

SUPPLEMENTARY MATERIAL

Supplementary Figure

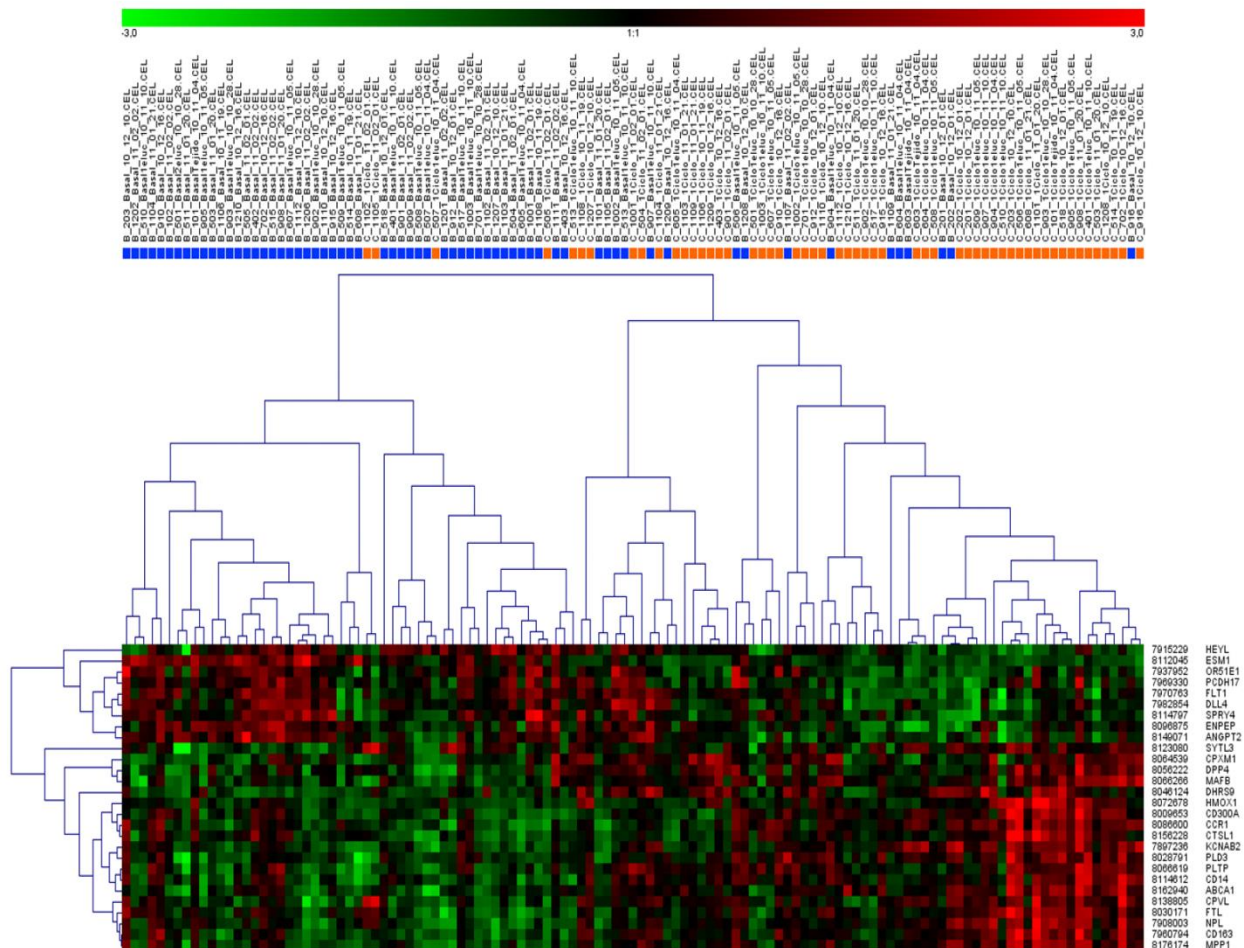


Figure S1: Hierarchical clustering of 119 samples according to expression of the top 28 differentially expressed probes (pre- and post-bevacizumab; baseline and after C1, respectively). Columns represent samples; rows represent individual probes; heat map depicts high (red) and low (green) relative levels of expression.

