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Supplementary information

Maladaptation, migration and extirpation fuel climate change risk in a forest tree species

In the format provided by the authors and unedited

Supplemental Materials

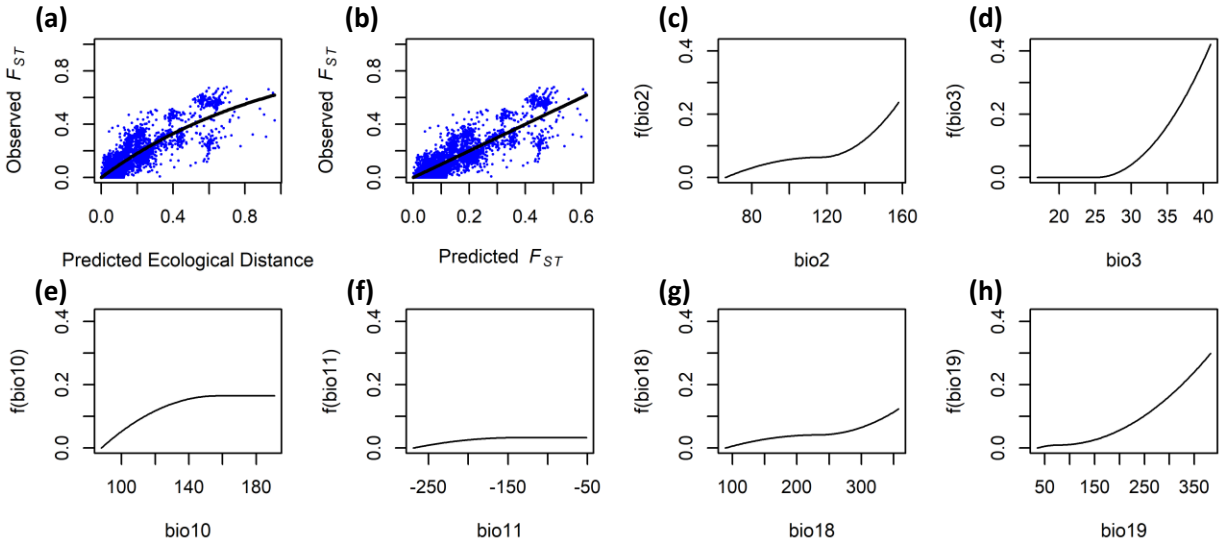

Fig. S1. (a & b) Generalized dissimilarity model (GDM) fit and (c-h) climatic response plots. GDM was fit to F_{ST} of 75 SNPs in the *Populus* flowering time network across 81 range-wide balsam poplar populations (bio2: mean diurnal range; bio3: isothermality; bio10: mean summer temperature; bio11: mean winter temperature; bio18: summer precipitation; bio19: winter precipitation). 'Observed F_{ST}' is the calculated F_{ST} between pairs of populations, and 'Predicted F_{ST}' is the predicted value from the GDM. Predicted ecological distance is the sum of transformed climate predictors between pairs of populations. I-spline functions transforming climate predictors (denoted as 'f()' on the y-axes) are shown in c – h. b shows the fit of the model, where the black line is a 1:1 line.

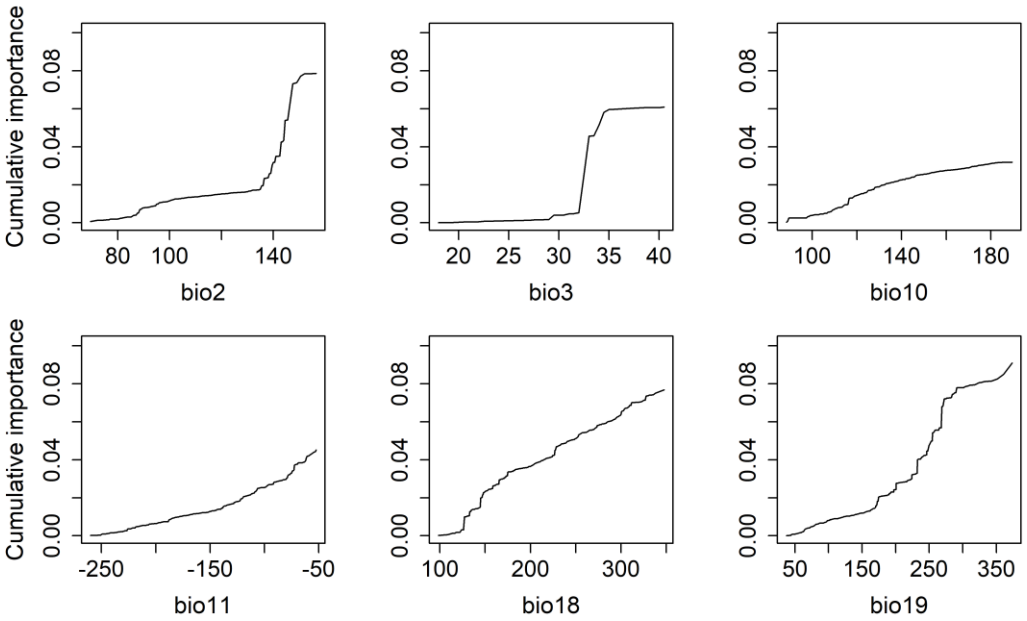

Fig. S2. Aggregate turnover functions for Gradient Forest for each climate variable (bio2: mean diurnal range; bio3: isothermality; bio10: mean summer temperature; bio11: mean winter temperature; bio18: summer precipitation; bio19: winter precipitation). The maximum height of each curve indicates the amount of turnover in allele frequencies along each climate variable, and the relative importance of each climate variable in explaining allele frequency turnover across 81 balsam poplar populations.

