

EGFR and PDGFR differentially promote growth in malignant epithelioid mesothelioma of short and long term survivors

H Kothmaier,¹ F Quehenberger,² I Halbwedl,¹ P Morbini,³ F Demirag,⁴ H Zeren,⁵ C E Comin,⁶ B Murer,⁷ P T Cagle,⁸ R Attanoos,⁹ A R Gibbs,⁹ F Galateau-Salle,¹⁰ H H Popper¹

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¹ Institute of Pathology, Statistics and Documentation, Medical University of Graz, Austria; ² Institute for Medical Informatics, Statistics and Documentation, Medical University of Graz, Austria; ³ Istituto di Anatomia Patologica, IRCCS Policlinico S Matteo, Pavia, Italy;

⁴ Department of Pathology, Ataturk Chest Disease and Chest Surgery Education and Research Hospital, Ankara, Turkey; ⁵ Pathology, Adana University, Adana, Turkey;

⁶ Department of Human Pathology and Oncology, University of Florence, Italy;

⁷ Department of Anatomic Pathology, Mestre, Italy;

⁸ Department of Pathology, The Methodist Hospital and Cornell University Houston, Houston, Texas, USA; ⁹ Department of Histopathology, Cardiff and Vale NHS Trust, Llandough Hospital, Penarth Vale of Glamorgan, Cardiff, UK; ¹⁰ Laboratoire d'Anatomie Pathologique, CHU Cote de Nacre, Caen Cedex, France

Correspondence to:
Dr H H Popper, Institute of Pathology, Medical University of Graz, Auenbruggerplatz 25, A-8036 Graz, Austria;
helmut.popper@meduni-graz.at

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ABSTRACT

Background: Malignant pleural mesothelioma (MPM) is an asbestos related tumour difficult to detect early and treat effectively. Asbestos causes genetic modifications and cell signalling events that favour the resistance of MPM to apoptosis and chemotherapy. Only a small number of patients, approximately 10%, survive more than 3 years. The aim of our study was to assess possible differences within signalling pathways between short term survivors (survival <3 years; STS) and long term survivors (survival >3 years; LTS) of MPM.

Methods: 37 antibodies detecting proteins engaged in cell signalling pathways, enforcing proliferation, anti-apoptosis, angiogenesis and other cellular activities were investigated by tissue microarray (TMA) technology.

Results: Epidermal growth factor receptor (EGFR) was expressed stronger in LTS whereas platelet derived growth factor receptor (PDGFR) signalling was more abundant in STS. Expression of TIE2/Tek, a receptor for tyrosine kinases involved in angiogenesis, was differentially regulated via PDGFR and thus is more important in STS. Antiapoptosis was upregulated in STS by signal transducer and activator of transcription 1 (STAT1)—survivin and related molecules, but not in LTS. Our study provides novel insights into the regulatory mechanisms of signalling pathways in MPM, which differentially promote tumour growth in LTS and STS.

Conclusion: We have demonstrated that small scale proteomics can be carried out by powerful linkage of TMA, immunohistochemistry and statistical methods to identify proteins which might be relevant targets for therapeutic intervention.

Malignant pleural mesothelioma (MPM) is an asbestos related tumour difficult to detect early and treat effectively.¹ Although MPM in general is a rare tumour, its incidence is increasing worldwide. It is estimated that in Europe, Australia and Japan, MPM will peak between 2015 and 2025, whereas in the USA, MPM reached its peak incidence in 2004.²

Most cases are a direct consequence of asbestos exposure 30–40 years earlier. From the onset of symptoms, survival is a few weeks to a few years,³ median survival being 4–12 months in treated or untreated patients.⁴ Only a small number of patients (approximately 10%) survive more than 3 years, which seems to be restricted to the epithelioid subtype.^{5,6} Immunohistochemical analysis of Ki-67/MIB-1,⁷ p27^{kip1},⁸ p21^{cip1} and cyclooxygenase-2^{5,9} have been correlated with survival in

MPM, but their significance has not been entirely clarified.

Asbestos causes genetic modifications and cell signalling events, most notably the upregulation of cell survival and growth pathways, as well as other proteins that favour the resistance of MPM to apoptosis and chemotherapy.¹⁰ Various studies have confirmed the importance of signalling pathways in MPM, including the epidermal growth factor (EGF), platelet derived growth factor (PDGF), hepatocyte growth factor and insulin-like growth factor (IGF) pathways and their downstream signalling molecules, such as the mitogen activating protein kinase and phosphatidylinositol 3-kinase (PI3-K)/Akt kinase, respectively.^{11,12}

The aim of our study was to compare the role of signalling pathways between short term survivors (<3 years; STS) and long term survivors (>3 years; LTS) of MPM, assessing possible differences correlated to the corresponding phenotype. To do this, a large panel of antibodies detecting proteins engaged in these cell signalling pathways, enforcing proliferation, antiapoptosis, angiogenesis and other cellular activities in MPM were investigated by tissue microarray (TMA) technology. Because of the extreme rarity of LTS in MPM, a comparison between STS and LTS with regard to signalling pathways has never been investigated previously.

METHODS

Histological examination and clinical data

Seventy MPM were derived from surgically resected material, either open biopsies or pleurectomies. The cases were diagnosed between 1987 and 2003 and classification was made according to the World Health Organisation (WHO 2004) by each of the contributing authors (PM, FD, HZ, CEC, BM, PTC, RA, ARG., FGS, HHP). At least three positive and two negative markers were applied to confirm the diagnosis of a mesothelioma according to published recommendations.¹³ Forty-eight of 70 cases of epithelioid MPM (collected in USA, UK, Turkey, Italy, France and Austria) with available clinical information and sufficient formalin fixed, paraffin embedded material were selected for TMA construction. Asbestos exposure was confirmed in one-third of the patients in both groups; in the others no exposure data were available. Informed consent from patients was provided with the data sheet submitted with the

Table 1 Clinical data for the 48 patients with epithelioid malignant pleural mesothelioma involved in the study

MPM (n = 48)	Males	Females	Age (y) (range (mean))	Survival (months) (range (mean))	MIB1/Ki-67
LTS (n = 26)	11	15	41–78 (63.7)	36–116 (50.7)	Cases <30% 24/26 (92.3%)
	17	5	30–71 (57.4)	<1–31 (9.1)	Cases >30% 13/22 (40.9%)

36 months was taken as the cut-off level for survival; 26 patients were identified as LTS and 22 as STS.

MIB-1/Ki-67 proliferation index (<30% or >30%) was associated with STS and LTS.

LTS, long term survivors; MPM, malignant pleural mesothelioma; STS, short term survivors.

tissue. In addition, the study was approved by the local Ethical Commission.

Taking 36 months as a cut-off level for survival, 26 patients were identified as LTS and 22 as STS. Survival time was determined from the time of diagnosis until the last follow-up or death. Fifteen of 20 females and 11 of 28 males were LTS. Clinical data were collected for all patients (table 1).

Tissue microarray construction

For TMA construction, a haematoxylin–eosin (H&E) stained section was cut from each paraffin block and re-examined by an experienced pathologist (HP). Five representative tumour regions were morphologically identified and marked on the H&E stained sections. Tissue cylinders with a diameter of 0.6 mm were punched from the marked areas of each block and brought into a recipient paraffin block, using a manual instrument (Beecher Instruments, Sun Prairie, Wisconsin, USA). Sections (5 µm thick) were cut from each TMA and prepared for immunohistochemistry as previously described.¹⁴ Every 15th section was stained with H&E and controlled for the presence of the epithelioid subtype. To overcome the problem of tumour heterogeneity and increase the number of accessible slides, each donor tissue block was punched 6–10 times for construction of two recipient blocks, each containing 243 tissue cores. In these 243 tissue cores, 13 adjacent parenchyma cores were also included.

Immunohistochemistry

Immunohistochemical staining with 37 antibodies was performed on TMA sections, according to the manufacturer's recommendations. In addition, antibodies were pretested on different tissues prior to their use on TMA. Antibodies used in the study for simplicity of reading are given in the abbreviated form (in alphabetically order): AMPKα2, β-catenin, CREB binding protein, c-Fos, c-Jun, c-Met, c-Myc, cyclin D1, epidermal growth factor receptor (EGFR)1, extracellular signal regulated kinase 2 (ERK2), Gab1, Grb2, glycogen synthase kinase 3 (GSK3), IGF1R, IGF1Rα, Janus kinase 1 (JAK1), MAP4K-1, methyl-CpG binding protein 2 (MECP2), p-m-Tor (Ser2448), NFκB p65, pAKT (Ser473), proliferating cell nuclear antigen (PCNA), Src, p27kip1, platelet derived growth factor receptor (PDGFR)α, PDGFRβ, PI3K p110α, p-ELK, p-p70S6K(Ser411), p-Paxillin, signal transducer and transcription factor (STAT)1, STAT3, STAT5, survivin, transforming growth factor (TGF)β, TIE2 and VEGF. A list of the antibodies with additional information about source, dilution, antigen retrieval and detection is given in supplementary table 1 (available online).

Scoring

Immunohistochemical analysis was carried out by one pathologist (HP) without knowledge of patient survival data or core

distribution within the TMA. Protein expression was recorded semiquantitatively. For each core, staining intensity (0, no staining; 1+, weak; 2+, moderate; 3+, strong) together with the percentage (0–100%, in 10% increments) of cells expressing the protein was recorded. Staining scores were calculated by multiplying the percentage of positive cells by the staining intensity. The obtained product scores, ranging from 0 to 300, were used for statistical analysis.

Statistics

The null hypothesis that there is no difference in immunohistochemical parameters between LTS and STS was assessed with Goeman's global test, the R-package globaltest 3.0.2 (<http://www.bioconductor.org/repository/release1.5/package/html/globaltest.html>) with a simulated permutation test criterion. Individual immunohistochemical parameters were tested for differences using Wilcoxon's rank sums test. Correlation coefficients were calculated using Spearman's rank correlation coefficient of the product score. Tests of differences between correlation coefficients of LTS and STS were based on differences between z transformed Spearman correlation coefficients. p Values were calculated from simulated permutation tests.

The statistically relevant correlations and differences between correlations were displayed as network graphics with antibodies as nodes and correlation as edges (see fig 3). p Values below 0.05 were considered to be statistically significant. All permutation tests comprised 10 000 replications.

Correlations between immunohistochemical parameters were displayed as network graphic using Graphviz graph visualisation software (<http://www.graphviz.org>). The absolute values of correlations determined the strength of springs between nodes. The neato algorithm placed the nodes such that the energy of the system was minimised.

RESULTS

Clinical features

Forty-eight MPM cases used for the TMA construction were histologically classified as epithelioid mesotheliomas. Survival of the 26 LTS (survival >36 months) ranged from 36 to 116 months, with a mean of 50.7 months, whereas the 22 STS (<36 months) ranged from <1 to 31 months with a mean of 9.4 months. The mean survival time in the LTS group was 5.4 times longer than that in the STS group (table 1). Sex was neither significantly correlated to survival nor to immunohistochemical reactions.

Immunohistochemistry and statistical evaluation

MIB-1 immunostaining revealed diffuse nuclear staining. In line with published data, the proliferative activity, detected by MIB-1

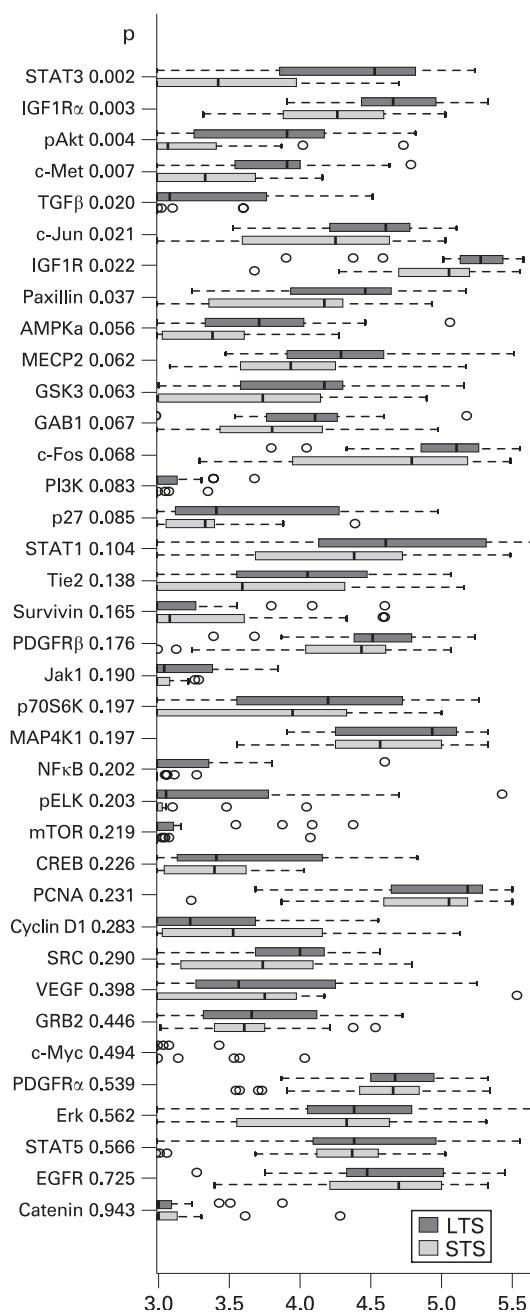


Figure 1 Box and whisker plots of all antibody measurements for long term survivors (LTS) and short term survivors (STS). The $\log_2(x+20)$ transformed product score is shown on the horizontal axis. On the vertical axis for each antibody is the p value of the Wilcoxon rank sum test which compares the median of the product score in LTS and STS. In LTS, significantly higher values ($p<0.05$) were found for STAT3, IGF1Ra, pAkt, c-Met, TGF β , c-Jun, IGF1R and paxillin.

immunoreactivity, was significantly different between LTS and STS ($p=0.014$, Fisher's exact test) (table 1).

Many of the proteins analysed on the TMA were characterised by low expression in the parenchyma and increased expression in the tumour tissue. Comparison of protein expression profiles between LTS and STS showed a significant difference ($p<0.009$, Goeman's global test).

In the comparison of expression levels of single proteins detected by the corresponding antibodies, significantly higher values were found in LTS only for STAT3, IGF1Ra, pAkt,

c-Met, TGF β , c-Jun, IGF1R and paxillin ($p<0.05$, Wilcoxon's rank sum test) (fig 1).

Representative immunohistochemical stains for EGFR, PDGFR, TIE2, STAT1, STAT3 and survivin are shown in fig 2A–F.

Correlations and correlation differences between LTS and STS are displayed in the network graphic (fig 3) and the corresponding correlation differences are summarised in table 2. Differences in correlations indicate differences in the underlying regulatory network.¹⁵ The complete statistical data set, including correlation and p values, is given for LTS and STS and the differences in correlations between LTS and STS (z transformed correlations) in supplementary table 2A–C (available online).

DISCUSSION

We have explored differences in signalling pathways by defining correlation differences in protein expression between LTS and STS (table 2). Only those differences for which a rationale to signalling pathways exist are included in the discussion below. These differences indicate alterations in the underlying regulatory pathway, including proliferation (EGFR or PDGFR), angiogenesis (TIE2) and antiapoptosis (STAT1, survivin), which seem differentially regulated in both groups. A simplified schema showing interactions of EGFR and PDGFR signalling is given in fig 4.

