

## **Supplementary Information**

### **Network Biology of Tumor Stem-like Cells Identified a Regulatory Role of Cbx5 in Lung Cancer**

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Figure S2 – Consensus TSLC networks

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Table S1 – Description of the used in the analysis to come up with the concordant consensus gene signature

Table S2&3 – Consensus TSLC networks

Table S4&5 – Lung TSLC networks

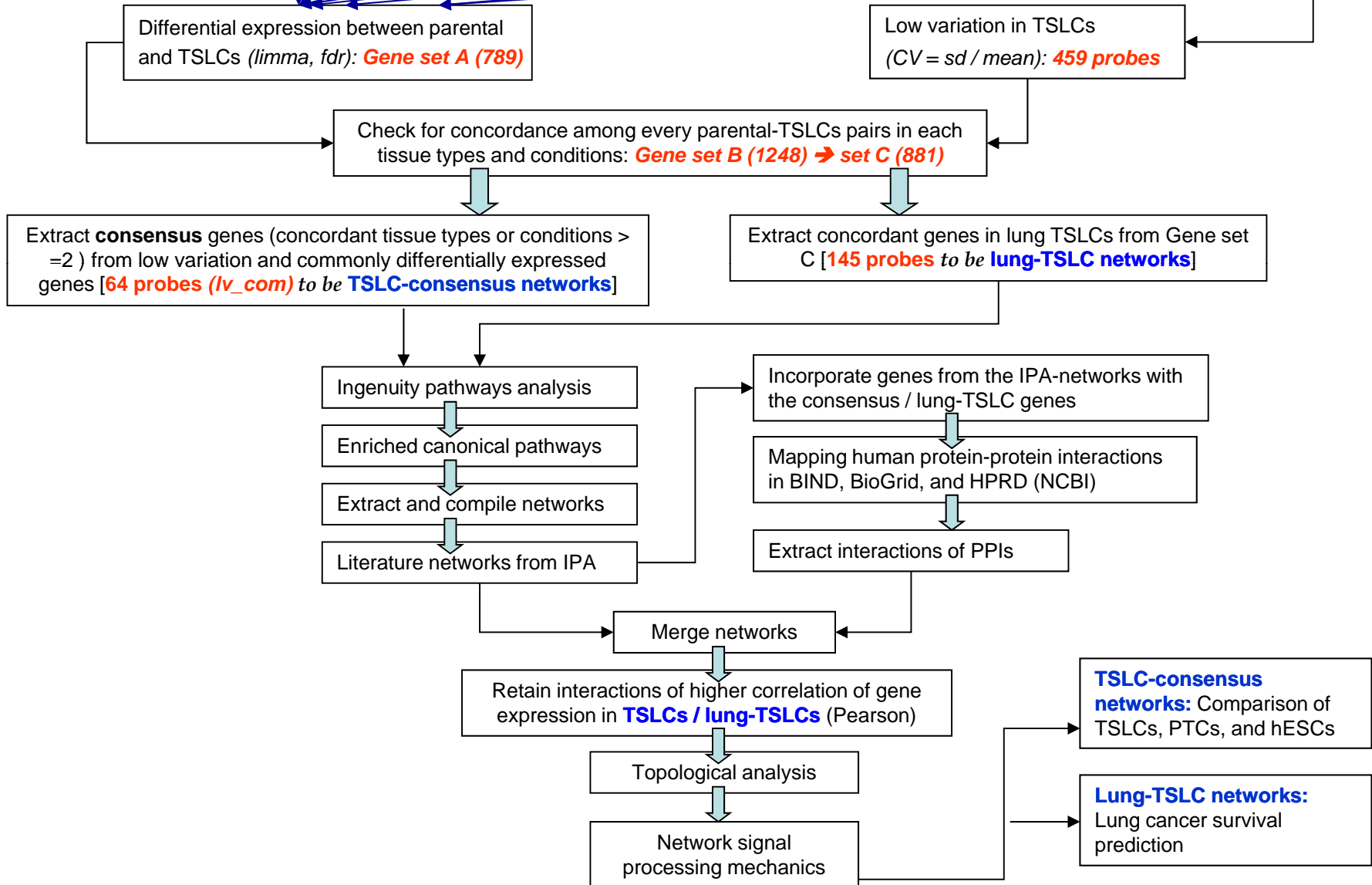
Table S6 –Survival analysis of lung cancer transcriptome using the consensus and lung TSLC network models

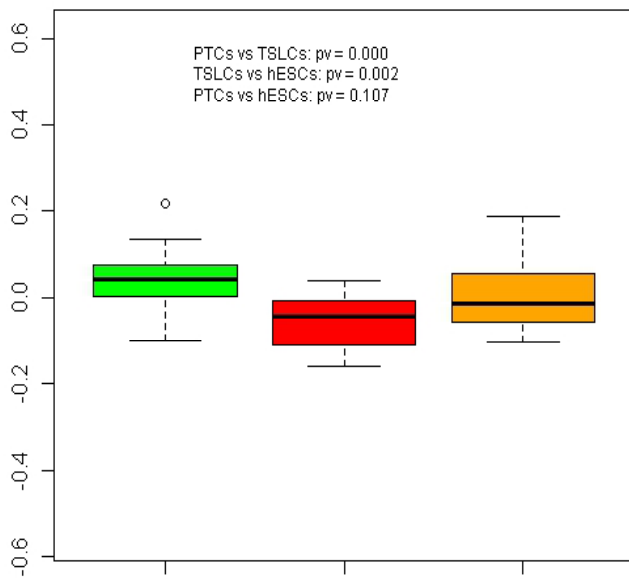
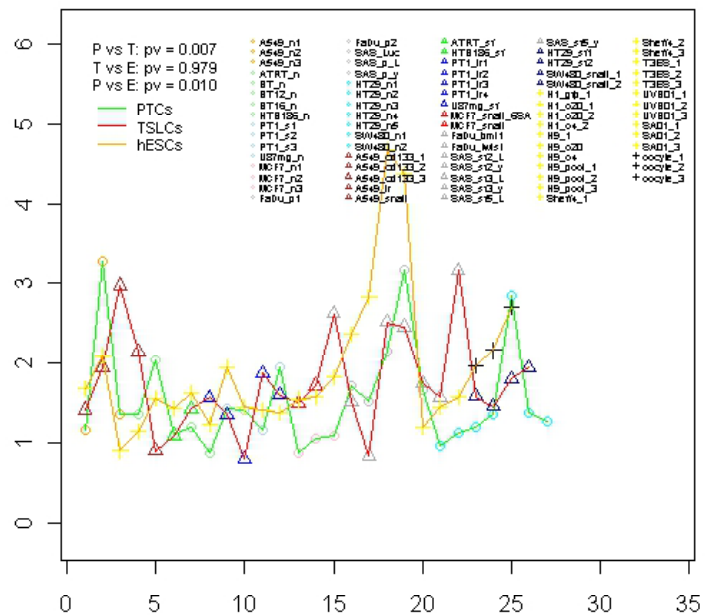
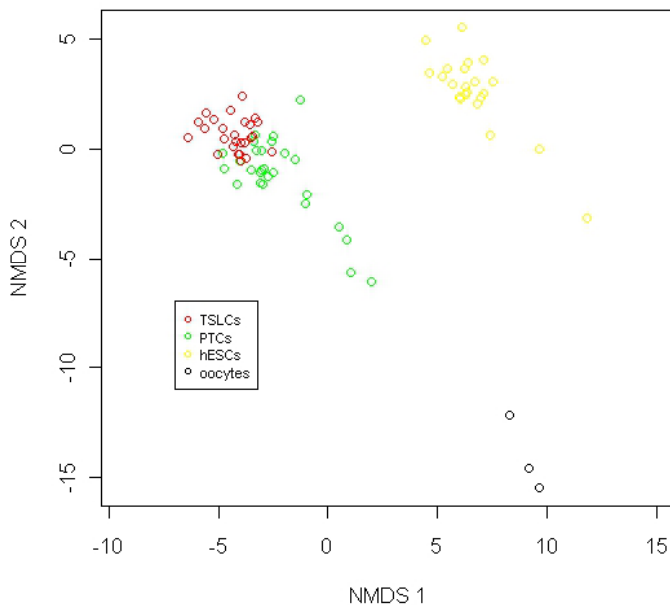
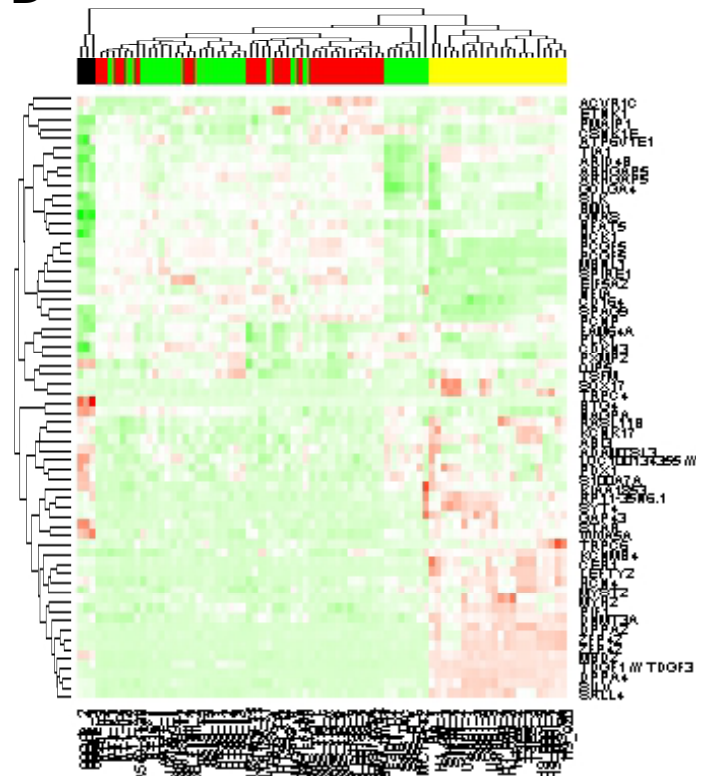
Table S7 – Clinicopathological characteristics of 125 patients with lung adenocarcinoma