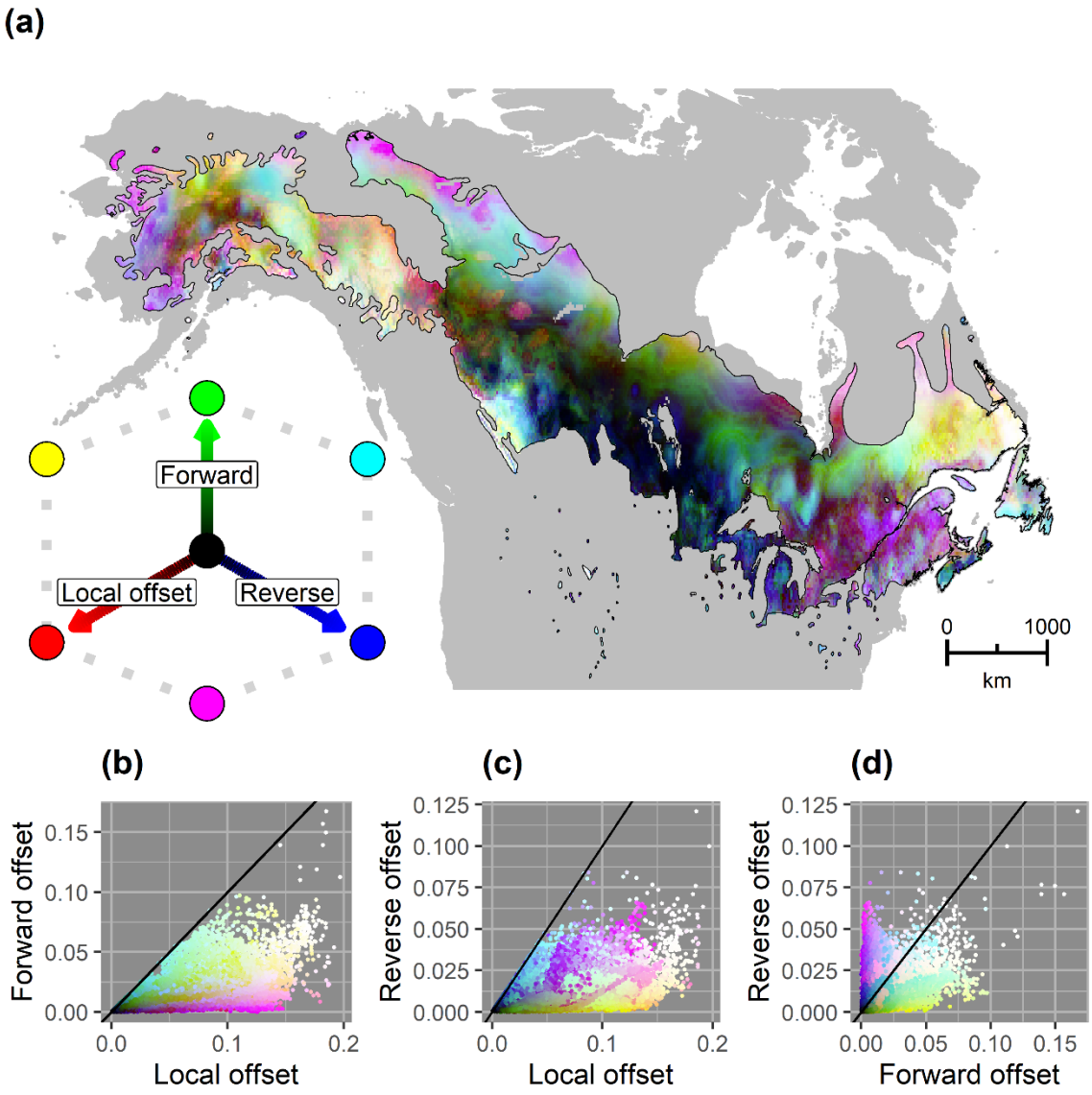

Fig. S3. Red-green-blue map of local (red), forward (green), and reverse (blue) offsets. Offset values were calculated from generalized dissimilarity models throughout the range of balsam poplar for 2070 and RCP 4.5. Brighter cells, closer to white, have relatively high values along each of the three axes while darker cells, closer to black, have relatively lower values. (b-d) Bivariate scattergrams of (a), with 1:1 lines. Individual maps used in (a) are shown in Extended Fig. 3.

