Figure S2: Fosmid Clone Tiling Paths. The browser snapshots (http://hgsv.washington.edu) show the clone ID and mapping location of concordant (black) and discordant (red) fosmid end-sequences mapped against the human genome (hg17) for each library. a) Clone tiling path across the leptin (*LEP*) locus is shown for two individual libraries, G248 and ABC7; all clones are concordant by length and orientation; b) A putative heterozygous deletion is shown for an individual library (ABC7) where both concordant and discordant clones are identified; note discordant clones from third library (ABC9) predict an insertion allele over the *CYP2D6* locus; c) The *GSTM1*shows an example of locus complexity. Analysis of the ABC9 library predicts a homozygous deletion (absence of concordant clones) and another genomic library (ABC10) predicts the presence of two non-overlapping insertions in the heterozygous state. Any region of interest in the human genome can be accessed using a UCSC browser interface (http://hgsv.washington.edu) and the corresponding fosmid clones, end-sequences, and alignments retrieved for further characterization.

Fig. S2 a) Clone Tiling path across LEP locus (1 clone/5 kb)

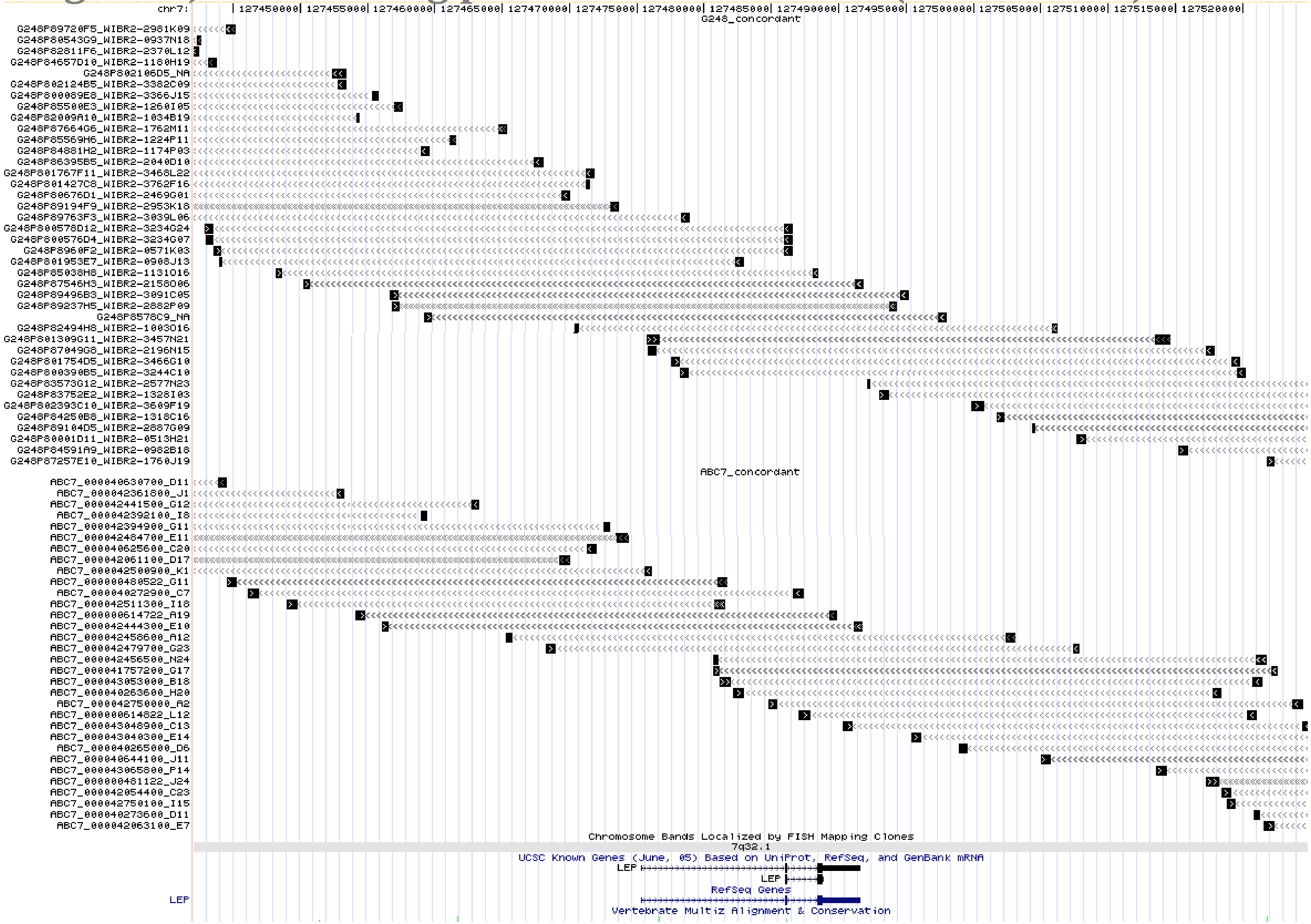


Fig. S2 b) CYP2D6 Deletion

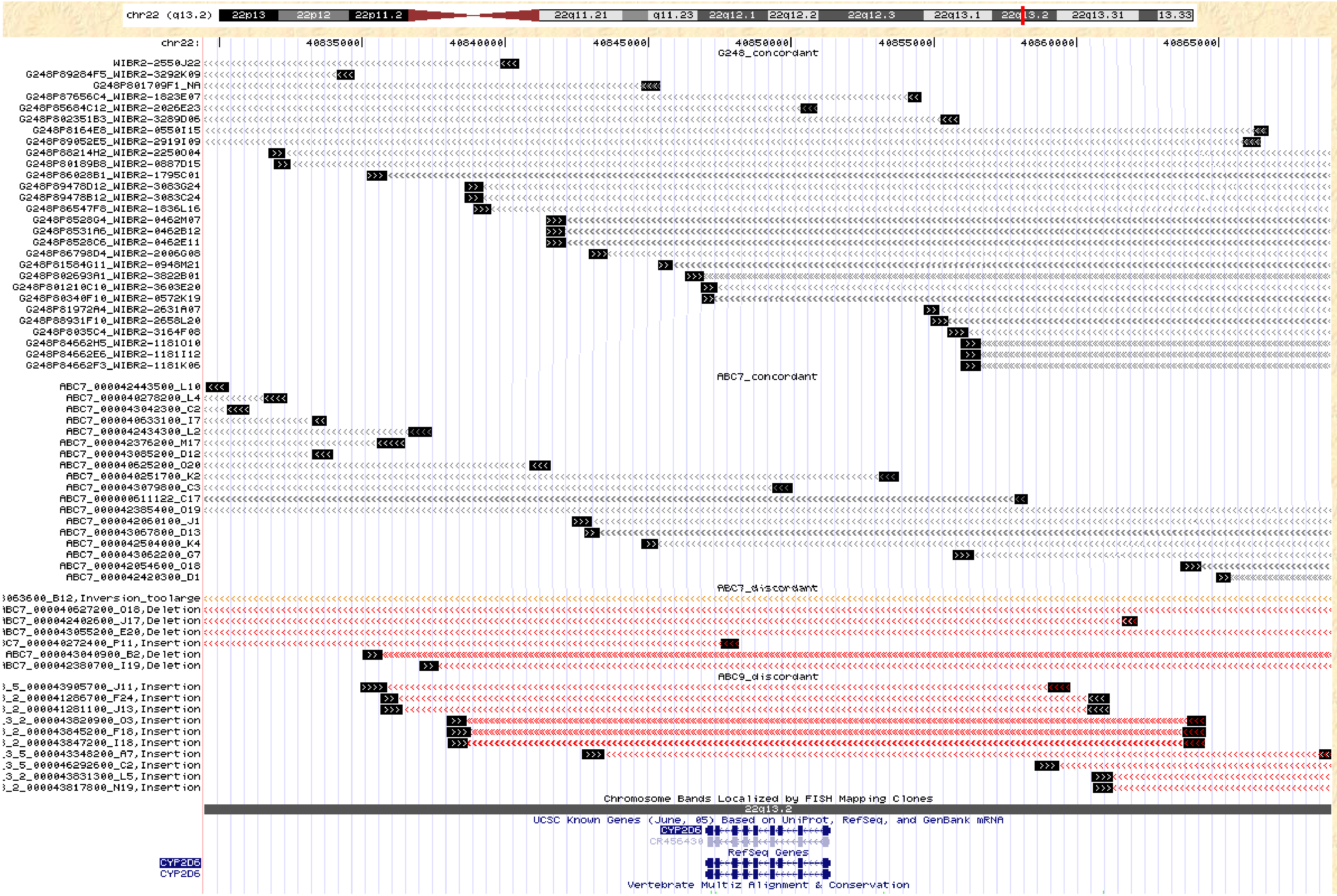
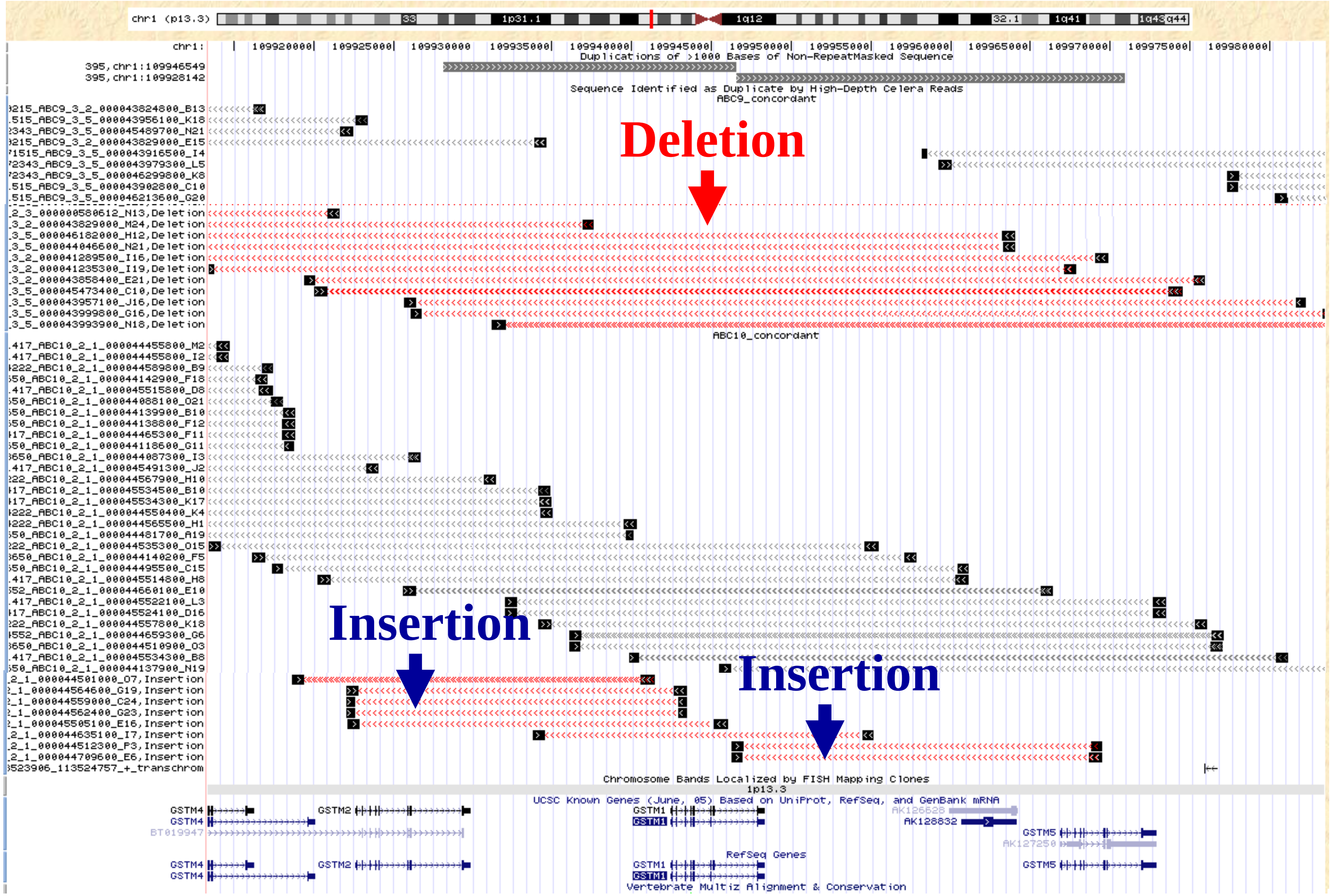


Fig. S2 c) GSTM1 Locus Complexity



Deletion

Japanese Sample NA18956

Insertion

Insertion

Yoruba Sample NA19240