Supplementary Table

Table S1: Differential change in gene expression from baseline after bevacizumab treatment (after C1) using Linear Models for Microarray data.

Gene description [gene symbol]	Molecular function	Log-fold change in gene expression
Endothelial cell-specific molecule 1 [<i>ESM1</i>]	Extracellular region	−0.72
FMS-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) [<i>FLT1</i>]	Angiogenesis, blood vessel development, response to hypoxia	−0.43
Angiopoietin 2 [<i>ANGPT2</i>]	Angiogenesis, blood vessel development, extracellular region, regulation of angiogenesis	−0.36
Sprouty homolog 4 [<i>SPRY4</i>]	Cell projection, plasma membrane	−0.34
Glutamyl aminopeptidase (aminopeptidase A) [<i>ENPEP</i>]	Aminopeptidase activity, angiogenesis, blood vessel development, cell motility	−0.34
Delta-like 4 [<i>DLL4</i>]	Angiogenesis, blood vessel development, cell motility, endothelial cell migration, NOTCH pathway signalling	−0.33
Olfactory receptor, family 51, subfamily E, member 1 [<i>OR51E1</i>]	Intrinsic to membrane	−0.27
Protocadherin 17 [<i>PCDH17</i>]	Intrinsic to membrane	−0.24

Hairy/enhancer-of-split related with YRPW motif-like [<i>HEYL</i>]	NOTCH pathway signalling	-0.20
Synaptotagmin-like 3 [<i>SYTL3</i>]	Not specified	+0.22
Phospholipase D family, member 3 [<i>PLD3</i>]	Intrinsic to membrane, phospholipase D activity	+0.24
Ferritin, light polypeptide [<i>FTL</i>]	Intracellular ferritin complex, iron ion homeostasis	+0.24
CD300a molecule [<i>CD300A</i>]	Intrinsic to membrane	+0.25
Potassium voltage-gated channel, shaker-related subfamily, beta member 2 [<i>KCNAB2</i>]	Cell projection, intrinsic to membrane	+0.29
Carboxypeptidase, vitellogenic-like [<i>CPVL</i>]	Carboxypeptidase activity (serine-type), peptidase activity (L-amino peptides)	+0.33
V-maf musculoaponeurotic fibrosarcoma oncogene homolog B [<i>MAFB</i>]	Erythrocyte homeostasis	+0.33
Membrane protein, palmitoylated 1, 55 kDa [<i>MMP1</i>]	Cell fraction, intrinsic to membrane	+0.38
Cathepsin 1 [<i>CTSL1</i>]	Aminopeptidase activity	+0.41
N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) [<i>NPL</i>]	Not specified	+0.42
CD14 molecule [<i>CD14</i>]	Cytokine production, inflammatory response, phagocytosis	+0.43
ATP-binding cassette, subfamily A (ABC1), member 1 [<i>ABCA1</i>]	Cdc42 protein signal transduction, cytokine production, phagocytosis, platelet dense granule organisation	+0.43
Chemokine (C-C motif) receptor 1 [<i>CCR1</i>]	Inflammatory response, peptide binding	+0.43
Carboxypeptidase X (M14 family), member 1 [<i>CPXM1</i>]	Metalloexopeptidase activity, peptidase activity	+0.43

Dehydrogenase/reductase (SDR family) member 9 [<i>DHRS9</i>]	9-cis-retinoic acid biosynthesis process	+0.49
Phospholipid transfer protein [<i>PLTP</i>]	Extracellular region	+0.53
Dipeptidyl-peptidase 4 [<i>DPP4</i>]	Aminopeptidase activity, endothelial cell migration, peptidase activity, regulation of leukocyte-mediated immunity, response to hypoxia	+0.56
CD163 molecule [<i>CD163</i>]	Inflammatory response	+0.59
Haem oxygenase (decycling) 1 [<i>HMOX1</i>]	Angiogenesis, blood vessel development, haem oxidation, inflammatory response, response to hypoxia	+0.84