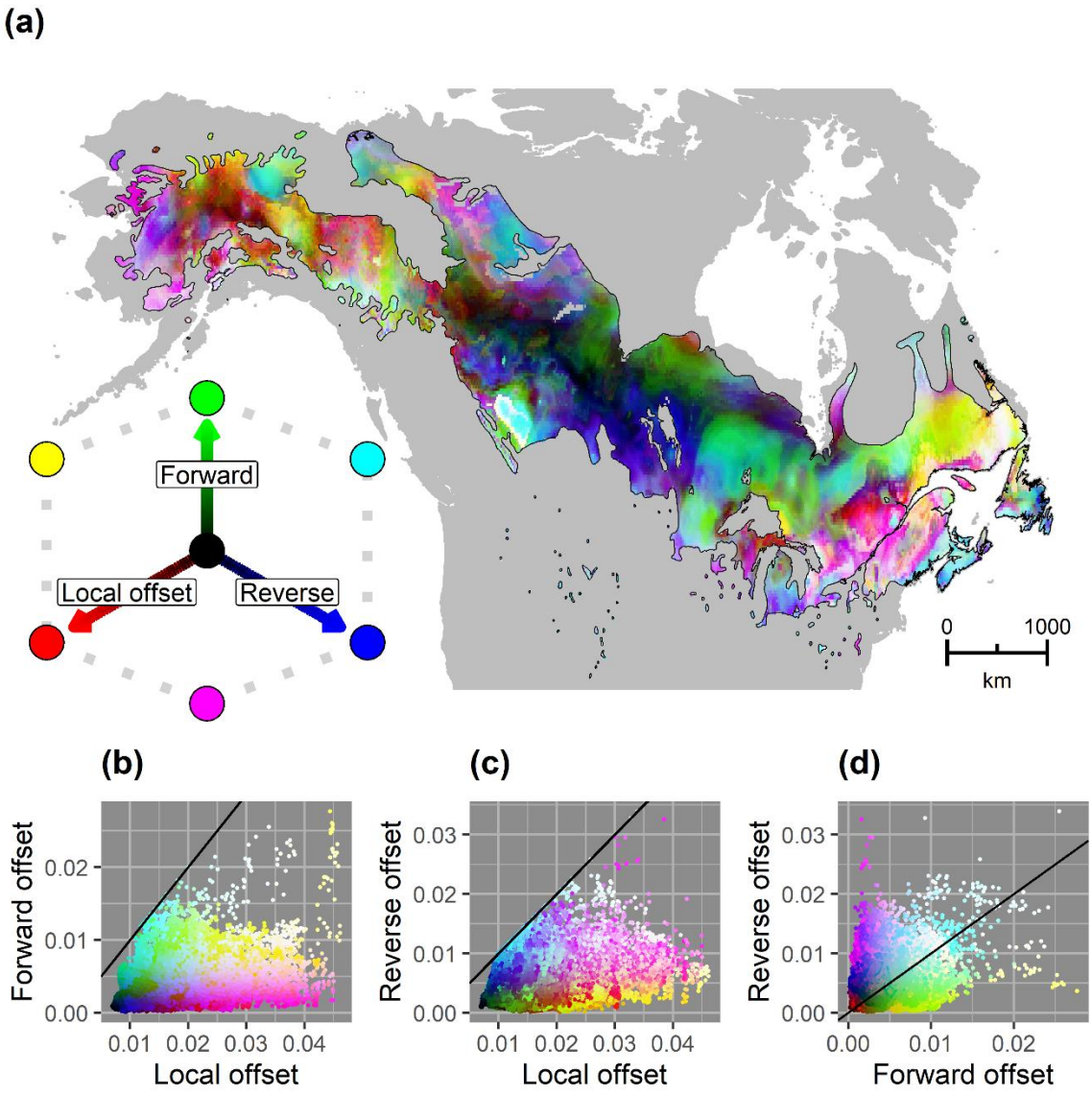

Fig. S4. Red-green-blue map of local (red), forward (green), and reverse (blue) offsets. Offset values were calculated from Gradient Forest throughout the range of balsam poplar for 2070 and RCP 4.5. Brighter cells, closer to white, have relatively high values along each of the three axes while darker cells, closer to black, have relatively lower values. (b-d) Bivariate scattergrams of (a), with 1:1 lines. Individual maps used in (a) are shown in Extended Fig. 4.

