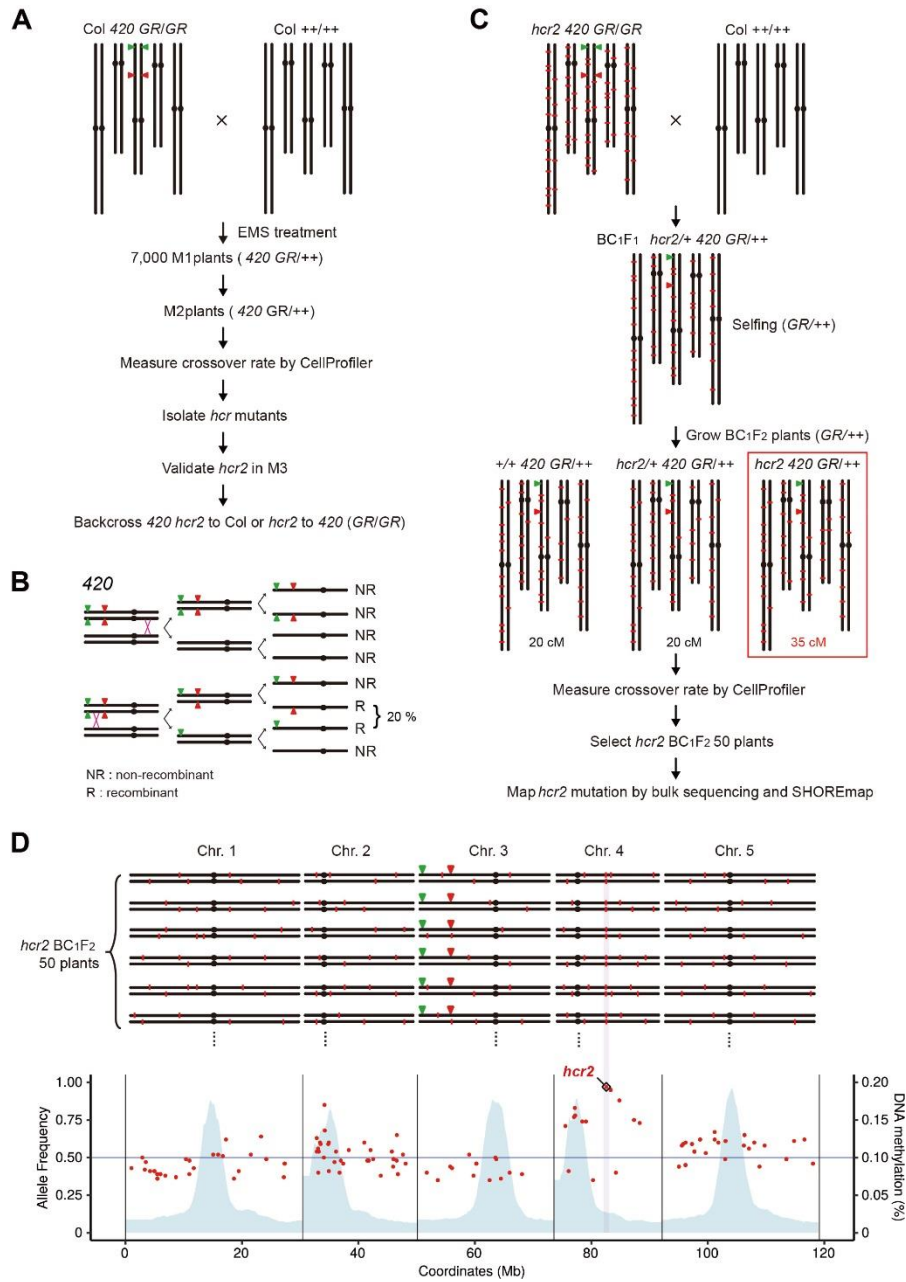# *Arabidopsis* HEAT SHOCK FACTOR BINDING PROTEIN is required to limit meiotic crossovers and *HEI10* transcription

Juhyun Kim[1§], Jihye Park[1§], Heejin Kim[1], Namil Son[1], Eun-Jung Kim[1], Jaeil Kim[1], Dohwan Byun[1], Youngkyung Lee[1], Yeong Mi Park[1], Divyashree C. Nageswaran[2], Pallas Kuo[2], Teresa Rose[3], Tuong Vi T. Dang[1], Ildoo Hwang[1], Christophe Lambing[2, 3], Ian R. Henderson[2] and Kyuha Choi[1]*
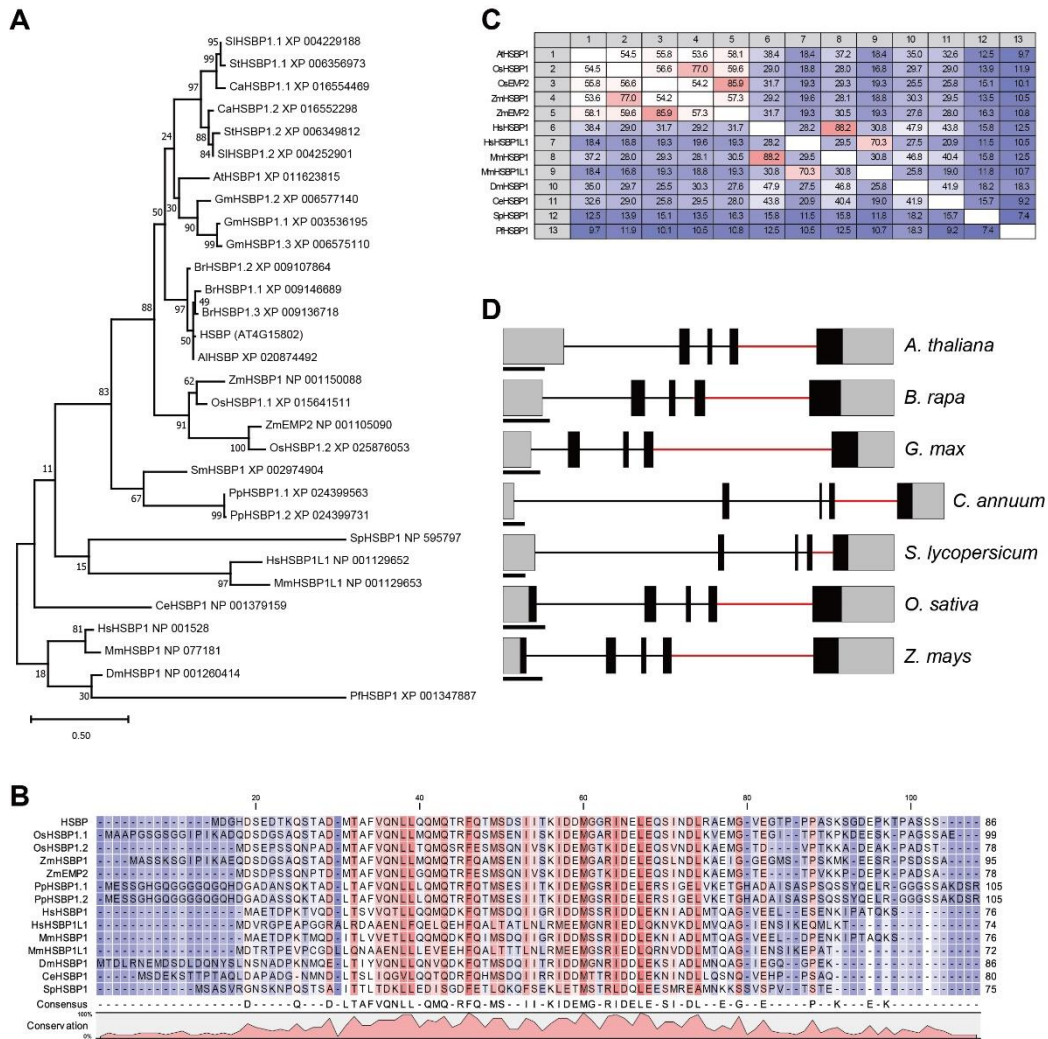
Appendix- Table of contents

Appendix Figure S1. Isolation and mapping of *hcr2*. A. Schematic diagram of the genetic screen conducted to isolate *high crossover rate* (*hcr*) mutants using the *420* seed fluorescence reporter (Nageswaran *et al*, 2021). **B.** Segregation of fluorescent reporters during meiosis in the *420/++* reporter line. **C.** Schematic diagram illustrating the generation of the *hcr2 420* BC$_1$F$_2$ mapping population. Red lines indicate EMS-type mutations. **D.** Mapping of *hcr2* using bulk sequencing and the SHOREmap pipeline (Schneeberger *et al*, 2009). Upper diagram, representative BC$_1$F$_2$ individuals with high crossover rates, like *hcr2*. Lower diagram, allele frequency of EMS-type mutations (red dots) along the genome. The position of *hcr2* is highlighted by the pink line and marked by a diamond.

A

C

		1	2	3	4	5	6	7	8	9	10	11	12	13
AtHSBP1	1		54.5	55.8	53.6	58.1	38.4	18.4	37.2	18.4	35.0	32.6	12.5	9.7
OsHSBP1	2	54.5		56.6	77.0	59.6	29.0	18.8	28.0	16.8	29.7	29.0	13.9	11.9
OsEMP2	3	55.8	56.6		54.2	85.9	31.7	19.3	29.3	19.3	25.5	25.8	15.1	10.1
ZmHSBP1	4	53.6	77.0	54.2		57.3	29.2	19.6	28.1	18.8	30.3	29.5	13.5	10.5
ZmEMP2	5	58.1	59.6	85.9	57.3		31.7	19.3	30.5	19.3	27.6	28.0	16.3	10.8
HsHSBP1	6	38.4	29.0	31.7	29.2	31.7		28.2	88.2	30.8	47.9	43.8	15.8	12.5
HsHSBP1L1	7	18.4	18.8	19.3	19.6	19.3	28.2		29.5	70.3	27.5	20.9	11.5	10.5
MmHSBP1	8	37.2	28.0	29.3	28.1	30.5	88.2	29.5		30.8	46.8	40.4	15.8	12.5
MmHSBP1L1	9	18.4	16.8	19.3	18.8	19.3	30.8	70.3	30.8		25.8	19.0	11.8	10.7
DmHSBP1	10	35.0	29.7	25.5	30.3	27.6	47.9	27.5	46.8	25.8		41.9	18.2	18.3
CeHSBP1	11	32.6	29.0	25.8	29.5	28.0	43.8	20.9	40.4	19.0	41.9		15.7	9.2
SpHSBP1	12	12.5	13.9	15.1	13.5	16.3	15.8	11.5	15.8	11.8	18.2	15.7		7.4
PfHSBP1	13	9.7	11.9	10.1	10.5	10.8	12.5	10.5	12.5	10.7	18.3	9.2	7.4	

D

B

Appendix Figure S2. HSBP orthologs and gene structure from diverse eukaryotes. A. Phylogenetic tree based on an alignment of protein sequences of HSBP homologs. The scale bar indicates the number of changes per amino acid position. **B.** Protein sequence alignment of Arabidopsis HSBP and its homologs from diverse eukaryotic species. **C.** As in B, showing percent identity of protein sequence between HSBP homologs. **D.** Schematic representation of *HSBP* and homologous gene models from diverse plant species. Exons, black boxes; gray boxes, untranslated regions [UTRs]). Horizontal lines indicate introns, and red lines represents AT-AC class introns. Scale bars, 200 bp.

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A. *420*

B.

CTL	Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR
420	Col	236	228	1891	507	2862	17.8	2.89	2.85
	Col	276	297	1934	463	2970	21.6	2.91	3.02
	Col	290	298	2058	479	3125	21.0	3.02	3.06
	Col	232	189	1601	410	2432	19.1	3.06	2.79
	hsbp-3	504	536	2231	380	3651	34.4	2.99	3.13
	hsbp-3	525	535	2174	396	3630	35.5	2.90	2.94
	hsbp-3	566	502	2252	412	3732	34.6	3.08	2.82
	hsbp-3	486	488	1915	345	3234	36.9	2.88	2.89
	hsbp-3/hsbp-2 F₁	242	647	1593	615	3097	34.74	1.45	2.61
	hsbp-3/hsbp-2 F₁	166	488	1215	649	2518	30.68	1.21	2.09
	hsbp-3/hsbp-2 F₁	232	513	1385	463	2593	34.78	1.66	2.73
	hsbp-3/hsbp-2 F₁	187	524	1285	482	2478	34.72	1.46	2.70
	hsbp-3/hsbp-2 F₁	242	503	1656	513	2914	30.09	1.87	2.86

C. *hsbp-3 420*

hsbp-3/hsbp-2 F₁ *420*

D. *hsbp-2 420* — *hsbp-2 CTL5.14*

E. Col *I3bc* — *hsbp-3/hsbp-2 I3bc*

hsbp-3 I3bc — *hsbp-2 I3bc*

Appendix Figure S3. The *hsbp-2* T-DNA insertion mutant causes gene silencing of fluorescent reporters in seeds but not in pollen grains. A. *420* crossover frequency (cM) in Col, *hsbp-3*, and *hsbp-3/hsbp-2* F₁ hybrid plants. Red dots and horizontal lines indicate mean ± s.d. of cM values from individual plants. Black dots represent cM values of individual plants. Significance was assessed by one-sided Welch's t-tests. **B.** Altered ratios of fluorescence reporters in seeds from *hsbp-3/hsbp-2* F₁ hybrid plants, compared to Col and *hsbp-3* plants. **C.** Representative fluorescent seed images, non-color and color ratio plots, and scatterplots from *420 hsbp-3* and *hsbp-3/hsbp-2* F₁ hybrid plants. Scale bars, 1 mm. **D.** Representative images showing silencing of fluorescent reporters in *hsbp-2* seeds. Scale bars, 1 mm. **E.** Representative images of pollen tetrads of *I3bc* from Col, *hsbp-3*, *hsbp-2*, and *hsbp-3/hsbp-2* F₁ hybrid plants. Scale bars, 1 mm.

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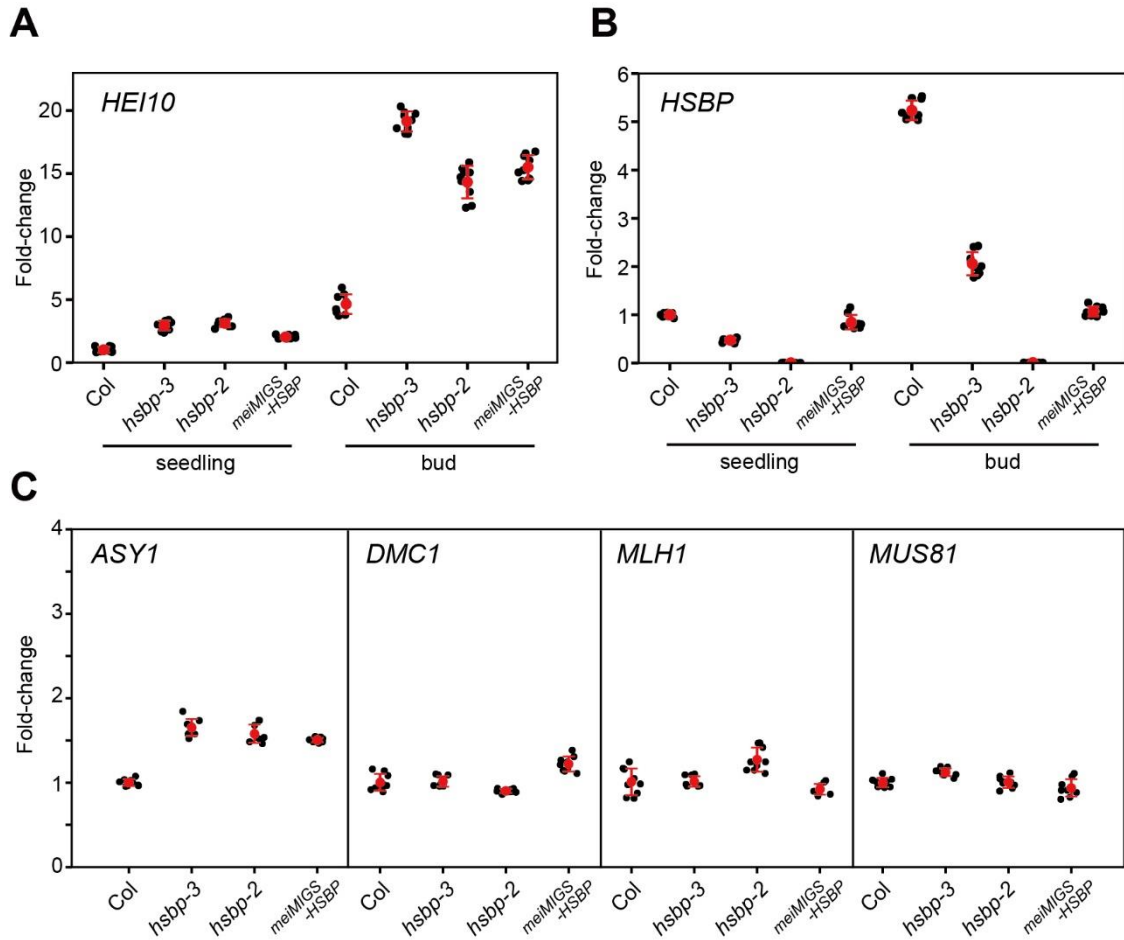
Appendix Figure S4. *hsbp-3* **leads to higher** *HEI10* **transcription during meiosis. A.** RT-qPCR analysis of relative *HEI10* transcript levels in Col, *hsbp-3*, *hsbp-2*, and *meiMIGS-HSBP* transgenic lines. Relative fold-changes of *HEI10* transcript levels in *hsbp-3*, *hsbp-2*, and *meiMIGS-HSBP* relative to Col were examined in seedlings and buds. *TUB2* was used as a reference. Data points (black) represent three biological replicates and three technical repeats per replicate. Red dots and horizontal lines indicate mean ± s.d. values (one-sided Welch's *t*-test). **B.** As in A, showing relative *HSBP* transcript levels. **C.** As in A, showing relative *ASY1*, *DMC1*, *MLH1*, and *MUS81* transcript levels. Experiments were repeated at least three times.
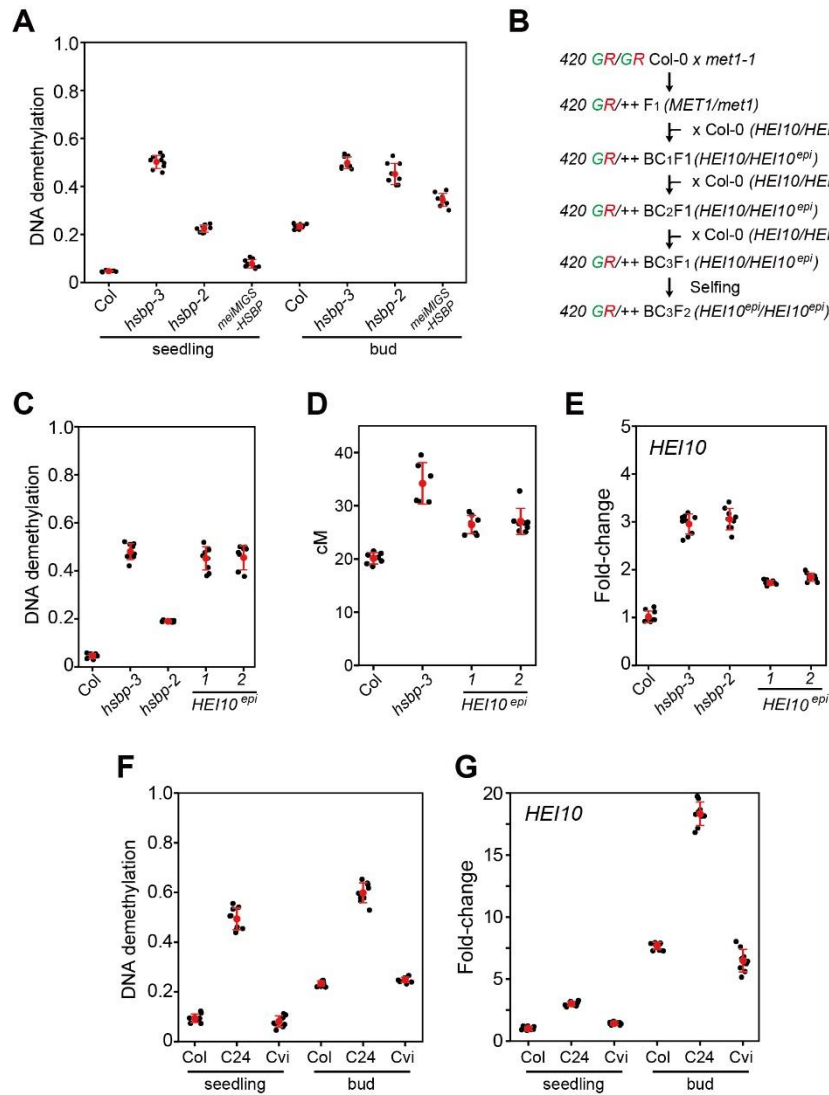
Appendix Figure S5. HSBP represses *HEI10* transcription by maintaining DNA methylation. A. McrBC assay followed by qPCR (McrBC-qPCR) analysis of *HEI10* 5′ UTR in Col, *hsbp-3*, *hsbp-2*, and *meiMIGS-HSBP* seedlings and buds. Only cytosine-methylated DNA is digested by McrBC. Relative DNA demethylation (undigested DNA) levels to input DNA were quantified by qPCR. Higher qPCR signals indicate lower methylation levels. Data points (black) represent fold-changes of qPCR (+McrBC/–McrBC) for three biological replicates and three technical repeats per replicate. Red dots and horizontal lines indicate mean ± s.d. values. **B.** Schematic diagram showing the generation of *HEI10^epi^* lines by crossing the *420* reporter to the *met1* mutant and backcrossing. **C.** McrBC-qPCR analysis of the *HEI10* 5′ UTR in Col and *HEI10^epi^* lines. **D.** As in C, showing *420* crossover frequency. **E.** As in C, showing relative *HEI10* transcript levels. **F.** McrBC assay followed by qPCR analysis of *HEI10* 5′ UTR in Col, C24, and Cvi accessions. **G.** As in F, showing relative *HEI10* transcript levels. Experiments were repeated at least three times (A,C, E-G). Data points indicate two or three technical duplicates of three biological replicates. Significance between genotypes was assessed by one-sided Welch's *t*-tests.
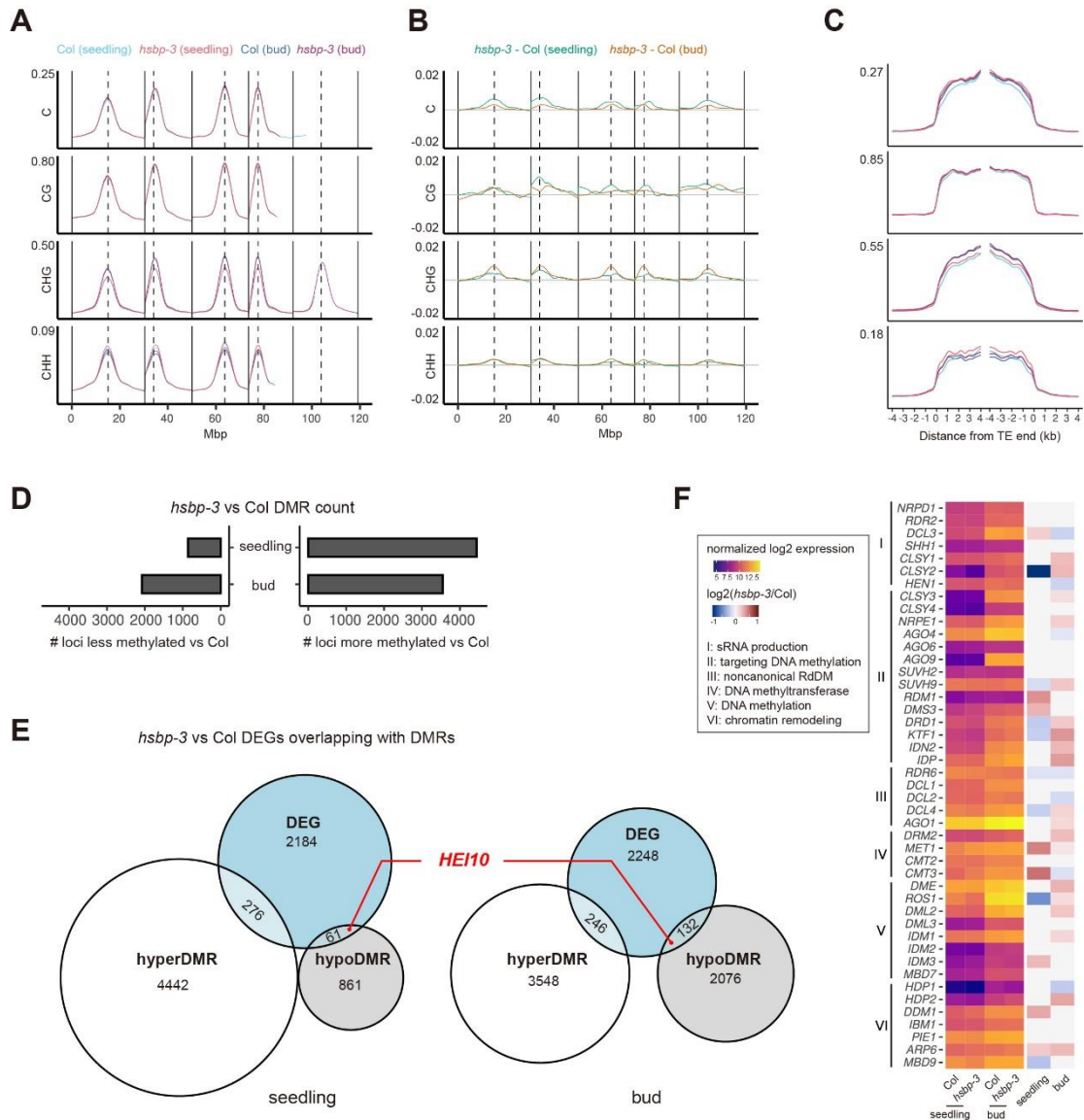
Appendix Figure S6. Genome-wide DNA methylation and RNA-seq analyses of *hsbp-3* seedlings and buds. A. Genomic DNA methylation landscapes of Col and *hsbp-3*. Solid line, chromosome end. Dotted line, centromere. **B.** As in A, but showing difference in DNA methylation levels between Col and *hsbp-3* in seedlings and buds. **C.** As in A, but showing transposable elements (TEs). DNA methylation was plotted around the 5′ end or 3′ end of TEs, with average methylation levels in 10 bp bins. **D.** Number of DMRs (differentially methylated regions) in *hsbp-3* compared with Col. **E.** Number of DEGs (differentially expressed genes) of *hsbp-3* and the number of DEGs overlapping with DMRs. The regions ±2 kb from the start and end of DEGs were used for DMR overlapping analysis. **F.** Heatmap representation of transcript levels in *hsbp-3* for DNA methylation (group I to IV) and chromatin modifying genes (group V) from RNA-seq data. Fold-change (Log2) of genes with false discovery rate (FDR) < 0.05 were considered as 0.

