Table S1

Complete list of 317 CAM genes induced by VEGF

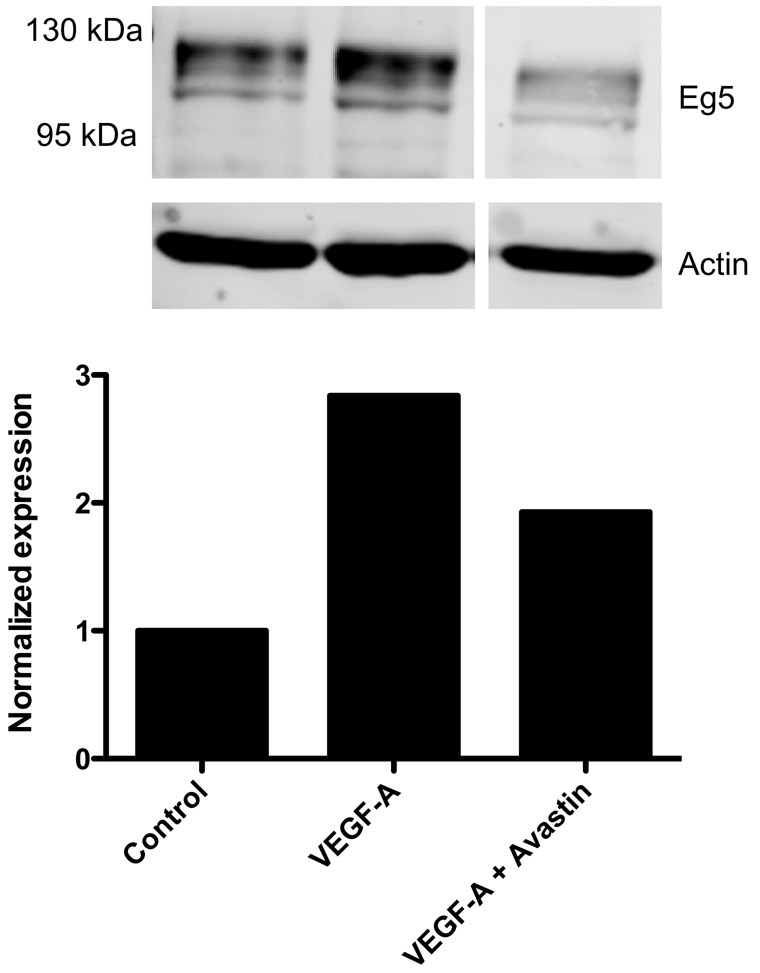
(provided as Microsoft Excel file)

The table contains the list of 317 probe sets detecting significantly up regulated transcripts in at least two out of three biological replicates. The five kinesins motor protein encoding genes are marked in red (KIF4A, KIF11, KIF15, KIF20A and KIF23).

I = Increased.

Figure S1

Expression of Eg5 protein in endothelial cells is stimulated by VEGF-A *in vitro* and inhibited by Avastin



HUVECs were treated with 10 ng/ml recombinant human VEGF-A for 24 h and Eg5 protein expression is analyzed by Western Blot. Note that co-treatment with VEGF-A blocking antibody Avastin abolishes Eg5 expression.

Table S2

Biological themes significantly enriched in genes up regulated by VEGF

Annotation Cluster 1	**Enrichment Score: 11.6**											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
SP_PIR_KEYWORDS	mitosis	22	10.68	5.37E-16	KIF23, KIF11, CDC2, NUF2, NUSAP1, NDC80, CENPE, CDC20, SMC2, SMC4, NCAPD2, FAM83D, NCAPH, CCNB2, PLK1, NCAPG, NCAPG2, BUB1, BUB1B, CCNA2, HELLS, CDCA3	206	183	19235	11.22526	1.68E-13	1.68E-13	7.44E-13
GOTERM_BP_FAT	GO:0048285~organelle fission	25	12.136	1.53E-15	KIF23, FAM83D, NCAPH, NCAPG2, NCAPG, BUB1, CCNA2, HELLS, CDCA3, KIF11, OPA1, CDC2, KIF15, NUF2, TPX2, NUSAP1, CENPE, NDC80, CDC20, SMC2, NCAPD2, SMC4, CCNB2, PLK1, BUB1B	174	229	13528	8.487678	2.64E-12	2.64E-12	2.62E-12
GOTERM_BP_FAT	GO:0000280~nuclear division	24	11.65	6.74E-15	KIF23, KIF11, CDC2, KIF15, TPX2, NUF2, NUSAP1, NDC80, CENPE, CDC20, SMC2, SMC4, NCAPD2, FAM83D, NCAPH, CCNB2, PLK1, NCAPG, NCAPG2, BUB1, BUB1B, CCNA2, HELLS, CDCA3	174	220	13528	8.481505	1.15E-11	5.74E-12	1.14E-11
GOTERM_BP_FAT	GO:0007067~mitosis	24	11.65	6.74E-15	KIF23, KIF11, CDC2, KIF15, TPX2, NUF2, NUSAP1, NDC80, CENPE, CDC20, SMC2, SMC4, NCAPD2, FAM83D, NCAPH, CCNB2, PLK1, NCAPG, NCAPG2, BUB1, BUB1B, CCNA2, HELLS, CDCA3	174	220	13528	8.481505	1.15E-11	5.74E-12	1.14E-11
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	24	11.65	9.98E-15	KIF23, KIF11, CDC2, KIF15, TPX2, NUF2, NUSAP1, NDC80, CENPE, CDC20, SMC2, SMC4, NCAPD2, FAM83D, NCAPH, CCNB2, PLK1, NCAPG, NCAPG2, BUB1, BUB1B, CCNA2, HELLS, CDCA3	174	224	13528	8.330049	1.69E-11	5.65E-12	1.69E-11
SP_PIR_KEYWORDS	cell cycle	30	14.563	1.36E-14	KIF23, E2F1, FAM83D, NCAPH, CDC45L, NCAPG2, NCAPG, BUB1, CCNA2, HELLS, CDCA3, CKAP2, RBBP4, KIF11, CDC2, NUF2, NUSAP1, CENPE, NDC80, CDC20, MCM2, SMC2, SMC4, GAK, MCM6, NCAPD2, CCNB2, RGS2, PLK1, BUB1B	206	461	19235	6.076385	4.10E-12	2.05E-12	1.81E-11
GOTERM_BP_FAT	GO:0000279~M phase	27	13.107	8.52E-14	KIF23, FAM83D, NCAPH, NCAPG2, NCAPG, BUB1, CCNA2, HELLS, CDCA3, MSH6, KIF11, CDC2, KIF15, NUF2, TPX2, NUSAP1, CENPE, NDC80, CDC20, SMC2, SMC4, RAD51, NCAPD2, CCNB2, PLK1, TOP3A, BUB1B	174	329	13528	6.380463	1.44E-10	3.61E-11	1.44E-10
SP_PIR_KEYWORDS	cell division	23	11.165	9.44E-14	KIF23, KIF11, CDC2, NUF2, NUSAP1, NDC80, CENPE, CDC20, SMC2, MCM5, SMC4, NCAPD2, FAM83D, NCAPH, CCNB2, PLK1, NCAPG, NCAPG2, BUB1, BUB1B, CCNA2, HELLS, CDCA3	206	264	19235	8.134837	2.86E-11	7.15E-12	1.26E-10
GOTERM_BP_FAT	GO:0007049~cell cycle	39	18.932	4.48E-13	KIF23, E2F1, FAM83D, NCAPH, CDC45L, NCAPG2, NCAPG, PSMD1, BUB1, CCNA2, HELLS, CDCA3, CKAP2, GPS1, MSH6, RBBP4, KIF11, UPF1, CDC2, KIF15, TPX2, NUF2, NUSAP1, CDC20, CENPE, NDC80, MCM2, SMC2, SMC4, GAK, NCAPD2, RAD51, MCM6, CCNB2, RGS2, PLK1, TOP3A, BUB1B, BARD1	174	776	13528	3.907394	7.60E-10	1.52E-10	7.56E-10
GOTERM_BP_FAT	GO:0022403~cell cycle phase	28	13.592	2.69E-12	KIF23, E2F1, FAM83D, NCAPH, NCAPG2, NCAPG, BUB1, CCNA2, HELLS, CDCA3, MSH6, KIF11, CDC2, KIF15, NUF2, TPX2, NUSAP1, CENPE, NDC80, CDC20, SMC2, SMC4, RAD51, NCAPD2, CCNB2, PLK1, TOP3A, BUB1B	174	414	13528	5.25826	4.56E-09	7.60E-10	4.53E-09
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	26	12.621	8.72E-12	KIF23, E2F1, FAM83D, NCAPH, NCAPG2, NCAPG, PSMD1, BUB1, CCNA2, HELLS, CDCA3, KIF11, CDC2, KIF15, NUF2, TPX2, NUSAP1, CENPE, NDC80, CDC20, SMC2, NCAPD2, SMC4, CCNB2, PLK1, BUB1B	174	370	13528	5.463312	1.48E-08	2.11E-09	1.47E-08
GOTERM_BP_FAT	GO:0051301~cell division	23	11.165	2.54E-11	KIF23, KIF11, CDC2, NUF2, NUSAP1, NDC80, CENPE, CDC20, SMC2, MCM5, SMC4, NCAPD2, FAM83D, NCAPH, CCNB2, PLK1, NCAPG, NCAPG2, BUB1, BUB1B, CCNA2, HELLS, CDCA3	174	295	13528	6.06164	4.31E-08	5.39E-09	4.29E-08
GOTERM_BP_FAT	GO:0022402~cell cycle process	30	14.563	1.33E-10	KIF23, E2F1, FAM83D, NCAPH, NCAPG2, NCAPG, PSMD1, BUB1, CCNA2, HELLS, CDCA3, MSH6, KIF11, CDC2, KIF15, TPX2, NUF2, NUSAP1, CENPE, NDC80, CDC20, SMC2, SMC4, RAD51, NCAPD2, CCNB2, PLK1, TOP3A, BUB1B, BARD1	174	565	13528	4.128166	2.26E-07	2.51E-08	2.24E-07
GOTERM_CC_FAT	GO:0000793~condensed chromosome	13	6.3107	6.76E-08	NUF2, NDC80, CENPE, SMC2, RAD51, NCAPD2, SMC4, NCAPH, BAZ1B, NCAPG, CENPC1, BUB1, BUB1B	160	129	12782	8.050678	1.99E-05	9.93E-06	9.00E-05
GOTERM_CC_FAT	GO:0005819~spindle	13	6.3107	2.86E-07	CKAP2, KIF23, KIF11, CDC2, KIF15, TPX2, NUSAP1, CDC20, CENPE, FAM83D, PLK1, BUB1, BUB1B	160	147	12782	7.064881	8.40E-05	2.80E-05	3.80E-04
Annotation Cluster 2	**Enrichment Score: 8.2**											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0000279~M phase	27	13.107	8.52E-14	KIF23, FAM83D, NCAPH, NCAPG2, NCAPG, BUB1, CCNA2, HELLS, CDCA3, MSH6, KIF11, CDC2, KIF15, NUF2, TPX2, NUSAP1, CENPE, NDC80, CDC20, SMC2, SMC4, RAD51, NCAPD2, CCNB2, PLK1, TOP3A, BUB1B	174	329	13528	6.380463	1.44E-10	3.61E-11	1.44E-10
GOTERM_BP_FAT	GO:0007049~cell cycle	39	18.932	4.48E-13	KIF23, E2F1, FAM83D, NCAPH, CDC45L, NCAPG2, NCAPG, PSMD1, BUB1, CCNA2, HELLS, CDCA3, CKAP2, GPS1, MSH6, RBBP4, KIF11, UPF1, CDC2, KIF15, TPX2, NUF2, NUSAP1, CDC20, CENPE, NDC80, MCM2, SMC2, SMC4, GAK, NCAPD2, RAD51, MCM6, CCNB2, RGS2, PLK1, TOP3A, BUB1B, BARD1	174	776	13528	3.907394	7.60E-10	1.52E-10	7.56E-10
GOTERM_CC_FAT	GO:0005694~chromosome	23	11.165	5.67E-08	MSH6, RBBP4, CENPL, UPF1, NUF2, NDC80, CENPE, MCM2, SMC2, SMC4, RAD51, NCAPD2, NCAPH, BAZ1B, NCAPG, CENPC1, HNRNPD, TOP3A, BUB1, BUB1B, BCL6, TOP2A, HELLS	160	460	12782	3.994375	1.67E-05	1.67E-05	7.56E-05

