

Table S1. Bivalent shape and calculated chiasma frequency

Line (ploidy)	Cell#	Rods	Rings	Multi.	Uni.	Chiasmata/pair
SN23 (2X)	1	7	1	0	0	1.125
	2	6	2	0	0	1.25
	3	5	3	0	0	1.375
	4	4	4	0	0	1.5
	5	5	3	0	0	1.375
	6	3	5	0	0	1.625
	7	3	3	1	0	
	8	8	0	0	0	1
	9	8	0	0	0	1
	10	6	0	1	0	
	11	7	1	0	0	1.125
	12	5	3	0	0	1.375
	13	6	2	0	0	1.25
	14	5	3	0	0	1.375
	15	4	4	0	0	1.5
	16	2	6	0	0	1.75
	17	2	6	0	0	1.75
	18	5	3	0	0	1.375
	19	7	1	0	0	1.125
	20	4	4	0	0	1.5
	21	5	3	0	0	1.375
	22	1	7	0	0	1.875
	23	0	8	0	0	2
	24	5	3	0	0	1.375
	25	5	2	0	2	1.125
	26	4	4	0	0	1.5
	27	6	2	0	0	1.25
	28	7	1	0	0	1.125
	29	7	1	0	0	1.125
	28	3	5	0	0	1.625
	29	5	3	0	0	1.375
	30	4	4	0	0	1.5
	31	5	3	0	0	1.375
	32	7	1	0	0	1.125
	33	4	4	0	0	1.5
34	6	2	0	0	1.25	
35	4	4	0	0	1.5	
SN29 (2X)	1	8	0	0	0	1
	2	5	3	0	0	1.375
	3	6	1	0	2	1
2X average		4.98	2.88	0.05	0.1	1.36
TBG 1 (4X)	1	10	0	1	1	
	2	15	0	0	2	0.9375
	3	12	1	0	6	0.875
	4	8	4	1	0	
	5	14	2	0	0	1.125
	6	15	1	0	0	1.0625
	7	14	2	0	0	1.125
	8	15	2	0	0	1.1875
	9	12	2	0	4	1
	10	14	1	0	2	1
	11	15	1	0	0	1.0625
	12	13	2	0	2	1.0625
	13	15	0	0	2	0.9375
	14	14	2	0	0	1.125
	15	14	2	0	2	1.125
	16	15	0	0	2	0.9375
TBG 6 (4X)	1	14	1	0	2	1
TBG 2 (4X)	1	14	2	0	0	1.125
	2	14	2	0	0	1.125
	3	15	1	0	0	1.0625

	4	12	3	0	2	1.125
	5	14	2	0	0	1.125
Line (ploidy)	Cell#	Rods	Rings	Multi.	Uni.	Chiasmata/pair
	6	14	2	0	0	1.125
	7	15	0	0	2	0.9375
	8	14	2	0	0	1.125
	9	13	3	0	0	1.1875
	10	16	0	0	0	1
	11	12	4	0	0	1.25
	12	13	3	0	0	1.1875
	13	12	3	0	2	1.125
	14	16	0	0	0	1
	15	13	3	0	0	1.1875
	16	15	1	0	0	1.0625
	17	16	0	0	0	1
	18	15	1	0	0	1.0625
	19	6	5	2	0	
	20	14	1	0	2	1
	21	14	2	0	0	1.125
	22	13	3	0	0	1.1875
	23	14	2	0	0	1.125
	24	13	3	0	0	1.1875
	25	15	1	0	0	1.0625
	26	12	4	0	0	1.25
	27	13	3	0	0	1.1875
	28	11	3	1	0	
4X average		13.5	1.8	0.11	0.72	1.09
C 22 (neo 4x)	1	0	0	1	0	n/a
	2	0	0	1	0	n/a
	3	2	0	1	0	n/a
	4	2	1	1	0	n/a
	5	0	1	1	0	n/a
	6	0	0	1	0	n/a
	7	0	0	1	0	n/a
	8	0	0	1	0	n/a
	9	0	0	1	0	n/a
	10	0	0	1	0	n/a
	11	2	0	1	0	n/a
C 41 (neo 4X)	1	0	0	1	0	n/a
	2	0	0	1	0	n/a
	3	0	0	1	0	n/a
	4	0	0	1	0	n/a
	5	0	0	1	0	n/a
	6	0	0	1	0	n/a
	7	0	0	1	0	n/a
	8	0	0	1	0	n/a
	9	0	0	1	0	n/a
	10	0	0	1	0	n/a
	11	0	0	1	0	n/a
	12	0	0	1	0	n/a
neo4X average		0.26	0.1	1	0	n/a