Appendix Table S1. *420* **crossover frequency (cM) in wild-type Col, *hcr1, hcr2, hcr3* and *hcr4* mutants**. *420* crossover frequency was measured using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). To examine for significant differences between wild type and mutants, *P* values were calculated using Welch's t-tests. G/nG indicates the ratio of green color seed number (G) to non-green seed number (nG). R/nR repesents the ratio of red color seed number to non-red seed number.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col	177	220	1508	361	2266	19.4	2.90	3.21			
Col	216	221	1356	303	2096	23.6	3.00	3.04			
Col	229	201	1462	293	2185	22.1	3.42	3.19			
Col	202	134	1153	259	1748	21.5	3.45	2.79	21.61	1.78	
Col	129	158	1087	294	1668	19.0	2.69	2.94			
Col	148	173	1003	263	1587	22.8	2.64	2.86			
Col	159	150	978	235	1522	22.9	2.95	2.86			
hcr1	253	235	1360	353	2201	25.4	2.74	2.63			
hcr1	234	244	1206	248	1932	28.9	2.93	3.01			
hcr1	244	233	1313	290	2080	26.4	2.98	2.90			
hcr1	122	142	729	155	1148	26.5	2.87	3.14	27.00	1.19	4.21×10^{-5}
hcr1	127	121	683	159	1090	26.2	2.89	2.81			
hcr1	188	206	992	225	1611	28.5	2.74	2.90			
hcr1	261	245	1342	295	2143	27.4	2.97	2.85			
hcr1	203	247	1242	255	1947	26.7	2.88	3.25			
hcr2	128	146	582	88	944	35.2	3.03	3.37			
hcr2	280	284	1229	207	2000	34.0	3.07	3.11			
hcr2	169	203	822	173	1367	32.5	2.64	3.00			
hcr2	463	449	1960	415	3287	33.3	2.80	2.74	34.49	1.56	7.62×10^{-9}
hcr2	474	452	1997	386	3309	33.6	2.95	2.85			
hcr2	332	322	1342	221	2217	36.0	3.08	3.01			
hcr2	388	388	1527	280	2583	36.8	2.87	2.87			
hcr3	432	446	1020	58	1956	32.0	2.88	2.99			
hcr3	258	265	1281	230	2034	30.3	3.11	3.17			
hcr3	281	293	1268	229	2071	33.2	2.97	3.06			
hcr3	253	257	1168	269	1947	31.0	2.70	2.73	31.57	1.33	1.19×10^{-7}
hcr3	288	258	1270	241	2057	31.5	3.12	2.89			
hcr3	278	282	1374	274	2208	29.8	2.97	3.00			
hcr3	299	265	1244	229	2037	33.2	3.12	2.86			
hcr4	279	274	1068	200	1821	37.3	2.84	2.80			
hcr4	206	191	819	138	1354	35.7	3.12	2.94			
hcr4	263	256	959	174	1652	39.0	2.84	2.78			
hcr4	228	265	915	147	1555	39.5	2.77	3.15	37.70	1.72	8.22×10^{-10}
hcr4	265	282	1017	182	1746	38.9	2.76	2.91			
hcr4	256	246	1040	193	1735	35.1	2.95	2.86			
hcr4	241	217	869	148	1475	38.4	3.04	2.79			

Appendix Table S2. *420* **crossover frequency (cM) in Col, *hcr2*, *hcr2/+* and high recombination *hcr1* BC$_1$F$_2$ individuals.** *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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 × (1- [1-2(N_{Green}+N_{Red})/N_{Total}]$^{1/2}$) (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild type and genotypes, *P* values were calculated using Welch's t-tests. G/nG indicates the ratio of green color seed number (G) to non-green seed number (nG). R/nR repesents the ratio of red color seed number to non-red seed number.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col	297	276	1934	463	2970	21.63	2.91	3.02			
Col	298	290	2058	479	3125	21.03	3.02	3.06			
Col	189	232	1601	410	2432	19.14	3.06	2.79	20.46	0.98	
Col	238	262	1801	477	2778	20.00	2.89	2.76			
Col	274	263	1846	446	2829	21.24	2.93	2.99			
Col	274	226	1876	438	2814	19.71	2.95	3.24			
hcr2/+	222	242	1824	487	2775	18.42	2.91	2.81			
hcr2/+	196	217	1466	354	2233	20.62	2.91	3.06			
hcr2/+	220	212	1462	345	2239	21.63	3.02	2.96	20.91	1.93	0.629
hcr2/+	197	226	1382	306	2111	22.59	2.97	3.20			
hcr2/+	209	244	1430	325	2208	23.21	2.88	3.13			
hcr2/+	204	200	1567	383	2354	18.96	3.04	3.01			
hcr2	452	445	1789	350	3036	36.04	2.79	2.82			
hcr2	364	379	1539	299	2581	34.87	2.89	2.81			
hcr2	412	419	1788	345	2964	33.72	2.92	2.88	35.11	0.91	1.32×10^{-10}
hcr2	396	501	1770	359	3026	36.19	3.01	2.52			
hcr2	437	395	1709	339	2880	35.02	2.71	2.92			
hcr2	475	477	2055	304	3311	34.81	3.25	3.24			
hcr2 BC$_1$F$_2$	206	191	819	138	1354	35.69	3.12	2.94			
hcr2 BC$_1$F$_2$	331	292	1341	197	2161	34.93	3.42	3.09			
hcr2 BC$_1$F$_2$	212	232	927	171	1542	34.88	2.83	3.03			
hcr2 BC$_1$F$_2$	287	295	1309	235	2126	32.73	3.01	3.07			
hcr2 BC$_1$F$_2$	363	328	1397	257	2345	35.92	3.01	2.78			
hcr2 BC$_1$F$_2$	228	230	941	141	1540	36.35	3.15	3.17	34.81	1.29	1.23×10^{-12}
hcr2 BC$_1$F$_2$	326	346	1333	267	2272	36.09	2.71	2.83			
hcr2 BC$_1$F$_2$	333	311	1435	237	2316	33.38	3.23	3.06			
hcr2 BC$_1$F$_2$	287	295	1309	235	2126	32.73	3.01	3.07			
hcr2 BC$_1$F$_2$	130	128	524	112	894	34.98	2.73	2.69			
hcr2 BC$_1$F$_2$	239	152	806	130	1327	35.91	3.71	2.6			
hcr2 BC$_1$F$_2$	237	200	973	134	1544	34.13	3.62	3.16			

Appendix Table S3. EMS mutations identified from sequencing high *420* recombination *hcr2* BC₁F₂ plants. SHORE pipeline was used for mapping EMS mutations (Schneeberger *et al*, 2009; Sun & Schneeberger, 2015). Sequencing quality score (Qual score) indicates 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 represents 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	Sequence feature	Gene ID	Type of Change	Ref aa	Mut aa
1	1031530	C	T	22	0.43	40	UTR	AT1G04010.1			
1	2892436	C	T	40	0.5	40	CDS	AT1G09000.1	Nonsyn	P	S
1	3318260	G	A	32	0.42	40	CDS	AT1G10130.1	Syn	G	G
1	3493292	G	A	55	0.47	40	CDS	AT1G10580.1	Nonsyn	P	L
1	4227606	G	A	45	0.41	40	CDS	AT1G12420.1	Nonsyn	A	V
1	4972879	C	T	28	0.41	40	CDS	AT1G14530.1	Syn	L	L
1	4972879	C	T	28	0.41	40	CDS	AT1G14530.2	Syn	L	L
1	5472453	C	T	31	0.39	40	intronic	AT1G15930.1			
1	5472453	C	T	31	0.39	40	intronic	AT1G15930.2			
1	5481316	C	T	12	0.36	40	intronic	AT1G15950.1			
1	5481316	C	T	12	0.36	40	intronic	AT1G15950.2			
1	6005658	C	T	30	0.39	40	CDS	AT1G17470.1	Nonsyn	P	S
1	6005658	C	T	30	0.39	40	CDS	AT1G17470.2	Nonsyn	P	S
1	6846162	C	T	22	0.38	40	intergenic				
1	8669892	C	T	28	0.37	40	intronic	AT1G24460.1			
1	8669892	C	T	28	0.37	40	intronic	AT1G24460.2			
1	10383572	C	T	17	0.49	40	intergenic				
1	10962603	C	T	26	0.39	40	intronic	AT1G30825.1			
1	10989207	C	T	31	0.48	40	CDS	AT1G30860.1	Nonsyn	D	N
1	11729488	C	T	27	0.43	40	intergenic				
1	15061362	C	T	55	0.52	40	intergenic				
1	15925613	C	T	17	0.52	40	intergenic				
1	16716347	C	T	42	0.51	40	UTR	AT1G44020.1			
1	17261817	C	T	48	0.62	40	intergenic				
1	18629738	C	T	20	0.36	40	CDS	AT1G50300.1	Nonsyn	G	D
1	19450673	C	T	26	0.41	40	intergenic				
1	21524149	G	A	13	0.52	40	intergenic				
1	23280529	C	T	30	0.64	40	intergenic				
1	24173119	C	T	43	0.49	40	intronic	AT1G65070.1			

1	24173119	C	T	43	0.49	40	CDS	AT1G65070.2	Syn	K	K
1	27192559	C	T	16	0.37	40	intergenic				
1	27317714	C	T	25	0.46	40	intergenic				
1	27352157	C	T	43	0.46	40	CDS	AT1G72650.1	Nonsyn	S	F
1	27352157	C	T	43	0.46	40	CDS	AT1G72650.2	Nonsyn	S	F
2	2414053	G	A	40	0.63	40	intergenic				
2	2426364	G	A	42	0.54	40	CDS	AT2G06200.1	Nonsyn	E	K
2	2646255	C	T	53	0.56	40	intergenic				
2	2680417	G	A	44	0.4	40	intergenic				
2	2773331	G	A	49	0.54	40	intergenic				
2	2988024	G	A	24	0.6	40	splice_site_change	AT2G07190.1			
2	3082719	G	A	69	0.59	40	intergenic				
2	3637495	G	A	44	0.5	40	intergenic				
2	3756150	G	A	44	0.85	40	intergenic				
2	3799792	G	A	23	0.68	40	intergenic				
2	4400393	C	T	56	0.59	40	intergenic				
2	4489446	C	T	61	0.6	40	intergenic				
2	4505198	G	A	47	0.41	40	intergenic				
2	5464826	G	A	30	0.47	40	intergenic				
2	5732638	G	A	15	0.54	40	intergenic				
2	6329810	C	T	23	0.4	40	intergenic				
2	6550072	G	A	46	0.48	40	intergenic				
2	6963454	C	T	35	0.46	40	intergenic				
2	7915022	G	A	52	0.55	40	CDS	AT2G18190.1	Nonsyn	A	V
2	10583637	G	A	24	0.6	40	CDS	AT2G24850.1	Nonsyn	P	L
2	11096892	G	A	11	0.48	40	intergenic				
2	11312320	G	A	30	0.48	40	CDS	AT2G26590.1	Syn	D	D
2	11312320	G	A	30	0.48	40	CDS	AT2G26590.2	Syn	D	D
2	11312320	G	A	30	0.48	40	CDS	AT2G26590.3	Syn	D	D
2	11649451	G	A	29	0.55	40	CDS	AT2G27229.1	Nonsyn	R	K
2	12114302	G	A	29	0.49	40	intergenic				
2	13417156	C	T	24	0.38	40	CDS	AT2G31510.1	Syn	L	L
2	15319340	C	T	60	0.54	40	CDS	AT2G36500.1	Nonsyn	L	F
2	15534145	G	A	17	0.44	40	intergenic				
2	15605181	G	A	51	0.49	40	CDS	AT2G37150.1	Nonsyn	T	I
2	15605181	G	A	51	0.49	40	CDS	AT2G37150.2	Nonsyn	T	I
2	15605181	G	A	51	0.49	40	CDS	AT2G37150.3	Nonsyn	T	I

2	16140093	G	A	26	0.48	40	CDS	AT2G38580.1	Nonsyn	E	K
2	16174290	G	A	26	0.65	40	intronic	AT2G38680.1			
2	16355346	G	A	34	0.39	40	UTR	AT2G39190.1			
2	16355346	G	A	34	0.39	40	CDS	AT2G39190.2	Syn	G	G
2	17221038	G	A	12	0.52	40	intergenic				
2	17682792	G	A	31	0.46	40	intronic	AT2G42470.1			
3	1611832	C	T	23	0.4	40	CDS	AT3G05545.1	Nonsyn	S	F
3	3504948	C	T	22	0.35	40	CDS	AT3G11180.1	Syn	Y	Y
3	3504948	C	T	22	0.35	40	CDS	AT3G11180.2	Syn	Y	Y
3	5651178	G	A	24	0.44	40	intergenic				
3	5957417	C	T	51	0.43	40	CDS	AT3G17410.1	Syn	L	L
3	8901306	G	A	11	0.52	40	CDS	AT3G24480.1	Nonsyn	P	S
3	9644950	C	T	35	0.38	40	CDS	AT3G26320.1	Nonsyn	W	*
3	10129789	C	T	44	0.46	40	CDS	AT3G27360.1	Syn	R	R
3	10129789	C	T	44	0.46	40	UTR	AT3G27380.1			
3	10129789	C	T	44	0.46	40	UTR	AT3G27380.2			
3	12397197	G	A	42	0.35	40	intergenic				
3	13403049	G	A	14	0.5	40	intergenic				
3	13555948	C	T	39	0.49	40	intergenic				
3	14347712	C	T	19	0.36	40	intergenic				
3	15848416	C	T	32	0.4	40	intergenic				
3	17971822	C	T	21	0.39	40	intergenic				
4	1967265	G	A	62	0.71	40	intergenic				
4	2508965	G	A	14	0.41	40	intergenic				
4	3437643	G	A	64	0.77	40	intergenic				
4	3580503	G	A	68	0.83	40	intergenic				
4	3646746	C	T	53	0.78	40	intergenic				
4	4856197	G	A	79	0.74	40	intergenic				
4	5487407	G	A	45	0.74	40	intergenic				
4	6700268	C	T	14	0.35	40	intergenic				
4	8987414	G	A	69	0.97	40	intronic	AT4G15802.1			
4	9742963	G	A	71	0.95	40	CDS	AT4G17470.1	Nonsyn	Q	*
4	9742963	G	A	71	0.95	40	CDS	AT4G17470.2	Nonsyn	Q	*
4	9742963	G	A	71	0.95	40	CDS	AT4G17470.3	Nonsyn	Q	*
4	10632917	C	T	17	0.4	40	intergenic				
4	11231903	G	A	53	0.88	40	CDS	AT4G21030.1	Nonsyn	D	N
4	13747409	G	A	70	0.75	40	CDS	AT4G27510.1	Nonsyn	S	F
4	13747409	G	A	70	0.75	40	CDS	AT4G27510.2	Nonsyn	S	F

4	14718117	G	A	77	0.73	40	CDS	AT4G30100.1	Nonsyn	G	D
5	2876441	C	T	31	0.44	40	intronic	AT5G09250.1			
5	2876441	C	T	31	0.44	40	intronic	AT5G09250.2			
5	3372488	C	T	49	0.58	40	intergenic				
5	3585603	C	T	41	0.59	40	intronic	AT5G11240.1			
5	4004534	G	A	73	0.45	40	intronic	AT5G12370.1			
5	4004534	G	A	73	0.45	40	intronic	AT5G12370.2			
5	4004534	G	A	73	0.45	40	intronic	AT5G12370.3			
5	4020078	C	T	30	0.6	40	intronic	AT5G12400.1			
5	5116642	C	T	36	0.59	40	CDS	AT5G15700.1	Nonsyn	E	K
5	5116642	C	T	36	0.59	40	CDS	AT5G15700.2	Nonsyn	E	K
5	5526181	C	T	47	0.54	40	CDS	AT5G16800.1	Nonsyn	E	K
5	5526181	C	T	47	0.54	40	CDS	AT5G16800.2	Nonsyn	E	K
5	5526181	C	T	47	0.54	40	CDS	AT5G16800.3	Nonsyn	E	K
5	6509610	C	T	50	0.62	40	CDS	AT5G19330.1	Nonsyn	V	I
5	6509610	C	T	50	0.62	40	CDS	AT5G19330.2	Nonsyn	V	I
5	7481761	C	T	48	0.53	40	CDS	AT5G22540.1	Nonsyn	D	N
5	9013739	C	T	24	0.67	40	intergenic				
5	9013798	C	T	18	0.62	40	intergenic				
5	9644532	G	A	12	0.6	40	intergenic				
5	10816741	C	T	42	0.49	40	intergenic				
5	10877866	C	T	36	0.61	40	CDS	AT5G28850.1	Nonsyn	G	E
5	10877866	C	T	36	0.61	40	CDS	AT5G28850.2	Nonsyn	G	E
5	14030275	C	T	31	0.58	40	CDS	AT5G35910.1	Nonsyn	E	K
5	14132164	C	T	45	0.65	40	CDS	AT5G35980.1	Nonsyn	P	S
5	14132164	C	T	45	0.65	40	CDS	AT5G35980.2	Nonsyn	P	S
5	14900735	C	T	25	0.56	40	intergenic				
5	15809558	G	A	26	0.6	40	intergenic				
5	16710225	C	T	30	0.44	40	intergenic				
5	17593307	C	T	57	0.58	40	CDS	AT5G43790.1	Nonsyn	A	T
5	21318563	G	A	88	0.49	40	CDS	AT5G52530.1	Nonsyn	V	M
5	21318563	G	A	88	0.49	40	CDS	AT5G52530.2	Nonsyn	V	M
5	21318563	G	A	88	0.49	40	CDS	AT5G52530.3	Nonsyn	V	M
5	22646827	C	T	31	0.61	40	intronic	AT5G55920.1			
5	24420186	C	T	40	0.62	40	CDS	AT5G60720.1	Nonsyn	D	N
5	25894245	C	T	33	0.46	40	CDS	AT5G64760.1	Nonsyn	E	K