(table continues on next page)

Table S2

Biological themes significantly enriched in genes up regulated by VEGF

Annotation Cluster 3	**Enrichment Score: 6.7**												
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
UP_SEQ_FEATURE	nucleotide phosphate-binding region:ATP	35	16.99	7.84E-10	KIF23, FES, MYO9A, N4BP2, LONP1, TEK, BUB1, TOP2A, NSF, HELLS, SYK, MSH6, KIF11, FLT1, UPF1, MYO1C, LYN, CDC2, KIF15, CENPE, MCM2, SMC2, MCM4, MCM5, SMC4, ABCG2, RAD51, MCM6, KDR, PLK1, HIPK2, BMP2K, BUB1B, JAK2, KIF20A	206	962	19113	3.375628	6.53E-07	6.53E-07	1.21E-06
SP_PIR_KEYWORDS	atp-binding	40	19.417	5.88E-09	KIF23, FES, MYO9A, N4BP2, LONP1, TEK, BUB1, TOP2A, NSF, HELLS, SYK, MSH6, KIF11, FLT1, UPF1, MYO1C, LYN, CDC2, KIF15, CENPE, RBKS, MCM2, MCM4, SMC2, MCM5, SMC4	206	1326	19235	2.816705	1.78E-06	3.56E-07	7.87E-06
SP_PIR_KEYWORDS	nucleotide-binding	45	21.845	1.91E-08	KIF23, GNAI2, FES, MYO9A, N4BP2, LONP1, TEK, LSG1, BUB1, RAPGEF3, TOP2A, NSF, HELLS, SYK, MSH6, KIF11, FLT1, UPF1, OPA1, MYO1C, LYN, CDC2, KIF15, RBKS, CENPE, MCM2, MCM4, SMC2, MCM5, SMC4, GAK, KDR, ABCG2, RAD51, MCM6, BAZ1B, PLK1, HIPK2, RAB22A, RRM1, BMP2K, TOP3A, BUB1B, JAK2, KIF20A	206	1686	19235	2.492183	5.79E-06	9.65E-07	2.56E-05
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	44	21.359	1.59E-07	KIF23, STEAP4, FES, MYO9A, N4BP2, LONP1, TEK, BUB1, RAPGEF3, TOP2A, NSF, HELLS, DUS3L, SYK, MSH6, KIF11, FLT1, UPF1, MYO1C, LYN, CDC2, KIF15, TPX2, CENPE, RBKS, MCM2, MCM4, SMC2, MCM5, SMC4, GAK, KDR, ABCG2, RAD51, MCM6, BAZ1B, PLK1, HIPK2, RRM1, BMP2K, TOP3A, BUB1B, JAK2, KIF20A	158	1577	12983	2.292656	5.93E-05	5.93E-05	2.20E-04
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	44	21.359	2.44E-07	KIF23, STEAP4, FES, MYO9A, N4BP2, LONP1, TEK, BUB1, RAPGEF3, TOP2A, NSF, HELLS, DUS3L, SYK, MSH6, KIF11, FLT1, UPF1, MYO1C, LYN, CDC2, KIF15, TPX2, CENPE, RBKS, MCM2, MCM4, SMC2, MCM5, SMC4, GAK, KDR, ABCG2, RAD51, MCM6, BAZ1B, PLK1, HIPK2, RRM1, BMP2K, TOP3A, BUB1B, JAK2, KIF20A	158	1601	12983	2.258288	9.09E-05	4.54E-05	3.36E-04
GOTERM_MF_FAT	GO:0001882~nucleoside binding	44	21.359	2.95E-07	KIF23, STEAP4, FES, MYO9A, N4BP2, LONP1, TEK, BUB1, RAPGEF3, TOP2A, NSF, HELLS, DUS3L, SYK, MSH6, KIF11, FLT1, UPF1, MYO1C, LYN, CDC2, KIF15, TPX2, CENPE, RBKS, MCM2, MCM4, SMC2, MCM5, SMC4, GAK, KDR, ABCG2, RAD51, MCM6, BAZ1B, PLK1, HIPK2, RRM1, BMP2K, TOP3A, BUB1B, JAK2, KIF20A	158	1612	12983	2.242878	1.10E-04	3.67E-05	4.08E-04
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	42	20.388	3.03E-07	KIF23, FES, MYO9A, N4BP2, LONP1, TEK, BUB1, RAPGEF3, TOP2A, NSF, HELLS, SYK, MSH6, KIF11, FLT1, UPF1, MYO1C, LYN, CDC2, KIF15, TPX2, CENPE, RBKS, MCM2, MCM4, SMC2, MCM5, SMC4, GAK, KDR, ABCG2, RAD51, MCM6, BAZ1B, PLK1, HIPK2, RRM1, BMP2K, TOP3A, BUB1B, JAK2, KIF20A	158	1497	12983	2.305396	1.13E-04	2.83E-05	4.19E-04
GOTERM_MF_FAT	GO:0005524~ATP binding	41	19.903	5.95E-07	KIF23, FES, MYO9A, N4BP2, LONP1, TEK, BUB1, TOP2A, NSF, HELLS, SYK, MSH6, KIF11, FLT1, UPF1, MYO1C, LYN, CDC2, KIF15, TPX2, CENPE, RBKS, MCM2, MCM4, SMC2, MCM5, SMC4, GAK, KDR, ABCG2, RAD51, MCM6, BAZ1B, PLK1, HIPK2, RRM1, BMP2K, TOP3A, BUB1B, JAK2, KIF20A	158	1477	12983	2.280979	2.22E-04	4.44E-05	8.22E-04
Annotation Cluster 4	**Enrichment Score: 5.5**											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0001568~blood vessel development	17	8.2524	9.84E-08	CCM2, FLT1, LMO2, COL3A1, ELK3, PROX1, GJA5, CDH5, KDR, CDH13, MEOX2, NARG1, ID1, FOXC2, SOX18, COL1A1, SOX17	174	245	13528	5.394699	1.67E-04	1.52E-05	1.66E-04
GOTERM_BP_FAT	GO:0001944~vasculature development	17	8.2524	1.38E-07	CCM2, FLT1, LMO2, COL3A1, ELK3, PROX1, GJA5, CDH5, KDR, CDH13, MEOX2, NARG1, ID1, FOXC2, SOX18, COL1A1, SOX17	174	251	13528	5.265742	2.34E-04	1.95E-05	2.32E-04
Annotation Cluster 5	**Enrichment Score: 5.4**											
Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0030261~chromosome condensation	8	3.8835	1.96E-08	NCAPH, NCAPG2, NCAPG, NUSAP1, TOP2A, SMC2, NCAPD2, SMC4	174	25	13528	24.87908	3.33E-05	3.33E-06	3.31E-05
GOTERM_CC_FAT	GO:0005694~chromosome	23	11.165	5.67E-08	MSH6, RBBP4, CENPL, UPF1, NUF2, NDC80, CENPE, MCM2, SMC2, SMC4, RAD51, NCAPD2, NCAPH, BAZ1B, NCAPG, CENPC1, HNRNPD, TOP3A, BUB1, BUB1B, BCL6, TOP2A	160	460	12782	3.994375	1.67E-05	1.67E-05	7.56E-05
GOTERM_CC_FAT	GO:0000793~condensed chromosome	13	6.3107	6.76E-08	NUF2, NDC80, CENPE, SMC2, RAD51, NCAPD2, SMC4, NCAPH, BAZ1B, NCAPG, CENPC1, BUB1, BUB1B	160	129	12782	8.050678	1.99E-05	9.93E-06	9.00E-05
SP_PIR_KEYWORDS	dna condensation	6	2.9126	9.76E-08	NCAPH, NCAPG2, NCAPG, SMC2, NCAPD2, SMC4	206	12	19235	46.68689	2.96E-05	4.22E-06	1.31E-04
GOTERM_BP_FAT	GO:0000070~mitotic sister chromatid segregation	8	3.8835	3.02E-07	NCAPH, NCAPG, NUSAP1, CENPE, NDC80, SMC2, NCAPD2, SMC4	174	36	13528	17.27714	5.13E-04	3.95E-05	5.10E-04
GOTERM_CC_FAT	GO:0000796~condensin complex	5	2.4272	3.39E-07	NCAPH, NCAPG, SMC2, NCAPD2, SMC4	160	6	12782	66.57292	9.97E-05	2.49E-05	4.52E-04
GOTERM_BP_FAT	GO:0000819~sister chromatid segregation	8	3.8835	3.69E-07	NCAPH, NCAPG, NUSAP1, CENPE, NDC80, SMC2, NCAPD2, SMC4	174	37	13528	16.81019	6.26E-04	4.47E-05	6.22E-04
GOTERM_BP_FAT	GO:0007076~mitotic chromosome condensation	6	2.9126	3.82E-07	NCAPH, NCAPG, NUSAP1, SMC2, NCAPD2, SMC4	174	13	13528	35.88329	6.48E-04	4.32E-05	6.45E-04

Out of the 317 probe sets, which detected up regulated transcripts in VEGF-treated CAMs, 206 unique orthologs were submitted to gene ontology analysis. Note that significantly enriched GO-terms identify cell proliferation and blood vessel development as main biological processes (>5-fold enrichment, FDR<0.001).