EGFR signalling in LTS

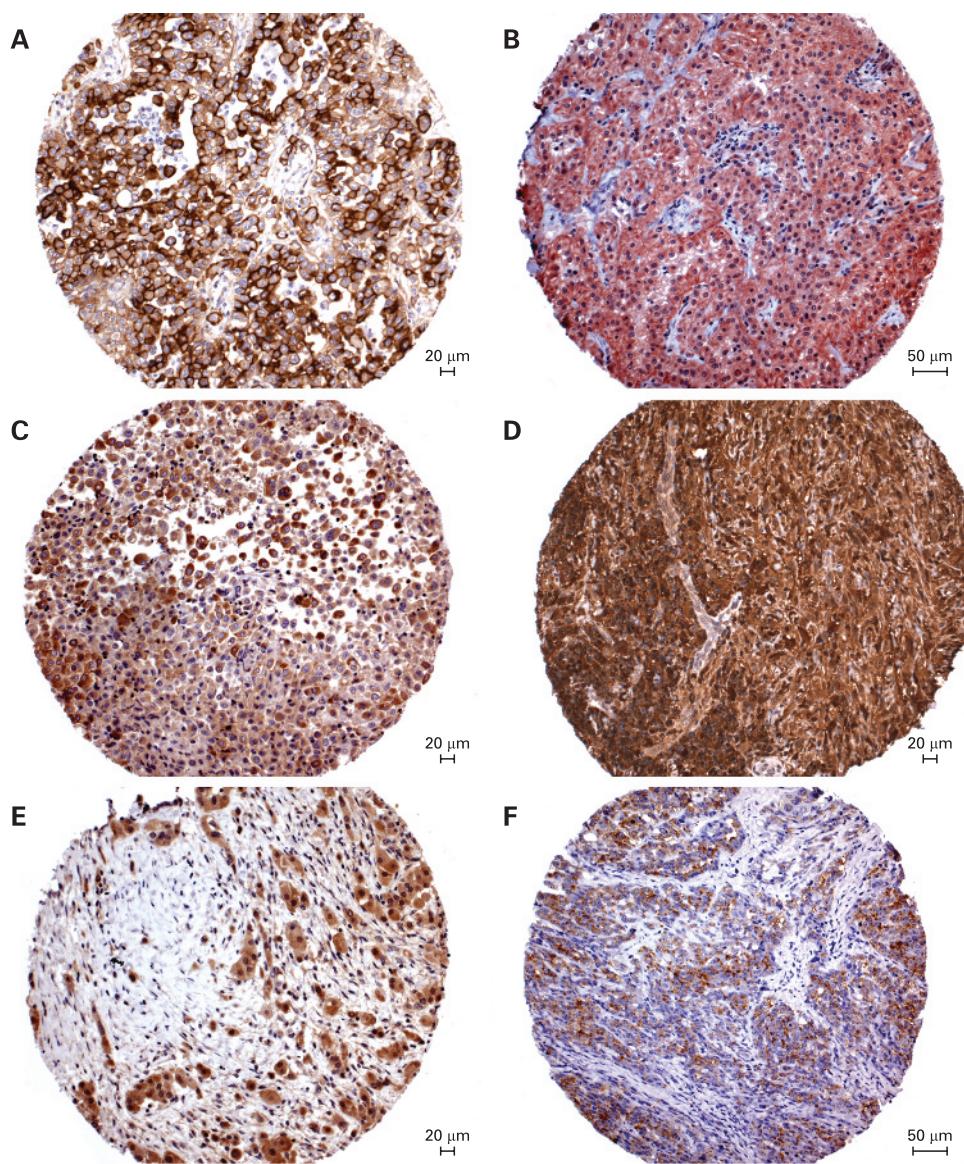
In the LTS, EGFR is correlated with downstream acting STAT3, the proto-oncogenes c-Fos and c-Jun, and proliferating cell nuclear antigen (PCNA). Further EGFR downstream acting proteins including GAB1, Janus kinase 1 (JAK1), plays a pivotal role in phosphorylating STAT3, extracellular signal regulated kinase 2 (ERK2), pAkt and pELK are highly correlated in LTS but not detected in STS. These results indicate that cell survival pathways in LTS are preferentially driven through EGFR. ERK, Akt and STAT3 are on signal transduction pathways triggered by EGFR¹⁶ and the subsequent activation of c-Fos, c-Jun and PCNA is caused by EGFR activation also.¹⁷ Blocking EGFR signalling with the EGFR inhibitors gefitinib and erlotinib in early phase II trials of patients with MPM had limited or no effect,¹⁸ suggesting that EGFR is a therapeutic target only for a minority of mesothelioma patients.¹⁶ From our findings we suppose that this minority belongs to the LTS.

Our data demonstrate that TGF β promotes EGFR signalling in the LTS. It is known that TGF β activates EGFR by inducing expression of the EGFR ligands TGF α and heparin binding EGF-like growth factor.¹⁹ The ligands form dimers and after receptor binding EGFR will be activated for further downstream signalling. TGF β might be responsible for EGFR activation in LTS because of the higher expression value in LTS ($p=0.02$, fig 1) compared with STS as well as TGF β which is correlated with PCNA and IGF1R. The latter is also more highly expressed in LTS ($p=0.003$, fig 1).

PDGFR signalling in STS

Non-neoplastic mesothelial cells express predominantly the PDGFR α subunit and less PDGFR β , while MPM prefers PDGFR β expression.²⁰ In our cases both PDGFR α and PDGFR β were expressed equally in LTS and STS. PDGFR α expression in MPM could be induced by interferon gamma (IFN γ). In THP1 cells it was shown that IFN γ stimulation resulted in augmented expression of PDGFR α through transient STAT1 promoter

Figure 2 Immunohistochemical stains. Immunohistochemical stainings for (A) epidermal growth factor receptor (EGFR), (B) platelet derived growth factor receptor (PDGFR), (C) TIE2, (D) signal transducer and activator of transcription (STAT1), (E) STAT3 and (F) survivin of different cores from the epithelioid malignant pleural mesothelioma tissue microarray (original magnification $\times 200$). Small bars represent 20 μm , large bars 50 μm .



binding,²¹ and IFN γ was described as inducing STAT1 overexpression.²²

Only in STS did we find PDGFR α and PDGFR β associated with downstream glycogen synthase kinase 3 (GSK3), TIE2, c-Fos, cyclin D1 and PCNA. Some of these downstream acting proteins (TIE2, c-fos and PCNA) were also important in LTS. But in LTS these three proteins were associated with EGFR expression. Analysis of correlation differences indicates that PDGFR and EGFR pathways were differentially activated in both groups. Although STS and LTS show similar expression levels of EGFR and PDGFR, correlation analysis showed that LTS prefer EGFR whereas STS prefer PDGFR signalling pathways with different downstream proteins.

PCNA could be a key player in MPM proliferation in both STS and LTS. Interestingly, it is known that binding of EGF, PDGF and IGF1 to their corresponding receptors induces PCNA expression and stabilisation of the resulting mRNA.²³ Taking this into account, our results imply that PCNA expression benefits from EGFR and/or PDGFR activation in LTS and STS. Blocking key proteins acting within several signalling pathways might be potential targets for further translational approaches in MPM. PCNA alone or in combination with PDGFR could be one of these targets.

TIE2 and angiogenesis in MPM

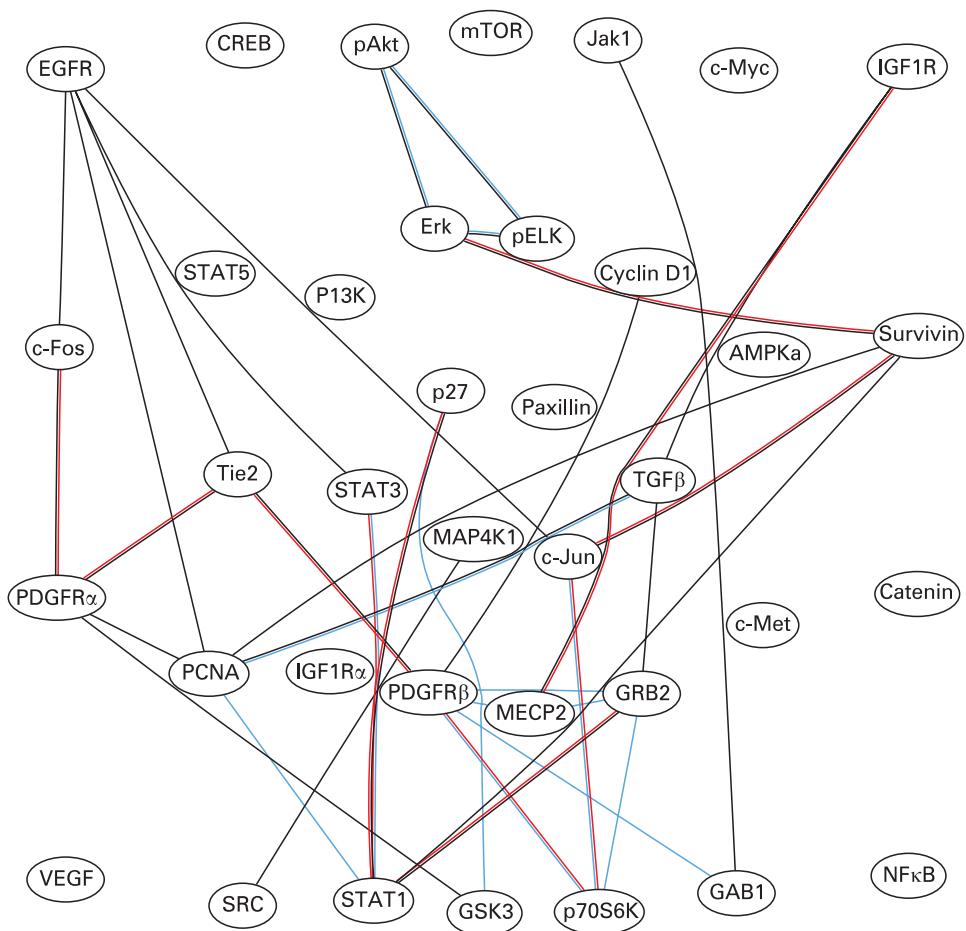
TIE2/Tek, a recently identified RTK principally expressed on vascular endothelium, induces angiogenesis on stimulation through one of the four angiopoietin ligands (Ang1–4). To date, TIE2 protein expression has not been studied in MPM but TIE2 involvement has been reported for breast,²⁴ lung²⁵ and liver tumours.²⁶ In STS we found TIE2 highly associated with PDGFR α and PDGFR β . In contrast with LTS, TIE2 was associated with EGFR. Hence we conclude that PDGFR expression in STS and EGFR in LTS leads to a subsequent upregulation of TIE2 in MPM.

Antiapoptosis induced by survivin and STAT1 in STS

Survivin, a member of the inhibitor of apoptosis protein family, is specifically upregulated in a variety of human cancers and undetectable in normal tissue.²⁷

In our cases, survivin was also exclusively expressed in the tumour tissue whereas it was not detected in adjacent normal pleura. Lower expression of survivin was found in LTS compared with STS (fig 1). Xia and colleagues²⁷ previously reported that overexpression of survivin in mesothelioma cell

Figure 3 Network graphic. The network graphic shows the correlations between antibodies using the Spearman rank correlation of the product score. There are 666 possible correlations between the antibodies but only correlations higher than 0.7 are shown. Blue edges indicate correlations within long term survivors (LTS), red edges indicate correlations within short term survivors (STS). Black edges represent differences in correlations between LTS and STS with a p value below 0.05. Nodes represent the proteins detected by the antibody. The neato algorithm placed correlated antibodies close to each other.



lines and fresh tumour samples contribute to the poor response of MPM cells to chemo- and radiation therapy.

Survivin in STS is highly correlated with ERK2, STAT1, c-Jun and PCNA. The correlation between survivin and STAT1 indicates a novel role for STAT1 promoting antiapoptosis

through survivin upregulation. For chemotherapy resistant breast carcinomas it was reported that survivin was induced by STAT3. In addition, the authors showed that direct inhibition of STAT3 signalling blocked survivin expression.²⁸ Contrary to breast carcinomas, our findings provide a strong

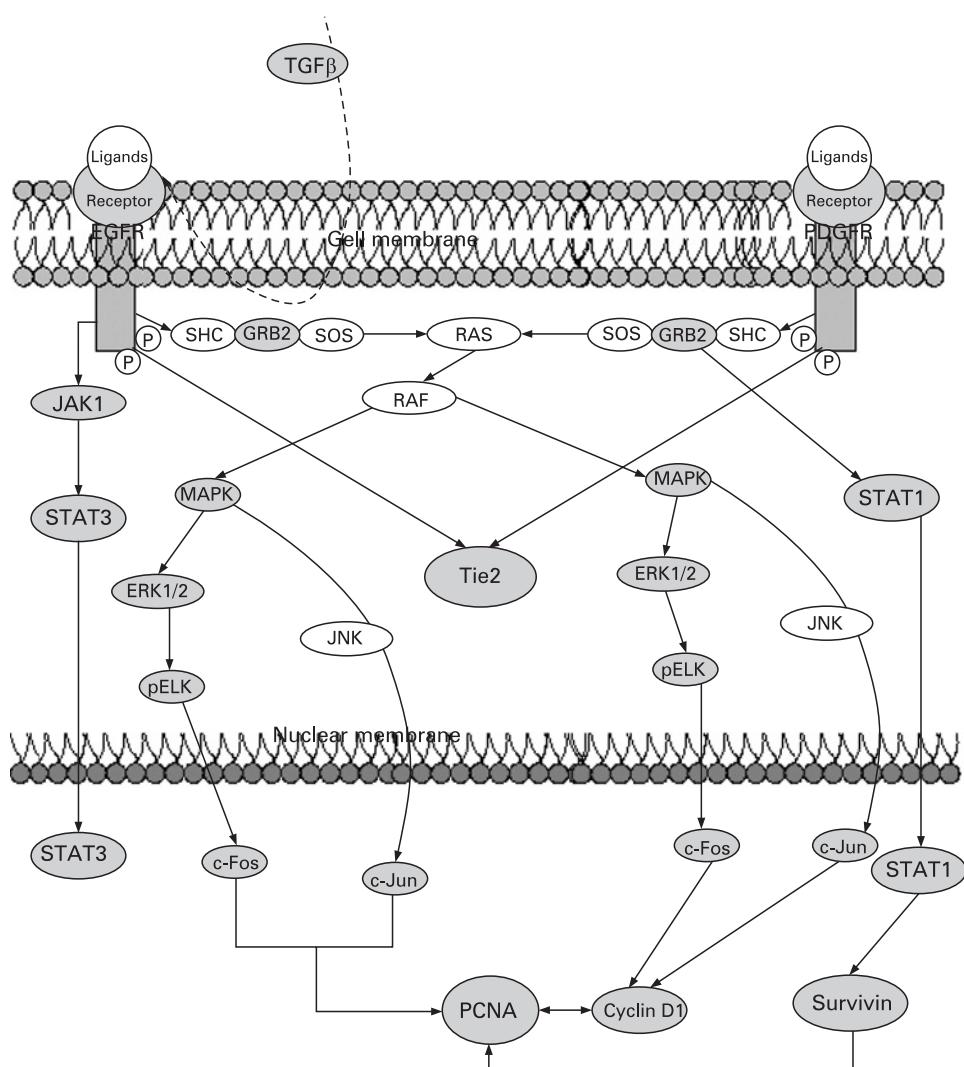
Table 2 Differentially correlated proteins in STS and LTS with $p < 0.05$

Higher correlations in STS				Higher correlations in LTS			
Protein 1	Protein 2	Correlation difference	p Value	Protein 1	Protein 2	Correlation difference	p Value
PDGFR α	Tie2	0.77	0.036	EGFR	PCNA	1.01	0.004
PDGFR β	Tie2	0.78	0.045	EGFR	STAT3	0.80	0.027
PDGFR α	GSK3	0.73	0.039	EGFR	c-Jun	0.70	0.038
PDGFR α	c-Fos	0.73	0.035	EGFR	Tie2	0.86	0.013
PDGFR α	PCNA	0.70	0.045	EGFR	c-Fos	0.65	0.046
PDGFR β	Cyclin D1	0.67	0.049	Erk	pAkt	0.84	0.027
STAT1	p27	0.96	0.013	Erk	pELK	0.82	0.047
STAT1	Survivin	0.76	0.025	GAB1	Jak1	0.67	0.047
STAT1	GRB2	0.77	0.029	IGF1R	TGF β	0.87	0.005
Survivin	Erk	0.91	0.012	PCNA	TGF β	0.87	0.007
Survivin	c-Jun	0.85	0.022				
Survivin	PCNA	0.73	0.032				
IGF1R	MECP2	0.87	0.017				
MAP4K1	SRC	0.69	0.042				

The resulting differences between correlations are given either in the left or right section of the table, depending on whether correlations were higher in STS or LTS, respectively.

EGFR, epidermal growth factor receptor; GSK3, glycogen synthase kinase 3; IGF1R, insulin-like growth factor receptor 1; LTS, long term survivors; MECP2, methyl-CpG binding protein 2; PCNA, proliferating cell nuclear antigen; PDGFR, platelet derived growth factor receptor; STAT, signal transducer and activator of transcription; STS, short term survivors; TGF β , transforming growth factor β .

Figure 4 Schema showing the different interactions of epidermal growth factor receptor (EGFR) and platelet derived growth factor receptor (PDGFR) signalling with respect to long term (LTS) and short term (STS) survivors in malignant pleural mesothelioma (MPM). All molecules shaded in grey have been tested on the tissue microarray and molecules not tested in white; arrows indicate activation, P indicates phosphorylation. For simplicity, only major key proteins are included.



argument that in STS of MPM, survivin upregulation is induced by STAT1, instead of STAT3. Survivin disrupts the intrinsic apoptosis pathway, most probably by blocking activation of caspase 9.²⁹ Enhanced STAT1–survivin and PCNA–survivin interactions imply that in STS, proliferation is promoted and apoptosis is blocked via survivin expression, while in LTS survivin plays no significant role.

STAT1 and MECP2, a novel role in MPM pathogenesis

STATs are a family of latent cytoplasmic signal transducers and activators of transcription with known opposing actions. While STAT3 and STAT5 are referred to as the oncogenic STATs, STAT1 is regarded as a tumour suppressor.³⁰ Curiously, we found STAT1 and STAT5 equally expressed in LTS and STS, whereas STAT3 was higher expressed in LTS ($p = 0.03$, fig 1). In LTS, we found STAT3 further associated with EGFR.

It appears that in MPM the tumour suppressor STAT1 acts similar to an oncogene. Exclusively in STS, STAT1 was correlated with survivin, p27 and Grb2. STAT1 overexpression has also been reported in breast, head and neck cancers, and in some haematological tumours, again suggesting a prosurvival mode of action,³¹ but its role has not been clarified. Only one report describes the role of STAT1 in mesothelioma.³² Buard *et al* reported that IFN γ induces STAT1 overexpression in mesothelioma cell lines.

STAT1 overexpression confers some tumours resistance against radiation and cisplatin treatment.³² Resistance against cisplatin and radiation based therapies is also frequent in MPM. Does increased STAT1 protein also induce resistance in MPM? Our data indicate that the axis STAT1–survivin can be associated with antiapoptotic and therapy resistant mechanisms in MPM, especially in patients with a poor prognosis, such as STS. Although similarly expressed in LTS, no similar association for STAT1 was found.

