

Appendix

The mutant p53-ID4 complex controls VEGFA isoforms production by recruiting lncRNA MALAT1

Table of content

p. 2-4	Appendix Table S1	List of mRNAs that resulted bound by ID4 protein by RIP-chip analysis in MDA-MB-468 cells
p.5	Appendix Table S2	Functional classification of genes whose transcripts were found to interact with ID4 protein through RIP-chip analysis in MDA-MB-468 cells
p.6-7	Appendix Table S3	Genes comprised in the 16-VEGFA signature used for GSEA and Kaplan-Meier analyses
p.8	Appendix Table S4	Characteristics of patients with basal-like breast cancer considered for GSEA and Kaplan-Meier analyses
p.9-11	Appendix Table S5	Oligonucleotides used in PCR analyses
p.12	Appendix Figure S1	
p.13	Appendix Figure S2	
p.14	Appendix Figure S3	
p.15	Appendix Figure Legends	

Appendix Table S1. List of mRNAs that resulted bound by ID4 protein by RIP-chip analysis in MDA-MB-468 cells. Ribonucleoprotein immunoprecipitation (RIP) was performed using 2 antibodies recognizing ID4 protein (H-70 from Santa Cruz and 49261 from Abcam); microarray analysis was performed on Affymetrix platform (Human Gene 1.0 ST arrays). Transcripts that were enriched >2.5-fold with both antibodies are reported.

Fold1 (H70)	Fold2 (Abcam)	Gene Symbol	To	Gene Name
2,93	2,64	ACTN4	786096	actinin, alpha 4
5,62	4,69	ADIPOR1	823710	adiponectin receptor 1
2,86	2,88	AKR1B1	782528	aldo-keto reductase family 1, member B1 (aldose reductase)
2,74	3,37	ALG8	782511	asparagine-linked glycosylation 8, alpha-1,3-glycosyltransferase homolog (S. cerevisiae)
2,75	2,83	ALG9	795413	asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae)
2,88	2,92	ANXA2	787053	annexin A2 pseudogene 3; annexin A2; annexin A2 pseudogene 1
2,88	3,11	ANXA3	812167	annexin A3
3,17	3,38	APP	810642	amyloid beta (A4) precursor protein
3,14	5,01	ATF2	796169	activating transcription factor 2
2,88	3,35	ATP6V0E1	819267	ATPase, H ⁺ transporting, lysosomal 9kDa, V0 subunit e1
4,11	3,42	AURKA	782105	aurora kinase A; aurora kinase A pseudogene 1
2,88	3,11	BAT1	810340	HLA-B associated transcript 1
3,74	2,58	BBOX1	813438	butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) 1
3,71	2,95	BTF3L4	812346	basic transcription factor 3-like 4; similar to hCG2008008
2,78	2,86	CALM3	776019	calmodulin 3 (phosphorylase kinase, delta); calmodulin 2 (phosphorylase kinase, delta); calmodulin 1 (phosphorylase kinase, delta)
4,12	2,97	CAPNS1	777192	calpain, small subunit 1
4,16	4,43	CASP14	826235	caspase 14, apoptosis-related cysteine peptidase
2,65	2,67	CCDC6	799583	coiled-coil domain containing 6
2,72	2,55	CCNI	825102	cyclin I
3,01	2,71	CD164	773106	CD164 molecule, sialomucin
3,86	3,43	CD24	805559	CD24 molecule; CD24 molecule-like 4
3,77	3,54	CD81	772612	CD81 molecule
2,78	2,58	CD9	813468	CD9 molecule
2,54	2,65	CDC123	825411	cell division cycle 123 homolog (S. cerevisiae)
2,95	2,75	CDC37	795814	cell division cycle 37 homolog (S. cerevisiae)
10,20	6,64	CDR1	821476	cerebellar degeneration-related protein 1, 34kDa
4,75	2,68	CHP	779833	calcium binding protein P22
2,72	3,47	CLINT1	790599	clathrin interactor 1
2,68	3,82	CNOT7	780576	CCR4-NOT transcription complex, subunit 7
3,55	3,20	COPS6	799250	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)
2,87	2,95	CSNK1D	814527	casein kinase 1, delta
2,67	4,46	CSNK2A1P	799522	casein kinase 2, alpha 1 polypeptide pseudogene; casein kinase 2, alpha 1 polypeptide
3,60	3,24	CSNK2B	818087	lymphocyte antigen 6 complex, locus G5B; casein kinase 2, beta polypeptide
2,64	3,24	DAD1	775593	defender against cell death 1
2,52	3,63	DDX17	775919	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
4,40	3,33	DHCR24	785925	24-dehydrocholesterol reductase
3,06	2,63	DHCR7	777080	7-dehydrocholesterol reductase
3,28	4,61	DHFR	812353	dihydrofolate reductase
3,42	4,24	DNAJC19	793565	similar to translocase of the inner mitochondrial membrane 14; DnaJ (Hsp40) homolog, subfamily C, member 19
5,36	3,76	ECH1	822387	enoyl Coenzyme A hydratase 1, peroxisomal
3,06	3,41	EGFR	816368	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)
2,98	3,19	EI24	806893	etoposide induced 2.4 mRNA
2,82	2,81	EIF2S3	776090	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
3,21	4,27	EIF4EBP2	792823	eukaryotic translation initiation factor 4E binding protein 2
3,02	3,35	EIF5A	773179	eukaryotic translation initiation factor 5A; eukaryotic translation initiation factor 5A-like 1
3,70	3,36	ELOVL1	818641	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1
3,27	2,78	EMP2	773898	epithelial membrane protein 2
6,34	3,88	ENO1	783039	enolase 1, (alpha)
2,98	2,66	EPR1	797117	effector cell peptidase receptor 1 (non-protein coding)
3,32	2,54	EPS15	818063	epidermal growth factor receptor pathway substrate 15
2,63	2,66	FBXO18	789822	F-box protein, helicase, 18
4,66	3,60	GABARAP	815063	GABA(A) receptor-associated protein
3,20	2,61	GATAD2A	793345	GATA zinc finger domain containing 2A
3,10	2,55	GDI1	809511	GDP dissociation inhibitor 1

