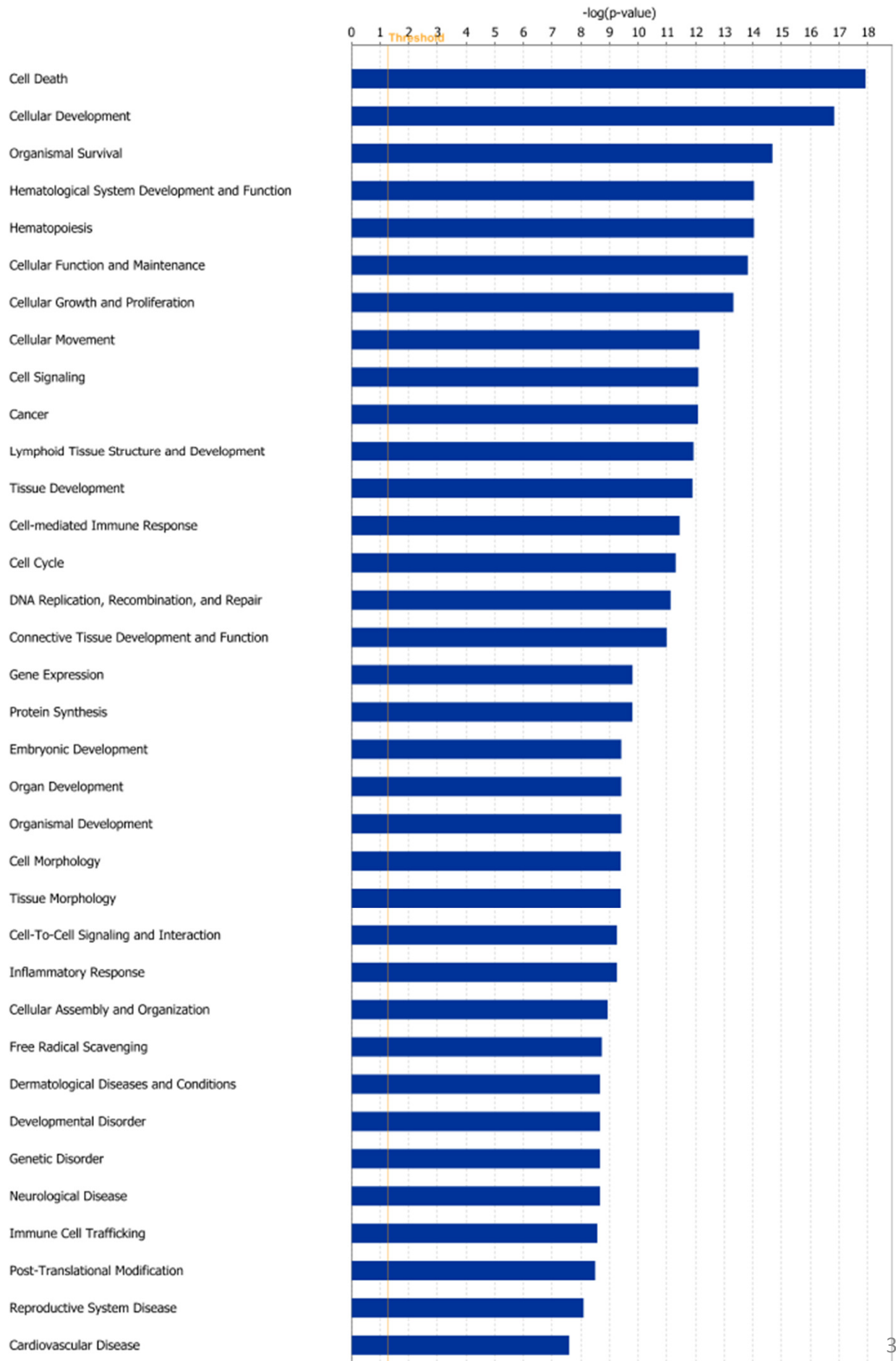
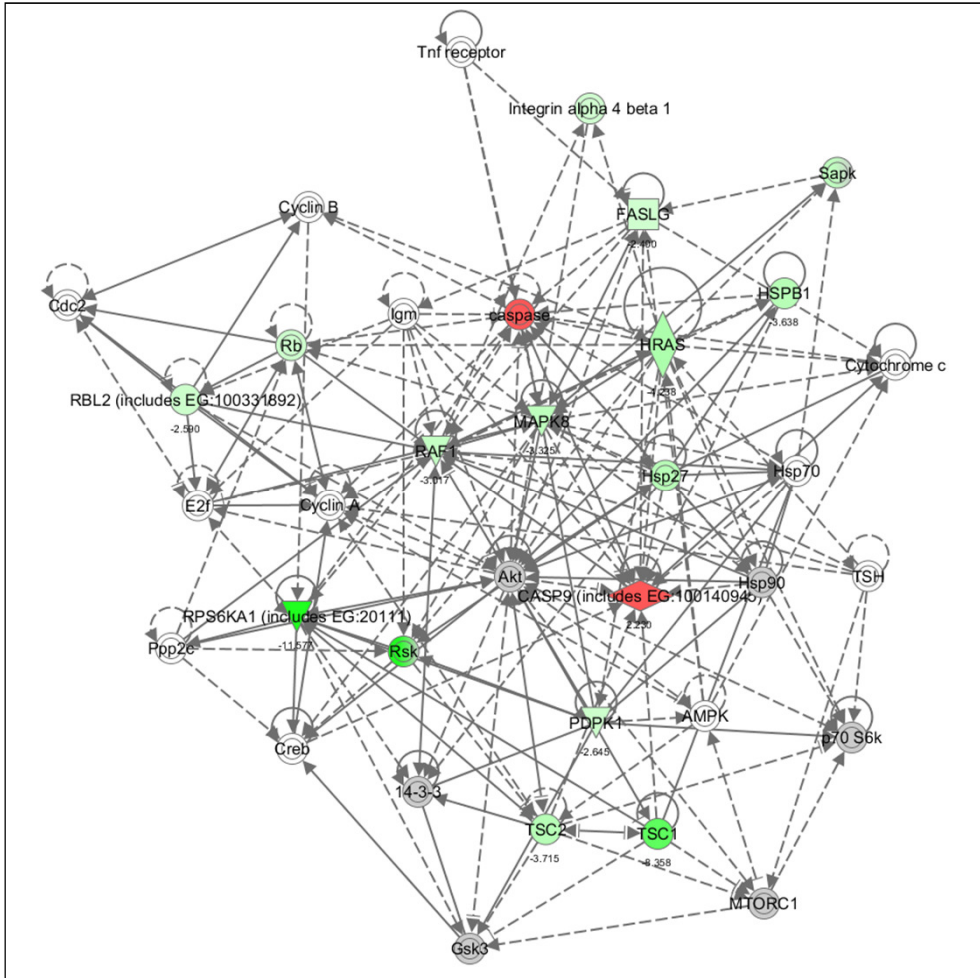


