Figure S2. UCSC Genome browser view of the *PDZK1* region.
Genome browser view showing the location of the target SNP *rs1967017* (highlighted in blue) in human hg19 assembly. The 'Transcription Factor ChIP-seq' track summarizes the presence of transcription factor clusters in different cell lines, denoted by gray boxes with the color intensity being proportional to the signal strength. A green highlight within a cluster is the highest scoring site of a canonical motif of the corresponding transcription factor; note that the SNP *rs1967017* sits on a canonical HNF4A site. The 'HepG2 Chromatin State Segmentation' track displays the presence of regulatory elements based on chromatin marks. Enhancers are defined by the presence of H3K4me1, H3K4me2 and H3K27ac; strong enhancers (orange boxes) and weak enhancers (yellow boxes) differ in expression of proximal genes. The 'DNaseI Hypersensitivity Clusters' track shows the presence of open chromatin regions in different cell lines, denoted by grey boxes with the colour intensity being proportional to the signal strength. The 'Multiz Alignments of 100 Vertebrates' track displays pairwise alignments of each species to the human genome in the form of green peaks, height of the peak is proportional to alignment score. The *rs1967017* enhancer element is conserved in mouse but not in zebrafish. Histone data that predict the presence of an enhancer were derived from: Ernst J, Kheradpour P, Mikkelsen TS, et al. Systematic analysis of chromatin state dynamics in nine human cell types. Nature. 2011;473(7345):43-49. doi:10.1038/nature09906.