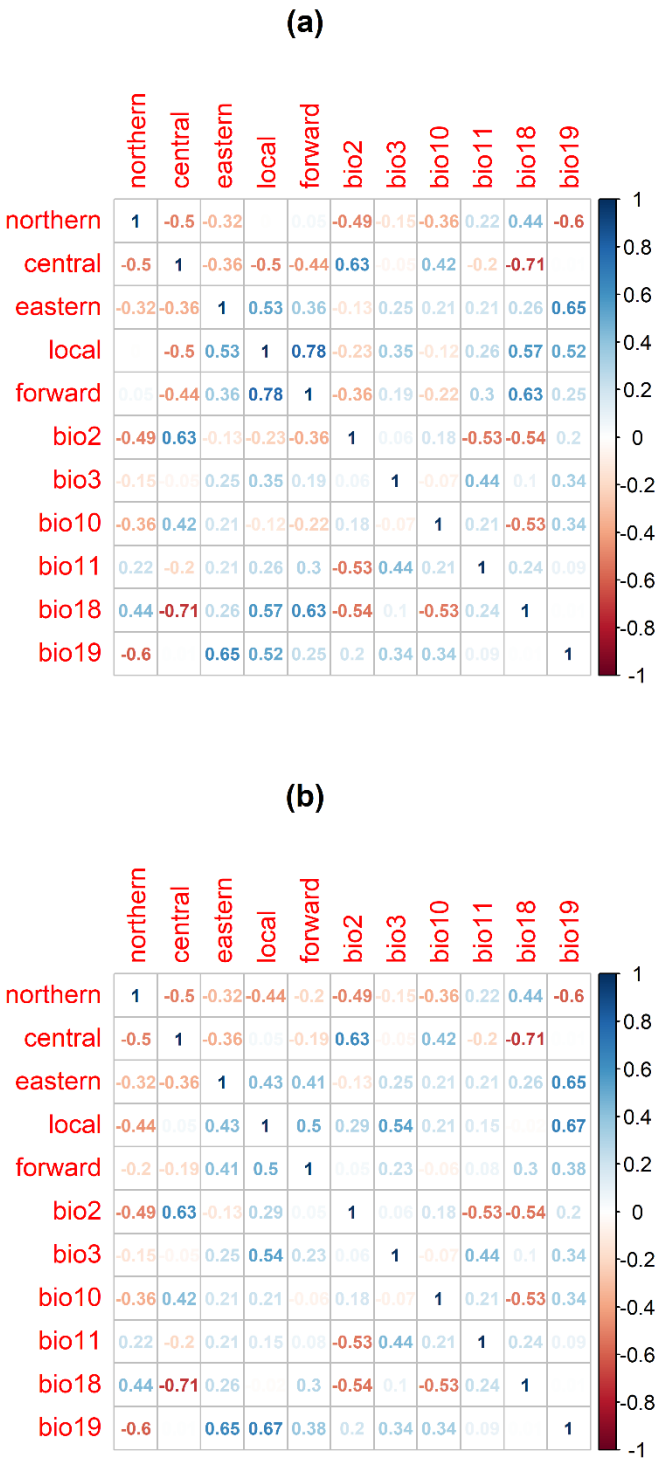

Fig. S5. Spearman rank correlation between local and forward offsets from (a) generalized dissimilarity model and (b) Gradient Forest, climatic shifts, and ancestry coefficients. Climatic shifts were calculated as future climate (2070, RCP 8.5) minus current climate, for each climate

variable (bio2: mean diurnal range; bio3: isothermality; bio10: mean summer temperature; bio11: mean winter temperature; bio18: summer precipitation; bio19: winter precipitation). Ancestry coefficients represent the relative affiliation of each population to three genetic clusters in balsam poplar's range ('northern', 'central' and 'eastern' clusters). Ancestry coefficients are meant to represent neutral population structure, and were collected from Gougherty et al. (2020) for 85 balsam poplar populations. Panels (a) and (b) differ only in the model used to calculate local and forward offsets (generalized dissimilarity models, and Gradient Forest, respectively) – ancestry coefficients, and climate shifts are identical.

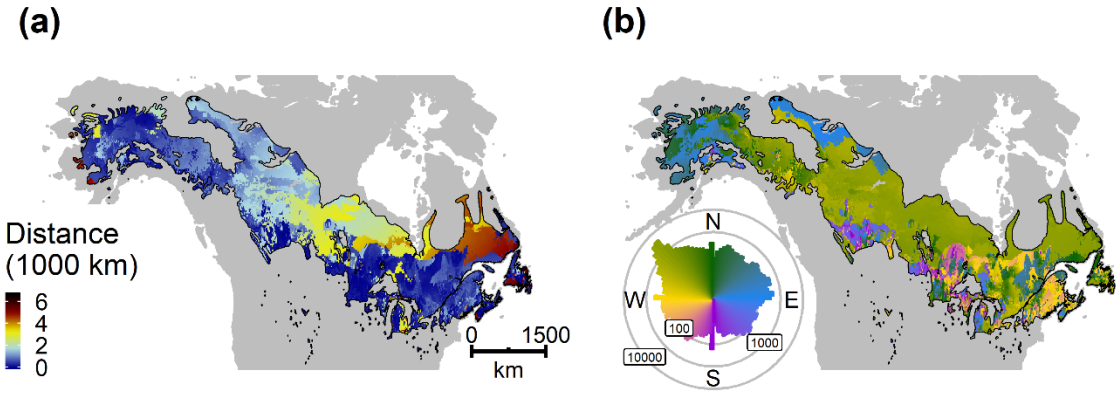

Fig. S6. Distance and initial bearing to locations that minimizes forward offset. (a) Distance and (b) initial bearing were calculated from the focal cell to the location in future North American climate (2070, RCP 4.5) that minimizes predicted F_{ST} from a generalized dissimilarity model. Polar histogram in (b) shows the log10 number of cells in each bearing bin.

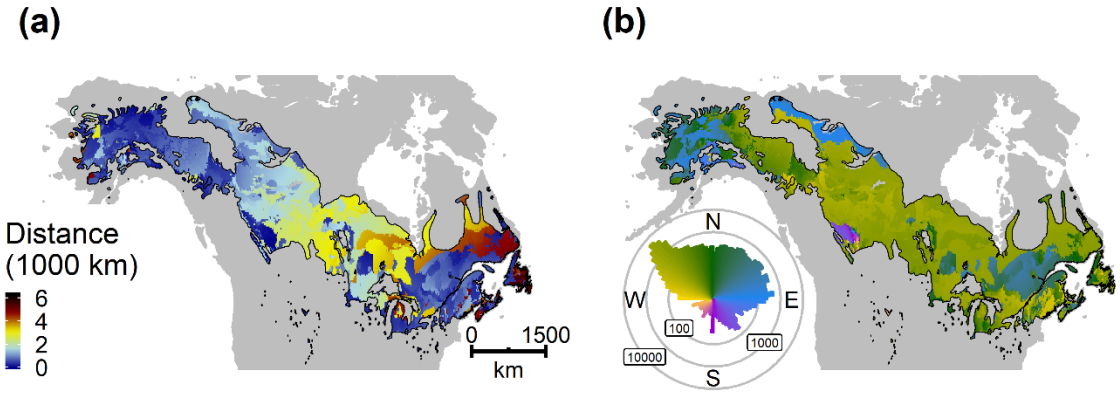

Fig. S7. Distance and initial bearing to locations that minimizes forward offset. (a) Distance and (b) initial bearing were calculated from the focal cell to the location in future North American climate (2070, RCP 4.5) that minimizes predicted offset from a Gradient Forest model. Polar histogram in (b) shows the log10 number of cells in each bearing bin.