Table S3

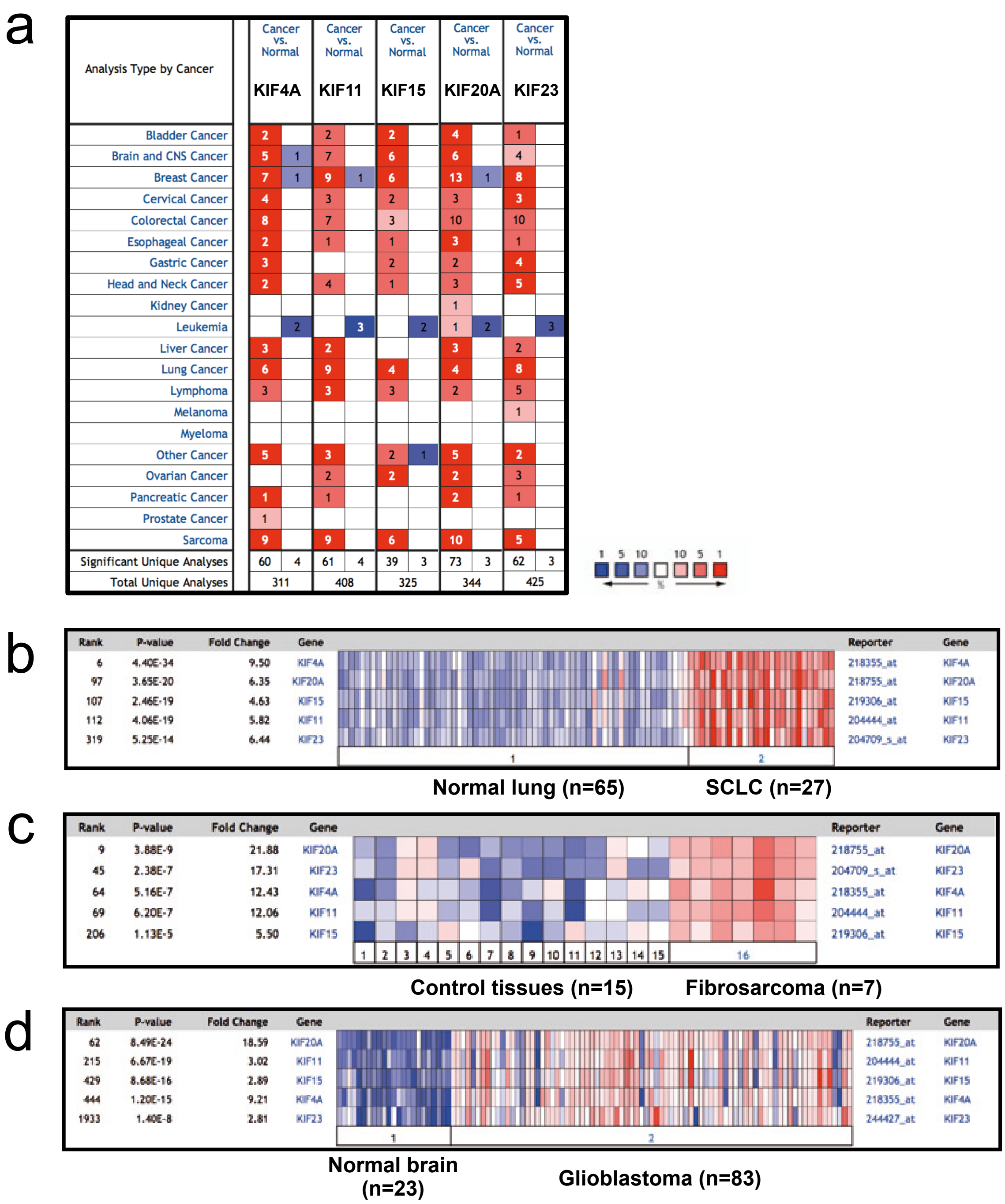
In silico prediction of endothelial versus non-endothelial enrichment of human kinesin family members

Gene symbol	Gene name	No. EC-EST	No. Non EC-EST	Enrichment EC-EST/Non EC-EST	FDR q-value	
KIF11	kinesin family member 11	2	0	-	0.10	Endothelial
KIF13B	kinesin family member 13B	3	2	6.59	0.26	
KIF18A	kinesin family member 18A	2	2	4.39	0.44	
KIF9	kinesin family member 9	1	1	4.39	0.57	
KIF15	kinesin family member 15	1	1	4.39	0.57	
KIF20A	kinesin family member 20A	5	6	3.66	0.26	
KIF2C	kinesin family member 2C	3	6	2.20	0.57	
KIF13A	kinesin family member 13A	1	2	2.20	0.62	
KIF1B	kinesin family member 1B	2	5	1.76	0.62	
KIF5B	kinesin family member 5B	3	8	1.65	0.62	
KIF3A	kinesin family member 3A	1	3	1.46	0.81	
KIF1C	kinesin family member 1C	1	4	1.10	0.94	
KIF22	kinesin family member 22	2	14	1.59	0.62	Non-Endothelial
KIF12	kinesin family member 12	0	3	-	0.53	
KIF17	kinesin family member 17	0	1	-	0.62	
KIF1A	kinesin family member 1A	0	3	-	0.53	
KIF21A	kinesin family member 21A	0	2	-	0.57	
KIF21B	kinesin family member 21B	0	4	-	0.49	
KIF23	kinesin family member 23	0	1	-	0.62	
KIF24	kinesin family member 24	0	1	-	0.62	
KIF27	kinesin family member 27	0	1	-	0.62	
KIF3B	kinesin family member 3B	0	7	-	0.33	
KIF3C	kinesin family member 3C	0	4	-	0.49	
KIF4A	kinesin family member 4A	0	3	-	0.53	
KIF5C	kinesin family member 5C	0	9	-	0.29	
KIFC1	kinesin family member C1	0	2	-	0.57	
KIFC2	kinesin family member C2	0	2	-	0.57	
KIFC3	kinesin family member C3	0	8	-	0.29	
				(no restriction for q-value)		

Genes encoding for kinesins were extracted from the Affymetrix chicken GeneChip by their gene symbol (KIFxx), subjected to ortholog screen and *in silico* assignment of endothelial vs. non-endothelial enrichment. Out of 36 unique kinesin genes, 12 showed preferential endothelial expression, whereas 16 were enriched in non-endothelial cells.

Figure S2

Expression and co-expression analysis of five VEGF-induced kinesins in various human tumors



Analysis Type by Cancer	Cancer vs. Normal KIF4A		Cancer vs. Normal KIF11		Cancer vs. Normal KIF15		Cancer vs. Normal KIF20A		Cancer vs. Normal KIF23	
Bladder Cancer	2		2		2		4		1	
Brain and CNS Cancer	5	1	7		6		6		4	
Breast Cancer	7	1	9	1	6		13	1	8	
Cervical Cancer	4		3		2		3		3	
Colorectal Cancer	8		7		3		10		10	
Esophageal Cancer	2		1		1		3		1	
Gastric Cancer	3				2		2		4	
Head and Neck Cancer	2		4		1		3		5	
Kidney Cancer							1			
Leukemia		2		3		2	1	2		3
Liver Cancer	3		2				3		2	
Lung Cancer	6		9		4		4		8	
Lymphoma	3		3		3		2		5	
Melanoma									1	
Myeloma										
Other Cancer	5		3		2	1	5		2	
Ovarian Cancer			2		2		2		3	
Pancreatic Cancer	1		1				2		1	
Prostate Cancer	1									
Sarcoma	9		9		6		10		5	
Significant Unique Analyses	60	4	61	4	39	3	73	3	62	3
Total Unique Analyses	311		408		325		344		425	

Rank	P-value	Fold Change	Gene	Reporter	Gene
6	4.40E-34	9.50	KIF4A	218355_at	KIF4A
97	3.65E-20	6.35	KIF20A	218755_at	KIF20A
107	2.46E-19	4.63	KIF15	219306_at	KIF15
112	4.06E-19	5.82	KIF11	204444_at	KIF11
319	5.25E-14	6.44	KIF23	204709_s_at	KIF23

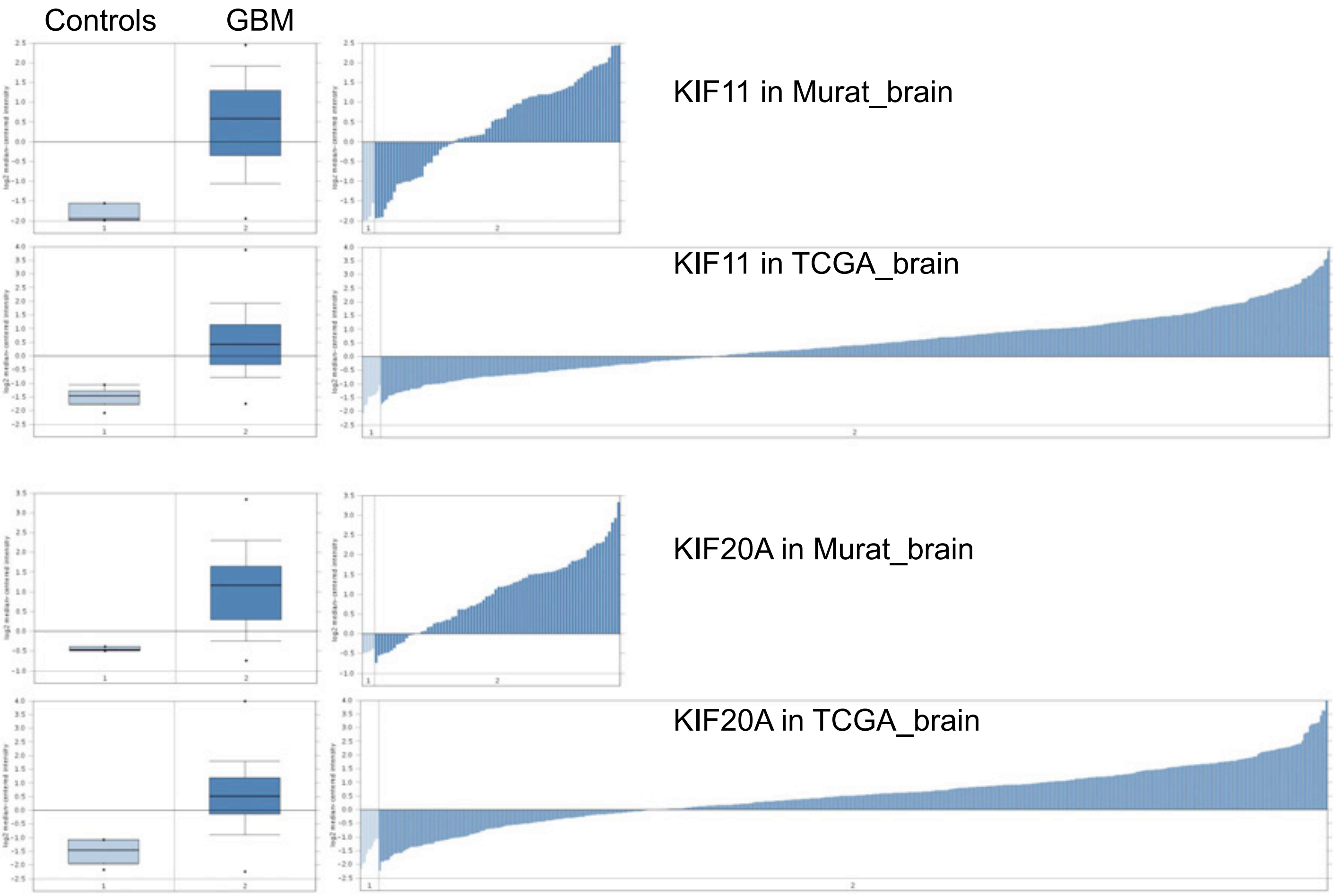
Rank	P-value	Fold Change	Gene	Reporter	Gene
9	3.88E-9	21.88	KIF20A	218755_at	KIF20A
45	2.38E-7	17.31	KIF23	204709_s_at	KIF23
64	5.16E-7	12.43	KIF4A	218355_at	KIF4A
69	6.20E-7	12.06	KIF11	204444_at	KIF11
206	1.13E-5	5.50	KIF15	219306_at	KIF15

Rank	P-value	Fold Change	Gene	Reporter	Gene
62	8.49E-24	18.59	KIF20A	218755_at	KIF20A
215	6.67E-19	3.02	KIF11	204444_at	KIF11
429	8.68E-16	2.89	KIF15	219306_at	KIF15
444	1.20E-15	9.21	KIF4A	218355_at	KIF4A
1933	1.40E-8	2.81	KIF23	244427_at	KIF23

(a) Oncomine database was queried for expression of indicated kinesins in human malignancies compared to normal tissue. The numbers in the cases indicated in how many different studies significant over expression was found. Intensity of the red and blue colour indicates rank-order of the gene by over expression and under expression in cancer versus normal tissue (eg. top 1%, 5% and 10%). Co-expression of five VEGF-induced kinesins was observed in three different cancer types. In all cases, kinesins were significantly over expressed in cancer tissues. (b) SCLC = squamous cell lung carcinoma; Hou_Lung study. (c) Fibrosarcoma; Detwiller_sarcoma study. (d) Glioblastoma; Sun_Brain study.