#### **Data and code repository:**

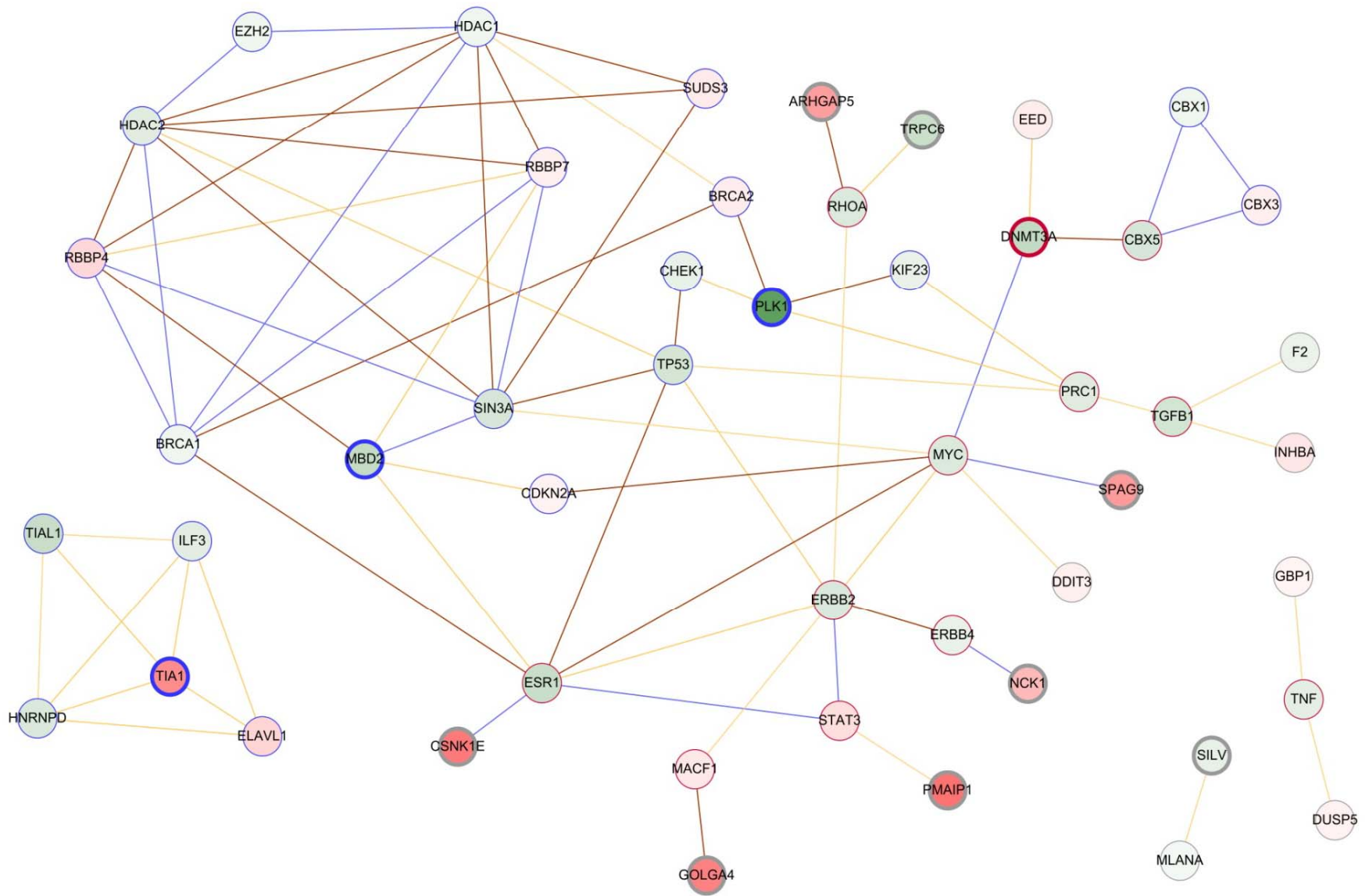
<https://sites.google.com/site/nwtoposignalincancer/>

Tissue / Condition	Lung	GBM	ATRT	Breast	Head Neck	Colon	Snail-over	SF-sphere
G_stemCaEMT	13048 probes (5812 geneIDs)							
Cancer-specific alternative splicing	801	628	628	706	171	511	0	0
Total probes	13849	13676	13676	13754	13219	13559	13048	13048

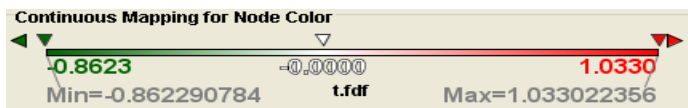


**A****Inter-modular Hubs Expression****B****Inter-modular Hubs SNR****C****Kruskal's Non-metric Multidimensional Scaling****D**

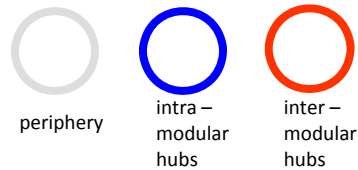
(A) Box plots of averaged expression levels and (B) dynamic ranges of SNR of inter-modular hubs in the consensus TSLC networks were plotted for PTCs, TSLCs and hESCs. Clustering of oocytes, hESCs, TSLCs, and PTCs displayed (C) in the 2-D NMDS plot and (D) heatmap using gene signatures of *lv\_com*.