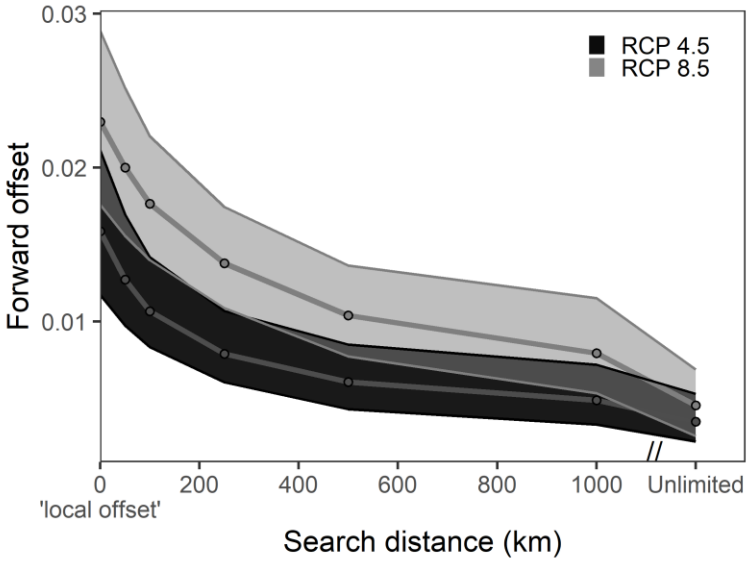

Fig. S8. Relationship between maximum allowable migration distance (i.e., search distance) and minimized forward offset from Gradient Forest for 2070. Bands extend between the 25th and 75th percentiles, and points are median values.