We also found high levels of MECP2 protein in LTS and STS. MECP2 particularly binds to methylated CpG islands in the genome and can be linked to DNA methylation and histone deacetylation. The implication of MECP2 in neoplasms has already been reported for a variety of human tumours.³³ The prominent interaction between MECP2 and IGFR1 was detected in STS but not in LTS. At present, we are not able to explain the role of MECP2 in STS or in MPM generally. Interestingly, Gordon *et al* detected high levels of FMR1 mRNA (fragile X mental retardation 1), another X-linked gene, in MPM.³⁴ The role of these X-linked genes, MECP2 and FMR1, in MPM is unknown, but involvement in the epigenetic silencing network is indicated.

Our study provides novel insights into the regulatory mechanisms of signalling pathways in MPM, which differentially promote tumour growth in LTS and STS. As shown,

EGFR signalling is activated more strongly in LTS, whereas PDGFR signalling is more abundant in STS. Antiapoptosis is upregulated in STS by STAT1-survivin and related molecules, but not in LTS. We have demonstrated that small scale proteomics can be carried out by a powerful linkage of TMA, immunohistochemistry and statistical methods, to identify differences in protein expression. Nevertheless, these tools were used to generate a hypothesis. Additional in vitro studies are needed to evaluate multiple targeting strategies, including EGFR, PDGFR, TIE2, STAT1 and PCNA. This may provide new treatment options of these aggressive neoplasms. To the best of our knowledge, we have provided the first evidence of an immunohistochemistry based comparison with regard to signalling pathways in MPM between STS and LTS in a large series of LTS.

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Competing interests: None.

Ethics approval: The study was approved by the local Ethical Commission.

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Supplementary table 1. Antibodylist. 37 antibodies (enclosed methodological application) related to different signalling pathways were used for the IHC staining. Antibodies are listed alphabetically.

Antibody	Source	Order number	Dilution	Antigen retrieval*	Detection*
AMPKα2	Santa Cruz	Sc-19129	1:200	MW, 9.0	CM DAB Str.AB/428
β-Catenin	Dako	M3539	1:100	WB	LSAB AEC
CREB binding protein	Chemicon	MAB1133	1:100	KT, 6.0	CM AEC
c-Fos	Santa Cruz	Sc-253	1:200	MW, 9.0	CM DAB
c-Jun	Santa Cruz	Sc-1694	1:200	MW, 9.0	CM DAB
c-Met	Santa Cruz	Sc-161	1:100	Ventana	DAB
c-Myc	Chemicon	MAB8864	1:100	MW, Tris	CM AEC
Cyclin D1	Neomarker	RM-9104	1:25	MW, Prot K	DAB HRP Kit
EGFR1	Dako	K1494	Dako Kit	Dako Kit	Dako Kit
ERK2	Santa Cruz	Sc-1647	1:200	Ventana CC1	Ventana iViewDAB
Gab1	Santa Cruz	Sc-9049	1:200	MW, 6.0	Env DAB
Grb2	Santa Cruz	Sc-255	1:50	Ventana CC1	Ventana iViewDAB
GSK3	Chemicon	AB9295	1:100	MW, 6.0	Env DAB
IGF1R	Neomarker	Ms-641	1:50	MW, EDTA 8.0	CM AEC
IGF1Ra	Santa Cruz	Sc-7952	1:200	MW, 9.0	CM DAB
JAK1	Santa Cruz	Sc-7228	1:500	MW, 9.0	Env DAB
MAP4K-1	Abcam	Ab2646	1:200	WB40	ML AEC
MECP2	Santa Cruz	Sc-20700	1:50	MW, 6.0	CM DAB
p-m-Tor (Ser2448)	Cell Signaling	2971	1:40	MW, Tris 9.5 Urea	Env AEC
NFκB p65	Santa Cruz	Sc-8008	1:2000	MW, 6.0	Dako HRP Kit
p-AKT (Ser473)	Cell Signaling	4051	1:100	MW, 9.0	CM AEC

PCNA	Dako	M0879	1:20	P	CM AEC
p27Kip1	Novocastra	NCL-p27	1:20	MW, 6.0	LSAB AEC
PDGFR-α	Neomarker	Rb-1691	1:50	KT, 6.0	CM AEC
PDGFR-β	Neomarker	Rb-1692	1:100	MW, 9.0	Env AEC
PI3K p110α	Cell Signaling	4254	1:50	MW, 9.0	CM AEC
p-ELK-1	Santa Cruz	Sc-8404	1:50	MW, EDTA 8.0	CM DAB
p-p70S6K (Ser411)	Santa Cruz	Sc-8416	1:200	Ventana CC1	Ventana iViewDAB
p-Paxillin	Neomarker	MS404 P0	1:150	Ventana CC1	Ventana iViewDAB
Src	Cell Signaling	2108	1:50	Ventana CC1	Ventana iViewDAB
STAT 1	Santa Cruz	Sc-592	1:1000	Ventana	DAB
STAT 3	Santa Cruz	Sc-7179	1:100	Ventana	DAB
STAT 5	Santa Cruz	Sc-836	1:100	Ventana	DAB
Survivin	Neomarker	9245	1:200	MW, 6.0	Env DAB
TGF-β	Cymbus	A75-2.1	1:150	MW, 6.0	CM DAB
TIE2	Santa Cruz	Sc-9026	1:50	Ventana CC1	Ventana CC1
VEGF	Santa Cruz	Sc-152	1:500	MW, 9.0	CM DAB

***Abbreviations:**

CM= ChemoMate Dako; MW= Microwave; KT= Heat steamer; 6.0= citrate buffer ph 6.0;

Tris= TrisHCl + 5% Urea, pH9.5; P= Protease Tap XXIV, 0.1 % in PBS

WB 40= waterbath 40min, 90°C epitope retrieval solution; 9.0= target retrieval solution, pH 9.0, Dako

LSAB + AEC= LSAB Peroxidase Blocking Solution and AEC Substrate Chromogen, Dako

CM DAB= ChemoMate Detection Kit Peroxidase/ DAB rabbit/ mouse Chromogen

Env DAB= ChemoMate Dako Envision, HRP, rabbit/mouse

Supplementary table 2a: Correlations (r) and related p-values (p) between antibodies (Protein 1 & 2) for LTS of epithelioid malignant pleural mesothelioma. The correlations were calculated using the Spearman's rank correlation coefficient of the product score.
LTS: long-term survivors (survival >36 months)

LTS	Protein 1	Protein 2	r	p-value
	c.fos	c.jun	0.750	0.00025
	c.fos	c.Met	0.556	0.00498
	c.fos	c.Myc	-0.186	0.09779
	c.fos	cyclinD1	0.516	0.00773
	c.fos	EGFR	-0.006	0.20296
	c.fos	pELK	0.459	0.01397
	c.fos	Erk	0.389	0.02601
	c.fos	GSK3	0.594	0.00321
	c.fos	IGF1Ra	0.453	0.01475
	c.fos	IGF1R	0.360	0.03274
	c.fos	MAP4K1	0.528	0.00687
	c.fos	mTOR	0.568	0.00434
	c.fos	pAkt	0.239	0.07314
	c.fos	PCNA	0.679	0.00098
	c.fos	PDGFRa	0.714	0.00044
	c.fos	PDGFRb	0.581	0.00372
	c.fos	PI3K	0.451	0.01496
	c.fos	STAT1	0.552	0.00526
	c.fos	STAT3	0.549	0.00544
	c.fos	STAT5	0.540	0.00602
	c.fos	TGFb	0.077	0.15886
	c.fos	Tie2	0.647	0.00168
	c.fos	VEGF	0.303	0.04889
	c.fos	AMPKa	0.514	0.00787
	c.fos	GRB2	0.563	0.00463
	c.fos	p70S6K	0.718	0.00042
	c.fos	Catenin	0.134	0.12545
	c.fos	GAB1	0.293	0.05232
	c.fos	NFkB	0.455	0.01449
	c.fos	Jak1	0.344	0.03680
	c.fos	MECP2	0.569	0.00428
	c.fos	CREB	0.625	0.00223
	c.fos	p27	0.354	0.03423
	c.fos	Survivin	0.472	0.01233
	c.fos	Paxillin	0.622	0.00231
	c.fos	SRC	0.494	0.00977
	c.jun	c.Met	0.426	0.01885
	c.jun	c.Myc	-0.187	0.09736
	c.jun	cyclinD1	0.431	0.01804
	c.jun	EGFR	-0.261	0.06376
	c.jun	pELK	0.508	0.00833
	c.jun	Erk	0.568	0.00434
	c.jun	GSK3	0.752	0.00024
	c.jun	IGF1Ra	0.395	0.02485
	c.jun	IGF1R	0.433	0.01762
	c.jun	MAP4K1	0.572	0.00413
	c.jun	mTOR	0.499	0.00925
	c.jun	pAkt	0.347	0.03589
	c.jun	PCNA	0.686	0.00085

c.jun	PDGFRa	0.663	0.00130
c.jun	PDGFRb	0.638	0.00192
c.jun	PI3K	0.599	0.00300
c.jun	STAT1	0.628	0.00216
c.jun	STAT3	0.577	0.00389
c.jun	STAT5	0.408	0.02209
c.jun	TGFb	0.147	0.11826
c.jun	Tie2	0.592	0.00329
c.jun	VEGF	0.341	0.03737
c.jun	AMPKa	0.571	0.00421
c.jun	GRB2	0.792	0.00010
c.jun	p70S6K	0.742	0.00027
c.jun	Catenin	0.254	0.06686
c.jun	GAB1	0.238	0.07346
c.jun	NFkB	0.345	0.03636
c.jun	Jak1	0.578	0.00385
c.jun	MECP2	0.640	0.00186
c.jun	CREB	0.465	0.01323
c.jun	p27	0.608	0.00271
c.jun	Survivin	0.811	0.00006
c.jun	Paxillin	0.789	0.00011
c.jun	SRC	0.455	0.01449
c.Met	c.Myc	-0.104	0.14279
c.Met	cyclinD1	0.610	0.00265
c.Met	EGFR	0.206	0.08820
c.Met	pELK	0.514	0.00792
c.Met	Erk	0.386	0.02678
c.Met	GSK3	0.544	0.00578
c.Met	IGF1Ra	0.472	0.01232
c.Met	IGF1R	0.328	0.04063
c.Met	MAP4K1	0.674	0.00108
c.Met	mTOR	0.153	0.11525
c.Met	pAkt	0.159	0.11183
c.Met	PCNA	0.387	0.02655
c.Met	PDGFRa	0.492	0.00999
c.Met	PDGFRb	0.522	0.00732
c.Met	PI3K	0.616	0.00248
c.Met	STAT1	0.739	0.00028
c.Met	STAT3	0.777	0.00014
c.Met	STAT5	0.611	0.00263
c.Met	TGFb	0.006	0.20299
c.Met	Tie2	0.611	0.00261
c.Met	VEGF	0.149	0.11727
c.Met	AMPKa	0.467	0.01287
c.Met	GRB2	0.543	0.00581
c.Met	p70S6K	0.448	0.01541
c.Met	Catenin	0.148	0.11774
c.Met	GAB1	0.282	0.05603
c.Met	NFkB	0.481	0.01114
c.Met	Jak1	0.330	0.04018
c.Met	MECP2	0.401	0.02339
c.Met	CREB	0.540	0.00603
c.Met	p27	0.485	0.01077
c.Met	Survivin	0.301	0.04937
c.Met	Paxillin	0.546	0.00564
c.Met	SRC	0.480	0.01135

c.Myc	cyclinD1	-0.160	0.11116
c.Myc	EGFR	0.500	0.00909
c.Myc	pELK	0.106	0.14151
c.Myc	Erk	-0.073	0.16151
c.Myc	GSK3	-0.265	0.06223
c.Myc	IGF1Ra	-0.047	0.17799
c.Myc	IGF1R	0.079	0.15763
c.Myc	MAP4K1	-0.168	0.10697
c.Myc	mTOR	0.209	0.08679
c.Myc	pAkt	0.035	0.18529
c.Myc	PCNA	-0.227	0.07853
c.Myc	PDGFRa	-0.093	0.14938
c.Myc	PDGFRb	-0.335	0.03902
c.Myc	PI3K	0.219	0.08238
c.Myc	STAT1	-0.287	0.05442
c.Myc	STAT3	-0.110	0.13917
c.Myc	STAT5	-0.149	0.11731
c.Myc	TGFb	-0.098	0.14666
c.Myc	Tie2	-0.164	0.10940
c.Myc	VEGF	0.127	0.12912
c.Myc	AMPKa	0.036	0.18448
c.Myc	GRB2	-0.139	0.12281
c.Myc	p70S6K	-0.193	0.09452
c.Myc	Catenin	0.195	0.09362
c.Myc	GAB1	-0.136	0.12406
c.Myc	NFkB	0.366	0.03126
c.Myc	Jak1	0.140	0.12192
c.Myc	MECP2	-0.144	0.11975
c.Myc	CREB	-0.120	0.13328
c.Myc	p27	-0.275	0.05866
c.Myc	Survivin	-0.254	0.06672
c.Myc	Paxillin	-0.084	0.15503
c.Myc	SRC	-0.031	0.18768
cyclinD1	EGFR	-0.101	0.14481
cyclinD1	pELK	0.280	0.05667
cyclinD1	Erk	0.265	0.06221
cyclinD1	GSK3	0.347	0.03598
cyclinD1	IGF1Ra	0.137	0.12361
cyclinD1	IGF1R	0.194	0.09405
cyclinD1	MAP4K1	0.520	0.00746
cyclinD1	mTOR	0.211	0.08608
cyclinD1	pAkt	0.485	0.01076
cyclinD1	PCNA	0.610	0.00266
cyclinD1	PDGFRa	0.462	0.01354
cyclinD1	PDGFRb	0.577	0.00390
cyclinD1	PI3K	0.376	0.02896
cyclinD1	STAT1	0.519	0.00755
cyclinD1	STAT3	0.518	0.00762
cyclinD1	STAT5	0.197	0.09233
cyclinD1	TGFb	0.136	0.12441
cyclinD1	Tie2	0.809	0.00006
cyclinD1	VEGF	-0.071	0.16312
cyclinD1	AMPKa	0.260	0.06417
cyclinD1	GRB2	0.510	0.00820
cyclinD1	p70S6K	0.502	0.00885
cyclinD1	Catenin	0.277	0.05808

cyclinD1	GAB1	0.287	0.05431
cyclinD1	NFkB	0.551	0.00532
cyclinD1	Jak1	0.329	0.04039
cyclinD1	MECP2	0.351	0.03487
cyclinD1	CREB	0.344	0.03676
cyclinD1	p27	0.461	0.01369
cyclinD1	Survivin	0.328	0.04070
cyclinD1	Paxillin	0.545	0.00567
cyclinD1	SRC	0.325	0.04150
EGFR	pELK	0.190	0.09571
EGFR	Erk	-0.149	0.11727
EGFR	GSK3	-0.159	0.11206
EGFR	IGF1Ra	0.339	0.03786
EGFR	IGF1R	0.135	0.12471
EGFR	MAP4K1	0.125	0.13035
EGFR	mTOR	0.220	0.08163
EGFR	pAkt	-0.013	0.19875
EGFR	PCNA	-0.257	0.06567
EGFR	PDGFRa	0.083	0.15524
EGFR	PDGFRb	-0.289	0.05361
EGFR	PI3K	0.122	0.13208
EGFR	STAT1	0.050	0.17627
EGFR	STAT3	0.075	0.16059
EGFR	STAT5	0.272	0.05957
EGFR	TGFb	0.020	0.19434
EGFR	Tie2	-0.099	0.14590
EGFR	VEGF	0.200	0.09112
EGFR	AMPKa	0.123	0.13196
EGFR	GRB2	-0.021	0.19398
EGFR	p70S6K	-0.194	0.09380
EGFR	Catenin	0.013	0.19864
EGFR	GAB1	-0.061	0.16905
EGFR	NFkB	0.308	0.04703
EGFR	Jak1	0.074	0.16080
EGFR	MECP2	0.003	0.20444
EGFR	CREB	0.219	0.08233
EGFR	p27	-0.043	0.18058
EGFR	Survivin	-0.296	0.05100
EGFR	Paxillin	-0.036	0.18464
EGFR	SRC	0.255	0.06637
pELK	Erk	0.264	0.06249
pELK	GSK3	0.520	0.00746
pELK	IGF1Ra	0.591	0.00332
pELK	IGF1R	0.599	0.00301
pELK	MAP4K1	0.534	0.00640
pELK	mTOR	0.430	0.01818
pELK	pAkt	0.328	0.04079
pELK	PCNA	0.321	0.04270
pELK	PDGFRa	0.280	0.05694
pELK	PDGFRb	0.328	0.04078
pELK	PI3K	0.542	0.00585
pELK	STAT1	0.528	0.00690
pELK	STAT3	0.577	0.00390
pELK	STAT5	0.325	0.04149
pELK	TGFb	0.186	0.09757
pELK	Tie2	0.325	0.04164

pELK	VEGF	0.533	0.00651
pELK	AMPKa	0.625	0.00223
pELK	GRB2	0.378	0.02859
pELK	p70S6K	0.451	0.01499
pELK	Catenin	0.278	0.05760
pELK	GAB1	0.008	0.20160
pELK	NFkB	0.451	0.01501
pELK	Jak1	0.667	0.00122
pELK	MECP2	0.583	0.00364
pELK	CREB	0.335	0.03895
pELK	p27	0.420	0.01996
pELK	Survivin	0.442	0.01626
pELK	Paxillin	0.542	0.00589
pELK	SRC	0.392	0.02549
Erk	GSK3	0.736	0.00030
Erk	IGF1Ra	0.158	0.11256
Erk	IGF1R	0.104	0.14293
Erk	MAP4K1	0.528	0.00686
Erk	mTOR	0.440	0.01650
Erk	pAkt	0.110	0.13923
Erk	PCNA	0.486	0.01061
Erk	PDGFRa	0.492	0.00994
Erk	PDGFRb	0.362	0.03212
Erk	PI3K	0.467	0.01292
Erk	STAT1	0.470	0.01251
Erk	STAT3	0.360	0.03271
Erk	STAT5	0.129	0.12794
Erk	TGFb	-0.029	0.18902
Erk	Tie2	0.373	0.02967
Erk	VEGF	0.429	0.01837
Erk	AMPKa	0.024	0.19223
Erk	GRB2	0.472	0.01226
Erk	p70S6K	0.468	0.01279
Erk	Catenin	0.247	0.06974
Erk	GAB1	0.274	0.05892
Erk	NFkB	-0.122	0.13202
Erk	Jak1	0.168	0.10711
Erk	MECP2	0.235	0.07471
Erk	CREB	0.418	0.02029
Erk	p27	0.375	0.02919
Erk	Survivin	0.746	0.00026
Erk	Paxillin	0.450	0.01507
Erk	SRC	0.462	0.01360
GSK3	IGF1Ra	0.465	0.01315
GSK3	IGF1R	0.386	0.02677
GSK3	MAP4K1	0.651	0.00159
GSK3	mTOR	0.483	0.01094
GSK3	pAkt	0.101	0.14463
GSK3	PCNA	0.584	0.00360
GSK3	PDGFRa	0.624	0.00225
GSK3	PDGFRb	0.577	0.00388
GSK3	PI3K	0.627	0.00219
GSK3	STAT1	0.745	0.00026
GSK3	STAT3	0.621	0.00233
GSK3	STAT5	0.369	0.03056
GSK3	TGFb	0.054	0.17355

