Supplementary Table 1 Sampling localities for accessions from the *M. guttatus* complex included in our genetic, phenotypic, and redundancy analyses. Accessions are ordered first by state/province from north to south, then alphabetically. AL = Alaska; BC = British Columbia; WA = Washington; OR = Oregon; CA = California; ID = Idaho; NV = Nevada; CO = Colorado; AZ = Arizona

Species	Accession ID	State or Province	Latitude (N)	Longitude (W)	Elevation (m)	Annual/Perennial
M. arvensis	CVP	CA	38.372	-123.055	224	A
	NAP	CA	38.752	-122.615	335	A
	POT	CA	37.925	-122.609	622	A
M. cupriphilus	SEC	CA	37.915	-120.725	297	A
M. guttatus	NKL	BC	50.358	-126.930	96	A
	SKZ	BC	48.782	-123.953	125	A
	TAY	BC	49.299	-125.292	59	A
	WLD	BC	49.898	-124.550	286	A
	AWP	WA	48.495	-122.702	22	A
	LCU	WA	47.495	-123.277	230	A
	RFA	WA	46.631	-123.230	83	A
	BSP	OR	43.712	-124.099	13	A
	BVG	OR	43.059	-123.571	476	A
	FEV	OR	44.400	-122.298	490	A
	IM	OR	44.401	-122.150	1582	A
	LIN	OR	45.136	-123.896	18	A
	MAR	OR	43.479	-123.294	183	A
	MED	OR	37.809	-120.302	288	A
	RGR	OR	42.489	-124.208	17	A
	S2G	OR	43.982	-123.096	580	A
	SAG	OR	44.797	-122.544	243	A
	SAM	OR	45.959	-123.680	545	A
	SWC	OR	43.959	-123.902	38	A
	BHI	CA	41.155	-123.890	777	A
	BHT	CA	37.977	-120.639	293	A
	CAV	CA	38.343	-122.485	118	A

Species	Accession ID	State or Province	Latitude (N)	Longitude (W)	Elevation (m)	Annual/Perennial
M. guttatus	GCC	CA	37.874	-120.434	392	A
	GTR	CA	38.580	-122.197	144	A
	KLM	CA	41.270	-123.606	227	A
	LON	CA	38.044	-120.648	512	A
	LQH	CA	37.921	-120.717	279	A
	OAE	CA	38.411	-122.960	280	A
	PCR	CA	40.641	-123.892	702	A
	RNC	CA	38.911	-123.245	314	A
	SEX	CA	37.915	-120.725	297	A
	SGS	CA	34.301	-118.107	1164	A
	SHO	CA	37.931	-120.733	204	A
	SSR	CA	38.676	-123.240	333	A
	STO	CA	38.439	-122.940	212	A
	USK	CA	38.672	-123.210	125	A
	CMF	CA	38.443	-122.974	87	A
	KRR	CA	38.580	-123.117	106	A
	AGG	BC	52.626	-131.422	15	P
	ATT	AL	52.936	-123.245	1200	P
	BAM	BC	48.837	-125.144	3	P
	CPB	BC	53.171	-131.785	10	P
	GPT	BC	49.052	-125.722	0	P
	PCL	BC	53.689	-132.184	5	P
	SCC	BC	48.412	-124.012	1	P
	TSG	BC	53.419	-131.916	17	P
	CHR	WA	46.780	-121.779	1118	P
	GBS	OR	42.425	-124.410	26	P
	HEC	OR	44.135	-124.123	11	P
	MWV	OR	44.419	-121.773	1215	P
	OSW	OR	45.761	-123.983	0	P

Species	Accession ID	State or Province	Latitude (N)	Longitude (W)	Elevation (m)	Annual/Perennial
	OTT	OR	44.753	-124.057	76	P
	THR	OR	44.101	-121.623	1992	P
	ANR	CA	39.737	-123.631	397	P
	BCB	CA	36.063	-121.592	8	P
	BSR	CA	40.529	-124.163	16	P
	BUL	CA	34.921	-120.436	73	P
	CAB	CA	39.359	-123.817	5	P
	CAN	CA	36.069	-121.551	573	P
	DAV	CA	37.025	-122.218	4	P
	GBM	CA	41.379	-124.069	21	P
	MRR	CA	38.456	-123.141	8	P
	ORO	CA	35.273	-120.889	10	P
	SBC	CA	36.484	-121.196	647	P
	SMO	CA	38.323	-122.590	494	P
	STB	CA	37.891	-122.635	9	P
	SVH	CA	41.616	-120.104	1408	P
	SWB	CA	39.036	-123.690	4	P
	USB	CA	39.832	-123.849	11	P
	WEV	CA	35.423	-120.789	108	P
	WFM	ID	44.710	-114.335	1992	P
	YJS	ID	44.951	-114.584	1656	P
	ALL	NV	39.006	-114.219	2076	P
	BOB	NV	48.529	-124.451	4	P
	BOG	NV	41.924	-118.804	1308	P
	DHS	NV	41.051	-119.029	1208	P
	SOL	NV	40.051	-116.985	1597	P
	CC	CO	38.986	-106.948	3214	P
	COT	CO	38.839	-106.419	3517	P
	EML	CO	39.007	-107.040	3193	P