**Color bar of differential gene expression:**



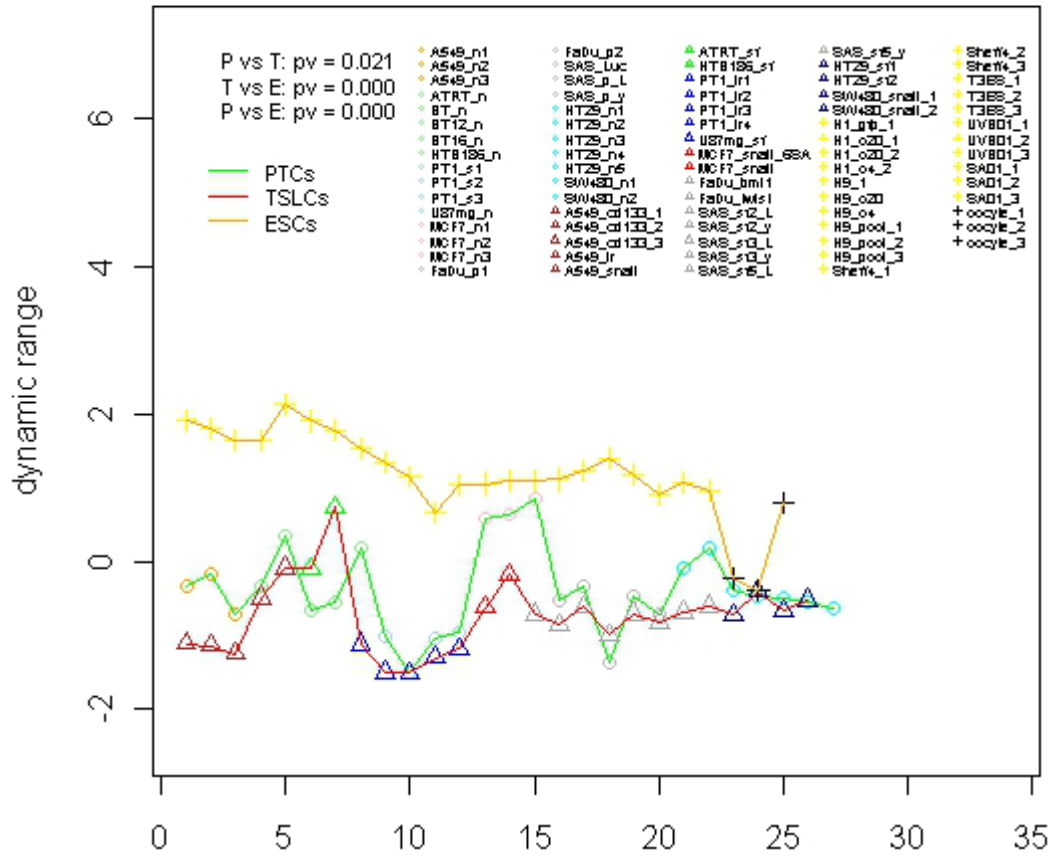
**Topological classification:**



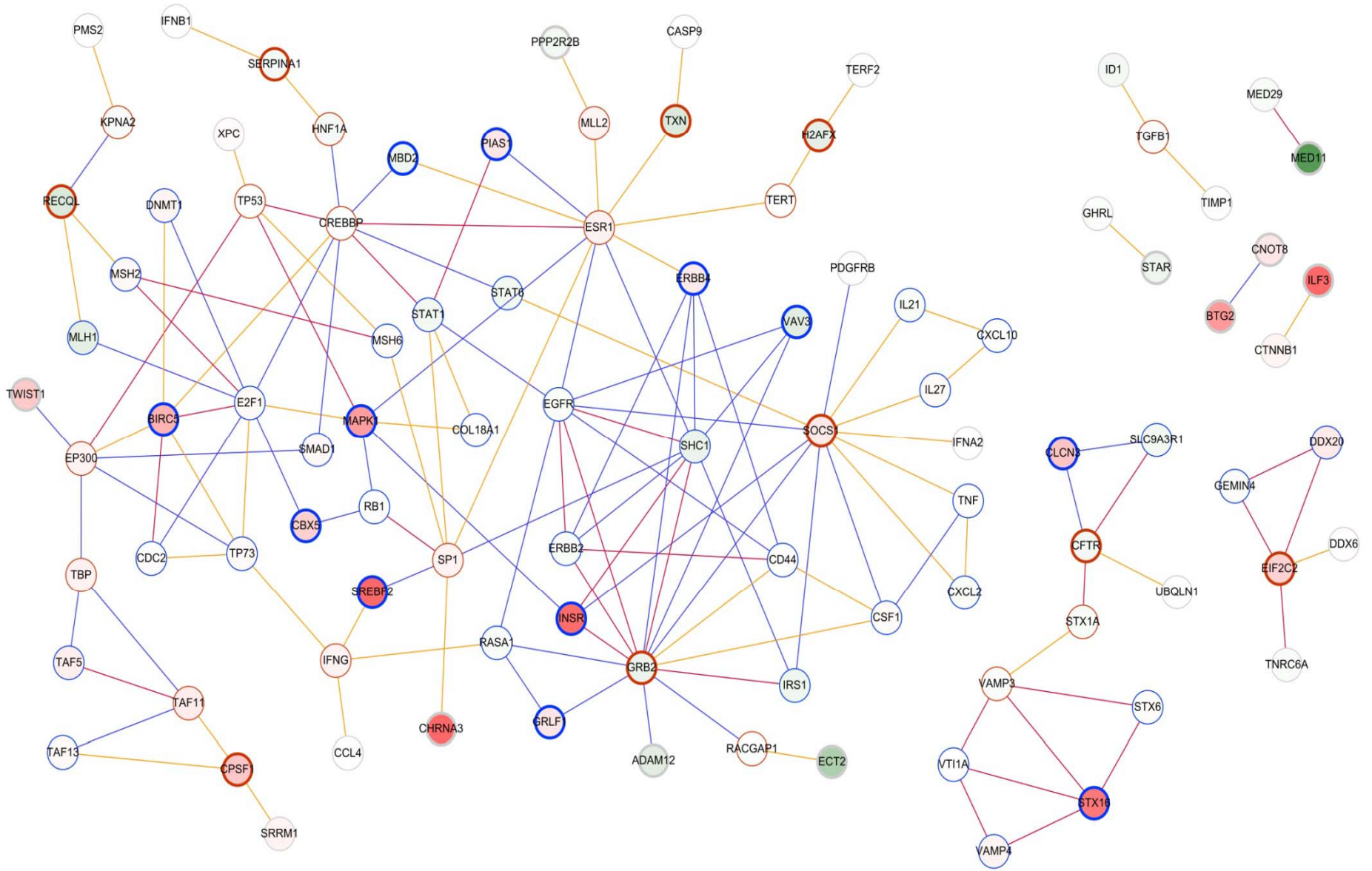
**Functional association reported from various databases:**



## Gene expression - DNMT3A



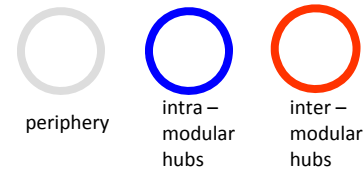
Dynamic ranges of averaged expression levels of DNMT3A in the consensus TSLC networks were plotted for PTCs, TSLCs and hESCs.



**Color bar of differential gene expression:**



**Topological classification:**



**Functional association reported from various databases:**



Table S1 Microarray Data Sets

Cancer tissue types / Experimental conditions	Parental Tumor Cells (PTCs)	No.	Tumor Stem-Like Cells (TSLCs)	No.	Human Embryonic Stem Cells (hESCs)	Feeder_cond	No.
<b>Glioblastoma</b> (gbm)	PT1-s	3	PT1-ir	4	H1		5
	U87-n	1	U87-sf	1	H1	4% and 20% O2	4
<b>ATRT</b>	atrt-n	1	atrt-sf	1	H9		8
<b>Medulloblastoma</b> (atrt)	HTB186-n	1	HTB186-sf	1	H9	4% and 20% O2	2
	BT16-s	1					
	BT	1					
	BT12-s	1					
<b>HNSCC</b> (oral_or)	sas-n	3	sas-sf (2,3,5)	6	Sheff 4 hesc	MEFs	3
	FaDu	2	FaDu_twist, bmi1	2			
<b>Breast</b> (br)	MCF7	3	MCF7_snail	2	SA01		3
<b>Colon</b> (cn)	SW480	2	SW480_snail	2	VUB01		3
	HT29-n	5	HT29-sf	2			
<b>Lung</b> (lq)	A549-n	3	A549-ir	1	T3ES		3
			A549_cd133	3			
			A549_snail	1			
<b>Serum-free sphere</b> (sf)	U87-n	1	U87-sf		oocyte		3
	atrt-n	1	atrt-sf	1			
	HTB186-n	1	HTB186-sf	1			
	sas-n	3	sas-sf (2,3,5)	6			
	HT29-n	5	HT29-sf	2			
<b>Over-expression of</b> (snail)	FaDu	2	FaDu_twist, bmi1	2			
	MCF7	3	MCF7_snail	2			
	SW480	2	SW480_snail	2			
	A549	3	A549_snail	1			

<b>Tissue Types / Conditions</b>	<b>Abbreviation</b>	<b>Number of Chips</b>	<b>87.5% of Absolute Values of Fold Changes</b>
Glioblastoma	gbm	9	1.37
AT/RT and Medulloblastoma	atrt	7	1.68
HNSCC	or	13	1.79
Breast	br	5	1.67
Colon	cn	11	1.71
Lung	lng	8	1.62
Over-expression of Snail, Bmi1, Twist	snail	17	1.23
Serum free sphere forming	sf	22	1.32



Table S2 Consensus TSLC networks (Edges)

a.sym	b.sym	a.gid	b.gid	#dbs	database	a.pb	b.pb	corr
ESR1	MYC	2099	4609	2	BIND-IPA.n1	211234_x_at	202431_s_at	0.4448037
ESR1	TP53	2099	7157	4	BioGRID-HPRD-BIND-IPA.n1	217163_at	201746_at	0.4623676
BRCA1	ESR1	672	2099	3	BioGRID-HPRD-IPA.n1	211851_x_at	215551_at	0.4634535
TP53	SIN3A	7157	25942	2	BIND-IPA.n1	211300_s_at	225135_at	0.4099827
HDAC2	RBBP4	3066	5928	3	BioGRID-HPRD-IPA.n1	201833_at	210371_s_at	0.7315502
HDAC1	RBBP4	3065	5928	4	BioGRID-HPRD-BIND-IPA.n1	201209_at	210371_s_at	0.7248656
BRCA1	BRCA2	672	675	4	BioGRID-HPRD-BIND-IPA.n1	211851_x_at	214727_at	0.7893156
SIN3A	SUDS3	25942	64426	2	BioGRID-IPA.n1	225135_at	233841_s_at	0.6568272
RBBP4	MBD2	5928	8932	3	BioGRID-HPRD-IPA.n1	217301_x_at	214396_s_at	0.4646377
HDAC1	RBBP7	3065	5931	2	BioGRID-IPA.n1	201209_at	201092_at	0.4255271
HDAC2	RBBP7	3066	5931	2	BioGRID-IPA.n1	201833_at	201092_at	0.5747854
ERBB2	ERBB4	2064	2066	2	BioGRID-IPA.n2	216836_s_at	233494_at	0.4383003
RHOA	ARHGAP5	387	394	2	BioGRID-IPA.n2	1555814_a_at	217936_at	0.4060502
BRCA2	PLK1	675	5347	2	BioGRID-IPA.n1	208368_s_at	202240_at	0.742489
CDKN2A	MYC	1029	4609	2	BIND-IPA.n1	209644_x_at	202431_s_at	0.5367128
CHEK1	TP53	1111	7157	3	BioGRID-HPRD-IPA.n1	205393_s_at	211300_s_at	0.5828072
DNMT3A	CBX5	1788	23468	2	BioGRID-IPA.n2	244428_at	242069_at	0.7219506
GOLGA4	MACF1	2803	23499	3	BIND-HPRD-IPA.n2	215203_at	232168_x_at	0.770862
HDAC1	HDAC2	3065	3066	3	BioGRID-HPRD-IPA.n1	201209_at	201833_at	0.7017465
HDAC1	SIN3A	3065	25942	4	BioGRID-BIND-HPRD-IPA.n1	201209_at	238005_s_at	0.6020143
HDAC1	SUDS3	3065	64426	2	BioGRID-IPA.n1	201209_at	224974_at	0.6532894
HDAC2	SIN3A	3066	25942	4	BioGRID-BIND-HPRD-IPA.n1	201833_at	238005_s_at	0.6187318
HDAC2	SUDS3	3066	64426	2	BioGRID-IPA.n1	201833_at	224974_at	0.5477465
PLK1	KIF23	5347	9493	2	HPRD-IPA.n1	202240_at	204709_s_at	0.8933461
CHEK1	PLK1	1111	5347	1		1 205393_s_at	202240_at	0.6306712
TP53	PRC1	7157	9055	1		1 211300_s_at	218009_s_at	0.472979
ESR1	ERBB2	2099	2064	1		1 217163_at	216836_s_at	0.5622145
TGFB1	PRC1	7040	9055	1		1 203084_at	218009_s_at	-0.445663
TNF	DUSP5	7124	1847	1		1 207113_s_at	209457_at	0.4055571
TNF	GBP1	7124	2633	1		1 207113_s_at	231578_at	0.4390259
ERBB2	MYC	2064	4609	1		1 234354_x_at	244089_at	0.5345625
ERBB2	TP53	2064	7157	1		1 216836_s_at	201746_at	0.5287188
STAT3	PMAIP1	6774	5366	1		1 243213_at	204285_s_at	0.4541879
TP53	HDAC2	7157	3066	1		1 211300_s_at	201833_at	0.5072621
SIN3A	MYC	25942	4609	1		1 238189_at	244089_at	0.4375127
HDAC1	BRCA2	3065	675	1		1 201209_at	214727_at	0.4556454
MYC	DDIT3	4609	1649	1		1 244089_at	209383_at	0.4326038
MBD2	ESR1	8932	2099	1		1 202485_s_at	211233_x_at	0.5747414
MBD2	CDKN2A	8932	1029	1		1 214396_s_at	207039_at	0.5026108
KIF23	PRC1	9493	9055	1		1 204709_s_at	218009_s_at	0.7708755
PRC1	PLK1	9055	5347	1		1 218009_s_at	202240_at	0.8164269
RBBP7	RBBP4	5931	5928	1		1 201092_at	217301_x_at	0.7137153
MBD2	RBBP7	8932	5931	1		1 214396_s_at	201092_at	0.5314243

