATACATCTGCGTTAGATCA
FANCM-2R-1	CACCTTGGATGGCAATGTCTG
FANCM-2R-2	CTGGAAAGCTGGAGTCTCAGTG
ppx1-F3	AGCAGGCAAATCACACAGGT
ppx1-R3	TCCACAACAGCTGAAAGACTCA
ppx2-F3	CCGGCAGATTACGCAGGTAT
ppx2-R3	AGCCCTGATCTGGTCTAGAGT
pp4r2-F5	CGACCACGAGTGAGAGTGAG
pp4r2-R5	ACGTTGTAGGCAACCGTGAA
GAPC-RTF1	CGAGAAAGCTGCTACCTACGAT
GAPC-RTR1	GTTGTGCTACCATGACACCAAT
ppx2-2 genotyping LP	GGCAGATCAGGG TATTGATCG
ppx2-2 genotyping RP	AACGATGACCTTGCAATTTTG
meiMIGS-PPX1-Lv0-AATG-F	CCGAAGACGGCTCAAATGGTGATTTTCTCTACAAGCGAAGCCCCGTGCTACTTTATGTGGTG ACATCCATGGGCAGTTCTATGATATG
meiMIGS-PPX1-Lv0-ACCT-R	TTGTGGTCTCAACCTCACTGCCACCAAAAAGGAAT
meiMIGS-PPX2-Lv0-AGGT-F	TTGTGGTCTCAAGGTGTGATTTTTCTCTACAAGCGAACGAGGCTTTGAAGGAATCAG

meiMIGS-PPX2-Lv0-AAGC-R	CCGAAGACGGCTCGAAGCCGACAAGAGCTGAAAGACTCAAGTAGTCAAAGATATC
meiMIGS-PPX1-Lv0-AAGC-R	CCGAAGACGGCTCGAAGCCACTGCCACCAAAAAGGAATCCGGCACCACGAGGGCTC
meiMIGS-PPX2-Lv0-AATG-F	CCGAAGACGGCTCAAATGGTGATTTTTCTCTACAAGCGAACGAGGCTTTGAAGGAATCAGAA GTGAAGGCTCTTTGTCTTAAAGC
DMC1-1p_1.5kb-Lv0-GGAG-F	CCGAAGACGGCTCAGGAGAAAGAAACCAAGTTCCATGTCCAT
DMC1-1p_1.5kb-Lv0-CATT-R	CCGAAGACGGCTCGCATTCCGATCACTGACACAAGCAAAAATAAA
DMC1-qPCR-F	TGAAGAAACGAGCCAGATGC
DMC1-qPCR-R	GCGTTTATACCTTGTCGATCA
PPX1-qPCR-F	AATGGGCAAACTTCGAAAA
PPX1-qPCR-R	CAACCCAGTTTCGATCAGTC
PPX2-qPCR-F	CCAAGAAACCTGCACCTGAT
PPX2-qPCR-R	TCTCTTTGGCAACACATGGA
pGADT7-PPX1 CDS GA F	CGGGTGGGCATCGATACGGGATCCATGTCAGACCTAGATCGGCAA
pGADT7-PPX1 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTTATAGGAAGTAATCAGGGGCC
pGBKT7-PPX1 CDS GA F	GGAGGCCGAATTCGCGGATCCATGTCAGACCTAGATCGGCAA
pGBKT7-PPX1 CDS GA R	GGGGTTATGCTAGTTATGCAGGCCTTTATAGGAAGTAATCAGGGGCC
pGADT7-PP4R2L GA F	CGGGTGGGCATCGATACGGATCCATGGAGAATCCGTCATCATCGG
pGADT7-PP4R2L GA R	CAGTATCTACGATTCATCTGCAGGCCTTAGGCACACGTTGTAGGC
pGADT7-PP4R3A GA F	CGGGTGGGCATCGATACGGATCCATGGGCGCTCCGAAAAGTC
pGADT7-PP4R3A GA R	CAGTATCTACGATTCATCTGCAGGCCTTCAGGATCCATTTACAGCCATTTCC
pGADT7-PP4R3A-N GA R	CAGTATCTACGATTCATCTGCAGGCCTTCAAATAAGTTTCAAGTTAGGC
pGADT7-HEI10 CDS GA F	CGGGTGGGCATCGATACGGGATCCATGAGATGCAACGCGTGTTG
pGADT7-HEI10 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTATAGCGTGAACAGCTGAGG
pGBKT7-HEI10 CDS GA F	GGAGGCCGAATTCGCGGATCCATGAGATGCAACGCGTGTTG
pGBKT7-HEI10 CDS GA R	GGGGTTATGCTAGTTATGCAGGCCTTATAGCGTGAACAGCTGAGG
pGADT7-MSH5 CDS GA F	CGGGTGGGCATCGATACGGATCCATGGAGGAAATGGAAGACACTG
pGADT7-MSH5 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTAGGAAGTGAAGATATCTTGAAG