2,54	2,73	GDI2	787514	GDP dissociation inhibitor 2
2,96	2,62	GPSN2		TECR trans-2,3-enoyl-CoA reductase
3,01	2,77	HCCS	798837	holocytochrome c synthase (cytochrome c heme-lyase)
2,99	3,13	HDAC1	775085	histone deacetylase 1
2,85	2,50	HDLBP	810749	high density lipoprotein binding protein
8,42	7,16	HIATL1	800934	hippocampus abundant transcript-like 1
3,52	2,51	HIST1H2BH	821062	histone cluster 1, H2bh
2,62	3,08	HIST1H4L	784692	histone cluster 1, H4l
2,61	2,96	HIST2H2AB	820180	histone cluster 2, H2ab
6,08	4,12	HIST2H2AC	814981	histone cluster 2, H2ac
2,53	2,54	HNRPF		
4,53	4,70	HRB		
2,51	2,89	HSP90AB1	807045	heat shock protein 90kDa alpha (cytosolic), class B member 1
3,04	2,99	ILF2	775229	interleukin enhancer binding factor 2, 45kDa
2,75	3,15	ILF3	810501	interleukin enhancer binding factor 3, 90kDa
4,37	3,11	IPO9	826586	importin 9
4,33	3,31	KDEL2	795959	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
5,86	3,00	KLK5	783622	kallikrein-related peptidase 5
4,09	2,90	KRT18	819470	keratin 18; keratin 18 pseudogene 26; keratin 18 pseudogene 19
2,65	2,59	KRT5	808801	keratin 5
3,54	2,71	KRT8	796258	keratin 8 pseudogene 9; similar to keratin 8; keratin 8
3,93	2,61	LAMP1	773945	lysosomal-associated membrane protein 1
2,75	4,73	LAPTM4A	808988	lysosomal protein transmembrane 4 alpha
3,24	2,61	LOC729843		
2,81	3,57	LRRC37A4	821668	leucine rich repeat containing 37, member A4 (pseudogene)
4,22	4,10	LSM14A	792918	LSM14A, SCD6 homolog A (S. cerevisiae)
4,48	2,77	LY6E	803722	lymphocyte antigen 6 complex, locus E
4,48	9,93	MALAT1	807518	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
2,59	4,13	MAPK9	783020	mitogen-activated protein kinase 9
3,55	3,93	MBOAT5		
3,61	2,64	MCFD2	776539	multiple coagulation factor deficiency 2
3,44	2,52	MCM5	807548	minichromosome maintenance complex component 5
2,78	2,75	MED27	800566	similar to cofactor required for Sp1 transcriptional activation, subunit 8, 34kDa; mediator complex subunit 27; CRSP8 pseudogene
2,86	6,07	METAP1	785625	methionyl aminopeptidase 1
3,65	2,81	MPDU1	803697	mannose-P-dolichol utilization defect 1
2,78	3,10	MSN	799778	moesin
3,94	2,99	MT1F	794395	metallothionein 1F
2,92	3,01	MTA2	809718	metastasis associated 1 family, member 2
3,11	2,56	NFE2L2	813212	nuclear factor (erythroid-derived 2)-like 2
3,30	2,78	NQO1	781597	NAD(P)H dehydrogenase, quinone 1
2,68	7,80	NUCKS1	799600	nuclear casein kinase and cyclin-dependent kinase substrate 1
2,96	4,17	NUP155	784280	nucleoporin 155kDa
2,67	3,30	PAICS	819408	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
3,98	3,23	PAK1	795823	p21 protein (Cdc42/Rac)-activated kinase 1
2,79	4,41	PICALM	804797	phosphatidylinositol binding clathrin assembly protein
3,10	2,78	PLP2	813393	proteolipid protein 2 (colonic epithelium-enriched)
3,65	2,70	POLDIP2	810304	polymerase (DNA-directed), delta interacting protein 2
3,93	3,44	POLR2J3	795460	polymerase (RNA) II (DNA directed) polypeptide J3; polymerase (RNA) II (DNA directed) polypeptide J2
6,93	5,16	POLR2J4	795688	polymerase (RNA) II (DNA directed) polypeptide J4, pseudogene
3,15	2,50	POLR3K	802491	polymerase (RNA) III (DNA directed) polypeptide K, 12.3 kDa
5,17	2,63	POTE2		
2,59	4,24	PPP1CC	778740	protein phosphatase 1, catalytic subunit, gamma isoform
2,76	2,60	PRDX3	791180	peroxiredoxin 3
3,23	3,01	PRMT5	820833	protein arginine methyltransferase 5
2,79	3,08	PRPS1	816631	phosphoribosyl pyrophosphate synthetase 1; phosphoribosyl pyrophosphate synthetase 1-like 1
2,52	3,08	PTDSS1	792506	phosphatidylserine synthase 1
4,37	2,52	PXMP2	812524	hypothetical LOC100129532; peroxisomal membrane protein 2, 22kDa
4,75	3,52	RAB1B	819977	RAB1B, member RAS oncogene family
4,77	5,22	RAB31	804323	RAB31, member RAS oncogene family
4,68	2,65	RAB5C	775592	RAB5C, member RAS oncogene family
3,38	3,22	RAB7A	796982	RAB7A, member RAS oncogene family
3,11	3,30	RAD23B	815871	RAD23 homolog B (S. cerevisiae)
2,93	3,16	RAF1	781513	v-raf-1 murine leukemia viral oncogene homolog 1
3,16	3,22	RAG1AP1	774129	recombination activating gene 1 activating protein 1
2,82	2,56	RANBP1	810677	similar to RAN binding protein 1; RAN binding protein 1
2,56	2,55	RCE1	797957	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)
2,58	3,25	RCN1	782629	reticulocalbin 1, EF-hand calcium binding domain
3,66	2,91	RNF26	814167	ring finger protein 26
2,81	2,87	RPL18A	778688	ribosomal protein L18a pseudogene 6; ribosomal protein L18a