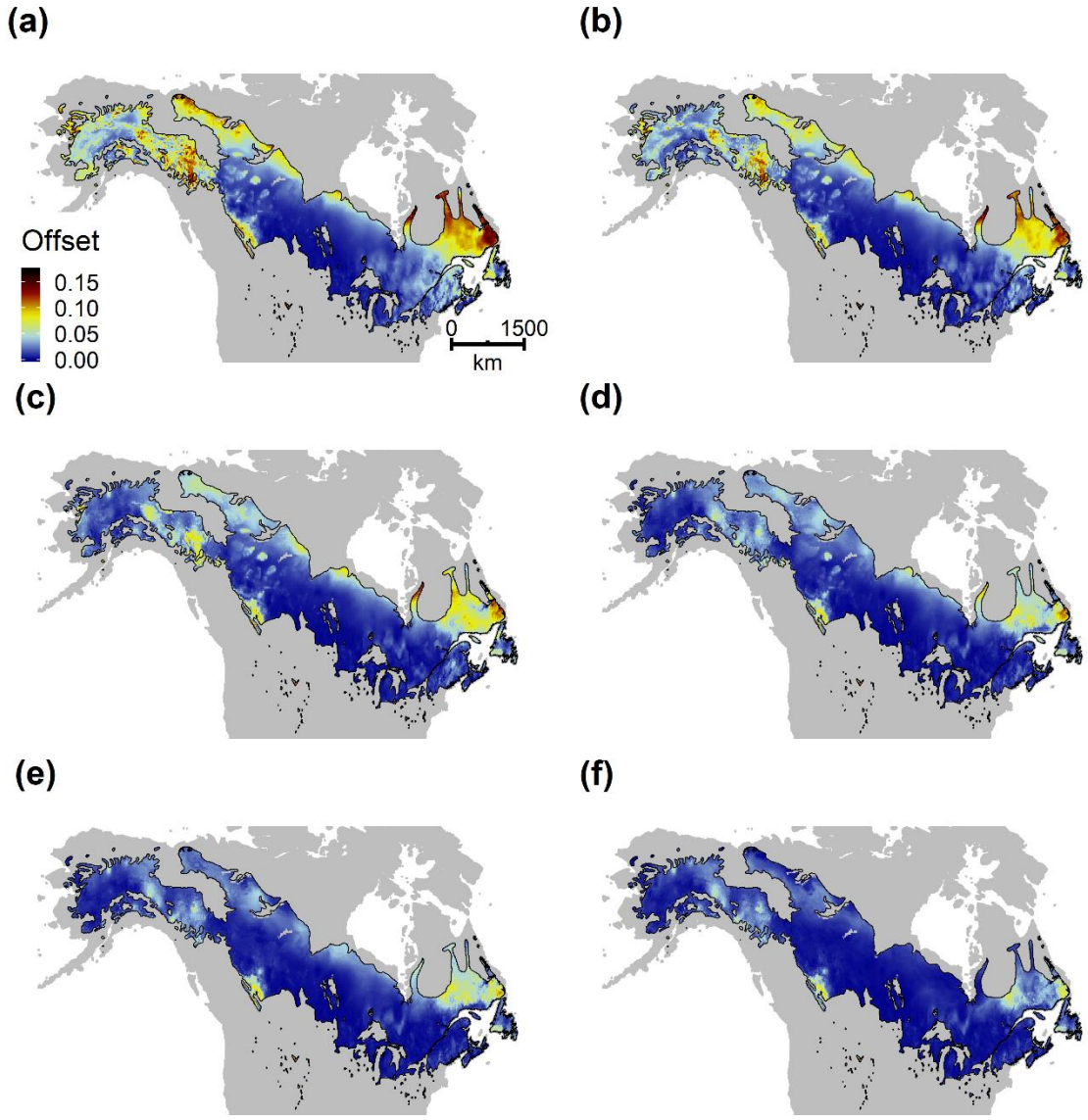

Fig. S9. Effect of search distance on forward offset from generalized dissimilarity models for RCP 4.5 in 2070. Distance classes included (a) 50 km, (b) 100 km, (c) 250 km, (d) 500 km, (e) 1000 km, and (f) unlimited.

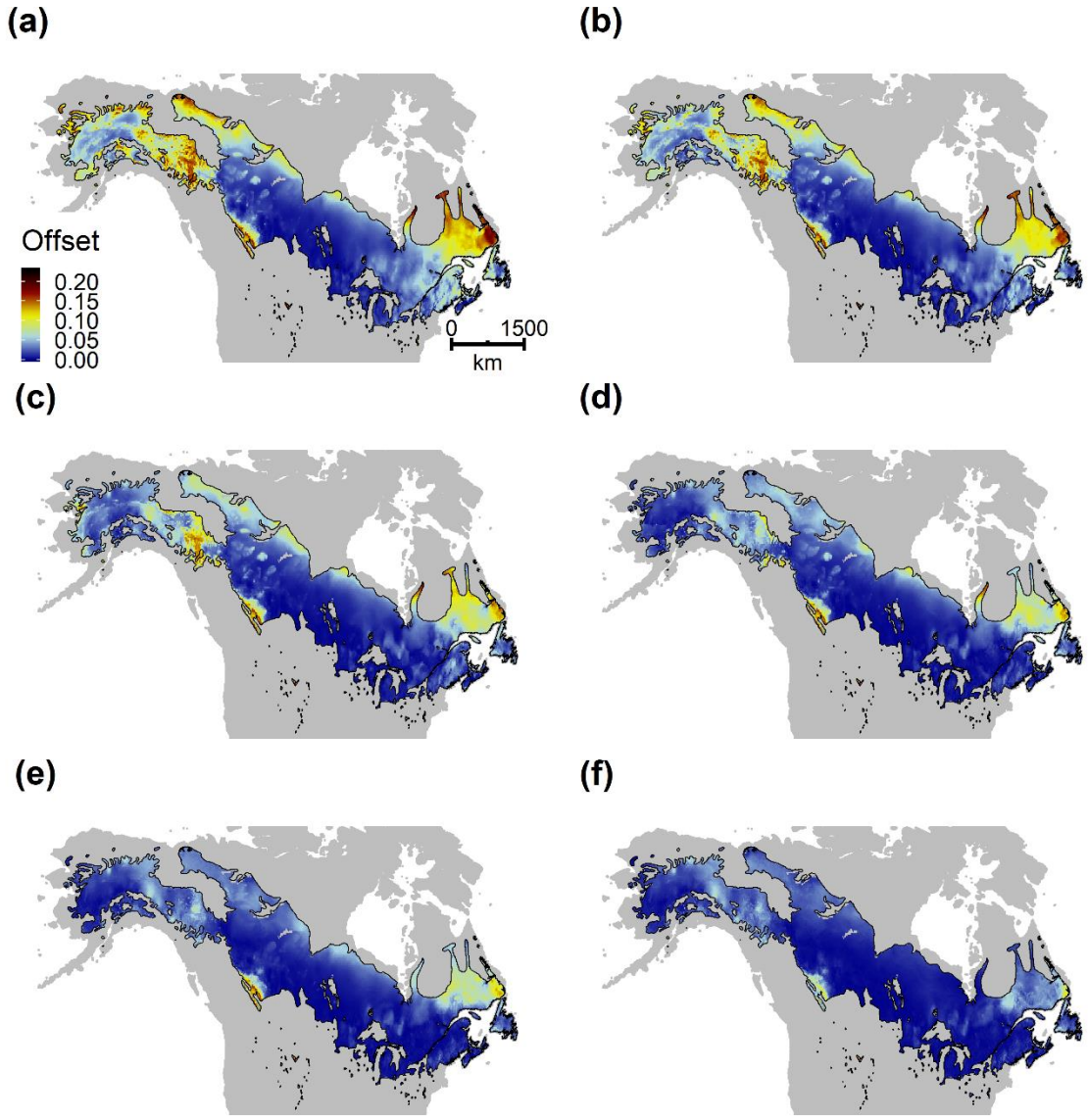

Fig. S10. Effect of search distance on forward offset from generalized dissimilarity models for RCP 8.5 in 2070. Distance classes included (a) 50 km, (b) 100 km, (c) 250 km, (d) 500 km, (e) 1000 km, and (f) unlimited.