Species	Accession ID	State or Province	Latitude (N)	Longitude (W)	Elevation (m)	Annual/Perennial
	PGA	CO	38.964	-107.094	3259	P
	SCH	CO	39.018	-107.035	3448	P
	STR	CO	39.025	-107.031	3377	P
	PED	AZ	32.711	-110.628	727	P
M. laciniatus	GB	OR	37.136	-122.133	1865	A
	TRT	OR	37.716	-119.705	1479	A
	CECL	CA	37.309	-119.495	1302	A
	DNK	CA	37.085	-119.218	1880	A
	PETL	CA	37.056	-119.369	1250	A
	SHL	CA	37.145	-119.306	1603	A
	SNB	CA	37.042	-119.404	1043	A
	TIGR	CA	37.812	-119.506	2584	A
	WLF	CA	37.842	-119.594	2405	A
M. micranthus	LGR	CA	39.140	-123.286	622	A
M. nasutus	WSK	WA	45.754	-121.518	148	A
	HCN	OR	42.547	-123.502	360	A
	NFN	OR	45.241	-122.261	218	A
	SBN	OR	45.261	-121.033	241	A
	SF	OR	45.262	-121.030	242	A
	BCR	CA	37.823	-120.258	867	A
	MEN	CA	37.809	-120.302	288	A
	MHA	CA	37.340	-121.657	962	A
	SHI	CA	39.877	-123.732	225	A
	SMC	CA	36.062	-121.554	696	A
	SQP	CA	36.565	-118.766	1965	A
M. nudatus	GUN	CA	38.752	-122.615	335	A
M. pardalis	DPP	CA	37.661	-120.456	94	A
M. tilingii	BAG	WA	48.873	-121.688	1186	P
	RAN	WA	47.010	-121.760	1354	P

Species	Accession ID	State or Province	Latitude (N)	Longitude (W)	Elevation (m)	Annual/Perennial
	STV	WA	46.802	-121.714	1910	P
	TWN	WA	48.950	-121.636	1594	P
	ICE	OR	45.226	-117.268	2402	P
	LPI	CA	38.289	-119.638	3167	P
	LVR	CA	37.951	-119.226	2774	P
	SAB	CA	37.212	-118.610	2793	P
	SOP	CA	40.362	-120.510	1251	P

Supplementary Table 2 Primers for the 1 microsatellite and 15 intron-length polymorphic markers used in our genetic analyses. All primers are written 5’ to 3’. Positions given are based on the genome sequence for *M. guttatus* IM62. PCR protocols are found in Kelly and Willis (1998). LG = linkage group.