GSK3	Tie2	0.524	0.00718
GSK3	VEGF	0.348	0.03576
GSK3	AMPKa	0.466	0.01309
GSK3	GRB2	0.563	0.00461
GSK3	p70S6K	0.690	0.00079
GSK3	Catenin	0.160	0.11124
GSK3	GAB1	0.342	0.03713
GSK3	NFkB	0.119	0.13394
GSK3	Jak1	0.434	0.01756
GSK3	MECP2	0.417	0.02039
GSK3	CREB	0.362	0.03235
GSK3	p27	0.548	0.00549
GSK3	Survivin	0.842	0.00002
GSK3	Paxillin	0.724	0.00037
GSK3	SRC	0.469	0.01268
IGF1Ra	IGF1R	0.210	0.08640
IGF1Ra	MAP4K1	0.579	0.00380
IGF1Ra	mTOR	0.395	0.02475
IGF1Ra	pAkt	0.278	0.05752
IGF1Ra	PCNA	0.300	0.04965
IGF1Ra	PDGFRa	0.443	0.01608
IGF1Ra	PDGFRb	0.510	0.00823
IGF1Ra	PI3K	0.603	0.00284
IGF1Ra	STAT1	0.690	0.00079
IGF1Ra	STAT3	0.684	0.00090
IGF1Ra	STAT5	0.420	0.01990
IGF1Ra	TGFb	0.417	0.02035
IGF1Ra	Tie2	0.434	0.01749
IGF1Ra	VEGF	0.480	0.01129
IGF1Ra	AMPKa	0.722	0.00039
IGF1Ra	GRB2	0.391	0.02571
IGF1Ra	p70S6K	0.617	0.00244
IGF1Ra	Catenin	-0.092	0.14993
IGF1Ra	GAB1	0.410	0.02171
IGF1Ra	NFkB	0.280	0.05679
IGF1Ra	Jak1	0.517	0.00766
IGF1Ra	MECP2	0.433	0.01775
IGF1Ra	CREB	0.399	0.02396
IGF1Ra	p27	0.566	0.00446
IGF1Ra	Survivin	0.293	0.05232
IGF1Ra	Paxillin	0.595	0.00317
IGF1Ra	SRC	0.333	0.03952
IGF1R	MAP4K1	0.509	0.00828
IGF1R	mTOR	0.387	0.02653
IGF1R	pAkt	0.382	0.02756
IGF1R	PCNA	0.164	0.10926
IGF1R	PDGFRa	0.006	0.20319
IGF1R	PDGFRb	0.302	0.04901
IGF1R	PI3K	0.303	0.04867
IGF1R	STAT1	0.286	0.05463
IGF1R	STAT3	0.345	0.03641
IGF1R	STAT5	0.388	0.02621
IGF1R	TGFb	-0.248	0.06925
IGF1R	Tie2	0.073	0.16127
IGF1R	VEGF	0.193	0.09438
IGF1R	AMPKa	0.453	0.01479

IGF1R	GRB2	0.344	0.03664
IGF1R	p70S6K	0.328	0.04085
IGF1R	Catenin	0.416	0.02052
IGF1R	GAB1	0.026	0.19056
IGF1R	NFkB	0.626	0.00220
IGF1R	Jak1	0.540	0.00600
IGF1R	MECP2	0.756	0.00022
IGF1R	CREB	0.248	0.06955
IGF1R	p27	0.353	0.03444
IGF1R	Survivin	0.380	0.02803
IGF1R	Paxillin	0.416	0.02068
IGF1R	SRC	0.340	0.03770
MAP4K1	mTOR	0.388	0.02633
MAP4K1	pAkt	0.370	0.03042
MAP4K1	PCNA	0.451	0.01497
MAP4K1	PDGFRa	0.433	0.01765
MAP4K1	PDGFRb	0.646	0.00172
MAP4K1	PI3K	0.631	0.00210
MAP4K1	STAT1	0.761	0.00020
MAP4K1	STAT3	0.727	0.00036
MAP4K1	STAT5	0.505	0.00857
MAP4K1	TGFb	0.235	0.07502
MAP4K1	Tie2	0.560	0.00477
MAP4K1	VEGF	0.279	0.05736
MAP4K1	AMPKa	0.423	0.01945
MAP4K1	GRB2	0.625	0.00222
MAP4K1	p70S6K	0.703	0.00058
MAP4K1	Catenin	0.087	0.15315
MAP4K1	GAB1	0.337	0.03857
MAP4K1	NFkB	0.378	0.02852
MAP4K1	Jak1	0.602	0.00288
MAP4K1	MECP2	0.607	0.00273
MAP4K1	CREB	0.527	0.00696
MAP4K1	p27	0.611	0.00261
MAP4K1	Survivin	0.589	0.00339
MAP4K1	Paxillin	0.729	0.00035
MAP4K1	SRC	0.590	0.00336
mTOR	pAkt	0.437	0.01710
mTOR	PCNA	0.512	0.00807
mTOR	PDGFRa	0.452	0.01491
mTOR	PDGFRb	0.269	0.06086
mTOR	PI3K	0.375	0.02908
mTOR	STAT1	0.208	0.08706
mTOR	STAT3	0.335	0.03886
mTOR	STAT5	0.187	0.09726
mTOR	TGFb	0.023	0.19281
mTOR	Tie2	0.356	0.03366
mTOR	VEGF	0.432	0.01776
mTOR	AMPKa	0.390	0.02574
mTOR	GRB2	0.302	0.04890
mTOR	p70S6K	0.532	0.00659
mTOR	Catenin	0.103	0.14338
mTOR	GAB1	0.372	0.02996
mTOR	NFkB	0.303	0.04867
mTOR	Jak1	0.508	0.00837
mTOR	MECP2	0.494	0.00974

mTOR	CREB	0.221	0.08145
mTOR	p27	0.141	0.12140
mTOR	Survivin	0.392	0.02542
mTOR	Paxillin	0.408	0.02203
mTOR	SRC	0.310	0.04629
pAkt	PCNA	0.503	0.00878
pAkt	PDGFRa	0.059	0.17007
pAkt	PDGFRb	0.607	0.00272
pAkt	PI3K	0.214	0.08469
pAkt	STAT1	0.304	0.04839
pAkt	STAT3	0.404	0.02289
pAkt	STAT5	0.143	0.12049
pAkt	TGFb	0.249	0.06875
pAkt	Tie2	0.400	0.02367
pAkt	VEGF	0.302	0.04904
pAkt	AMPKa	0.340	0.03771
pAkt	GRB2	0.447	0.01555
pAkt	p70S6K	0.529	0.00680
pAkt	Catenin	0.413	0.02119
pAkt	GAB1	0.389	0.02606
pAkt	NFkB	0.363	0.03198
pAkt	Jak1	0.516	0.00774
pAkt	MECP2	0.695	0.00070
pAkt	CREB	0.211	0.08606
pAkt	p27	0.521	0.00740
pAkt	Survivin	0.217	0.08291
pAkt	Paxillin	0.446	0.01565
pAkt	SRC	0.274	0.05892
PCNA	PDGFRa	0.572	0.00414
PCNA	PDGFRb	0.669	0.00117
PCNA	PI3K	0.506	0.00854
PCNA	STAT1	0.547	0.00559
PCNA	STAT3	0.566	0.00443
PCNA	STAT5	0.273	0.05924
PCNA	TGFb	0.182	0.09971
PCNA	Tie2	0.635	0.00199
PCNA	VEGF	0.107	0.14093
PCNA	AMPKa	0.200	0.09095
PCNA	GRB2	0.538	0.00617
PCNA	p70S6K	0.741	0.00028
PCNA	Catenin	0.226	0.07888
PCNA	GAB1	0.417	0.02035
PCNA	NFkB	0.237	0.07394
PCNA	Jak1	0.414	0.02104
PCNA	MECP2	0.431	0.01796
PCNA	CREB	0.320	0.04300
PCNA	p27	0.486	0.01059
PCNA	Survivin	0.495	0.00958
PCNA	Paxillin	0.620	0.00236
PCNA	SRC	0.368	0.03072
PDGFRa	PDGFRb	0.400	0.02365
PDGFRa	PI3K	0.526	0.00702
PDGFRa	STAT1	0.633	0.00203
PDGFRa	STAT3	0.532	0.00657
PDGFRa	STAT5	0.282	0.05613
PDGFRa	TGFb	0.222	0.08070

PDGFRa	Tie2	0.713	0.00045
PDGFRa	VEGF	0.251	0.06814
PDGFRa	AMPKa	0.413	0.02117
PDGFRa	GRB2	0.603	0.00286
PDGFRa	p70S6K	0.571	0.00422
PDGFRa	Catenin	-0.081	0.15633
PDGFRa	GAB1	0.338	0.03823
PDGFRa	NFkB	0.190	0.09567
PDGFRa	Jak1	0.293	0.05225
PDGFRa	MECP2	0.230	0.07731
PDGFRa	CREB	0.505	0.00865
PDGFRa	p27	0.440	0.01651
PDGFRa	Survivin	0.512	0.00804
PDGFRa	Paxillin	0.692	0.00076
PDGFRa	SRC	0.310	0.04646
PDGFRb	PI3K	0.461	0.01371
PDGFRb	STAT1	0.714	0.00044
PDGFRb	STAT3	0.784	0.00012
PDGFRb	STAT5	0.507	0.00847
PDGFRb	TGFb	0.303	0.04886
PDGFRb	Tie2	0.728	0.00035
PDGFRb	VEGF	0.210	0.08643
PDGFRb	AMPKa	0.557	0.00496
PDGFRb	GRB2	0.641	0.00183
PDGFRb	p70S6K	0.893	0.00000
PDGFRb	Catenin	0.278	0.05743
PDGFRb	GAB1	0.666	0.00124
PDGFRb	NFkB	0.280	0.05697
PDGFRb	Jak1	0.426	0.01890
PDGFRb	MECP2	0.674	0.00107
PDGFRb	CREB	0.506	0.00855
PDGFRb	p27	0.667	0.00122
PDGFRb	Survivin	0.481	0.01124
PDGFRb	Paxillin	0.772	0.00016
PDGFRb	SRC	0.520	0.00745
PI3K	STAT1	0.645	0.00175
PI3K	STAT3	0.640	0.00188
PI3K	STAT5	0.268	0.06135
PI3K	TGFb	0.254	0.06676
PI3K	Tie2	0.465	0.01313
PI3K	VEGF	0.149	0.11717
PI3K	AMPKa	0.480	0.01126
PI3K	GRB2	0.600	0.00294
PI3K	p70S6K	0.643	0.00178
PI3K	Catenin	0.203	0.08966
PI3K	GAB1	0.163	0.10993
PI3K	NFkB	0.496	0.00949
PI3K	Jak1	0.620	0.00236
PI3K	MECP2	0.322	0.04234
PI3K	CREB	0.218	0.08286
PI3K	p27	0.538	0.00612
PI3K	Survivin	0.445	0.01578
PI3K	Paxillin	0.761	0.00020
PI3K	SRC	0.381	0.02782
STAT1	STAT3	0.773	0.00016
STAT1	STAT5	0.440	0.01653

STAT1	TGFb	0.364	0.03178
STAT1	Tie2	0.613	0.00257
STAT1	VEGF	0.300	0.04976
STAT1	AMPKa	0.586	0.00352
STAT1	GRB2	0.708	0.00051
STAT1	p70S6K	0.678	0.00100
STAT1	Catenin	0.182	0.09959
STAT1	GAB1	0.360	0.03274
STAT1	NFkB	0.236	0.07469
STAT1	Jak1	0.527	0.00695
STAT1	MECP2	0.469	0.01261
STAT1	CREB	0.524	0.00714
STAT1	p27	0.826	0.00004
STAT1	Survivin	0.631	0.00208
STAT1	Paxillin	0.782	0.00013
STAT1	SRC	0.567	0.00438
STAT3	STAT5	0.641	0.00185
STAT3	TGFb	0.264	0.06249
STAT3	Tie2	0.761	0.00020
STAT3	VEGF	0.295	0.05136
STAT3	AMPKa	0.656	0.00147
STAT3	GRB2	0.608	0.00270
STAT3	p70S6K	0.736	0.00030
STAT3	Catenin	0.059	0.17037
STAT3	GAB1	0.663	0.00130
STAT3	NFkB	0.410	0.02162
STAT3	Jak1	0.557	0.00493
STAT3	MECP2	0.592	0.00327
STAT3	CREB	0.577	0.00388
STAT3	p27	0.556	0.00500
STAT3	Survivin	0.391	0.02559
STAT3	Paxillin	0.752	0.00024
STAT3	SRC	0.444	0.01595
STAT5	TGFb	-0.161	0.11100
STAT5	Tie2	0.373	0.02970
STAT5	VEGF	0.251	0.06822
STAT5	AMPKa	0.409	0.02184
STAT5	GRB2	0.331	0.03992
STAT5	p70S6K	0.445	0.01578
STAT5	Catenin	0.027	0.19033
STAT5	GAB1	0.365	0.03162
STAT5	NFkB	0.333	0.03936
STAT5	Jak1	0.191	0.09532
STAT5	MECP2	0.485	0.01075
STAT5	CREB	0.491	0.01000
STAT5	p27	0.268	0.06130
STAT5	Survivin	0.178	0.10173
STAT5	Paxillin	0.409	0.02183
STAT5	SRC	0.518	0.00757
TGFb	Tie2	0.250	0.06848
TGFb	VEGF	0.088	0.15217
TGFb	AMPKa	0.304	0.04850
TGFb	GRB2	0.401	0.02354
TGFb	p70S6K	0.350	0.03521
TGFb	Catenin	0.013	0.19865
TGFb	GAB1	0.108	0.14035

TGFb	NFkB	-0.091	0.15061
TGFb	Jak1	0.443	0.01612
TGFb	MECP2	0.111	0.13846
TGFb	CREB	0.202	0.09006
TGFb	p27	0.220	0.08179
TGFb	Survivin	0.025	0.19123
TGFb	Paxillin	0.374	0.02929
TGFb	SRC	0.271	0.06009
Tie2	VEGF	0.177	0.10223
Tie2	AMPKa	0.515	0.00781
Tie2	GRB2	0.596	0.00311
Tie2	p70S6K	0.718	0.00042
Tie2	Catenin	-0.007	0.20233
Tie2	GAB1	0.604	0.00283
Tie2	NFkB	0.408	0.02211
Tie2	Jak1	0.320	0.04296
Tie2	MECP2	0.423	0.01938
Tie2	CREB	0.555	0.00507
Tie2	p27	0.463	0.01337
Tie2	Survivin	0.423	0.01939
Tie2	Paxillin	0.718	0.00042
Tie2	SRC	0.290	0.05313
VEGF	AMPKa	0.368	0.03084
VEGF	GRB2	0.134	0.12515
VEGF	p70S6K	0.291	0.05303
VEGF	Catenin	0.071	0.16263
VEGF	GAB1	0.246	0.07039
VEGF	NFkB	-0.020	0.19479
VEGF	Jak1	0.285	0.05507
VEGF	MECP2	0.341	0.03735
VEGF	CREB	0.382	0.02766
VEGF	p27	0.227	0.07864
VEGF	Survivin	0.475	0.01198
VEGF	Paxillin	0.217	0.08296
VEGF	SRC	0.182	0.09942
AMPKa	GRB2	0.548	0.00552
AMPKa	p70S6K	0.568	0.00433
AMPKa	Catenin	0.131	0.12702
AMPKa	GAB1	0.350	0.03527
AMPKa	NFkB	0.515	0.00784
AMPKa	Jak1	0.606	0.00277
AMPKa	MECP2	0.626	0.00221
AMPKa	CREB	0.394	0.02502
AMPKa	p27	0.488	0.01038
AMPKa	Survivin	0.352	0.03477
AMPKa	Paxillin	0.639	0.00190
AMPKa	SRC	0.323	0.04217
GRB2	p70S6K	0.637	0.00193
GRB2	Catenin	0.338	0.03822
GRB2	GAB1	0.208	0.08728
GRB2	NFkB	0.348	0.03572
GRB2	Jak1	0.509	0.00829
GRB2	MECP2	0.673	0.00110
GRB2	CREB	0.634	0.00201
GRB2	p27	0.713	0.00045
GRB2	Survivin	0.578	0.00384