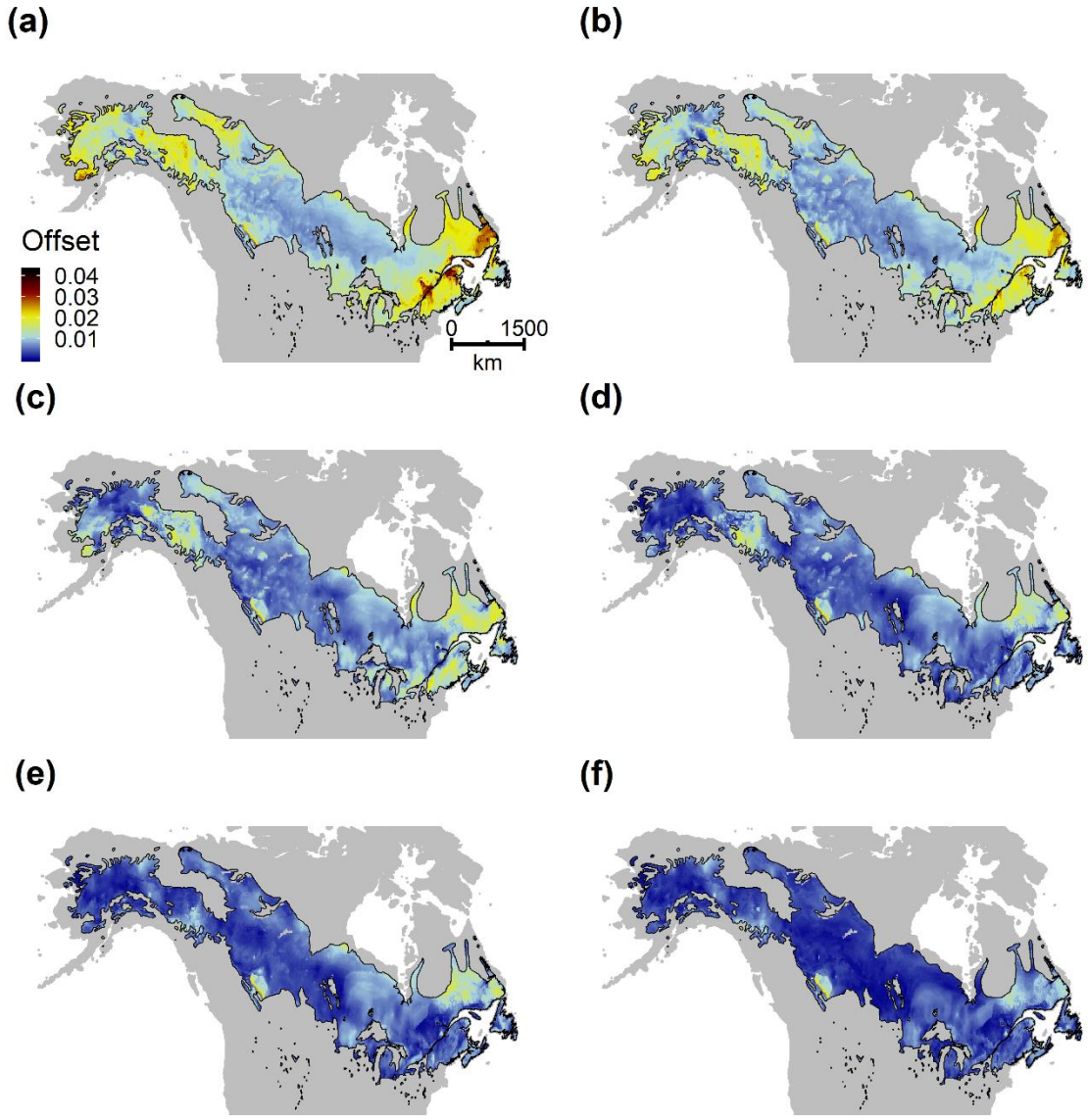

Fig. S11. Effect of search distance on forward offset from Gradient Forest for RCP 4.5 in 2070. Distance classes included (a) 50 km, (b) 100 km, (c) 250 km, (d) 500 km, (e) 1000 km, and (f) unlimited.

