Abstract: Ets-related gene (ERG), a member of Ets family of Transcription factor, is highly expressed in endothelial cells (ECs). It has role in the development of lymphocytes, activation of platelets, angiogenesis, signal transduction mitogenic pathways and differentiation of ECs. ERG is overexpressed as a fusion protein in prostate cancer. During metastasis, the pathological role of ERG is associated with cell proliferation, invasion, and angiogenesis. Micro RNAs (miRNAs) are the small, non-coding RNAs consisting of approximately 18-25bp nucleotides and regulating about 60% of genes in humans. The miRNAs bind to 3′untranslated region (3′UTR), 5′untranslated region (5′UTR), promoters, introns and coding regions of the target mRNAs with 5-8 nucleotide sequence named as seed sequence. Their binding leads to the complete degradation of respective mRNA and sometimes even imperfect binding to target would result in inhibition of translation process. Here, we hypothesized that miRNAs regulate ERG expression through its 3′UTR, coding region or both. Several bioinformatics tools were used to identify miRNAs and their binding sites on 3′UTR and coding region of ERG. The selected miRNAs basal expression in prostate cancer samples was analysed by qPCR. The ectopic miRNAs expression was induced in prostate cancer cell lines (VCaP) and endothelial cell (HUVECs) to analyze ERG expression. Reporter gene assay was performed to evaluate the ERG activity in response to selected miRNAs. The expression of ERG downstream target genes was also investigated through qPCR after miRNAs overexpression. To observe the effects of selected miRNAs on cell proliferation and migration, scratch assay was performed to calculate the cell migration rate. VE-cadherin and VCAM-1are the endothelial-specific ERG targets and were analyzed after miRs overexpression. To observe the effect of selected miRNA on the cell cytotoxicity the colony formation assay was performed. From bioinformatics analysis, miR-4482 and miR-3912 were selected to investigate the 3′UTR of ERG; miR-6756 and miR-3190 were selected to investigate the coding region of ERG; and miR-361 was selected to investigate the both 3′UTR and coding region of ERG. The miR-4482 ($p<0.05$), miR-3912 ($p<0.001$), miR-361 ($p<0.001$), miR-6756 and miR-3190 ($p<0.001$) expression were decreased in prostate cancer samples, as compared to controls. Overexpression of miR-4482 and miR-3912, miR-361, miR-6756 and miR-3190 significantly reduced ERG mRNA ($p<0.001$, $p<0.01$, $p<0.001$, $p<0.001$ *and* $p<0.001$), respectively) and protein ($p<0.01$ $p<0.01$, $p<0.01$, $p<0.001$ and $p<0.001$ *respectively*). The transcriptional activity of ERG was significantly reduced ($p<0.01$, $p<0.01$, $p<0.01$, $p<0.001$ and $p<0.001$ respectively) in response to miR-4482, miR-3912, miR-361, miR-6756 and miR3190. ERG angiogenic targets and cell migration rate was also reduced significantly ($p<0.001$) after miR-4482, miR-3912, miR-361, miR-6756 and miR3190 over-expression. VE-cadherin and VCAM-1 showed significantly reduced protein expression and activity, after miR-4482, miR-3912, miR-361, miR-6756 and miR3190 over-expression. Overexpression of miR-4482, miR-3912, miR-361, miR-6756 and miR3190 significantly reduced ($p<0.001$) the colony formation ability of cancerous cells. This study indicates that miR-4482, miR-3912, miR-361, miR-6756 and miR3190 can suppress the ERG expression and its target genes, thereby, halt cancer progression and angiogenesis. These miRNAs may be employed as a potential therapeutic target for the miRNA-based therapy against cancer and angiogenesis.