Figure S3

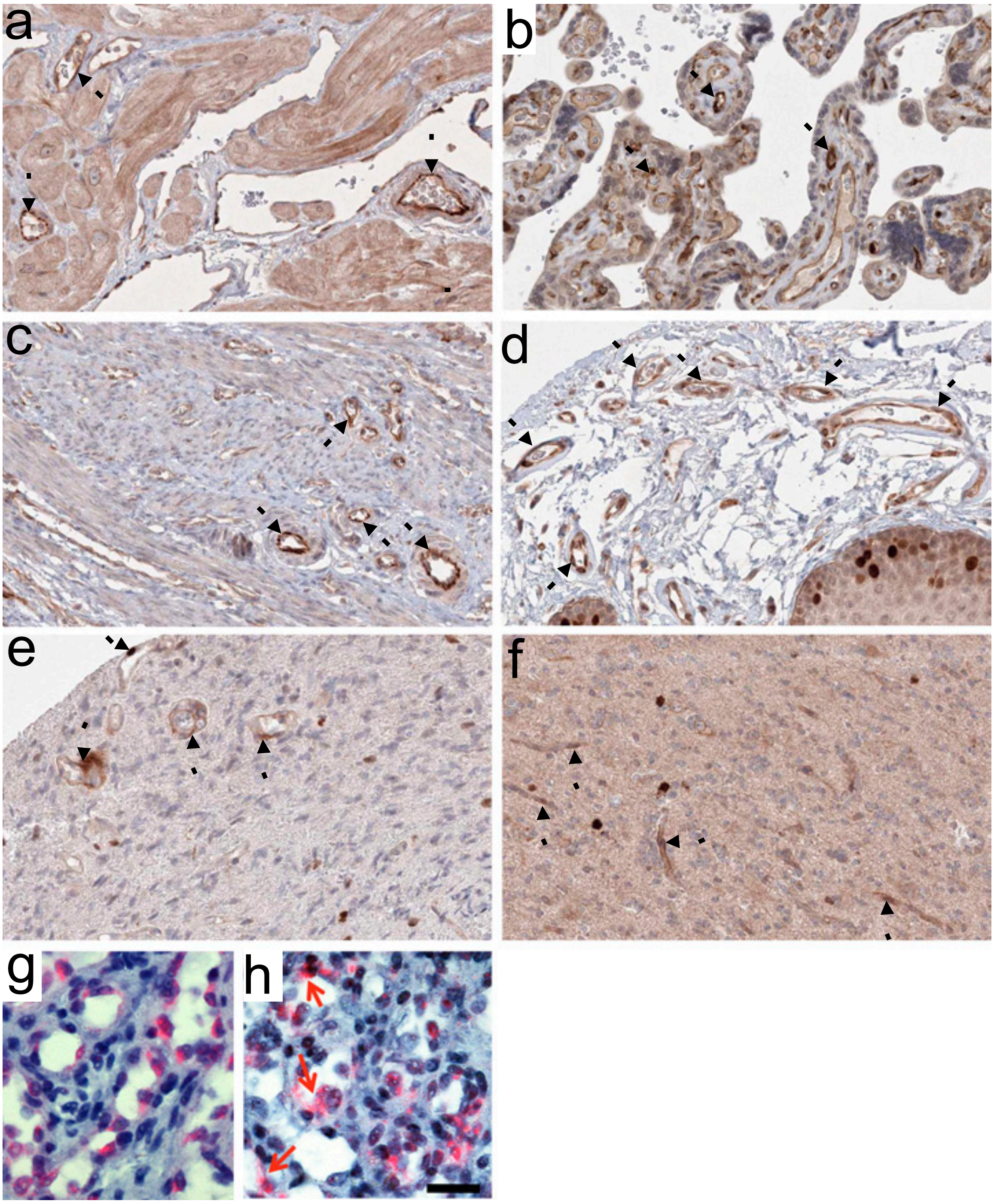
Heterogeneous expression of KIF11 and KIF20A in glioblastoma



Even though over expression of KIF11 and KIF20A seems obvious from box plot presentation, visualization of the whole dataset (expression per patient) shows heterogeneity of expression in two independent glioblastoma studies (Murat_brain: 4 controls, 80 GBMs; TCGA_brain: 10 controls, 515 GBMs) with approximately two-thirds of patients over expressing.

Figure S4

Vascular expression of KIF20A/Mklp2 in normal tissues and glioblastoma

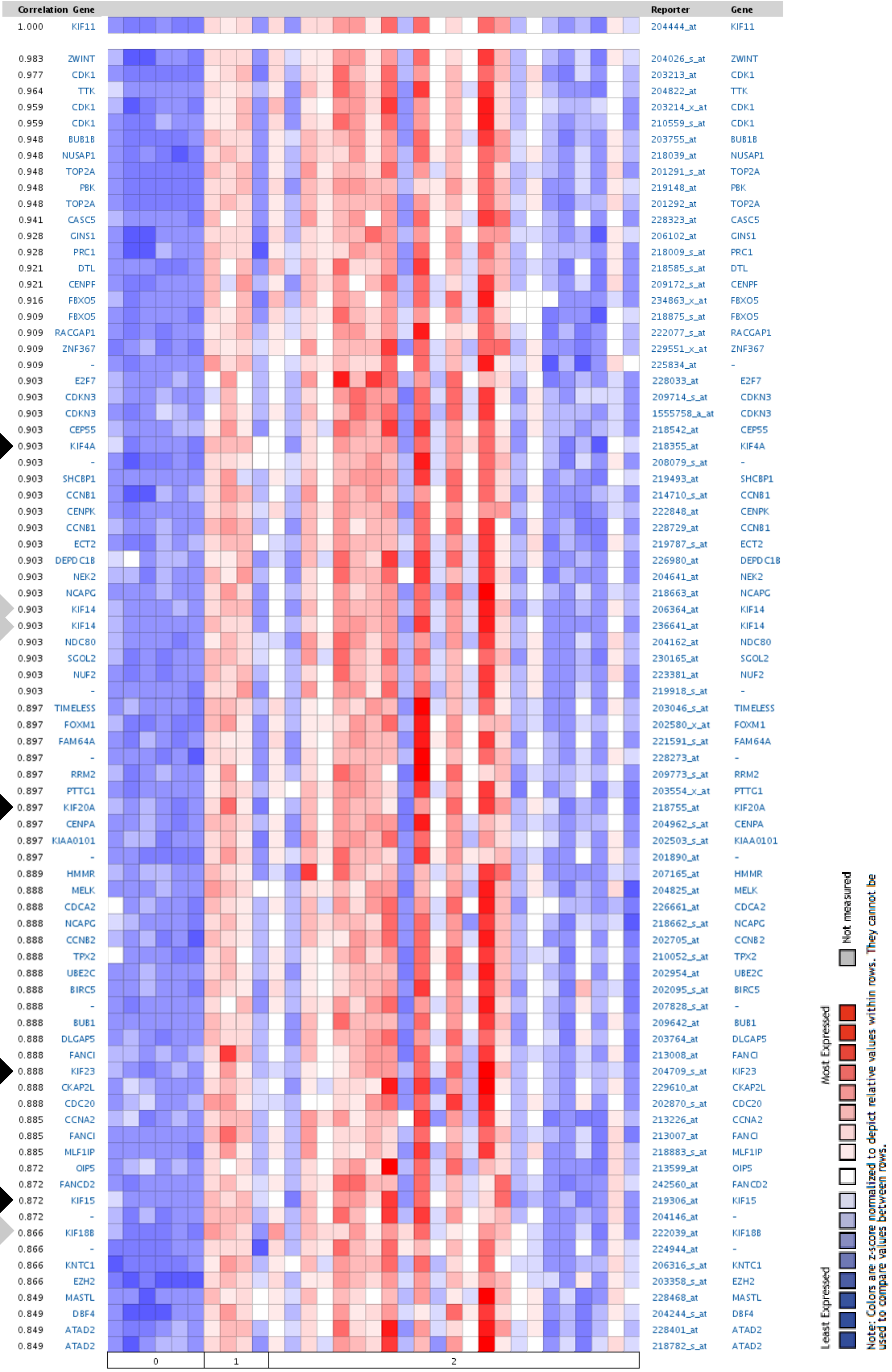


Mklp2 protein is expressed with varying intensities in endothelial cells (black arrows) in several normal tissues: (a) heart, (b) placenta, (c) endometrium and oral mucosa (d). In glioblastoma (e, f) a diffuse background signal is found in all cells, but several tumor capillaries can be recognized by stronger Mklp2 expression in the endothelium (black arrows). (g) Endothelial cells in tumor capillaries can be identified by in situ hybridization using a PECAM1 probe (in red). (h) KIF20A transcripts exhibit a very similar expression pattern in tumor capillaries in glioblastoma (in red, arrows point to endothelial cells). Serial sections are shown (a-f: bar = 30 μm; g, h: bar = 30 μm).

Figure S5

Co-expression of VEGF-induced kinesins in brain tumors

a



Correlation	Gene	Reporter	Gene
1.000	KIF11	204444_at	KIF11
0.983	ZWINT	204026_s_at	ZWINT
0.977	CDK1	203213_at	CDK1
0.964	TTK	204822_at	TTK
0.959	CDK1	203214_x_at	CDK1
0.959	CDK1	210559_s_at	CDK1
0.948	BUB1B	203755_at	BUB1B
0.948	NUSAP1	218039_at	NUSAP1
0.948	TOP2A	201291_s_at	TOP2A
0.948	PBK	219148_at	PBK
0.948	TOP2A	201292_at	TOP2A
0.941	CASC5	228323_at	CASC5
0.928	GINS1	206102_at	GINS1
0.928	PRC1	218009_s_at	PRC1
0.921	DTL	218585_s_at	DTL
0.921	CENPF	209172_s_at	CENPF
0.916	FBXO5	234863_x_at	FBXO5
0.909	FBXO5	218875_s_at	FBXO5
0.909	RACGAP1	222077_s_at	RACGAP1
0.909	ZNF367	229551_x_at	ZNF367
0.909	-	225834_at	-
0.903	E2F7	228033_at	E2F7
0.903	CDKN3	209714_s_at	CDKN3
0.903	CDKN3	1555758_a_at	CDKN3
0.903	CEP55	218542_at	CEP55
0.903	KIF4A	218355_at	KIF4A
0.903	-	208079_s_at	-
0.903	SHCBP1	219493_at	SHCBP1
0.903	CCNB1	214710_s_at	CCNB1
0.903	CENPK	222848_at	CENPK
0.903	CCNB1	228729_at	CCNB1
0.903	ECT2	219787_s_at	ECT2
0.903	DEPDC1B	226980_at	DEPDC1B
0.903	NEK2	204641_at	NEK2
0.903	NCAPG	218663_at	NCAPG
0.903	KIF14	206364_at	KIF14
0.903	KIF14	236641_at	KIF14
0.903	NDC80	204162_at	NDC80
0.903	SGOL2	230165_at	SGOL2
0.903	NUF2	223381_at	NUF2
0.903	-	219918_s_at	-
0.897	TIMELESS	203046_s_at	TIMELESS
0.897	FOXM1	202580_x_at	FOXM1
0.897	FAM64A	221591_s_at	FAM64A
0.897	-	228273_at	-
0.897	RRM2	209773_s_at	RRM2
0.897	PTTG1	203554_x_at	PTTG1
0.897	KIF20A	218755_at	KIF20A
0.897	CENPA	204962_s_at	CENPA
0.897	KIAA0101	202503_s_at	KIAA0101
0.897	-	201890_at	-
0.889	HMMR	207165_at	HMMR
0.888	MELK	204825_at	MELK
0.888	CDCA2	226661_at	CDCA2
0.888	NCAPG	218662_s_at	NCAPG
0.888	CCNB2	202705_at	CCNB2
0.888	TPX2	210052_s_at	TPX2
0.888	UBE2C	202954_at	UBE2C
0.888	BIRC5	202095_s_at	BIRC5
0.888	-	207828_s_at	-
0.888	BUB1	209642_at	BUB1
0.888	DLGAP5	203764_at	DLGAP5
0.888	FANCI	213008_at	FANCI
0.888	KIF23	204709_s_at	KIF23
0.888	CKAP2L	229610_at	CKAP2L
0.888	CDC20	202870_s_at	CDC20
0.885	CCNA2	213226_at	CCNA2
0.885	FANCI	213007_at	FANCI
0.885	MLF1IP	218883_s_at	MLF1IP
0.872	OIP5	213599_at	OIP5
0.872	FANCD2	242560_at	FANCD2
0.872	KIF15	219306_at	KIF15
0.872	-	204146_at	-
0.866	KIF18B	222039_at	KIF18B
0.866	-	224944_at	-
0.866	KNTC1	206316_s_at	KNTC1
0.866	EZH2	203358_s_at	EZH2
0.849	MASTL	228468_at	MASTL
0.849	DBF4	204244_s_at	DBF4
0.849	ATAD2	228401_at	ATAD2
0.849	ATAD2	218782_s_at	ATAD2

Note: Colors are z-score normalized to depict relative values within rows. They cannot be used to compare values between rows.

