



Supplemental Figure S3. eQTL and the transcript abundance patterns they regulate. Each blue bar is a unique introgression. When the transcript abundance pattern of gene 1 is correlated with bin-A, then bin-A contains a *cis*-eQTL. When the transcript abundance pattern of gene 1 is correlated with bin-E, then bin-E contains a *trans*-eQTL. When gene 2 has a *cis*-eQTL designated for bin-D and the transcript abundance pattern of gene 2 is also correlated with bin-B, then this secondary correlation is not designated as an eQTL, since these bins share overlapping introgression regions. When the transcript abundance pattern of gene 2 is correlated with bin-B and gene 2 does not have a *cis*-eQTL designated for bin-D, then bin-B is designated as a *trans*-eQTL. All eQTLs for genes that lie in the unassembled portion of the genome (not on any chromosome) cannot be designated as either *cis* or *trans* and are designated *chromo0*-eQTL.