TGFB1	INHBA	7040	3624	1		2 203084_at	210511_s_at	0.4625732
TRPC6	RHOA	7225	387	1		2 206528_at	240337_at	0.5669307
F2	TGFB1	2147	7040	1		2 205754_at	203085_s_at	0.4145961
ERBB2	RHOA	2064	387	1		2 210930_s_at	1555814_a_at	0.4800704
ERBB2	MACF1	2064	23499	1		2 216836_s_at	241896_at	0.4428346
DNMT3A	EED	1788	8726	1		2 244428_at	209572_s_at	0.6196614
MLANA	SILV	2315	6490	1		2 206427_s_at	209848_s_at	0.4420115
TIA1	ILF3	7072	3609	1		2 201447_at	217804_s_at	0.6419677
TIA1	ELAVL1	7072	1994	1		2 201449_at	244660_at	0.6890435
TIA1	TIAL1	7072	7073	1		2 201446_s_at	202405_at	0.7581311
HNRNPD	TIAL1	3184	7073	1		2 227744_s_at	202405_at	0.4516152
HNRNPD	TIA1	3184	7072	1		2 221481_x_at	201450_s_at	0.6862381
HNRNPD	ILF3	3184	3609	1		2 209330_s_at	208931_s_at	0.9188382
HNRNPD	ELAVL1	3184	1994	1		2 209330_s_at	201726_at	0.7109695
TIAL1	ILF3	7073	3609	1		2 202405_at	217804_s_at	0.4189879
ELAVL1	ILF3	1994	3609	1		2 201726_at	208931_s_at	0.791773
BRCA1	RBBP7	672	5931	3	BioGRID-HPRD-BIND	211851_x_at	201092_at	0.7789275
BRCA1	RBBP4	672	5928	3	BioGRID-HPRD-BIND	211851_x_at	217301_x_at	0.7852398
BRCA1	HDAC1	672	3065	3	BioGRID-HPRD-BIND	204531_s_at	201209_at	0.5243523
BRCA1	HDAC2	672	3066	3	BioGRID-HPRD-BIND	211851_x_at	201833_at	0.6763091
CSNK1E	ESR1	1454	2099	1	BIND	222015_at	215551_at	0.7100838
DNMT3A	MYC	1788	4609	3	BioGRID-HPRD-BIND	244428_at	202431_s_at	0.482701
ERBB2	STAT3	2064	6774	1	BioGRID	210930_s_at	208992_s_at	0.4799372
ERBB4	NCK1	2066	4690	1	BioGRID	233494_at	204725_s_at	0.6337783
ESR1	STAT3	2099	6774	1	BioGRID	217190_x_at	208991_at	0.5839479
EZH2	HDAC1	2146	3065	2	BioGRID-HPRD	203358_s_at	201209_at	0.6080015
EZH2	HDAC2	2146	3066	1	BioGRID	203358_s_at	201833_at	0.6718183
MYC	SPAG9	4609	9043	1	HPRD	202431_s_at	206748_s_at	0.5381877
RBBP4	SIN3A	5928	25942	2	BioGRID-HPRD	217301_x_at	225135_at	0.5493761
RBBP7	SIN3A	5931	25942	1	BioGRID	201092_at	225135_at	0.6468258
MBD2	SIN3A	8932	25942	1	BioGRID	214397_at	238189_at	0.4267213
CBX1	CBX3	10951	11335	2	BioGRID-HPRD	201518_at	200037_s_at	0.4047979
CBX1	CBX5	10951	23468	2	BioGRID-HPRD	201518_at	209715_at	0.6985717
CBX3	CBX5	11335	23468	2	BioGRID-HPRD	200037_s_at	209715_at	0.6567468

Table S3 Consensus TSLC networks (Nodes)

label	type	nb	focality	cc_Loc	g_family	probe	fold change	index	geneID
ERBB2	1	7	58.25			210930_s_at	-0.490105011	ipa	2064
MYC	1	7	57	Nucleus	transcription regulator	244089_at	-0.478447564	ipa	4609
PRC1	1	4	52.5	Nucleus	other	218009_s_at	-0.43201027	ipa	9055
DNMT3A	1	3	46.33333			222640_at	-0.319093984	focus	1788
CBX5	1	3	36	Nucleus	other	209715_at	-0.534017606	ipa	23468
RHOA	1	3	24.33333			240337_at	-0.478698961	ipa	387
TGFB1	1	3	24.33333	Extracellular Space	growth factor	203084_at	-0.590310818	ipa	7040
ESR1	1	7	18.5			211233_x_at	-0.722288804	ipa	2099
STAT3	1	3	18.5			243213_at	0.531044846	ipa	6774
ERBB4	1	2	18.5			233498_at	-0.284633595	ipa	2066
MACF1	1	2	18.5	Cytoplasm	other	215222_x_at	0.374446584	ipa	23499
TNF	1	2	0.5	Extracellular Space	cytokine	207113_s_at	-0.355577155	ipa	7124
HDAC2	2	8	0	Nucleus	transcription regulator	242141_at	-0.405956984	ipa	3066
HDAC1	2	8	0	Nucleus	transcription regulator	201209_at	-0.221716938	ipa	3065
SIN3A	2	8	0	Nucleus	transcription regulator	238189_at	-0.535936661	ipa	25942
BRCA1	2	6	0			204531_s_at	-0.191922572	ipa	672
TP53	2	6	0	Nucleus	transcription regulator	201746_at	-0.571994042	ipa	7157
RBBP4	2	6	0	Nucleus	enzyme	244872_at	0.626296521	ipa	5928
RBBP7	2	6	0	Nucleus	transcription regulator	201092_at	0.233202447	ipa	5931
MBD2	2	5	0	Nucleus	transcription regulator	202485_s_at	-0.315019855	focus	8932
PLK1	2	4	0	Nucleus	kinase	202240_at	-0.850044083	focus	5347
TIA1	2	4	0	Nucleus	other	1554889_at	0.726609853	focus	7072
HNRNPD	2	4	0	Nucleus	transcription regulator	205183_at	-0.49328733	ipa	3184
ILF3	2	4	0	Nucleus	transcription regulator	217804_s_at	-0.385495338	ipa	3609
BRCA2	2	3	0			208368_s_at	0.286383076	ipa	675
TIAL1	2	3	0	Nucleus	transcription regulator	217500_at	-0.733605585	ipa	7073
ELAVL1	2	3	0			227746_at	0.675569985	ipa	1994
SUDS3	2	3	0	Nucleus	other	224974_at	0.31989142	ipa	64426
CDKN2A	2	2	0			209644_x_at	0.21253652	ipa	1029
CHEK1	2	2	0			205394_at	-0.289269415	ipa	1111
KIF23	2	2	0	Cytoplasm	other	244427_at	-0.282312247	ipa	9493
EZH2	2	2	0			203358_s_at	-0.199232459	ipa	2146
CBX1	2	2	0	Nucleus	other	201518_at	-0.207006629	ipa	10951
CBX3	2	2	0	Nucleus	other	1555920_at	0.256790796	ipa	11335
GOLGA4	3	1	0	Cytoplasm	other	201567_s_at	0.796419343	focus	2803
TRPC6	3	1	0	Plasma Membrane	ion channel	217287_s_at	-0.275099599	focus	7225
F2	3	1	0			205754_at	-0.277487108	ipa	2147
MLANA	3	1	0			206426_at	-0.151041801	ipa	2315
CSNK1E	3	1	0			226858_at	0.839604727	lvcom	1454
ARHGAP5	3	1	0			235635_at	0.620410459	focus	394
DUSP5	3	1	0			209457_at	0.217890443	ipa	1847
GBP1	3	1	0	Cytoplasm	enzyme	231578_at	0.156580214	ipa	2633
PMAIP1	3	1	0	Cytoplasm	other	204285_s_at	0.892757243	focus	5366
DDIT3	3	1	0			209383_at	0.235709901	ipa	1649
INHBA	3	1	0	Extracellular Space	growth factor	210511_s_at	0.386399436	ipa	3624
EED	3	1	0	Nucleus	transcription regulator	210656_at	0.293971429	ipa	8726
SILV	3	1	0	Plasma Membrane	enzyme	209848_s_at	-0.119821454	focus	6490
NCK1	3	1	0	Cytoplasm	kinase	204725_s_at	0.436825922	focus	4690
SPAG9	3	1	0	Plasma Membrane	other	1554543_at	0.635588561	focus	9043

