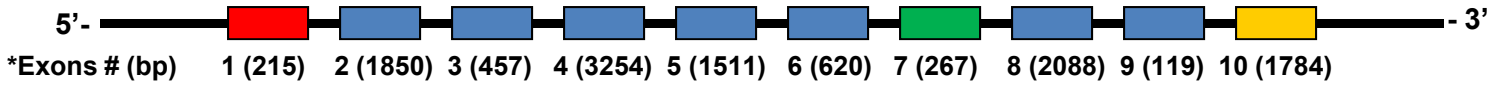
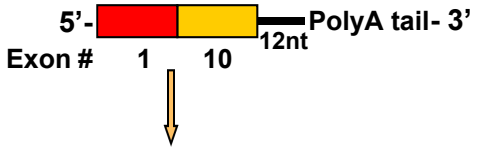
Figure S1*a*

LOCUS : 5q23.1, Chromosome: 5; NC_000005.9 (118604418..118730294) (Genomic TNFAIP8, 125,877 bp)
mRNA ACCESSION No: NM_001077654.1 (Transcript Variant 2); NM_014350.2 (Transcript Variant 1)
Protein Accession No:NP_001071122.1 (Protein Isoform b); NP_055165.2 (Protein Isoform a)
http://www.ncbi.nlm.nih.gov/sites/entrez?db=gene&cmd=Retrieve&dopt=full_report&list_uids=25816#



*http://www.ncbi.nlm.nih.gov/sutils/evv.cgi?taxid=9606&contig=NT_034772.6&gene=TNFAIP8&lid=25816

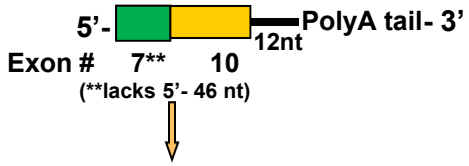
Transcript Variant 2 (2012 bp, includes 5'UTR 214 bp and 3'UTR 1233 bp)



Protein Isoform b (188aa, 21.8 kDa)
*****SCC-S2, GG2-1, NDED, MDC-3.13 (Uniprot: O95379-3)**
***** Kumar *et al*., J. Biol. Chem. 275:2973-2978, 2000**

MATDVFNSKNLAVQAQKKILGKMVSKSIATTLIDDTSSEVLDELYRVTREYTQNK KEAEKIIKNLIKTVIKLAILYRNNQFNQDELALMEKFKKKVHQLAMTVVSFHQVD YTFDRNVLSRLLNECREMLHQIIQRHLTAK SHGRVNNVFDHFSDCEFLAALYN PFGNFKPHLQKLCDGINKMLDEENI

Transcript Variant 1 (2017 bp, includes 5'UTR 190 bp and 3'UTR 1233bp)



Protein Isoform a (198aa, 23 kDa)
MDC-3.13-2 (Uniprot: O95379-1)

MHSEAEESKEVATDVFNSKNLAVQAQKKILGKMVSKSIATTLIDDTSSE VLDELYRVTREYTQNKKEAEKIIKNLIKTVIKLAILYRNNQFNQDELALM EKFKKKVHQLAMTVVSFHQVDYTFDRNVLSRLLNECREMLHQIIQRHL TAKSHGRVNNVFDHFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLD EENI

Figure S1*b*

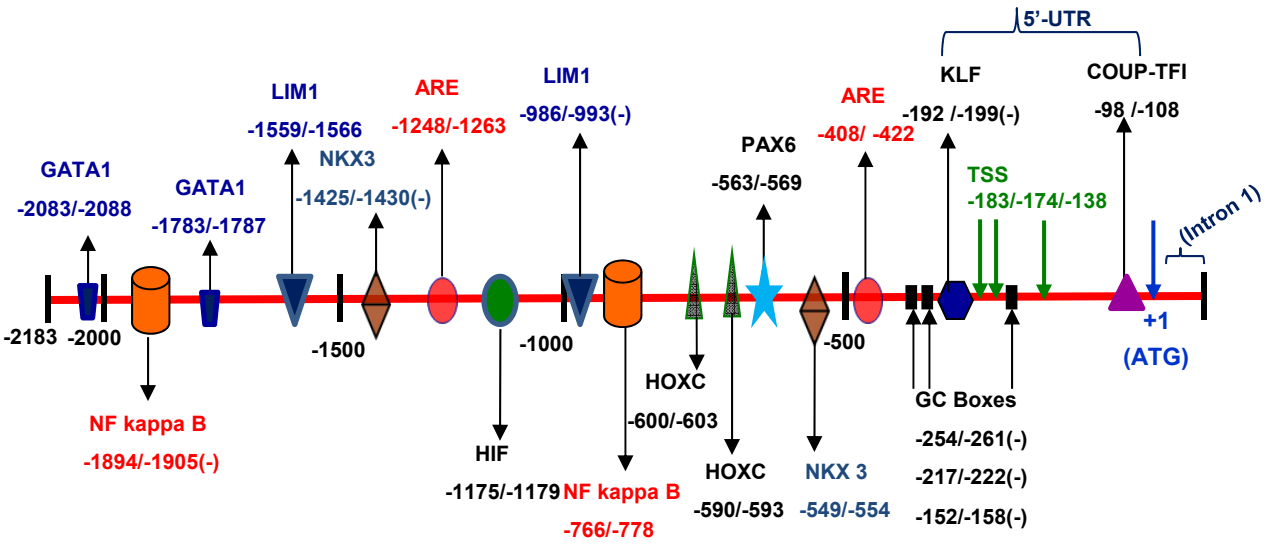

5'-UTR
KLF
-192 /-199(-)
COUP-TFI
-98 /-108
ARE
-408/ -422
PAX6
-563/-569
TSS
-183/-174/-138
(Intron 1)
LIM1
-1559/-1566
NKX3
-1425/-1430(-)
ARE
-1248/-1263
LIM1
-986/-993(-)
GATA1
-2083/-2088
GATA1
-1783/-1787
-2183
-2000
-1500
-1000
-500
+1
(ATG)
HOXC
-600/-603
GC Boxes
-254/-261(-)
-217/-222(-)
-152/-158(-)
NF kappa B
-1894/-1905(-)
HIF
-1175/-1179
NF kappa B
-766/-778
HOXC
-590/-593
NKX 3
-549/-554