Appendix Table S4. *420* **crossover frequency (cM) in Col,** *hsbp-3* **and** *hsbp-3* **transformed with** *HSBP* **transgenes.** *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler(van Tol *et al*, 2018; Carpenter *et al*, 2006). 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: $cM = 100 \times (1 - [1 - 2(N_{Green}+N_{Red})/N_{Total}]^{1/2})$(Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild type and genotypes, *P* values were calculated using Welch's t-tests. G/nG indicates the ratio of green color seed number (G) to non-green seed number (nG). R/nR repesents the ratio of red color seed number to non-red seed number.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col	113	102	730	255	1200	19.90	2.36	2.26			
Col	152	228	1196	379	1955	21.82	2.22	2.68			
Col	90	78	631	163	962	19.33	2.99	2.80	20.52	1.00	
Col	111	131	799	239	1280	21.14	2.46	2.66			
Col	274	263	1846	446	2829	21.24	2.93	2.99			
Col	274	226	1876	438	2814	19.71	2.95	3.24			
hsbp-3	426	456	1879	440	3201	33.00	2.70	2.57			
hsbp-3	387	384	1561	302	2634	35.61	2.82	2.84			
hsbp-3	121	150	533	111	915	36.15	2.94	2.51	35.13	1.19	8.22×10^{-10}
hsbp-3	396	501	1770	359	3026	36.19	3.01	2.52			
hsbp-3	437	395	1709	339	2880	35.02	2.71	2.92			
hsbp-3	475	477	2055	304	3311	34.81	3.25	3.24			
hsbp-3 HSBP	264	241	1885	429	2819	19.89	3.21	3.07			versus Col =0.192
hsbp-3 HSBP	143	155	941	273	1512	22.17	2.53	2.63			
hsbp-3 HSBP	221	194	1360	350	2125	21.94	2.91	2.72			
hsbp-3 HSBP	215	271	1648	392	2526	21.57	2.81	3.16	21.30	0.99	
hsbp-3 HSBP	259	262	1821	468	2810	20.68	2.85	2.87			versus *hsbp-3* = 8.53×10^{-10}
hsbp-3 HSBP	304	306	1987	461	3058	22.47	2.99	3.00			
hsbp-3 HSBP	253	259	1848	440	2800	20.36	3.01	3.04			
hsbp-3 HCR2-myc	268	246	2089	541	3144	17.96	2.99	2.89			versus Col =0.436
hsbp-3 HCR2-myc	329	323	1968	456	3076	24.10	2.95	2.92			
hsbp-3 HCR2-myc	264	318	1952	499	3033	21.50	2.71	2.98			
hsbp-3 HCR2-myc	255	322	2119	542	3238	19.77	2.75	3.06	21.25	2.09	
hsbp-3 HCR2-myc	354	300	1999	529	3182	23.26	2.84	2.60			versus *hsbp-3* = 4.91×10^{-8}
hsbp-3 HCR2-myc	306	249	1840	468	2863	21.75	2.99	2.70			
hsbp-3 HCR2-myc	300	293	2102	541	3236	20.41	2.88	2.85			

Appendix Table S5. *420* crossover frequency (cM) in Col, *hsbp-3* and *meiMIGS-HSBP* transgenic lines. *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler(van Tol *et al*, 2018; Carpenter *et al*, 2006). 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 × (1- [1- 2(N_{Green}+N_{Red})/N_{Total}]$^{1/2}$)(Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild type and genotypes, *P* values were calculated using Welch's t-tests. G/nG indicates the ratio of green color seed number (G) to non-green seed number (nG). R/nR repesents the ratio of red color seed number to non-red seed number.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col	111	77	631	158	977	21.57	3.16	2.63			
Col	96	130	191	897	1314	19.01	3.09	3.58			
Col	210	183	1448	324	2165	20.19	3.27	3.05	20.29	0.96	
Col	202	193	1439	358	2192	20.03	2.98	2.91			
Col	274	263	1846	446	2829	21.24	2.93	2.99			
Col	274	226	1876	438	2814	19.71	2.95	3.24			
hsbp-3	418	430	1975	378	3201	31.43	2.96	3.02			
hsbp-3	134	125	552	95	906	34.56	3.12	2.96			
hsbp-3	263	274	1089	194	1820	35.98	2.89	2.98	33.98	1.92	$6.51×10^{-7}$
hsbp-3	375	383	1601	275	2634	34.85	3.00	3.05			
hsbp-3	301	338	1307	252	2198	35.30	2.73	2.97			
hsbp-3	254	268	1185	248	1955	31.74	2.79	2.89			
meiMIGS-HSBP	281	255	1419	293	2248	27.67	3.10	2.92			
meiMIGS-HSBP	345	335	1638	319	2637	30.41	3.03	2.97			
meiMIGS-HSBP	320	326	1659	341	2646	28.47	2.97	3.00			
meiMIGS-HSBP	287	293	1523	316	2419	27.86	2.97	3.01			
meiMIGS-HSBP	364	363	1547	257	2531	34.77	3.08	3.08	30.38	2.57	$7.22×10^{-8}$
meiMIGS-HSBP	219	244	1219	268	1950	27.53	2.81	3.00			
meiMIGS-HSBP	343	297	1552	257	2449	30.91	3.42	3.08			
meiMIGS-HSBP	306	282	1431	260	2279	30.43	3.20	3.03			
meiMIGS-HSBP	389	403	1713	314	2819	33.81	2.93	3.01			
meiMIGS-HSBP	289	292	1327	256	2164	31.95	2.95	2.97			

Appendix Table S6. Pollen-based FTL crossover frequency (cM) of *I3bc* in Col, *hsbp-3, hsbp-3/hsbp-2* and *hsbp-2*. Pollen-based FTL crossover frequency was measured by DeepTetrad using 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*) (Berchowitz & Copenhaver, 2008). Fluorescent tetrad states were identified using DeepTetrad and crossover frequency (cM) was calculated using the Perkin's equations (Perkins, 1962; Lim *et al*, 2020). *P* values were calculated using Welch's t-tests, which assessed significant differences between wild type and mutants (Berchowitz & Copenhaver, 2008).

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	*I3b*(cM)	*I3c*(cM)	*I3bc*(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col	829	416	99	5	2	8	1	5	0	0	0	0	1365	16.92	4.21	20.55	0.18	0.07	0.39	1.54
Col	641	374	127	2	7	9	7	9	2	2	0	0	1180	19.70	7.03	26.57	0.21	0.12	0.57	3.22
Col	343	193	58	3	1	1	2	4	1	0	0	0	606	18.48	5.86	24.34	0.20	0.05	0.26	1.98
Col	413	206	58	0	0	3	1	3	0	1	0	0	685	17.08	4.60	21.31	0.18	0.08	0.44	1.17
Col	441	291	71	4	2	2	7	7	1	0	0	0	826	21.07	5.57	27.60	0.23	0.09	0.38	2.78
Col	846	437	87	3	2	5	5	4	0	0	0	0	1389	17.13	3.67	21.06	0.18	0.07	0.41	1.37
Col	710	355	86	3	2	3	4	7	2	0	0	0	1172	17.45	4.69	22.35	0.19	0.06	0.32	1.79
Mean														18.26	5.09	23.40	0.19	0.08	0.40	1.98
SD														1.59	1.14	2.82	0.02	0.02	0.10	0.76
hsbp-3	283	320	110	13	4	5	5	10	2	2	0	0	754	27.79	10.01	36.01	0.31	0.14	0.45	5.44
hsbp-3	325	342	123	17	4	16	9	13	1	3	2	0	855	28.42	11.11	36.73	0.31	0.19	0.61	7.60
hsbp-3	194	232	93	2	2	8	6	5	1	1	0	0	544	26.29	10.85	37.50	0.30	0.11	0.35	4.60
hsbp-3	154	230	75	12	17	7	19	10	0	1	0	0	525	33.43	12.48	48.00	0.37	0.23	0.63	12.57
hsbp-3	208	299	91	11	20	19	20	6	2	3	0	0	679	31.15	12.96	44.18	0.33	0.27	0.81	11.93
hsbp-3	176	247	84	10	17	17	17	9	0	2	0	0	579	32.30	12.69	45.16	0.35	0.25	0.71	12.44
Mean														29.89	11.68	41.26	0.33	0.20	0.59	9.10
SD														2.81	1.19	5.13	0.03	0.06	0.17	3.66
P value														$2.52{\times}10^{-5}$	$9.20{\times}10^{-7}$	$8.79{\times}10^{-5}$			0.0372	0.00457
hsbp-3/hsbp-2	276	323	109	16	17	17	17	12	1	1	0	0	789	29.66	11.60	41.00	0.32	0.21	0.63	10.27

hsbp-3/hsbp-2	270	337	116	20	16	18	24	12	2	1	0	0	816	30.21	12.68	43.87	0.33	0.21	0.65	11.40
hsbp-3/hsbp-2	551	851	272	35	37	38	43	40	5	5	2	0	1897	33.63	12.44	45.68	0.38	0.21	0.56	10.81
hsbp-3/hsbp-2	477	545	167	24	25	18	19	23	1	2	0	0	1301	30.02	10.03	39.01	0.33	0.19	0.59	8.61
hsbp-3/hsbp-2	298	351	117	16	19	18	18	12	1	1	0	0	851	29.38	11.46	40.66	0.32	0.20	0.63	9.99
Mean														30.58	11.64	42.04	0.34	0.20	0.61	10.21
SD														1.74	1.04	2.68	0.02	0.01	0.04	1.05
P value (versus Col)														1.17×10^{-6}	2.24×10^{-6}	9.65×10^{-7}			5.80×10^{-4}	1.58×10^{-6}
P value (versus *hsbp-3*)														0.634	0.952	0.755			0.813	0.503
hsbp-2	296	410	136	13	23	21	30	17	3	2	1	0	952	32.14	13.08	46.90	0.35	0.22	0.62	11.55
hsbp-2	154	230	75	12	17	7	19	10	0	1	0	0	625	28.08	10.48	40.32	0.37	0.23	0.63	10.56
hsbp-2	333	545	151	28	22	17	31	23	2	1	2	1	1156	34.39	12.11	46.45	0.38	0.22	0.58	10.99
hsbp-2	160	224	54	7	18	14	14	9	2	1	0	0	503	33.50	11.93	45.83	0.35	0.27	0.76	12.92
hsbp-2	194	275	79	4	10	8	10	11	0	0	0	0	591	31.56	9.39	42.13	0.36	0.14	0.41	7.28
hsbp-2	265	341	97	5	10	9	10	11	0	0	0	0	748	29.48	8.76	38.97	0.33	0.13	0.39	6.02
Mean														31.52	10.96	43.43	0.36	0.20	0.56	9.89
SD														2.39	1.69	3.41	0.02	0.05	0.14	2.66
P value (versus Col)														1.71×10^{-6}	6.47×10^{-5}	5.67×10^{-7}			0.0368	5.18×10^{-4}
P value (versus *hsbp-3*)														0.305	0.412	0.411			0.751	0.679

Appendix Table S7. Crossover frequency (cM) of fluorescent seed reporter lines (CTLs) in Col and *hsbp-3*. CTL crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from *CTL/++* plants, using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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: $cM = 100 \times (1-[1-2(N_{Green}+N_{Red})/N_{Total}]^{1/2})$ (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). *P* values were calculated using Welch's t-test ,which assessed significant differences between wild type and *hcr2* in each CTL line (Wu *et al*, 2015).

CTL	Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
1.17	Col	275	259	1488	332	2354	26.09	2.98	2.88			
1.17	Col	270	292	1480	345	2387	27.26	2.75	2.88			
1.17	Col	275	271	1647	372	2565	24.22	2.99	2.96			
1.17	Col	236	318	1553	361	2468	25.77	2.63	3.13			
1.17	Col	273	331	1662	407	2673	25.97	2.62	2.93			
1.17	Col	263	257	1594	363	2477	23.83	3.00	2.96			
1.17	Col	268	328	1591	396	2583	26.62	2.57	2.89			
1.17	Col	295	333	1429	369	2426	30.55	2.46	2.65			
1.17	Col	276	343	1592	356	2567	28.05	2.67	3.06			
1.17	Col	304	305	1508	316	2433	29.33	2.92	2.92	27.17	1.73	
1.17	Col	248	271	1383	307	2209	27.19	2.82	2.98			
1.17	Col	271	307	1386	291	2255	30.19	2.77	3.01			
1.17	Col	255	318	1478	300	2351	28.41	2.80	3.24			
1.17	Col	233	227	1283	286	2029	26.07	2.96	2.91			
1.17	Col	249	274	1382	290	2195	27.65	2.89	3.07			
1.17	Col	250	246	1250	300	2046	28.23	2.75	2.72			
1.17	Col	248	257	1263	321	2089	28.13	2.61	2.67			
1.17	Col	257	285	1458	344	2344	26.68	2.73	2.90			
1.17	Col	207	249	1209	332	1997	26.29	2.44	2.71			
1.17	Col	239	242	1337	247	2065	26.92	3.22	3.25			
1.17	*hsbp-3*	377	353	1250	186	2166	42.91	3.02	2.85			
1.17	*hsbp-3*	410	411	1454	203	2478	41.92	3.04	3.04			
1.17	*hsbp-3*	449	431	1364	194	2438	47.27	2.90	2.79			
1.17	*hsbp-3*	418	440	1417	189	2464	44.90	2.92	3.06	43.13	2.34	1.05×10^{-7}
1.17	*hsbp-3*	347	404	1371	221	2343	40.09	2.75	3.13			
1.17	*hsbp-3*	321	378	1228	189	2116	41.75	2.73	3.15			
1.17	*hsbp-3*	350	444	1337	218	2349	43.08	2.55	3.14			
1.5	Col	436	454	1960	372	3222	33.10	2.90	2.99			
1.5	Col	427	525	2056	383	3391	33.78	2.73	3.19			
1.5	Col	419	422	1974	415	3230	30.77	2.86	2.87			
1.5	Col	426	415	2049	388	3278	30.22	3.08	3.03			
1.5	Col	408	469	2066	423	3366	30.80	2.77	3.05			
1.5	Col	373	405	2060	389	3227	28.04	3.06	3.23	30.07	2.01	
1.5	Col	403	399	2079	480	3361	27.70	2.82	2.81			
1.5	Col	411	421	2173	402	3407	28.47	3.14	3.19			
1.5	Col	445	414	2026	436	3321	30.52	2.91	2.77			
1.5	Col	412	385	2073	389	3259	28.52	3.21	3.07			
1.5	Col	445	404	2131	455	3435	28.89	3.00	2.82			
1.5	*hsbp-3*	440	467	2164	399	3470	30.92	3.01	3.14			
1.5	*hsbp-3*	324	269	1490	311	2394	28.97	3.13	2.77			
1.5	*hsbp-3*	445	430	2097	457	3429	30.03	2.87	2.80			
1.5	*hsbp-3*	113	112	549	103	877	30.22	3.08	3.06	29.94	0.81	0.847
1.5	*hsbp-3*	429	421	2014	408	3272	30.69	2.95	2.91			
1.5	*hsbp-3*	426	435	2093	459	3413	29.61	2.82	2.86			
1.5	*hsbp-3*	405	407	1942	381	3135	30.58	2.98	2.99			

1.5	hsbp-3	432	401	2149	429	3411	28.48	3.11	2.96			
1.5	hsbp-3	429	459	2178	417	3483	29.99	2.98	3.12			
1.11	Col	247	244	1680	405	2576	21.34	2.97	2.95			
1.11	Col	334	290	1919	503	3046	23.17	2.84	2.64			
1.11	Col	314	340	2174	554	3382	21.69	2.78	2.90			
1.11	Col	328	308	2121	544	3301	21.60	2.87	2.79			
1.11	Col	326	291	2092	527	3236	21.34	2.96	2.79			
1.11	Col	305	353	2184	515	3357	22.03	2.87	3.09			
1.11	Col	223	239	1788	447	2697	18.92	2.93	3.03			
1.11	Col	242	292	1790	458	2782	21.51	2.71	2.97			
1.11	Col	300	278	1966	456	3000	21.60	3.09	2.97			
1.11	Col	224	250	1640	381	2495	21.26	2.95	3.12	20.99	1.50	
1.11	Col	298	250	2071	472	3091	19.66	3.28	3.01			
1.11	Col	266	294	1948	469	2977	21.02	2.90	3.05			
1.11	Col	208	188	1725	391	2512	17.25	3.34	3.19			
1.11	Col	306	302	1957	531	3096	22.07	2.72	2.70			
1.11	Col	282	270	1991	530	3073	19.95	2.84	2.78			
1.11	Col	265	237	1798	468	2768	20.17	2.93	2.78			
1.11	Col	308	314	1930	537	3089	22.72	2.63	2.66			
1.11	Col	80	62	556	131	829	18.92	3.30	2.93			
1.11	Col	298	274	1846	436	2854	22.59	3.02	2.89			
1.11	hsbp-3	328	345	2050	458	3181	24.05	2.96	3.05			
1.11	hsbp-3	316	380	2009	448	3153	25.27	2.81	3.13			
1.11	hsbp-3	379	336	1812	480	3007	27.58	2.69	2.50	23.53	1.85	3.62×10^{-4}
1.11	hsbp-3	303	358	1909	484	3054	24.69	2.63	2.88			
1.11	hsbp-3	376	383	2048	471	3278	26.73	2.84	2.87			
1.11	hsbp-3	145	101	624	126	996	28.86	3.39	2.68			
1.13	Col	366	349	2095	461	3271	24.98	3.04	2.96			
1.13	Col	320	252	1892	455	2919	22.02	3.13	2.77			
1.13	Col	356	308	2043	459	3166	23.81	3.13	2.88			
1.13	Col	361	345	2240	480	3426	23.33	3.15	3.07			
1.13	Col	343	356	2010	495	3204	24.92	2.76	2.82	23.75	0.98	
1.13	Col	394	322	2140	499	3355	24.29	3.09	2.76			
1.13	Col	299	371	2087	509	3266	23.21	2.71	3.04			
1.13	Col	344	359	2094	518	3315	24.11	2.78	2.85			
1.13	Col	346	330	1998	488	3162	24.34	2.87	2.79			
1.13	Col	339	348	2245	504	3436	22.53	3.03	3.08			
1.13	hsbp-3	423	495	2168	398	3484	31.22	2.90	3.24			
1.13	hsbp-3	464	451	1931	396	3242	34.01	2.83	2.77			
1.13	hsbp-3	460	431	2103	436	3430	30.68	2.96	2.83			
1.13	hsbp-3	426	461	2106	345	3338	31.55	3.14	3.33	31.52	1.40	1.33×10^{-8}
1.13	hsbp-3	403	402	2015	390	3210	29.40	3.05	3.05			
1.13	hsbp-3	354	416	1817	383	2970	30.61	2.72	3.03			
1.13	hsbp-3	401	423	1842	376	3042	32.31	2.81	2.92			
1.13	hsbp-3	429	410	1884	370	3093	32.36	2.97	2.87			
1.22	Col	225	302	1788	554	2869	20.46	2.35	2.68			
1.22	Col	246	388	1967	522	3123	22.93	2.43	3.07			
1.22	Col	181	326	1416	480	2403	23.97	1.98	2.64			
1.22	Col	249	269	1862	396	2776	20.83	3.17	3.30	22.25	1.26	
1.22	Col	315	268	1959	451	2993	21.87	3.16	2.91			
1.22	Col	374	197	1851	391	2813	22.93	3.78	2.68			
1.22	Col	353	247	1937	440	2977	22.74	3.33	2.75			
1.22	hsbp-3	420	425	1948	362	3155	31.86	3.01	3.03			
1.22	hsbp-3	473	439	1901	395	3208	34.32	2.85	2.70	33.16	0.84	2.29×10^{-9}
1.22	hsbp-3	399	322	1653	262	2636	32.70	3.51	2.99			

1.22	*hsbp-3*	407	370	1713	292	2782	33.56	3.20	2.98			
1.22	*hsbp-3*	430	396	1834	339	2999	32.98	3.08	2.90			
1.22	*hsbp-3*	319	282	1316	237	2154	33.52	3.15	2.87			
2.1	Col	286	281	1941	440	2948	21.56	3.09	3.06			
2.1	Col	216	251	1868	463	2798	18.38	2.92	3.12			
2.1	Col	288	309	1834	463	2894	23.36	2.75	2.85			
2.1	Col	200	228	1499	394	2321	20.55	2.73	2.91			
2.1	Col	294	263	1940	461	2958	21.04	3.09	2.92			
2.1	Col	317	326	2225	501	3369	21.37	3.07	3.12			
2.1	Col	281	308	1887	494	2970	22.32	2.70	2.83			
2.1	Col	268	318	1963	454	3003	21.92	2.89	3.16			
2.1	Col	236	250	1524	405	2415	22.70	2.69	2.77			
2.1	Col	321	307	2145	579	3352	20.92	2.78	2.72	21.04	1.18	
2.1	Col	317	310	2252	569	3448	20.23	2.92	2.89			
2.1	Col	233	241	1709	392	2575	20.51	3.07	3.12			
2.1	Col	260	247	1729	442	2678	21.17	2.89	2.81			
2.1	Col	257	273	1870	521	2921	20.18	2.68	2.75			
2.1	Col	266	303	2030	534	3133	20.20	2.74	2.92			
2.1	Col	269	291	2143	530	3233	19.16	2.94	3.05			
2.1	Col	269	270	1870	490	2899	20.74	2.81	2.82			
2.1	Col	285	277	1967	492	3021	20.76	2.93	2.89			
2.1	Col	191	209	1290	320	2010	22.41	2.80	2.93			
2.1	Col	232	243	1637	376	2488	21.38	3.02	3.09			
2.1	*hsbp-3*	256	284	2086	515	3141	19.00	2.93	3.07			
2.1	*hsbp-3*	182	171	1536	371	2260	17.08	3.17	3.09			
2.1	*hsbp-3*	287	263	1960	481	2991	20.49	3.02	2.89			
2.1	*hsbp-3*	299	303	2165	564	3331	20.09	2.84	2.86	19.27	1.11	4.28×10^{-3}
2.1	*hsbp-3*	241	239	1860	455	2795	18.97	3.03	3.02			
2.1	*hsbp-3*	192	184	1415	354	2145	19.41	2.99	2.93			
2.1	*hsbp-3*	280	283	2070	520	3153	19.82	2.93	2.94			
2.8	Col	280	342	1698	426	2746	26.04	2.58	2.89			
2.8	Col	355	363	1838	443	2999	27.81	2.72	2.76			
2.8	Col	362	408	1868	424	3062	29.50	2.68	2.90			
2.8	Col	322	337	1975	432	3066	24.49	2.99	3.07			
2.8	Col	354	306	1824	419	2903	26.16	3.00	2.76			
2.8	Col	321	376	1757	430	2884	28.12	2.58	2.84			
2.8	Col	321	286	1945	427	2979	23.03	3.18	2.98			
2.8	Col	324	376	1893	462	3055	26.40	2.65	2.89			
2.8	Col	347	338	1888	394	2967	26.63	3.05	3.00			
2.8	Col	377	355	2036	454	3222	26.13	2.98	2.88			
2.8	Col	315	336	1796	391	2838	26.43	2.90	3.02			
2.8	Col	301	301	1591	412	2605	26.66	2.65	2.65	26.36	1.41	
2.8	Col	313	305	1740	442	2800	25.26	2.75	2.71			
2.8	Col	335	308	1869	424	2936	25.03	3.01	2.87			
2.8	Col	363	352	2001	424	3140	26.20	3.05	2.99			
2.8	Col	374	353	2033	458	3218	25.96	2.97	2.87			
2.8	Col	388	363	2106	470	3327	25.94	2.99	2.88			
2.8	Col	374	427	2051	507	3359	27.68	2.60	2.81			
2.8	Col	331	364	2020	431	3146	25.29	2.96	3.13			
2.8	Col	356	388	1950	451	3145	27.41	2.75	2.90			
2.8	Col	361	357	2108	487	3313	24.73	2.93	2.91			
2.8	Col	336	396	1864	425	3021	28.21	2.68	2.97			
2.8	Col	360	444	2166	458	3428	27.14	2.80	3.19			
2.8	*hsbp-3*	459	422	1847	370	3098	34.33	2.91	2.74	32.03	1.19	2.09×10^{-8}
2.8	*hsbp-3*	402	454	2105	375	3336	30.23	3.02	3.29			