GRB2	Paxillin	0.809	0.00006
GRB2	SRC	0.591	0.00331
p70S6K	Catenin	0.190	0.09600
p70S6K	GAB1	0.563	0.00463
p70S6K	NFkB	0.313	0.04540
p70S6K	Jak1	0.538	0.00612
p70S6K	MECP2	0.651	0.00160
p70S6K	CREB	0.453	0.01468
p70S6K	p27	0.597	0.00310
p70S6K	Survivin	0.557	0.00491
p70S6K	Paxillin	0.877	0.00000
p70S6K	SRC	0.530	0.00674
Catenin	GAB1	-0.037	0.18393
Catenin	NFkB	0.335	0.03894
Catenin	Jak1	0.236	0.07444
Catenin	MECP2	0.365	0.03154
Catenin	CREB	0.169	0.10668
Catenin	p27	0.349	0.03534
Catenin	Survivin	0.206	0.08802
Catenin	Paxillin	0.266	0.06190
Catenin	SRC	0.602	0.00288
GAB1	NFkB	0.078	0.15814
GAB1	Jak1	0.181	0.10004
GAB1	MECP2	0.333	0.03939
GAB1	CREB	0.381	0.02773
GAB1	p27	0.241	0.07253
GAB1	Survivin	0.165	0.10843
GAB1	Paxillin	0.378	0.02851
GAB1	SRC	0.173	0.10439
NFkB	Jak1	0.499	0.00924
NFkB	MECP2	0.473	0.01219
NFkB	CREB	0.237	0.07423
NFkB	p27	0.243	0.07130
NFkB	Survivin	0.065	0.16663
NFkB	Paxillin	0.420	0.01987
NFkB	SRC	0.207	0.08760
Jak1	MECP2	0.540	0.00602
Jak1	CREB	0.082	0.15605
Jak1	p27	0.445	0.01586
Jak1	Survivin	0.435	0.01734
Jak1	Paxillin	0.618	0.00240
Jak1	SRC	0.342	0.03724
MECP2	CREB	0.586	0.00351
MECP2	p27	0.567	0.00441
MECP2	Survivin	0.428	0.01846
MECP2	Paxillin	0.634	0.00201
MECP2	SRC	0.496	0.00956
CREB	p27	0.378	0.02841
CREB	Survivin	0.323	0.04215
CREB	Paxillin	0.476	0.01185
CREB	SRC	0.559	0.00485
p27	Survivin	0.620	0.00235
p27	Paxillin	0.739	0.00028
p27	SRC	0.454	0.01463
Survivin	Paxillin	0.620	0.00236
Survivin	SRC	0.349	0.03544

Paxillin SRC 0.556 0.00499

and Protein 2'

Supplementary table 2b: Correlations (r) and related p-values (p) between antibodies (Protein 1 and Protein 2) for STS of epithelioid malignant pleural mesothelioma. The correlations were calculated using the Spearman's rank correlation coefficient of the product score.
 STS: short-term survivors (survival <36 months)

STS	Protein 1	Protein 2	r	p-value
c.fos	c.jun	0.514	0.00728	
c.fos	c.Met	0.158	0.44060	
c.fos	c.Myc	0.383	0.05318	
c.fos	cyclinD1	0.305	0.12999	
c.fos	EGFR	0.499	0.00940	
c.fos	pELK	0.541	0.00432	
c.fos	Erk	0.393	0.04692	
c.fos	GSK3	0.220	0.28040	
c.fos	IGF1Ra	0.436	0.02600	
c.fos	IGF1R	0.467	0.01620	
c.fos	MAP4K1	0.234	0.25081	
c.fos	mTOR	0.589	0.00156	
c.fos	pAkt	0.546	0.00394	
c.fos	PCNA	0.674	0.00016	
c.fos	PDGFRa	0.131	0.52340	
c.fos	PDGFRb	0.323	0.10762	
c.fos	PI3K	0.337	0.09202	
c.fos	STAT1	0.390	0.04864	
c.fos	STAT3	0.533	0.00506	
c.fos	STAT5	0.305	0.12978	
c.fos	TGFb	0.610	0.00093	
c.fos	Tie2	0.554	0.00329	
c.fos	VEGF	0.144	0.48379	
c.fos	AMPKa	0.132	0.51907	
c.fos	GRB2	0.067	0.74471	
c.fos	p70S6K	0.446	0.02243	
c.fos	Catenin	0.556	0.00317	
c.fos	GAB1	0.072	0.72597	
c.fos	NFkB	0.290	0.15058	

c.fos	Jak1	0.347	0.08283
c.fos	MECP2	0.200	0.32792
c.fos	CREB	0.572	0.00225
c.fos	p27	0.366	0.06612
c.fos	Survivin	0.205	0.31466
c.fos	Paxillin	0.596	0.00133
c.fos	SRC	0.443	0.02350
c.jun	c.Met	0.212	0.29891
c.jun	c.Myc	0.197	0.33412
c.jun	cyclinD1	0.408	0.03873
c.jun	EGFR	0.354	0.07593
c.jun	pELK	0.276	0.17207
c.jun	Erk	0.263	0.19453
c.jun	GSK3	0.262	0.19589
c.jun	IGF1Ra	0.354	0.07577
c.jun	IGF1R	0.019	0.92779
c.jun	MAP4K1	0.479	0.01323
c.jun	mTOR	0.331	0.09809
c.jun	pAkt	0.408	0.03847
c.jun	PCNA	0.407	0.03890
c.jun	PDGFRa	0.252	0.21513
c.jun	PDGFRb	0.561	0.00286
c.jun	PI3K	0.509	0.00791
c.jun	STAT1	0.350	0.08009
c.jun	STAT3	0.397	0.04437
c.jun	STAT5	0.263	0.19437
c.jun	TGFb	0.218	0.28413
c.jun	Tie2	0.402	0.04158
c.jun	VEGF	0.455	0.01962
c.jun	AMPKa	0.516	0.00692
c.jun	GRB2	0.511	0.00764
c.jun	p70S6K	0.752	0.00001
c.jun	Catenin	0.660	0.00024
c.jun	GAB1	0.490	0.01097
c.jun	NFkB	0.524	0.00605
c.jun	Jak1	0.548	0.00377

c.jun	MECP2	0.500	0.00929
c.jun	CREB	0.668	0.00019
c.jun	p27	0.264	0.19172
c.jun	Survivin	0.190	0.35381
c.jun	Paxillin	0.442	0.02369
c.jun	SRC	0.330	0.09937
c.Met	c.Myc	0.393	0.04685
c.Met	cyclinD1	0.247	0.22309
c.Met	EGFR	0.151	0.46292
c.Met	pELK	0.329	0.10113
c.Met	Erk	0.429	0.02857
c.Met	GSK3	0.187	0.36016
c.Met	IGF1Ra	0.302	0.13354
c.Met	IGF1R	0.110	0.59258
c.Met	MAP4K1	0.098	0.63471
c.Met	mTOR	0.181	0.37648
c.Met	pAkt	0.247	0.22403
c.Met	PCNA	0.282	0.16250
c.Met	PDGFRa	0.234	0.25087
c.Met	PDGFRb	0.440	0.02436
c.Met	PI3K	0.021	0.91750
c.Met	STAT1	0.418	0.03372
c.Met	STAT3	0.418	0.03358
c.Met	STAT5	0.142	0.48897
c.Met	TGFb	0.300	0.13688
c.Met	Tie2	0.367	0.06537
c.Met	VEGF	0.255	0.20779
c.Met	AMPKa	0.542	0.00423
c.Met	GRB2	0.138	0.50105
c.Met	p70S6K	0.151	0.46211
c.Met	Catenin	0.208	0.30810
c.Met	GAB1	0.322	0.10922
c.Met	NFkB	0.247	0.22361
c.Met	Jak1	0.350	0.07923
c.Met	MECP2	0.141	0.49215
c.Met	CREB	0.372	0.06133

c.Met	p27	0.247	0.22328
c.Met	Survivin	0.240	0.23683
c.Met	Paxillin	0.117	0.56773
c.Met	SRC	0.505	0.00856
c.Myc	cyclinD1	0.294	0.14515
c.Myc	EGFR	0.286	0.15659
c.Myc	pELK	0.205	0.31570
c.Myc	Erk	0.332	0.09709
c.Myc	GSK3	0.328	0.10189
c.Myc	IGF1Ra	0.026	0.89977
c.Myc	IGF1R	0.232	0.25492
c.Myc	MAP4K1	0.034	0.86962
c.Myc	mTOR	0.198	0.33177
c.Myc	pAkt	0.295	0.14340
c.Myc	PCNA	0.132	0.52180
c.Myc	PDGFRa	0.065	0.75375
c.Myc	PDGFRb	0.034	0.86901
c.Myc	PI3K	0.025	0.90270
c.Myc	STAT1	0.081	0.69301
c.Myc	STAT3	0.151	0.46076
c.Myc	STAT5	0.198	0.33314
c.Myc	TGFb	0.232	0.25381
c.Myc	Tie2	0.444	0.02308
c.Myc	VEGF	0.282	0.16263
c.Myc	AMPKa	0.221	0.27848
c.Myc	GRB2	0.002	0.99159
c.Myc	p70S6K	0.144	0.48305
c.Myc	Catenin	0.354	0.07578
c.Myc	GAB1	-0.031	0.87951
c.Myc	NFkB	0.006	0.97616
c.Myc	Jak1	0.131	0.52237
c.Myc	MECP2	0.071	0.73088
c.Myc	CREB	0.279	0.16676
c.Myc	p27	0.308	0.12554
c.Myc	Survivin	0.392	0.04751
c.Myc	Paxillin	0.157	0.44451

c.Myc	SRC	-0.009	0.96498
cyclinD1	EGFR	0.455	0.01953
cyclinD1	pELK	0.446	0.02223
cyclinD1	Erk	0.577	0.00202
cyclinD1	GSK3	0.267	0.18778
cyclinD1	IGF1Ra	0.274	0.17495
cyclinD1	IGF1R	0.123	0.54975
cyclinD1	MAP4K1	0.179	0.38256
cyclinD1	mTOR	0.310	0.12356
cyclinD1	pAkt	0.628	0.00059
cyclinD1	PCNA	0.658	0.00026
cyclinD1	PDGFRa	-0.156	0.44702
cyclinD1	PDGFRb	-0.018	0.93064
cyclinD1	PI3K	0.329	0.10115
cyclinD1	STAT1	0.683	0.00012
cyclinD1	STAT3	0.417	0.03425
cyclinD1	STAT5	0.322	0.10876
cyclinD1	TGFb	0.405	0.04024
cyclinD1	Tie2	0.575	0.00211
cyclinD1	VEGF	0.249	0.22020
cyclinD1	AMPKa	0.080	0.69637
cyclinD1	GRB2	-0.038	0.85457
cyclinD1	p70S6K	0.316	0.11542
cyclinD1	Catenin	0.171	0.40293
cyclinD1	GAB1	-0.037	0.85764
cyclinD1	NFkB	0.340	0.08961
cyclinD1	Jak1	0.309	0.12490
cyclinD1	MECP2	0.037	0.85577
cyclinD1	CREB	0.597	0.00128
cyclinD1	p27	0.126	0.54008
cyclinD1	Survivin	0.187	0.36014
cyclinD1	Paxillin	0.251	0.21610
cyclinD1	SRC	0.143	0.48694
EGFR	pELK	0.522	0.00629
EGFR	Erk	0.482	0.01272
EGFR	GSK3	0.217	0.28774

EGFR	IGF1Ra	0.433	0.02714
EGFR	IGF1R	0.436	0.02587
EGFR	MAP4K1	0.293	0.14664
EGFR	mTOR	0.268	0.18590
EGFR	pAkt	0.344	0.08550
EGFR	PCNA	0.526	0.00579
EGFR	PDGFRa	-0.077	0.70809
EGFR	PDGFRb	0.338	0.09103
EGFR	PI3K	0.193	0.34431
EGFR	STAT1	0.425	0.03048
EGFR	STAT3	0.593	0.00141
EGFR	STAT5	0.585	0.00171
EGFR	TGFb	0.451	0.02066
EGFR	Tie2	0.569	0.00243
EGFR	VEGF	-0.034	0.86802
EGFR	AMPKa	0.209	0.30491
EGFR	GRB2	-0.009	0.96529
EGFR	p70S6K	0.348	0.08149
EGFR	Catenin	0.220	0.27960
EGFR	GAB1	0.355	0.07482
EGFR	NFKB	0.397	0.04482
EGFR	Jak1	0.585	0.00171
EGFR	MECP2	0.381	0.05472
EGFR	CREB	0.447	0.02202
EGFR	p27	0.254	0.20965
EGFR	Survivin	-0.103	0.61678
EGFR	Paxillin	0.281	0.16470
EGFR	SRC	0.111	0.58914
pELK	Erk	0.759	0.00001
pELK	GSK3	0.472	0.01497
pELK	IGF1Ra	0.656	0.00028
pELK	IGF1R	0.357	0.07369
pELK	MAP4K1	0.479	0.01333
pELK	mTOR	0.456	0.01925
pELK	pAkt	0.807	0.00000
pELK	PCNA	0.572	0.00228

pELK	PDGFRa	0.123	0.54809
pELK	PDGFRb	0.374	0.05946
pELK	PI3K	0.528	0.00560
pELK	STAT1	0.521	0.00636
pELK	STAT3	0.551	0.00354
pELK	STAT5	0.488	0.01143
pELK	TGFb	0.321	0.10976
pELK	Tie2	0.575	0.00210
pELK	VEGF	0.248	0.22194
pELK	AMPKa	0.208	0.30869
pELK	GRB2	0.271	0.18136
pELK	p70S6K	0.479	0.01329
pELK	Catenin	0.190	0.35246
pELK	GAB1	0.166	0.41849
pELK	NFkB	0.439	0.02473
pELK	Jak1	0.477	0.01376
pELK	MECP2	0.350	0.07944
pELK	CREB	0.438	0.02517
pELK	p27	0.496	0.00992
pELK	Survivin	0.148	0.46939
pELK	Paxillin	0.632	0.00053
pELK	SRC	0.455	0.01941
Erk	GSK3	0.499	0.00940
Erk	IGF1Ra	0.608	0.00099
Erk	IGF1R	0.322	0.10848
Erk	MAP4K1	0.499	0.00942
Erk	mTOR	0.412	0.03641
Erk	pAkt	0.734	0.00002
Erk	PCNA	0.609	0.00097
Erk	PDGFRa	0.081	0.69320
Erk	PDGFRb	0.281	0.16373
Erk	PI3K	0.429	0.02875
Erk	STAT1	0.689	0.00010
Erk	STAT3	0.537	0.00466
Erk	STAT5	0.493	0.01048
Erk	TGFb	0.433	0.02731

Erk	Tie2	0.670	0.00018
Erk	VEGF	0.318	0.11325
Erk	AMPKa	0.381	0.05489
Erk	GRB2	0.148	0.47165
Erk	p70S6K	0.408	0.03854
Erk	Catenin	0.032	0.87513
Erk	GAB1	0.132	0.52063
Erk	NFkB	0.191	0.34875
Erk	Jak1	0.550	0.00357
Erk	MECP2	0.152	0.45972
Erk	CREB	0.356	0.07394
Erk	p27	0.423	0.03135
Erk	Survivin	0.087	0.67172
Erk	Paxillin	0.566	0.00260
Erk	SRC	0.268	0.18618
GSK3	IGF1Ra	0.268	0.18597
GSK3	IGF1R	-0.186	0.36235
GSK3	MAP4K1	0.443	0.02340
GSK3	mTOR	0.455	0.01941
GSK3	pAkt	0.438	0.02512
GSK3	PCNA	0.026	0.90137
GSK3	PDGFRa	-0.047	0.82107
GSK3	PDGFRb	0.340	0.08905
GSK3	PI3K	0.215	0.29056
GSK3	STAT1	0.294	0.14436
GSK3	STAT3	0.337	0.09192
GSK3	STAT5	0.540	0.00439
GSK3	TGFb	-0.038	0.85414
GSK3	Tie2	0.266	0.18849
GSK3	VEGF	0.142	0.48896
GSK3	AMPKa	0.216	0.28977
GSK3	GRB2	0.544	0.00409
GSK3	p70S6K	0.487	0.01163
GSK3	Catenin	-0.120	0.55874
GSK3	GAB1	0.214	0.29459
GSK3	NFkB	0.140	0.49552