Figure S2*a*

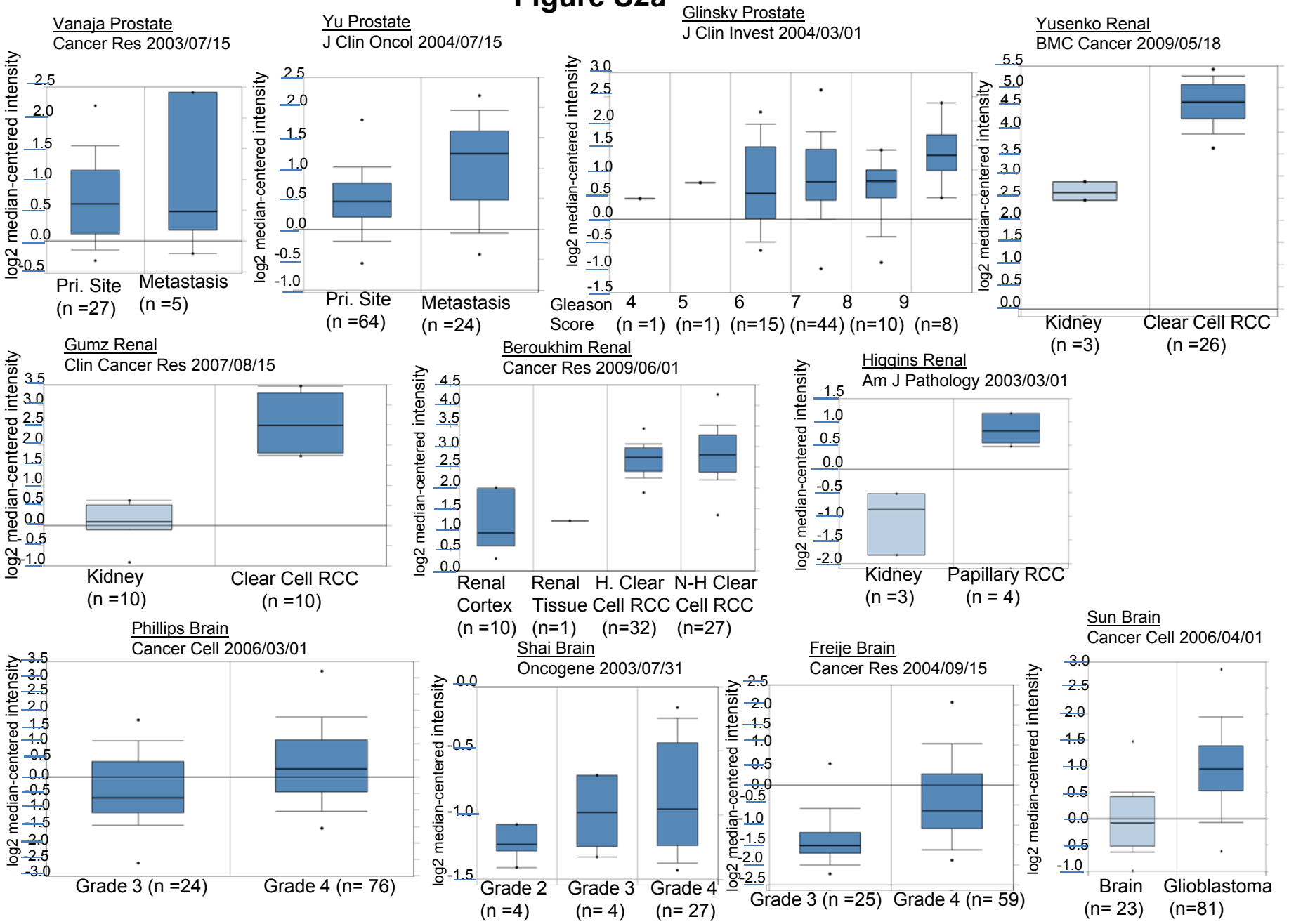

Vanaja Prostate
Cancer Res 2003/07/15
log2 median-centered intensity
Pri. Site (n =27)
Metastasis (n =5)
Yu Prostate
J Clin Oncol 2004/07/15
log2 median-centered intensity
Pri. Site (n =64)
Metastasis (n =24)
Glinsky Prostate
J Clin Invest 2004/03/01
log2 median-centered intensity
Gleason Score
4 (n =1)
5 (n=1)
6 (n=15)
7 (n=44)
8 (n=10)
9 (n=8)
Yusenko Renal
BMC Cancer 2009/05/18
log2 median-centered intensity
Kidney (n =3)
Clear Cell RCC (n =26)
Gumz Renal
Clin Cancer Res 2007/08/15
log2 median-centered intensity
Kidney (n =10)
Clear Cell RCC (n =10)
Beroukhim Renal
Cancer Res 2009/06/01
log2 median-centered intensity
Renal Cortex (n =10)
Renal Tissue (n=1)
H. Clear Cell RCC (n=32)
N-H Clear Cell RCC (n=27)
Higgins Renal
Am J Pathology 2003/03/01
log2 median-centered intensity
Kidney (n =3)
Papillary RCC (n = 4)
Phillips Brain
Cancer Cell 2006/03/01
log2 median-centered intensity
Grade 3 (n =24)
Grade 4 (n= 76)
Shai Brain
Oncogene 2003/07/31
log2 median-centered intensity
Grade 2 (n =4)
Grade 3 (n= 4)
Grade 4 (n= 27)
Freije Brain
Cancer Res 2004/09/15
log2 median-centered intensity
Grade 3 (n =25)
Grade 4 (n= 59)
Sun Brain
Cancer Cell 2006/04/01
log2 median-centered intensity
Brain (n= 23)
Glioblastoma (n=81)

Figure S2*a* (contd.)