2.8	*hsbp-3*	401	383	1731	383	2898	32.26	2.78	2.70			
2.8	*hsbp-3*	360	413	1793	356	2922	31.38	2.80	3.08			
2.8	*hsbp-3*	426	479	2031	385	3321	32.55	2.84	3.09			
2.8	*hsbp-3*	409	440	1916	388	3153	32.07	2.81	2.96			
2.8	*hsbp-3*	466	467	2105	418	3456	32.17	2.91	2.91			
2.8	*hsbp-3*	415	446	2010	398	3269	31.21	2.87	3.02			
2.2	Col	330	337	2273	478	3418	21.92	3.19	3.23			
2.2	Col	298	291	1865	467	2921	22.75	2.85	2.82			
2.2	Col	335	307	2234	484	3360	21.40	3.25	3.10			
2.2	Col	291	356	2146	477	3270	22.26	2.93	3.26			
2.2	Col	361	378	2164	507	3410	24.73	2.85	2.93			
2.2	Col	355	325	2186	516	3382	22.68	3.02	2.88			
2.2	Col	275	285	1944	482	2986	20.95	2.89	2.94			
2.2	Col	301	340	2099	475	3215	22.46	2.94	3.14			
2.2	Col	282	288	1819	405	2794	23.06	3.03	3.07			
2.2	Col	307	307	1912	454	2980	23.32	2.92	2.92			
2.2	Col	293	294	2033	487	3107	21.12	2.98	2.98	22.37	1.10	
2.2	Col	279	285	1840	459	2863	22.15	2.85	2.88			
2.2	Col	295	311	1848	428	2882	23.88	2.90	2.99			
2.2	Col	299	310	2009	470	3088	22.18	2.96	3.02			
2.2	Col	286	292	1897	460	2935	22.15	2.90	2.93			
2.2	Col	268	255	1718	416	2657	22.13	2.96	2.88			
2.2	Col	251	248	1730	460	2689	20.70	2.80	2.78			
2.2	Col	247	312	1954	476	2989	20.88	2.79	3.13			
2.2	Col	310	332	2139	516	3297	21.86	2.89	2.99			
2.2	Col	301	320	1948	517	3086	22.70	2.69	2.77			
2.2	Col	315	314	1885	416	2930	24.46	3.01	3.01			
2.2	*hsbp-3*	439	488	2050	379	3356	33.10	2.87	3.10			
2.2	*hsbp-3*	457	453	1865	365	3140	35.16	2.84	2.82			
2.2	*hsbp-3*	378	409	1834	355	2976	31.36	2.90	3.06			
2.2	*hsbp-3*	378	461	1826	349	3014	33.42	2.72	3.15	33.22	1.23	3.51×10^{-9}
2.2	*hsbp-3*	394	448	1797	334	2973	34.15	2.80	3.08			
2.2	*hsbp-3*	425	441	1916	356	3138	33.06	2.94	3.02			
2.2	*hsbp-3*	404	439	1916	356	3115	32.27	2.92	3.10			
2.7	Col	296	349	2255	535	3435	20.98	2.89	3.13			
2.7	Col	295	325	2090	543	3253	21.34	2.75	2.88			
2.7	Col	391	392	2196	595	3574	25.04	2.62	2.62			
2.7	Col	303	333	2291	562	3489	20.29	2.90	3.03			
2.7	Col	362	347	2215	494	3418	23.51	3.06	2.99			
2.7	Col	306	403	2189	501	3399	23.66	2.76	3.21			
2.7	Col	294	351	2247	516	3408	21.17	2.93	3.21			
2.7	Col	358	334	2314	555	3561	21.81	3.01	2.90			
2.7	Col	315	414	2248	540	3517	23.49	2.69	3.11			
2.7	Col	321	342	2077	484	3224	23.27	2.90	3.00	22.49	1.45	
2.7	Col	319	307	2081	506	3213	21.88	2.95	2.89			
2.7	Col	320	364	2072	488	3244	23.95	2.81	3.01			
2.7	Col	293	326	2065	437	3121	22.33	3.09	3.28			
2.7	Col	371	370	2182	472	3395	24.93	3.03	3.03			
2.7	Col	360	372	2350	603	3685	22.37	2.78	2.83			
2.7	Col	312	335	2401	545	3593	20.01	3.08	3.19			
2.7	Col	348	369	2308	593	3618	22.31	2.76	2.84			
2.7	Col	319	335	2015	480	3149	23.54	2.86	2.94			
2.7	Col	291	333	2222	497	3343	20.84	3.03	3.24			
2.7	Col	338	377	2300	490	3505	23.06	3.04	3.23			
2.7	*hsbp-3*	546	597	2102	339	3584	39.82	2.83	3.05	38.84	0.91	$2.20 \times 10^{-}$

2.7	*hsbp-3*	533	520	2008	325	3386	38.52	3.01	2.95			16
2.7	*hsbp-3*	491	494	1949	337	3271	36.93	2.94	2.95			
2.7	*hsbp-3*	476	517	1930	294	3217	38.14	2.97	3.18			
2.7	*hsbp-3*	572	546	2061	343	3522	39.57	2.96	2.85			
2.7	*hsbp-3*	595	575	2146	367	3683	39.61	2.91	2.83			
2.7	*hsbp-3*	547	614	2223	338	3722	38.67	2.91	3.21			
2.7	*hsbp-3*	552	563	2139	347	3601	38.30	2.96	3.01			
2.7	*hsbp-3*	546	599	2136	323	3604	39.62	2.91	3.15			
2.7	*hsbp-3*	571	550	2087	348	3556	39.21	2.96	2.87			
3.2	Col	278	234	1833	472	2817	20.22	2.99	2.76			
3.2	Col	226	251	2103	569	3149	16.51	2.84	2.96			
3.2	Col	242	287	2148	564	3241	17.93	2.81	3.02			
3.2	Col	186	189	1662	443	2480	16.48	2.92	2.94			
3.2	Col	211	232	1989	591	3023	15.92	2.67	2.77			
3.2	Col	78	104	888	236	1306	15.07	2.84	3.16			
3.2	Col	237	223	1726	459	2645	19.24	2.88	2.80			
3.2	Col	265	245	2345	657	3512	15.76	2.89	2.81			
3.2	Col	90	128	1024	273	1515	15.61	2.78	3.17	16.41	1.72	
3.2	Col	259	187	2207	616	3269	14.73	3.07	2.74			
3.2	Col	223	204	2172	626	3225	14.26	2.89	2.80			
3.2	Col	287	273	2346	588	3494	17.57	3.06	2.99			
3.2	Col	263	248	2277	568	3356	16.61	3.11	3.04			
3.2	Col	239	266	2346	564	3415	16.08	3.11	3.25			
3.2	Col	235	240	1917	515	2907	17.95	2.85	2.88			
3.2	Col	216	224	2299	676	3415	13.84	2.79	2.83			
3.2	Col	228	208	2079	586	3101	15.22	2.91	2.81			
3.2	*hsbp-3*	398	428	1911	317	3054	32.25	3.10	3.27			
3.2	*hsbp-3*	462	425	2118	428	3433	30.48	3.02	2.86			
3.2	*hsbp-3*	383	398	2105	408	3294	27.49	3.09	3.16			
3.2	*hsbp-3*	419	439	2153	465	3476	28.84	2.85	2.93	30.39	1.73	3.42×10^{-11}
3.2	*hsbp-3*	421	448	1898	389	3156	32.97	2.77	2.90			
3.2	*hsbp-3*	418	430	2064	384	3296	30.33	3.05	3.11			
3.2	*hsbp-3*	398	477	2140	400	3415	30.17	2.89	3.28			
3.2	*hsbp-3*	322	337	1591	293	2543	30.59	3.04	3.13			
3.6	Col	90	99	1781	582	2552	7.70	2.75	2.80			
3.6	Col	123	117	2117	661	3018	8.30	2.88	2.85			
3.6	Col	108	96	1904	560	2668	7.96	3.07	2.99			
3.6	Col	85	105	1889	579	2658	7.42	2.89	3.00			
3.6	Col	99	83	2079	648	2909	6.47	2.98	2.89			
3.6	Col	121	88	2101	637	2947	7.36	3.06	2.89			
3.6	Col	76	136	1875	574	2661	8.31	2.75	3.09			
3.6	Col	85	83	1798	569	2535	6.86	2.89	2.88			
3.6	Col	83	104	2117	650	2954	6.54	2.92	3.03			
3.6	Col	103	128	1997	614	2842	8.49	2.83	2.96	7.66	0.68	
3.6	Col	98	121	2064	664	2947	7.73	2.75	2.87			
3.6	Col	106	118	1995	622	2841	8.22	2.84	2.90			
3.6	Col	124	119	2359	755	3357	7.52	2.84	2.82			
3.6	Col	119	106	2000	621	2846	8.25	2.91	2.85			
3.6	Col	117	129	2171	651	3068	8.37	2.93	2.99			
3.6	Col	99	138	2147	696	3080	8.02	2.69	2.87			
3.6	Col	65	86	1605	481	2237	6.99	2.95	3.10			
3.6	Col	109	116	1978	614	2817	8.33	2.86	2.90			
3.6	Col	83	98	2008	633	2822	6.63	2.86	2.94			
3.6	*hsbp-3*	243	226	2049	565	3083	16.59	2.90	2.82	14.83	0.76	4.76×10^{-13}
3.6	*hsbp-3*	210	183	1886	547	2826	15.04	2.87	2.73			

3.6	*hsbp-3*	169	199	1871	549	2788	14.21	2.73	2.88			
3.6	*hsbp-3*	194	227	2008	586	3015	15.10	2.71	2.87			
3.6	*hsbp-3*	179	183	1857	504	2723	14.32	2.96	2.99			
3.6	*hsbp-3*	66	73	700	186	1025	14.63	2.96	3.07			
3.6	*hsbp-3*	180	211	2010	531	2932	14.37	2.95	3.12			
3.6	*hsbp-3*	205	188	1888	550	2831	15.01	2.84	2.75			
3.6	*hsbp-3*	177	195	1965	489	2826	14.17	3.13	3.24			
3.8	Col	311	311	1361	256	2239	33.34	2.95	2.95			
3.8	Col	394	423	1756	395	2968	32.96	2.63	2.76			
3.8	Col	323	328	1519	305	2475	31.16	2.91	2.94			
3.8	Col	374	446	1788	385	2993	32.76	2.60	2.94			
3.8	Col	390	423	1784	378	2975	32.66	2.71	2.87			
3.8	Col	433	405	1965	400	3203	30.95	2.98	2.85			
3.8	Col	393	411	1714	373	2891	33.38	2.69	2.77			
3.8	Col	268	271	1257	257	2053	31.09	2.89	2.91			
3.8	Col	440	472	1979	394	3285	33.31	2.79	2.94			
3.8	Col	439	452	2079	427	3397	31.05	2.86	2.92			
3.8	Col	349	339	1762	351	2801	28.67	3.06	3.00	31.53	1.59	
3.8	Col	424	438	1888	396	3146	32.77	2.77	2.84			
3.8	Col	369	401	1799	367	2936	31.05	2.82	2.99			
3.8	Col	366	408	1891	399	3064	29.66	2.80	3.01			
3.8	Col	441	432	1899	342	3114	33.72	3.02	2.98			
3.8	Col	426	457	1989	410	3282	32.04	2.79	2.93			
3.8	Col	390	358	1787	368	2903	30.38	3.00	2.83			
3.8	Col	292	333	1608	369	2602	27.92	2.71	2.94			
3.8	Col	387	379	1878	339	2983	30.26	3.15	3.11			
3.8	Col	444	464	2083	462	3453	31.15	2.73	2.81			
3.8	Col	402	480	1989	417	3288	31.92	2.67	3.01			
3.8	*hsbp-3*	264	284	1416	301	2265	28.16	2.87	3.01			
3.8	*hsbp-3*	440	439	2024	433	3336	31.22	2.83	2.82			
3.8	*hsbp-3*	404	484	2099	444	3431	30.55	2.70	3.05			
3.8	*hsbp-3*	387	462	2118	453	3420	29.04	2.74	3.07	30.03	1.90	0.0920
3.8	*hsbp-3*	414	543	2024	516	3497	32.72	2.30	2.76			
3.8	*hsbp-3*	384	430	1874	408	3096	31.14	2.69	2.91			
3.8	*hsbp-3*	330	311	1757	314	2712	27.39	3.34	3.21			
3.9	Col	323	271	2545	716	3855	16.82	2.91	2.71			
3.9	Col	260	308	2360	614	3542	17.58	2.84	3.05			
3.9	Col	269	302	2479	639	3689	16.91	2.92	3.06			
3.9	Col	288	343	2465	677	3773	18.42	2.70	2.91			
3.9	Col	312	328	2505	710	3855	18.27	2.71	2.77			
3.9	Col	310	254	2418	655	3637	16.94	3.00	2.77			
3.9	Col	286	308	2627	709	3930	16.47	2.86	2.95			
3.9	Col	324	291	2631	698	3944	17.05	2.99	2.86			
3.9	Col	315	339	2552	659	3865	18.66	2.87	2.97			
3.9	Col	259	234	2504	733	3730	14.23	2.86	2.76	17.37	1.12	
3.9	Col	347	328	2600	659	3934	18.95	2.99	2.91			
3.9	Col	329	275	2623	730	3957	16.65	2.94	2.74			
3.9	Col	300	351	2582	719	3952	18.11	2.69	2.88			
3.9	Col	324	284	2672	721	4001	16.57	2.98	2.83			
3.9	Col	361	304	2602	706	3973	18.44	2.93	2.72			
3.9	Col	320	336	2590	669	3915	18.46	2.90	2.96			
3.9	Col	341	280	2538	744	3903	17.43	2.81	2.60			
3.9	Col	298	327	2605	653	3883	17.65	2.96	3.08			
3.9	Col	305	292	2623	723	3943	16.50	2.88	2.84			
3.9	*hsbp-3*	216	218	2537	761	3732	12.40	2.81	2.82	10.63	1.06	$2.97 \times 10^{-}$

3.9	hsbp-3	178	218	2606	809	3811	11.00	2.71	2.86			[11]
3.9	hsbp-3	159	191	2659	805	3814	9.64	2.83	2.96			
3.9	hsbp-3	202	187	2749	809	3947	10.40	2.96	2.90			
3.9	hsbp-3	208	166	2631	828	3833	10.29	2.86	2.70			
3.9	hsbp-3	206	193	2845	788	4032	10.44	3.11	3.06			
3.9	hsbp-3	225	225	2714	770	3934	12.18	2.95	2.95			
3.9	hsbp-3	179	178	2588	825	3770	9.97	2.76	2.75			
3.9	hsbp-3	175	173	2741	830	3919	9.31	2.91	2.90			
3.15	Col	288	297	1657	391	2633	25.46	2.83	2.88			
3.15	Col	277	285	1649	355	2566	25.04	3.01	3.06			
3.15	Col	266	282	1640	346	2534	24.67	3.04	3.14			
3.15	Col	247	269	1579	345	2440	24.04	2.97	3.12			
3.15	Col	236	264	1621	367	2488	22.66	2.94	3.13			
3.15	Col	278	266	1621	377	2542	24.37	2.95	2.88			
3.15	Col	286	259	1557	372	2474	25.21	2.92	2.76			
3.15	Col	263	259	1528	353	2403	24.80	2.93	2.90	24.38	1.21	
3.15	Col	230	240	1471	329	2270	23.46	2.99	3.06			
3.15	Col	253	264	1464	325	2306	25.73	2.92	2.99			
3.15	Col	226	293	1579	358	2456	24.02	2.77	3.21			
3.15	Col	268	286	1592	344	2490	25.50	2.95	3.07			
3.15	Col	261	259	1739	389	2648	22.07	3.09	3.07			
3.15	Col	272	288	1621	366	2547	25.15	2.89	2.99			
3.15	Col	304	311	1772	362	2749	25.67	3.08	3.13			
3.15	Col	261	266	1722	417	2666	22.24	2.90	2.93			
3.15	hsbp-3	421	433	1478	218	2550	42.54	2.92	2.99			
3.15	hsbp-3	472	461	1714	242	2889	40.49	3.11	3.05			
3.15	hsbp-3	396	431	1415	233	2475	42.41	2.73	2.93			
3.15	hsbp-3	420	388	1425	236	2469	41.22	2.96	2.76	41.09	1.27	8.61×10^{-12}
3.15	hsbp-3	341	414	1435	223	2413	38.83	2.79	3.28			
3.15	hsbp-3	444	465	1636	218	2763	41.52	3.05	3.17			
3.15	hsbp-3	457	453	1657	243	2810	40.64	3.04	3.01			
4.1	Col	228	226	1280	323	2057	25.26	2.75	2.73			
4.1	Col	247	393	1517	443	2600	28.75	2.11	2.77			
4.1	Col	291	392	1553	435	2671	30.10	2.23	2.68			
4.1	Col	308	303	1450	377	2438	29.38	2.59	2.56			
4.1	Col	246	205	1173	307	1931	27.00	2.77	2.49			
4.1	Col	237	309	1389	366	2301	27.51	2.41	2.82			
4.1	Col	216	239	1216	285	1956	26.87	2.73	2.90			
4.1	Col	298	225	1440	366	2329	25.78	2.94	2.51			
4.1	Col	324	270	1585	428	2607	26.22	2.73	2.47			
4.1	Col	194	152	813	243	1402	28.84	2.55	2.21			
4.1	Col	289	373	1711	453	2826	27.10	2.42	2.81			
4.1	Col	195	214	950	317	1676	28.45	2.16	2.27			
4.1	Col	186	154	761	236	1337	29.90	2.43	2.17	27.19	1.61	
4.1	Col	187	178	978	254	1597	26.32	2.70	2.62			
4.1	Col	300	423	1945	489	3157	26.38	2.46	3.00			
4.1	Col	414	357	2011	467	3249	27.52	2.94	2.69			
4.1	Col	241	257	1323	428	2249	25.36	2.28	2.36			
4.1	Col	295	256	1510	438	2499	25.23	2.60	2.41			
4.1	Col	387	312	1827	399	2925	27.75	3.11	2.72			
4.1	Col	378	320	1762	489	2949	27.43	2.65	2.40			
4.1	Col	289	294	1504	398	2485	27.15	2.59	2.62			
4.1	Col	164	169	967	240	1540	24.67	2.77	2.81			
4.1	Col	267	347	1756	502	2872	24.34	2.38	2.73			
4.1	Col	232	268	1220	410	2130	27.16	2.14	2.32			

4.1	Col	330	386	1589	521	2826	29.77	2.12	2.32			
4.1	Col	259	259	1296	427	2241	26.67	2.27	2.27			
4.1	hsbp-3	125	134	875	256	1390	20.80	2.56	2.65			
4.1	hsbp-3	124	133	684	174	1115	26.58	2.63	2.74			
4.1	hsbp-3	147	135	860	196	1338	23.94	3.04	2.90			
4.1	hsbp-3	214	161	1012	249	1636	26.41	2.99	2.53			
4.1	hsbp-3	156	163	862	218	1399	26.25	2.67	2.74	24.52	2.27	7.78×10^{-3}
4.1	hsbp-3	121	120	809	197	1247	21.68	2.93	2.92			
4.1	hsbp-3	179	159	887	213	1438	27.21	2.87	2.67			
4.1	hsbp-3	196	147	1002	263	1608	24.28	2.92	2.50			
4.1	hsbp-3	315	273	1757	488	2833	23.52	2.72	2.53			
4.7	Col	347	336	2236	510	3429	22.43	3.05	3.00			
4.7	Col	314	247	1868	461	2890	21.78	3.08	2.73			
4.7	Col	173	212	1287	325	1997	21.61	2.72	3.01			
4.7	Col	292	315	2192	528	3327	20.31	2.95	3.06			
4.7	Col	322	295	2061	505	3183	21.75	2.98	2.85			
4.7	Col	287	279	2120	492	3178	19.76	3.12	3.08	20.83	1.02	
4.7	Col	306	335	2413	560	3614	19.67	3.04	3.17			
4.7	Col	278	260	1986	532	3056	19.51	2.86	2.77			
4.7	Col	352	292	2245	592	3481	20.63	2.94	2.69			
4.7	Col	353	341	2314	605	3613	21.53	2.82	2.77			
4.7	Col	311	320	2232	613	3476	20.19	2.73	2.76			
4.7	hsbp-3	589	599	2162	379	3729	39.76	2.81	2.85			
4.7	hsbp-3	548	478	2099	363	3488	35.84	3.15	2.83			
4.7	hsbp-3	545	465	1993	338	3341	37.12	3.16	2.78	36.83	1.79	2.44×10^{-7}
4.7	hsbp-3	561	419	2069	386	3435	34.47	3.27	2.63			
4.7	hsbp-3	498	572	2076	365	3511	37.51	2.75	3.07			
4.7	hsbp-3	520	517	2082	372	3491	36.29	2.93	2.91			
5.1	Col	429	436	2653	572	4090	24.04	3.06	3.09			
5.1	Col	374	384	2755	664	4177	20.18	2.99	3.02			
5.1	Col	411	452	2649	629	4141	23.63	2.83	2.98	21.89	1.60	
5.1	Col	359	358	2361	609	3687	21.83	2.81	2.81			
5.1	Col	316	403	2528	610	3857	20.81	2.81	3.17			
5.1	Col	336	382	2506	617	3841	20.87	2.84	3.03			
5.1	hsbp-3	567	595	2397	409	3968	35.63	2.95	3.07			
5.1	hsbp-3	512	614	2296	457	3879	35.24	2.62	3.00			
5.1	hsbp-3	514	604	2306	455	3879	34.92	2.66	3.00			
5.1	hsbp-3	594	602	2593	466	4255	33.83	2.98	3.01			
5.1	hsbp-3	520	532	2248	440	3740	33.86	2.85	2.90			
5.1	hsbp-3	567	510	2233	448	3758	34.67	2.92	2.70	34.89	1.38	3.58×10^{-8}
5.1	hsbp-3	532	550	2349	431	3862	33.69	2.94	3.01			
5.1	hsbp-3	426	402	1586	283	2697	37.87	2.94	2.80			
5.1	hsbp-3	339	404	1684	272	2699	32.96	2.99	3.42			
5.1	hsbp-3	413	413	1706	247	2779	36.32	3.21	3.21			
5.1	hsbp-3	377	343	1527	257	2504	34.81	3.17	2.95			
5.2	Col	186	220	1527	419	2352	19.08	2.68	2.89			
5.2	Col	197	208	1576	416	2397	18.63	2.84	2.91			
5.2	Col	179	194	1604	426	2403	16.96	2.88	2.97			
5.2	Col	184	194	1535	415	2328	17.83	2.82	2.89			
5.2	Col	180	163	1643	451	2437	15.24	2.97	2.86	16.78	1.46	
5.2	Col	157	187	1550	420	2314	16.17	2.81	3.01			
5.2	Col	186	193	1552	430	2361	17.60	2.79	2.83			
5.2	Col	144	135	1488	398	2165	13.85	3.06	2.99			
5.2	Col	175	205	1504	405	2289	18.27	2.75	2.95			
5.2	Col	170	154	1444	399	2167	16.28	2.92	2.81			

