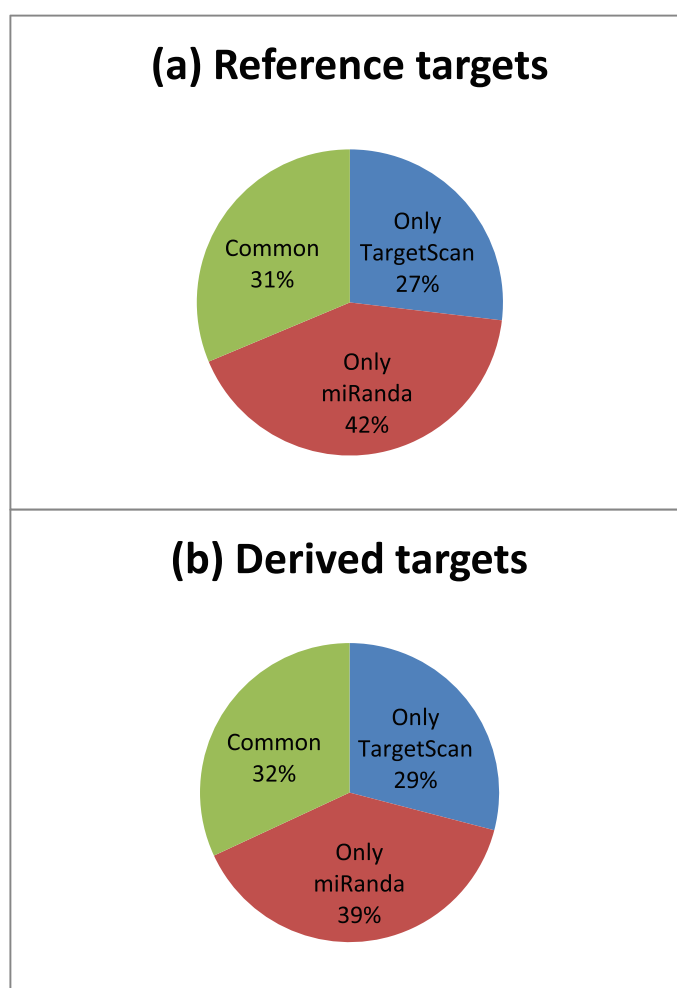


Knowledge-based analysis of functional impacts of mutations in microRNA seed regions

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Supplementary material



Supplementary figure 1. Summary of predicted miRNA targets from TargetScan and miRanda for all the SNPs in miRNA seeds. Percentages of miRNA targets found from only TargetScan, from only miRanda and from both TargetScan and miRanda are shown in pie chart (a) for the average number of reference targets and in pie chart (b) for the average number of derived targets.

Supplementary table 1. All naturally occurred SNPs in seed regions of human miRNAs. The information of the columns is given in the second sheet. Highly expressed miRNAs are represented in bold font.