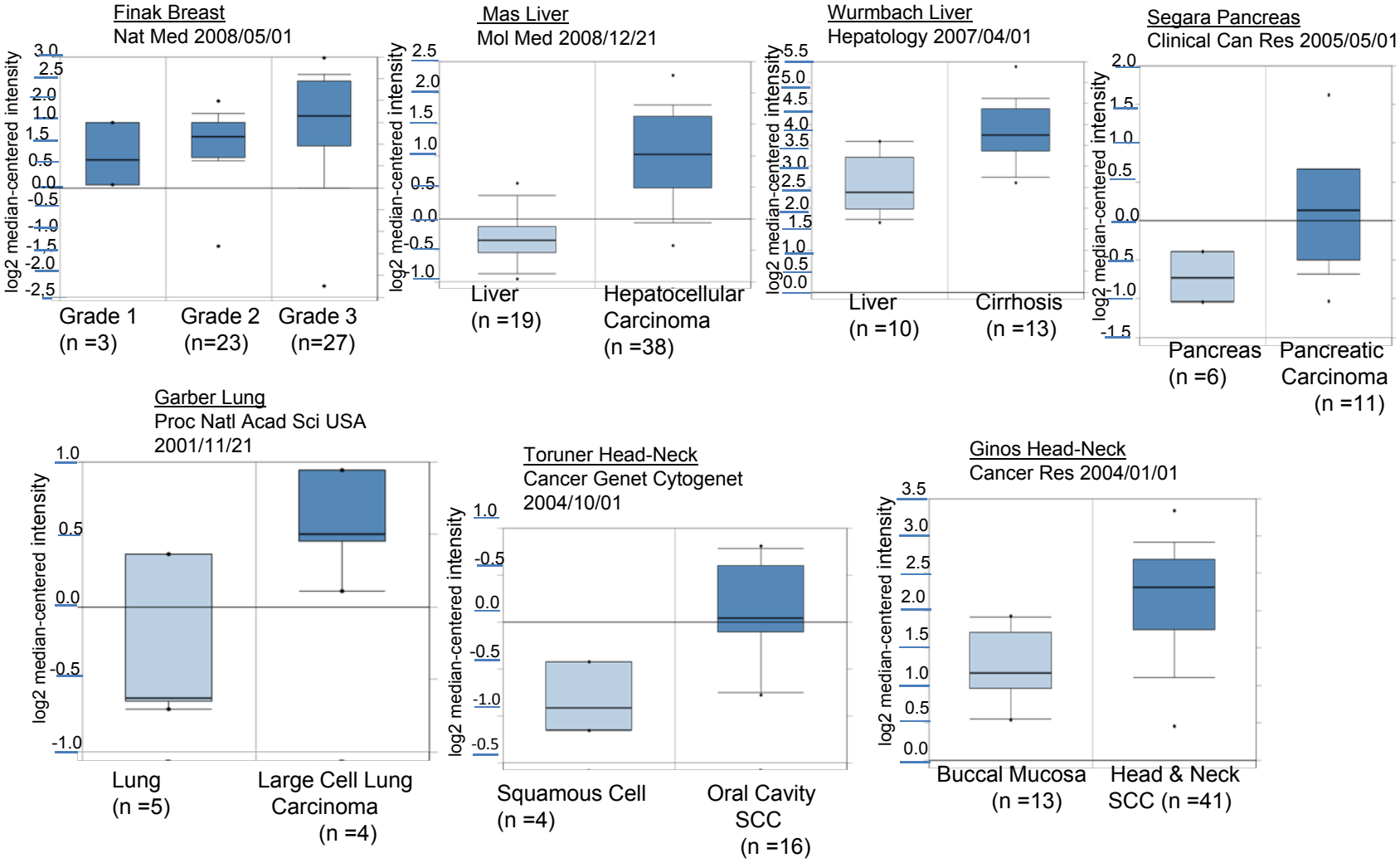
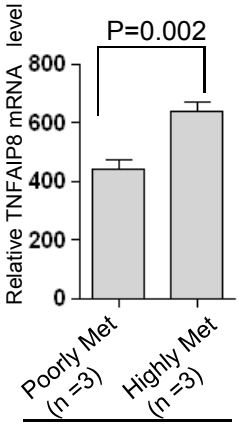
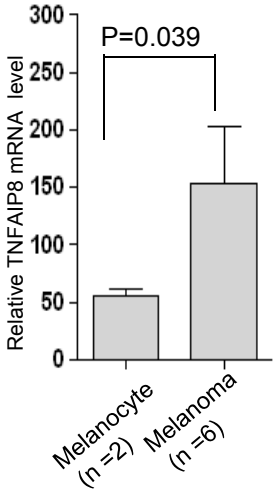


Figure S2*b*

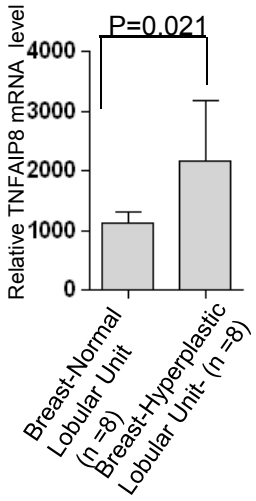
GDS2865/208296_x_at
(Wong et al., Proc Natl Acad Sci USA 2007,104:12784)



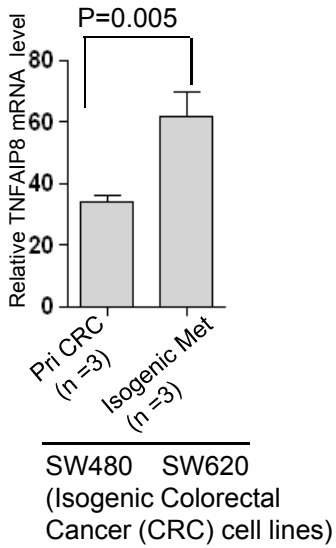
GDS1965/210260_s_at
(Hoek et al., Cancer Res 2004,64:5270)



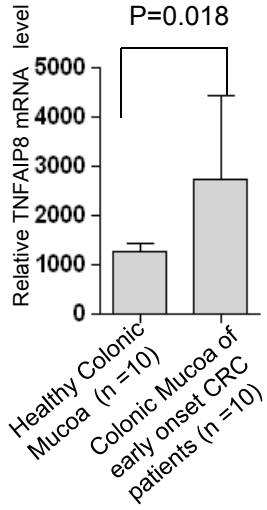
GDS2739/g7657123_3p_a_at
(Lee et al., Am J Pathol 2007,171:252)