3,79	3,11	RPL28	820040	ribosomal protein L28
3,02	3,19	RPL8	801125	ribosomal protein L8; ribosomal protein L8 pseudogene 2
2,54	2,52	S100A10	772988	S100 calcium binding protein A10
2,86	2,89	SAR1A	825692	SAR1 homolog A (<i>S. cerevisiae</i>)
3,33	3,10	SCD	802025	stearoyl-CoA desaturase (delta-9-desaturase)
2,57	3,21	SEC61A1	779432	Sec61 alpha 1 subunit (<i>S. cerevisiae</i>)
4,72	5,79	SELT	801358	selenoprotein T; similar to Selenoprotein T
3,16	4,37	SERINC3	801618	serine incorporator 3
3,01	2,57	SLC34A2	810578	solute carrier family 34 (sodium phosphate), member 2
2,77	2,61	SLC35B1	799141	solute carrier family 35, member B1
3,15	3,53	SLC44A2	784643	solute carrier family 44, member 2
2,68	2,70	SORT1	818683	sortilin 1
3,22	2,68	SOSTDC1	826633	sclerostin domain containing 1
4,13	2,90	ST6GALNAC2	779265	ST6 (alpha-N-acetyl-neuraminy1-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
4,11	5,89	STT3A	813322	STT3, subunit of the oligosaccharyltransferase complex, homolog A (<i>S. cerevisiae</i>)
4,06	3,22	SURF4	805447	surfeit 4
3,19	2,53	SYVN1	826957	synovial apoptosis inhibitor 1, synoviolin
6,57	3,26	TECR	800114	glycoprotein, synaptic 2
2,73	2,89	TEGT		
4,60	3,53	TEX261	805716	testis expressed 261
2,80	3,06	TIMP3	775480	TIMP metalloproteinase inhibitor 3
2,66	2,52	TMED2	776789	transmembrane emp24 domain trafficking protein 2
3,46	2,62	TMED3	822010	transmembrane emp24 protein transport domain containing 3
7,30	3,65	TMEM106C	821072	transmembrane protein 106C
3,18	2,90	TMEM97	820211	transmembrane protein 97
2,90	3,97	TOB2	796992	transducer of ERBB2, 2
2,89	3,49	TOX4	812256	TOX high mobility group box family member 4
4,25	2,70	TPD52L1	786887	tumor protein D52-like 1
4,99	3,41	TUBB	800083	tubulin, beta;
3,19	2,54	TUBB2A	801263	tubulin, beta 2A
3,32	4,05	TUBB2C	776899	tubulin, beta 2C
2,63	2,82	TWSG1	818639	twisted gastrulation homolog 1 (<i>Drosophila</i>)
4,22	2,56	UBC	790215	ubiquitin C
2,94	2,97	UBE2MP1	819741	ubiquitin-conjugating enzyme E2M (UBC12 homolog, yeast); ubiquitin-conjugating enzyme E2M pseudogene 1
3,40	2,58	UBL4A	823016	ubiquitin-like 4A
2,72	2,62	USP10	818267	ubiquitin specific peptidase 10
2,61	2,82	USP39	821075	ubiquitin specific peptidase 39
3,68	2,63	VGLL1	781113	vestigial like 1 (<i>Drosophila</i>)
2,51	3,05	WDR77	804920	WD repeat domain 77
2,69	3,07	YWHAE	790173	similar to 14-3-3 protein epsilon (14-3-3E) (Mitochondrial import stimulation factor L subunit) (MSF L); tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
5,59	6,68	ZFAND6	811925	zinc finger, AN1-type domain 6
2,51	3,54	ZNF852	825862	zinc finger protein 852; zinc finger protein 167

Appendix Table S2. Functional classification of genes whose transcripts were found to interact with ID4 protein through RIP-chip analysis in MDA-MB-468 cells. Enrichment for specific pathways was evaluated by using the ConsensusPathDB at <http://cpdb.molgen.mpg.de> (geneset analysis > enrichment analysis), setting as cut-off the presence of at least 8 genes for the pathway.

pathway name	set size	candidates contained	p-value	q-value	pathway source
EGFR1	453	17 (3.8%)	0,00001	0,00014	NetPath
Membrane Trafficking	157	9 (5.7%)	0,00005	0,00053	Reactome
Protein processing in endoplasmic reticulum	169	9 (5.4%)	0,00008	0,00060	KEGG
Cell Cycle, Mitotic	432	14 (3.3%)	0,00020	0,00092	Reactome
Vesicle-mediated transport	195	9 (4.6%)	0,00024	0,00093	Reactome
Chromatin modifying enzymes	253	10 (4.0%)	0,00038	0,00110	Reactome
Chromatin organization	253	10 (4.0%)	0,00038	0,00110	Reactome
Cell Cycle	502	14 (2.8%)	0,00091	0,00210	Reactome
TNFalpha	234	9 (3.8%)	0,00091	0,00210	NetPath
TCR	244	9 (3.7%)	0,00119	0,00249	NetPath
Disease	483	13 (2.7%)	0,00194	0,00371	Reactome
Metabolism of proteins	687	16 (2.3%)	0,00262	0,00464	Reactome
Cellular responses to stress	367	10 (2.7%)	0,00579	0,00951	Reactome

Appendix Table S3. Genes comprised in the 16-VEGFA signature used for GSEA and Kaplan-Meier analyses.

