Microarray analysis of TIE-2-activated Endothelial Cells

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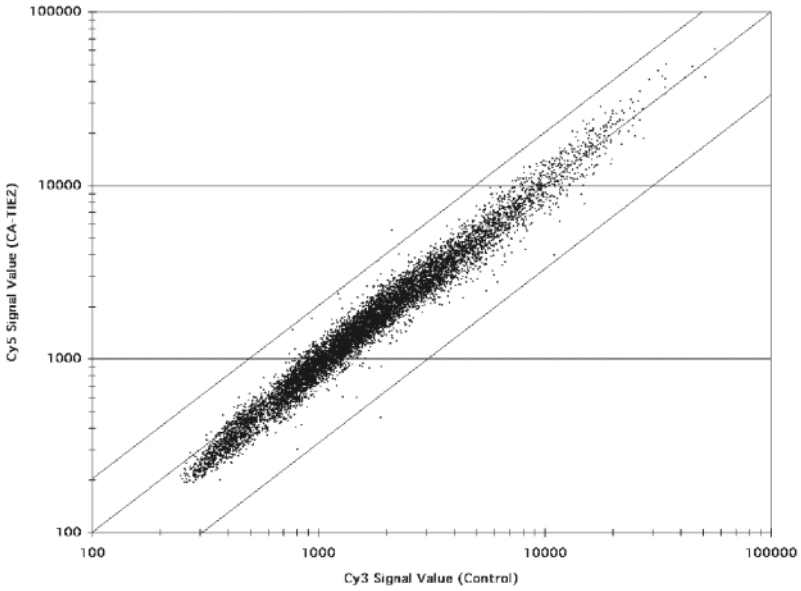
Growth and metastasis of solid tumors depend on the formation of new blood vessels by a process called angiogenesis. These blood vessels grow into the tumor and provide the nutrients and growth factors for tumor progression. Thus, there is considerable interest in understanding the mechanisms of angiogenesis for therapeutic purposes. Angiopoietin-1 (Ang-1) and their tyrosine kinase receptor Tie2 have been shown to play a pivotal role in normal as well as tumor angiogenesis. To understand the downstream of Ang-1/Tie2 signal pathway, we established a constitutively activated (CA)-Tie2 expressed subclone (#41) from an endothelial-like cell line, bEND3, and performed microarray gene expression analysis of 9364 genes between parental bEND3 and #41. Eight genes are up-regulated in #41, and 18 genes are repressed. Genes involved in membrane protein and protease are among those up-regulated, whereas genes involved in tight junction protein are predominantly repressed. We are analyzing each gene, whether gene(s) are participate in tumor angiogenesis.



Cloning and Characterlstic of a novel gene, *#E11*

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To better understand the molecular regulatory mechanisms of the hematopoietic stem cells, we performed a PCR-based subtraction methods and identified novel genes, *#E11*. This gene encodes highly conserved protein and its transcripts are found specifically in bone marrow and testis. In *C. elegans, #E11*-deficient embryo arrest with no sign gastrulation and show abnormal chromatin division. We are analyzing the function of *#E11* in hematopoietic stem cell.