Figure S5 (cont'd)

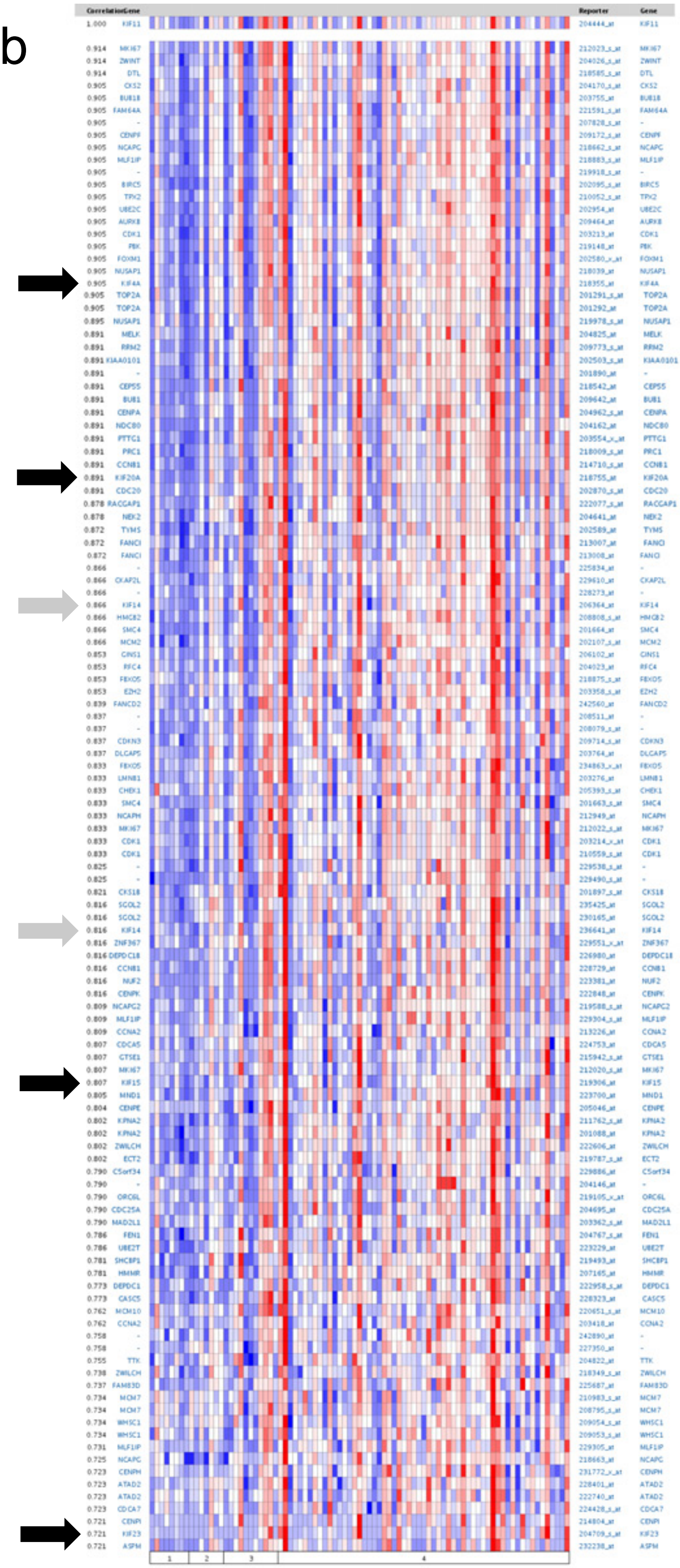
Co-expression of VEGF-induced kinesins in brain tumors

(a) French_brain study. Note that all kinesins induced by VEGF are highly co-expressed (KIF11 as a bait), with correlation values ranging from 0.903 for KIF4A to 0.872 for KIF15 (black arrows). Other kinesins such as KIF14 and KIF18B also show co-regulation (grey arrows). Legend: 0: Normal brain (n=6), 1: Anaplastic Oligoastrocytoma (n=4), 2: Anaplastic Oligodendroglioma (n=23).

Figure S5 (cont'd)