Table S3 Consensus TSLC networks (Nodes)

label	type	nb	focality	cc_Loc	g_family	probe	fold change	index	geneID
ERBB2	1	7	58.25			210930_s_at	-0.490105011	ipa	2064
MYC	1	7	57	Nucleus	transcription regulator	244089_at	-0.478447564	ipa	4609
PRC1	1	4	52.5	Nucleus	other	218009_s_at	-0.43201027	ipa	9055
DNMT3A	1	3	46.33333			222640_at	-0.319093984	focus	1788
CBX5	1	3	36	Nucleus	other	209715_at	-0.534017606	ipa	23468
RHOA	1	3	24.33333			240337_at	-0.478698961	ipa	387
TGFB1	1	3	24.33333	Extracellular Space	growth factor	203084_at	-0.590310818	ipa	7040
ESR1	1	7	18.5			211233_x_at	-0.722288804	ipa	2099
STAT3	1	3	18.5			243213_at	0.531044846	ipa	6774
ERBB4	1	2	18.5			233498_at	-0.284633595	ipa	2066
MACF1	1	2	18.5	Cytoplasm	other	215222_x_at	0.374446584	ipa	23499
TNF	1	2	0.5	Extracellular Space	cytokine	207113_s_at	-0.355577155	ipa	7124
HDAC2	2	8	0	Nucleus	transcription regulator	242141_at	-0.405956984	ipa	3066
HDAC1	2	8	0	Nucleus	transcription regulator	201209_at	-0.221716938	ipa	3065
SIN3A	2	8	0	Nucleus	transcription regulator	238189_at	-0.535936661	ipa	25942
BRCA1	2	6	0			204531_s_at	-0.191922572	ipa	672
TP53	2	6	0	Nucleus	transcription regulator	201746_at	-0.571994042	ipa	7157
RBBP4	2	6	0	Nucleus	enzyme	244872_at	0.626296521	ipa	5928
RBBP7	2	6	0	Nucleus	transcription regulator	201092_at	0.233202447	ipa	5931
MBD2	2	5	0	Nucleus	transcription regulator	202485_s_at	-0.315019855	focus	8932
PLK1	2	4	0	Nucleus	kinase	202240_at	-0.850044083	focus	5347
TIA1	2	4	0	Nucleus	other	1554889_at	0.726609853	focus	7072
HNRNPD	2	4	0	Nucleus	transcription regulator	205183_at	-0.49328733	ipa	3184
ILF3	2	4	0	Nucleus	transcription regulator	217804_s_at	-0.385495338	ipa	3609
BRCA2	2	3	0			208368_s_at	0.286383076	ipa	675
TIAL1	2	3	0	Nucleus	transcription regulator	217500_at	-0.733605585	ipa	7073
ELAVL1	2	3	0			227746_at	0.675569985	ipa	1994
SUDS3	2	3	0	Nucleus	other	224974_at	0.31989142	ipa	64426
CDKN2A	2	2	0			209644_x_at	0.21253652	ipa	1029
CHEK1	2	2	0			205394_at	-0.289269415	ipa	1111
KIF23	2	2	0	Cytoplasm	other	244427_at	-0.282312247	ipa	9493
EZH2	2	2	0			203358_s_at	-0.199232459	ipa	2146
CBX1	2	2	0	Nucleus	other	201518_at	-0.207006629	ipa	10951
CBX3	2	2	0	Nucleus	other	1555920_at	0.256790796	ipa	11335
GOLGA4	3	1	0	Cytoplasm	other	201567_s_at	0.796419343	focus	2803
TRPC6	3	1	0	Plasma Membrane	ion channel	217287_s_at	-0.275099599	focus	7225
F2	3	1	0			205754_at	-0.277487108	ipa	2147
MLANA	3	1	0			206426_at	-0.151041801	ipa	2315
CSNK1E	3	1	0			226858_at	0.839604727	lvcom	1454
ARHGAP5	3	1	0			235635_at	0.620410459	focus	394
DUSP5	3	1	0			209457_at	0.217890443	ipa	1847
GBP1	3	1	0	Cytoplasm	enzyme	231578_at	0.156580214	ipa	2633
PMAIP1	3	1	0	Cytoplasm	other	204285_s_at	0.892757243	focus	5366
DDIT3	3	1	0			209383_at	0.235709901	ipa	1649
INHBA	3	1	0	Extracellular Space	growth factor	210511_s_at	0.386399436	ipa	3624
EED	3	1	0	Nucleus	transcription regulator	210656_at	0.293971429	ipa	8726
SILV	3	1	0	Plasma Membrane	enzyme	209848_s_at	-0.119821454	focus	6490
NCK1	3	1	0	Cytoplasm	kinase	204725_s_at	0.436825922	focus	4690
SPAG9	3	1	0	Plasma Membrane	other	1554543_at	0.635588561	focus	9043

Table S4 Lung TSLC Network (Edges)

