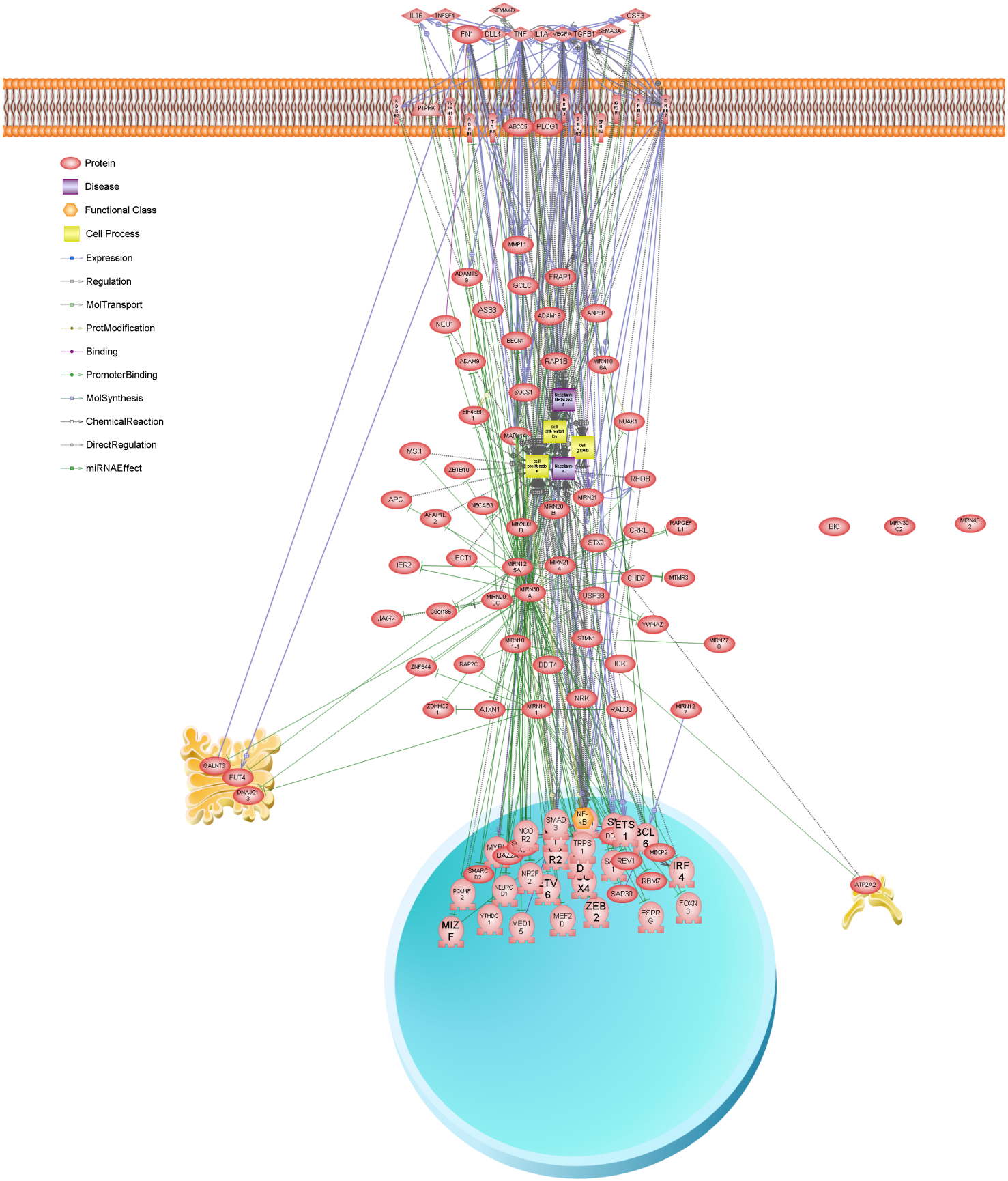

Figure S5 Network of common altered microRNAs on predicted risk regions in variety of cancers. Network was constructed using pathway studio 9 software (shortest path algorithm). This network comprises 383 entities and 1121 relations and various type of transcription factors, protein kinases, small molecules, mrnas and mirnas serve as either validated or putative regulators.