Co-expression of VEGF-induced kinesins in brain tumors

b

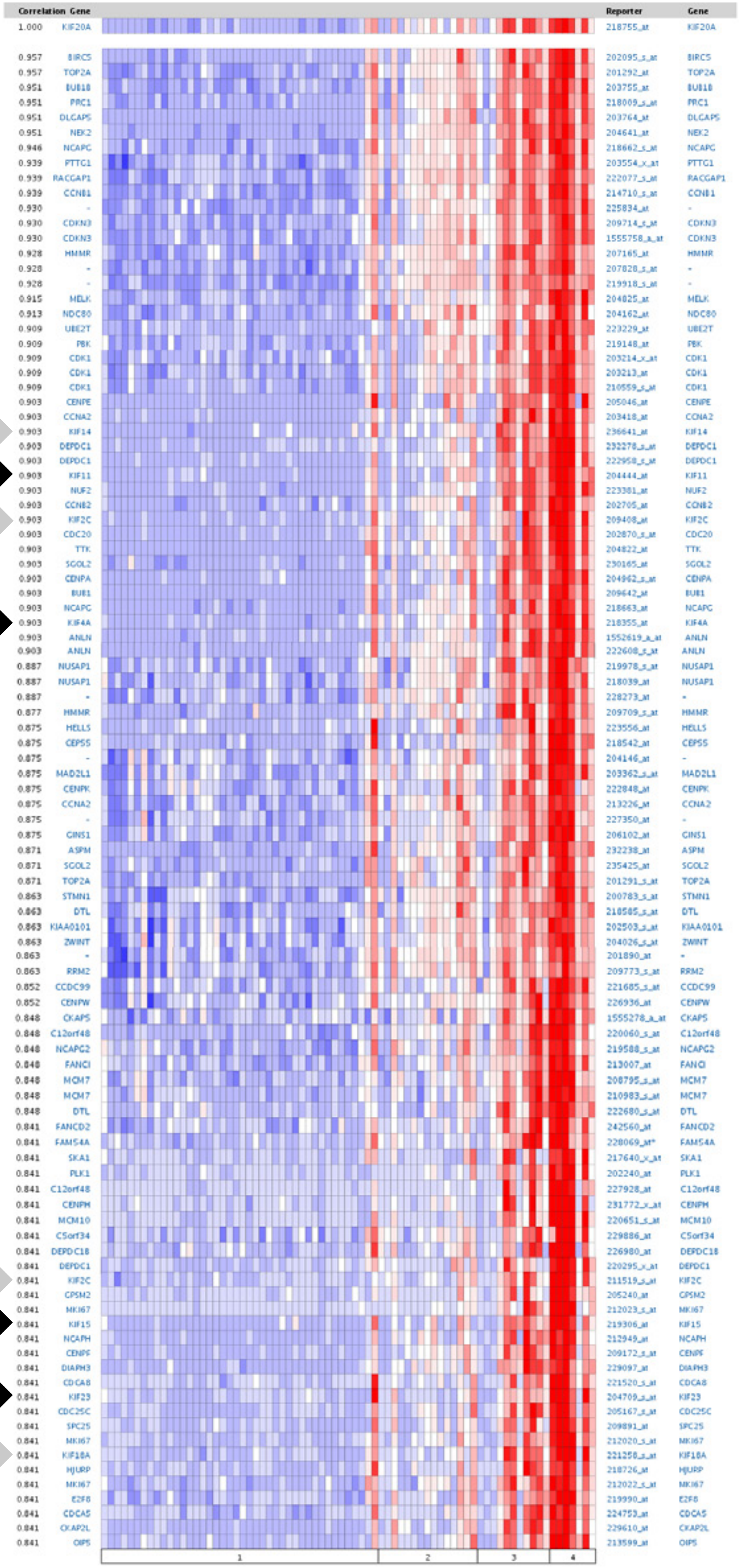


Correlation	Gene	Reporter	Gene
1.000	KIF11	204444_at	KIF11
0.914	MKI67	212023_s_at	MKI67
0.914	ZWINT	204026_s_at	ZWINT
0.914	DTL	218585_s_at	DTL
0.905	CKS2	204170_s_at	CKS2
0.905	BUB1B	203755_at	BUB1B
0.905	FAM64A	221591_s_at	FAM64A
0.905	-	207828_s_at	-
0.905	CENPF	209172_s_at	CENPF
0.905	NCAPG	218662_s_at	NCAPG
0.905	MLF1IP	218883_s_at	MLF1IP
0.905	-	219918_s_at	-
0.905	BIRC5	202095_s_at	BIRC5
0.905	TPX2	210052_s_at	TPX2
0.905	UBE2C	202954_at	UBE2C
0.905	AURKB	209464_at	AURKB
0.905	CDK1	203213_at	CDK1
0.905	PBK	219148_at	PBK
0.905	FOXM1	202580_x_at	FOXM1
0.905	NUSAP1	218039_at	NUSAP1
0.905	KIF4A	218355_at	KIF4A
0.905	TOP2A	201291_s_at	TOP2A
0.905	TOP2A	201292_at	TOP2A
0.895	NUSAP1	219978_s_at	NUSAP1
0.891	MELK	204825_at	MELK
0.891	RRM2	209773_s_at	RRM2
0.891	KIAA0101	202503_s_at	KIAA0101
0.891	-	201890_at	-
0.891	CEP55	218542_at	CEP55
0.891	BUB1	209642_at	BUB1
0.891	CENPA	204962_s_at	CENPA
0.891	NDC80	204162_at	NDC80
0.891	PTTG1	203554_x_at	PTTG1
0.891	PRC1	218009_s_at	PRC1
0.891	CCNB1	214710_s_at	CCNB1
0.891	KIF20A	218755_at	KIF20A
0.891	CDC20	202870_s_at	CDC20
0.878	RACGAP1	222077_s_at	RACGAP1
0.878	NEK2	204641_at	NEK2
0.872	TYMS	202589_at	TYMS
0.872	FANCI	213007_at	FANCI
0.872	FANCI	213008_at	FANCI
0.866	-	225834_at	-
0.866	CKAP2L	229610_at	CKAP2L
0.866	-	228273_at	-
0.866	KIF14	206364_at	KIF14
0.866	HMGB2	208808_s_at	HMGB2
0.866	SMC4	201664_at	SMC4
0.866	MCM2	202107_s_at	MCM2
0.853	GINS1	206102_at	GINS1
0.853	RFC4	204023_at	RFC4
0.853	FBXO5	218875_s_at	FBXO5
0.853	EZH2	203358_s_at	EZH2
0.839	FANCD2	242560_at	FANCD2
0.837	-	208511_at	-
0.837	-	208079_s_at	-
0.837	CDKN3	209714_s_at	CDKN3
0.837	DLGAP5	203764_at	DLGAP5
0.833	FBXO5	234863_x_at	FBXO5
0.833	LMNB1	203276_at	LMNB1
0.833	CHEK1	205393_s_at	CHEK1
0.833	SMC4	201663_s_at	SMC4
0.833	NCAPH	212949_at	NCAPH
0.833	MKI67	212022_s_at	MKI67
0.833	CDK1	203214_x_at	CDK1
0.833	CDK1	210559_s_at	CDK1
0.825	-	229538_s_at	-
0.825	-	229490_s_at	-
0.821	CKS1B	201897_s_at	CKS1B
0.816	SGOL2	235425_at	SGOL2
0.816	SGOL2	230165_at	SGOL2
0.816	KIF14	236641_at	KIF14
0.816	ZNF367	229551_x_at	ZNF367
0.816	DEPDC1B	226980_at	DEPDC1B
0.816	CCNB1	228729_at	CCNB1
0.816	NUF2	223381_at	NUF2
0.816	CENPK	222848_at	CENPK
0.809	NCAPG2	219588_s_at	NCAPG2
0.809	MLF1IP	229304_s_at	MLF1IP
0.809	CCNA2	213226_at	CCNA2
0.807	CDCA5	224753_at	CDCA5
0.807	GTSE1	215942_s_at	GTSE1
0.807	MKI67	212020_s_at	MKI67
0.807	KIF15	219306_at	KIF15
0.805	MND1	223700_at	MND1
0.804	CENPE	205046_at	CENPE
0.802	KPNA2	211762_s_at	KPNA2
0.802	KPNA2	201088_at	KPNA2
0.802	ZWILCH	222606_at	ZWILCH
0.802	ECT2	219787_s_at	ECT2
0.790	C5orf34	229886_at	C5orf34
0.790	-	204146_at	-
0.790	ORC6L	219105_x_at	ORC6L
0.790	CDC25A	204695_at	CDC25A
0.790	MAD2L1	203362_s_at	MAD2L1
0.786	FEN1	204767_s_at	FEN1
0.786	UBE2T	223229_at	UBE2T
0.781	SHCBP1	219493_at	SHCBP1
0.781	HMMR	207165_at	HMMR
0.773	DEPDC1	222958_s_at	DEPDC1
0.773	CASC5	228323_at	CASC5
0.762	MCM10	220651_s_at	MCM10
0.762	CCNA2	203418_at	CCNA2
0.758	-	242890_at	-
0.758	-	227350_at	-
0.755	TTK	204822_at	TTK
0.738	ZWILCH	218349_s_at	ZWILCH
0.737	FAM83D	225687_at	FAM83D
0.734	MCM7	210983_s_at	MCM7
0.734	MCM7	208795_s_at	MCM7
0.734	WHSC1	209054_s_at	WHSC1
0.734	WHSC1	209053_s_at	WHSC1
0.731	MLF1IP	229305_at	MLF1IP
0.725	NCAPG	218663_at	NCAPG
0.723	CENPH	231772_x_at	CENPH
0.723	ATAD2	228401_at	ATAD2
0.723	ATAD2	222740_at	ATAD2
0.723	CDCA7	224428_s_at	CDCA7
0.721	CENPI	214804_at	CENPI
0.721	KIF23	204709_s_at	KIF23
0.721	ASPM	232238_at	ASPM

(b) Freje_brain study: Correlation ranges from 0.905 for KIF4A to 0.71 for KIF23 (black arrows). Again, KIF14 was also co-regulated (grey arrows). Legend: 1: Anaplastic Astrocytoma (n=8), 2: Anaplastic Oligoastrocytoma (n=7), 3: Anaplastic Oligodendroglioma (n=11), 4: Glioblastoma (n=59).

Figure S6

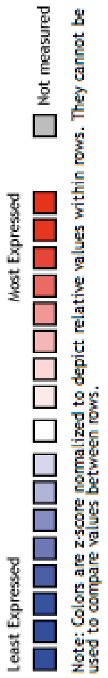
Expression of VEGF-induced kinesins depends on the vascularization status in hepatocellular carcinoma (HCC)



Correlation	Gene	Reporter	Gene
1.000	KIF20A	218755_at	KIF20A
0.957	BIRC5	202095_s_at	BIRC5
0.957	TOP2A	201292_at	TOP2A
0.951	BUB1B	203755_at	BUB1B
0.951	PRC1	218009_s_at	PRC1
0.951	DLGAP5	203764_at	DLGAP5
0.951	NEK2	204641_at	NEK2
0.946	NCAPG	218662_s_at	NCAPG
0.939	PTTG1	203554_x_at	PTTG1
0.939	RACGAP1	222077_s_at	RACGAP1
0.939	CCNB1	214710_s_at	CCNB1
0.930	-	225834_at	-
0.930	CDKN3	209714_s_at	CDKN3
0.930	CDKN3	1555758_a_at	CDKN3
0.928	HMMR	207165_at	HMMR
0.928	-	207828_s_at	-
0.928	-	219918_s_at	-
0.915	MELK	204825_at	MELK
0.913	NDC80	204162_at	NDC80
0.909	UBE2T	223229_at	UBE2T
0.909	PBK	219148_at	PBK
0.909	CDK1	203214_x_at	CDK1
0.909	CDK1	203213_at	CDK1
0.909	CDK1	210559_s_at	CDK1
0.903	CENPE	205046_at	CENPE
0.903	CCNA2	203418_at	CCNA2
0.903	KIF14	236641_at	KIF14
0.903	DEPDC1	232278_s_at	DEPDC1
0.903	DEPDC1	222958_s_at	DEPDC1
0.903	KIF11	204444_at	KIF11
0.903	NUF2	223381_at	NUF2
0.903	CCNB2	202705_at	CCNB2
0.903	KIF2C	209408_at	KIF2C
0.903	CDC20	202870_s_at	CDC20
0.903	TTK	204822_at	TTK
0.903	SGOL2	230165_at	SGOL2
0.903	CENPA	204962_s_at	CENPA
0.903	BUB1	209642_at	BUB1
0.903	NCAPG	218663_at	NCAPG
0.903	KIF4A	218355_at	KIF4A
0.903	ANLN	1552619_a_at	ANLN
0.903	ANLN	222608_s_at	ANLN
0.887	NUSAP1	219978_s_at	NUSAP1
0.887	NUSAP1	218039_at	NUSAP1
0.887	-	228273_at	-
0.877	HMMR	209709_s_at	HMMR
0.875	HELLS	223556_at	HELLS
0.875	CEP55	218542_at	CEP55
0.875	-	204146_at	-
0.875	MAD2L1	203362_s_at	MAD2L1
0.875	CENPK	222848_at	CENPK
0.875	CCNA2	213226_at	CCNA2
0.875	-	227350_at	-
0.875	GINS1	206102_at	GINS1
0.871	ASPM	232238_at	ASPM
0.871	SGOL2	235425_at	SGOL2
0.871	TOP2A	201291_s_at	TOP2A
0.863	STMN1	200783_s_at	STMN1
0.863	DTL	218585_s_at	DTL
0.863	KIAA0101	202503_s_at	KIAA0101
0.863	ZWINT	204026_s_at	ZWINT
0.863	-	201890_at	-
0.863	RRM2	209773_s_at	RRM2
0.852	CCDC99	221685_s_at	CCDC99
0.852	CENPW	226936_at	CENPW
0.848	CKAP5	1555278_a_at	CKAP5
0.848	C12orf48	220060_s_at	C12orf48
0.848	NCAPG2	219588_s_at	NCAPG2
0.848	FANCI	213007_at	FANCI
0.848	MCM7	208795_s_at	MCM7
0.848	MCM7	210983_s_at	MCM7
0.848	DTL	222680_s_at	DTL
0.841	FANCD2	242560_at	FANCD2
0.841	FAM54A	228069_at*	FAM54A
0.841	SKA1	217640_x_at	SKA1
0.841	PLK1	202240_at	PLK1
0.841	C12orf48	227928_at	C12orf48
0.841	CENPM	231772_x_at	CENPM
0.841	MCM10	220651_s_at	MCM10
0.841	C5orf34	229886_at	C5orf34
0.841	DEPDC1B	226980_at	DEPDC1B
0.841	DEPDC1	220295_x_at	DEPDC1
0.841	KIF2C	211519_s_at	KIF2C
0.841	GPSM2	205240_at	GPSM2
0.841	MKI67	212023_s_at	MKI67
0.841	KIF15	219306_at	KIF15
0.841	NCAPH	212949_at	NCAPH
0.841	CENPF	209172_s_at	CENPF
0.841	DIAPH3	229097_at	DIAPH3
0.841	CDCA8	221520_s_at	CDCA8
0.841	KIF23	204709_s_at	KIF23
0.841	CDC25C	205167_s_at	CDC25C
0.841	SPC25	209891_at	SPC25
0.841	MKI67	212020_s_at	MKI67
0.841	KIF18A	221258_s_at	KIF18A
0.841	HJURP	218726_at	HJURP
0.841	MKI67	212022_s_at	MKI67
0.841	E2F8	219990_at	E2F8
0.841	CDCA5	224753_at	CDCA5
0.841	CKAP2L	229610_at	CKAP2L
0.841	OIP5	213599_at	OIP5

KIF11 (0.903), KIF4A (0.903) and KIF15 (0.841) expression correlates with KIF20A expression (data from the Wurmbach_liver study). Notably, these kinesins are over expressed in highly vascularized HCC samples, compared to controls.