gene.a	gene.b	geneID.a	geneID.b	#db	database	probe.a	probe.b	Correlation
CD44	EGFR	960	1956	3	BioGRID-HPRD-BIND	209835_x_at	211607_x_at	0.99992185
IFNA2	SOCS1	3440	8651	1	IPA.n2	211338_at	209999_x_at	0.99849356
CTNNB1	ILF3	1499	3609	1	IPA.n3	223679_at	211375_s_at	0.99761243
EGFR	STAT1	1956	6772	2	BioGRID-HPRD	201983_s_at	AFFX-HUMISGF3A/M97935_MB_at	0.99718719
EP300	SMAD1	2033	4086	2	BioGRID-HPRD	202221_s_at	227798_at	0.9966831
EGFR	SHC1	1956	6464	4	BioGRID-BIND-HPRD-IPA.n1	211607_x_at	214853_s_at	0.9946332
E2F1	TP73	1869	7161	1	IPA.n2	204947_at	232546_at	0.99436015
EGFR	VAV3	1956	10451	2	BioGRID-HPRD	211550_at	224221_s_at	0.99282514
EGFR	ERBB2	1956	2064	4	BioGRID-HPRD-BIND-IPA.n3	201984_s_at	210930_s_at	0.99276028
IRS1	SHC1	3667	6464	3	BioGRID-HPRD-BIND	204686_at	214853_s_at	0.99262096
CREBBP	TP53	1387	7157	4	BioGRID-HPRD-BIND-IPA.n1	228177_at	201746_at	0.99193726
CREBBP	STAT1	1387	6772	4	BioGRID-HPRD-BIND-IPA.n1	211808_s_at	AFFX-HUMISGF3A/M97935_MB_at	0.99141449
CD44	CSF1	960	1435	1	IPA.n3	229221_at	209716_at	0.99110969
SHC1	VAV3	6464	10451	2	BioGRID-HPRD	201469_s_at	218806_s_at	0.99051204
CDC2	E2F1	983	1869	1	BIND	203213_at	204947_at	0.98959017
BIRC5	CDC2	332	983	2	HPRD-IPA.n1	210334_x_at	231534_at	0.98938474
STX16	STX6	8675	10228	2	HPRD-IPA.n4	218822_s_at	212800_at	0.98818302
CDC2	TP73	983	7161	1	IPA.n2	203213_at	232546_at	0.98695704
CD44	ERBB2	960	2064	2	BioGRID-IPA.n3	212063_at	210930_s_at	0.9862118
VAMP3	STX6	9341	10228	2	BioGRID-IPA.n1	201337_s_at	212800_at	0.98527358
KPNA2	RECQL	3838	5965	2	BioGRID-HPRD	201088_at	212917_x_at	0.98448425
TGFB1	TIMP1	7040	7076	1	IPA.n2	203085_s_at	201666_at	0.98401838
IFNG	TP73	3458	7161	1	IPA.n2	210354_at	1554379_a_at	0.98301829
EP300	TP73	2033	7161	1	BIND	202221_s_at	232546_at	0.98230869
GRB2	RACGAP1	2885	29127	1	BioGRID	228572_at	224272_at	0.98202449
ERBB2	SHC1	2064	6464	2	BioGRID-HPRD	210930_s_at	214853_s_at	0.98054627
RECQL	MLH1	5965	4292	1	IPA.n1	210568_s_at	202520_s_at	0.98049163
CSF1	SOCS1	1435	8651	1	HPRD	211839_s_at	213337_s_at	0.98001357
EP300	TBP	2033	6908	1	BIND	202221_s_at	203135_at	0.97978613
E2F1	MAPK1	1869	5594	1	IPA.n1	204947_at	224621_at	0.97964449
DNMT1	E2F1	1786	1869	1	BioGRID	201697_s_at	204947_at	0.97960639
GRB2	VAV3	2885	10451	2	BioGRID-HPRD	215075_s_at	218807_at	0.97935493
ERBB4	GRB2	2066	2885	1	BioGRID	206794_at	215075_s_at	0.97928233
BIRC5	E2F1	332	1869	3	BIND-IPA.n1	202095_s_at	2028_s_at	0.97856914
MAPK1	RB1	5594	5925	1	BIND	208351_s_at	211540_s_at	0.97828946
CD44	ERBB4	960	2066	2	BioGRID-HPRD	229221_at	206794_at	0.97815941
VAMP3	VT1A	9341	143187	2	BioGRID-IPA.n1	201337_s_at	235923_at	0.977110459
CREBBP	SMAD1	1387	4086	1	BioGRID	202160_at	210993_s_at	0.97692954
SP1	STAT1	6667	6772	1	IPA.n1	214732_at	AFFX-HUMISGF3A/M97935_5_at	0.97543318
SHC1	SP1	6464	6667	1	HPRD	201469_s_at	214732_at	0.97286578
TP53	XPC	7157	7508	1	IPA.n1	201746_at	209375_at	0.97036456
ESR1	PIAS1	2099	8554	2	HPRD-BIND	211234_x_at	217864_s_at	0.96791505
MSH6	MSH2	2956	4436	4	BioGRID-HPRD-BIND-IPA.n1	202911_at	209421_at	0.96719338
VAMP4	STX16	8674	8675	3	BioGRID-HPRD-IPA.n4	213480_at	221500_s_at	0.96490985
ERBB4	SHC1	2066	6464	1	BioGRID	206794_at	214853_s_at	0.96459712
ESR1	MAPK1	2099	5594	2	BioGRID-HPRD	211627_x_at	224620_at	0.96401021
GRLF1	RASA1	2909	5921	1	BioGRID	202046_s_at	210621_s_at	0.96388052
TGFB1	ID1	7040	3397	1	IPA.n2	203085_s_at	208937_s_at	0.96349901
COL18A1	MAPK1	80781	5594	1	IPA.n1	209081_s_at	224620_at	0.96295819
STX16	VAMP3	8675	9341	3	BioGRID-HPRD-IPA.n4	218822_s_at	201337_s_at	0.96178359
ESR1	TERT	2099	7015	1	IPA.n1	211234_x_at	1555271_a_at	0.96090159
TAF5	TAF11	6877	6882	3	BioGRID-HPRD-IPA.n4	210053_at	1558136_s_at	0.96034622
DDX20	GEMIN4	11218	50628	2	BioGRID-IPA.n1	223331_s_at	217099_s_at	0.95930209
GRB2	GRLF1	2885	2909	1	BioGRID	215075_s_at	229397_s_at	0.95916294
MLL2	ESR1	8085	2099	1	IPA.n1	216382_s_at	211233_x_at	0.95884696
MBD2	ESR1	8932	2099	1	IPA.n1	202485_s_at	211233_x_at	0.95874665
CFTR	CLCN3	1080	1182	1	BioGRID	215703_at	201733_at	0.95734999
GRB2	IRS1	2885	3667	3	BioGRID-HPRD-IPA.n1	215075_s_at	204686_at	0.95622984
SOCS1	CXCL2	8651	2920	1	IPA.n2	213337_s_at	209774_x_at	0.95582855
TXN	ESR1	7295	2099	1	IPA.n1	208864_s_at	211627_x_at	0.95335455
COL18A1	STAT1	80781	6772	1	IPA.n1	209082_s_at	AFFX-HUMISGF3A/M97935_MB_at	0.95236669
TXN	CASP9	7295	842	1	IPA.n1	216609_at	210775_x_at	0.95194107
CREBBP	MBD2	1387	8932	1	HPRD	211808_s_at	202484_s_at	0.95029479
TAF11	TBP	6882	6908	2	BioGRID-HPRD	1558136_s_at	203135_at	0.95017968
IL27	CXCL10	246778	3627	1	IPA.n2	1552995_at	204533_at	0.95004652
RB1	CBX5	5925	23468	1	BioGRID	211540_s_at	234990_at	0.94895941
TAF5	TBP	6877	6908	2	BioGRID-HPRD	210053_at	203135_at	0.94815388
EGFR	SOCS1	1956	8651	2	BioGRID-HPRD	210984_x_at	213337_s_at	0.94715926
EP300	TWIST1	2033	7291	2	BioGRID-HPRD	202221_s_at	213943_at	0.9453108
CSF1	GRB2	1435	2885	1	IPA.n3	209716_at	215075_s_at	0.94002163
RB1	SP1	5925	6667	3	BioGRID-HPRD-IPA.n1	211540_s_at	214732_at	0.93488739
CREBBP	STAT6	1387	6778	2	BioGRID-HPRD	211808_s_at	201331_s_at	0.93464983
INSR	SHC1	3643	6464	4	BioGRID-BIND-HPRD-IPA.n3	226450_at	217048_at	0.93142407
EGFR	ESR1	1956	2099	2	BioGRID-HPRD	211551_at	211627_x_at	0.93062295

GRB2	CD44	2885	960	1	IPA.n3	215075_s_at	210916_s_at	0.93057158
E2F1	MSH2	1869	4436	2	BIND-IPA.n1	204947_at	209421_at	0.92812721
CREBBP	BIRC5	1387	332	2	IPA.n1月2日	235858_at	202094_at	0.92801297
IFNB1	SERPINA1	3456	5265	1	IPA.n3	208173_at	211428_at	0.92552906
SP1	CHRNA3	6667	1136	1	IPA.n1	224754_at	211587_x_at	0.92384532
EGFR	GRB2	1956	2885	4	BioGRID-BIND-HPRD-IPA.n3	201983_s_at	215075_s_at	0.92371344
GRB2	SHC1	2885	6464	4	BioGRID-BIND-HPRD-IPA.n3	215075_s_at	214853_s_at	0.92282236
CREBBP	HNF1A	1387	6927	3	BioGRID-HPRD-BIND	211808_s_at	210515_at	0.92246709
DDX6	EIF2C2	1656	27161	1	IPA.n4	225549_at	225569_at	0.91570674
TNF	SOCS1	7124	8651	1	IPA.n2	207113_s_at	209999_x_at	0.91526933
GRB2	ADAM12	2885	8038	1	HPRD	228572_at	204943_at	0.91470651
STX16	VT11A	8675	143187	2	HPRD-IPA.nIPA.n4	218822_s_at	235923_at	0.91419594
CFTR	SLC9A3R1	1080	9368	4	BioGRID-HPRD-BIND-IPA.n4	205043_at	201349_at	0.9139189
GRB2	SOCS1	2885	8651	3	BioGRID-HPRD-BIND	228572_at	209999_x_at	0.91320869
DDX20	EIF2C2	11218	27161	3	BioGRID-HPRD-IPA.n4	223331_s_at	225569_at	0.91156212
GRB2	INSR	2885	3643	2	BioGRID-IPA.nIPA.n3	228572_at	226450_at	0.9113859
IFNG	SREBF2	3458	6721	1	IPA.n2	210354_at	201247_at	0.90869244
EIF2C2	GEMIN4	27161	50628	2	BioGRID-IPA.n4	225569_at	217099_s_at	0.90837564
CREBBP	ESR1	1387	2099	2	BioGRID-IPA.n1	235858_at	217190_x_at	0.90757023
EGFR	RASA1	1956	5921	3	BioGRID-HPRD-BIND	201983_s_at	210621_s_at	0.90572326
ESR1	ERBB4	2099	2066	1	IPA.n1	211627_x_at	206794_at	0.90477497
CFTR	STX1A	1080	6804	4	BioGRID-HPRD-BIND-IPA.nIPA.n4	234706_x_at	204729_s_at	0.90474984
ESR1	SHC1	2099	6464	2	BioGRID-HPRD	211235_s_at	217048_at	0.9029758
SP1	ESR1	6667	2099	1	IPA.n1	224754_at	211233_x_at	0.90224676
VAMP3	STX1A	9341	6804	1	IPA.n4	201337_s_at	204729_s_at	0.89942194
EIF2C2	TNRC6A	27161	27327	2	BioGRID-IPA.n4	213310_at	1553346_a_at	0.89908096
ERBB2	ERBB4	2064	2066	1	BioGRID	210930_s_at	206794_at	0.89779145
BTG2	CNOT8	7832	9337	2	BioGRID-HPRD	201235_s_at	202162_s_at	0.89766634
IL21	SOCS1	59067	8651	1	IPA.n2	221271_at	209999_x_at	0.89413839
STAT1	PIAS1	6772	8554	3	BioGRID-HPRD-IPA.nIPA.n1	AFFX-HUMISGF217862_at		0.89305307
IRS1	SOCS1	3667	8651	2	BioGRID-HPRD	204686_at	213337_s_at	0.88625226
PDGFRB	SOCS1	5159	8651	1	BIND	202273_at	210000_s_at	0.88426858
BIRC5	TP73	332	7161	1	IPA.n2	202095_s_at	232546_at	0.87922305
EP300	BIRC5	2033	332	1	IPA.n1	202221_s_at	202095_s_at	0.87318735
INSR	MAPK1	3643	5594	1	BioGRID	207851_s_at	224621_at	0.87184012
INSR	SOCS1	3643	8651	1	BIND	226450_at	209999_x_at	0.87054663
DNMT1	BIRC5	1786	332	1	IPA.n1	201697_s_at	202095_s_at	0.87009235
TERF2	H2AFX	7014	3014	1	IPA.n1	1555185_x_at	212524_x_at	0.86685461
SP1	MSH6	6667	2956	1	IPA.n1	224754_at	211449_at	0.86344667
GRB2	RASA1	2885	5921	2	BioGRID-HPRD	215075_s_at	210621_s_at	0.86060807
RECQL	MSH2	5965	4436	1	IPA.n1	212918_at	209421_at	0.86033785
TNF	CXCL2	7124	2920	1	IPA.n2	207113_s_at	230101_at	0.85869582
TAF13	CPSF1	6884	29894	1	IPA.n4	205966_at	201638_s_at	0.85782377
GHRL	STAR	51738	6770	1	IPA.n4	237647_at	204548_at	0.85541653
IL27	SOCS1	246778	8651	1	IPA.n2	1552995_at	209999_x_at	0.85422625
MED29	MED11	55588	400569	3	BioGRID-HPRD-IPA.n4	225708_at	226958_s_at	0.85299997
VAMP4	VT11A	8674	143187	2	BioGRID-IPA.nIPA.n4	213480_at	1552536_at	0.85051308
SP1	SREBF2	6667	6721	2	BioGRID-HPRD	1553685_s_at	201248_s_at	0.84864892
TP53	MSH6	7157	2956	1	IPA.n1	201746_at	211450_s_at	0.84699558
IL21	CXCL10	59067	3627	1	IPA.n2	221271_at	204533_at	0.84685918
MAPK1	TP53	5594	7157	2	BioGRID-IPA.nIPA.n1	212271_at	201746_at	0.84399718
CFTR	UBQLN1	1080	29979	1	IPA.n4	234702_x_at	222991_s_at	0.83859762
TERT	H2AFX	7015	3014	1	IPA.n1	207199_at	205436_s_at	0.83462337
ERBB2	GRB2	2064	2885	3	BioGRID-HPRD-IPA.nIPA.n3	210930_s_at	215075_s_at	0.83391447
KPNA2	PMS2	3838	5395	1	IPA.n4	201088_at	216039_at	0.82969324
CPSF1	SRRM1	29894	10250	1	IPA.n4	201639_s_at	201224_s_at	0.82859094
EP300	TP53	2033	7157	4	BioGRID-HPRD-BIND-IPA.n1	213579_s_at	201746_at	0.82832229
E2F1	CBX5	1869	23468	1	BIND	2028_s_at	242069_at	0.82800423
TAF11	CPSF1	6882	29894	1	IPA.n4	1558136_s_at	33132_at	0.82769656
STAT6	SOCS1	6778	8651	1	IPA.n2	201331_s_at	213337_s_at	0.82678845
IFNG	CCL4	3458	6351	1	IPA.n2	210354_at	204103_at	0.82448473
CREBBP	E2F1	1387	1869	1	BioGRID	202160_at	204947_at	0.82345875
ECT2	RACGAP1	1894	29127	1	IPA.n4	237241_at	224272_at	0.82237249
CSF1	TNF	1435	7124	1	HPRD	207082_at	207113_s_at	0.82208815
MLL2	PPP2R2B	8085	5521	1	IPA.n1	216382_s_at	205643_s_at	0.81663086
HNF1A	SERPINA1	6927	5265	1	IPA.n3	210515_at	211429_s_at	0.81470722
CLCN3	SLC9A3R1	1182	9368	2	BioGRID-HPRD	201734_at	201349_at	-0.81366656
TAF11	TAF13	6882	6884	2	BioGRID-HPRD	1558136_s_at	205966_at	-0.81956655
E2F1	MLH1	1869	4292	1	BIND	204947_at	202520_s_at	-0.8543077
IFNG	RASA1	3458	5921	1	IPA.n2	210354_at	210621_s_at	-0.8553362