5.2	Col	152	217	1622	412	2403	16.76	2.82	3.26			
5.2	Col	145	168	1353	375	2041	16.74	2.76	2.93			
5.2	Col	170	209	1607	417	2403	17.26	2.84	3.09			
5.2	Col	183	191	1479	392	2245	18.34	2.85	2.90			
5.2	Col	158	173	1673	450	2454	14.55	2.94	3.04			
5.2	Col	161	161	1538	416	2276	15.32	2.94	2.94			
5.2	Col	172	197	1446	417	2232	18.19	2.64	2.79			
5.2	Col	162	182	1649	428	2421	15.39	2.97	3.10			
5.2	Col	185	188	1688	427	2488	16.32	3.05	3.07			
5.2	*hsbp-3*	245	257	1504	364	2370	24.08	2.82	2.89			
5.2	*hsbp-3*	248	253	1555	363	2419	23.46	2.93	2.96			
5.2	*hsbp-3*	238	248	1424	332	2242	24.74	2.87	2.93			
5.2	*hsbp-3*	239	254	1371	370	2234	25.26	2.58	2.67			
5.2	*hsbp-3*	231	232	1441	318	2222	23.63	3.04	3.05	24.48	0.80	6.67×10^{-16}
5.2	*hsbp-3*	260	268	1484	323	2335	25.99	2.95	3.01			
5.2	*hsbp-3*	199	227	1265	283	1974	24.61	2.87	3.10			
5.2	*hsbp-3*	284	226	1533	328	2371	24.51	3.28	2.87			
5.2	*hsbp-3*	252	248	1541	326	2367	24.00	3.12	3.10			
5.5	Col	325	453	2039	507	3324	27.07	2.46	3.00			
5.5	Col	418	376	1883	361	3038	30.91	3.12	2.90			
5.5	Col	387	423	2066	477	3353	28.11	2.73	2.88			
5.5	Col	330	358	1834	399	2921	27.27	2.86	3.01			
5.5	Col	396	390	2030	429	3245	28.20	2.96	2.93			
5.5	Col	380	382	1963	384	3109	28.60	3.06	3.07			
5.5	Col	409	362	2007	496	3274	27.27	2.82	2.62	27.37	1.47	
5.5	Col	369	362	2187	430	3348	24.95	3.23	3.19			
5.5	Col	386	388	2247	438	3459	25.67	3.19	3.20			
5.5	Col	378	354	2015	431	3178	26.56	3.05	2.93			
5.5	Col	347	356	1982	415	3100	26.08	3.02	3.07			
5.5	Col	429	370	2119	434	3352	27.66	3.17	2.88			
5.5	Col	370	429	2175	499	3473	26.52	2.74	3.00			
5.5	Col	403	434	2191	420	3448	28.27	3.04	3.19			
5.5	*hsbp-3*	325	361	2165	467	3318	23.42	3.01	3.19			
5.5	*hsbp-3*	327	340	2300	497	3464	21.58	3.14	3.20			
5.5	*hsbp-3*	330	294	2218	480	3322	20.99	3.29	3.10			
5.5	*hsbp-3*	297	266	1789	395	2747	23.18	3.16	2.97	22.04	1.19	2.51×10^{-7}
5.5	*hsbp-3*	362	352	2481	543	3738	21.39	3.18	3.13			
5.5	*hsbp-3*	329	280	2259	438	3306	20.53	3.60	3.31			
5.5	*hsbp-3*	285	285	1821	392	2783	23.16	3.11	3.11			
5.13	Col	423	372	2073	396	3264	28.39	3.25	2.99			
5.13	Col	391	450	2036	499	3376	29.16	2.56	2.79			
5.13	Col	390	423	2072	442	3327	28.50	2.85	3.00			
5.13	Col	423	368	2190	475	3456	26.36	3.10	2.85			
5.13	Col	369	375	1906	359	3009	28.90	3.10	3.13			
5.13	Col	397	382	2025	392	3196	28.41	3.13	3.05			
5.13	Col	351	352	1999	372	3074	26.34	3.25	3.25			
5.13	Col	400	422	1984	385	3191	30.37	2.95	3.06	28.18	1.51	
5.13	Col	429	359	1933	325	3046	30.53	3.45	3.04			
5.13	Col	372	391	2021	380	3164	28.05	3.10	3.21			
5.13	Col	402	368	1969	336	3075	29.35	3.37	3.17			
5.13	Col	365	368	2064	338	3135	27.04	3.44	3.46			
5.13	Col	388	325	1990	376	3079	26.73	3.39	3.03			
5.13	Col	430	377	2035	406	3248	29.07	3.15	2.89			
5.13	Col	361	318	2000	378	3057	25.45	3.39	3.14			
5.13	*hsbp-3*	518	450	2181	464	3613	31.87	2.95	2.68	31.01	1.31	2.40

5.13	hsbp-3	414	467	1981	420	3282	31.95	2.70	2.94			$\times 10^{-4}$
5.13	hsbp-3	404	427	2193	379	3403	28.47	3.22	3.35			
5.13	hsbp-3	418	386	1896	359	3059	31.13	3.11	2.94			
5.13	hsbp-3	415	458	1965	342	3180	32.85	2.98	3.20			
5.13	hsbp-3	427	446	2088	402	3363	30.66	2.97	3.06			
5.13	hsbp-3	495	474	2354	429	3752	30.47	3.16	3.06			
5.13	hsbp-3	441	454	2168	386	3449	30.65	3.11	3.17			
5.14	Col	113	133	1873	709	2828	9.11	2.36	2.44			
5.14	Col	152	109	1974	795	3030	9.02	2.35	2.20			
5.14	Col	116	91	1712	647	2566	8.42	2.48	2.36			
5.14	Col	130	135	1753	789	2807	9.93	2.04	2.05			
5.14	Col	129	124	1839	752	2844	9.33	2.25	2.23			
5.14	Col	116	114	1691	662	2583	9.34	2.33	2.32			
5.14	Col	121	112	1977	835	3045	7.97	2.22	2.19			
5.14	Col	117	87	1893	737	2834	7.48	2.44	2.32			
5.14	Col	122	116	1722	715	2675	9.33	2.22	2.20			
5.14	Col	119	126	1783	771	2799	9.17	2.12	2.14			
5.14	Col	121	141	1939	834	3035	9.04	2.11	2.18	8.94	0.92	
5.14	Col	148	109	1923	780	2960	9.10	2.33	2.19			
5.14	Col	111	104	1738	717	2670	8.41	2.25	2.22			
5.14	Col	137	102	1890	783	2912	8.58	2.29	2.17			
5.14	Col	148	124	1901	823	2996	9.53	2.16	2.09			
5.14	Col	136	136	1825	786	2883	9.93	2.13	2.13			
5.14	Col	153	99	1745	732	2729	9.71	2.28	2.08			
5.14	Col	120	108	1849	808	2885	8.24	2.15	2.11			
5.14	Col	99	94	1810	798	2801	7.15	2.14	2.12			
5.14	Col	111	109	1837	830	2887	7.94	2.07	2.07			
5.14	Col	112	124	1378	568	2182	11.47	2.15	2.21			
5.14	Col	115	100	1739	701	2655	8.46	2.31	2.25			
5.14	Col	144	114	1972	807	3037	8.89	2.30	2.19			
5.14	hsbp-3	239	241	1385	422	2287	23.83	2.45	2.46			
5.14	hsbp-3	210	248	1463	548	2469	20.69	2.10	2.26			
5.14	hsbp-3	259	261	1799	623	2942	19.59	2.33	2.34	20.95	1.83	7.17×10^{-6}
5.14	hsbp-3	232	236	1635	618	2721	19.01	2.19	2.20			
5.14	hsbp-3	194	251	1280	510	2235	22.42	1.94	2.17			
5.14	hsbp-3	238	276	1706	616	2836	20.16	2.18	2.32			

Appendix Table S8. Crossover frequency (cM) of fluorescent seed reporter lines (CTLs) in Col and *meiMIGS-HSBP*. *CTL* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from *CTL/++* plants, using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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: $cM = 100 \times (1-[1-2(N_{Green}+N_{Red})/N_{Total}]^{1/2})$ (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). *P* values were calculated using Welch's t-test ,which assessed significant differences between Col and *meiMIGS-HSBP* in each CTL line (Wu *et al*, 2015).

CTL	Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	P value
1.13	Col	242	240	1533	361	2376	22.91	2.95	2.94			
1.13	Col	205	191	1331	337	2064	21.50	2.91	2.81			
1.13	Col	344	354	2117	516	3331	23.78	2.83	2.87			
1.13	Col	384	370	2240	523	3517	24.42	2.94	2.88	23.32	1.02	
1.13	Col	337	328	2025	479	3169	23.82	2.93	2.88			
1.13	Col	394	340	2277	531	3542	23.48	3.07	2.83			
1.13	*meiMIGS-HSBP*	241	212	1234	302	1989	26.21	2.87	2.66			
1.13	*meiMIGS-HSBP*	291	285	1412	291	2279	29.68	2.96	2.92			
1.13	*meiMIGS-HSBP*	372	372	1950	380	3074	28.17	3.09	3.09			
1.13	*meiMIGS-HSBP*	367	374	2051	447	3239	26.35	2.95	2.98	27.80	1.12	6.41×10^{-6}
1.13	*meiMIGS-HSBP*	221	205	1080	258	1764	28.10	2.81	2.68			
1.13	*meiMIGS-HSBP*	250	240	1308	265	2063	27.55	3.09	3.01			
1.13	*meiMIGS-HSBP*	401	379	2032	397	3209	28.32	3.14	3.02			
1.13	*meiMIGS-HSBP*	368	406	2059	380	3213	28.01	3.09	3.30			
1.5	Col	390	414	2026	432	3262	28.78	2.86	2.97			
1.5	Col	451	480	2143	414	3488	31.73	2.90	3.03			
1.5	Col	410	414	2040	393	3257	29.71	3.04	3.06	29.50	1.31	
1.5	Col	393	378	1928	369	3068	29.47	3.11	3.03			
1.5	Col	423	445	2126	454	3448	29.52	2.83	2.93			
1.5	Col	362	369	1911	415	3057	27.77	2.90	2.93			
1.5	*meiMIGS-HSBP*	393	389	1991	405	3178	28.74	3.00	2.98			
1.5	*meiMIGS-HSBP*	388	390	2044	424	3246	27.84	2.99	3.00			
1.5	*meiMIGS-HSBP*	432	411	1887	363	3093	32.55	3.00	2.89	29.97	1.68	0.598
1.5	*meiMIGS-HSBP*	406	387	1949	388	3130	29.77	3.04	2.94			
1.5	*meiMIGS-HSBP*	396	368	1868	382	3014	29.78	3.02	2.87			
1.5	*meiMIGS-HSBP*	427	458	2086	394	3365	31.15	2.95	3.10			
1.26	Col	27	28	1454	501	2010	2.77	2.80	2.81			
1.26	Col	29	26	1548	517	2120	2.63	2.90	2.88			
1.26	Col	23	17	1143	404	1587	2.55	2.77	2.72			
1.26	Col	21	23	1457	500	2001	2.22	2.83	2.84	2.54	0.28	
1.26	Col	39	42	2144	697	2922	2.81	2.95	2.97			
1.26	Col	35	46	2029	736	2846	2.89	2.64	2.69			
1.26	Col	28	15	1441	532	2016	2.16	2.69	2.60			
1.26	Col	24	22	1443	515	2004	2.32	2.73	2.72			
1.26	*meiMIGS-HSBP*	50	56	1641	512	2259	4.81	2.98	3.02			
1.26	*meiMIGS-HSBP*	55	38	1692	504	2289	4.15	3.22	3.09			
1.26	*meiMIGS-HSBP*	44	37	1663	523	2267	3.64	3.05	3.00			
1.26	*meiMIGS-HSBP*	70	80	2047	652	2849	5.41	2.89	2.95	4.77	1.10	5.64×10^{-4}
1.26	*meiMIGS-HSBP*	144	74	2348	676	3242	6.97	3.32	2.95			
1.26	*meiMIGS-HSBP*	40	38	1625	549	2252	3.53	2.84	2.82			
1.26	*meiMIGS-HSBP*	53	58	1689	598	2398	4.74	2.66	2.68			
1.26	*meiMIGS-HSBP*	81	72	2323	715	3191	4.92	3.05	3.01			

2.7	Col	225	195	1574	343	2337	19.96	3.34	3.11			
2.7	Col	207	188	1443	355	2193	20.01	3.04	2.90			
2.7	Col	211	224	1425	381	2241	21.78	2.70	2.79	21.58	1.32	
2.7	Col	309	347	2192	509	3357	21.95	2.92	3.10			
2.7	Col	290	336	1998	451	3075	23.00	2.91	3.15			
2.7	Col	340	370	2269	539	3518	22.78	2.87	3.00			
2.7	*meiMIGS-HSBP*	249	293	1469	357	2368	26.36	2.64	2.91			
2.7	*meiMIGS-HSBP*	481	427	2170	435	3513	30.50	3.08	2.84			
2.7	*meiMIGS-HSBP*	502	428	2126	390	3446	32.16	3.21	2.86			
2.7	*meiMIGS-HSBP*	406	345	1979	395	3125	27.93	3.22	2.90	27.99	2.56	2.37×10^{-4}
2.7	*meiMIGS-HSBP*	420	406	2417	557	3800	24.82	2.95	2.89			
2.7	*meiMIGS-HSBP*	431	461	2450	562	3904	26.31	2.82	2.93			
2.7	*meiMIGS-HSBP*	435	450	2278	529	3692	27.85	2.77	2.83			

Appendix Table S9. *420* **crossover frequency (cM) of male and female meiosis in Col,** *hsbp-3* **and** ***meiMIGS-HSBP.*** *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds from *420/++* plants, using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). Genetic distances of *420* male and female meiosis were separately measured by reciprocally crossing Col, *hcr2* and *meiMIGS-HSBP* of *420* plants with Ler or Ler *ms* (*male sterile1*) 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: $cM = 100 \times (N_{Green} + N_{Red})/N_{Total}$. *P* values were calculated using Welch's t-test which assessed significant differences between Col, *hcr2* and *meiMIGS-HSBP* (Wu *et al*, 2015).

Genotype	Green n	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col male	165	178	551	546	1440	23.82	0.99	1.03			
Col male	187	193	596	674	1650	23.03	0.90	0.92			
Col male	229	223	604	675	1731	26.11	0.93	0.91	25.46	1.62	
Col male	183	183	469	527	1362	26.87	0.92	0.92			
Col male	264	247	650	764	1925	26.55	0.90	0.87			
Col male	145	162	409	447	1163	26.40	0.91	0.96			
hsbp-3 male	175	200	273	348	996	37.65	0.82	0.90			
hsbp-3 male	180	187	287	366	1020	35.98	0.84	0.87			
hsbp-3 male	281	254	384	437	1356	39.45	0.96	0.89	38.01	1.33	1.87×10^{-7}
hsbp-3 male	96	110	131	203	540	38.15	0.73	0.81			
hsbp-3 male	114	79	127	177	497	38.83	0.94	0.71			
Col female	52	39	469	446	1006	9.05	1.07	1.02			
Col female	50	53	563	481	1147	8.98	1.15	1.16			
Col female	57	55	497	460	1069	10.48	1.08	1.07	9.38	0.72	
Col female	34	46	427	413	920	8.70	1.00	1.06			
Col female	39	50	427	400	916	9.72	1.04	1.09			
hsbp-3 female	100	111	294	284	789	26.74	1.00	1.05			
hsbp-3 female	104	112	316	271	803	26.90	1.10	1.14			
hsbp-3 female	67	84	228	232	611	24.71	0.93	1.04	26.6	0.98	1.15×10^{-10}
hsbp-3 female	98	100	289	257	744	26.61	1.08	1.10			
hsbp-3 female	205	210	513	576	1504	27.59	0.91	0.93			
hsbp-3 female	165	191	463	499	1318	27.01	0.91	0.98			

Appendix Table S10. Pollen-based FTL crossover frequency (cM) in Col and *hsbp-3*. Pollen-based FTL crossover frequency was measured by DeepTetrad using 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*) (Berchowitz & Copenhaver, 2008). Fluorescent tetrad states were identified using DeepTetrad and crossover frequency (cM) was calculated using the Perkin's equations (Perkins, 1962; Lim *et al*, 2020). *P* values were calculated using Welch's t-tests, which assessed significant differences between wild type and mutants (Berchowitz & Copenhaver, 2008).

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	$I1b$(cM)	$I1c$(cM)	$I1bc$(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col	472	119	345	10	5	8	1	2	10	0	2	0	974	8.06	22.64	28.59	0.11	0.03	0.31	3.90
Col	918	267	667	18	9	17	19	1	12	0	5	0	1933	8.82	21.52	29.93	0.12	0.05	0.40	4.19
Col	162	45	136	3	3	4	2	0	2	0	0	0	357	7.98	22.41	29.69	0.11	0.04	0.37	3.92
Col	339	120	257	8	7	4	3	0	8	0	0	0	746	9.52	21.92	30.43	0.13	0.04	0.29	4.02
Col	307	76	175	4	2	3	2	0	4	0	0	0	573	7.59	18.32	25.48	0.10	0.03	0.29	2.62
Mean														8.39	21.36	28.82	0.11	0.04	0.33	3.73
SD														0.77	1.75	1.99	0.01	0.01	0.05	0.63
hsbp-3	253	145	327	19	22	25	14	3	4	0	3	0	815	15.09	27.55	39.75	0.20	0.10	0.49	11.04
hsbp-3	466	280	547	42	29	30	34	3	16	4	1	0	1452	15.77	27.13	41.63	0.20	0.11	0.57	10.95
hsbp-3	266	164	407	27	24	19	27	1	13	0	6	0	954	14.31	32.39	45.39	0.20	0.10	0.50	12.26
hsbp-3	256	155	338	31	26	19	18	1	15	0	2	0	861	14.92	31.01	43.21	0.20	0.11	0.55	13.01
hsbp-3	131	53	131	13	7	10	9	0	6	0	0	0	360	12.78	28.61	40.42	0.14	0.11	0.77	12.50
Mean														14.57	29.34	42.08	0.19	0.11	0.58	11.95
SD														1.13	2.28	2.27	0.02	0.01	0.11	0.91
P value														1.92×10^{-5}	3.32×10^{-4}	1.09×10^{-5}			5.55×10^{-3}	6.12×10^{-7}

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	$I3b$(cM)	$I3c$(cM)	$I3bc$(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col	234	124	25	1	0	1	0	2	0	0	0	0	387	17.83	3.49	20.93	0.19	0.04	0.20	1.03
Col	543	277	76	2	3	2	0	9	2	0	0	0	914	18.49	5.20	23.19	0.20	0.04	0.21	1.97
Col	411	184	55	3	1	2	2	4	0	0	0	0	662	16.31	4.76	21.00	0.17	0.06	0.37	1.81
Col	534	267	82	2	1	2	3	8	1	1	0	0	901	18.26	5.38	23.58	0.19	0.08	0.39	2.00

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	$I5a$(cM)	$I5b$(cM)	$I5ab$(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col	356	175	48	2	0	2	3	3	2	0	0	0	591	16.92	5.67	23.10	0.18	0.06	0.34	2.03
Mean														17.56	4.90	22.36	0.19	0.06	0.30	1.77
SD														0.92	0.86	1.29	0.01	0.02	0.09	0.42
hsbp-3	283	320	110	13	4	5	5	10	2	2	0	0	754	27.79	10.01	36.01	0.31	0.14	0.45	5.44
hsbp-3	325	342	123	17	4	16	9	13	1	3	2	0	855	28.42	11.11	36.73	0.31	0.19	0.61	7.60
hsbp-3	426	453	170	19	6	19	10	17	1	2	2	0	1126	27.66	10.83	36.41	0.31	0.15	0.48	6.75
hsbp-3	154	230	75	12	17	7	19	10	0	1	0	0	525	33.43	12.48	48.00	0.37	0.23	0.63	12.57
hsbp-3	176	247	84	10	17	17	17	9	0	2	0	0	579	32.30	12.69	45.16	0.35	0.25	0.71	12.44
Mean														29.92	11.43	40.46	0.33	0.19	0.58	8.96
SD														2.73	1.14	5.68	0.03	0.05	0.11	3.33
P value														2.35×10^{-4}	1.18×10^{-5}	1.56×10^{-3}			2.86×10^{-3}	8.02×10^{-3}

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	$I5a$(cM)	$I5b$(cM)	$I5ab$(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col	279	292	184	14	14	15	18	3	2	0	0	0	821	22.59	15.65	39.16	0.27	0.12	0.46	8.04
Col	164	134	90	10	2	5	13	3	4	0	0	0	425	21.41	16.94	41.29	0.25	0.12	0.48	8.71
Col	254	227	132	17	10	16	11	6	3	1	2	0	679	23.93	15.98	37.41	0.27	0.16	0.60	9.72
Col	529	536	339	30	35	34	24	13	4	1	1	0	1546	24.06	15.94	38.55	0.28	0.14	0.49	9.18
Col	558	499	365	26	31	30	22	8	11	3	1	0	1554	21.72	17.66	37.81	0.26	0.13	0.51	8.49
Col	291	269	187	12	15	17	12	5	5	0	0	0	813	21.83	16.79	38.13	0.26	0.11	0.43	8.12
Col	425	353	218	29	12	19	9	12	6	2	1	0	1086	23.34	15.24	35.31	0.27	0.14	0.51	8.29
Mean														22.70	16.32	38.24	0.27	0.13	0.50	8.65
SD														1.09	0.85	1.81	0.01	0.02	0.05	0.61
hsbp-3	213	456	296	50	36	48	37	15	10	4	4	0	1169	31.86	23.74	52.01	0.40	0.21	0.51	17.45
hsbp-3	119	198	145	42	38	32	34	11	4	5	3	0	631	35.10	26.78	56.66	0.40	0.30	0.73	26.78
hsbp-3	161	197	149	34	27	31	27	11	7	5	3	0	652	31.83	25.54	52.30	0.36	0.27	0.75	22.24
hsbp-3	161	290	190	46	46	47	46	15	6	8	3	0	858	35.90	25.47	57.46	0.41	0.30	0.74	25.29
hsbp-3	153	260	181	48	50	59	39	10	7	12	4	0	823	35.97	27.64	54.80	0.38	0.34	0.90	27.83
hsbp-3	121	211	133	40	24	36	33	9	6	4	7	0	624	34.38	27.88	56.33	0.39	0.29	0.75	25.48
hsbp-3	110	237	143	42	37	38	36	6	4	2	7	0	662	33.61	27.49	55.89	0.39	0.28	0.72	25.98
Mean														34.09	26.36	55.06	0.39	0.28	0.73	24.44
SD														1.74	1.52	2.14	0.02	0.04	0.11	3.53
P value														3.94×10^{-8}	5.78×10^{-8}	2.95×10^{-9}			9.18×10^{-4}	1.59×10^{-5}

Appendix Table S11. Pollen-based FTL crossover frequency (cM) of *I3bc* in Col and *meiMIGS-HSBP* lines. *I3bc* crossover frequency was measured by DeepTetrad using three-color *I3bc* 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*) (Berchowitz & Copenhaver, 2008). Fluorescent tetrad states were identified using DeepTetrad and crossover frequency (cM) was calculated using the Perkin's equations (Perkins, 1962; Lim *et al*, 2020). *P* values were calculated using Welch's t-tests, which assessed significant differences between wild-type Col and *meiMIGS-HSBP* transgenic lines (Berchowitz & Copenhaver, 2008).