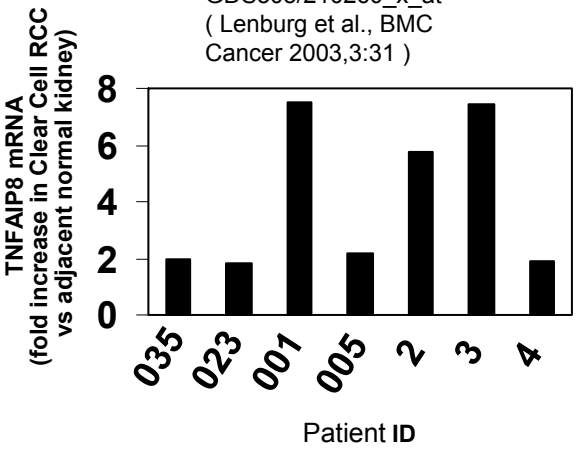
GDS1780/208296_x_at
(Provenzani et al., Carcinogenesis 2006,27:1323)



GDS2609/210260_s_at
(Hong et al., Clin Cancer Res 2007,13:1107)

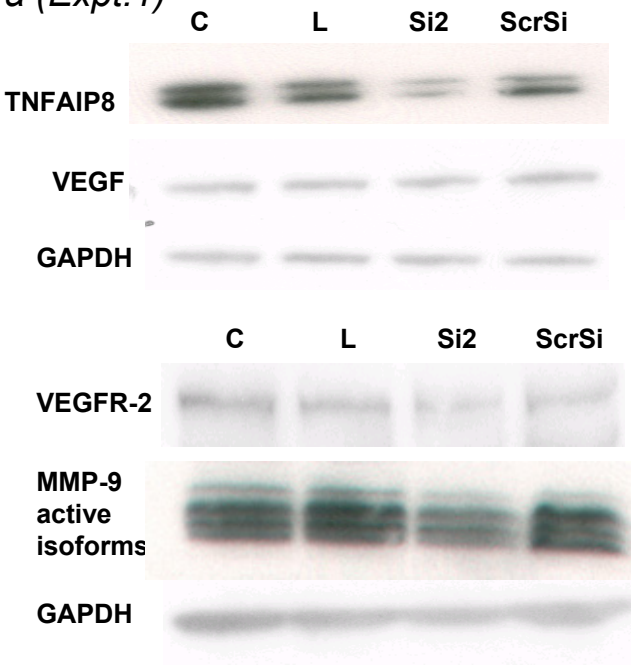


GDS505/210260_x_at
(Lenburg et al., BMC Cancer 2003,3:31)

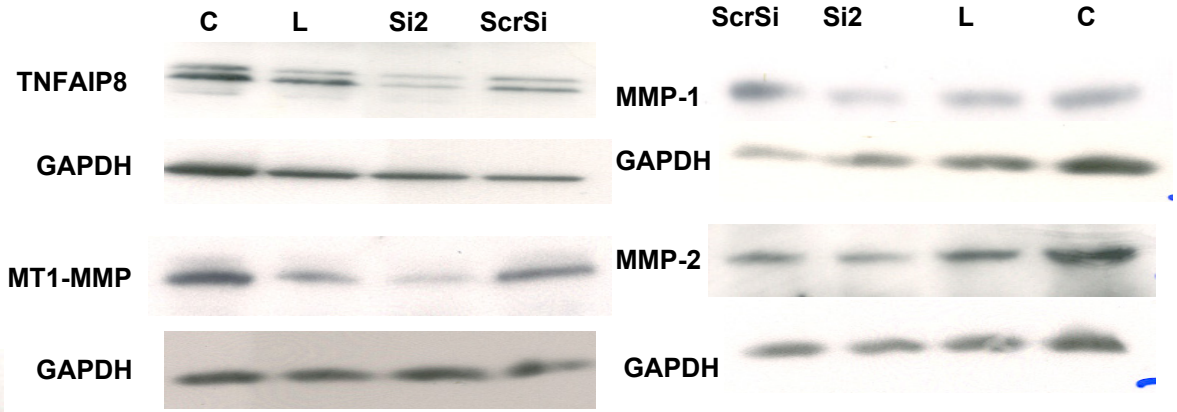


Figures S3*a*- S3*c*

a (Expt.1)



b (Expt.2)



c

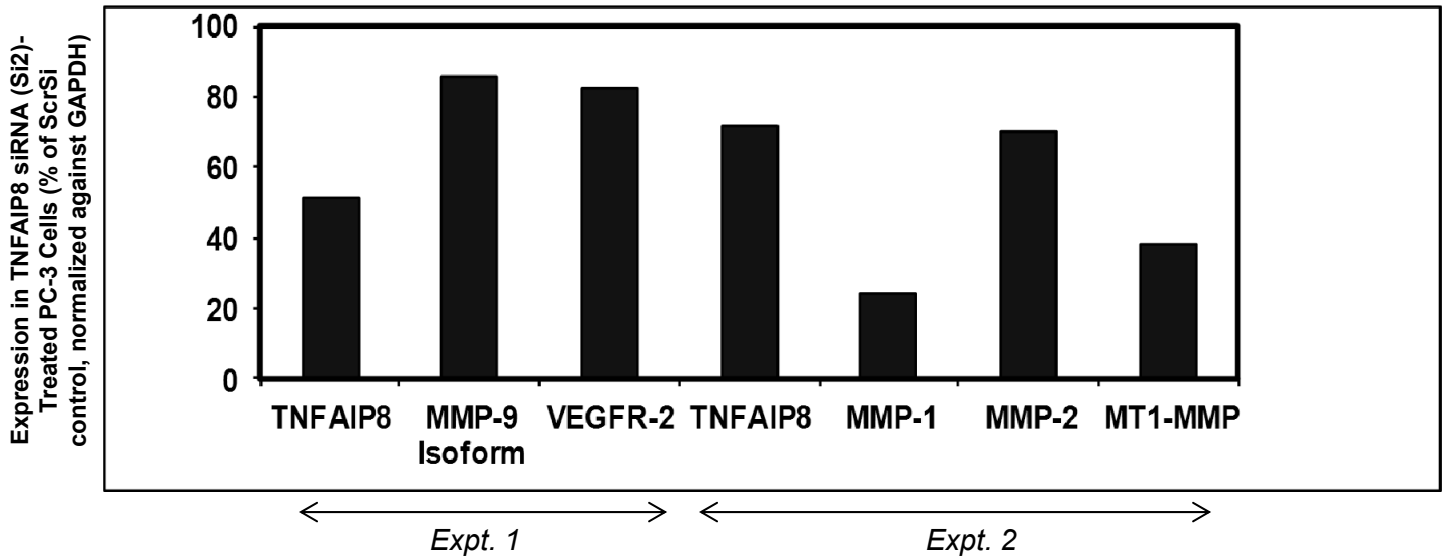
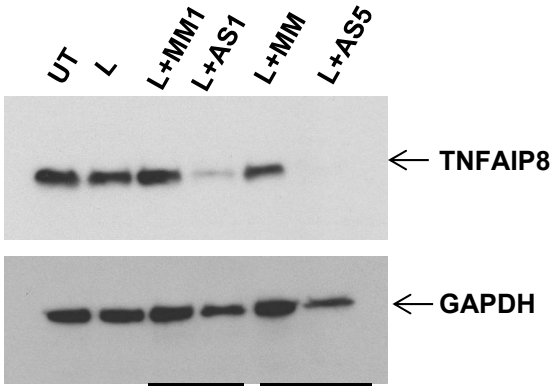