Gene Symbol	Gene Name	References
<i>PTGS2</i>	Prostaglandin-Endoperoxide Synthase 2	Abe et al., 2001
<i>RCAN1</i>	Regulator Of Calcineurin 1	Abe et al., 2001; Iizuka et al., 2004; Suehiro et al., 2010
<i>ESM1</i>	Endothelial Cell-Specific Molecule 1	Rennel et al., 2007
<i>CD55</i>	CD55 Molecule, Decay Accelerating Factor For Complement (Cromer Blood Group)	Mason et al., 2001
<i>EGR3</i>	Early Growth Response 3	Liu et al., 2003; Suehiro et al., 2010
<i>EGR2</i>	Early Growth Response 2	Liu et al., 2003
<i>EGR1</i>	Early Growth Response 1	Suehiro et al., 2010
<i>ETS1</i>	V-Ets Avian Erythroblastosis Virus E26 Oncogene Homolog 1	Sato et al., 2000; Suehiro et al., 2010
<i>MMP1</i>	Matrix Metalloproteinase 1	Sato et al., 2000
<i>FLT1</i>	Fms-Related Tyrosine Kinase 1	Sato et al., 2000
<i>SNAIL</i>	Snail Family Zinc Finger 1	Wanami et al., 2008
<i>NR4A1</i>	Nuclear Receptor Subfamily 4, Group A, Member 1	Liu et al., 2003
<i>NR4A2</i>	Nuclear Receptor Subfamily 4, Group A, Member 2	Liu et al., 2003
<i>NR4A3</i>	Nuclear Receptor Subfamily 4, Group A, Member 3	Liu et al., 2003
<i>F3</i>	Coagulation Factor III (Thromboplastin, Tissue Factor)	Liu et al., 2003; Suehiro et al., 2010
<i>TNFSF11</i>	Tumor Necrosis Factor (Ligand) Superfamily, Member 11	Guan et al., 2009

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Appendix Table S4. Characteristics of patients with basal-like breast cancer considered for GSEA and Kaplan-Meier analyses.

Age_class		T		Stage		Grade		TP53 status		Metastasis event		Death event	
<i>Age</i>	<i>n</i> ^o	<i>T</i>	<i>n</i> ^o	<i>Stage</i>	<i>n</i> ^o	<i>G</i>	<i>n</i> ^o	<i>TP53</i>	<i>n</i> ^o	<i>M</i>	<i>n</i> ^o		<i>n</i> ^o
<40	40	1	46	1	6	1	4	MUT	34	0	138	0	150
>60	21	2	81	2	23	2	20	WT	14	1	48	1	51
40-60	84	3	2	3	1	3	126	NA	153	NA	15		
NA	56	4	5	4	1	NA	51						
		NA	67	NA	170	1	4						

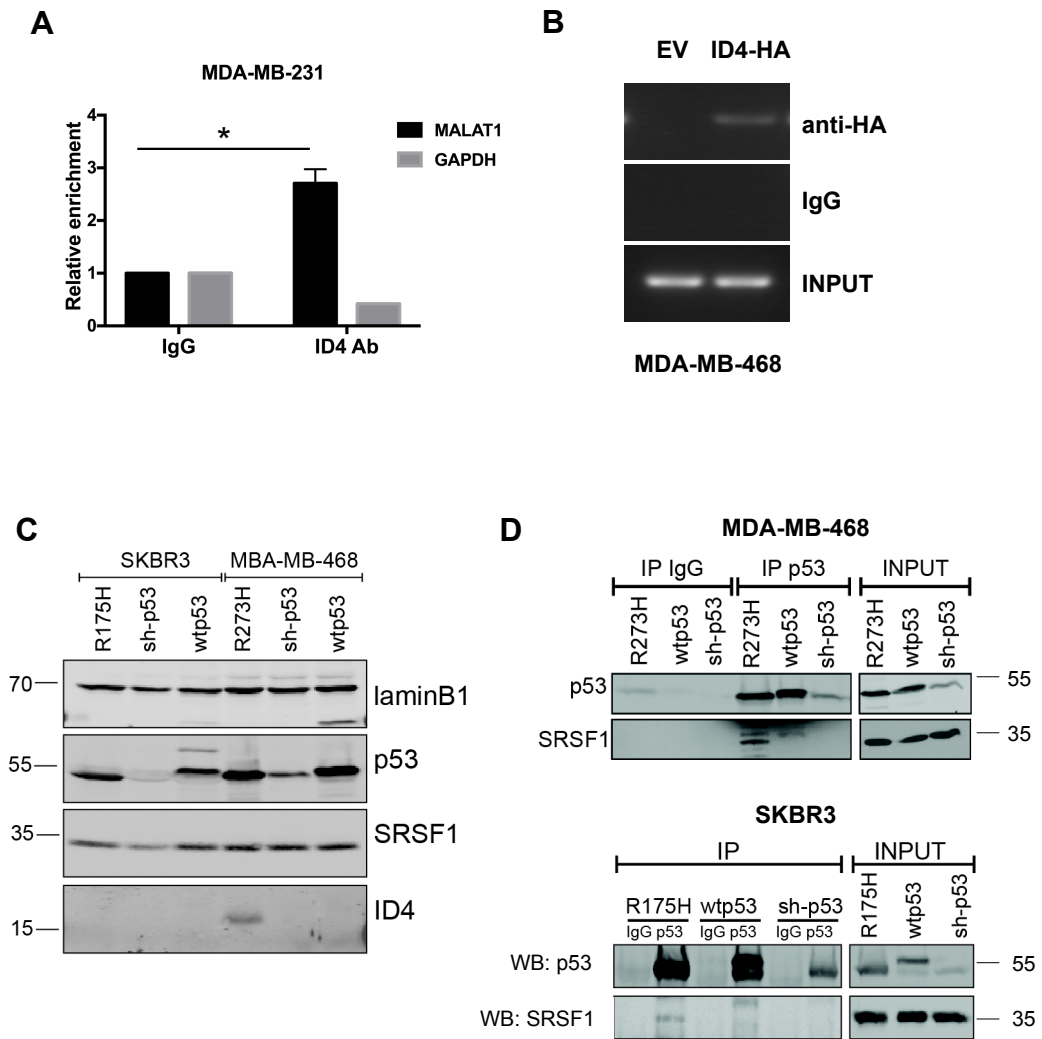
T: Tumor size; NA: not assessed.

