Table S1Parallel divergence in all fifteen divergence comparisons.

| Divergence Comparison ^a | Parallel Divergent SNPs ^b | Major Orientation ^c | Skew ^d | GO BP term ^e |
|------------------------------------|--------------------------------------|--------------------------------|-------------------|---|
| PY-EU vs. OC-SA | 96.1** | PY/OC, EU/SA | 0.61* | n/a |
| PY-EU vs. OC-EA | 93.8** | PY/OC, EU/EA | 0.85** | n/a |
| PY-OC vs. EA-SA | 92.8** | PY/SA, OC/EA | 0.83** | homeostatic process; cell cycle |
| WA-EU vs. OC-SA | 92.4** | WA/OC, EU/SA | 0.62* | synaptic transmission |
| WA-EU vs. OC-EA | 89.5* | WA/OC, EU/EA | 0.82** | proteolysis |
| PY-WA vs. EU-SA | 86.6* | PY/SA, WA/EU | 0.71* | n/a |
| WA-OC vs. EA-SA | 86.1* | WA/SA, OC/EA | 0.83** | n/a |
| PY-WA vs. EU-EA | 85.6* | PY/EA, WA/EU | 0.60 | cognition; sensory perception |
| PY-EU vs. EA-SA | 79.1 | PY/SA, EU/EA | 0.82** | transmembrane receptor protein tyrosine |
| | | | | kinase signaling pathway; protein |
| | | | | phosphorylation |
| PY-WA vs. OC-EA | 75.8 | PY/OC, WA/EA | 0.59 | n/a |
| PY-WA vs. EU-OC | 75.8 | PY/OC, WA/EU | 0.68* | n/a |
| PY-WA vs. OC-SA | 75.1 | PY/SA, WA/OC | 0.55 | regulation of transcription, DNA-dependent; proteolysis |
| PY-WA vs. EA-SA | 73.9 | PY/SA, WA/EA | 0.64* | neuron projection development |
| WA-EU vs. EA-SA | 69.1 | WA/SA, EU/EA | 0.78* | cell surface receptor linked signal transduction; transmembrane receptor protein tyrosine kinase signaling pathway; |
| | | | | protein phosphorylation; homeostatic process |
| EU-OC vs. EA-SA | 58.1 | EU/SA, OC/EA | 0.57 | n/a |

^aF_{ST} at all SNPs between the first pair of groups is compared to F_{ST} at all SNPs between the second pair of groups

^bMean number of parallel divergent SNPs in 1000 replicates (expected number is 67.2).

^cMore frequently observed of the two possible orientations. Each orientation unites each group from the first divergence comparison with one of the groups from the second divergence comparison, according to which groups had relatively similar allele frequencies. ^dThe proportion of parallel divergent SNPs showing the major orientation.

^eEnriched Gene Ontology Biological Process terms. All terms showing at least 2-fold enrichment and a mean of at least three SNPs per replicate for that divergence comparison are shown, with redundant terms eliminated. "n/a" indicates no terms met the criteria. *p<0.05 in comparison to simulation *standard*

^{**}p<0.05 in comparison to simulation standard and in Bonferroni-corrected Fisher's exact test