Figure S4*a*-S4*c*

a. *In vitro*

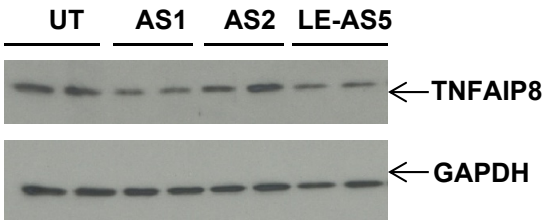


c.

TNFAIP8 antisense oligonucleotides tested *in vitro/in vivo* (14-mers; AS1 and AS5 are identical sequences)

All bases phosphorothioated	
AS1	5’-GsTsGsGsCsCsAsTsCsGsGsAsGsG-3’
AS2	5’- GsCsCsCsTsAsTsTsAsAsAsAsAsG-3’
Only one base at each end phosphorothioated	
AS5	5’-GsTGGCCATCGGAGsG-3’

b. *In vivo*



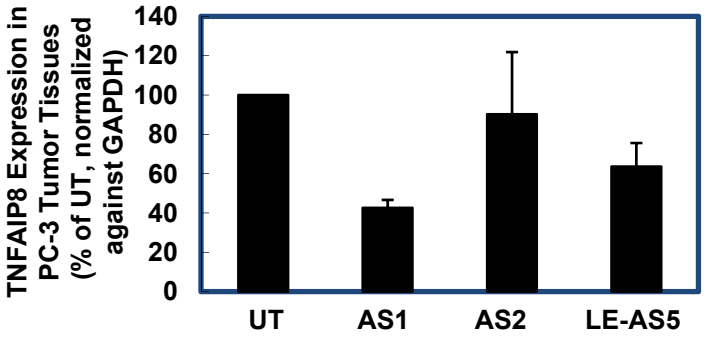


Figure S5*a*

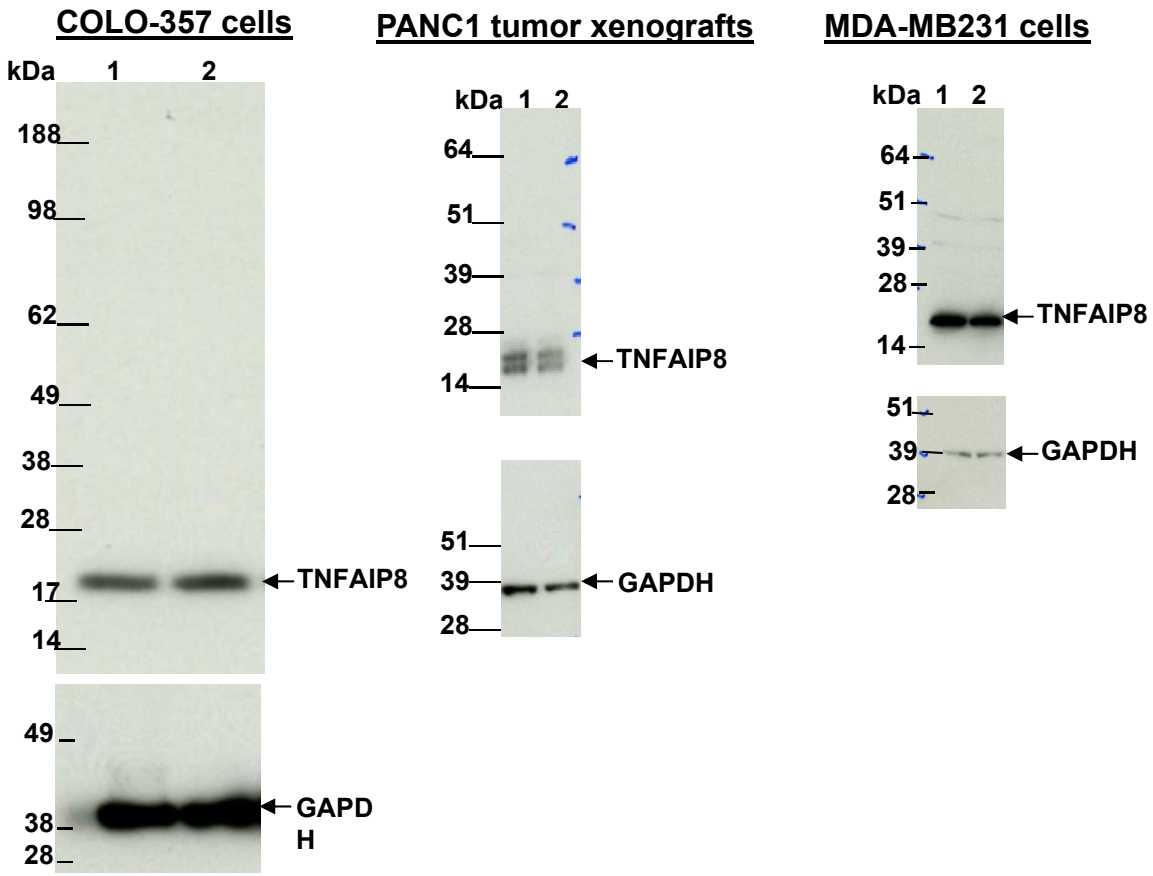

COLO-357 cells
kDa
1
2
188
98
62
49
38
28
17
14
TNFAIP8
49
38
28
GAPDH
PANC1 tumor xenografts
kDa
1
2
64
51
39
28
14
TNFAIP8
51
39
28
GAPDH
MDA-MB231 cells
kDa
1
2
64
51
39
28
14
TNFAIP8
51
39
28
GAPDH