MSH5 CDS-pGBKT7 GA F	GGAGGCCGAATTCGCGGATCCATGGAGGAAATGGAAGACACTG
MSH5 CDS-pGBKT7 GA R	GGGGTTATGCTAGTTATGCAGGCCTTAGGAAGTGAAGATATCTTGAAG
pGADT7-PTD CDS GA F	CGGGTGGGCATCGATACGGATCCATGGCGACGGCGGGATC
pGADT7-PTD CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTCAGTTGAATTTGGGACTGAGG
PTD CDS-pGBKT7 GA F	GGAGGCCGAATTCGCGGATCCATGGCGACGGCGGGATC
PTD CDS-pGBKT7 GA R	GGGGTTATGCTAGTTATGCAGGCCTCAGTTGAATTTGGGACTGAGG
pGAD-SHOC1-C CDS GA F	CGGGTGGGCATCGATACGGATCCAGTCTCAAATGATAAAGGGAGAC
pGAD-SHOC1-C CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTACTTGAGCTGTGTATCAGCAAA
pGADT7-MER3 CDS GA F-2	CGGGTGGGCATCGATACGGATCCATGGATACACACACGCTCAAATCTGTCTCAGATTTG
pGADT7-MER3 CDS GA R-2	AGTATCTACGATTCATCTGCAGGCCTTCACAGAAAAGAGAAGATGCTTTTAAATCCAAG
pGADT7-ZIP4 CDS GA F	CGGGTGGGCATCGATACGGATCCATGAGAATCGCCGAGATCAC
pGADT7-ZIP4 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTAAGCAGAAGAACTTTGGTCT

ZYP1a CDS-pGADT7 GA F	CGGGTGGGCATCGATACGGATCCATGCAGAAGTTAGGGTTTCCGG
ZYP1a CDS-pGADT7 GA R	CAGTATCTACGATTCATCTGCAGGCCTTCAATCAAATGCATAGGGATCATCAGC
pGADT7-MLH1 CDS GA F	CGGGTGGGCATCGATACGGATCCATGATCGACGATTCGTCTCTTAC
pGADT7-MLH1 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTTAGCATCGTTTCAATATCTTGTAC
pGADT7-HEIP1 CDS GA F	CGGGTGGGCATCGATACGGGATCCATGCTGCAATGGATGGGAGG
pGADT7-HEIP1 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTAAAGTTTTAAAGAGTCAAGAAGC
pGBKT7-ASY1 CDS GA F	GGAGGCCGAATTCCCGGGATCCATGGTGATGGCTCAGAAGCTG
pGBKT7-ASY1 CDS GA R	GGGGTTATGCTAGTTATGCAGGCCTTCAATTAGCTTGAGATTCTGACG
pGBKT7-ASY3 CDS GA F	GGAGGCCGAATTCCCGGGATCCATGAGCGACTATAGAAGCTTCG
pGBKT7-ASY3 CDS GA R	GGGGTTATGCTAGTTATGCAGGCCTTCAATCATCCCTCAAACATTCTGC
pGADT7-REC8 CDS GA F	CGGGTGGGCATCGATACGGATCCATGTTGAGACTGGAGAGTTTG
pGADT7-REC8 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTACATGTTGGGTCCTCTTGC
SWI1 CDS-pGBKT7 GA F	GGAGGCCGAATTCCCGGGATCCATGAGTAGTACGATGTTCTG
SWI1 CDS-pGBKT7 GA R	GGGGTTATGCTAGTTATGCAGGCCTTCAAACGTTGAAGAGATTCTTGG
pGAD-SPO11-1 CDS GA F	CGGGTGGGCATCGATACGGATCCATGGAGGGAAAATTCGCTATTTCC
pGAD-SPO11-1 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTCAAGGAGAGCTTACTTCACGAC
pGBK-MTOPVIB CDS GA F	GGAGGCCGAATTCCCGGGATCCATGGAAAACAATGCTCCGGTTCGG
pGBK-MTOPVIB CDS GA R	GGGGTTATGCTAGTTATGCAGGCCTTATTCTCGCAGCATAGTCGC
PRD2 CDS-pGBKT7 GA F	GGAGGCCGAATTCCCGGGATCCATGAGTTCAAGCGTAGCTGAAG
PRD2 CDS-pGBKT7 GA R	GGGGTTATGCTAGTTATGCAGGCCTTCAATCTATTCTTGGTAGGCTAAG