Appendix table S5

Oligonucleotides used in PCR analyses		
RT	RPL-19 For	CGGAAGGGCAGGCACAT
	RPL-19 Rev	GGCGCAAATCCTCATTCTC
RT	GAPDH For	GAGTCAACGGATTTGGTCGT
	GAPDH Rev	GACAAGCTTCCCGTTCTCAG
RT	18S rRNA	TaqMan assay from Life Technologies
VEGFA pre-mRNA RT and Int7/Ex8 ChIP	VEGFA_Int7-Ex8 For	CTCCTCACTTGGCCCTAACC
	VEGFA_Int7-Ex8 Rev	TCAGTCTTTCCTGGTGAGAGAT
VEGFA ChIP Int7	VEGFA_Int7 For	ACTGAAAACCCTCCTCAGCA
	VEGFA_Int7 Rev	AAGAGCTGATGGGTGACCAG
total VEGFA RT	VEGF-A all isoforms F	CTTCTACAGCACAACAATGTG
	VEGF-A all isoforms R	GTCTTGCTCTATCTTTCTTTGG
VEGFA ₁₂₁ TaqMan assay RT	VEGFA_Ex3 For	CCCACTGAGGAGTCCAACAT
	VEGFA_Ex5-8 Rev	CCTCGGCTTGTCACATTTTTCTTGTC
	VEGFA_Ex4 probe FAM	AAGGCCAGCACATAGGAGAGAT
VEGFA _{121b} TaqMan assay RT	VEGFA_Ex3 For	CCCACTGAGGAGTCCAACAT
	VEGFA_Ex5-8B_Rev	CTTCTGCTGAGAGATTTTTCTTGT C
	VEGFA_Ex4 probe FAM	AAGGCCAGCACATAGGAGAGAT
VEGFA ₁₆₅ TaqMan assay RT	VEGFA_Ex7 For	CGCAGACGTGTAATGTTCTT
	VEGFA_Ex8 Rev	GCCTCGGCTTGTCACATC
	VEGFA_Ex7 probe FAM	CAAGGCGAGGCAGCTTGAGTTAAA
VEGFA _{165b} TaqMan assay RT	VEGFA_Ex7 For	CGCAGACGTGTAATGTTCTT
	VEGFA_Ex7-8B_Rev	CCTGGTGAGAGATCTGCAAGTAC
	VEGFA_Ex7 probe FAM	CAAGGCGAGGCAGCTTGAGTTAAA
RT ALDOA isoforms	ALDOA-Ex2F	ACCCAGCACCAGACAGAGTT
	ALDOA-Ex1-Ex3F	TCTCCTGTGCCAGGAAGTTG
	ALDOA-Ex3R	GGGTCAGTGCTGGATATTGG
RT	ID4 TaqMan assay	Hs.PT.49a.3494489.g (IDT)
	ID4 For	GTGCGATATGAACGACTGCT
	ID4 Rev	CAGGATCTCCACTTTGCTGA
	U2 snRNA For	CTCGGCCTTTTGGCTAAGAT
	U2 snRNA Rev	TATTCCATCTCCCTGCTCCA
	NEAT1 For	TCGGGTATGCTGTTGTGAAA
	NEAT1 Rev	TGACGTAACAGAATTAGTTCTTACC A
	MALAT1 For	GGGAAGGCGAAGAAAAGAAT
	MALAT1 Rev	TGCCCTTAGCTTTTTGTTTCC
	MALAT1_bis For	GAGGTCTTTGGTGGGTGAA
	MALAT1_bis Rev	CCCACCCAGCATTACAGTTC
	MALAT1 For (365-544)	AAGCAGACCCAGAGCAGTGT
	MALAT1 Rev	TTTTCAGCTTCCAGGCTCTC
	MALAT1 For (nt 664-832)	GTGGGATTGAGGCGTTTTCC

