**S3 Fig. Whole-genome sequence identifies similar patterns of population genetic differentiation.** Data corresponding to the 28 studied genes were extracted from a set of 81 *A. coluzzii* and 84 *A. gambiae* wild mosquitoes from Burkina Faso that were whole-genome sequenced by the *Anopheles* *gambiae* 1000 Genomes (Ag1k) project at the Wellcome Trust Sanger Institute (VCF files from pre-publication data release provided by kind permission of the Ag1k project. Source: The *Anopheles* *gambiae* 1000 Genomes Consortium (2014): Ag1000G phase 1 AR2 data release. MalariaGEN. http://www.malariagen.net/data/ag1000g-phase1-AR2). The same methods of analysis were applied as those described in Methods for Fig 1. This result replicates the main analysis using an independent sample set from a different site sympatric for *A. coluzzii* and *A. gambiae*, using nucleotide variation data generated by a different sequencing technology. Patterns of gene sequence differentiation are strikingly similar, with all but one gene (LRR7059) exhibiting patterns of differentiation similar to those detected by manual Sanger sequencing of *A. coluzzii* and *A. gambiae* samples in the current study (Fig 1).

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