Table S1 notes: Observed cytological configurations in diploids (2X), tetraploids (4X), and colchicine-doubled lines (neo4X). Diploids and tetraploids have a significantly different number of rod and ring bivalents (One-way ANOVA $p < 0.0001$).

Table S2. Sampling and sequencing information

<u>individual</u>	<u>Site</u>	<u>GPS</u>	<u>reads</u>	<u>read lqth</u>	<u>single or paired</u>
TBG8	Triberg, Germany	48° 8' 23" N, 8° 14' 12" E	95,657,023	101	single
US7	Bad Urach, Germany	48° 28' 31" N, 9° 23' 44" E	78,606,294	101	single
US24	Bad Urach, Germany	48° 28' 31" N, 9° 23' 44" E	88,087,206	101	single
BGS4	Berchtesgaden, Germany	47° 37' 41" N, 13° 0' 06" E	88,764,962	101	single
BGS11	Berchtesgaden, Germany	47° 37' 41" N, 13° 0' 06" E	71,286,294	101	single
BGS19	Berchtesgaden, Germany	47° 37' 41" N, 13° 0' 06" E	72,344,882	101	single
KA6	Kasparstein, Austria	46° 41' 18" N, 14° 52' 18" E	62,520,747	101	single
KA2	Kasparstein, Austria	46° 41' 18" N, 14° 52' 18" E	93,415,527	101	single
KA30	Kasparstein, Austria	46° 41' 18" N, 14° 52' 18" E	66,224,696	101	single
BE	Beuron, Germany	48° 03' 25" N, 8° 59' 05" E	22,994,132	85	single
RF	Neidlingen, Germany	48° 06' 04" N, 9° 03' 02" E	23,860,199	85	single
US1	Bad Urach, Germany	48° 28' 31" N, 9° 23' 44" E	21,625,553	85	single
MT	Seeburg, Germany	48° 26' 33" N, 9° 27' 54" E	19,949,301	85	single
DFS	Deadfalls, Sweden	62° 55' 20" N, 15° 57' 30" E	16,663,053	85	single
TB7	Triberg, Germany	48° 8' 23" N, 8° 14' 12" E	15,765,954	85	single
TBU3	Triberg, Germany	48° 8' 23" N, 8° 14' 12" E	15,621,195	85	single
CAI18	Hnilčák, Slovakia	48° 52' 21" N, 20° 31' 30" E	48,518,042	52	single
CAI21	Hnilčák, Slovakia	48° 52' 21" N, 20° 31' 30" E	57,701,492	52	single
CAI6	Hnilčák, Slovakia	48° 52' 21" N, 20° 31' 30" E	40,497,742	52	single
CAIX	Hnilčák, Slovakia	48° 52' 21" N, 20° 31' 30" E	35,905,817	52	single
SN23	Strečno, Slovakia	49° 10' 27" N, 18° 51' 42" E	46,356,422	52	single
SN3	Strečno, Slovakia	49° 10' 27" N, 18° 51' 42" E	68,707,978	52	single
SN9	Strečno, Slovakia	49° 10' 27" N, 18° 51' 42" E	36,489,721	52	single
SN8	Strečno, Slovakia	49° 10' 27" N, 18° 51' 42" E	104,755,747	101	paired

Table S2 notes: Data from individuals in rows 1-9, 12, 15, 16 are also described in [11]. Read number is the number of reads per sample that passed quality thresholds. All raw data are available through the NCBI SRA database under project SRP021057.