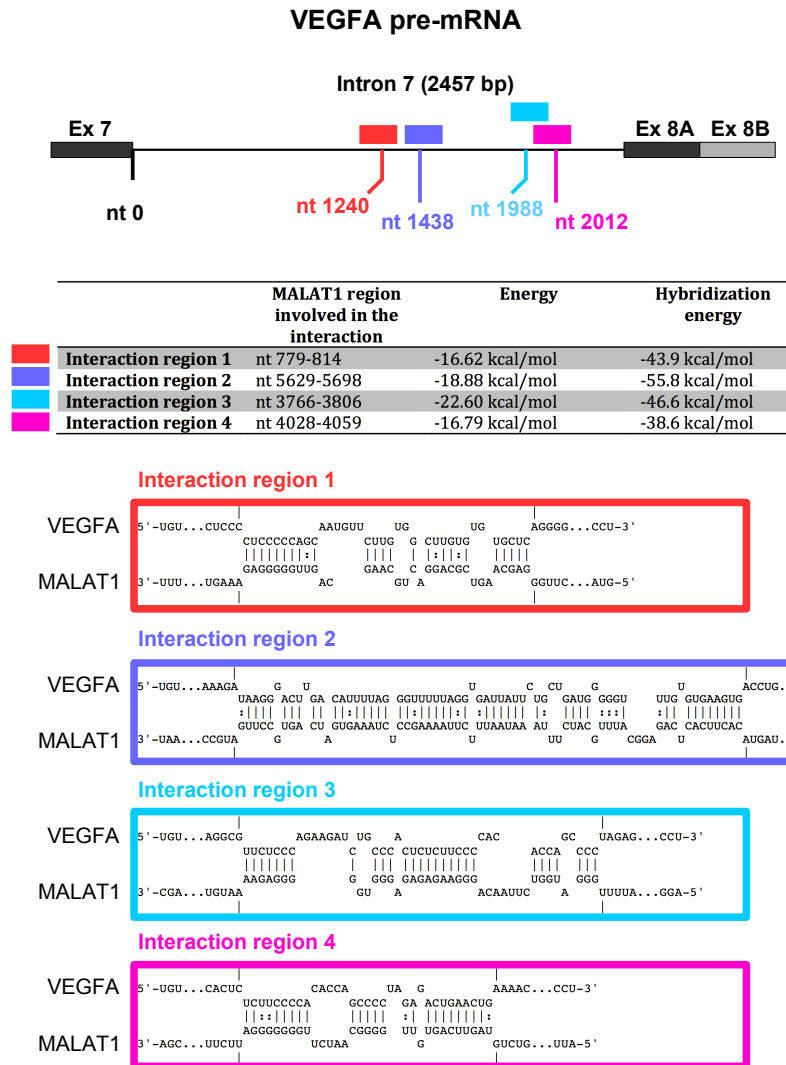
	MALAT1 Rev (nt 664-832)	TGGCAAATGGCGGACTTTC
	MALAT1 For (nt 1332-1515)	GCTTGAGGAAACCGCAGATA
	MALAT1 Rev (nt 1332-1515)	TTTCCTTCCTCATGCTACTCTTC
	MALAT1 For (nt 1922-2061)	GGGAAGGCGAAGAAAAGAAT
	MALAT1 Rev (nt 1922-2061)	TGCCCTTAGCTTTTTGTTTCC
	MALAT1 For (nt 2629-2698)	TGACCCAGGTGCTACACAGA
	MALAT1 Rev (nt 2629-2698)	TTCCTGGAATCCTGTCTGCT
	MALAT1 For (nt 3082-3223)	TGGGGGAGTTTCGTAAGTCTG
	MALAT1 Rev (nt 3082-3223)	TCTCCAGGACTTGGCAGTCT
	MALAT1 For (nt 3592-3645)	GGATAATCAGACCACCACAGG
	MALAT1 Rev (nt 3592-3645)	AGACCTCAACGTGAGAACTGC
	MALAT1 For (nt 3892-4123)	GAACACCTTCAGGGACTGGA
	MALAT1 Rev (nt 3892-4123)	GTAACAGGCCACTGCCAACT
	MALAT1 For (nt 4494-4585)	GGTAGTGTGTGGTTCTCTTTTGG
	MALAT1 Rev (nt 4494-4585)	AAGCCACTTCCTTTGCTCTG
	MALAT1 For (nt 4943-5192)	AACAGCTCCTTGGTGAATTGAT
	MALAT1 Rev (nt 4943-5192)	TGGACATTGCCTCTTCATTG
	MALAT1 For (nt 5919-6023)	GTTCAAGTGTGGGGCAATCT
	MALAT1 Rev (nt 5919-6023)	GTTCTTCCGCTCAAATCCTG
	MALAT1 For (nt 6866-7030)	GGAGGGGACTGAAGCCTTT
	MALAT1 Rev (nt 6866-7030)	GGGAGAGAGAAACCCACACA
	MALAT1 For (nt 7431-7500)	CTCACTAAAGGCACCGAAGG
	MALAT1 Rev (nt 7431-7500)	TGTTGTCTCTCCTGCCACAG
	MALAT1 For (nt 7916-8076)	GAGGTCTTTGGTGGGTTGAA
	MALAT1 Rev (nt 7916-8076)	CCCACCCAGCATTACAGTTC
	BCL2L1 For (Exon 2)	GTAAACTGGGGTCGCATTGT
	BCL2L1 Rev (Intron 2)	CACAAGGGGCTTGTTCTTA
	BIM For (Exon 2)	CAACACAAACCCCAAGTCCT
	BIM Rev (Intron 2)	CAGATTCAACCATCCACACG
Oligonucleotides used in ChIRP analysis		
MALAT1 ChIRP	Bio_MALAT1_1	GCTTCTGCGTTGCTAAAATG/3BioTEG/
	Bio_MALAT1_2	GCGAGGCGTATTTATAGACG/3BioTEG/
	Bio_MALAT1_3	ACGCTAAGCAATATCTTAGT/3BioTEG/
	Bio_MALAT1_4	TAAGCTGTTTAAGTCACCTT/3BioTEG/
	Bio_MALAT1_5	GGTCTTTTAATCACCTTCGG/3BioTEG/
	Bio_MALAT1_6	TCTTTCCATTTTCGTCTGCG/3BioTEG/
	Bio_MALAT1_7	GCCCTTAGCTTTTTGTTTCC/3BioTEG/
	Bio_MALAT1_8	TCTGGTCTACGTAAACACCC/3BioTEG/
	Bio_MALAT1_9	CTGGGTACAGCTGTCAATTAA/3BioTEG/
	Bio_MALAT1_10	TTGCTCCTCAGTCCTAGCTT/3BioTEG/
	Bio_MALAT1_11	TGGAATCCTTTTTCTAGCT/3BioTEG/
CTR ChIRP	Bio_CTR_1	GTAGTGGAGGAGAAACGGTGTGAGTAGTAC/3BioTEG/
	Bio_CTR_2	GTAGTGGAGGAGGCGGGTGTGAGTAGTAC/3BioTEG/
siRNA oligonucleotides		
	SCR	CTATAACGGCGCTCGATAT
	ID4	Ambion