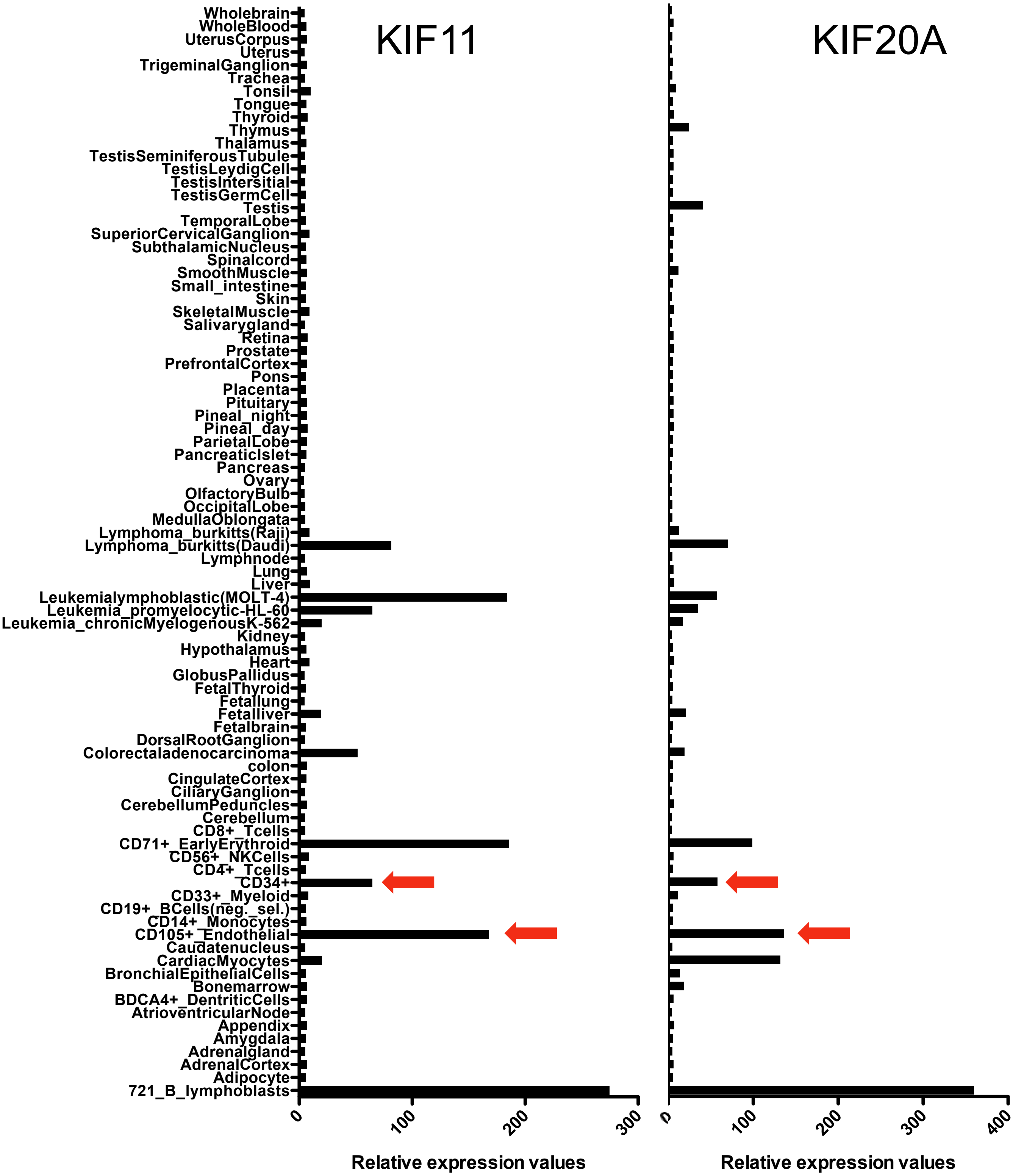
Legend: 0: normal liver (n=42), 1: No visible vascular invasion (n=15), 2: microscopic vascular invasion (n=11); macroscopic vascular invasion (n=7).



Note: Colors are z-score normalized to depict relative values within rows. They cannot be used to compare values between rows.

Figure S7

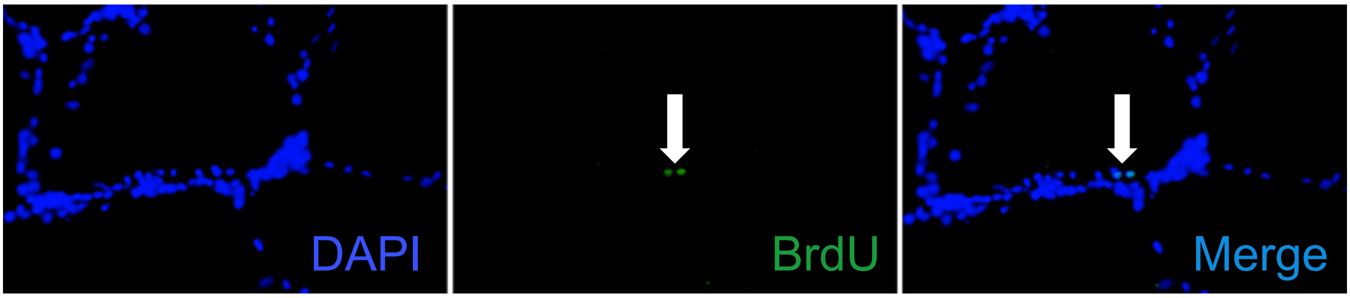
Relative expression levels of KIF11 and KIF20A transcripts in 84 human tissus and cell lines



High levels of KIF11 and KIF20A transcripts were essentially found in malignant lymphoma cells and CD105+ / CD34+ endothelial cells (red arrows). There is a high correlation of KIF11 and KIF20A expression levels throughout all tissues (Spearman r=0.84, P<0.0001). Data were obtained using the BioGPS project.

Figure S8

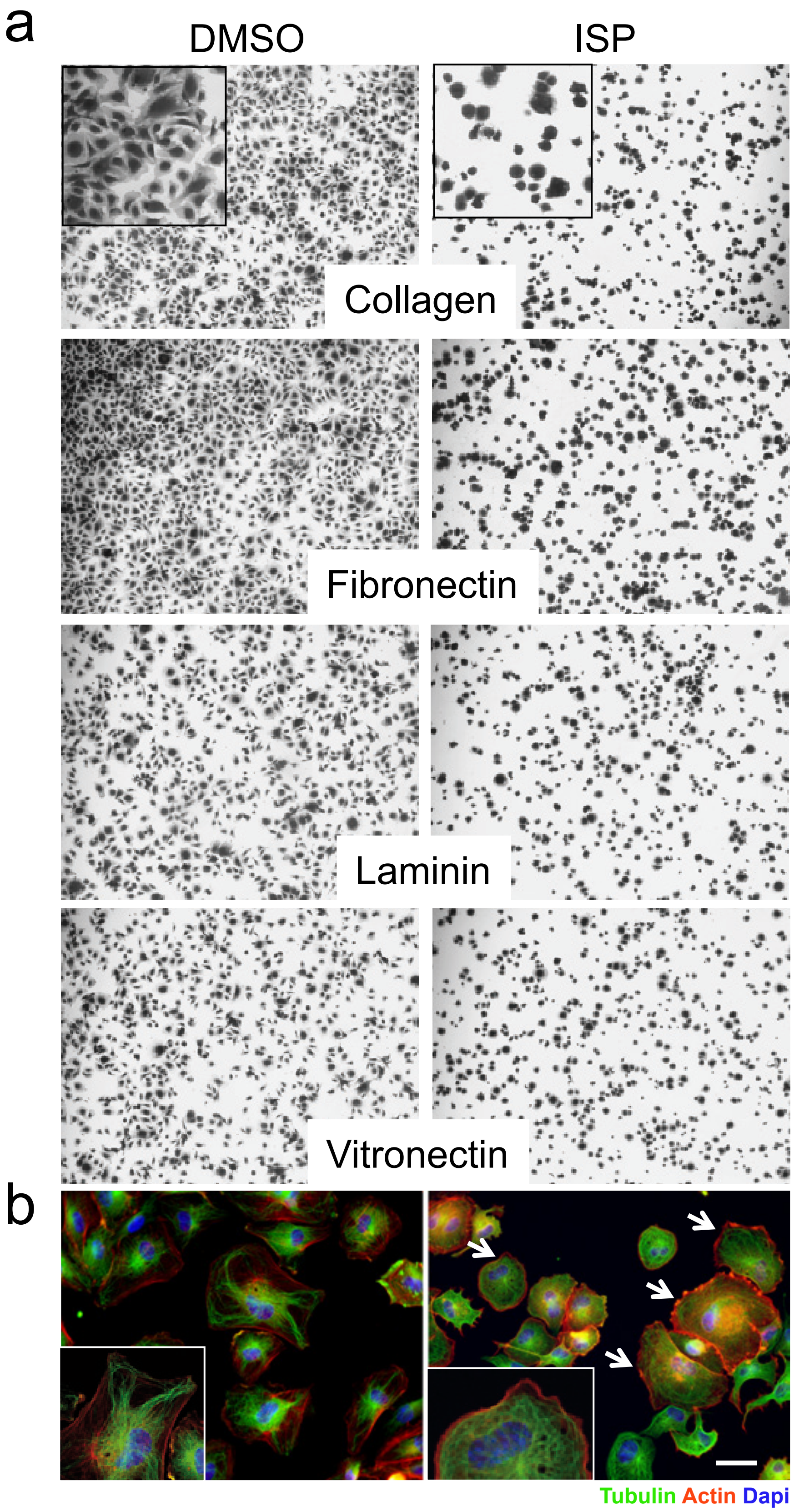
Cell proliferation is a rare occurrence in the tubulogenesis assay

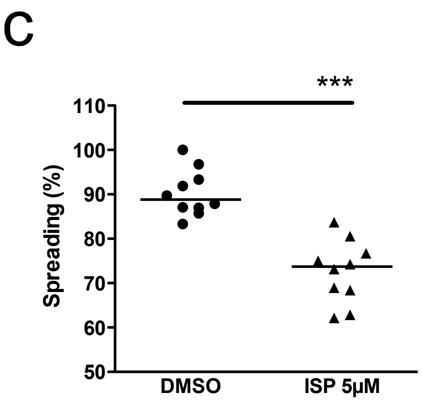


To exclude that endothelial cell proliferation occurs in our assay conditions, cells were incubated with BrdU and allowed to form tubes on matrigel for 14h30. Anti-BrdU antibody (in green) rarely detected BrdU signal in cells, one example is shown (arrows).

Figure S9

Eg5 inhibition impairs endothelial cell adhesion and spreading

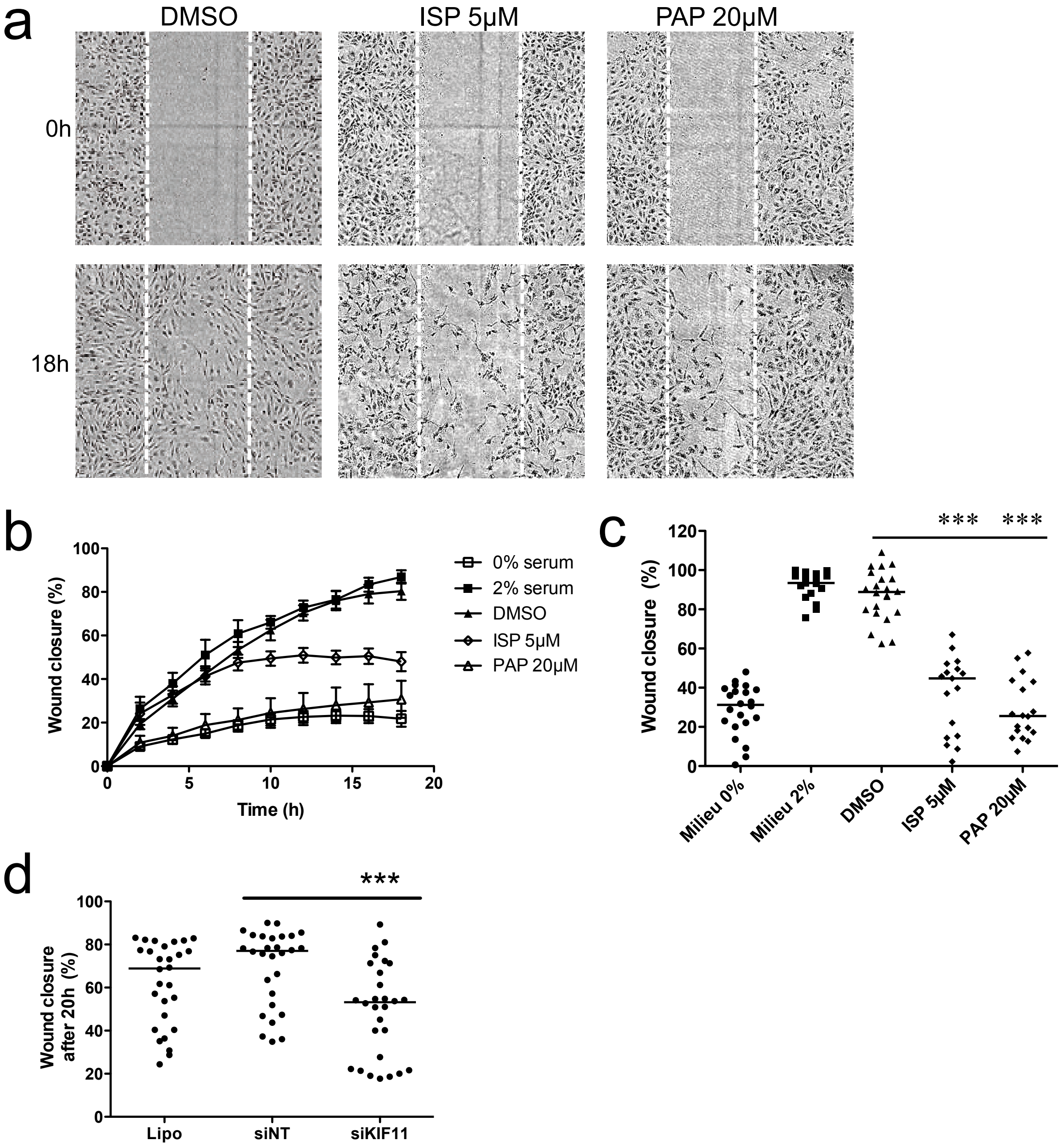




a) Inhibition of Eg5 by ispinesib reduces cell adhesion of endothelial cells plated on indicated matrix proteins b) Reorganization of the actin cytoskeleton: appearance of cortical actin and strong reduction of stress fibers (arrows and insert; bar in b=50μM) c) Cell spreading is reduced significantly after Eg5 blockade (p>0.0001).

