

Legends for Supplementary Tables

Table S1. Sampling information for all individuals included in the genomic analyses. The table provides sample ID, species identity, geographic coordinates (latitude and longitude), sampling location, and landscape classification at two hierarchical levels.

Table S2. Proportional cover of major land-use classes within each sampling location, including tree cover, cropland, built area, rangeland, and bare ground, derived from the ESRI Sentinel-2 Land Cover dataset.

Table S3. Description of the 23 metrics used to characterize landscape composition and configuration.

Table S4. Summary statistics of landscape metrics for each sampling location. Median, mean, and standard deviation values are presented for all landscape metrics calculated within the studied landscapes.

Table S5. Forward and reverse primers used for COI amplification in *Andrena flavipes*.

Table S6. Quality control and filtering results obtained from FastQC, FastP, STACKS (process_radtags and ref_map.pl), BWA/SAMtools, relatedness filtering, and missing data assessment for all samples included in the RADseq datasets.

Table S7. Genetic diversity statistics for each sampling location. Estimates include sample size (N), observed heterozygosity (H_o), expected heterozygosity (H_e), nucleotide diversity (π), number of segregating sites, number of private alleles, gene diversity (H_s), proportion of polymorphic loci, allelic richness, and inbreeding coefficient (F_{is}) for each species and location.

Table S8. Genetic diversity statistics grouped by landscape category level 1. Estimates of genetic diversity are shown separately for low-agricultural (LoA) and small-scale farming (SSF) landscapes for each species. Statistics include sample size (N), observed heterozygosity (H_o), expected heterozygosity (H_e), nucleotide diversity (π), number of segregating sites, private alleles, gene diversity (H_s), proportion of polymorphic loci, allelic richness, and inbreeding coefficient (F_{is}).

Table S9. Genetic diversity statistics grouped by landscape category level 2. Estimates are presented for small-scale farming (SSF), near low-agricultural (Near_LoA), and far low-agricultural (Far_LoA) populations. Statistics include sample size (N), observed heterozygosity (H_o), expected heterozygosity (H_e), nucleotide diversity (π), number of segregating sites, private alleles, gene diversity (H_s), proportion of polymorphic loci, allelic richness, and inbreeding coefficient (F_{is}).

Table S10. Candidate SNPs identified by PCAdapt in *Andrena flavipes*. For each candidate SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, raw and adjusted p-values, minor allele frequency (MAF), test statistic, and associated chi-square value. Candidate loci were identified after correction for multiple testing.

Table S11. Candidate SNPs identified by PCAdapt in *Bombus terrestris*. For each candidate SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, raw and adjusted p-values, minor allele frequency (MAF), test statistic, and associated chi-square value. Candidate loci were identified after correction for multiple testing.

Table S12. Candidate SNPs identified by PCAdapt in *Lasioglossum malachurum*. For each candidate SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, raw and adjusted p-values, minor allele frequency (MAF), test statistic, and associated chi-square value. Candidate loci were identified after correction

for multiple testing.

Table S13. Candidate SNPs identified by BayeScan in *Andrena flavipes*. For each candidate SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, posterior probability (Prob.), log posterior odds (LogPO), q-value, alpha coefficient, locus-specific F_{ST} estimate, and inferred mode of selection. Only diversifying SNPs were retained.

Table S14. Candidate SNPs identified by BayeScan in *Bombus terrestris*. For each candidate SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, posterior probability (Prob.), log posterior odds (LogPO), q-value, alpha coefficient, locus-specific F_{ST} estimate, and inferred mode of selection. Only diversifying SNPs were retained.

Table S15. Results of the BayPass C2 statistic for *Andrena flavipes*. For each SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, land-use contrast tested, C2 statistic, associated $-\log_{10}(p\text{-value})$, and outlier status. Candidate SNPs under selection were identified using the calibrated significance threshold described in the Methods section.

Table S16. Results of the BayPass C2 statistic for *Bombus terrestris*. For each SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, land-use contrast tested, C2 statistic, associated $-\log_{10}(p\text{-value})$, and outlier status. Candidate SNPs under selection were identified using the calibrated significance threshold described in the Methods section.

Table S17. Results of the BayPass C2 statistic for *Lasioglossum malachurum*. For each SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, land-use contrast tested, C2 statistic, associated $-\log_{10}(p\text{-value})$, and outlier status. Candidate SNPs under selection were identified using the calibrated significance threshold described in the Methods section.

Table S18. Results of the BayPass BF statistic for *Andrena flavipes*. For each SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, land-use contrast tested, Bayes Factor (BF), Pearson and Spearman correlation coefficients (means and standard deviations), regression coefficient (Beta IS) and its standard deviation, empirical Bayesian posterior inclusion probability (eBPis), and outlier status. Candidate SNPs were identified according to the significance criteria described in the Methods section.

Table S19. Results of the BayPass BF statistic for *Bombus terrestris*. For each SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, land-use contrast tested, Bayes Factor (BF), Pearson and Spearman correlation coefficients (means and standard deviations), regression coefficient (Beta IS) and its standard deviation, empirical Bayesian posterior inclusion probability (eBPis), and outlier status. Candidate SNPs were identified according to the significance criteria described in the Methods section.