Table S4: Overlap list of top 0.5% outliers for CLR and Diversity/differentiation residuals

Chr	start	end	A. lyrata identifier	ATG ID	Name	Description	Res	CLR
1	222786	223811	Al_scaffold_0001_57	AT1G01690	PRD3	Spo11-accessory protein	-0.075	211.5
1	6576455	6577852	fgenes2_kg.1_1711_AT1G15570.1	AT1G15570	CYCA2;3	Cyclin, regulator of endopolyploidy	-0.156	185.6
1	6577857	6579852	fgenes2_kg.1_1712_AT1G15580.1	AT1G15580	IAA5	Auxin-induced protein	-0.174	221.4
1	9779128	9780172	NA	AT1G22260	ZYP1a	Transverse filament of SC	-0.079	224.9
1	9780176	9781176	NA	AT1G22260	ZYP1a	Transverse filament of SC	-0.125	223.4
1	9781180	9783857	NA	AT1G22260	ZYP1a	Transverse filament of SC	-0.215	260.6
1	9783922	9787727	scaffold_102525.1	AT1G22275	ZYP1b	Transverse filament of SC	-0.133	234.5
1	12958080	12958873	fgenes2_kg.1_3100_AT1G29370.1	AT1G29370	-	Kinase-related protein	-0.105	187.6
1	12959745	12960507	fgenes2_kg.1_3100_AT1G29370.1	AT1G29370	-	Kinase-related protein	-0.126	189.6
1	12960508	12961616	fgenes2_kg.1_3100_AT1G29370.1	AT1G29370	-	Kinase-related protein	-0.118	189.6
1	12961617	12963831	Al_scaffold_0001_2996	AT1G29380	-	Carbohydrate-binding X8	-0.104	197.4
1	14235903	14260051	fgenes1_pg.C_scaffold_1002808	NA	-	-	-0.078	209.2
2	289714	292779	Al_scaffold_0002_48	NA	-	-	-0.141	205.6
2	795302	796894	fgenes2_kg.2_121_AT1G63640.1	AT1G63640	-	P-loop hydrolase; microtubule motor	-0.079	196.5
2	12428843	12430439	scaffold_201546.1	AT1G67370	ASY1	Axis-associated protein	-0.146	193.8
2	13554321	13555490	fgenes1_pg.C_scaffold_2001247	AT1G69070	-	unknown	-0.113	200.1
2	17692431	17694023	Al_scaffold_0002_2462	AT1G77550	-	tubulin-tyrosine ligase	-0.084	184.9
2	17706277	17708050	scaffold_202722.1	AT1G77600	PDS5	ARM-repeat / PDS5-like, cohesin	-0.181	221.3
2	17712959	17714821	scaffold_202722.1	AT1G77600	PDS5	ARM-repeat / PDS5-like, cohesin	-0.196	222.5
3	1299873	1304202	NA	NA	-	-	-0.157	270.1
3	1491312	1493335	fgenes1_pm.C_scaffold_3000324	AT3G04450	-	Homeodomain protein	-0.133	192.7
3	1568349	1570637	fgenes2_kg.3_418_AT3G04590.2	AT3G04590	-	AT hook DNA-binding family	-0.101	204.3
3	1842291	1844544	NA	NA	-	-	-0.099	209.1
3	5073655	5076483	fgenes2_kg.3_1330_AT3G12690.1	AT3G12690	AGC1.5	Serine/threonine kinase, pollen-specific	-0.123	185.7
3	7247564	7249853	fgenes1_pm.C_scaffold_3001478	NA	-	-	-0.193	267.4
4	11129868	11131556	fgenes1_pg.C_scaffold_4000806	AT2G27170	SMC3	Member of A. th cohesin complex	-0.074	193.8
4	14217398	14218895	fgenes1_pm.C_scaffold_4000859	AT2G30480	-	unknown	-0.155	217.3
4	14218903	14219870	fgenes1_pm.C_scaffold_4000859	AT2G30480	-	unknown	-0.148	233.9
4	14219874	14220748	fgenes1_pm.C_scaffold_4000859	AT2G30480	-	unknown	-0.124	206.2
4	16059402	16061575	fgenes2_kg.4_1400_AT2G33845.1	AT2G33845	-	Nucleic acid-binding, OB-fold-like	-0.110	192.8