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	*I3b* (cM)	*I3c* (cM)	*I3bc* (cM)
Col	521	229	48	4	2	2	0	2	0	0	0	0	808	15.41	3.47	18.13
Col	378	148	35	2	2	0	2	5	0	0	0	0	572	16.08	3.58	19.84
Col	642	356	73	1	3	1	3	7	1	0	0	0	1087	18.68	4.00	22.95
Col	336	175	36	3	3	1	2	6	1	0	0	0	563	19.54	4.53	23.89
Col	259	113	33	0	2	0	2	3	1	0	0	0	413	16.34	5.21	22.28
Col	667	303	75	4	0	2	4	2	6	0	0	0	1063	15.29	5.69	21.26
Mean														16.89	4.41	21.39
SD														1.78	0.90	2.12
DMC1p:meiMIGS HSBP	344	343	99	35	7	7	10	15	6	6	2	1	875	30.63	12.46	37.14
DMC1p:meiMIGS HSBP	377	325	100	12	10	21	10	7	1	1	0	0	864	24.65	9.26	32.70
DMC1p:meiMIGS HSBP	210	215	89	13	4	7	10	7	4	2	0	1	562	27.49	13.79	39.41
DMC1p:meiMIGS HSBP	202	189	82	11	3	8	5	5	3	1	0	0	509	24.75	12.57	35.46
DMC1p:meiMIGS HSBP	214	112	36	0	4	3	3	4	0	0	0	0	376	19.41	6.12	26.20
Mean														25.39	10.84	34.18
SD														4.14	3.13	5.09
P value														7.17×10^{-3}	8.38×10^{-3}	3.03×10^{-3}
HEI10p:meiMIGS HSBP	237	206	97	28	15	16	17	16	5	2	2	0	641	30.58	16.93	44.15
HEI10p:meiMIGS HSBP	346	359	148	17	8	10	9	13	7	6	0	0	923	28.01	13.00	38.19
HEI10p:meiMIGS HSBP	295	279	117	29	6	20	22	10	6	2	0	0	786	27.23	14.76	41.48
HEI10p:meiMIGS HSBP	228	215	79	8	5	13	6	5	1	0	0	0	560	24.73	10.45	34.29
HEI10p:meiMIGS HSBP	334	295	106	18	9	9	11	9	3	3	0	1	798	26.32	11.28	35.09

HEI10p:meiMIGS HSBP	170	162	63	6	8	6	5	4	0	0	3	0	427	25.06	12.41	34.66
Mean														26.99	13.14	37.98
SD														2.16	2.38	4.08
P value														6.18×10^{-6}	1.09×10^{-4}	3.14×10^{-5}
ASY1p:mei-MIGS HSBP	387	224	63	13	5	6	7	5	4	0	1	0	715	20.00	8.67	27.62
ASY1p:mei-MIGS HSBP	573	501	146	11	13	15	12	16	3	2	2	1	1295	25.79	9.07	33.40
ASY1p:mei-MIGS HSBP	374	206	90	31	10	7	7	5	4	0	3	0	737	19.95	12.69	27.95
ASY1p:mei-MIGS HSBP	234	207	63	10	10	13	5	3	1	4	0	1	551	26.59	10.62	31.85
ASY1p:mei-MIGS HSBP	450	384	120	14	6	10	15	10	2	2	1	0	1014	24.75	9.12	33.78
Mean														23.42	10.03	30.92
SD														3.21	1.66	2.95
P value														6.66×10^{-3}	5.34×10^{-4}	4.91×10^{-4}

Appendix Table S12. *420* crossover frequency (cM) in Col, *hsbp-3, fancm, zip4, fancm hsbp-3, zip4 hsbp-3,* and *zip4 fancm*. *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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 = $100 \times (1- [1-2(N_{Green}+N_{Red})/N_{Total}]^{1/2})$ (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild type and mutants, *P* values were calculated using Welch's t-tests. G/nG indicates the ratio of green color seed number (G) to non-green seed number (nG). R/nR repesents the ratio of red color seed number to non-red seed number.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col	237	225	439	1602	2503	20.57	2.77	2.70			
Col	257	230	401	1627	2515	21.72	2.99	2.82			
Col	251	285	417	1820	2773	21.68	2.95	3.15	21.44	0.70	
Col	296	287	461	1905	2949	22.24	2.94	2.90			
Col	284	253	453	1919	2909	20.58	3.12	2.95			
Col	291	253	457	1792	2793	21.87	2.93	2.73			
hsbp-3	382	360	441	1652	2835	30.97	2.54	2.44			
hsbp-3	392	379	339	1611	2721	34.17	2.79	2.72			
hsbp-3	461	407	375	1882	3125	33.33	3.00	2.74	32.66	1.44	2.48×10^{-9}
hsbp-3	280	316	1365	231	2192	32.46	3.01	3.29			
hsbp-3	292	317	1280	267	2156	34.04	2.69	2.86			
hsbp-3	330	357	335	1603	2625	30.97	2.79	2.95			
fancm	423	402	1831	335	2991	33.04	3.06	2.95			
fancm	435	429	1801	368	3033	34.41	2.81	2.78			
fancm	404	399	1769	317	2889	33.36	3.03	3.01			
fancm	402	422	1584	332	2740	36.87	2.63	2.73	34.01	1.37	3.84×10^{-9}
fancm	427	400	1843	344	3014	32.83	3.05	2.91			
fancm	431	396	1820	302	2949	33.73	3.22	3.02			
fancm	422	367	1706	313	2808	33.82	3.13	2.82			
zip4	74	44	889	269	1276	9.72	3.08	2.72			
zip4	48	38	876	230	1192	7.50	3.45	3.29			
zip4	77	35	1010	231	1353	8.65	4.09	3.39	8.53	0.87	1.42×10^{-10}
zip4	51	53	956	252	1312	8.27	3.30	3.33			
zip4	53	41	908	259	1261	7.76	3.20	3.04			
zip4	43	54	757	240	1094	9.30	2.72	2.87			
fancm hsbp-3	507	493	1782	302	3084	40.71	2.88	2.81			versus *hsbp-3*= 0.0134
fancm hsbp-3	507	536	1770	300	3113	42.56	2.72	2.86			
fancm hsbp-3	412	412	1703	292	2819	35.55	3.00	3.00	39.11	3.01	
fancm hsbp-3	416	423	1555	259	2653	39.38	2.89	2.93			versus *fancm*= 0.0120
fancm hsbp-3	455	487	1806	289	3037	38.38	2.91	3.08			
zip4 hsbp-3	60	96	1410	392	1958	8.31	3.01	3.33			versus *hsbp-3*= 3.03×10^{-10}
zip4 hsbp-3	36	46	613	192	887	9.72	2.73	2.89	8.51	1.21	
zip4 hsbp-3	19	50	738	153	960	7.47	3.73	4.58			

zip4 hsbp-3	29	41	739	191	1000	7.26	3.31	3.55			versus *zip4*= 0.977
zip4 hsbp-3	44	45	662	203	954	9.81	2.85	2.86			
zip4 fancm	404	417	1950	394	3165	30.63	2.90	2.97	32.60	1.38	versus *fancm*= 0.0180 versus *zip4*= 2.13×10^{-15}
zip4 fancm	450	466	2088	448	3452	31.50	2.78	2.84			
zip4 fancm	441	458	1861	444	3204	33.76	2.55	2.62			
zip4 fancm	349	378	1586	348	2661	32.65	2.67	2.82			
zip4 fancm	377	391	1807	356	2931	31.01	2.92	3.00			
zip4 fancm	309	363	1535	315	2522	31.66	2.72	3.04			
zip4 fancm	343	407	1627	399	2776	32.20	2.44	2.74			
zip4 fancm	323	356	1506	340	2525	32.02	2.63	2.81			
zip4 fancm	313	290	1265	248	2116	34.42	2.93	2.77			

Appendix Table S13. *CTL1.26* **crossover frequency (cM) in Col, *hcr1, hsbp-3, fancm, hcr1 hsbp-3*, and *fancm hsbp-3*.** *CTL1.26* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). To examine for significant differences between wild type and genotypes, *P* values were calculated using Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col	21	18	1518	513	2070	1.90	2.90	2.88			
Col	15	25	1516	506	2062	1.96	2.88	2.96			
Col	21	21	1520	470	2032	2.09	3.14	3.14			
Col	18	17	1200	367	1602	2.21	3.17	3.16			
Col	23	26	1432	493	1974	2.51	2.80	2.83	2.26	0.33	
Col	14	17	1209	394	1634	1.92	2.98	3.00			
Col	25	33	1603	572	2233	2.63	2.69	2.74			
Col	23	20	1471	508	2022	2.15	2.83	2.81			
Col	24	20	1412	455	1911	2.33	3.02	2.99			
Col	24	33	1471	492	2020	2.86	2.85	2.91			
hcr1	84	71	2263	750	3168	5.02	2.86	2.80			
hcr1	58	85	2538	813	3494	4.18	2.89	3.01			
hcr1	74	69	2587	842	3572	4.09	2.92	2.90			
hcr1	66	79	2552	816	3513	4.22	2.93	2.98	4.25	0.35	4.10×10^{-8}
hcr1	75	64	2565	809	3513	4.04	3.02	2.97			
hcr1	57	72	2392	788	3309	3.98	2.85	2.92			
hcr1	71	62	2347	741	3221	4.22	3.01	2.97			
hsbp-3	76	107	2461	817	3461	5.44	2.75	2.88			
hsbp-3	59	54	1752	508	2373	4.88	3.22	3.19			
hsbp-3	59	40	1257	442	1798	5.67	2.73	2.59			
hsbp-3	38	38	1222	427	1725	4.51	2.71	2.71	5.41	0.84	2.42×10^{-5}
hsbp-3	109	76	1961	584	2730	7.02	3.14	2.94			
hsbp-3	65	63	2004	625	2757	4.76	3.01	3.00			
hsbp-3	83	92	2258	773	3206	5.62	2.71	2.75			
fancm	39	58	1309	402	1808	5.52	2.93	3.10			
fancm	62	58	1356	428	1904	6.51	2.92	2.89			
fancm	71	61	1443	433	2008	6.81	3.06	2.98			
fancm	55	80	1376	423	1934	7.24	2.84	3.05	6.07	1.31	7.01×10^{-4}
fancm	50	40	1427	483	2000	4.61	2.82	2.75			
fancm	70	62	430	1248	1810	7.58	2.68	2.62			
fancm	18	12	517	182	729	4.20	2.76	2.65			
hcr1 hsbp-3	75	74	1371	446	1966	7.89	2.78	2.77			
hcr1 hsbp-3	78	97	1328	453	1956	9.39	2.56	2.68			versus *hcr1*= 4.97×10^{-5}
hcr1 hsbp-3	63	38	1090	355	1546	6.76	2.93	2.70	8.23	0.93	
hcr1 hsbp-3	76	45	1102	385	1608	7.83	2.74	2.49			versus *hsbp-3*= 1.85×10^{-4}
hcr1 hsbp-3	80	91	1441	458	2070	8.63	2.77	2.85			
hcr1 hsbp-3	90	78	1334	480	1982	8.87	2.55	2.48			
fancm hsbp-3	62	51	1017	301	1431	8.24	3.07	2.94			
fancm hsbp-3	75	45	1103	321	1544	8.10	3.22	2.90			versus *hsbp-3*= 1.43×10^{-5}
fancm hsbp-3	93	78	1429	417	2017	8.87	3.07	2.95	8.79	0.95	
fancm hsbp-3	97	79	1164	384	1724	10.79	2.72	2.58			versus *fancm*= 3.63×10^{-4}
fancm hsbp-3	166	142	2453	839	3600	8.96	2.67	2.58			

fancm hsbp-3	141	121	2376	690	3328	8.21	3.10	3.00			
fancm hsbp-3	114	113	1962	653	2842	8.33	2.71	2.71			

Appendix Table S14. Pollen-based FTL crossover frequency (cM) of *I3bc* in Col, *hsbp-3, recq4a recq4b,* and *recq4a recq4b hsbp-3.* Pollen-based FTL crossover frequency was measured by DeepTetrad using 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, no-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*) (Berchowitz & Copenhaver, 2008). Fluorescent tetrad states were identified using DeepTetrad and crossover frequency (cM) was calculated using the Perkin's equations (Perkins, 1962; Lim *et al*, 2020). *P* values were calculated using Welch's t-tests, which assessed significant differences between wild type and mutants (Berchowitz & Copenhaver, 2008)

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	*I3b*(cM)	*I3c*(cM)	*I3bc*(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col	661	362	120	6	3	4	2	9	3	0	0	0	1170	18.42	6.54	24.49	0.20	0.05	0.27	2.31
Col	313	145	35	1	1	1	0	2	0	0	0	0	498	16.06	3.82	19.48	0.17	0.04	0.23	1.00
Col	830	533	180	4	2	7	7	10	0	0	0	0	1573	19.49	6.36	26.19	0.22	0.05	0.23	1.91
Col	550	309	83	1	2	3	2	6	0	0	0	0	956	18.46	4.76	23.27	0.20	0.04	0.22	1.46
Col	959	536	133	2	2	3	8	9	1	1	1	0	1655	18.49	4.86	23.69	0.20	0.07	0.37	1.63
Mean														18.18	5.27	23.42	0.20	0.05	0.26	1.66
SD														1.27	1.15	2.47	0.02	0.01	0.06	0.49
hsbp-3	561	577	235	21	16	17	25	23	4	4	3	0	1486	27.62	12.11	39.17	0.31	0.16	0.53	7.60
hsbp-3	549	508	192	18	13	19	25	26	3	4	0	0	1357	28.11	10.65	39.06	0.31	0.18	0.59	7.96
hsbp-3	572	559	175	20	15	27	24	23	5	5	0	0	1425	28.53	10.39	38.35	0.30	0.21	0.71	8.35
hsbp-3	590	577	245	21	16	17	26	23	3	4	4	0	1526	26.97	12.16	38.50	0.30	0.16	0.53	7.47
hsbp-3	535	523	203	12	21	17	26	10	4	3	1	0	1355	25.02	11.51	37.20	0.27	0.17	0.61	6.94
Mean														27.25	11.36	38.45	0.30	0.18	0.59	7.66
SD														1.38	0.82	0.79	0.01	0.02	0.07	0.53
P value														4.89×10^{-6}	2.26×10^{-5}	6.44×10^{5}			7.17×10^{-5}	7.77×10^{-8}
recq4	126	184	89	45	28	35	35	20	12	23	12	1	610	49.43	33.20	63.36	0.53	0.46	1.16	34.59
recq4	193	283	100	36	31	49	34	31	5	17	7	3	789	47.28	22.62	57.48	0.49	0.46	1.06	27.00
recq4	286	363	126	45	38	50	35	52	12	17	8	3	1035	46.91	21.69	57.78	0.44	0.48	0.92	25.12
recq4	246	288	101	34	33	36	43	32	8	17	8	2	848	44.10	21.93	57.84	0.48	0.42	1.12	25.12
recq4	127	221	75	43	32	44	35	31	3	29	6	3	649	58.47	25.42	63.25	0.65	0.54	1.21	34.82
recq4	119	196	70	48	31	45	32	32	3	27	8	2	613	59.22	27.00	63.54	0.64	0.56	1.14	37.19
recq4	173	187	57	16	21	26	25	27	12	12	2	0	558	45.79	21.59	61.74	0.47	0.45	1.05	25.27

Mean														50.17	24.78	60.71	0.53	0.48	1.09	29.87
SD														6.14	4.25	2.88	0.08	0.05	0.10	5.40
P value														4.40×10^{-6}	6.75×10^{-6}	7.40×10^{-10}			5.35×10^{-9}	7.68×10^{-6}
recq4 hsbp-3	53	99	46	30	43	41	40	24	7	27	15	4	429	69.70	44.64	81.24	0.70	0.69	1.02	53.85
recq4 hsbp-3	89	166	57	27	34	20	39	49	3	26	10	9	529	75.61	31.66	81.19	0.76	0.76	1.00	41.02
recq4 hsbp-32	97	185	61	34	30	28	45	51	3	24	9	7	574	71.69	29.27	81.10	0.69	0.74	0.93	40.24
recq4 hsbp-3	163	212	85	40	32	34	35	55	6	28	4	3	697	62.63	23.82	69.66	0.62	0.63	0.98	34.00
recq4 hsbp-3	171	231	89	47	28	42	41	57	6	26	3	1	742	60.38	22.44	70.28	0.57	0.62	0.91	33.83
Mean														68.00	30.37	76.69	0.67	0.69	0.97	40.59
SD														6.35	8.84	6.14	0.07	0.06	0.04	8.14
P value (versus *recq4*)														1.03×10^{-3}	0.244	2.49×10^{-3}			0.0136	0.0397
P value (versus *hsbp-3*)														8.40×10^{-5}	8.36×10^{-3}	1.30×10^{-4}			3.66×10^{-5}	8.04×10^{-4}

Appendix Table S15. Seed number per silique in wild-type Col, *fancm, zip4, hsbp-3, zip4 fancm*, and *zip4 hsbp-3. P* values were calculated using a Wilcoxon test.

number	Col	*fancm*	*zip4*	*hsbp-3*	*zip4 fancm*	*zip4 hsbp-3*
1	54	47	1	39	48	5
2	42	47	4	49	49	5
3	52	51	1	39	46	3
4	61	52	2	36	47	4
5	61	53	3	49	47	3
6	60	54	2	26	45	4
7	65	55	4	39	48	4
8	62	48	3	36	49	3
9	60	49	4	50	57	4
10	61	49	1	37	58	4
11	41	50	3	45	59	2
12	41	50	3	44	49	2
13	54	56	1	51	50	2
14	50	57	3	33	47	3
15	46	58	3	35	50	2
16	49	59	3	36	50	2
17	49	60	4	46	50	3
18	64	61	4	44	51	4
19	60	50	1	37	51	3
20	63	51	5	46	51	3
21	55	51	4	47	51	3
22	59	52	3	46	52	3
23	54	52	5	48	53	2
24	57	53	3	63	53	3
25	56	53	3	45	53	3
26	54	53	2	46	53	2
27	55	53	3	47	54	2
28	56	54	3	48	54	2
29	55	54	4	57	54	3
30	54	54	4	58	54	2
31	54	54	3	49	55	3
32	56	55	3	49	55	2
33	53	56	4	57	55	3
34	52	56	3	59	56	3
35	53	56	4	57	57	2
36	56	56	4	49	60	3
37	54	57	4	42	62	2
38	52	57	4	49	61	2
39	49	64	4	39	62	3
40	49	65	3	43	63	3
Mean	54.80	53.23	3.03	45.51	51.74	2.94
S.D.	6.111	3.465	1.098	8.319	3.576	0.873
P value (versus Col)		0.463	9.16×10^{-15}	6.24×10^{-7}	0.1071	8.22×10^{-15}
P value (versus *zip4*)					9.29×10^{-15}	0.1120

Appendix Table S16. Univalent and bivalent counts from meiotic chromosome spreads in wild type (Col), *hsbp-3*, *zip4,* and *zip4 hsbp-3*. *P* values were calculated using a Wilcoxon test.

Col			*hsbp-3*			*zip4*			*hsbp-3 zip4*		
number	uni	bi	number	uni	bi	number	uni	bi	number	uni	bi
1	0	5	1	0	5	1	8	1	1	6	2
2	0	5	2	0	5	2	8	1	2	8	1
3	0	5	3	0	5	3	10	0	3	6	2
4	0	5	4	0	5	4	10	0	4	6	2
5	0	5	5	0	5	5	4	3	5	10	0
6	0	5	6	0	5	6	8	1	6	6	2
7	0	5	7	0	5	7	10	0	7	8	1
8	0	5	8	0	5	8	10	0	8	6	2
9	0	5	9	0	5	9	10	0	9	8	1
10	0	5	10	0	5	10	6	2	10	6	2
11	0	5	11	0	5	11	6	2	11	6	2
12	0	5	12	0	5	12	6	2	12	8	1
13	0	5	13	0	5	13	8	1	13	10	0
14	0	5	14	0	5	14	6	2	14	8	1
15	0	5	15	0	5	15	6	2	15	8	1
16	0	5	16	0	5	16	10	0	16	6	2
17	0	5	17	0	5	17	6	2	17	6	2
18	0	5	18	0	5	18	4	3	18	8	1
19	0	5	19	0	5	19	6	2	19	8	1
20	0	5	20	0	5	20	8	1	20	8	1
21	0	5	21	0	5	21	4	3	21	4	3
22	0	5	22	0	5	22	10	0	22	2	4
23	0	5	23	0	5	23	6	2	23	8	1
24	0	5	Mean	0	5	24	6	2	24	4	3
25	0	5	S.D.	0	0	25	10	0	25	8	1
26	0	5	*P* value	1	1	26	6	2	26	6	2
27	0	5				27	6	2	27	4	3
28	0	5				28	8	1	28	4	3
29	0	5				29	10	0	29	6	2
30	0	5				30	8	1	30	8	1
Mean	0	5				Mean	7.47	1.27	Mean	6.67	1.67
S.D.	0	0				S.D.	2.03	1.015	S.D.	1.845	0.922
						P value	8.71×10^{-13}	8.71×10^{-13}	*P* value	7.89×10^{-13}	7.89×10^{-13}
									P value (versus *zip4)*	0.1681	0.1681

Appendix Table S17. *420* **crossover frequency (cM) in wild-type and *meiMIGS-HSBP* Col/Ler F$_1$ hybrids.** *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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 × (1- [1-2(N$_{Green}$+N$_{Red}$)/N$_{Total}$]$^{1/2}$) (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild-type Col/Ler F$_1$ and *meiMIGS-HSBP* Col/Ler F$_1$, *P* value was calculated using Welch's t-tests. G/nG indicates the ratio of green color seed number (G) to non-green seed number (nG). R/nR repesents the ratio of red color seed number to non-red seed number.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col/Ler F$_1$	165	165	2077	668	3075	11.38	2.69	2.69			
Col/Ler F$_1$	148	139	1682	472	2441	12.54	3.00	2.94			
Col/Ler F$_1$	145	175	1930	616	2866	11.87	2.62	2.77			
Col/Ler F$_1$	150	166	1864	525	2705	12.46	2.91	3.01			
Col/Ler F$_1$	159	219	2104	663	3145	12.84	2.57	2.83			
Col/Ler F$_1$	143	149	1498	464	2254	13.92	2.68	2.71	12.63	1.03	
Col/Ler F$_1$	134	189	1888	567	2778	12.40	2.67	2.96			
Col/Ler F$_1$	173	177	1884	568	2802	13.39	2.76	2.78			
Col/Ler F$_1$	155	204	1864	600	2823	13.65	2.51	2.74			
Col/Ler F$_1$	151	205	1827	575	2758	13.87	2.54	2.80			
Col/Ler F$_1$	131	148	1558	499	2336	12.76	2.61	2.71			
Col/Ler F$_1$	139	174	2146	682	3141	10.52	2.67	2.83			
meiMIGS-HSBP Col/Ler F$_1$	389	495	1484	229	2597	43.50	2.59	3.20			
meiMIGS-HSBP Col/Ler F$_1$	379	506	1473	239	2597	43.57	2.49	3.20			
meiMIGS-HSBP Col/Ler F$_1$	382	389	1544	396	2711	34.33	2.45	2.48			
meiMIGS-HSBP Col/Ler F$_1$	403	478	1532	238	2651	42.09	2.70	3.14			
meiMIGS-HSBP Col/Ler F$_1$	341	352	1688	329	2710	30.10	2.98	3.04			
meiMIGS-HSBP Col/Ler F$_1$	304	305	1519	362	2490	28.53	2.73	2.74			
meiMIGS-HSBP Col/Ler F$_1$	258	291	1365	327	2241	28.58	2.63	2.83			
meiMIGS-HSBP Col/Ler F$_1$	561	422	2010	284	3277	36.75	3.64	2.88			
meiMIGS-HSBP Col/Ler F$_1$	397	439	1488	231	2555	41.21	2.81	3.07	35.53	6.62	8.44×10^{-11}
meiMIGS-HSBP Col/Ler F$_1$	330	443	1468	216	2457	39.11	2.73	3.50			
meiMIGS-HSBP Col/Ler F$_1$	316	309	1341	261	2227	33.77	2.91	2.86			
meiMIGS-HSBP Col/Ler F$_1$	435	496	1617	253	2801	42.10	2.74	3.07			
meiMIGS-HSBP Col/Ler F$_1$	413	517	1605	248	2783	42.41	2.64	3.21			
meiMIGS-HSBP Col/Ler F$_1$	438	508	1825	272	3043	38.50	2.90	3.29			
meiMIGS-HSBP Col/Ler F$_1$	339	271	1599	351	2560	27.65	3.12	2.71			
meiMIGS-HSBP Col/Ler F$_1$	323	321	1975	382	3001	24.45	3.27	3.26			
meiMIGS-HSBP Col/Ler F$_1$	259	289	1436	342	2326	27.28	2.69	2.87			

Appendix Table S18. Crossover numbers identified by sequencing Col/Ler and *meiMIGS-HSBP* Col/Ler F$_2$ populations. To test for significant differences in crossover number between Col/Ler F$_2$ and *meiMIGS-HSBP* Col/Ler F$_2$, *P* values were calculated using a Wilcoxon test.