GSK3	Jak1	0.271	0.18015
GSK3	MECP2	0.409	0.03807
GSK3	CREB	0.164	0.42264
GSK3	p27	0.728	0.00002
GSK3	Survivin	0.507	0.00823
GSK3	Paxillin	0.687	0.00011
GSK3	SRC	0.062	0.76516
IGF1Ra	IGF1R	0.295	0.14321
IGF1Ra	MAP4K1	0.374	0.05963
IGF1Ra	mTOR	0.295	0.14350
IGF1Ra	pAkt	0.417	0.03386
IGF1Ra	PCNA	0.534	0.00498
IGF1Ra	PDGFRa	0.409	0.03824
IGF1Ra	PDGFRb	0.460	0.01811
IGF1Ra	PI3K	0.388	0.05038
IGF1Ra	STAT1	0.648	0.00034
IGF1Ra	STAT3	0.583	0.00179
IGF1Ra	STAT5	0.461	0.01771
IGF1Ra	TGFb	0.581	0.00184
IGF1Ra	Tie2	0.414	0.03554
IGF1Ra	VEGF	0.227	0.26564
IGF1Ra	AMPKa	0.406	0.03933
IGF1Ra	GRB2	0.268	0.18549
IGF1Ra	p70S6K	0.477	0.01366
IGF1Ra	Catenin	0.274	0.17550
IGF1Ra	GAB1	0.381	0.05504
IGF1Ra	NFkB	0.467	0.01616
IGF1Ra	Jak1	0.697	0.00008
IGF1Ra	MECP2	0.296	0.14268
IGF1Ra	CREB	0.305	0.12976
IGF1Ra	p27	0.356	0.07459
IGF1Ra	Survivin	-0.189	0.35562
IGF1Ra	Paxillin	0.433	0.02708
IGF1Ra	SRC	0.376	0.05847
IGF1R	MAP4K1	0.319	0.11163
IGF1R	mTOR	0.378	0.05704

IGF1R	pAkt	0.338	0.09151
IGF1R	PCNA	0.383	0.05328
IGF1R	PDGFRa	0.004	0.98476
IGF1R	PDGFRb	0.099	0.62979
IGF1R	PI3K	0.350	0.07993
IGF1R	STAT1	0.128	0.53477
IGF1R	STAT3	0.247	0.22456
IGF1R	STAT5	0.025	0.90484
IGF1R	TGFb	0.572	0.00228
IGF1R	Tie2	0.377	0.05738
IGF1R	VEGF	0.133	0.51759
IGF1R	AMPKa	0.211	0.30141
IGF1R	GRB2	-0.235	0.24732
IGF1R	p70S6K	0.035	0.86418
IGF1R	Catenin	0.157	0.44322
IGF1R	GAB1	0.042	0.83770
IGF1R	NFkB	0.143	0.48690
IGF1R	Jak1	0.402	0.04153
IGF1R	MECP2	0.027	0.89414
IGF1R	CREB	0.104	0.61475
IGF1R	p27	-0.038	0.85508
IGF1R	Survivin	-0.126	0.53912
IGF1R	Paxillin	-0.066	0.74702
IGF1R	SRC	-0.060	0.77157
MAP4K1	mTOR	0.494	0.01041
MAP4K1	pAkt	0.545	0.00396
MAP4K1	PCNA	0.186	0.36358
MAP4K1	PDGFRa	0.312	0.12098
MAP4K1	PDGFRb	0.615	0.00083
MAP4K1	PI3K	0.623	0.00067
MAP4K1	STAT1	0.258	0.20242
MAP4K1	STAT3	0.278	0.16878
MAP4K1	STAT5	0.388	0.05045
MAP4K1	TGFb	0.085	0.67876
MAP4K1	Tie2	0.374	0.05993
MAP4K1	VEGF	0.401	0.04231

MAP4K1	AMPKa	0.527	0.00569
MAP4K1	GRB2	0.554	0.00333
MAP4K1	p70S6K	0.707	0.00005
MAP4K1	Catenin	0.241	0.23657
MAP4K1	GAB1	0.350	0.07958
MAP4K1	NFkB	0.363	0.06802
MAP4K1	Jak1	0.577	0.00201
MAP4K1	MECP2	0.492	0.01072
MAP4K1	CREB	0.280	0.16621
MAP4K1	p27	0.326	0.10428
MAP4K1	Survivin	0.183	0.37128
MAP4K1	Paxillin	0.536	0.00474
MAP4K1	SRC	0.038	0.85295
mTOR	pAkt	0.436	0.02583
mTOR	PCNA	0.516	0.00697
mTOR	PDGFRa	0.035	0.86683
mTOR	PDGFRb	0.284	0.16045
mTOR	PI3K	0.517	0.00678
mTOR	STAT1	0.397	0.04452
mTOR	STAT3	0.495	0.01022
mTOR	STAT5	0.389	0.04951
mTOR	TGFb	0.482	0.01268
mTOR	Tie2	0.566	0.00258
mTOR	VEGF	0.036	0.85977
mTOR	AMPKa	0.108	0.59884
mTOR	GRB2	0.288	0.15381
mTOR	p70S6K	0.393	0.04701
mTOR	Catenin	0.105	0.60949
mTOR	GAB1	0.212	0.29855
mTOR	NFkB	0.377	0.05749
mTOR	Jak1	0.215	0.29185
mTOR	MECP2	0.128	0.53288
mTOR	CREB	0.203	0.31986
mTOR	p27	0.368	0.06458
mTOR	Survivin	0.322	0.10878
mTOR	Paxillin	0.578	0.00199

mTOR	SRC	0.249	0.21912
pAkt	PCNA	0.563	0.00274
pAkt	PDGFRa	0.112	0.58490
pAkt	PDGFRb	0.227	0.26383
pAkt	PI3K	0.590	0.00151
pAkt	STAT1	0.552	0.00347
pAkt	STAT3	0.457	0.01895
pAkt	STAT5	0.389	0.04926
pAkt	TGFb	0.283	0.16198
pAkt	Tie2	0.496	0.00995
pAkt	VEGF	0.372	0.06108
pAkt	AMPKa	0.199	0.32917
pAkt	GRB2	0.140	0.49522
pAkt	p70S6K	0.543	0.00418
pAkt	Catenin	0.237	0.24324
pAkt	GAB1	-0.084	0.68275
pAkt	NFkB	0.303	0.13198
pAkt	Jak1	0.377	0.05731
pAkt	MECP2	0.164	0.42356
pAkt	CREB	0.629	0.00057
pAkt	p27	0.340	0.08874
pAkt	Survivin	0.252	0.21357
pAkt	Paxillin	0.634	0.00050
pAkt	SRC	0.411	0.03716
PCNA	PDGFRa	-0.008	0.96813
PCNA	PDGFRb	0.209	0.30635
PCNA	PI3K	0.407	0.03908
PCNA	STAT1	0.724	0.00003
PCNA	STAT3	0.619	0.00074
PCNA	STAT5	0.277	0.16999
PCNA	TGFb	0.767	0.00000
PCNA	Tie2	0.586	0.00166
PCNA	VEGF	0.134	0.51247
PCNA	AMPKa	0.097	0.63840
PCNA	GRB2	-0.069	0.73629
PCNA	p70S6K	0.316	0.11524

PCNA	Catenin	0.367	0.06542
PCNA	GAB1	0.048	0.81428
PCNA	NFkB	0.402	0.04160
PCNA	Jak1	0.352	0.07765
PCNA	MECP2	0.075	0.71740
PCNA	CREB	0.549	0.00367
PCNA	p27	0.069	0.73841
PCNA	Survivin	-0.179	0.38168
PCNA	Paxillin	0.362	0.06913
PCNA	SRC	0.406	0.03973
PDGFRa	PDGFRb	0.482	0.01263
PDGFRa	PI3K	0.118	0.56752
PDGFRa	STAT1	0.253	0.21189
PDGFRa	STAT3	0.154	0.45318
PDGFRa	STAT5	0.250	0.21821
PDGFRa	TGFb	0.035	0.86540
PDGFRa	Tie2	0.174	0.39488
PDGFRa	VEGF	0.149	0.46804
PDGFRa	AMPKa	0.272	0.17813
PDGFRa	GRB2	0.345	0.08466
PDGFRa	p70S6K	0.363	0.06809
PDGFRa	Catenin	0.371	0.06235
PDGFRa	GAB1	0.301	0.13491
PDGFRa	NFkB	0.275	0.17392
PDGFRa	Jak1	0.310	0.12329
PDGFRa	MECP2	0.057	0.78336
PDGFRa	CREB	0.147	0.47414
PDGFRa	p27	0.015	0.94243
PDGFRa	Survivin	0.096	0.64052
PDGFRa	Paxillin	0.271	0.18077
PDGFRa	SRC	0.269	0.18461
PDGFRb	PI3K	0.139	0.49742
PDGFRb	STAT1	0.276	0.17203
PDGFRb	STAT3	0.379	0.05646
PDGFRb	STAT5	0.271	0.18067
PDGFRb	TGFb	0.121	0.55760

PDGFRb	Tie2	0.256	0.20767
PDGFRb	VEGF	0.179	0.38153
PDGFRb	AMPKa	0.606	0.00105
PDGFRb	GRB2	0.744	0.00001
PDGFRb	p70S6K	0.714	0.00004
PDGFRb	Catenin	0.423	0.03112
PDGFRb	GAB1	0.714	0.00004
PDGFRb	NFkB	0.393	0.04674
PDGFRb	Jak1	0.649	0.00033
PDGFRb	MECP2	0.762	0.00001
PDGFRb	CREB	0.379	0.05613
PDGFRb	p27	0.455	0.01952
PDGFRb	Survivin	0.119	0.56258
PDGFRb	Paxillin	0.424	0.03077
PDGFRb	SRC	0.335	0.09459
PI3K	STAT1	0.320	0.11135
PI3K	STAT3	0.278	0.16971
PI3K	STAT5	0.234	0.25042
PI3K	TGFb	0.233	0.25112
PI3K	Tie2	0.378	0.05665
PI3K	VEGF	0.513	0.00737
PI3K	AMPKa	0.274	0.17591
PI3K	GRB2	0.257	0.20498
PI3K	p70S6K	0.427	0.02969
PI3K	Catenin	0.276	0.17275
PI3K	GAB1	0.129	0.53145
PI3K	NFkB	0.485	0.01199
PI3K	Jak1	0.278	0.16949
PI3K	MECP2	0.121	0.55643
PI3K	CREB	0.261	0.19715
PI3K	p27	0.010	0.96241
PI3K	Survivin	-0.023	0.91076
PI3K	Paxillin	0.358	0.07290
PI3K	SRC	0.050	0.80802
STAT1	STAT3	0.744	0.00001
STAT1	STAT5	0.512	0.00752

STAT1	TGFb	0.612	0.00089
STAT1	Tie2	0.504	0.00867
STAT1	VEGF	0.083	0.68619
STAT1	AMPKa	0.137	0.50552
STAT1	GRB2	0.079	0.70294
STAT1	p70S6K	0.369	0.06329
STAT1	Catenin	0.122	0.55374
STAT1	GAB1	0.231	0.25719
STAT1	NFkB	0.416	0.03457
STAT1	Jak1	0.520	0.00645
STAT1	MECP2	0.001	0.99429
STAT1	CREB	0.392	0.04775
STAT1	p27	0.132	0.52037
STAT1	Survivin	-0.076	0.71277
STAT1	Paxillin	0.448	0.02167
STAT1	SRC	0.372	0.06158
STAT3	STAT5	0.675	0.00015
STAT3	TGFb	0.657	0.00027
STAT3	Tie2	0.496	0.01001
STAT3	VEGF	0.077	0.70940
STAT3	AMPKa	0.272	0.17821
STAT3	GRB2	0.051	0.80288
STAT3	p70S6K	0.340	0.08926
STAT3	Catenin	0.226	0.26680
STAT3	GAB1	0.423	0.03128
STAT3	NFkB	0.557	0.00315
STAT3	Jak1	0.611	0.00090
STAT3	MECP2	0.263	0.19493
STAT3	CREB	0.396	0.04549
STAT3	p27	0.250	0.21775
STAT3	Survivin	-0.043	0.83621
STAT3	Paxillin	0.528	0.00554
STAT3	SRC	0.499	0.00946
STAT5	TGFb	0.324	0.10640
STAT5	Tie2	0.483	0.01241
STAT5	VEGF	-0.164	0.42387

STAT5	AMPKa	0.211	0.29969
STAT5	GRB2	0.151	0.46149
STAT5	p70S6K	0.445	0.02277
STAT5	Catenin	0.018	0.93055
STAT5	GAB1	0.272	0.17834
STAT5	NFkB	0.293	0.14702
STAT5	Jak1	0.514	0.00726
STAT5	MECP2	0.213	0.29721
STAT5	CREB	0.310	0.12324
STAT5	p27	0.452	0.02033
STAT5	Survivin	0.104	0.61209
STAT5	Paxillin	0.626	0.00062
STAT5	SRC	0.269	0.18431
TGFb	Tie2	0.480	0.01313
TGFb	VEGF	0.006	0.97540
TGFb	AMPKa	0.203	0.31916
TGFb	GRB2	-0.230	0.25787
TGFb	p70S6K	0.148	0.47144
TGFb	Catenin	0.307	0.12771
TGFb	GAB1	0.070	0.73531
TGFb	NFkB	0.273	0.17708
TGFb	Jak1	0.462	0.01761
TGFb	MECP2	-0.015	0.94113
TGFb	CREB	0.302	0.13426
TGFb	p27	0.097	0.63736
TGFb	Survivin	-0.274	0.17515
TGFb	Paxillin	0.150	0.46461
TGFb	SRC	0.231	0.25537
Tie2	VEGF	0.261	0.19798
Tie2	AMPKa	0.358	0.07220
Tie2	GRB2	0.109	0.59525
Tie2	p70S6K	0.335	0.09395
Tie2	Catenin	0.271	0.18089
Tie2	GAB1	0.216	0.28926
Tie2	NFkB	0.364	0.06755
Tie2	Jak1	0.433	0.02721

Tie2	MECP2	0.119	0.56363
Tie2	CREB	0.411	0.03710
Tie2	p27	0.340	0.08884
Tie2	Survivin	0.246	0.22544
Tie2	Paxillin	0.446	0.02255
Tie2	SRC	0.246	0.22607
VEGF	AMPKa	0.583	0.00178
VEGF	GRB2	0.198	0.33183
VEGF	p70S6K	0.193	0.34381
VEGF	Catenin	0.450	0.02115
VEGF	GAB1	0.116	0.57261
VEGF	NFkB	0.368	0.06464
VEGF	Jak1	0.256	0.20649
VEGF	MECP2	0.251	0.21607
VEGF	CREB	0.280	0.16539
VEGF	p27	-0.066	0.74695
VEGF	Survivin	0.211	0.30058
VEGF	Paxillin	0.134	0.51302
VEGF	SRC	-0.034	0.86988
AMPKa	GRB2	0.379	0.05630
AMPKa	p70S6K	0.453	0.02004
AMPKa	Catenin	0.382	0.05419
AMPKa	GAB1	0.528	0.00559
AMPKa	NFkB	0.198	0.33277
AMPKa	Jak1	0.668	0.00019
AMPKa	MECP2	0.537	0.00472
AMPKa	CREB	0.384	0.05305
AMPKa	p27	0.295	0.14397
AMPKa	Survivin	0.079	0.70280
AMPKa	Paxillin	0.164	0.42253
AMPKa	SRC	0.174	0.39454
GRB2	p70S6K	0.726	0.00003
GRB2	Catenin	0.279	0.16767
GRB2	GAB1	0.631	0.00055
GRB2	NFkB	0.241	0.23640
GRB2	Jak1	0.375	0.05917

GRB2	MECP2	0.732	0.00002
GRB2	CREB	0.109	0.59699
GRB2	p27	0.536	0.00476
GRB2	Survivin	0.296	0.14238
GRB2	Paxillin	0.420	0.03287
GRB2	SRC	0.071	0.72961
p70S6K	Catenin	0.551	0.00350
p70S6K	GAB1	0.430	0.02845
p70S6K	NFkB	0.258	0.20276
p70S6K	Jak1	0.626	0.00063
p70S6K	MECP2	0.664	0.00022
p70S6K	CREB	0.618	0.00078
p70S6K	p27	0.555	0.00328
p70S6K	Survivin	0.242	0.23384
p70S6K	Paxillin	0.628	0.00060
p70S6K	SRC	0.337	0.09233
Catenin	GAB1	0.215	0.29095
Catenin	NFkB	0.288	0.15432
Catenin	Jak1	0.373	0.06047
Catenin	MECP2	0.440	0.02441
Catenin	CREB	0.595	0.00136
Catenin	p27	0.060	0.77100
Catenin	Survivin	0.118	0.56617
Catenin	Paxillin	0.199	0.33068
Catenin	SRC	0.291	0.14864
GAB1	NFkB	0.468	0.01594
GAB1	Jak1	0.640	0.00042
GAB1	MECP2	0.646	0.00037
GAB1	CREB	0.069	0.73908
GAB1	p27	0.295	0.14343
GAB1	Survivin	-0.020	0.92086
GAB1	Paxillin	0.183	0.37028
GAB1	SRC	0.168	0.41189
NFkB	Jak1	0.362	0.06939
NFkB	MECP2	0.265	0.19067
NFkB	CREB	0.309	0.12434

NFkB	p27	0.039	0.84819
NFkB	Survivin	0.011	0.95918
NFkB	Paxillin	0.293	0.14612
NFkB	SRC	0.281	0.16390
Jak1	MECP2	0.588	0.00160
Jak1	CREB	0.371	0.06188
Jak1	p27	0.376	0.05814
Jak1	Survivin	-0.030	0.88344
Jak1	Paxillin	0.329	0.10074
Jak1	SRC	0.224	0.27230
MECP2	CREB	0.320	0.11077
MECP2	p27	0.497	0.00972
MECP2	Survivin	0.104	0.61185
MECP2	Paxillin	0.280	0.16528
MECP2	SRC	0.072	0.72613
CREB	p27	0.302	0.13397
CREB	Survivin	0.266	0.18974
CREB	Paxillin	0.442	0.02360
CREB	SRC	0.570	0.00237
p27	Survivin	0.446	0.02225
p27	Paxillin	0.648	0.00034
p27	SRC	0.317	0.11412
Survivin	Paxillin	0.431	0.02787
Survivin	SRC	0.170	0.40668
Paxillin	SRC	0.515	0.00709

Supplementary table 2c: Differences in correlations (*r*) and related p-values (*p*) between antibodies (Protein 1 and Protein 2) for LTS and STS of epithelioid malignant pleural mesothelioma. The differences between correlation coefficients of LTS and STS were based on differences between z-transformed Spearman correlation coefficients.