4	20155641	20162893	Al_scaffold_0004_2751	NA	-	-	-0.111	308.3
4	21984594	21985882	fgenes1_pm.C_scaffold_4002225	AT1G65680	-	Expansin B2	-0.134	251.9
4	21985898	21988588	fgenes1_pm.C_scaffold_4002225	AT1G65680	-	Expansin B2	-0.140	226.1
4	21988589	21990711	NA	NA	-	-	-0.073	187.1
4	22000277	22001034	fgenes2_kg.4_2707_AT2G45140.1	AT2G45140	PVA12	ER-localized VAMP-associated	-0.072	196.5
4	22843177	22846825	fgenes2_kg.4_2929_AT2G46980.2	AT2G46980	ASY3	required for normal meiosis	-0.125	187.8
4	22846865	22848680	fgenes2_kg.4_2929_AT2G46980.2	AT2G46980	ASY3	required for normal meiosis	-0.274	275.6
4	22846865	22851541	fgenes2_kg.4_2929_AT2G46980.2	AT2G46980	ASY3	required for normal meiosis	-0.297	313.1
5	9482240	9483838	fgenes1_pm.C_scaffold_5000607	AT3G42640	HA8	H+ ATPase	-0.122	206.2
5	9483841	9485667	fgenes1_pm.C_scaffold_5000607	AT3G42640	HA8	H+ ATPase	-0.211	290.5
5	16015301	16017248	fgenes2_kg.5_1585_AT3G52280.1	AT3G52280	GTE6	General transcription factor	-0.206	223.8
6	987180	994021	fgenes2_kg.6_252_AT5G03430.1	AT5G03430	-	PAPS reductase	-0.082	190.3
6	2002848	2004254	fgenes1_pm.C_scaffold_6000400	AT5G05490	SYN1	REC8/RAD21-like, essential for meiosis	-0.130	201.9
6	2004261	2005868	fgenes1_pm.C_scaffold_6000400	AT5G05490	SYN1	REC8/RAD21-like, essential for meiosis	-0.140	261.2
6	8101667	8103395	scaffold_602007.1	AT5G19180	ECR1	Part of ubiquitin-activating complex	-0.075	203.2
6	8862067	8865140	scaffold_602187.1	AT5G20890	-	TCP-1/cpn60 chaperonin protein	-0.068	187.6
6	14370559	14373157	fgenes2_kg.6_2803_AT5G28900.1	AT5G28850	-	Calcium-binding EF-hand protein	-0.095	263.0
7	36874	39896	fgenes2_kg.7_13_AT4G38210.1	AT4G38210	EXPA20	Expansin A20	-0.074	207.7
7	7507538	7509803	fgenes2_kg.7_1815_AT4G24610.1	AT4G24610	-	unknown	-0.074	191.7
7	10777841	10778735	fgenes2_kg.7_2443_AT4G18490.1	AT4G18490	-	unknown	-0.136	248.6
7	10779762	10780840	fgenes2_kg.7_2443_AT4G18490.1	AT4G18490	-	unknown	-0.150	207.3
7	11029171	11030985	Al_scaffold_0007_2373	AT4G18150	-	Kinase-related protein	-0.218	247.7
7	11030986	11034624	fgenes2_kg.7_2486_AT4G18140.1	AT4G18140	SSP4A	SCP1-like phosphatase	-0.189	213.9
8	12441481	12445896	fgenes2_kg.8_780_AT5G49020.1	AT5G49020	PRMT4A	Arginine methyltransferase	-0.071	192.5
8	12445966	12447861	fgenes2_kg.8_780_AT5G49020.1	AT5G49020	PRMT4A	Arginine methyltransferase	-0.101	228.9
8	14783639	14792924	Al_scaffold_0008_1558	AT5G51870	AGL71	MADS box transcription factor	-0.192	243.3
8	17033171	17034749	fgenes2_kg.8_1438_AT5G55390.1	AT5G55390	EDM2	Enhanced downy mildew resistance	-0.096	220.1
8	17034761	17036048	fgenes2_kg.8_1438_AT5G55390.1	AT5G55390	EDM2	Enhanced downy mildew resistance	-0.095	234.4
8	20213189	20214339	fgenes2_kg.8_2171_AT5G61865.1	AT5G61865	-	unknown	-0.089	206.5
8	20610244	20612898	fgenes2_kg.8_2263_AT5G62640.2	AT5G62640	ELF5	Flowering time regulator	-0.095	196.8