Marker	LG	Position	Primer Sequences	
DIV1 Inversion				
MgSTS299	8	1844602	F: CTTGATCTTCATGCTCACACG	R: TAATCACATTCGGCAACTCG
MgSTS675	8	2044482	F: TCGTTGGTGGAAATCAAAGC	R: CCGGATCCTTGTTGAGTAGC
MgSTS173	8	2444182	F: GGCAATCTTCAACCTTTTCC	R: AGGCTGGTGGCTTATCTTCC
MgSTS059	8	2636431	F: TTTCCGATTGGAGATTCGAC	R: ACTCCAGGAACGTTTGGATG
MgSTS084	8	2943772	F: CCACCGAAGAAGTTGAAACC	R: GCCTTAATAGGACCCCCAAC
MgSTS278	8	3605725	F: ACGTCAGCCCTTTGTACACC	R: ACTCAGTTGTGCCAGTCACC
MgSTS563	8	3695076	F: AAACTGGTGTGCTGAAAGAGC	R: GCTTCCACCGTAAATTCTCC
MgSTS069	8	3717111	F: GAGGAAGTGGGAGACGACAA	R: CCTTCCAACGATCCAATCAT
Noninversion				
MgSTS665	1	5030756	F: CATTGCAAAGCGATTACCC	R: ATGCAAAGCCTGAAAAGTGC
MgSTS617	2	2505570	F: CGCCTTGGAAGAGTTAATCG	R: ATCGTTGGATCTCGTTGTCC
MgSTS423	6	4650184	F: TCTGATCTCTCGAACCTCTCG	R: ATCTAGCTCGCACCAACTCC
MgSTS571	8	8885823	F: TGCTTTCTCTGCATCACTCG	R: CTCTACCCCGGTTGTATTGC
MgSTS837	10	357023	F: AATGACGCACGATCTCTCG	R: GGAACCCCTATCATCACTTTCC
MgSTS332	10	18598693	F: GTGGTGTGCAATTCATTATCC	R: AAATTCATCACTGGACATTTCG
MgSTS672	14	25799001	F: AATCAACCGCAATTCTGACC	R: GGGAATTAATCCTCAACAAAGC
AAT217	17	727542	F: ACCTGGACTACCATGTACCG	R: CCTTGAGTACGGCTTCTTCG

Supplementary Table 3 Missing alleles for *M. guttatus* sp. – indicates number of accessions with missing data.

	Inversion markers							
	278	59	69	84	173	299	563	675
M. arvensis	–	–	–	–	–	–	–	–
M. cupriphilus	–	–	–	–	–	–	–	–
M. guttatus annuals	–	–	1	–	–	–	–	–
M. guttatus perennials	3	1	–	–	–	–	–	–
M. laciniatus	–	–	–	–	–	–	–	–
M. micranthus	–	–	–	–	–	–	–	–
M. nasutus	–	–	–	–	–	–	–	–
M. nudatus	–	–	–	–	–	–	–	–
M. pardalis	–	–	–	–	–	–	–	–
M. tilingii	–	–	–	–	–	–	–	–

	Non inversion markers							
	217	332	423	571	617	665	672	837
M. arvensis	–	–	–	–	–	–	–	–
M. cupriphilus	–	–	–	–	–	–	–	–
M. guttatus annuals	2	–	–	–	2	–	1	1
M. guttatus perennials	2	–	2	1	1	2	1	1
M. laciniatus	–	–	–	–	–	–	1	–
M. micranthus	–	–	–	–	–	–	–	–
M. nasutus	–	–	–	–	1	–	–	–
M. nudatus	–	–	–	–	–	–	–	–
M. pardalis	–	–	–	1	–	–	–	–
M. tilingii	–	–	–	–	–	–	–	–

Supplementary Table 4 Genetic diversity indices for each locus for members of the *M. guttatus* sp. complex and for *M. guttatus* annuals and perennials. N_a = Number of alleles; H_e = expected heterozygosity; H_o = observed heterozygosity; F_{IS} = inbreeding coefficient; Inv = inverted region; NI = non-inverted region. Indices are given with standard error. Indices for which the inversion markers exhibit lower diversity than the noninversion markers are in bold. NA = insufficient data.

Taxon	Inv Locus	N_a	H_o	H_e	F_{IS}
M. guttatus annuals	69	38	0.421	0.883	0.522
	278	38	0.421	0.928	0.551
	675	19	0.421	0.872	0.517
	59	6	0.263	0.759	0.653
	299	18	0.395	0.897	0.560
	173	11	0.395	0.800	0.506
	563	9	0.211	0.765	0.725
	84	19	0.421	0.889	0.526
M. guttatus perennials	69	12	0.227	0.830	0.723
	278	21	0.405	0.902	0.551
	675	15	0.267	0.877	0.692
	59	7	0.364	0.791	0.540
	299	18	0.333	0.893	0.627
	173	7	0.222	0.613	0.637
	563	10	0.244	0.724	0.662
	84	15	0.341	0.759	0.551
M. guttatus all accessions	69	16	0.317	0.885	0.642
	278	31	0.413	0.938	0.560
	675	24	0.337	0.896	0.624
	59	9	0.317	0.792	0.600
	299	24	0.361	0.914	0.605
	173	12	0.301	0.779	0.613
	563	13	0.229	0.770	0.703
	84	26	0.378	0.850	0.555

