**Data Archive Files:**

**Script\_01-Power simulation.R.txt** R script used for power simulation for gene expression

**Script\_get\_anc\_for\_variable\_sites.py.txt** Python script used to identify ancestral alleles of variable SNPs

**Script\_MANOVA\_permutation.R.txt** R script used for MANOVA permutation and generation of Figure 5.

**Script\_Transf\_vcf2fas.py.txt** Python script for VCF reformatting

**Script\_Variant\_discovery.txt** SLURM script for GATK analysis of polymorphisms

**Sup Data Boechera Libraries.xlsx** Identifying information for Boechera libraries

**Sup Data Experimental Crosses.docx** Summary information on experimental crosses used in these analyses. Pedigree, Designation, Genotype origins, Collinearity, and Location.

**Sup Data Expression.xlsx** Expression levels for each gene near the inversion breakpoints, for individuals that are homozygous for INV and STD.

**Sup Data Genotype\_Information.xlsx** Information on genotypes used in this study. ID, East-West admixture, principal component scores, presence in the inversion region (Y/N), population group, population name, state, latitude, longitude, elevation in meters

**Sup Data Genotype\_Matrix\_For\_RILs.xlsx** Genotype matrix with columns: scaffold number, Bin\_ID, genome position, number of RILS with data, heterozygosity, followed by one column for each genotype. The genotypes are coded as -1 = LTM homozygote, 0 = heterozygous, 1 = SAD12 homozygote, 9 = missing

**Sup Data INV122\_RP83.snp.geno.xlsx** Genotype matrix with columns: scaffold ID, position on scaffold, Reference\_Allele, Alternate\_Allele, followed by one column for each genotype. The genotypes are coded as -1 = missing, 0 = homozygous of reference allele (2 reference alleles), 1 = heterozygous (1 reference allele), 2 = homozygous for alternative allele (0 reference alleles).

**Sup Data Inversion\_SNP\_annotation.xlsx** Annotation of SNPs with minor allele frequency >=0.05 in the inversion region of chromosome 1. Columns: Chr, chromosome number; Pos1, position on chromosome; Scaffold, Scaffold number, Pos2, position on scaffold; Ref, reference allele; Alt, alternative allele; Anc, ancestral state; Frequency, frequency of derived allele or reference allele if ancestral state is unknown; Arabidopsis thaliana orthology; Putative\_function.

**Sup Data JGI\_Libraries.xlsx** Detailed information on JGI library, nomenclature, and methods.

**Sup Data Locations of breakpoints and related primers.docx** Genomic locations of breakpoints and related primers.

**Sup Data LTMxSAD12\_Inferred\_Crossovers.xlsx** Location information on all inferred crossovers. Format: Scaffold ID, left flanking bin ID, right flanking bin ID, RIL ID, left flanking bin genotype, right flanking bin genotype. LTM = -1, SAD12 = 1.

**Sup Data LTMxSAD12\_NIL\_Flowering\_time.xlsx** Flowering times in the NIL experiment. Columns indicate: Individual Genotype, Flowering\_June\_date, Family, Flowering\_day\_after\_vernalization, Flowering\_day\_plant\_age

**Sup Data LTMxSAD12\_RIL\_IDS.xlsx** Recombinant Inbred Lines used for the linkage map. Columns indicate: ID numbers (TMO\_ID, JGI\_ID, UffeID\_2015), Proportion.Heterozygous. Usage groups indicated in: Use\_for\_best\_125\_RILs\_Final, Final.use.150

**Sup Data LTMxSDM\_Trait\_Matrix.xlsx** Phenotypic values for LTM x SDM F2 cross. Columns indicate: Genotype\_Name, ID\_all, Cross, Survival\_after\_vern, Flowering, Width\_4week, Width\_10week, Flower\_day\_after\_vern, Flower-W, Flower-H, Flower-RosNum, Flower-LN, Fruit\_num, Lifetime\_fitness. Inversion genotype (last column) has A = Standard homozygote; H = Heterozygote; B = Inversion homozygote

**Sup Data Map\_For\_LTMxSAD\_RILs.xlsx** Map information for the SAD x LTM recombinant inbred lines (RILs). Columns give: Linkage\_Group, Scaffold centiMorgans, bin\_end (Physical position in LG [nucleotides]), Start and End (coordinates on scaffold, with 1-offset; If start > end, use reverse complement), Mapped\_or\_Inferred indicates method used to identify location ("M" if mapped, "I" if inferred based on context).

**Sup Data ParkerxRuby-KAS6\_GH\_flowering\_20120804-Indiv-Data\_3-Blks.xlsx**Genotype, ID, and experimental data for the collinear cross, followed by trait data. This greenhouse experiment has 12 blocks: 9 used for flowering-time related measurements (next file), and 3 blocks for destructive leaf harvesting measurement (this file).

**Sup Data ParkerxRuby-KAS6\_GH\_flowering\_20120804-Indiv-Data\_9-Blks.xlsx**  
Genotype, ID, and experimental data for the collinear cross, followed by trait data. This greenhouse experiment has 12 blocks: 9 used for flowering-time related measurements (this file), and 3 blocks for destructive leaf harvesting measurement (previous file).

**Sup Data ParkerxRuby-KAS6\_GH\_Trait\_Matrix-Family\_Means.xlsx** Family-mean trait data from the collinear cross.

**Sup Data PARxRUBY\_Linkage\_Map.xlsx** Linkage map data for the collinear cross (Parker x Ruby). Bin\_Name, cM, and Chromosome.

**Sup Data Primers for gene expression.docx** Primers used for for gene expression analysis.

**Sup Data Whole Genome Profiling.xlsx** Sheets provide: summary information, Sequence of the WGP tags (FASTA), WGP tags alignment to the Scaffolds, BAC End Sequence (BES) alignment to the Scaffolds, Contig position (cM) on the physical map, Scaffold and Contig position (cM) on the physical map, Markers derived from Scaffolds linked on the genetic map.