Figure S5*b*

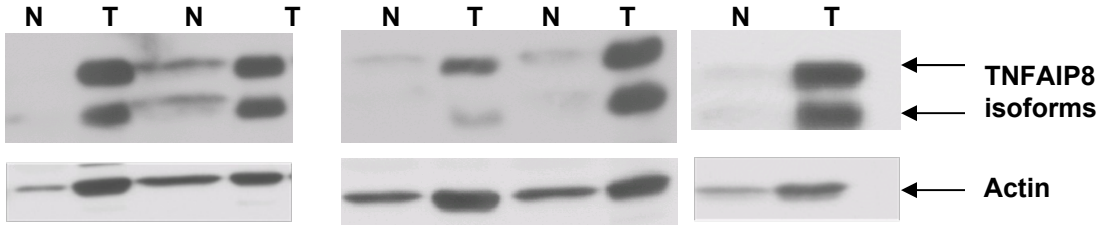


Figure S5*c*

Immunoprecipitation (IP):
Lane 1. anti-TNFAIP8
Lane 2. anti-Raf-1 (polyclonal)
Lane 3. Normal rabbit IgG

Immunoblotting(IB):
anti-TNFAIP8

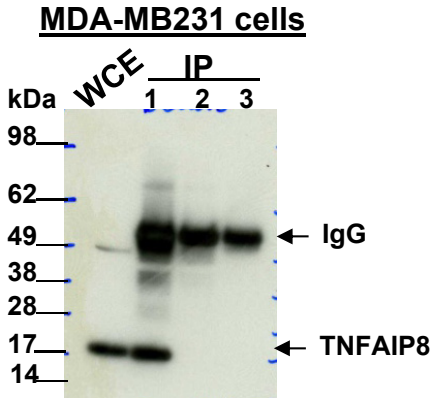
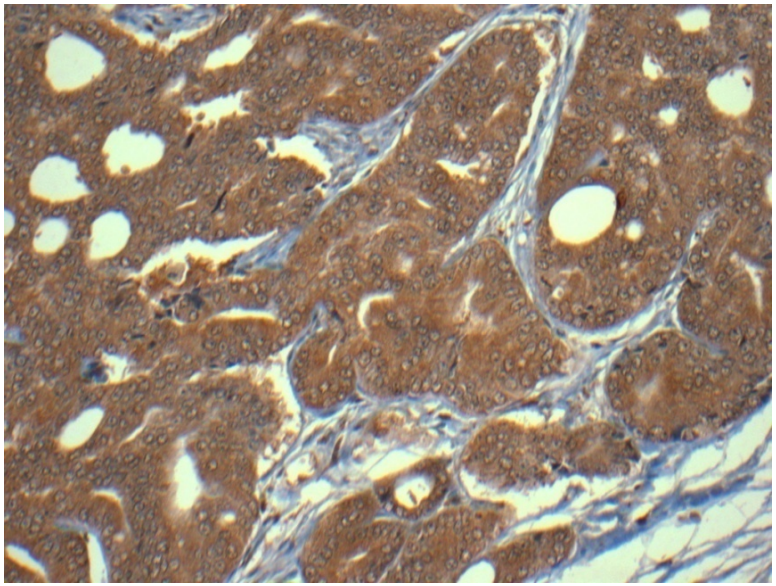
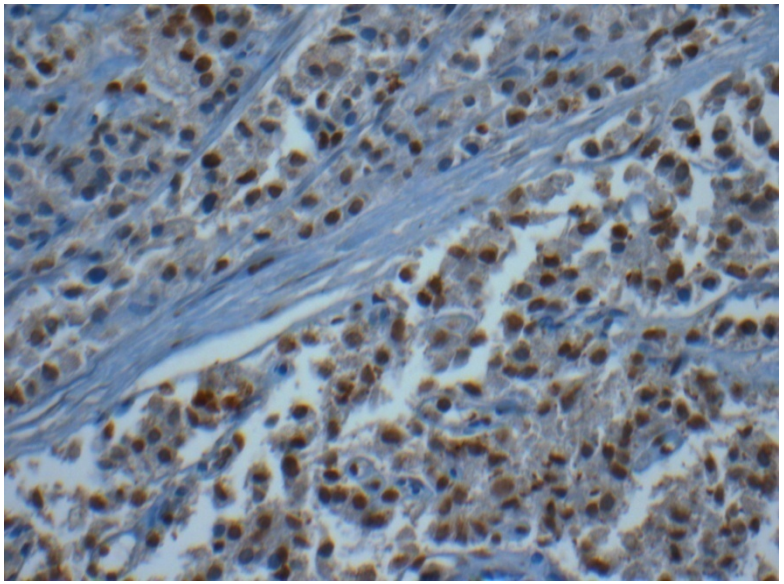


Figure S6*a*





Immunohistochemical analysis of TNFAIP8 in prostate tumor TMA

PAC Grade	Cytoplasmic TNFAIP8		Nuclear TNFAIP8	
	Weak	Moderate to Intense	Weak	Moderate to Intense
Low (n =26)	15/26 (58%)	11/26 (42%)	0/26	1/26 (4%)
Intermediate/ High (n =38)	4/38 (11%)	34/38 (89%)	0/38	5/38 (13%)