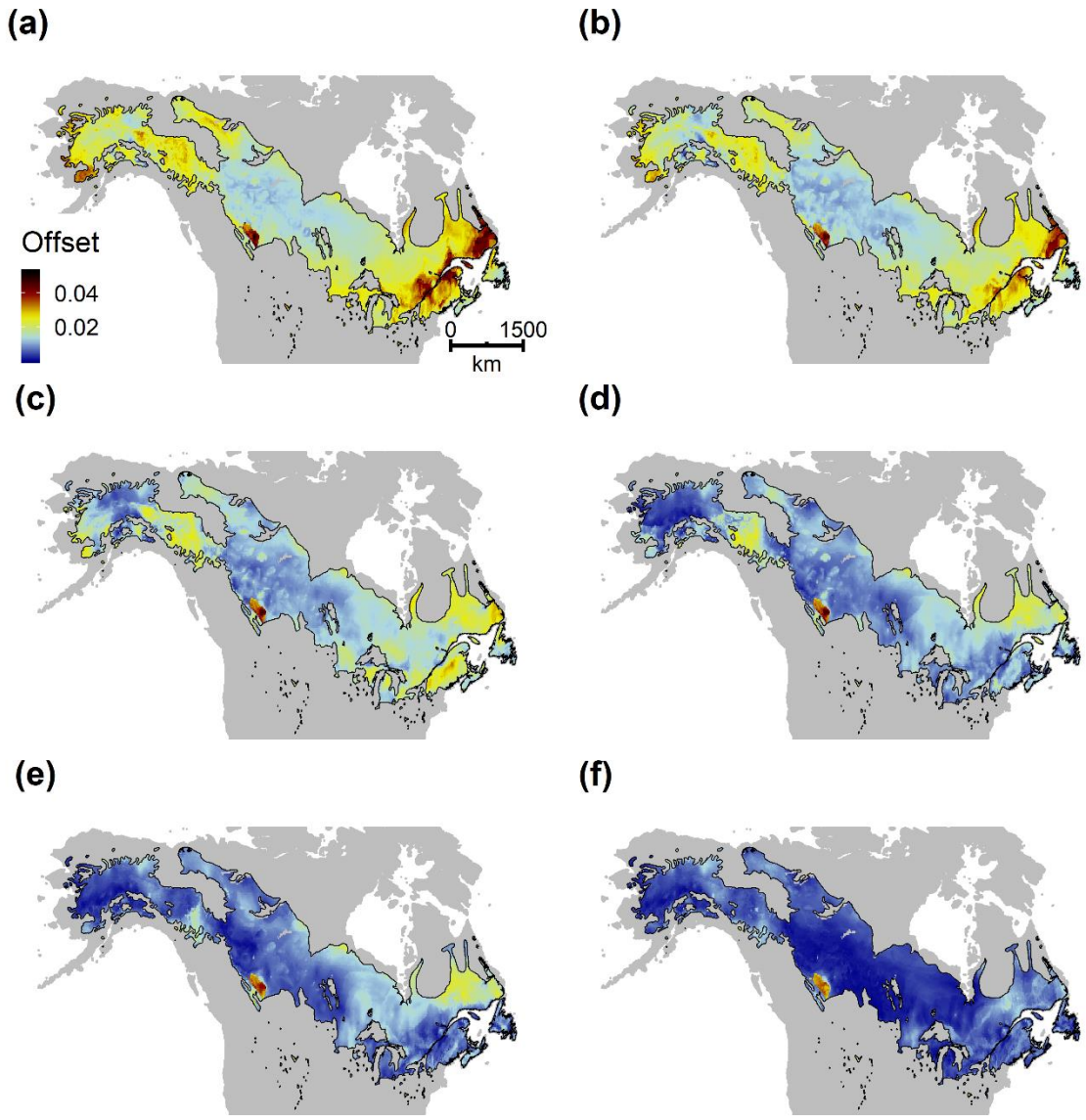

Fig. S12. Effect of search distance on forward offset from Gradient Forest for RCP 8.5 in 2070. Distance classes included (a) 50 km, (b) 100 km, (c) 250 km, (d) 500 km, (e) 1000 km, and (f) unlimited.

Table S1. Flowering time genes and number of SNPs used in Gradient Forest and generalized dissimilarity models.

Gene	Gene ID	Annotation	No. SNPs
ABA insensitive-1B	ABI1B	Abscisic acid	2
ABA insensitive-1D	ABI1D	Abscisic acid	3
ABA insensitive-1D	ABI3	Abscisic acid	2
Casein kinase-2 subunit β 3.4	CKB3.4	Peripheral circadian clock	2
Constans-1	CO1	Downstream target	6
Constans-2	CO2	Downstream target	3
Cryptochrome-1.1	CRY1.1	Photoreceptor	5
Cryptochrome-1.2	CRY1.2	Photoreceptor	2
Early bolting in short days	EBS	Downstream target	2
Early flowering-3	ELF3	Peripheral circadian clock	15
Gigantea-2	GI2	Peripheral circadian clock	2
Gigantea-5	GI5	Peripheral circadian clock	10
Heme oxygenase-1.1	HY1.1	Photoreceptor	1
Heme oxygenase-1.2	HY1.2	Photoreceptor	2
Heme oxygenase-2.1	HY2.1	Photoreceptor	2
Heme oxygenase-2.2	HY2.2	Photoreceptor	1
Leafy	LFY	Downstream target	1
Phytochome-B1	PHYB1	Photoreceptor	1
Phytochome-B2	PHYB2	Photoreceptor	2
Phytochome interacting factor-3	PIF3	Photoreceptor	3
Flowering locus T-1	PtFT1	Downstream target	2
Terminal flowering-1.1	TFL1.1	Downstream target	1
Timing of cab-1	TOC1	Central circadian clock	2
ZEITLUPE-2.9	ZTL2.9	Photoreceptor	3

Table S2. Variable importance from generalized dissimilarity model. Importance is calculated as the decrease in deviance explained when the variable is permuted. Permutations fit indicates the number of iterations when the model is successfully fit when variables are permuted.

Climate variable	Variable ID	Importance (%)	Significance	Permutations fit (of 100)
Mean diurnal range	bio2	1.308	0.03	100
Isothermality	bio3	4.389	< 0.01	99
Mean summer temperature	bio10	4.593	< 0.01	100
Mean winter temperature	bio11	0.271	0.17	100
Summer precipitation	bio18	2.075	< 0.01	100
Winter precipitation	bio19	10.912	< 0.01	100