Table S4 notes: Chr = Chromosome number, start = 100 SNP window start position in base pairs, based on A. lyrata v1 genome annotation, end = end of 100 SNP window. A. lyrata identifier = gene name of A. lyrata locus within which 100 SNP window falls, ATG ID = A. thaliana gene identifier based on TAIR10 annotation. Res = residual value from diversity/divergence linear regression, CLR = value from site frequency spectrum analysis. Names of meiosis genes are indicated in bold. Alternating grey and white shading indicates distinct peak regions.

Table S5: Annotated meiosis-related genes from TAIR 10

<i>A. lyrata</i> gene name	ATG ID	Name	Description
Al_scaffold_0001_57	AT1G01690	PRD3	plant-specific protein involved in meiotic DSB formation.
scaffold_100662.1	AT1G06660	JASON	Mutant produces diploid male gametes
scaffold_100916.1	AT1G08880	H2AX	(Poorly aligned in <i>A. arenosa</i>) Meiosis-specific histone
Al_scaffold_0001_1062	AT1G10710	PHS1	regulates recombination and pairing
fgenes2_kg.1_1185_AT1G10930.1	AT1G10930	RECQ4A	DNA damage response, suppression of hom. recombination.
scaffold_102523.1	AT1G22260	ZYP1a	SC transverse filament protein
scaffold_102525.1	AT1G22275	ZYP1b	SC transverse filament protein
scaffold_103117.1	AT1G27900		(Poorly aligned in <i>A. arenosa</i>) predicted - DSB formation/repair
fgenes2_kg.1_3543_AT1G34355.1	AT1G34355	PS1	Mutant produces 2N pollen (Meiosis II defect)
fgenes2_kg.1_3636_AT1G35530.1	AT1G35530	FANCM	helicase - limits meiotic crossover formation.
Al_scaffold_0001_4789	AT1G53490	HEI10	Belongs to a group of ZMM proteins well conserved among species
scaffold_704114.1	AT1G54690	HTA3	(Poorly aligned in <i>A. arenosa</i>) HTA3, a histone H2A protein.
Al_scaffold_0002_448	AT1G60930	RECQ4B	Involved in homologous recombination
fgenes2_kg.2_87_AT1G63990.1	AT1G63990	AtSPO11-2	DSB induction, Required for meiotic recombination.
scaffold_201325.1	AT1G66170	MMD1	DNA binding, male meiosis, microsporogenesis
scaffold_201546.1	AT1G67370	ASY1	Chiasma assembly
scaffold_202694.1	AT1G77320	MEI1	Mutant defective in meiosis and produces abnormal microspores.
fgenes2_kg.2_2033_AT1G77390.1	AT1G77390	CYCA1;2	core cell cycle gene involved in meiosis II
scaffold_202722.1	AT1G77600		Homologous to animal sister chromatid cohesion protein PDS5
scaffold_303391.1	AT2G06510	RPA1A	(Poorly aligned in <i>A. arenosa</i>) meiosis I in pollen mother cells.
fgenes1_pg.C_scaffold_400806	AT2G27170	SMC3	Member of the cohesin complex, partner of SMC1
fgenes1_pg.C_scaffold_4001300	AT2G31970	RAD50	Involved in double strand break repair.
scaffold_403468.1	AT2G45280	ATRAD51C	(Poorly aligned in <i>A. arenosa</i>) RAD51 homolog, DNA repair
fgenes2_kg.4_2929_AT2G46980.2	AT2G46980	ASY3	ASY3, coiled-coil domain protein required for normal meiosis.
scaffold_403776.1	AT2G47980	SCC3	monopolar orientation of the kinetochores during meiosis.
fgenes2_kg.3_209_AT3G02680.1	AT3G02680	NBS1	DNA repair and meiotic recombination protein
fgenes2_kg.3_245_AT3G02980.1	AT3G02980	MCC1	required in meiosis for normal chiasma number and distribution
fgenes2_kg.3_538_AT3G05480.1	AT3G05480	RAD9	DNA repair and homologous recombination
Al_scaffold_0003_1340	AT3G13170	AtSPO11-1	DSB induction, Required for meiotic recombination.
fgenes2_kg.3_2059_AT3G18524.1	AT3G18524	MSH2	MutS-homolog, required for normal levels of recombination in yeast
fgenes2_kg.3_2137_AT3G19210.1	AT3G19210	ATRAD54	RAD54, functions in DNA repair via homologous recombination.
fgenes2_kg.3_2273_AT3G20475.1	AT3G20475	MSH5	MutS-homolog, required for normal levels of recombination in yeast