	ID4_1	GATCCTGCAGCACGTTATC
	ID4_2	TTACAGAGCTCTTGATATC
	p53	Ambion
	p53_1	GACUCCAGUGGUAUUCUAC (CDS)
	p53_2	GGUGAACCUUAGUACCUAA (3'-UTR)
	SRSF1	NM_006924 duplex 3 (IDT)
	SRSF1_1	GAAAGAAGATATGACCTAT (from Ezponda et al., 2010)
	SRSF1_2	TGAAGCAGGTGATGTATGT (from Ezponda et al., 2010)
	SRSF1_3	NM_006924 duplex 1 (IDT)
	si SCR-2	mC*mU*mA*mU*mA*A*C*G*G*C*G*C*T*C*G*mA*mU*mG*mA*mU
	si MALAT1-2	mG*mG*mG*mA*mG*T*T*A*C*T*T*G*C*C*A*mA*mC*mU*mU*mG (from Tripathi, Mol Cell 2010)
	si-MALAT1_1	GATCCATAATCGGTTTCAA (from Miyagawa et al., 2012)
	si-MALAT1	CACAGGGAAAGCGAGTGGTTGGTAA (from Miyagawa et al., 2012)
	si-hnRNP A1	Trifecta 29-mer oligo from Origene
	NC1	Trifecta negative ctr from Origene

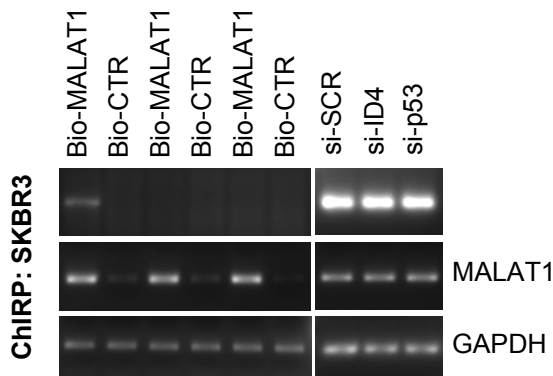


A

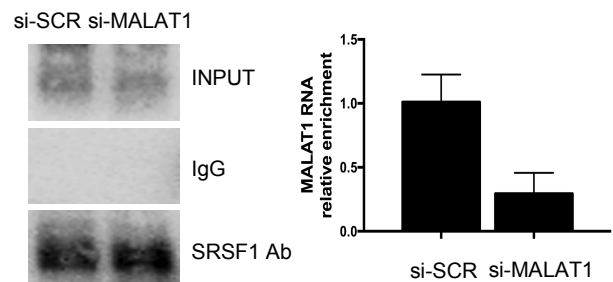
Putative interaction regions between VEGFA pre-mRNA and MALAT1 IncRNA