pGADT7-PRD3 CDS GA F	CGGGTGGGCATCGATACGGATCCATGAAGATGAATATTAACAAAGCCTG
pGADT7-PRD3 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTCAATTAATTATTATGGGGTTACCG
pGADT7-PRD1-N GA F	CGGGTGGGCATCGATACGGATCCATGTTCTTCCAACACTCACAGTTG
pGADT7-PRD1-N GA R	CAGTATCTACGATTCATCTGCAGGCCTTCAATGCGGCATAGTTGTCTCC
pGADT7-RPA1A GA F	CGGGTGGGCATCGATACGGATCCATGCCGGTGAGTTTGACTCC
pGADT7-RPA1A GA R	CAGTATCTACGATTCATCTGCAGGCCTTCACTTACGAGCAAATCAAGCATG
RAD51 CDS pGADT7 GA F	CGGGTGGGCATCGATACGGATCCATGACGACGATGGAGCAGC
RAD51 CDS pGADT7 GA R	CAGTATCTACGATTCATCTGCAGGCCTTCAATCCTTGCAATCTGTTACACCTTCTG
pGADT7-CDKA;1 CDS GA F	CGGGTGGGCATCGATACGGATCCATGGATCAGTACGAGAAAGTTG
pGADT7-CDKA;1 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTAAAGCATGCCTCCAAGA
pGADT7-DMC1 CDS GA F	CGGGTGGGCATCGATACGGATCCATGATGGCTTCTCTTAAAGCTGAA
pGADT7-DMC1 CDS GA R	CAGTATCTACGATTCATCTGCAGGCCTTAAATCCTTCGCGTCAGCAATG
PPX1 CDS1-Lv0- AATG-F	CCGAAGACGGCTCAAATGATGTCAGACCTAGATCGGCAAATAGGGCAGC
PPX1 CDS1ns-Lv0- TTCG-R	CCGAAGACGGCTCGCGAACCTAGGAAGTAATCAGGGGCCGGCTTTTTGGCGGG
HEI10 CDS1-Lv0- AATG-F	CCCGAAGACGGCTCAAATGATGAGATGCAACGCGTGTGGA
HEI10 CDS1ns-Lv0- ggTTCG-R	CCGAAGACGGCTCGCGAACCTAGCGTGAACAGCTGAGGGCCGGGAA
HEI10 CDS OL F1	GAACAGAGAAACCATTCGCAA

HEI10 CDS OL R1	TTGCGAATGGTTTCTCTGTTC
MSH5 CDS1-Lv0-AATG-F	CCGAAGACGGCTCAAATGATGGAGGAAATGGAGGACACTG
MSH5 CDS1ns-Lv0-ggTTCG-R	CCGAAGACGGCTCGCGAACCGGAAGTGAAGATATCTTGAAAG
MSH5 CDS OL F1	CGTGTTAGTGGTGGACTTCTTGCTATATT
MSH5 CDS OL R1	AATATAGCAAGAAGTCCACCACTAACACG
MSH5 CDS OL F2	AAGCTGGTTTATGAAACCAATTTAGATC
MSH5 CDS OL R2	GATCTAAAATTGGTTTCATAAACCCAGCTT
MSH5 CDS OL F3	TACCATACCTCGAAAACACGAGAGTTAGA
MSH5 CDS OL R3	TCTAACTCTCGTGTTCGAGGTATGGTA
PTD CDS1-Lv0-AATG-F	CCGAAGACGGCTCAAATGATGGCGACGGCGGGATCA
PTD CDS1ns-Lv0-ggTTCG-R-2	CCGAAGACGGCTCGCGAACCTCAGTTGAATTTGGGACTGAG
PTD ORF OL F1	TCTATCGCAAACCTCCTATATGTGTTCTGA
PTD ORF OL R1	TCAGAACACATATAGGAGTTTGCGATAGA
PTD ORF OL F2	TTACTTCCAGTGAGTGGTGTCTACTCTT
PTD ORF OL R2	AAGAGTAGAACACCACTCACTGGAAGTAA
PTD ORF OL F3-2	GAAGCAATCGCTAAAGCATCCAAAGAGGACATTTAGCAAACACAG
PTD ORF OL R3	TTTGCTAAAATGTCCTCTTTGGATGCTTT
eYFP CT-Lv0-TTCG-F	CCGAAGACGGCTCATTGATGGTGAGCAAGGGCGAGGAGCTGTTCCACC
eYFP CT-Lv0-GCTT-R	CCGAAGACGGCTCGAAGCTCATGATCTAATAGCCGCGTNTTGTACAG
eCFP CT-Lv0-TTCG-F	AAGAAGACAACCTCATTGCGTGAGCAAGGGCGAG
eCFP CT-Lv0-GCTT-R	CCGAAGACAACCTCGAAGCTTACTTGTACAGCTCGT
Lv0-seq_F	GGGAAACGCCTGGTATCTTT