scaffold_302741.1	AT3G22880	DMC1	(Poorly aligned in <i>A. arenosa</i>) Chiasma assembly / DNA repair
fgenes2_kg.3_2716_AT3G25100.1	AT3G25100	CDC45	Required for normal meiosis
fgenes1_pm.C_scaffold_5000623	AT3G43210	TETRASPORE	Required for cytokinesis in pollen.
fgenes1_pm.C_scaffold_5000964	AT3G48190	ATM	homolog of human ataxia telangiectasia mutated
fgenes1_pm.C_scaffold_5001305	AT3G52115	AtCOM1	Sae2 like, DNA repair
fgenes1_pm.C_scaffold_5001543	AT3G54670	SMC1	member of cohesin complex.
scaffold_502896.1	AT3G57300	INO80	SWI/SNF ATPase. Positive regulator of homologous recombination
fgenes2_kg.6_43_AT4G00020.1	AT4G00020	BRCA2A	Ortholog of BRCA2. Essential at meiosis.
scaffold_604079.1	AT4G02070	MSH6	Homolog of MSH6
scaffold_603241.1	AT4G09140	MLH1	Encodes protein similar to Mut1 DNA mismatch repair protein.
fgenes2_kg.7_2921_AT4G14220.1	AT4G14220	RHF1A	RING-type E3 ubiquitin ligase implicated in gametogenesis.
fgenes2_kg.7_2572_AT4G17380.1	AT4G17380	MSH4	meiosis-specific member of MutS-homolog family.
fgenes1_pm.C_scaffold_7001736	AT4G20900	MS5	In ms5 mutants, pollen tetrads undergo an extra round of division
scaffold_702296.1	AT4G21270	ATK1	kinesin-like motor protein heavy chain involved in spindle formation
fgenes2_kg.7_2002_AT4G22970.1	AT4G22970	ESP	Encodes a separase (ESP)
fgenes2_kg.7_1706_AT4G25540.1	AT4G25540	MSH3	DNA mismatch repair
fgenes2_kg.7_1273_AT4G29170.1	AT4G29170	ATMND1	might play a role in DSB repair during meiosis.
fgenes2_kg.7_1096_AT4G30870.1	AT4G30870	MUS81	Associates with noninterfering crossovers
fgenes1_pm.C_scaffold_7000779	AT4G32200	ASY2	(Poorly aligned in <i>A. arenosa</i>) homolog of ASY1
fgenes2_kg.6_43_AT4G00020.1	AT5G01630	BRCA2B	Ortholog of BRCA2. Essential at meiosis.
fgenes1_pm.C_scaffold_6000400	AT5G05490	SYN1	Encodes a RAD21-like gene essential for meiosis.
fgenes2_kg.6_735_AT5G07660.1	AT5G07660	SMC6a	SMC5/6 complex; sister chromatid alignment, hom. recombination
scaffold_601585.1	AT5G15540	SCC2	Encodes Adherin SCC2. Sister chromatid cohesion
fgenes1_pm.C_scaffold_6001261	AT5G15920	SMC5	SMC5/6 complex; sister chromatid alignment, hom. recombination
scaffold_601664.1	AT5G16270	SYN4	Rad21 homolog
fgenes2_kg.6_1963_AT5G19400.1	AT5G19400	SMG7	Required for exit from meiosis.
fgenes2_kg.6_2181_AT5G22000.1	AT5G22000	RHF2A	allows the mitoses associated with gametogenesis
Al_scaffold_0006_2318	AT5G24280	GMI1	Involved in somatic homologous recombination.
scaffold_703887.1	AT5G40820	ATR	
fgenes2_kg.8_17_AT5G47690.1	AT5G47690	PDS5-like	Homologous to animal sister chromatid cohesion protein PDS5
fgenes1_pm.C_scaffold_8000591	AT5G48390	AtSPO22	Involved in crossover formation.
fgenes2_kg.8_753_AT5G48720.1	AT5G48720	XRI1	resolution of meiotic recombination intermediates
fgenes2_kg.8_1020_AT5G51330.1	AT5G51330	DYAD/SW1	sister chromatid cohesion and meiotic chromosome organization
fgenes2_kg.271_2_AT5G52290.1	AT5G52290	SHOC1	(Poorly aligned in <i>A. arenosa</i>) Mutants have defects in meiosis.
fgenes2_kg.8_1327_AT5G54260.1	AT5G54260	MRE11	DNA repair / meiotic recombination protein, MRE11 complex
scaffold_8021318.1	AT5G57450	XRCC3	(Poorly aligned in <i>A. arenosa</i>) homologous recombination / repair.
fgenes2_kg.8_2121_AT5G61460.1	AT5G61460	SMC6b	SMC5/6 complex; sister chromatid alignment, hom. recombination
fgenes2_kg.8_2400_AT5G63920.1	AT5G63920	TOP3a	Encodes topoisomerase 3alpha
Al_scaffold_0008_3317	AT5G66130	RAD17	regulation of DNA damage repair and homologous recombination.