LTS: long-term survivors (survival >36 months)

STS: short-term survivors (survival <36 months)

LTS - STS	Protein 1	Protein 2	<i>r</i>	p-value
	EGFR	PCNA	1.014	0.00440
	IGF1R	TGFb	0.873	0.00502
	PCNA	TGFb	0.867	0.00784
	Erk	Survivin	-0.906	0.01200
	STAT1	p27	-0.965	0.01340
	EGFR	Tie2	0.862	0.01360
	IGF1R	MECP2	-0.871	0.01700
	c.jun	Survivin	-0.847	0.02240
	STAT1	Survivin	-0.760	0.02560
	EGFR	STAT3	0.795	0.02740
	Erk	pAkt	0.838	0.02780
	pELK	Erk	0.808	0.02820
	STAT1	GRB2	-0.774	0.02980
	PCNA	Survivin	-0.734	0.03240
	c.fos	PDGFRa	-0.733	0.03540
	PDGFRa	Tie2	-0.769	0.03620
	c.jun	EGFR	0.698	0.03820
	GSK3	PDGFRa	-0.734	0.03920
	MAP4K1	SRC	-0.686	0.04200
	PCNA	PDGFRa	-0.704	0.04540
	PDGFRb	Tie2	-0.778	0.04580
	c.fos	EGFR	0.655	0.04700
	GAB1	Jak1	0.669	0.04720
	pELK	pAkt	0.823	0.04760
	TGFb	GRB2	-0.652	0.04883
	cyclinD1	PDGFRb	-0.669	0.04940
	Tie2	p70S6K	-0.752	0.05160
	c.fos	TGFb	0.567	0.05184
	PDGFRb	STAT3	-0.799	0.05280

STAT3	p70S6K	-0.651	0.05320
STAT3	GRB2	-0.683	0.05360
EGFR	Erk	0.695	0.05380
c.Myc	Tie2	0.738	0.05435
GSK3	Survivin	-0.659	0.05520
PCNA	p70S6K	-0.709	0.05780
c.Myc	p27	0.743	0.06016
c.jun	GSK3	-0.701	0.06020
PCNA	PDGFRb	-0.745	0.06180
STAT1	AMPKa	-0.591	0.06440
PCNA	GRB2	-0.706	0.06460
EGFR	PDGFRb	0.621	0.06660
cyclinD1	EGFR	0.610	0.06940
PDGFRb	STAT1	-0.692	0.07400
EGFR	Jak1	0.578	0.07560
pAkt	MECP2	-0.644	0.07600
c.jun	Catenin	0.593	0.07820
mTOR	TGFb	0.633	0.08253
c.Met	MAP4K1	-0.688	0.08280
EGFR	p70S6K	0.576	0.08300
cyclinD1	PDGFRa	-0.609	0.08380
c.Met	c.Myc	0.625	0.08383
STAT5	TGFb	0.571	0.08399
GRB2	CREB	-0.605	0.08460
PI3K	p27	-0.503	0.08664
c.fos	c.Myc	0.675	0.08804
pAkt	PI3K	0.600	0.08805
IGF1R	SRC	-0.591	0.08880
PDGFRa	STAT1	-0.576	0.09200
GSK3	PCNA	-0.593	0.09240
PDGFRa	Paxillin	-0.578	0.09260
c.Myc	Survivin	0.631	0.09425
c.Myc	GSK3	0.644	0.09907
PDGFRb	p70S6K	-0.612	0.09940
cyclinD1	GRB2	-0.539	0.10200
PDGFRa	STAT3	-0.545	0.10220

GSK3	PI3K	-0.517	0.10313
pAkt	PDGFRb	-0.567	0.10360
MAP4K1	STAT1	-0.646	0.10640
c.Met	PI3K	-0.549	0.10875
STAT1	MECP2	-0.555	0.10920
IGF1R	Survivin	-0.534	0.11000
Erk	TGFb	0.505	0.11534
IGF1R	GRB2	-0.568	0.11560
STAT3	TGFb	0.528	0.11574
GRB2	SRC	-0.585	0.11580
GSK3	IGF1R	-0.529	0.11980
Tie2	GRB2	-0.562	0.12160
Catenin	CREB	0.582	0.12680
MECP2	SRC	-0.554	0.12700
GSK3	STAT1	-0.554	0.12740
MAP4K1	Survivin	-0.519	0.12780
Erk	IGF1Ra	0.524	0.13540
EGFR	pELK	0.500	0.13580
p70S6K	Paxillin	-0.583	0.13780
PI3K	Survivin	-0.456	0.13851
PI3K	Paxillin	-0.497	0.14011
PDGFRb	Paxillin	-0.593	0.14220
Erk	STAT5	0.517	0.14240
pELK	STAT5	0.521	0.14420
c.jun	Paxillin	-0.603	0.14680
EGFR	STAT5	0.460	0.14780
IGF1Ra	Catenin	0.510	0.14800
EGFR	STAT1	0.492	0.14980
GRB2	Paxillin	-0.616	0.15040
STAT1	Paxillin	-0.557	0.15060
cyclinD1	STAT1	0.547	0.15120
GRB2	GAB1	0.500	0.15140
mTOR	PDGFRa	-0.454	0.15246
c.jun	PCNA	-0.590	0.15360
PI3K	VEGF	0.471	0.16102
PDGFRa	PI3K	-0.446	0.16183

GAB1	NFkB	0.468	0.16223
cyclinD1	TGFb	0.437	0.16317
AMPKa	Paxillin	-0.465	0.16400
c.Met	GRB2	-0.470	0.16460
IGF1Ra	Survivin	-0.444	0.16700
pAkt	CREB	0.467	0.16720
STAT1	p70S6K	-0.491	0.16760
GSK3	SRC	-0.497	0.16800
p70S6K	Catenin	0.470	0.16860
VEGF	NFkB	0.507	0.17004
pELK	PCNA	0.463	0.17340
Erk	NFkB	0.506	0.17865
c.fos	Catenin	0.467	0.18100
c.fos	p70S6K	-0.497	0.18100
mTOR	VEGF	-0.440	0.18211
TGFb	NFkB	0.412	0.18251
pAkt	GAB1	-0.434	0.18340
c.fos	GSK3	-0.484	0.18400
c.fos	GRB2	-0.501	0.18720
Tie2	Paxillin	-0.484	0.18760
Erk	PDGFRa	-0.484	0.18760
c.jun	PDGFRa	-0.460	0.18980
MAP4K1	STAT3	-0.522	0.19120
EGFR	GSK3	0.442	0.19140
IGF1Ra	NFkB	0.528	0.19187
c.Met	Paxillin	-0.461	0.19360
IGF1R	Paxillin	-0.454	0.19500
c.jun	GRB2	-0.495	0.19760
PDGFRa	Survivin	-0.453	0.19860
IGF1Ra	AMPKa	-0.415	0.19900
STAT5	Jak1	0.448	0.20160
c.fos	MECP2	-0.486	0.20420
STAT3	Survivin	-0.425	0.20760
c.jun	c.Myc	0.514	0.20776
c.Myc	CREB	0.451	0.20776
c.Myc	STAT1	0.499	0.20997

EGFR	GAB1	0.429	0.21120
pELK	Tie2	0.473	0.21160
STAT3	MECP2	-0.439	0.21180
VEGF	Catenin	0.460	0.21220
Erk	AMPKa	0.433	0.21220
STAT3	AMPKa	-0.445	0.21220
Erk	Jak1	0.433	0.21420
c.Myc	Erk	0.418	0.21598
c.Myc	TGFb	0.419	0.21600
PDGFRa	Catenin	0.444	0.21680
PCNA	p27	-0.431	0.21860
c.Myc	STAT3	0.457	0.22200
EGFR	MECP2	0.419	0.22360
Tie2	GAB1	-0.405	0.22360
c.Myc	cyclinD1	0.443	0.22400
STAT3	Tie2	-0.493	0.22440
c.fos	c.Met	-0.450	0.22480
Erk	GSK3	-0.409	0.22680
EGFR	TGFb	0.418	0.22687
PDGFRa	p27	-0.396	0.22760
c.fos	c.jun	-0.516	0.22780
IGF1R	p27	-0.379	0.22800
PCNA	MECP2	-0.435	0.22900
mTOR	MECP2	-0.395	0.23219
c.jun	Tie2	-0.451	0.23300
cyclinD1	Erk	0.474	0.23340
PCNA	STAT1	0.451	0.23660
MECP2	Paxillin	-0.423	0.24060
GAB1	CREB	-0.389	0.24400
c.Myc	PCNA	0.464	0.24606
VEGF	AMPKa	0.396	0.24740
c.jun	STAT1	-0.446	0.24800
pELK	AMPKa	-0.383	0.24860
GSK3	pAkt	0.414	0.25160
mTOR	STAT1	0.382	0.25563
Jak1	Survivin	-0.396	0.25640

IGF1R	PCNA	0.403	0.25720
Erk	STAT1	0.414	0.25900
STAT3	NFkB	0.430	0.25976
Catenin	SRC	-0.407	0.26000
PCNA	Paxillin	-0.413	0.26340
Erk	Tie2	0.444	0.26700
STAT3	Paxillin	-0.406	0.26760
STAT1	NFkB	0.374	0.26838
pAkt	STAT5	0.408	0.27140
pAkt	STAT1	0.376	0.27220
pAkt	Paxillin	0.349	0.27380
Tie2	MECP2	-0.374	0.27420
EGFR	p27	0.371	0.27520
mTOR	p27	0.360	0.27527
p70S6K	Survivin	-0.386	0.27740
STAT3	GAB1	-0.425	0.27820
GAB1	MECP2	0.387	0.27900
pAkt	GRB2	-0.359	0.28080
GSK3	p27	0.399	0.28300
PDGFRa	CREB	-0.392	0.28300
c.Myc	STAT5	0.384	0.28357
cyclinD1	MECP2	-0.381	0.28360
cyclinD1	VEGF	0.369	0.28420
PI3K	SRC	-0.337	0.28686
mTOR	STAT3	0.368	0.28689
c.Met	STAT1	-0.454	0.28960
PI3K	Jak1	-0.381	0.29028
c.fos	AMPKa	-0.390	0.29320
IGF1R	Tie2	0.359	0.29720
PDGFRb	Survivin	-0.377	0.29960
AMPKa	Catenin	0.354	0.30000
Jak1	CREB	0.348	0.30100
TGFb	Tie2	0.326	0.30684
c.fos	pAkt	0.346	0.30940
c.jun	Erk	-0.373	0.31000
pELK	Survivin	-0.335	0.31060

cyclinD1	pELK	0.362	0.31460
MAP4K1	p27	-0.332	0.31460
c.jun	p27	-0.378	0.31626
c.fos	PDGFRb	-0.416	0.31840
mTOR	STAT5	0.350	0.31914
STAT1	TGFb	0.305	0.32252
STAT3	p27	-0.336	0.32340
c.Met	p70S6K	-0.344	0.32360
c.Met	PDGFRa	-0.338	0.32580
IGF1Ra	IGF1R	0.366	0.32980
GSK3	Tie2	-0.335	0.33020
p70S6K	SRC	-0.340	0.33080
EGFR	Paxillin	0.334	0.33280
c.Myc	p70S6K	0.387	0.33310
c.Myc	EGFR	-0.308	0.33350
c.Myc	PDGFRb	0.384	0.33410
STAT5	p27	0.324	0.33540
c.jun	IGF1R	-0.343	0.33680
GSK3	p70S6K	-0.314	0.33760
PCNA	NFkB	0.323	0.33968
PDGFRb	PI3K	-0.300	0.34054
Erk	GRB2	-0.327	0.34060
mTOR	Tie2	0.324	0.34398
pELK	VEGF	-0.337	0.34480
STAT5	VEGF	-0.324	0.34560
PCNA	GAB1	-0.333	0.34560
PDGFRb	TGFb	-0.310	0.34703
c.Myc	pAkt	0.315	0.34814
IGF1R	NFkB	-0.340	0.34969
c.fos	MAP4K1	-0.348	0.35000
GSK3	STAT3	-0.334	0.35300
GSK3	MAP4K1	-0.358	0.35320
pELK	GAB1	0.321	0.35340
STAT5	Paxillin	0.337	0.35420
c.Myc	NFkB	-0.325	0.35597
MECP2	CREB	-0.344	0.35620

mTOR	PI3K	0.369	0.35699
c.fos	Survivin	-0.317	0.35760
TGFb	Catenin	0.279	0.35889
PI3K	GRB2	-0.297	0.36185
IGF1Ra	PCNA	0.322	0.36880
GSK3	STAT5	0.318	0.36940
GRB2	Survivin	-0.337	0.37000
c.fos	cyclinD1	-0.324	0.37060
STAT1	SRC	-0.355	0.37120
Jak1	Paxillin	-0.320	0.37260
EGFR	IGF1R	0.341	0.37320
PDGFRb	p27	-0.343	0.37340
PDGFRa	TGFb	-0.293	0.37536
PDGFRb	Jak1	0.317	0.37700
EGFR	pAkt	0.306	0.37780
PCNA	CREB	0.330	0.37860
IGF1Ra	p27	-0.284	0.37860
Erk	STAT3	0.322	0.37960
cyclinD1	Paxillin	-0.301	0.38760
c.Met	GSK3	-0.312	0.39080
Tie2	Survivin	-0.300	0.39200
EGFR	CREB	0.324	0.39340
IGF1Ra	pAkt	0.332	0.39680
Catenin	GAB1	0.307	0.39780
c.jun	NFkB	0.275	0.40116
STAT5	SRC	-0.290	0.40120
c.Met	STAT3	-0.368	0.40260
pELK	IGF1Ra	0.302	0.40360
c.jun	pELK	-0.283	0.40580
c.jun	CREB	0.305	0.40640
Catenin	Jak1	0.275	0.41140
c.jun	STAT3	-0.315	0.41220
mTOR	NFkB	0.303	0.41304
PDGFRa	GRB2	-0.277	0.41660
cyclinD1	CREB	0.280	0.41780
IGF1R	PI3K	0.311	0.41874

c.Myc	Paxillin	0.315	0.41893
c.Met	STAT5	-0.309	0.42360
c.Met	TGFb	0.250	0.42761
GSK3	PDGFRb	-0.300	0.42940
TGFb	p70S6K	-0.245	0.43002
IGF1Ra	Jak1	0.288	0.43020
c.fos	STAT1	-0.301	0.43180
PDGFRb	SRC	-0.310	0.43220
mTOR	Paxillin	0.285	0.43594
c.Myc	AMPKa	0.283	0.43738
Tie2	Catenin	0.265	0.44020
MECP2	Survivin	-0.277	0.44060
IGF1R	Catenin	-0.281	0.44080
c.jun	VEGF	0.293	0.44140
AMPKa	GAB1	0.300	0.44220
EGFR	MAP4K1	0.256	0.44260
AMPKa	NFkB	-0.246	0.44302
cyclinD1	pAkt	0.280	0.45040
cyclinD1	GAB1	-0.248	0.45060
STAT3	CREB	-0.257	0.45080
pELK	NFkB	0.290	0.45103
cyclinD1	mTOR	0.247	0.45257
STAT5	Tie2	0.269	0.45280
c.fos	Tie2	-0.292	0.45400
c.Myc	MECP2	0.288	0.45503
c.Met	cyclinD1	-0.311	0.45580
MAP4K1	Paxillin	-0.296	0.45720
pELK	STAT3	0.273	0.45740
cyclinD1	MAP4K1	-0.304	0.45920
GSK3	Catenin	-0.252	0.46040
c.jun	GAB1	0.263	0.46480
pELK	Jak1	-0.268	0.46760
cyclinD1	p70S6K	-0.250	0.46920
c.Met	CREB	-0.255	0.47180
p70S6K	CREB	0.243	0.47720
EGFR	NFkB	0.282	0.47827