Supplementary Figure 1



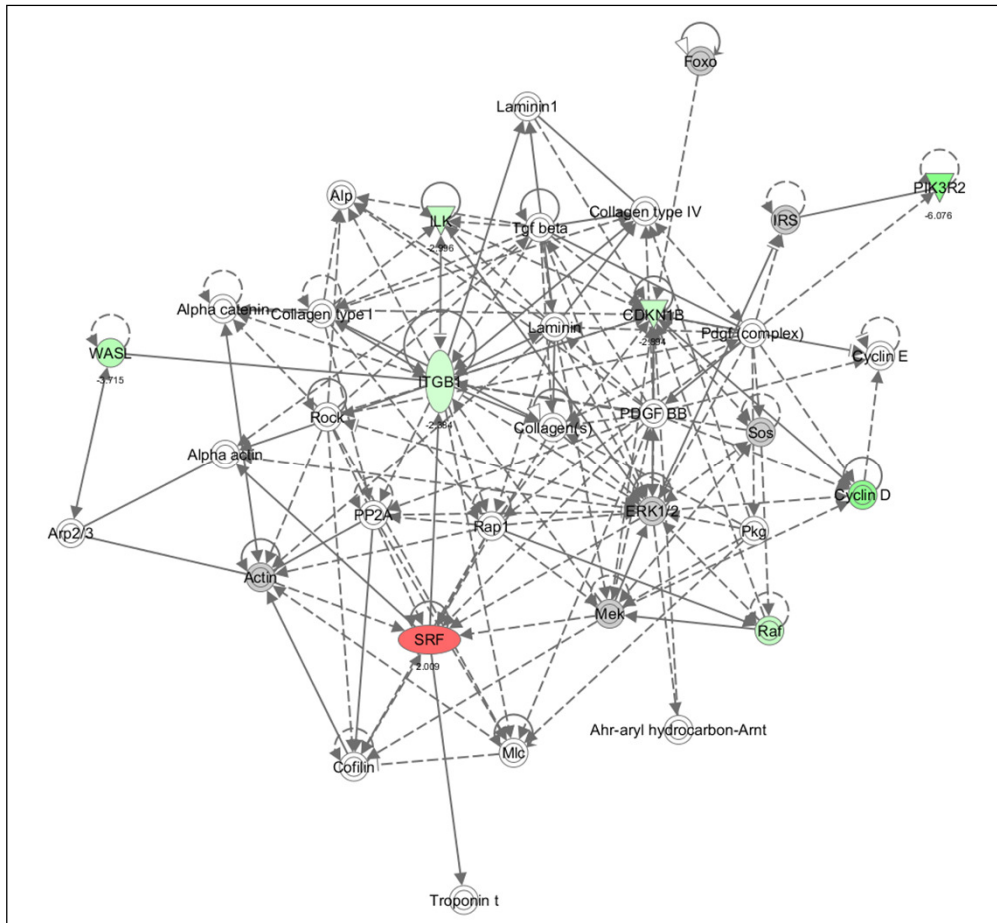
Supplementary Figure 2

A Network 1: Cell survival and differentiation



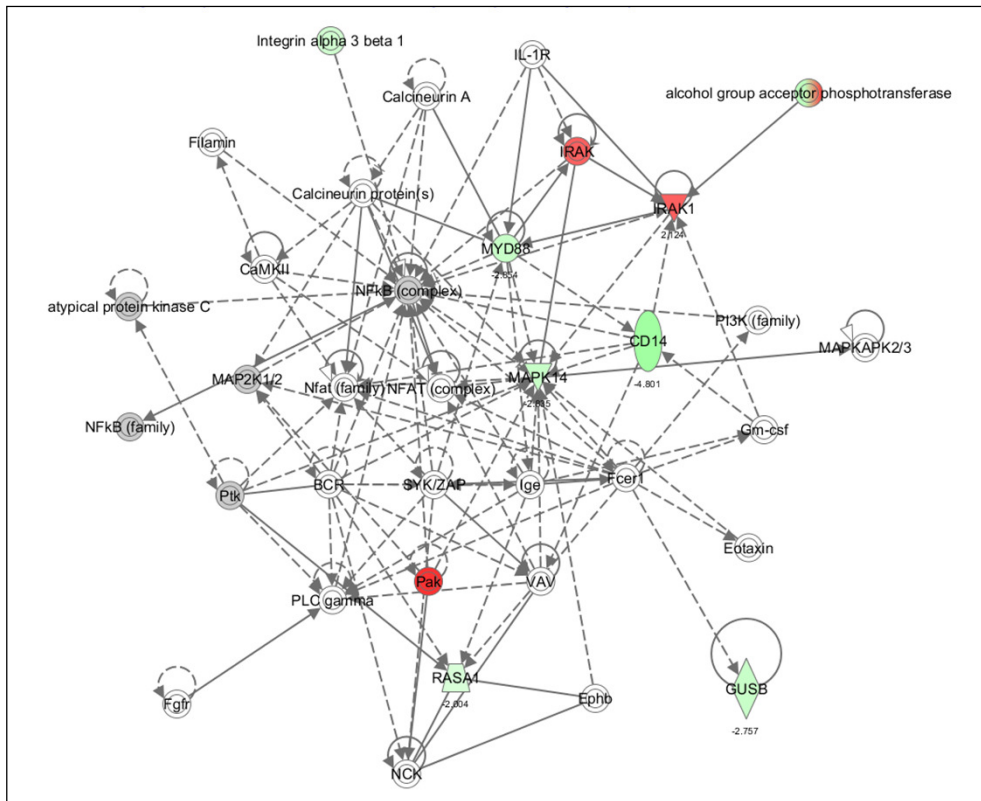
B

Network 2: Cell cycle and proliferation



C

Network 3: Innate immune signalling



Supplementary Figure Legends

Supplementary Figure 1. Predicted functional classifications of altered miRs and their potential targets. The data set containing the altered miRs obtained from miRCURY™ LNA array was uploaded into Ingenuity Pathway Analysis (IPA) software and the altered miRs classified into significantly enriched biological functions. Y axis values represent an IPA network score ($= -\log(p \text{ value})$), where a score of 1.3 (the threshold value; red line) is equivalent to $p=0.05$.) to indicate the probability that the miRs fall within these biological classifications; only cellular functions exceeding the threshold value were included. A right-tailed Fisher's exact test was used to determine the probability that each biological function identified is due to chance alone.

Supplementary Figure 2. Predicted functional networks of genes altered by miR-145 overexpression. Pre-miR-145 (500nM) was transfected into first trimester placental explants. 48 h later, total RNA was extracted and mRNA expression of multiple genes was assessed using PCR pathway arrays. Following normalisation and analysis, networks of known (solid lines) and inferred (dashed line) interacting molecules were created based on data within Ingenuity Knowledge Base. The colour intensity of protein species indicates the degree of up (red) or downregulated (green) genes. (A) Depicts a merged network predicted to regulate cell survival and differentiation, (B) is a network predicting a role for miR-145 in cell cycle regulation and proliferation, (C) suggests a role for miR-145 and its targets in regulation of innate immune signalling.