Table S5 notes: Meiosis-related genes in TAIR10 with *A. lyrata* gene names and locations in the *A. lyrata* genome assembly (from Plant Ensembl). Genes for which we have no data from *A. arenosa* due to poor read coverage are in grey.

Table S6. Top differentiating SNPs resulting in amino acid substitutions in selected meiosis genes.

Locus	Tetraploid High Frequency			Diploid High Frequency		
	substitution	excess	domain	substitution	excess	domain
PRD3	S103Y	0.70	(none)	V851L	-0.70	(none)
	T181S	0.73				
	K188E	0.72				
	V287G	0.55				
Zyp1a	E299K	0.95	(none)	(none)		
	V308M	0.95				
	I323M	0.71				
	E358A	0.98				
	G361S	0.98				
	T392A	0.53				
	E419V	0.98				
	N427S	0.98				
	L428V	1.00				
	N452K	0.98				
	K454E	0.98				
	A460V	0.98				
	A605E	0.94				
	N748S	0.66				
	S771A	0.98				
E797D	0.77					
Zyp1b	D100G	0.83	(none)	S232A	-0.56	(none)
	Q190R	0.95		K310N	-0.72	
	K789R	0.83		D341E	-0.55	
				F347Y	-0.55	
ASY1	K40E	0.77	HORMA	K405N	-0.66	(none)
	F272S	0.86				
	R313H	0.84				
PDS5	T300I	0.88	ARM repeat	V124A	-0.88	ARM repeat
	T335R	0.89	ARM repeat	C473W	-0.75	ARM repeat
	A341V	0.88	ARM repeat	T774I	-0.70	
	S527Y	0.86	ARM repeat	P1229T	-0.83	
	A588G	0.92	ARM repeat			
	Q841E	0.89				
	E949K	0.91				
	E983Q	0.88				
	V1102A	0.92				
	E1199A	0.92				

