Supplementary Material Legends

Table S1: Libraries

Table S2: Candidates Dropped due to Splice Sites Mismatches

Table S3: Expression Means and Number of Zambian Lines Expressed in Outgroup Filtered *vs*. Retained Candidates

Table S4: Candidate *de novo* Genes

Table S5: Candidates Frequencies

Table S6: Candidate *de novo* Genes At Different Cutoffs

Table S7: Single *vs*. Multi Exon *de novo* Candidates

Table S8: Single *vs*. Multi-Transcript *de novo* Candidates

Table S9: Singleton vs. non-Singleton Gene Features

Table S10: Distribution of Singleton vs. non-Singleton *de novo* Candidates in Zambia

Table S11: Counts of *de novo* Candidates in each Zambian Genome.

Table S12: π in 100 kb Windows

Table S13: Candidate *de novo* Genes by Data Set of Origin

Table S14: *de novo* Candidates by Population

Table S15: Overlap Between Candidate *de novo* Genes in Zambia and Raleigh

Table S16: Overlap in *de novo* Candidates between Zambian Subsets and Raleigh

Table S17: DE comparisons between Zambian subsets and Raleigh, Maine and Panama

Table S18: *de novo* Candidates in Regions of Selective Sweeps

Table S19: de novo Candidate Expression by Tissue in FlyAtlas2

File S1: Candidate *de novo* Transcripts