M. arvensis	69	1	0.000	0.000	NA
	278	1	0.000	0.000	NA
	675	2	0.000	0.444	1.000
	59	1	0.000	0.000	NA
	299	2	0.000	0.000	1.000
	173	1	0.000	0.000	NA
	563	2	0.000	0.444	1.000
	84	2	0.000	0.444	1.000
M. laciniatus	69	2	0.111	0.475	0.766
	278	4	0.333	0.599	0.443
	675	3	0.222	0.494	0.550
	59	3	0.000	0.370	1.000
	299	4	0.222	0.636	0.650
	173	3	0.222	0.204	-0.091
	563	5	0.222	0.728	0.695
	84	8	0.444	0.852	0.478
M. nasutus	69	6	0.167	0.719	0.768
	278	4	0.417	0.451	0.077
	675	5	0.250	0.361	0.308
	59	4	0.083	0.538	0.845
	299	4	0.000	0.583	1.000
	173	3	0.000	0.292	1.000
	563	4	0.295	0.308	0.435
	84	4	0.083	0.601	0.861
M. tilingii	69	5	0.111	0.772	0.856
	278	6	0.333	0.796	0.581
	675	5	0.444	0.765	0.419
	59	9	0.000	0.494	1.000
	299	8	0.333	0.809	0.588
	173	6	0.222	0.741	0.700
	563	2	0.111	0.500	0.778
	84	4	0.889	0.673	-0.321

Taxon	NI Locus	N_a	H_o	H_e	F_{IS}
M. guttatus annuals	217	14	0.528	0.858	0.385
	837	26	0.405	0.934	0.566
	672	24	0.447	0.928	0.518
	617	25	0.541	0.942	0.426
	665	26	0.237	0.929	0.745
	423	31	0.421	0.948	0.556
	571	17	0.474	0.859	0.449
M. guttatus perennials	217	7	0.279	0.813	0.657
	837	24	0.205	0.941	0.783
	672	19	0.395	0.890	0.556
	617	24	0.535	0.932	0.426
	665	22	0.279	0.917	0.696
	423	25	0.326	0.895	0.636
	571	10	0.273	0.778	0.649
	332	8	0.111	0.400	0.722
M. guttatus all accessions	217	13	0.380	0.842	0.549
	837	34	0.296	0.945	0.687
	672	30	0.420	0.919	0.543
	617	29	0.538	0.943	0.430
	665	34	0.259	0.938	0.724
	423	35	0.370	0.935	0.604
	571	19	0.378	0.833	0.546
	332	11	0.157	0.487	0.678
M. arvensis	217	1	0.000	0.000	NA
	837	3	0.000	0.667	1.000
	672	1	0.000	0.000	NA
	617	3	0.333	0.611	0.455
	665	2	0.000	0.444	1.000
	423	4	0.667	0.667	0.000
	571	2	0.000	0.444	1.000

	332	1	0.000	0.000	NA
M. laciniatus	217	4	0.222	0.568	0.609
	837	7	0.000	0.815	1.000
	672	5	0.125	0.758	0.835
	617	5	0.222	0.673	0.670
	665	7	0.333	0.710	0.530
	423	3	0.000	0.494	1.000
	571	5	0.333	0.623	0.465
	332	1	0.000	0.000	NA
M. nasutus	217	4	0.167	0.635	0.738
	837	7	0.083	0.767	0.891
	672	3	0.083	0.344	0.758
	617	5	0.364	0.587	0.380
	665	5	0.500	0.764	0.345
	423	4	0.083	0.358	0.767
	571	6	0.250	0.569	0.561
	332	3	0.083	0.392	0.788
M. tilingii	217	7	0.444	0.710	0.374
	837	6	0.000	0.741	1.000
	672	11	0.667	0.895	0.255
	617	10	0.556	0.883	0.371
	665	7	0.444	0.802	0.446
	423	6	0.111	0.772	0.856
	571	7	0.667	0.796	0.163
	332	3	0.000	0.370	1.000

Supplementary Table 5 Results of stepwise forward selection of variables for inclusion in RDA. CV = coefficient of variation. Mean diurnal range = mean of monthly (max temp – min temp). Temperature annual range = max temperature warmest month – min temperature coldest month. Isothermality = (mean diurnal range/temperature annual range)* 100. Temperature Seasonality (standard deviation *100). * p ≤ 0.050, ** p ≤ 0.010, *** p ≤ 0.001.