Table S5 Lung TSLC Networks (Nodes)

label	type	nbhood	focality	differential	probe	fold change	lv_consistent	lung TSLC	GeneID	g_family
TBP	1	3	160	.	203135_at	0.287551383	.	0.751982744	6908	transcription regulator
EP300	1	6	146.66667	.	202221_s_at	0.282407087	.	0.673816365	2033	transcription regulator
ESR1	1	11	112.5	.	215551_at	0.082793858	.	0.79818623	2099	ligand-dependent nuclear receptor
CREBBP	1	9	99	.	211808_s_at	0.095624117	.	-0.205538151	1387	transcription regulator
TAF11	1	4	99	.	1558135_at	0.431290153	.	1.093414667	6882	transcription regulator
SOCS1	1	12	81.75	lg	209999_x_at	-0.068025032	lung	0.313288221	8651	other
RECQL	1	3	67	atrt	205091_x_at	0.322937656	lung oral	-0.595630799	5965	enzyme
TERT	1	2	67	.	1555271_a_at	-0.019871004	.	-0.015934492	7015	enzyme
HNF1A	1	2	67	.	210515_at	-0.435404285	.	-0.939153104	6927	transcription regulator
GRB2	1	14	66.666667	snail	228572_at	0.017253845	lung breast	-0.290755352	2885	other
SP1	1	7	34	.	224754_at	0.514171963	.	0.710598752	6667	transcription regulator
TP53	1	5	34	.	211300_s_at	-0.498483886	.	-0.225716066	7157	transcription regulator
IFNG	1	4	34	.	210354_at	-0.125111301	.	0.724220169	3458	cytokine
CPSF1	1	3	34	atrt	201639_s_at	0.065009507	lung	0.81583748	29894	other
KPNA2	1	2	34	.	211762_s_at	-0.450958331	.	-0.703640227	3838	transporter
MLL2	1	2	34	.	227528_s_at	0.142852089	.	0.712940053	8085	transcription regulator
TXN	1	2	34	atrt	216609_at	0.04757852	lung	-0.867565811	7295	enzyme
RACGAP1	1	2	34	.	224272_at	-0.110018616	.	0.027009864	29127	transporter
SERPINA1	1	2	34	lg	211429_s_at	-0.08768584	lung	-0.23603667	5265	other
H2AFX	1	2	34	atrt	212524_x_at	-0.371707372	lung gbm	-0.416433395	3014	other
VAMP3	1	4	10	.	201336_at	0.09012197	.	-0.440880923	9341	other
STX1A	1	2	10	.	204729_s_at	-0.145838616	.	-0.652136806	6804	transporter
CFTR	1	4	6.666667	com	234702_x_at	-0.099860319	lung	-0.274374578	1080	ion channel
EIF2C2	1	4	1.666667	atrt	225827_at	0.29091523	lung breast	0.432941238	27161	translation regulator
TGFB1	1	2	0.5	.	203085_s_at	0.130741505	.	-0.439950196	7040	growth factor
EGFR	2	9	0	.	211607_x_at	0.4171874	.	-0.367135472	1956	kinase
E2F1	2	9	0	.	204947_at	-0.457846103	.	0.354955467	1869	transcription regulator
SHC1	2	9	0	.	214853_s_at	-0.052429192	.	-1.815286673	6464	other
BIRC5	2	6	0	cn	210334_x_at	-0.215221928	lung atrt	0.761308573	332	other
MAPK1	2	6	0	lg	1552263_at	0.355761603	lung breast	0.964369891	5594	kinase
CD44	2	5	0	.	216056_at	0.3155394	.	-0.151870383	960	other
ERBB2	2	5	0	.	234354_x_at	0.199512996	.	-0.536039887	2064	kinase
ERBB4	2	5	0	atrt	206794_at	-0.035414519	lung	0.304146378	2066	kinase
STAT1	2	5	0	.	AFFX-HUMISGF:	0.110893384	.	-1.1188445	6772	transcription regulator
TP73	2	5	0	.	220804_s_at	-0.18490816	.	0.30353359	7161	transcription regulator
STX16	2	4	0	atrt	221499_s_at	0.64421139	lung oral	1.327248307	8675	transporter
CSF1	2	4	0	.	210557_x_at	-0.179010437	.	0.225362698	1435	cytokine
INSR	2	4	0	atrt	226212_s_at	0.145780843	lung breast	1.455602753	3643	kinase
RASA1	2	4	0	.	210621_s_at	0.405472456	.	-0.484458084	5921	transporter
IRS1	2	3	0	.	235392_at	-0.485334283	.	-1.470380998	3667	other
CDC2	2	3	0	.	203214_x_at	0.024535323	.	0.120586658	983	kinase
MSH6	2	3	0	.	202911_at	0.298259263	.	0.256678316	2956	enzyme
RB1	2	3	0	.	203132_at	-0.065657187	.	-0.166067585	5925	transcription regulator
TNF	2	3	0	.	207113_s_at	-0.355577155	.	-0.332414373	7124	cytokine
VAV3	2	3	0	atrt	224221_s_at	0.190483744	lung	-0.728003029	10451	.
VT11A	2	3	0	.	242356_at	0.306646617	.	-0.03940389	143187	transporter