Genotype	Col/Ler F$_2$ (n=240)		*meiMIGS-HSBP* Col/Ler F$_2$ (n=288)		Fold change (*meiMIGS-HSBP*/wild type)	*P* value
Chromosome	Crossover number	Crossover number per individual	Crossover number	Crossover number per individual		
Chr1	440	1.83	798	2.77	1.51	2.20×10^{-16}
Chr2	323	1.35	528	1.83	1.36	4.093×10^{-5}
Chr3	373	1.55	553	1.92	1.24	8.363×10^{-4}
Chr4	299	1.25	526	1.83	1.47	1.431×10^{-9}
Chr5	415	1.73	746	2.59	1.50	1.635×10^{-13}
Total	1,850	7.71	3,151	10.94	1.42	2.20×10^{-16}

Appendix Table S19. *420* **crossover frequency (cM) in Col,** *hsbp-3, hei10, hei10 hsbp-3,* **and** *HEI10* **transgenic plants.** *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). To examine for significant differences between wild type and genotypes, *P* values were calculated using Welch's t-tests.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
Col	237	225	439	1602	2503	20.57	2.77	2.70			
Col	257	230	401	1627	2515	21.72	2.99	2.82			
Col	251	285	417	1820	2773	21.68	2.95	3.15	21.44	0.70	
Col	296	287	461	1905	2949	22.24	2.94	2.90			
Col	284	253	453	1919	2909	20.58	3.12	2.95			
Col	291	253	457	1792	2793	21.87	2.93	2.73			
hsbp-3	382	360	441	1652	2835	30.97	2.54	2.44			
hsbp-3	392	379	339	1611	2721	34.17	2.79	2.72			
hsbp-3	461	407	375	1882	3125	33.33	3.00	2.74	32.66	1.44	3.99×10^{-7}
hsbp-3	280	316	1365	231	2192	32.46	3.01	3.29			
hsbp-3	292	317	1280	267	2156	34.04	2.69	2.86			
hsbp-3	330	357	335	1603	2625	30.97	2.79	2.95			
hei10	128	149	462	1513	2252	13.17	2.69	2.82			
hei10	79	85	322	1157	1643	10.54	3.04	3.10			
hei10	156	151	465	1655	2427	13.57	2.94	2.91			
hei10	108	131	345	1344	1928	13.28	3.05	3.26			
hei10	131	141	491	1655	2418	11.96	2.83	2.89	12.32	1.00	1.31×10^{-10}
hei10	120	155	510	1829	2614	11.14	2.93	3.15			
hei10	147	162	526	1807	2642	12.47	2.84	2.93			
hei10	152	161	509	1879	2701	12.35	3.03	3.09			
hei10	151	141	461	1752	2505	12.43	3.16	3.09			
hei10 hsbp-3	155	131	482	1497	2265	13.54	2.69	2.56			
hei10 hsbp-3	136	141	531	1898	2706	10.82	3.03	3.06			versus *hsbp-3*= 2.22×10^{-10}
hei10 hsbp-3	115	94	358	1277	1844	12.06	3.08	2.90	12.23	1.34	
hei10 hsbp-3	123	140	420	1425	2108	13.37	2.76	2.88			
hei10 hsbp-3	158	164	518	1785	2625	13.13	2.85	2.88			versus *hei10*= 0.985
hei10 hsbp-3	84	134	465	1516	2199	10.46	2.67	3.01			
HEI10/+	345	336	364	1577	2622	30.68	2.75	2.70			
HEI10/+	363	372	333	1699	2767	31.54	2.92	2.98			
HEI10/+	383	358	348	1761	2850	30.72	3.04	2.90			
HEI10/+	316	377	410	1851	2954	27.14	2.75	3.07			
HEI10/+	279	306	359	1520	2464	27.53	2.71	2.86			
HEI10/+	303	338	409	1739	2789	26.49	2.73	2.92	28.58	2.23	2.23×10^{-7}
HEI10/+	372	347	334	1652	2705	31.56	2.97	2.83			
HEI10/+	321	325	369	1714	2729	27.44	2.93	2.96			
HEI10/+	295	359	425	1840	2919	25.71	2.72	3.05			
HEI10/+	305	353	432	1796	2886	26.24	2.68	2.92			
HEI10/+	349	327	359	1669	2704	29.29	2.94	2.82			
HEI10/+ hsbp-3	232	342	154	1129	1857	38.21	2.74	3.81			versus *hsbp-3*= 6.41×10^{-4}
HEI10/+ hsbp-3	220	226	137	865	1448	38.03	2.99	3.06			
HEI10/+ hsbp-3	411	468	290	1621	2790	39.18	2.68	2.98	39.06	2.07	
HEI10/+ hsbp-3	463	424	273	1487	2647	42.57	2.80	2.60			versus *HEI10*= 1.16×10^{-5}
HEI10/+ hsbp-3	412	351	237	1513	2513	37.33	3.27	2.87			

Appendix Table S20. *420* **crossover frequency (cM) in plants with different copy numbers of endogenous and transgene of** *HEI10.* *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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 = $100 \times (1- [1-2(N_{Green}+N_{Red})/N_{Total}]^{1/2})$ (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild type, genotype and *HEI10* overexpression transgenic plants, *P* values were calculated using Welch's t-tests. One way ANOVA test was used to calculate for significant differences between genotypes.

Genotype	Green	Red	Both	None	Total	cM	G/nG	R/nR	Mean	SD	*P* value
hei10/+	50	64	722	190	1026	11.81	3.04	3.28			
hei10/+	108	110	1168	309	1695	13.82	3.05	3.06			
hei10/+	100	115	1036	298	1549	15.01	2.75	2.89			
hei10/+	124	138	1216	370	1848	15.36	2.64	2.74	14.13	1.16	
hei10/+	54	58	562	159	833	14.50	2.84	2.91			
hei10/+	90	115	1040	283	1528	14.46	2.84	3.10			
hei10/+	121	119	1240	366	1846	13.98	2.81	2.79			
hei10;HEI10-myc/+	90	32	561	149	832	15.93	3.60	2.48			
hei10;HEI10-myc/+	149	91	1125	305	1670	15.59	3.22	2.68			
hei10;HEI10-myc/+	41	45	408	100	594	15.71	3.10	3.21			
hei10;HEI10-myc/+	35	59	422	147	663	15.36	2.22	2.64	15.88	0.45	
hei10;HEI10-myc/+	114	129	1097	272	1612	16.42	3.02	3.18			
hei10;HEI10-myc/+	52	86	635	188	961	15.57	2.51	3.00			
hei10;HEI10-myc/+	40	38	323	113	514	16.54	2.40	2.36			
hei10;HEI10-myc/HEI10-myc	123	132	953	213	1421	19.93	3.12	3.23			
hei10;HEI10-myc/HEI10-myc	204	203	1731	448	2586	17.22	2.97	2.97			
hei10;HEI10-myc/HEI10-myc	116	88	668	179	1051	21.78	2.94	2.56			
hei10;HEI10-myc/HEI10-myc	113	153	1007	270	1543	19.05	2.65	3.03	19.14	1.86	
hei10;HEI10-myc/HEI10-myc	132	103	1053	276	1564	16.36	3.13	2.83			
hei10;HEI10-myc/HEI10-myc	168	181	1359	308	2016	19.14	3.12	3.24			1.35×10^{-30}
hei10;HEI10-myc/HEI10-myc	132	132	924	247	1435	20.50	2.79	2.79			
Col	94	77	580	186	937	20.31	2.56	2.35			
Col	123	132	953	213	1421	19.93	3.12	3.23			
Col	190	184	1423	372	2169	19.06	2.90	2.86			
Col	77	109	742	200	1128	18.13	2.65	3.07	19.77	1.19	
Col	209	155	1391	300	2055	19.64	3.52	3.04			
Col	180	161	1146	257	1744	21.97	3.17	2.99			
Col	125	44	642	156	967	19.35	3.84	2.44			
hei10/+;HEI10-myc/+	124	142	1032	229	1527	19.28	3.12	3.33			
hei10/+;HEI10-myc/+	175	185	1335	337	2032	19.65	2.89	2.97			
hei10/+;HEI10-myc/+	117	197	945	319	1578	22.41	2.06	2.62			
hei10/+;HEI10-myc/+	204	224	1488	415	2331	20.45	2.65	2.77	20.27	1.17	
hei10/+;HEI10-myc/+	47	45	350	90	532	19.12	2.94	2.88			
hei10/+;HEI10-myc/+	57	80	477	151	765	19.89	2.31	2.68			
hei10/+;HEI10-myc/+	89	82	620	114	905	21.13	3.62	3.46			
hei10/+;HEI10-myc/HEI10-myc	222	153	847	217	1439	30.80	2.89	2.28			
hei10/+;HEI10-myc/HEI10-myc	142	107	631	150	1030	28.13	3.01	2.53	27.65	2.47	
hei10/+;HEI10-myc/HEI10-myc	255	251	1511	290	2307	25.08	3.26	3.23			

Genotype											
hei10/+;HEI10-myc/HEI10-myc	174	160	943	195	1472	26.09	3.15	2.99			
hei10/+;HEI10-myc/HEI10-myc	271	254	1445	274	2244	27.06	3.25	3.12			
hei10/+;HEI10-myc/HEI10-myc	85	142	607	192	1026	25.33	2.07	2.70			
hei10/+;HEI10-myc/HEI10-myc	296	276	1324	285	2181	31.05	2.89	2.75			
Col;*HEI10-myc/+*	217	239	1161	238	1855	28.70	2.89	3.08			
Col;*HEI10-myc/+*	127	189	775	193	1284	28.74	2.36	3.01			
Col;*HEI10-myc/+*	219	259	1265	256	1999	27.77	2.88	3.21	28.27	2.50	
Col;*HEI10-myc/+*	240	262	1429	306	2237	25.76	2.94	3.10			
Col;*HEI10-myc/+*	133	114	697	147	1091	26.03	3.18	2.90			
Col;*HEI10-myc/+*	289	277	1300	206	2072	32.65	3.29	3.19			
Col;*HEI10-myc/HEI10-myc*	269	341	1228	241	2079	35.72	2.57	3.08			
Col;*HEI10-myc/HEI10-myc*	344	305	1408	245	2302	33.96	3.19	2.91			
Col;*HEI10-myc/HEI10-myc*	68	78	272	60	478	37.62	2.46	2.73	36.19	1.67	
Col;*HEI10-myc/HEI10-myc*	118	90	439	76	723	34.84	3.36	2.73			
Col;*HEI10-myc/HEI10-myc*	316	306	1241	214	2077	36.67	2.99	2.92			
Col;*HEI10-myc/HEI10-myc*	79	89	299	75	542	38.35	2.30	2.52			
pDMC1:HEI10-myc /+	187	170	638	92	1087	41.42	3.15	2.90			
pDMC1:HEI10-myc /+	94	105	330	55	584	43.56	2.65	2.92			
pDMC1:HEI10-myc /+	196	208	643	101	1148	45.58	2.72	2.87			
pDMC1:HEI10-myc /+	177	277	679	157	1290	45.58	1.97	2.86	44.20	1.70	6.88×10^{-12}
pDMC1:HEI10-myc /+	190	200	629	96	1115	45.19	2.77	2.90			
pDMC1:HEI10-myc /+	180	141	596	41	958	42.57	4.26	3.33			
pDMC1:HEI10-myc /+	140	117	419	55	731	45.52	3.25	2.75			
pASY1:HEI10-myc /+	197	223	1201	224	1845	26.20	3.13	3.38			
pASY1:HEI10-myc /+	202	234	1144	242	1822	27.79	2.83	3.10			
pASY1:HEI10-myc /+	277	256	1407	335	2275	27.10	2.85	2.72			
pASY1:HEI10-myc /+	293	281	1551	352	2477	26.75	2.91	2.84	26.66	0.79	1.10×10^{-7}
pASY1:HEI10-myc /+	236	253	1407	320	2216	25.26	2.87	2.99			
pASY1:HEI10-myc /+	191	196	1061	216	1664	26.87	3.04	3.09			
pASY1:HEI10-myc /+	213	192	1109	240	1754	26.64	3.06	2.87			
pREC8:HEI10-myc /+	104	87	431	70	692	33.07	3.41	2.98			
pREC8:HEI10-myc /+	233	212	959	199	1603	33.31	2.90	2.71			
pREC8:HEI10-myc /+	220	184	1081	218	1703	27.51	3.24	2.89			
pREC8:HEI10-myc /+	93	99	471	109	772	29.11	2.71	2.82	30.52	2.87	1.61×10^{-5}
pREC8:HEI10-myc /+	143	157	730	174	1204	29.17	2.64	2.80			
pREC8:HEI10-myc /+	306	280	1256	232	2074	34.05	3.05	2.86			
pREC8:HEI10-myc /+	233	220	1174	288	1915	27.41	2.77	2.68			

Appendix Table S21. *420* **crossover frequency (cM) in Col and** *HSBP* **overexpression transgenic plants.** *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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: $cM = 100 \times (1- [1- 2(N_{Green}+N_{Red})/N_{Total}]^{1/2})$ (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild type and *HSBP* overexpression transgenic plants, *P* values were calculated using Welch's t-tests.

Genotype	green	red	both	none	total	cM	G/non G	R/non R	Mean	SD	*P* value
Col	73	71	145	506	795	20.14	2.68	2.65			
Col	118	139	260	838	1355	21.22	2.40	2.58			
Col	63	86	143	474	766	21.84	2.34	2.72			
Col	117	115	226	841	1299	19.83	2.81	2.79	20.63	0.71	
Col	35	38	73	249	395	20.60	2.56	2.66			
Col	53	78	129	446	706	20.70	2.41	2.88			
Col	21	35	60	194	310	20.08	2.26	2.83			
pSPO11-1_T₁	59	69	528	168	824	16.97	2.48	2.63			
pSPO11-1_T₁	103	105	197	904	1309	17.40	3.33	3.36			
pSPO11-1_T₁	30	36	268	83	417	17.33	2.50	2.69	16.95	0.75	$1.89×10^{-6}$
pSPO11-1_T₁	59	58	154	550	821	15.44	2.87	2.85			
pSPO11-1_T₁	78	84	646	214	1022	17.36	2.43	2.50			
pSPO11-1_T₁	27	43	298	78	446	17.17	2.69	3.25			
pHEI10_T₁	164	165	1648	428	2405	14.77	3.06	3.06			
pHEI10_T₁	190	170	1615	427	2402	16.32	3.02	2.89			
pHEI10_T₁	192	191	1651	428	2462	17.00	2.98	2.97			
pHEI10_T₁	182	177	1431	432	2222	17.73	2.65	2.62	16.09	1.50	$1.03×10^{-5}$
pHEI10_T₁	176	198	1553	439	2366	17.30	2.71	2.85			
pHEI10_T₁	95	65	697	229	1086	16.02	2.69	2.35			
pHEI10_T₁	172	105	1423	501	2201	13.50	2.63	2.27			
pDMC1_T₁	156	111	1212	229	1708	17.09	4.02	3.44			
pDMC1_T₁	101	73	725	172	1071	17.84	3.37	2.92			
pDMC1_T₁	111	92	961	168	1332	16.62	4.12	3.77			
pDMC1_T₁	68	61	549	115	793	17.86	3.51	3.33	16.90	0.71	$4.21×10^{-7}$
pDMC1_T₁	94	76	763	204	1137	16.28	3.06	2.82			
pDMC1_T₁	116	105	1003	258	1482	16.23	3.08	2.96			
pDMC1_T₁	94	98	847	237	1276	16.39	2.81	2.85			
pSPO11-1_T₂	181	162	1578	379	2300	16.23	3.25	3.11			
pSPO11-1_T₂	80	114	807	241	1242	17.08	2.50	2.87			
pSPO11-1_T₂	159	135	1387	346	2027	15.74	3.21	3.01			
pSPO11-1_T₂	149	142	1338	365	1994	15.85	2.93	2.88	16.61	0.81	$4.03×10^{-7}$
pSPO11-1_T₂	69	69	568	192	898	16.77	2.44	2.44			
pSPO11-1_T₂	196	162	1430	387	2175	18.10	2.96	2.73			
pSPO11-1_T₂	123	101	263	994	1481	16.48	3.07	2.84			
pHEI10_T₂	36	40	95	336	507	16.32	2.76	2.87			
pHEI10_T₂	22	20	55	220	317	14.27	3.23	3.12			
pHEI10_T₂	26	28	79	300	433	13.36	3.05	3.12			
pHEI10_T₂	16	27	60	186	289	16.19	2.32	2.80	15.00	1.23	$2.08×10^{-7}$
pHEI10_T₂	54	58	159	562	833	14.50	2.84	2.91			
pHEI10_T₂	22	27	63	216	328	16.26	2.64	2.86			
pHEI10_T₂	34	29	114	304	481	14.09	2.36	2.25			

Appendix Table S22. Pollen-based FTL crossover frequency (cM) of *I3bc* and *I5ab* in Col and *hsbp-3* grown in high temperature. Pollen-based FTL crossover frequency was measured by DeepTetrad using 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*) (Berchowitz & Copenhaver, 2008). Fluorescent tetrad states were identified using DeepTetrad and crossover frequency (cM) was calculated using the Perkin's equations (Perkins, 1962; Lim *et al*, 2020). *P* values were calculated using Welch's t-tests, which assessed significant differences between wild type and genotypes (Berchowitz & Copenhaver, 2008)

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	I3b(cM)	I3c(cM)	I3bc(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col 20 °C	418	245	59	4	0	4	3	2	0	0	0	0	735	18.23	4.76	22.99	0.193	0.079	0.41	0.018
Col 20 °C	645	316	88	5	0	3	5	4	0	1	0	0	1067	16.82	4.78	21.65	0.176	0.093	0.53	0.017
Col 20 °C	924	467	110	5	2	2	2	13	1	1	0	0	1527	18.40	4.19	22.20	0.194	0.069	0.36	0.017
Col 20 °C	859	461	114	8	2	2	5	5	2	0	0	0	1458	17.42	4.90	22.33	0.185	0.064	0.34	0.016
Mean														17.82	4.58	22.28	0.188	0.080	0.43	0.017
SD														0.87	0.33	0.68	0.010	0.012	0.09	0.000
Col 28 °C	629	341	98	4	3	4	14	6	0	2	1	0	1102	18.83	5.94	25.82	0.193	0.151	0.78	0.031
Col 28 °C	590	313	99	6	1	3	10	7	0	2	0	0	1031	18.77	5.87	25.22	0.195	0.132	0.68	0.028
Col 28 °C	598	350	87	4	2	0	7	10	3	0	1	0	1062	19.96	5.84	26.37	0.214	0.067	0.31	0.025
Col 28 °C	392	258	68	1	4	3	2	6	0	0	0	0	734	20.71	5.31	25.95	0.224	0.064	0.29	0.022
Col 28 °C	314	221	55	4	4	1	1	6	0	0	0	0	606	22.03	5.36	26.65	0.238	0.077	0.32	0.026
Mean														20.06	5.67	26.00	0.213	0.098	0.48	0.027
SD														1.37	0.30	0.55	0.019	0.040	0.23	0.003
P value														0.0156	2.45×10^{-3}	3.18×10^{-5}			0.5845	2.44×10^{-3}
hsbp-3 20 °C	612	630	241	35	15	42	21	39	4	8	6	0	1654	31.17	12.76	40.08	0.337	0.224	0.67	0.103
hsbp-3 20 °C	489	398	148	18	25	16	22	27	5	4	1	0	1153	28.88	11.67	39.72	0.306	0.222	0.72	0.102
hsbp-3 20 °C	437	550	185	25	21	12	24	20	2	3	0	0	1279	30.10	11.02	40.93	0.333	0.184	0.55	0.084
hsbp-3 20 °C	501	589	207	27	21	33	26	22	1	5	2	0	1434	29.99	11.75	40.13	0.324	0.216	0.67	0.096

Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	$I5a$(cM)	$I5b$(cM)	$I5ab$(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
hsbp-3 20 °C	584	477	146	21	8	15	21	29	3	3	0	0	1307	28.08	8.88	36.99	0.299	0.191	0.64	0.077
Mean														30.05	11.82	40.25	0.325	0.210	0.65	0.096
SD														1.14	0.88	0.62	0.017	0.023	0.09	0.011
hsbp-3 28 °C	536	525	195	17	6	14	11	15	6	4	0	0	1329	25.85	10.65	35.21	0.286	0.142	0.50	0.055
hsbp-3 28 °C	580	683	245	31	23	26	29	27	1	3	2	0	1651	29.50	11.36	40.10	0.328	0.179	0.55	0.086
hsbp-3 28 °C	602	700	254	29	23	36	27	26	1	4	2	0	1705	29.24	11.47	39.38	0.322	0.188	0.58	0.087
hsbp-3 28 °C	314	314	114	16	19	11	20	14	3	2	0	0	827	28.78	12.09	41.23	0.310	0.211	0.68	0.103
hsbp-3 28 °C	613	797	269	35	38	29	41	29	2	5	0	0	1858	30.79	11.54	42.25	0.337	0.206	0.61	0.096
Mean														28.83	11.42	39.64	0.317	0.185	0.58	0.085
SD														1.83	0.52	2.70	0.020	0.027	0.07	0.018
P value														0.433	0.776	0.965			0.148	0.494
Genotype	A	B	C	D	E	F	G	H	I	J	K	L	Total	$I5a$(cM)	$I5b$(cM)	$I5ab$(cM)	w/o_adj_CO	w_adj_CO	IFR	DCO ratio
Col 20 °C	343	289	194	10	11	14	11	8	3	0	0	0	883	21.69	14.61	36.24	0.263	0.095	0.36	0.065
Col 20 °C	574	470	259	30	16	18	22	8	10	1	2	1	1411	21.90	15.02	35.65	0.246	0.139	0.57	0.077
Col 20 °C	397	328	210	17	19	20	13	4	5	1	1	0	1015	21.08	15.57	35.02	0.241	0.133	0.55	0.079
Col 20 °C	704	699	386	28	24	16	20	11	5	2	0	0	1895	22.82	13.35	35.44	0.271	0.104	0.38	0.056
Col 20 °C	539	485	249	19	15	14	15	4	2	2	3	0	1347	21.79	12.77	33.18	0.248	0.122	0.49	0.055
Mean														21.87	14.64	35.59	0.255	0.118	0.46	0.069
SD														0.72	0.94	0.51	0.014	0.022	0.11	0.011
Col 28 °C	599	657	354	17	26	20	30	15	6	3	2	0	1729	24.87	14.40	39.56	0.294	0.123	0.42	0.069
Col 28 °C	689	753	441	34	32	37	32	15	7	5	2	0	2047	24.67	15.51	38.94	0.289	0.142	0.49	0.080
Col 28 °C	490	548	302	25	16	27	23	13	3	1	0	0	1448	24.97	14.23	38.95	0.298	0.122	0.41	0.075
Col 28 °C	218	220	142	10	11	12	11	3	3	1	1	0	632	22.86	16.69	38.69	0.270	0.134	0.49	0.082
Col 28 °C	270	285	182	10	10	12	15	8	3	1	1	0	797	24.28	15.93	40.59	0.296	0.115	0.39	0.075
Mean														24.34	15.21	39.03	0.288	0.130	0.45	0.076
SD														0.99	1.14	0.37	0.012	0.009	0.04	0.006
P value														1.12×10^{-3}	0.159	2.65×10^{-4}			0.555	0.131
hsbp-3 20 °C	349	697	455	106	85	108	81	35	13	10	12	3	1954	35.24	25.92	54.79	0.420	0.269	0.64	0.232

hsbp-3 20 °C	254	465	342	70	72	79	70	17	11	17	4	0	1401	34.40	26.41	55.92	0.385	0.298	0.77	0.243
hsbp-3 20 °C	215	353	263	81	65	58	60	21	7	7	5	0	1135	34.80	26.70	56.34	0.407	0.285	0.70	0.268
hsbp-3 20 °C	282	408	282	74	51	67	60	20	13	9	10	0	1276	33.07	26.68	54.27	0.372	0.279	0.75	0.238
hsbp-3 20 °C	271	527	333	88	83	85	82	21	10	10	10	0	1520	34.90	26.35	56.78	0.399	0.291	0.73	0.256
Mean														34.38	26.43	55.33	0.396	0.283	0.72	0.245
SD														0.93	0.36	0.97	0.021	0.012	0.06	0.016
hsbp-3 28 °C	162	279	212	51	35	46	47	7	8	6	10	1	864	31.94	29.57	55.56	0.358	0.278	0.77	0.244
hsbp-3 28 °C	174	320	231	62	48	40	47	11	5	2	3	0	943	31.71	25.34	54.19	0.382	0.242	0.63	0.231
hsbp-3 28 °C	150	297	236	60	51	43	46	15	10	7	5	1	921	34.74	29.26	57.82	0.419	0.276	0.66	0.258
hsbp-3 28 °C	157	331	233	47	40	52	44	19	9	3	6	0	941	34.64	27.05	58.29	0.439	0.238	0.54	0.234
hsbp-3 28 °C	130	246	216	28	22	37	24	7	10	8	1	1	730	31.10	27.88	53.15	0.376	0.239	0.64	0.189
hsbp-3 28 °C	271	391	313	39	37	36	47	11	9	5	4	0	1163	27.94	23.86	51.07	0.340	0.197	0.58	0.162
Mean														32.83	27.82	55.80	0.395	0.255	0.65	0.231
SD														1.73	1.72	2.23	0.033	0.020	0.08	0.026
P value														0.0633	0.453	0.638			0.0700	0.1332

Appendix Table S23. *420* **crossover frequency (cM) in plants with** *HEI10 epi* **allele.** *420* crossover frequency was measured by analyzing counts of fluorescence and non-fluorescent seeds using CellProfiler (van Tol *et al*, 2018; Carpenter *et al*, 2006). 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: $cM = 100 \times (1- [1-2(N_{Green}+N_{Red})/N_{Total}]^{1/2})$ (Melamed-Bessudo *et al*, 2005; Ziolkowski *et al*, 2015). To examine for significant differences between wild type and genotypes *P* values were calculated using Welch's t-tests. G/nG indicates the ratio of green color seed number (G) to non-green seed number (nG). R/nR repesents the ratio of red color seed number to non-red seed number.

genotype	green	red	both	none	total	cM	G/non G	R/non R	Mean	SD	*P* value
Col	192	229	1673	402	2496	18.60	2.96	3.20			
Col	203	171	1315	320	2009	20.77	3.09	2.84			
Col	217	207	1451	376	2251	21.05	2.86	2.80			
Col	176	202	1387	371	2136	19.62	2.73	2.90	20.13	1.06	
Col	170	202	1231	338	1941	21.47	2.59	2.82			
Col	218	203	1496	394	2311	20.27	2.87	2.78			
Col	160	161	1233	303	1857	19.11	3.00	3.01			
hsbp-3	407	387	1647	273	2714	35.59	3.11	2.99			
hsbp-3	434	428	1601	255	2718	39.53	2.98	2.94			
hsbp-3	372	428	1876	401	3077	30.72	2.71	2.98	34.19	3.89	1.92×10^{-4}
hsbp-3	508	458	1882	320	3168	37.54	3.07	2.83			
hsbp-3	396	444	1968	399	3207	31.00	2.80	3.03			
hsbp-3	430	418	2046	365	3259	30.75	3.16	3.10			
HEI10-Epi-1	147	164	228	909	1448	24.47	2.69	2.86			
HEI10-Epi-1	52	69	72	306	499	28.23	2.54	3.02			
HEI10-Epi-1	109	94	148	510	861	27.31	2.56	2.35			
HEI10-Epi-1	138	143	206	804	1291	24.85	2.70	2.75	26.44	1.51	1.64×10^{-6}
HEI10-Epi-1	129	134	160	719	1142	26.56	2.88	2.95			
HEI10-Epi-1	122	102	178	642	1044	24.44	2.73	2.48			
HEI10-Epi-1	131	131	156	712	1130	26.77	2.94	2.94			
HEI10-Epi-1	145	129	145	690	1109	28.88	3.05	2.82			
HEI10-Epi-2	145	89	125	495	854	32.77	2.99	2.16			
HEI10-Epi-2	255	251	1511	290	2307	25.08	3.26	3.23			
HEI10-Epi-2	277	256	1407	335	2275	27.10	2.85	2.72			
HEI10-Epi-2	293	281	1551	352	2477	26.75	2.91	2.84	27.05	2.58	2.85×10^{-5}
HEI10-Epi-2	236	253	1407	320	2216	25.26	2.87	2.99			
HEI10-Epi-2	191	196	1061	216	1664	26.87	3.04	3.09			
HEI10-Epi-2	213	192	1109	240	1754	26.64	3.06	2.87			
HEI10-Epi-2	264	258	1457	333	2312	25.94	2.91	2.87			

Appendix Table S24. Silique length in wild-type Col, *hsbp-3* and *hsbp-2*. Significance between wild type and mutant measurements were assessed by Welch's t-tests.

Silique number	Col	*hsbp-3*	*hsbp-2*
1	1.29	1.23	1.05
2	1.26	1.10	0.97
3	1.48	0.98	0.99
4	1.34	1.08	1.01
5	1.21	1.17	1.07
6	1.40	1.11	0.93
7	1.50	1.08	1.10
8	1.46	1.23	0.97
9	1.34	1.04	0.93
10	1.36	0.97	0.93
11	1.39	1.19	0.93
12	1.19	1.03	1.17
13	1.38	1.10	1.14
14	1.36	0.96	1.00
15	1.51	1.11	0.98
16	1.45	1.20	1.03
17	1.30	1.02	1.01
18	1.45	1.11	1.02
19	1.32	0.99	1.14
20	1.50	0.95	1.06
21	1.48	0.98	0.89
22	1.34	1.10	1.03
23	1.43	1.23	0.96
24	1.49	1.27	0.88
25	1.42	1.04	0.94
26	1.21	1.02	0.92
27	1.38	1.10	0.99
28	1.36	0.98	0.93
29	1.48	1.02	0.94
30	1.21	1.02	0.97
Mean (cm)	1.38	1.08	1.00
S.D.	0.096	0.092	0.074
P value		1.31×10^{-17}	1.43×10^{-23}

Appendix Table S25. Seed number per silique in wild-type Col, *hsbp-3* and *hsbp-2*. Significance between wild type and mutant measurements were assessed by Welch's t-tests.

Silique number	Col	*hsbp-3*	*hsbp-2*
1	53	50	20
2	52	56	20
3	58	48	25
4	51	54	23
5	50	50	19
6	56	54	21
7	58	42	19
8	56	46	19
9	59	46	18
10	50	54	16
11	60	47	17
12	56	42	23
13	45	55	17
14	50	43	16
15	62	53	23
16	55	44	23
17	63	40	21
18	58	53	12
19	57	43	27
20	60	55	15
21	59	41	16
22	56	51	23
23	51	54	11
24	55	52	15
25	56	41	22
26	47	44	19
27	54	41	27
28	58	43	18
29	50	58	22
30	51	52	18
Mean	54.87	48.40	19.50
S.D.	4.416	5.568	3.928
P value		6.53×10^{-6}	8.89×10^{-39}

Appendix Table S26. Pollen viability in wild-type Col, *hsbp-3* and *hsbp-2* measured using Alexander staining. Alexander staining of pollen was performed to measure pollen viability. Significance between wild type and mutant measurements were assessed by Welch's t-tests.

Measurement plant number	Col	*hsbp-3*	*hsbp-2*
1	99.42% (339/341)	99.03% (403/407)	98.98% (386/390)
2	98.78% (320/324)	98.98% (383/387)	99.05% (311/314)
3	99.12% (336/339)	99.60% (998/1002)	98.76% (314/318)
4	99.15% (349/352)	99.31% (1007/1014)	98.61% (350/355)
5	99.51% (405/407)	98.62% (565/573)	99.78% (463/464)
6	99.71% (337/338)	99.65% (563/565)	99.23% (385/388)
7	99.36% (309/311)	98.38% (536/545)	98.59% (344/349)
8	99.44% (354/356)	99.61% (1012/1016)	99.67% (301/302)
9	99.74% (377/378)	99.51% (1206/1212)	99.34% (298/300)
10		99.59% (1455/1461)	99.80% (494/495)
Mean	99.36%	99.23%	99.18%
S.D.	0.302	0.456	0.462
P value		0.465	0.334

Appendix Table S27. RAD51 foci number per cell in Col and *hsbp-3*. To test for significant differences in RAD51 foci number between Col and *hsbp-3*, *P* values were calculated using a Wilcoxon test.

Meiotic cell number	Col	*hsbp-3*
1	153	193
2	134	149
3	175	142
4	142	140
5	131	216
6	128	122
7	147	131
8	160	166
9	225	129
10	166	222
11	175	145
12	192	192
13	131	127
14	135	171
15	176	163
16	147	201
17	182	187
18	161	197
19	156	145
20	147	174
Mean	158.15	165.60
S.D.	24.399	30.981
P value		0.5883

Appendix Table S28. MLH1 foci number per cell in Col, *hsbp-3, hsbp-2*, Col/Ler and Col/Ler *meiMIGS-HSBP.* To test for significant differences in MLH1 foci number between Col, *hsbp-3, hsbp-2*, Col/Ler and Col/Ler *meiMIGS-HSBP*, *P* values were calculated using a Wilcoxon test.

Meiotic cell number	Col	*hsbp-3*	*hsbp-2*	Col/Ler	*meiMIGS-HSBP* Col/Ler
1	10	14	19	12	13
2	10	13	16	11	12
3	10	13	16	8	16
4	11	12	14	10	14
5	12	14	16	9	18
6	13	14	18	8	16
7	11	20	16	9	14
8	13	15	15	7	17
9	11	15	19	14	16
10	10	21	17	10	16
11	8	13	19	10	16
12	12	16	20	9	15
13	9	14	20	9	13
14	12	18	14	7	14
15	11	17	18	13	15
16	9	17	18	8	16
17	12	19	19	7	13
18	11	18	18	7	11
19	9	14	20	9	16
20	14	12	17	11	15
21	10	18	18	10	14
22	7	17	17	9	14
23	9	16	19	9	16
24	13	15	18	8	15
25	11	13	21	9	15
26	12	14	18	11	17
27	11	18	22	10	17
28	11	16	21	12	15
29	10	15	19	10	13
30	11	18	16	10	14
31	9	14	18	10	13
32	11	15	18	10	16
33	11	18		10	13
34	10	13		15	14
35	12	14		7	16
36	9			9	15
37	10			11	17
38	7			7	15
39	9			9	16
40	10			10	17
41	9			7	
42	11			9	
43	10			8	
44	13			10	
45	11			9	
46	8			11	
47	9			10	
48	12			10	

49	9			8	
50				9	
Mean	10.50	15.56	17.94	9.51	14.90
S.D.	1.57	2.34	1.97	1.77	1.55
P value		6.81×10^{-14}	2.95×10^{-14}		4.89×10^{-15}

Appendix Table S29. HEI10 foci number per cell in Col and *hsbp-3*. To test for significant differences in HEI10 foci number between Col and *hsbp-3, P* values were calculated using a Wilcoxon test.

Meiotic cell number	Col	*hsbp-3*
1	183	219
2	147	192
3	145	162
4	149	134
5	154	183
6	150	168
7	156	243
8	211	181
9	157	224
10	158	177
11	147	193
12	132	173
13	154	162
14	180	141
15	113	160
16	119	235
17	170	172
18	210	162
19	110	181
20	192	188
21	187	231
22	175	
23	154	
Mean	158.83	184.81
S.D.	27.112	30.190
P value		4.451×10^{-3}

Appendix Table S30. List of oligonucleotides used in this study.

Primer	Nucleotide sequence (5´ to 3´)
hcr2-geno_F	ACTTGGTTTATCACTGAATCC
hcr2-geno_R	ATAGAACCATGTGCTACTACC
HSBP-RT_F	CTCCGTCGTCTCTCATCG
HSBP-RT_R	TCTCAAGACCAAAATAGAAATGC
hsbp-2-geno_F	GTCCAAAATCTTCTCCAGCAG
hsbp-2-geno_R	CTAATACAGCTATGAGATTCG
LBb1.3	ATTTTGCCGATTTCGGAAC
HSBP-qPCR_F	CCGAGATGGGACTAGAAGG
HSBP-qPCR_R	AGAGGAACTAGCCGGTGTTTTG
HSBP-genomic_F	TGCAGGTCGACTCTAGAGTGGAAGCCGAGACTGTAG
HSBP-genomic_R	AGGCGCGCCCTCGAGTTGGGAAAATAAGAGAAGAGGC
HSBP-myc_R	AGGCGCGCCCTCGAGTTGAGAGGAACTAGCCGGTG
DMC1p_F	CCGAAGACGGCTCAGGAGAAAGAAACCAAAGTTCCATGTCCAT
DMC1p_R	CCGAAGACGGCTCGCATTccGATCACTGACACAAGCAAAAATAAA
meiMIGS-HSBP_F	CCGAAGACGGCTCAAATGGTGATTTTTCTCTACAAGCGAACATGATTCTGAGGATACTAAGCAGAGCAC
meiMIGS-HSBP_R	CCGAAGACGGCTCGAAGCCTAGCCGGTGTTTTGGGTTCATCGCCTGATTTG
meiMIGS-miR173_F	CCGAAGACGGCTCAAATGTAAGTACTTTCGCTTGCAGAGAGAAATC
meiMIGS-miR173_R	CCGAAGACGGCTCGAAGCCAAGCTCTTTCGCTTACACAGAGAATC
HEI10-qPCR_F	ACCCGCGACACCAAGAACC
HEI10-qPCR_R	GCAGGTGAGTCGGTGGAG
ASY1-qPCR_F	TGGTGGGATGCAGCAGAACG
ASY1-qPCR_R	CCTGCCACGTCTGTCCTGTG
DMC1-qPCR_F	GCAGCCACCATCAGGCTCTT
DMC1-qPCR_R	GCGTCAGCAATGCCTCCTTG
MLH1-qPCR_F	CCAAACCCATCGGGTGACG
MLH1-qPCR_R	CCATGGAAGCTGGTGGCT
MUS81-qPCR_F	TGCAGGTCCCGCAGGTAAC
MUS81-qPCR_R	AGACAAAGGTCAAAGGGACAC
TUB-qPCR_F	ATCGATTCCGTTCTCGATGT
TUB-qPCR_R	ATCCAGTTCCTCCTCCCAAC
HEI10-myc_F	CCCCGGATCCGTCTTCCTGCTGCTACTCCCATCAC
HEI10-myc_R	CCCCGGATCCCTAGCCTGAGAATAGAAGCAACAAA
pET-HSBP_F	GAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGGATGGTCATGATTCTGAGGATAC
pET-HSBP_R	GCCGGATCTCAGTGGTGGTGGTGGTGGTGCTCGAGAGAGGAACTAGCCGGTGTTTTGGGTTCATC
HSFA7a_F	CCCGAAGACGGCTCAAATGATGATGAACCCGTTTCTCCCG
HSFA7a_nsR	CCCGAAGACGGCTCGAAGCCCGGAGGTGGAAGCCAAACTCTCATCAC
HSFA7a_OLF1	CTCAATACTTATGTGAGCCTTCTCTGCTCTGTATTC
HSFA7a_OLF2	GAATACAGAGCAGAGAAGGCTCACATAAGTATTGAG
HSFA1a_F	CCCGAAGACGGCTCAAATGATGTTTGTAAATTTCAAATACTTCTCTT
HSFA1a_nsR	CCCGAAGACGGCTCGCGAACCGTGTTCTGTTTCTGATGTGAGTAGACCCAATT
HSFA1a_OLF1	AGCTTGAGGGAATACCCGAAGATCCCGAGATTGATGAACTAA
HSFA1a_OLR1	TTAGTTCATCAATCTCGGGATCTTCGGGTATTCCCTCAAGCT
HSBP_F	CCCGAAGACGGCTCAAATGATGGTAAATATCCGCCTCCTAATATCA
HSBP_R	CCCGAAGACGGCTCGAAGCCCTTAAGAGGAACTAGCCGGTGTTTTG
HSBP_OLF1	TTTATGTCTTTGTAGGCCTTGGAA
HSBP_OLR1	TTCCAAGGCCTACAAAGACATAAA
HSBP_OLF2	GATTATTTGTGTCTCCAAGGAAAG
HSBP_OLR2	CTTTCCTTGGAGACACAAATAATC

HSBP_nsR	CCCGAAGACGGCTCGCGAACCAGAGGAACTAGCCGGTGTTTTGGGTTCATCGCC
HEI10_F	CCCGAAGACGGCTCAAATGATGAGATGCAACGCGTGTTGGA
HEI10_R	CCCGAAGACGGCTCGAAGCCCCTATAGCCTGAGAATAGAAG
HEI10_OLF1	GAACAGAGAAACCATTCGCAA
HEI10_OLR1	TTGCGAATGGTTTCTCTGTTC
REC8p_F	CCCGAAGACGGCTCAGGAGATGGAGGTAGCGGGATAATTGA
REC8p_R	CCCGAAGACGGCTCGCATTCGCGTGCAATGTAGCGGCCATCCTTAAGAAGAAGAAA
REC8p_OLF1	GAATGAGGACGAAGTACAAGAATCAGAT
REC8p_OLR1	ATCTGATTCTTGTACTTCGTCCTCATTC
REC8p_OLF2	TTCGGTCCTCACTCTCTGCTCAAC
REC8p_OLR2	GTTGAGCAGAGAGTGAGGACCGAA
REC8p_OLF3	AACATTCGAGGACCCGTGATCTAACCAG
REC8p_ OLR3	CTGGTTAGATCACGGGTCCTCGAATGTT
ASY1p_F	CCCGAAGACGGCTCAGGAGTGGCAGGATATATTGTGGTG
ASY1p_R	CCCGAAGACGGCTCGCATTCCTTTTGCAGAAGTGTGAAACGA
SPO11-1p_F	CCCGAAGACGGCTCAGGAGGACCTCTCTGTTCTTAATTCC
SPO11-1p_R	CCCGAAGACGGCTCGCATTCCCTCTTTCGAGTTTCAAAACTGAAA
HEI10p_F	CCCGAAGACGGCTCAGGAGCACTGTATTTTTCCAACCAC
HEI10p_R	CCCGAAGACGGCTCGCATTCCGTCAACCTCTAATATAAGTATCTCA
RPS5Ap-F	CCGAAGACGGCTCAGGAGCCATAATCGTGAGTAGATATATTACTCAAC
RPS5Ap-R	CCGAAGACGGCTCGCATTGGCTGTGGTGAGAGAAACAGAGCGTGAGCTC
HEI10-ChIP_F1	CTTCTCCACCACAAGTGACTGTTG
HEI10-ChIP_R1	CTTAGAACCAGACCGCGAAAGC
HEI10-ChIP_F2	GGCAGTGAATTTTGAATAAGACAC
HEI10-ChIP_R2	CAGAGCACGTTTGTGCTCAGAAC
HEI10-ChIP_F3	CCCTTAATTTCGGGACTGTGCAG
HEI10-ChIP_R3	CGATTTAGAAAACGGAAACCCTAG
HEI10-ChIP_F4	GCAGTGACTCTTTGATGGAGAG
HEI10-ChIP_R4	GCAAAGGTCATTGTTGCTGCTC
HEI10-ChIP_F5	GCGATATCTCCTTTGACAAACTTG
HEI10-ChIP_R5	GTAACTATCCTGATTACAAGATCG
HEI10-ChIP_F	CGAAGGAGCTAGAAGCGATAAC
HEI10-ChIP_R	CGAGAACGTTCACGAGTAAAGATC
UBQ13-ChIP_F	AGTTAAGCTGATTTGTTGCCAAG
UBQ13-ChIP_R	GAATCTTCCAAATCTCCTGCC
TUB-ChIP_F	ACAAACACAGAGAGGAGTGAGCA
TUB-ChIP_R	GCATCTTCGGTTGGATGAGTGA
McrBC_HEI10p-qPCR_F	TCACAACCAAGCTCGAAAAC
McrBC_HEI10p-qPCR_R	TCTCAGATGGAGGTTCGTTG

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