Lv0-seq_R	GGTCAAGGTTCTGGACCAGTTGCCGTG
PP4R3A seq F1	CTATGGATGCTTTGGGATTAGC
MSH5 seq (1) F-2	GCCGTCTCAATGCTATTCC
MER3 CDS seq (1) F	GAAAAGCGCCTCCAAAATA
MER3 CDS seq (2) F	CAGCTCAGACGCAATGAGAA
ZIP4 seq (1) F-2	CATTACCTGTGTTGGCGATG
ZYP1a CDS seq R	GAATGGTCAGCAGTTGCCTC
MLH1 CDS seq (1) F	TCCTCTGTGACTCCTCTGG
ASY3 CDS seq (1) F	AGGGTAGGAGCCAAAGGTGT
RPA1A seq F1	ATTGTGGTGTCTGAACATGGAG
RAD51 SEQ F	GCTAGTTCCTCTGGGGTTCA

Supplementary References

1. van Tol, N., Rolloos, M., van Loon, P. & van der Zaal, B. J. MeioSeed: a CellProfiler-based program to count fluorescent seeds for crossover frequency analysis in *Arabidopsis thaliana*. *Plant Methods* **14**, 32 (2018).
2. Carpenter, A. E. *et al.* CellProfiler: image analysis software for identifying and quantifying cell phenotypes. *Genome Biol.* **7**, R100 (2006).
3. Melamed-Bessudo, C., Yehuda, E., Stuitje, A. R. & Levy, A. A. A new seed-based assay for meiotic recombination in *Arabidopsis thaliana*. *Plant J.* **43**, 458–66 (2005).
4. Ziolkowski, P. A. *et al.* Juxtaposition of heterozygosity and homozygosity during meiosis causes reciprocal crossover remodeling via interference. *Elife* **2015**, (2015).
5. Schneeberger, K. *et al.* SHOREmap: Simultaneous mapping and mutation identification by deep sequencing. *Nature Methods* vol. 6 550–551 (2009).
6. Sun, H. & Schneeberger, K. Shoremap v3.0: Fast and accurate identification of causal mutations from forward genetic screens. *Methods Mol. Biol.* **1284**, 381–395 (2015).
7. Wu, G., Rossivito, G., Hu, T., Berlyand, Y. & Poethig, R. S. Traffic lines: new tools for genetic analysis in *Arabidopsis thaliana*. *Genetics* **200**, 35–45 (2015).
8. Berchowitz, L. E. & Copenhaver, G. P. Fluorescent *Arabidopsis* tetrads: a visual assay for quickly developing large crossover and crossover interference data sets. *Nat. Protoc.* **3**, 41–50 (2008).
9. Lim, E. C. *et al.* DeepTetrad: high-throughput image analysis of meiotic tetrads by deep learning in *Arabidopsis thaliana*. *Plant J.* **101**, 473–483 (2020).
10. Perkins, D. D. Crossing-over and interference in a multiply marked chromosome arm of *Neurospora*. *Genetics* **47**, 1253–74 (1962).
11. Xue, Y. *et al.* GPS 2.1: Enhanced prediction of kinase-specific phosphorylation sites with an algorithm of motif length selection. *Protein Eng. Des. Sel.* **24**, 255–260 (2011).