Figure S6*b*

Patient ID	Grade 0=LG 1=HG	Cytoplasmic TNFAIP8 (Tumor vs Adjacent Benign)*
1	1	1
2	0	-1
3	1	1
6	1	1
11	0	-1
13	0	-1
20	1	1
25	1	1
35	0	-1
37	0	-1
39	1	1
41	0	-1
45	0	1
46	1	-1
50	0	-1
51	0	-1
52	0	-1
53	1	-1
	18	18

Patient ID	Grade 0=LG 1=HG	Nuclear TNFAIP8 (Tumor vs Adjacent Benign)*
3	1	1
4	0	1
5	1	1
6	1	1
14	1	1
17	1	1
18	1	1
20	1	1
21	1	1
22	1	1
23	1	1
24	1	1
25	1	1
31	1	1
37	0	1
45	0	1
	16	16

Figure S6*c*

Patient ID	0=Non-Recurrent 1= Recurrent	Nuclear TNFAIP8 (Tumor vs Adjacent Benign)*
3	1	1
4	0	1
5	1	1
6	1	1
7	0	0
8	1	0
9	1	0
10	1	0
12	1	0
14	1	1
15	1	0
16	0	0
17	1	1
18	1	1
19	0	0
20	0	1
21	1	1
22	1	1
23	1	1
24	0	1
25	1	1
26	0	0
27	0	0
28	0	0
29	1	0
30	1	0
31	1	1
32	0	0
33	0	0
34	0	0
36	1	0
37	0	1
38	1	0
40	0	0
42	0	0
43	1	0
44	0	0
45	0	1
47	0	0
48	0	0
49	0	0
54	0	0
	42	42

Figure S7

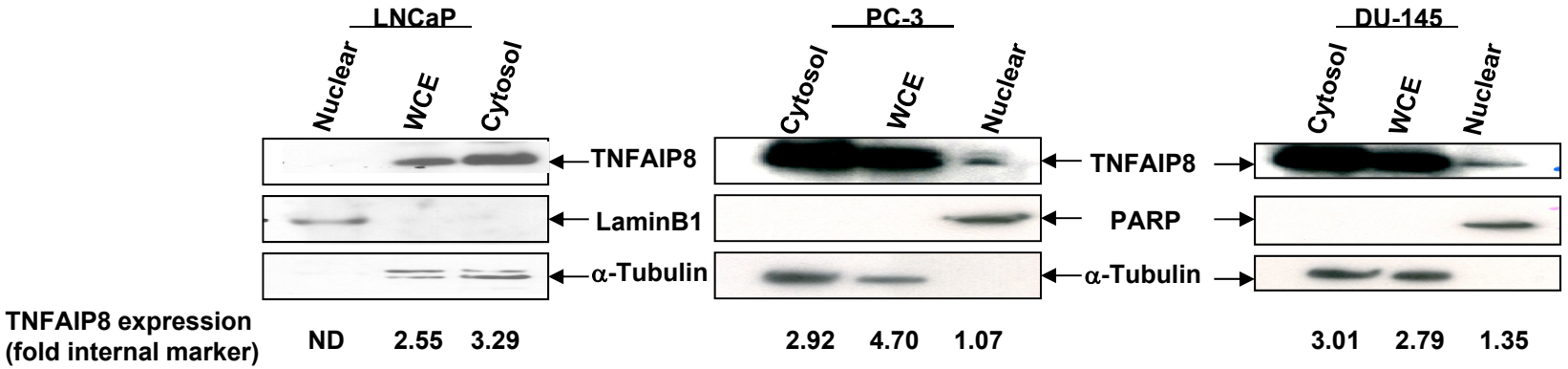

LNCaP
Nuclear
WCE
Cytosol
TNFAIP8
LaminB1
α-Tubulin
PC-3
Cytosol
WCE
Nuclear
TNFAIP8
PARP
α-Tubulin
DU-145
Cytosol
WCE
Nuclear
TNFAIP8 expression
(fold internal marker)
ND
2.55
3.29
2.92
4.70
1.07
3.01
2.79
1.35