Figure S10

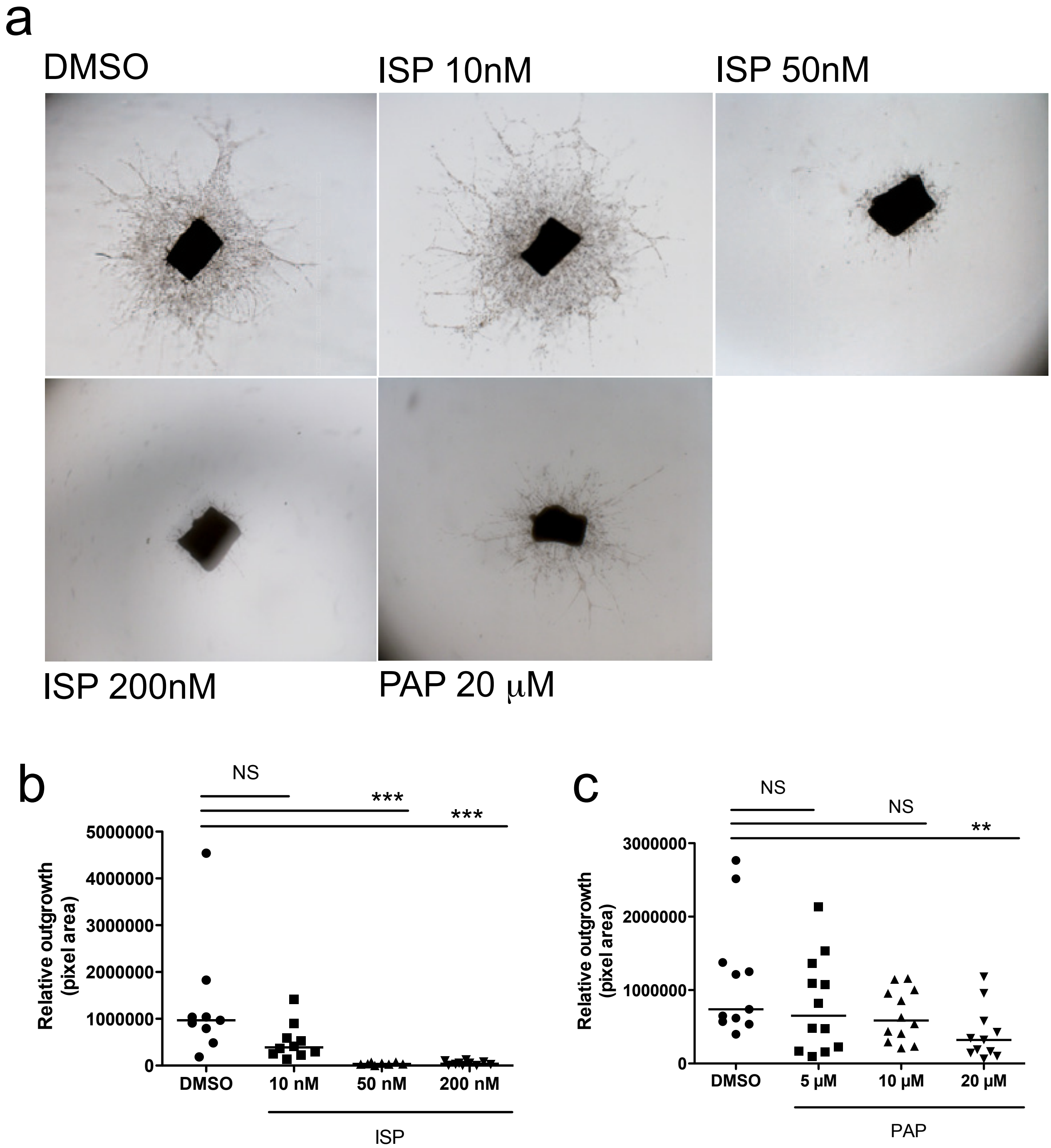
Kinesin inhibition impairs migration of HUVECs



a) Representative pictures of HUVEC migration treated with indicated drugs at 0h and 18h after wounding. b) Quantification of cell migration into the wounded area over time. Percentage is indicated as mean+/- SEM. Note strong inhibition of EC migration by ISP and PAP. c) For statistical analysis, four experiments were pooled and percentages of wound closure at the last time point were compared. ISP and PAP significantly block EC migration ($P<0.0001$). d) siRNA-mediated knock down of KIF11 also led to a significant reduction of endothelial cell migration ($P=0.0007$).

Figure S11

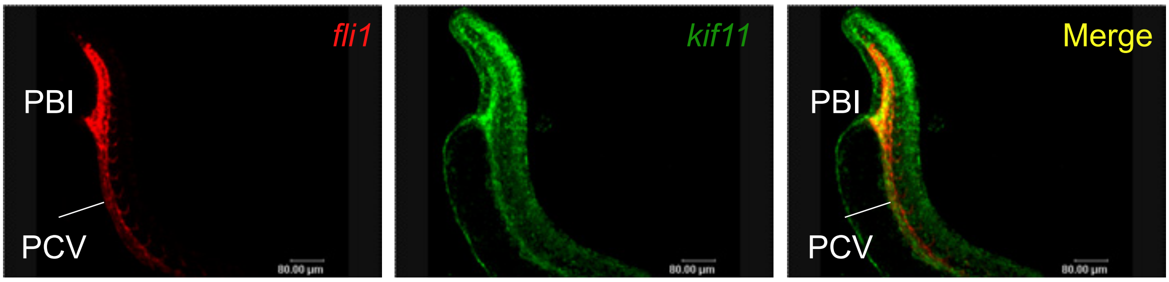
Eg5 and Mklp2 blockade inhibits angiogenic sprouting in the mouse aortic ring assay



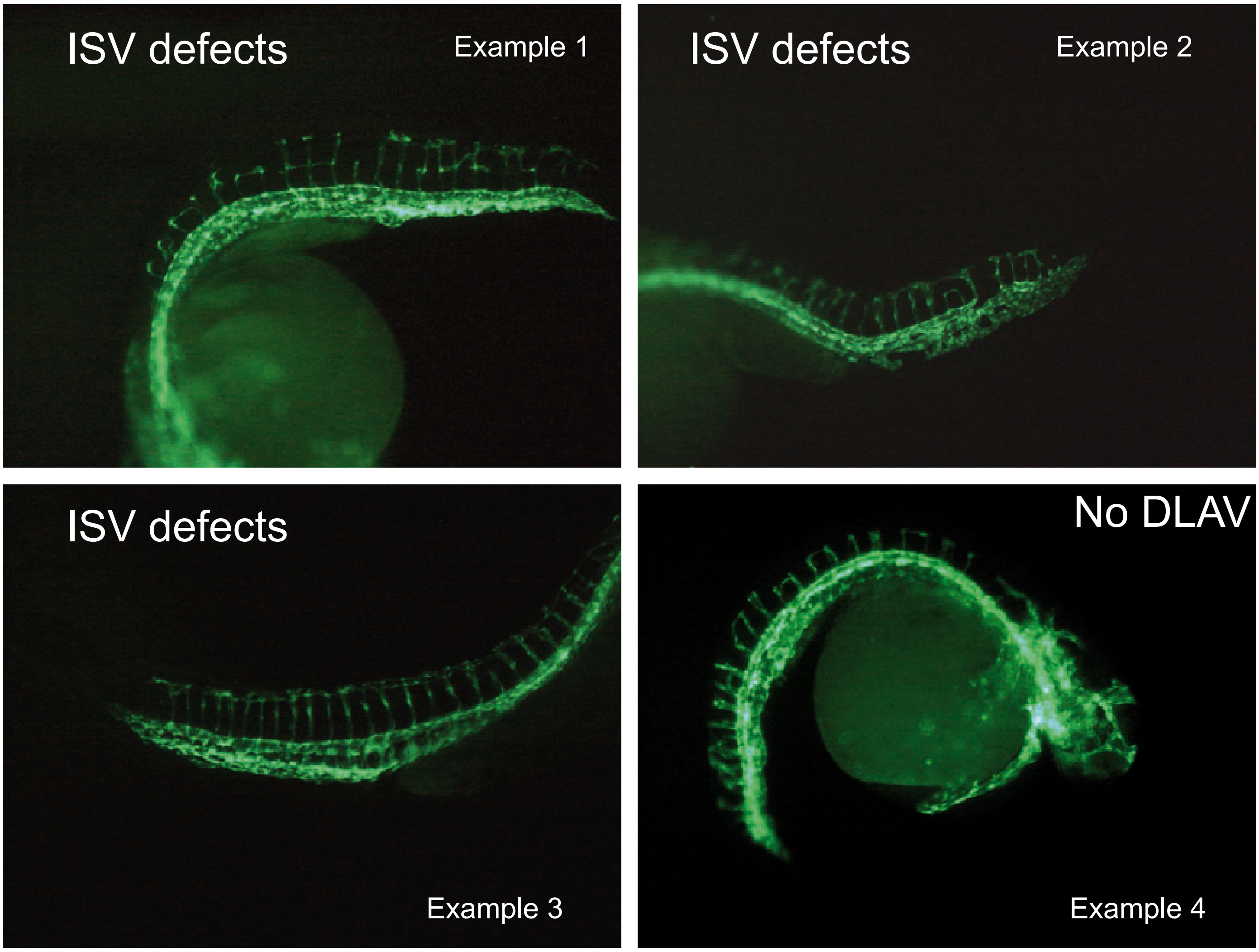
a) Representative pictures of mouse aortic rings in culture after 8 days. b) Quantification of cellular outgrowth around the aortic rings revealed significant reduction at doses around 50 nm for ispinesib and 20 μM for paprotrain.

Figure S12

a Fluorescence *in situ* hybridization; 24 hpf



b Vascular defects in *kif11* Tg(kdrl:EGFP)^{s843} morphants (48 hpf)



a) Zebrafish embryos at 24 hpf were hybridized with probes for the vascular/hematopoietic reporter transcript *fli1* (in red) or *kif11* mRNA (in green). Note that co-localisation occurs in the PBI and PCV. b) *kif11* knock-down embryos exhibited variable degrees of vascular malformation, mainly in the ISVs or the DLAV. Shown are four embryos with typical defects. Magnification x115.