Table S20. Results of the BayPass BF statistic for *Lasioglossum malachurum*. For each SNP, the table reports chromosome (CHR), genomic position (POS), SNP ID, land-use contrast tested, Bayes Factor (BF), Pearson and Spearman correlation coefficients (means and standard deviations), regression coefficient (Beta IS) and its standard deviation, empirical Bayesian posterior inclusion probability (eBPis), and outlier status. Candidate SNPs were identified according to the significance criteria described in the Methods section.

Table S21. Significant genomic regions identified by BayPass local score analyses in *Andrena flavipes*. Genomic regions are reported for each landscape contrast (SSF vs LoA, SSF vs Near_LoA, and SSF vs Far_LoA), including chromosome (CHR), start and end coordinates of the region, region size (bp), number of SNPs within the region, position and value of the maximum Lindley score, and position and value of the most significant SNP based on $-\log_{10}(p\text{-value})$.

Table S22. Significant genomic regions identified by BayPass local score

analyses in *Bombus terrestris*. Genomic regions are reported for each landscape contrast (SSF vs LoA, SSF vs Near_LoA, and SSF vs Far_LoA), including chromosome (CHR), start and end coordinates of the region, region size (bp), number of SNPs within the region, position and value of the maximum Lindley score, and position and value of the most significant SNP based on $-\log_{10}(p\text{-value})$.

Table S23. Significant genomic regions identified by BayPass local score analyses in *Lasioglossum malachurum*. Genomic regions are reported for each landscape contrast (SSF vs LoA, SSF vs Near_LoA, and SSF vs Far_LoA), including chromosome (CHR), start and end coordinates of the region, region size (bp), number of SNPs within the region, position and value of the maximum Lindley score, and position and value of the most significant SNP based on $-\log_{10}(p\text{-value})$.

Table S24. Overlap among candidate SNPs identified by different selection detection methods in *Andrena flavipes*. For each candidate SNP, chromosome (CHR), genomic position (POS), SNP ID, and outlier status across PCAdapt, BayeScan, BayPass C2, BayPass BF, and BayPass local score analyses are reported. The column "n Methods" indicates the number of selection detection methods that identified each SNP as a candidate locus under selection.

Table S25. Overlap among candidate SNPs identified by different selection detection methods in *Bombus terrestris*. For each candidate SNP, chromosome (CHR), genomic position (POS), SNP ID, and outlier status across PCAdapt, BayeScan, BayPass C2, BayPass BF, and BayPass local score analyses are reported. The column n Methods indicates the number of selection detection methods that identified each SNP as a candidate locus under selection.

Table S26. Overlap among candidate SNPs identified by different selection detection methods in *Lasioglossum malachurum*. For each candidate SNP, chromosome (CHR), genomic position (POS), SNP ID, and outlier status across PCAdapt, BayeScan, BayPass C2, BayPass BF, and BayPass local score analyses are reported. The column n Methods indicates the number of selection detection methods that identified each SNP as a candidate locus under selection.

Table S27. Candidate SNPs identified by BayPass AUX model GEA analyses in *Andrena flavipes*. For each candidate SNP, chromosome (CHR), genomic position (POS), SNP ID, median and mean Bayes Factor (BF), standard deviation (SD), associated environmental covariable, and the corresponding level of evidence are reported. Evidence categories follow the BayPass interpretation framework based on Bayes Factor values.

Table S28. Candidate SNPs identified by BayPass AUX model GEA analyses in *Bombus terrestris*. For each candidate SNP, chromosome (CHR), genomic position (POS), SNP ID, median and mean Bayes Factor (BF), standard deviation (SD), associated environmental covariable, and the corresponding level of evidence are reported. Evidence categories follow the BayPass interpretation framework based on Bayes Factor values.

Table S29. Candidate SNPs identified by BayPass AUX model GEA analyses in *Lasioglossum malachurum*. For each candidate SNP, chromosome (CHR), genomic position (POS), SNP ID, median and mean Bayes Factor (BF), standard deviation (SD), associated environmental covariable, and the corresponding level of evidence are reported. Evidence categories follow the BayPass interpretation framework based on Bayes Factor values.

Table S30. Functional annotation of candidate genes associated with candidate SNPs in *Andrena flavipes*. Candidate genes overlapping candidate SNPs are reported together with gene identifiers, gene names, functional descriptions, COG functional categories, corresponding category descriptions, annotation E-values, method support, and the relationship between the candidate SNP and the annotated gene.

Table S31. Functional annotation of candidate genes associated with candidate

SNPs in *Bombus terrestris*. Candidate genes overlapping candidate SNPs are reported together with gene identifiers, gene names, functional descriptions, COG functional categories, corresponding category descriptions, annotation E-values, method support, and the relationship between the candidate SNP and the annotated gene.

Table S32. Functional annotation of candidate genes associated with candidate SNPs in *Lasioglossum malachurum*. Candidate genes overlapping candidate SNPs are reported together with gene identifiers, gene names, functional descriptions, COG functional categories, corresponding category descriptions, annotation E-values, method support, and the relationship between the candidate SNP and the annotated gene.