Figure S8

Final Network 10

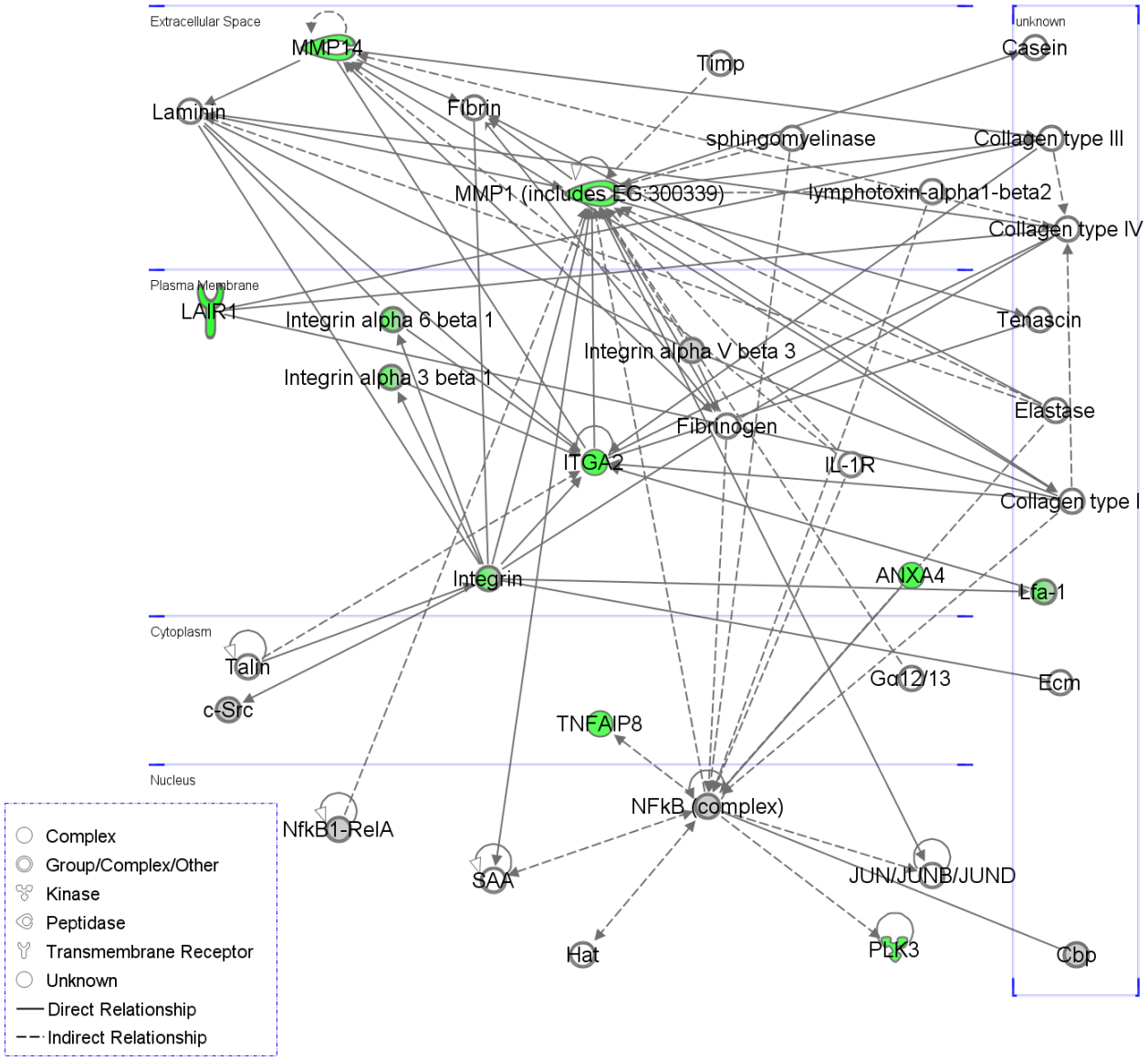
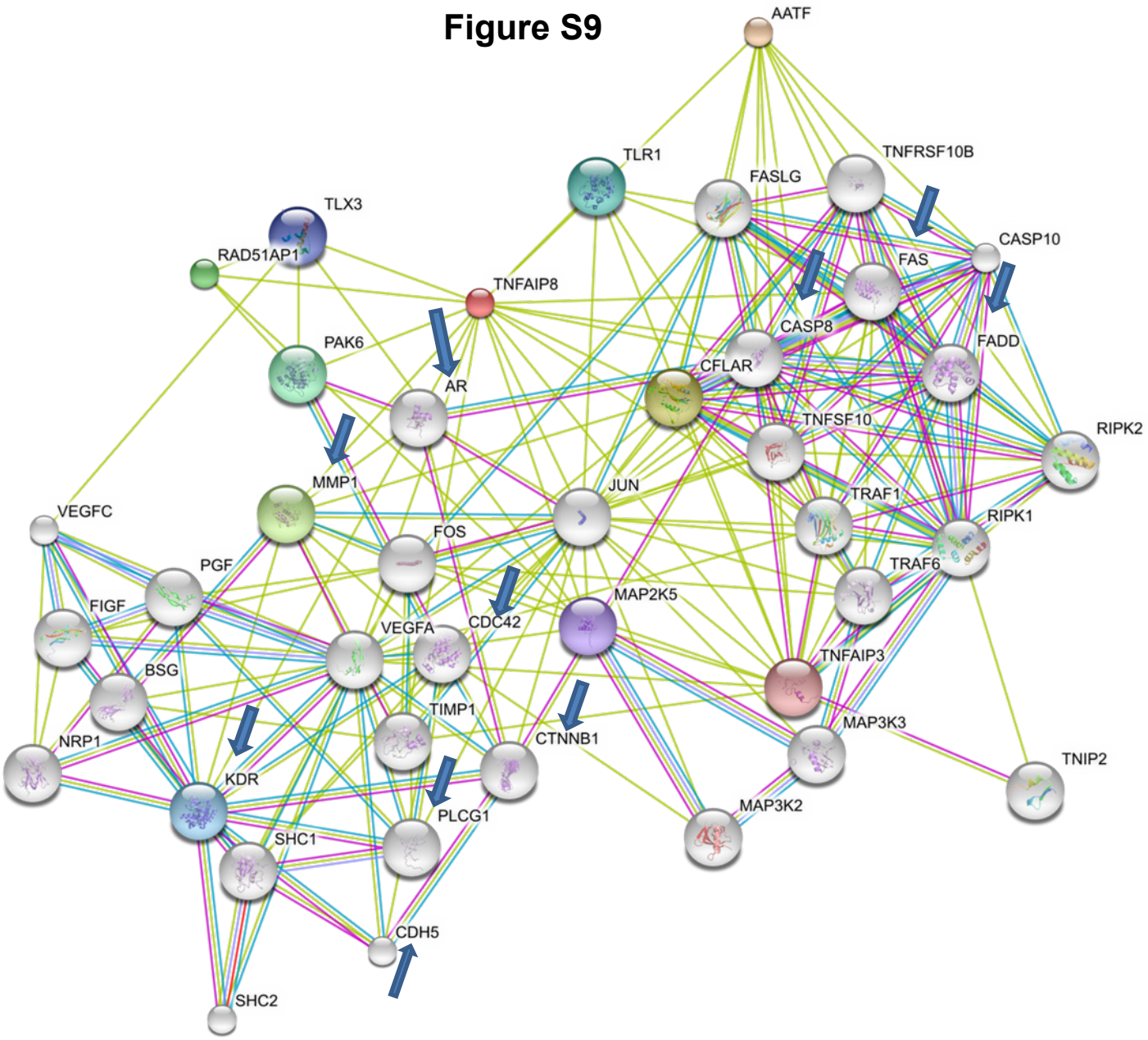


Figure S9


AATF
TLR1
TNFRSF10B
FASLG
TLX3
CASP10
RAD51AP1
FAS
TNFAIP8
CASP8
FADD
PAK6
CFLAR
AR
TNFSF10
RIPK2
MMP1
JUN
TRAF1
VEGFC
RIPK1
FOS
PGF
TRAF6
MAP2K5
FIGF
CDC42
VEGFA
TNFAIP3
BSG
TIMP1
MAP3K3
NRP1
CTNNB1
TNIP2
KDR
MAP3K2
PLCG1
SHC1
CDH5
SHC2