Model	AIC
Noninversion	
Mean temperature coldest quarter + Mean temperature driest quarter + Min. temperature coldest month + Temperature annual range + Temperature seasonality	121.23*
+ Precipitation CV	121.99
+ Mean temperature warmest quarter	121.98
+ Annual mean temperature	122.11
+ Isothermality	122.13
+ Annual precipitation	122.19
+ Precipitation coldest quarter	122.17
+ Precipitation wettest quarter	122.18
+ Precipitation wettest month	122.24
+ Precipitation warmest quarter	122.25
+ Precipitation driest month	122.27
+ Mean diurnal range (Mean of monthly (max temp - min temp))	122.36
+ Precipitation driest quarter	122.38
+ Mean temperature wettest quarter	122.58
+ Maximum temperature warmest month	121.23
Inversion	
Minimum temperature coldest month + Precipitation wettest month +Precipitation wettest quarter + Precipitation warmest quarter + Precipitation CV + Isothermality	132.91**
+ Precipitation driest month	133.56

+ Precipitation driest quarter	133.63
+ Mean temperature driest quarter	133.63
+ Maximum temperature warmest month	133.83
+ Mean diurnal range	133.79
+ Temperature annual range	133.83
+ Mean temperature wettest quarter	133.99
+ Annual precipitation	133.95
+ Mean temperature warmest quarter	133.98
+ Annual mean temperature	134.01
+ Precipitation coldest quarter	134.02
+ Mean temperature coldest quarter	134.02
+ Temperature seasonality	133.98

Appendix 1

We conducted a redundancy analysis (RDA) to determine whether variation in morphology and flowering time was correlated with variation in noninversion and inversion markers. We selected variables by first performing a RDA with stepwise forward addition of the morphological variables and flowering time and assessing their significance using AIC. We retained any variables that explained significant portions of genomic variation for full RDA and partial RDA (the latter where the annual/perennial status of *M. guttatus* accessions was held constant). We found that one variable (height in cm) was correlated with noninversion variation and one variable (diameter between the first and second true leaves) was correlated with inversion variation (Supplementary Table 6). In a full RDA, we found that annual/perennial status was significantly associated with both noninversion and inversion marker variation. Height was significantly correlated with noninversion variation and diameter between first and second true leaves and significantly correlated with inversion variation (Supplementary Table 7); these correlations did not change in a partial RDA where annual/perennial status was held constant.

Supplementary Table 6 Results of stepwise forward selection of morphological variables and flowering time for inclusion in RDA. * $p \leq 0.050$, ** $p \leq 0.010$, *** $p \leq 0.001$.

Model	AIC
Noninversion	
Height (cm)	104.98**
Flowering time post germination (days)	105.62
Length of first leaf (mm)	105.65
Width of first leaf (mm)	105.76
Length of first flower (mm)	105.75
Length of second internode (mm)	105.80
Number of pairs of leaves upon flowering	105.97
Width of first flower (mm)	106.01
Diameter btw 1st and 2nd true leaves (mm)	106.28
Presence of anthocyanin calyx spots	107.01
Inversion	
Diameter btw 1st and 2nd true leaves (mm)	117.43**
Length of first flower (mm)	118.12
Width of first flower (mm)	118.26
Flowering time post germination (days)	118.21
Number of pairs of leaves upon flowering	118.24
Presence of anthocyanin calyx spots	119.19
Length of second internode (mm)	118.33
Length of first leaf (mm)	118.43
Height (cm)	118.46
Width of first leaf (mm)	118.52

