



Category: Cancer Genomics

# Identification of genes responsible for anti-VEGF resistance in tumor cells

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## Abstract

Angiogenesis is the process of formation of new blood vessels from pre-existing vessels, which plays a key role in physiological as well as pathological conditions. It is a tightly regulated process involving the interplay of a number of pro and anti-angiogenic factors. Dysregulation of the balance between these factors lead to excess angiogenesis or inhibition of angiogenesis contributing to pathological conditions such as cancer, inflammation, atherosclerosis, tumor growth & rheumatoid arthritis. Vascular endothelial growth factor (VEGF) is an endothelial cell specific growth factor which is a critical mediator in angiogenesis and targeting VEGF signaling is considered a key therapeutic approach for blocking angiogenesis in anti-VEGF therapy. But recently it has been noted that certain tumors develop resistance to anti-VEGF therapy and develop capillaries by some alternative mechanisms. This may be due to the activation of other pathways which have a proper connection with the downstream signaling of VEGF mediated angiogenesis. To shed light on the mechanisms and mediators of resistance to anti-angiogenic therapy, we analysed a set of microarray expression data showing resistance to anti-VEGF therapy from databases and differentially expressed genes were identified. A total of 31 dataset were considered for the study, out of it one data set was used for the present study. The dataset contained 4 test and control samples, each having 34182 genes, out of which 796 genes were differentially expressed. Among the differentially expressed genes, 63 genes were 2 fold up regulated and 60 genes were 2 fold downregulated in both the sets. And these genes were classified based on the molecular function, cellular behavior and biological process. The results provide valuable biological insights into how tumors form resistance to anti- therapy.

## References

[1] Mitsuhashi, A., Goto, H., Saijo, A., Trung, V.T., Aono, Y., Ogino, H., et al. (2015) Fibrocyte-like cells mediate acquired resistance to anti-angiogenic therapy with bevacizumab. *Nat Commun* 6: 8792. <https://doi.org/10.1038/ncomms9792>

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