PI3K	p70S6K	-0.219	0.47864
cyclinD1	Tie2	-0.316	0.48120
MAP4K1	Tie2	-0.290	0.48500
cyclinD1	IGF1Ra	0.234	0.48600
cyclinD1	p27	-0.245	0.48640
TGFb	Survivin	-0.209	0.49071
Erk	Catenin	-0.242	0.49320
TGFb	CREB	0.199	0.49412
mTOR	Jak1	-0.231	0.49489
MAP4K1	CREB	-0.235	0.49560
cyclinD1	STAT5	0.242	0.49740
PDGFRb	STAT5	-0.246	0.49800
TGFb	Paxillin	-0.226	0.49975
STAT3	Catenin	0.230	0.50280
TGFb	MECP2	-0.200	0.50397
pELK	MECP2	-0.238	0.50580
c.jun	MECP2	-0.257	0.50760
MAP4K1	AMPKa	0.229	0.50980
GRB2	p70S6K	0.273	0.51000
pELK	IGF1R	-0.231	0.51760
STAT5	MECP2	-0.233	0.51860
PDGFRb	GAB1	0.228	0.52140
cyclinD1	NFkB	-0.233	0.52594
Erk	SRC	-0.226	0.52800
c.jun	c.Met	-0.230	0.52820
TGFb	AMPKa	-0.204	0.52828
IGF1R	STAT3	0.226	0.53220
PI3K	STAT1	-0.221	0.53272
Erk	PCNA	0.226	0.53280
MAP4K1	PCNA	-0.240	0.53500
EGFR	Survivin	0.213	0.53900
PDGFRb	NFkB	0.203	0.53956
VEGF	Survivin	-0.213	0.54220
c.fos	GAB1	-0.218	0.54380
pELK	TGFb	0.208	0.54476
c.Met	AMPKa	0.234	0.54600

GSK3	IGF1Ra	-0.184	0.54720
IGF1Ra	VEGF	-0.206	0.54780
c.Met	IGF1R	-0.229	0.55000
pELK	PDGFRa	-0.207	0.55080
PCNA	STAT3	0.249	0.55140
STAT1	STAT5	0.202	0.55400
GSK3	Jak1	-0.182	0.55440
pELK	mTOR	0.210	0.55480
c.Met	MECP2	-0.207	0.55580
MAP4K1	Catenin	0.204	0.55620
VEGF	SRC	-0.210	0.55640
PDGFRa	p70S6K	-0.223	0.55940
c.Myc	IGF1R	0.186	0.56172
pAkt	Jak1	-0.183	0.56320
Erk	IGF1R	0.213	0.56420
cyclinD1	SRC	-0.220	0.56600
c.Myc	MAP4K1	0.218	0.56633
c.jun	SRC	-0.211	0.56820
TGFb	p27	-0.171	0.56907
pELK	Catenin	-0.192	0.56960
PDGFRb	Catenin	0.198	0.57120
pELK	CREB	0.194	0.57260
EGFR	VEGF	-0.186	0.57700
PI3K	NFkB	0.228	0.57750
c.Met	mTOR	0.191	0.57878
EGFR	PDGFRa	-0.187	0.58100
IGF1R	PDGFRb	-0.192	0.58180
Jak1	MECP2	0.182	0.58520
c.Myc	VEGF	0.214	0.58558
PI3K	STAT3	-0.189	0.58619
c.Myc	GAB1	0.208	0.58899
Survivin	SRC	-0.192	0.59260
EGFR	PI3K	0.198	0.59343
NFkB	CREB	0.184	0.59403
STAT5	CREB	-0.175	0.59600
c.Myc	GRB2	0.218	0.59701

c.Met	Tie2	-0.231	0.59860
IGF1Ra	STAT5	0.182	0.60100
STAT5	GRB2	-0.166	0.60140
GAB1	Paxillin	-0.175	0.60240
AMPKa	SRC	-0.178	0.60600
GRB2	p27	-0.209	0.60640
p70S6K	Jak1	0.200	0.61000
MAP4K1	mTOR	0.176	0.61384
EGFR	SRC	-0.171	0.61440
MAP4K1	NFkB	0.172	0.61586
Catenin	p27	-0.168	0.62100
pAkt	Tie2	0.166	0.62400
EGFR	IGF1Ra	0.178	0.62620
MAP4K1	VEGF	0.173	0.62780
STAT1	VEGF	-0.164	0.62820
c.Met	VEGF	0.171	0.62940
mTOR	PCNA	0.153	0.62967
pAkt	STAT3	0.184	0.63060
GSK3	CREB	-0.172	0.63080
mTOR	p70S6K	-0.159	0.63248
c.Myc	Catenin	0.185	0.63371
pAkt	NFkB	0.176	0.63389
c.fos	NFkB	-0.150	0.63389
TGFb	GAB1	-0.148	0.63900
Jak1	SRC	-0.158	0.64200
Erk	Paxillin	0.165	0.64380
STAT1	GAB1	-0.160	0.64400
AMPKa	Survivin	-0.160	0.64400
c.Myc	IGF1Ra	0.174	0.64474
c.Myc	pELK	0.158	0.64554
c.jun	mTOR	-0.161	0.64630
IGF1Ra	STAT1	-0.180	0.65100
NFkB	MECP2	-0.154	0.65111
cyclinD1	Catenin	-0.151	0.65200
PDGFRa	MECP2	-0.158	0.65300
AMPKa	Jak1	0.161	0.65420

GSK3	VEGF	-0.149	0.65540
PI3K	AMPKa	-0.142	0.65675
pAkt	PCNA	0.147	0.65880
VEGF	GRB2	0.155	0.65900
pAkt	TGFb	0.140	0.66071
PCNA	Tie2	-0.199	0.66100
IGF1R	GAB1	0.142	0.66200
c.fos	STAT5	-0.158	0.66240
Survivin	Paxillin	-0.180	0.66320
PCNA	STAT5	0.158	0.66460
pELK	p27	0.146	0.66460
c.Myc	PI3K	-0.157	0.66882
MAP4K1	MECP2	-0.139	0.67260
EGFR	Catenin	0.158	0.67360
c.jun	MAP4K1	-0.142	0.67360
c.fos	SRC	-0.160	0.67480
Erk	p27	0.158	0.67540
c.jun	cyclinD1	-0.145	0.67600
mTOR	AMPKa	-0.151	0.67635
IGF1R	AMPKa	-0.140	0.68020
IGF1Ra	Paxillin	-0.147	0.68080
c.jun	PDGFRb	-0.165	0.68087
c.Met	PDGFRb	-0.158	0.68160
PDGFRb	AMPKa	0.141	0.68200
PDGFRb	GRB2	0.167	0.68580
pELK	Paxillin	0.139	0.68800
pELK	STAT1	0.138	0.69180
p70S6K	GAB1	-0.142	0.69340
Tie2	VEGF	0.142	0.69380
TGFb	SRC	-0.131	0.69386
PI3K	MECP2	-0.119	0.69414
EGFR	mTOR	0.137	0.69799
AMPKa	GRB2	-0.132	0.69800
MAP4K1	PDGFRa	-0.143	0.70220
IGF1R	STAT5	-0.128	0.70300
c.Myc	PDGFRa	0.144	0.70410

pAkt	SRC	0.126	0.70620
IGF1Ra	TGFb	0.108	0.70632
STAT1	CREB	-0.146	0.70700
Tie2	SRC	-0.142	0.70720
IGF1R	p70S6K	-0.134	0.70800
c.Met	SRC	-0.136	0.70860
IGF1Ra	p70S6K	-0.145	0.70860
STAT5	NFkB	0.135	0.71039
GSK3	NFkB	0.126	0.71100
mTOR	CREB	0.105	0.71221
c.Met	pAkt	0.132	0.71280
PDGFRa	NFkB	0.154	0.71300
GSK3	AMPKa	-0.132	0.71300
PI3K	CREB	0.117	0.71505
Tie2	NFkB	0.131	0.71660
IGF1R	CREB	-0.125	0.72000
Tie2	p27	-0.119	0.72020
pELK	GRB2	-0.120	0.72200
Tie2	AMPKa	-0.129	0.72200
c.jun	STAT5	-0.126	0.72300
PDGFRa	PDGFRb	0.137	0.72380
Erk	PDGFRb	-0.126	0.72420
c.fos	PI3K	-0.108	0.72530
cyclinD1	Survivin	-0.125	0.72620
STAT3	VEGF	-0.115	0.72940
STAT3	STAT5	0.124	0.73120
STAT3	Jak1	0.117	0.73240
EGFR	AMPKa	0.110	0.73400
c.Met	GAB1	0.117	0.73420
Paxillin	SRC	-0.122	0.73580
p27	Paxillin	-0.146	0.73740
STAT5	GAB1	-0.101	0.73920
Catenin	Survivin	-0.108	0.73960
Tie2	CREB	-0.119	0.74060
c.Met	p27	-0.108	0.74140
cyclinD1	AMPKa	-0.111	0.74140

PCNA	Catenin	0.117	0.74320
Erk	VEGF	-0.113	0.74680
MAP4K1	TGFb	-0.123	0.75033
mTOR	pAkt	0.114	0.75175
c.fos	pELK	0.107	0.75240
p70S6K	p27	-0.110	0.75260
VEGF	GAB1	-0.107	0.75420
c.fos	IGF1R	0.110	0.75440
PI3K	STAT5	0.117	0.75565
pELK	PI3K	0.126	0.75606
MAP4K1	GRB2	-0.089	0.75980
IGF1R	Jak1	-0.105	0.76020
TGFb	Jak1	-0.109	0.76098
MAP4K1	PI3K	0.105	0.76269
Catenin	MECP2	0.124	0.76280
AMPKa	p27	-0.108	0.76560
GAB1	p27	0.103	0.76680
mTOR	GAB1	-0.098	0.76750
pAkt	Catenin	-0.103	0.77000
c.fos	VEGF	-0.096	0.77200
IGF1Ra	PDGFRa	-0.099	0.77260
PDGFRb	CREB	-0.098	0.77440
IGF1Ra	GAB1	-0.095	0.77480
PDGFRb	MECP2	0.105	0.77660
c.fos	Paxillin	-0.108	0.77680
PDGFRa	STAT5	-0.085	0.77940
Tie2	Jak1	0.097	0.78020
mTOR	SRC	-0.099	0.78193
PDGFRa	AMPKa	-0.092	0.78220
p70S6K	NFkB	0.084	0.78410
Erk	mTOR	0.076	0.78534
VEGF	p27	-0.092	0.78620
STAT1	STAT3	0.095	0.78740
PI3K	Catenin	0.094	0.78822
STAT5	AMPKa	-0.101	0.78960
MAP4K1	PDGFRb	-0.092	0.78980

mTOR	Survivin	-0.091	0.79175
GRB2	Jak1	-0.090	0.79360
VEGF	CREB	0.092	0.79460
GAB1	Survivin	-0.092	0.79480
cyclinD1	PCNA	0.069	0.79560
pAkt	p70S6K	-0.072	0.80020
c.fos	PCNA	-0.097	0.80020
IGF1Ra	STAT3	-0.085	0.80180
STAT1	Jak1	-0.081	0.80840
NFKB	p27	-0.082	0.81114
IGF1R	pAkt	0.072	0.81360
c.Met	IGF1Ra	-0.092	0.81360
Catenin	Paxillin	-0.080	0.81420
PCNA	AMPKa	-0.083	0.81860
CREB	Survivin	-0.076	0.81980
EGFR	GRB2	0.085	0.82080
Erk	p70S6K	-0.070	0.82280
AMPKa	MECP2	0.082	0.82320
STAT1	Tie2	-0.100	0.82480
c.Met	Jak1	0.077	0.82500
PDGFRa	SRC	-0.076	0.82580
c.Met	Erk	0.076	0.82800
GSK3	Paxillin	-0.055	0.82800
Erk	GAB1	-0.070	0.82820
IGF1R	STAT1	-0.082	0.83040
IGF1R	mTOR	0.059	0.83282
MAP4K1	pAkt	0.077	0.83680
VEGF	p70S6K	-0.060	0.84080
IGF1R	PDGFRa	0.065	0.84100
IGF1Ra	PDGFRb	-0.054	0.84920
STAT1	Catenin	-0.061	0.85200
AMPKa	p70S6K	-0.063	0.85240
pAkt	p27	-0.044	0.85340
Erk	MECP2	-0.059	0.85580
c.fos	p27	0.068	0.85640
c.Myc	Jak1	0.061	0.85772

GSK3	MECP2	0.068	0.85860
IGF1R	MAP4K1	-0.069	0.85900
c.fos	mTOR	0.051	0.85946
AMPKa	CREB	0.059	0.86120
PCNA	Jak1	-0.060	0.86160
NFkB	SRC	0.053	0.86301
TGFb	VEGF	-0.048	0.86406
VEGF	Paxillin	0.064	0.86460
cyclinD1	IGF1R	-0.063	0.86460
PI3K	TGFb	0.058	0.87076
cyclinD1	Jak1	0.048	0.87300
PDGFRa	GAB1	-0.043	0.87420
mTOR	GRB2	0.050	0.87609
cyclinD1	STAT3	0.056	0.87960
GSK3	mTOR	-0.039	0.87970
IGF1Ra	MAP4K1	-0.059	0.88020
PCNA	SRC	-0.055	0.88240
IGF1Ra	PI3K	-0.062	0.88371
c.Myc	mTOR	0.056	0.88429
pAkt	VEGF	-0.044	0.88740
STAT5	p70S6K	0.044	0.88780
c.Met	Survivin	-0.050	0.89000
Erk	CREB	-0.053	0.89280
CREB	p27	0.052	0.89300
cyclinD1	PI3K	0.029	0.89738
PI3K	GAB1	0.038	0.89758
c.fos	STAT3	-0.046	0.89780
pELK	MAP4K1	0.037	0.90060
p70S6K	MECP2	0.037	0.90200
c.jun	PI3K	-0.048	0.90361
pELK	SRC	-0.045	0.90620
PDGFRa	Jak1	0.038	0.90920
pELK	GSK3	-0.024	0.90920
c.Met	EGFR	0.043	0.91080
PDGFRa	VEGF	-0.037	0.91500
MECP2	p27	0.035	0.91580

IGF1Ra	GRB2	-0.024	0.91640
GRB2	MECP2	0.034	0.91760
c.Met	Catenin	0.046	0.91900
c.Myc	SRC	0.035	0.91928
STAT3	SRC	-0.030	0.92200
MAP4K1	p70S6K	0.052	0.92240
IGF1Ra	mTOR	0.030	0.92397
GSK3	GAB1	-0.036	0.92680
Catenin	NFkB	-0.035	0.93251
cyclinD1	GSK3	-0.027	0.93320
PDGFRb	VEGF	0.039	0.93360
c.Met	PCNA	-0.038	0.93400
NFkB	Paxillin	-0.030	0.93411
c.jun	p70S6K	0.041	0.93500
IGF1Ra	SRC	0.028	0.93640
IGF1Ra	CREB	0.022	0.93640
PCNA	VEGF	0.031	0.93660
p27	Survivin	-0.045	0.93660
mTOR	Catenin	0.021	0.93739
mTOR	PDGFRb	-0.033	0.94180
pELK	PDGFRb	0.020	0.94280
c.jun	pAkt	-0.022	0.94340
IGF1Ra	MECP2	-0.023	0.94380
GRB2	Catenin	-0.021	0.94400
c.jun	AMPKa	-0.035	0.94520
Erk	PI3K	0.022	0.94542
c.Met	NFkB	-0.032	0.94572
GSK3	GRB2	-0.030	0.94720
p27	SRC	-0.024	0.94880
PI3K	Tie2	-0.030	0.94884
pELK	p70S6K	0.020	0.94920
pAkt	Survivin	-0.016	0.95520
GRB2	NFkB	-0.015	0.95534
STAT5	Survivin	-0.020	0.95740
Jak1	p27	-0.020	0.95780
c.jun	Jak1	0.011	0.95880

CREB	SRC	-0.021	0.95980
c.jun	IGF1Ra	-0.020	0.96360
PCNA	PI3K	-0.022	0.96713
NFkB	Survivin	0.014	0.96856
IGF1Ra	Tie2	-0.014	0.96920
pAkt	PDGFRa	-0.013	0.97000
c.fos	CREB	-0.006	0.97060
GSK3	TGFb	-0.013	0.97177
GAB1	SRC	-0.012	0.97180
Erk	MAP4K1	-0.032	0.97200
IGF1R	VEGF	-0.007	0.97400
STAT5	Catenin	0.008	0.97500
c.fos	Jak1	-0.014	0.97700
pAkt	AMPKa	-0.008	0.98100
c.fos	IGF1Ra	0.009	0.98140
c.Met	pELK	0.001	0.98420
MAP4K1	Jak1	0.020	0.98560
c.fos	Erk	-0.002	0.98800
MAP4K1	GAB1	-0.011	0.99020
CREB	Paxillin	-0.020	0.99040
NFkB	Jak1	0.003	0.99179
VEGF	MECP2	0.004	0.99380
c.jun	TGFb	-0.001	0.99387
VEGF	Jak1	0.000	0.99540
MAP4K1	STAT5	-0.007	0.99720