MSH2	2	3	0	.	209421_at	0.209219727 .	0.404763487	4436	enzyme
DNMT1	2	2	0	.	201697_s_at	-0.159234577 .	0.628881119	1786	enzyme
VAMP4	2	2	0	.	213480_at	0.693971537 .	0.656799858	8674	other
GRLF1	2	2	0	atrt	202044_at	0.231780126 lung	0.378941853	2909	.
COL18A1	2	2	0	.	209081_s_at	-0.037841289 .	-0.015347705	80781	other
TAF5	2	2	0	.	1553528_a_at	0.373159183 .	0.928668627	6877	transcription regulator
DDX20	2	2	0	.	223331_s_at	0.57211895 .	1.281605094	11218	transcription regulator
MBD2	2	2	0	x	202484_s_at	0.042601088 lung	-0.342293952	8932	transcription regulator
IL27	2	2	0	.	1552995_at	0.039994132 .	0.260998785	246778	cytokine
IL21	2	2	0	.	221271_at	-0.085991563 .	-0.521787528	59067	cytokine
TAF13	2	2	0	.	205966_at	0.043564356 .	0.311303517	6884	transcription regulator
STAT6	2	2	0	.	201331_s_at	-0.04032854 .	-1.193813016	6778	transcription regulator
CLCN3	2	2	0	atrt	201732_s_at	0.333145835 lung	0.866803302	1182	.
SMAD1	2	2	0	.	208015_at	0.261755793 .	0.39769438	4086	transcription regulator
STX6	2	2	0	.	212799_at	0.379527108 .	0.179865143	10228	transporter
MLH1	2	2	0	.	202520_s_at	-0.769251726 .	-3.099259205	4292	other
PIAS1	2	2	0	gbm	217864_s_at	0.616761964 lung oral	0.231453479	8554	transcription regulator
GEMIN4	2	2	0	.	205527_s_at	-0.132285795 .	-0.438877171	50628	other
CXCL2	2	2	0	.	230101_at	0.656182494 .	-0.465924854	2920	cytokine
CXCL10	2	2	0	.	204533_at	-0.311816102 .	-0.099371367	3627	cytokine
CBX5	2	2	0	atrt	234990_at	0.176982516 lung	0.705592144	23468	other
SLC9A3R1	2	2	0	.	201349_at	-0.868383063 .	-1.083493046	9368	other
SREBF2	2	2	0	atrt	201247_at	0.656182494 lung breast	1.626923677	6721	transcription regulator
IFNA2	3	1	0	.	211338_at	-0.191180578 .	-0.1392019	3440	cytokine
CTNNB1	3	1	0	.	223679_at	0.704111852 .	0.587887538	1499	transcription regulator
IFNB1	3	1	0	.	208173_at	-0.122798696 .	0.026418054	3456	cytokine
DDX6	3	1	0	.	225549_at	0.34485676 .	0.093643646	1656	enzyme
BTG2	3	1	0	atrt	201236_s_at	0.031756844 lung	1.585993018	7832	transcription regulator
PDGFRB	3	1	0	.	202273_at	-0.117418755 .	-0.32643221	5159	kinase
TERF2	3	1	0	.	203611_at	0.276757941 .	0.076128238	7014	other
GHRL	3	1	0	.	237647_at	-0.274866229 .	-0.356782491	51738	growth factor
MED29	3	1	0	.	225708_at	-0.003782209 .	-0.601559932	55588	other
ECT2	3	1	0	atrt	219787_s_at	0.175607613 lung oral breast	-0.78155886	1894	other
ILF3	3	1	0	sf	217805_at	0.224484872 lung colon	1.506583555	3609	transcription regulator
TIMP1	3	1	0	.	201666_at	0.129941232 .	-0.161337911	7076	other
XPC	3	1	0	.	209375_at	0.089357493 .	0.23955464	7508	other
ID1	3	1	0	.	208937_s_at	-0.631796535 .	-1.036089956	3397	transcription regulator
CASP9	3	1	0	.	240437_at	0.056179734 .	-0.167397365	842	peptidase
TWIST1	3	1	0	atrt	213943_at	0.319560235 lung	0.787541331	7291	transcription regulator
CHRNA3	3	1	0	atrt	211772_x_at	0.192560906 lung breast	1.60784574	1136	transmembrane receptor
ADAM12	3	1	0	atrt	202952_s_at	0.124916753 lung	-0.720607756	8038	.
TNRC6A	3	1	0	.	224705_s_at	0.350274687 .	-0.466245722	27327	other
CNOT8	3	1	0	atrt	202163_s_at	0.247264458 lung	0.361100008	9337	.
STAR	3	1	0	x	204548_at	-0.171699229 lung breast	-0.26826546	6770	transporter
MED11	3	1	0	atrt	226958_s_at	-0.558713911 lung breast gbn	-1.648572839	400569	other
UBQLN1	3	1	0	.	222990_at	0.587309974 .	-0.244566855	29979	other
PMS2	3	1	0	.	209805_at	0.032903456 .	0.014147032	5395	other
SRRM1	3	1	0	.	201225_s_at	0.243797948 .	0.69967427	10250	other
CCL4	3	1	0	.	204103_at	-0.459547058 .	-0.113533252	6351	cytokine
PPP2R2B	3	1	0	snail	205643_s_at	0.026537035 lung	-0.318493336	5521	phosphatase



Table S6 Survival Analyses

**Word color**    **Annotation:**  
 black            Only hub genes were included in the analysis (affecting spectrum and SNR).  
 purple            All genes were included in the analysis (affecting spectrum and SNR).  
 \* : data in HG\_U133plus2 platform; all others in HG-U133A

**Cell values: p-values of K-M survival analyses**

( ) : poorer prognosis quartiles  
 [ ] : better prognosis quartiles

**Topological weights (affecting wt.epx, mag, spec and SNR):**

upper row - degree, i.e. numbers of connected genes  
 lower row (foc) - for intermodular hubs only, estimated perturbed effect

**A. Overall Survival – Consensus TSLC Networks**

Merged Data	intra - 20 genes used					inter - 12					both intra + inter = 32					
N = 828	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	
Ed = 387 (47%)	x	x	x		0.02	0.04	x	0.049 (foc)	x	x	x	x	x		0.02	0.049 (foc)

**B. Overall Survival – Lung TSLC Networks**

Merged Data	intra = 44 genes (43 in HG-U133A)					inter - 25					both intra + inter =69 (68)				
N = 828	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR
Ed = 387 (47%)	x	x	x	x	x		0.01	x	x	x	x	x	x	x	x

**C. Metastasis-Free Survival – Consensus TSLC Networks**

Merged Data	intra - 20 genes used					inter - 12					both intra + inter = 32				
N = 374	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR
Em = 134 (36%)	x	x	x	x	0.01	x	x	0.03 (foc)	x	x	0.008	x	x	x	x

**D. Metastasis-Free Survival – Lung TSLC Networks**

Merged Data	intra = 44 genes (43 in HG-U133A)					inter - 25					both intra + inter =69 (68)					
N = 374	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	
Em = 134 (36%)	x	x	x	x	x		0.005	x	x	x		0.02	0.02	x	0.003	0.03

**E. Overall Survival – Lung TSLC Networks**

Data set	intra = 44 genes (43 in HG-U133A)					inter - 25					both intra + inter =69 (68)				
	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR
GSE3141*	N=111 (3); 0.007	x	x	x	x	x	x	x	x	(23,14];	x	x	x	(3); 0.02	x
	58/111=52%					<b>foc</b>	x	[3]; 0.04	x	x	<b>foc</b>	x	[3]; 0.03	x	x
GSE4573	N=130 67/130=52%	x	x	x	x	x (4); 0.04	x	(4); 0.03	(23,14];	x	x	x	[4]; 0.01	(1,23,4];	(4); 0.04
DFCI	N=82 35/82=43%	x	(24,13]; 0.04	x	x (1); 0.04	x	x	(34,12]; 0.02	(24,13]; 0.03	x	x	(3); 0.02	(23,14];0.005	x	x
HLM	N=92 70/92=76%	(3,14,2]; 0.01	x	x	(2); 0.01	x	[1]; 0.01	x	x	(2); 0.02	x	x	x	x	x
UMMI	N=177 102/177=58%	x	x	x	x	x (2); 0.003	(4); 0.01	x	x	[1]; 0.046	x	x	x	[2]; 0.03	x (3); 0.002
MSK1	N=107 31/107=29%	(34,12]; 0.01	(4,3,2,1];	x	x	x (2); 0.03	(34,12];	x	x	x	(34,12];	(34,12]; 0.0004	x	x	x
MSK2	N=129 24/129=19%	x	x	(2); 0.01	(23); 0.007	(2); 0.02	(34); 0.008	(3); 0.03	x	(23); 0.03	x	(34); 0.007	x	x	x
						<b>foc</b>	x	x	x	x	<b>foc</b>	x	x	x	x

**F. Metastasis-Free Survival – Lung TSLC Networks**

Data set	intra = 44 genes (43 in HG-U133A)					inter - 25					both intra + inter =69 (68)				
	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR	epx	wt.epx	mag	spec	SNR
GSE8894*	N=138 69/138=50%	x	x	x	(1); 0.001	x	x	x	x	x	x	(4); 0.03	x	(3); 0.02	(3,24,1];
MSK1	N=107 44/107=41%	(34,12]; 0.02	(4,23,1];	x	x	x	x	(4); 0.02	(1); 0.03	(34,12]; 0.002	(34,12]; 0.005	x	x	x	x
MSK2	N=129 21/129=16%	x	x	[1]; 0.04	(3); 0.04	x	x	x	x	(1); 0.04	<b>foc</b>	[3]; 0.006	x	x	(1); 0.04
						<b>foc</b>	x	x	x	x	<b>foc</b>	(4); 0.03	x	x	x

**Table S7** Clinicopathological characteristics of 125 patients with Lung adenocarcinoma

Patient characteristics	Total of 125 patients	
	Surgery + adjuvant therapy	Definitive CCRT
Numbers of patients	45	80
Age		
Range	40-83	37-79
Median	61	60
Cancer stage		
I-II	10	25
III-IV	35	55
OCT4 staining		
Negative	18	31
Positive	27	49
CBX5 staining		
Negative	17	32
Positive	28	48