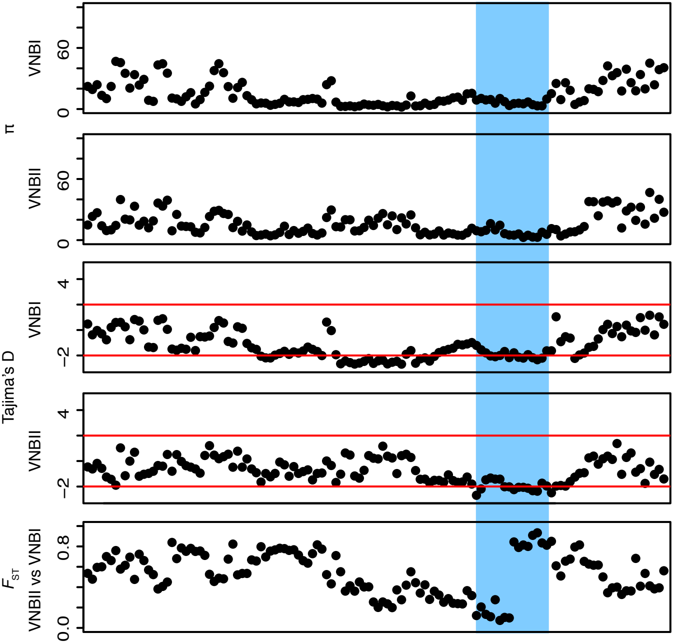

**low $F_{ST}$**
CNAG_07742 phosphatidylglycerol transfer protein
CNAG_07743 hypothetical protein
CNAG_01065 hypothetical protein
CNAG_01064 hypothetical protein
CNAG_01063 TOR protein KOG1

**high $F_{ST}$**
CNAG_01061 S/T protein kinase
CNAG_01060 hypothetical protein
CNAG_01059 vacuolar membrane protein
CNAG_01058 nitric oxide synthase-interacting protein
CNAG_01057 COP9 signalosome complex subunit 2

**in between $F_{ST}$**
CNAG_01062 CAMK/CAMKL/PASK protein kinase

**Supplemental Fig S5.** Region of chromosome 5 with abrupt change in FST between VNBI and VNBII. Genes in the low FST region, high FST region, and between the two regions are listed. The low FST region is the only region in the genome where loss of genetic diversity and a low Tajima's D is accompanied by a reduction in FST between two populations.