SYN1	A274V	0.89	(none)	(none)		
	A294T	0.88				
	E344D	0.89				
	R371H	0.88				
	Q388H	0.92				
	D454G	0.89				
ASY3	Q16H	0.84	(none)	I44L	-0.63	(none)
	T54P	0.94		L172Q	-0.95	
	L96S	0.98		Q380H	-0.97	
	N117T	0.77		R389Q	-0.63	
	Q133P	0.95		Q391K	-0.63	
	D193V	0.97		I433V	-0.98	
	P208T	0.94		A467V	-0.69	
	T265I	0.98		M482T	-0.94	
	L268V	0.98		N494T	-0.94	
	A275T	0.98		E511D	-0.95	
	N298D	0.97		K530N	-0.98	
	A567S	0.95		S538P	-1.00	
				G556S	-0.69	

Table S6 notes: Locus = Meiosis gene locus present on overlap list of windows found both among 0.5% outliers for 2dSFS and the residuals. All loci were annotated in the *A. lyrata* v1 genome annotation, except *Zyp1a*, which was manually curated from protein homology with *Arabidopsis thaliana* and the putative local duplicate, *Zyp1b*. Substitution = predicted amino acid change from *A. lyrata* v1 genome sequence at the locus. Excess = minor allele frequency in tetraploids minus minor allele frequency in diploids. Domain = if the substitution occurs in a conserved or otherwise identified domain (from Pfam and SMART searches), it is here indicated.

SUPPLEMENTAL METHODS

De novo sequencing of diploid *A. arenosa*

One diploid, SN8, was sequenced on three paired-end Illumina HiSeq lanes (as above) at 101 bp read length (21.2GB raw sequence). Reads were corrected with the kmer correction software SOAP Correction (<http://soap.genomics.org.cn/about.html>) and assembled with SOAP de novo 2 [47]. Multiple assemblies were compared, using a range of kmer lengths (25mer to 101mer) and an optimal assembly was chosen based on a combination of greatest mean contig size and total assembly length. Next, fragments smaller than 200bp were excluded and the resultant assembly was aligned with LASTZ [48] to the repeatmasked *Lyrata*1.0 genome [16]. Synteny of the two genomes in the regions of interest was determined by manual curation, visualized in IGV [49, 50].

Genomic analysis. Genome-wide polymorphism data from diploids and tetraploids were combined using custom PERL and R scripts. Sites with 1X or greater coverage in all individuals were retained for subsequent analysis. All analyses were implemented over 55,570 100-SNP sliding windows across each of the eight reference chromosome sequences, as described below. We calculated F_{ST} between diploids and tetraploids following [17]. To scan the genome for adaptive differentiation between diploid and tetraploid samples, we used two approaches: (1) a composite likelihood ratio test of the diploid-tetraploid two-dimensional Site Frequency Spectrum (2dSFS), and (2) a scan for regions with high allele frequency differentiation between diploids and tetraploids, but low diversity within tetraploids. (1) We implemented a composite likelihood ratio test of the 2dSFS, following the framework of [17, 51]. Briefly, we calculated the likelihoods of observing k SNPs at frequency i in the diploid sample and frequency j in the tetraploid sample, over all i and j , and compared the ratio of composite likelihoods for window-specific versus genome-wide models. The windows with the highest 0.5% ratios were retained as candidate selected regions. (2) To test for deviations from expected patterns of tetraploid diversity and divergence between diploids and tetraploids, we calculated nucleotide diversity in tetraploids and average allele frequency difference between diploids and tetraploids for each window. We then calculated the linear regression fit to these data. Residuals were calculated based on vertical deviations from the regression line fit and were used to identify outliers with the most negative regression values, which in this analysis identified regions with excess divergence relative to diversity, compared to the genome-wide relationship. Finally, we took the intersection of the 0.5% outliers from 1) and 2), above, for our final set of candidate selected regions. Candidate selected genes were identified by overlap between *A. lyrata* reference annotations and outlier windows. Gene functions/identities were determined by orthology with *A. thaliana* loci. All genome-wide analyses were performed using custom R scripts, implemented in R version 2.15.0. Annotations were based on the *A. lyrata* v1.0 release and hand edited for the eight meiosis genes as needed using Geneious R6.1 and IGV. Top differentiating SNPs resulting in amino acid substitutions in selected meiosis genes were predicted with SnpEff [52] and manually confirmed.

SUPPLEMENTAL REFERENCES

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