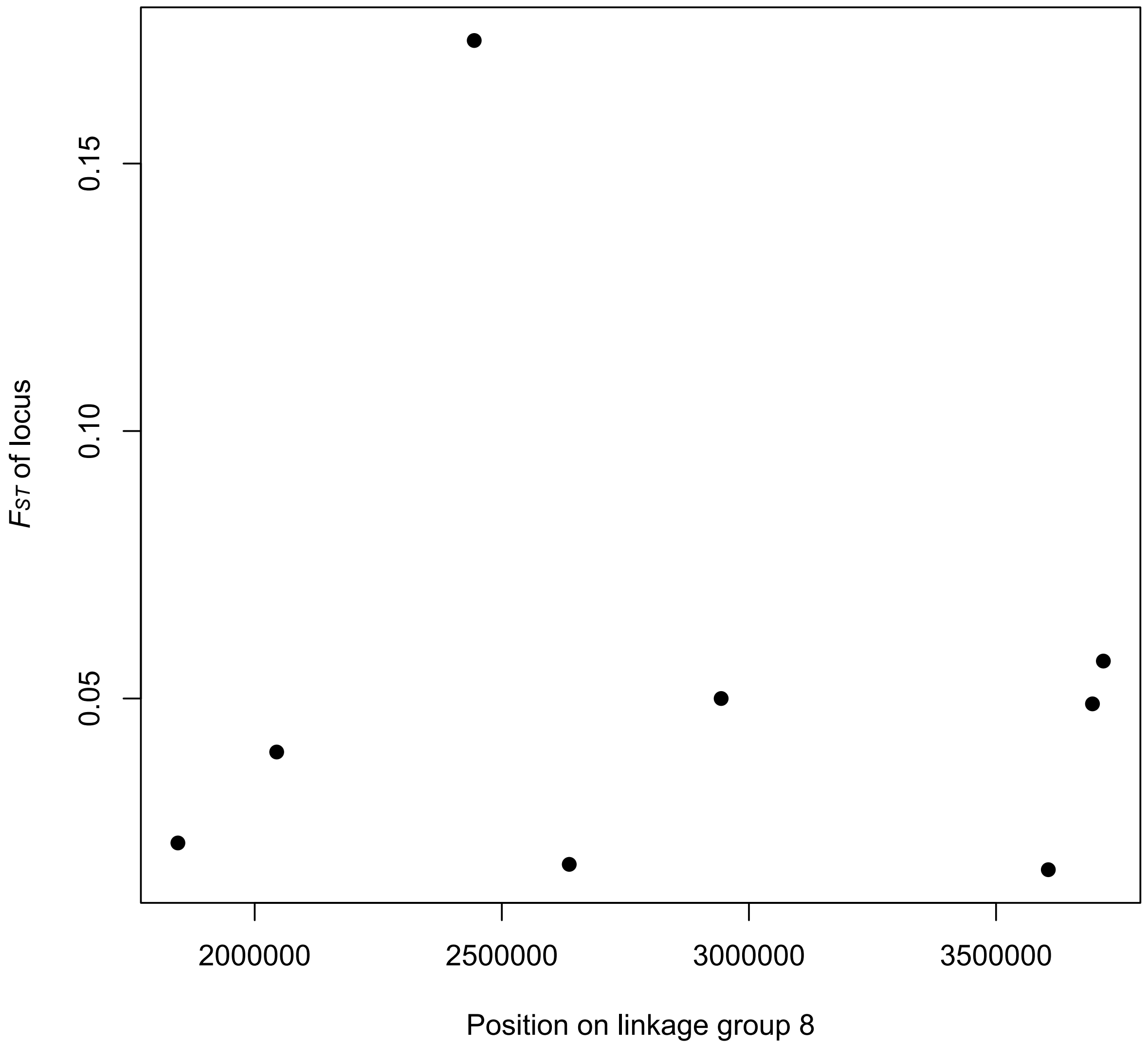
Supplementary Table 7 Results of redundancy analysis testing for associations between morphology variables and variation in the inversion and non-inversion markers within *M. guttatus*. All terms remain significant when annual/perennial status is held constant. Significance assessed with a minimum of 1,000 permutations: $^*p \leq 0.05$, $^{**}p \leq 0.01$, $^{***}p \leq 0.001$.

	% variance	*P*
<u>Inversion</u>		
Annual/Perennial	23.25	0.001***
Diameter btw 1st and 2nd true leaves	18.63	0.001***
<u>Noninversion</u>		
Annual/Perennial	12.78	0.022*
Height (cm)	20.22	0.001**

Appendix 2

We investigated whether F_{ST} and allelic variation in the DIV1 inversion markers could be a function of distance to the breakpoints. Plots of F_{ST} and number of alleles (N_a) of inversion markers with respect to their position on linkage group 8 show little evidence of an association (Supplementary Figures 1 and 2). There is no significant correlation between F_{ST} and distance to the leftmost breakpoint (as determined by recent mapping experiments (Friedman, unpublished data) ($r = 0.19$, $p = 0.68$; Spearman rank correlation coefficient). Similarly, there is no signficiant correlation between number of alleles and distance to the leftmost breakpoint. ($r = -0.13$, $p = 0.78$; Spearman rank correlation coefficient). Since F_{ST} can be impacted by the heterozygosity of the individual markers, and since we have so few markers, this analysis should be interpreted with caution. This question would be better addressed with genomic sequence data.

Supplementary Figure 1



Supplementary Figure 2