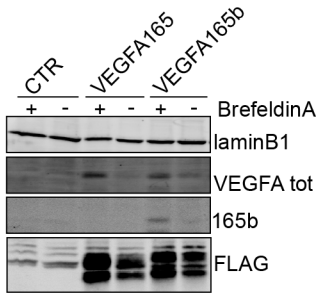
B si-SCR si-ID4 si-p53 INPUT



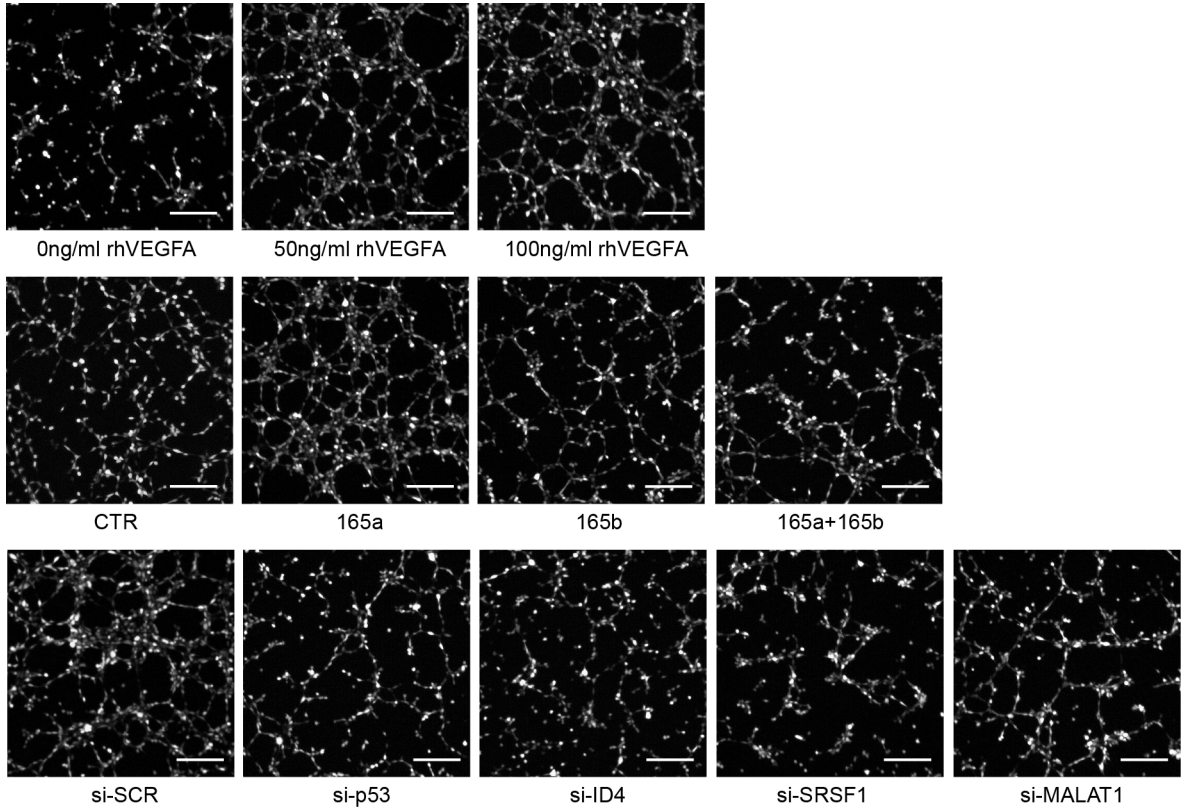
C



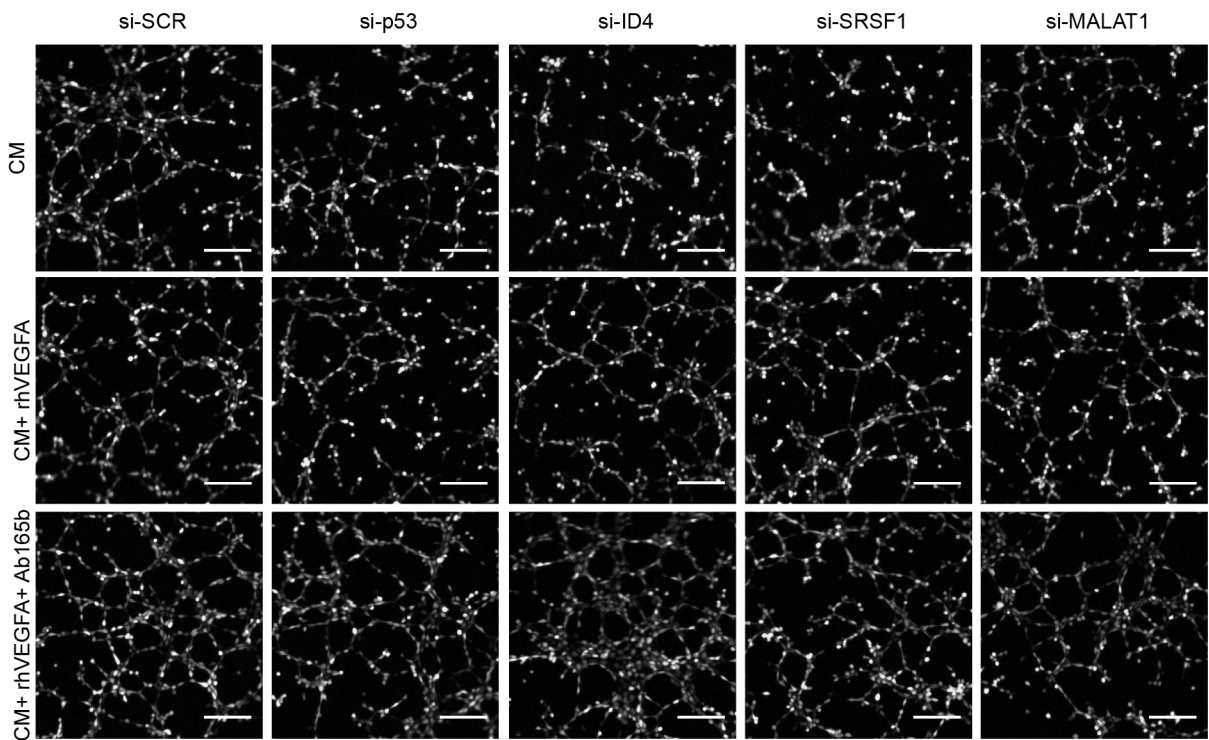
A



B



C



APPENDIX FIGURE LEGENDS

Appendix Figure S1. **A.** RIP (Ribonucleoprotein ImmunoPrecipitation) assay performed in MDA-MB-231 breast cancer cells using an antibody directed to ID4 or IgG as negative control. **B.** RIP assay performed in MDA-MB-468 breast cancer cells transfected with an empty vector (EV) or an ID4-HA expression vector (ID4-HA) using an antibody directed to HA tag (Santa Cruz) or IgG as negative control. MALAT1 RNA abundance was evaluated by RT-PCR. **C.** Characterization of stable cell lines carrying depletion of endogenous mutant p53 expression (sh-p53) or concomitant depletion of endogenous mutant p53 and replacement by flag-tagged wild-type p53 (FLAG wtp53), compared to parental cells SKBR3 (ATCC p53R175H) and MDA-MB-468 (ATCC p53R273H). **D.** SRSF1-p53 interaction evaluated by immunoprecipitation of p53 (and IgG as control) followed by western blot of SRSF1 using lysates from parental MDA-MB-468 cells (upper panel, indicated as R273H) or SKBR3 cells (lower panel, indicated as R175H) as well as in cells stably depleted of endogenous mutant p53 expression (sh-p53) or carrying wild-type p53 replacing endogenous mutant p53 (wtp53).

Appendix Figure S2. **A.** Putative interaction between MALAT1 lncRNA and VEGFA pre-mRNA was evaluated using the IntaRNA software (<http://rna.informatik.uni-freiburg.de/IntaRNA/Input.jsp>). **B.** ChIRP assay was performed to recover MALAT1 RNA and its associated RNAs by using a set of biotinylated oligonucleotides complementary to MALAT1 RNA sequence (Bio-MALAT1), or a set of control oligonucleotides (Bio-CTR), in lysates from control (si-SCR), ID4-depleted (si-ID4) and mutant p53-depleted (si-p53) SKBR3 cells. Enrichment for the indicated transcripts was evaluated by RT-PCR. **C.** Western blot analysis of SRSF1 protein immunoprecipitated in the RIP assay described in Figure 6E-F was performed to ensure efficient recovery of SRSF1 protein following depletion of MALAT1 in MDA-MB-468 cells. Efficiency of MALAT1 depletion after transfection of specific siRNAs is shown in right graph.

Appendix Figure S3. A. Western blot analysis of SKBR3 cells transfected with flag-tagged expression vectors for VEGF₁₆₅ or VEGF_{165b}. Antibodies recognizing total VEGF, VEGF_{165b} (165b) or FLAG tag were used. **B-C.** Representative images of the tube-formation assays reported in Figure 7. 0 ng/mL as well as 50-100 ng/mL of recombinant VEGFA (rhVEGFA) were used, respectively, as negative and positive controls for the assays. Experimental conditions are labeled as in Figure 7.