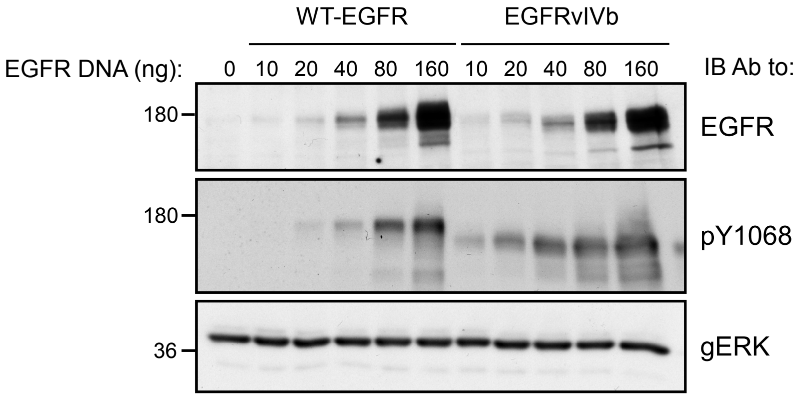
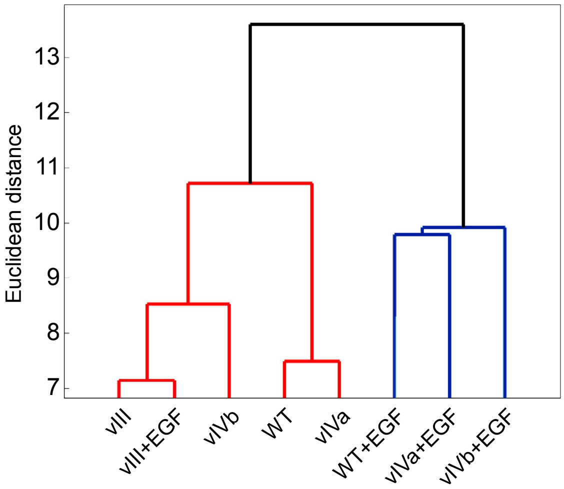
Supplementary Figure 1

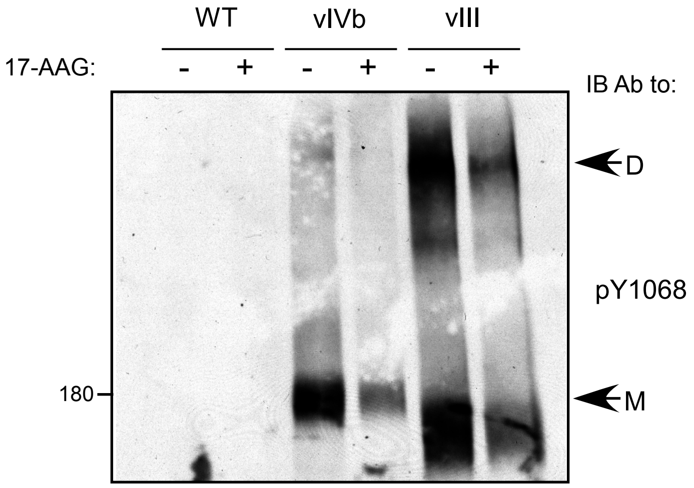


Supplementary Figure 2

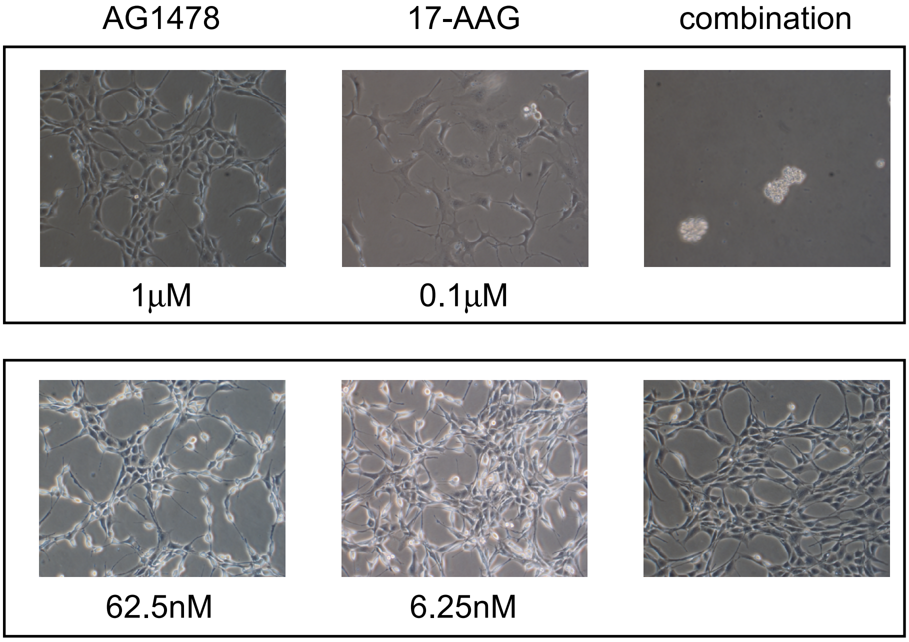


Supplementary Figure 3

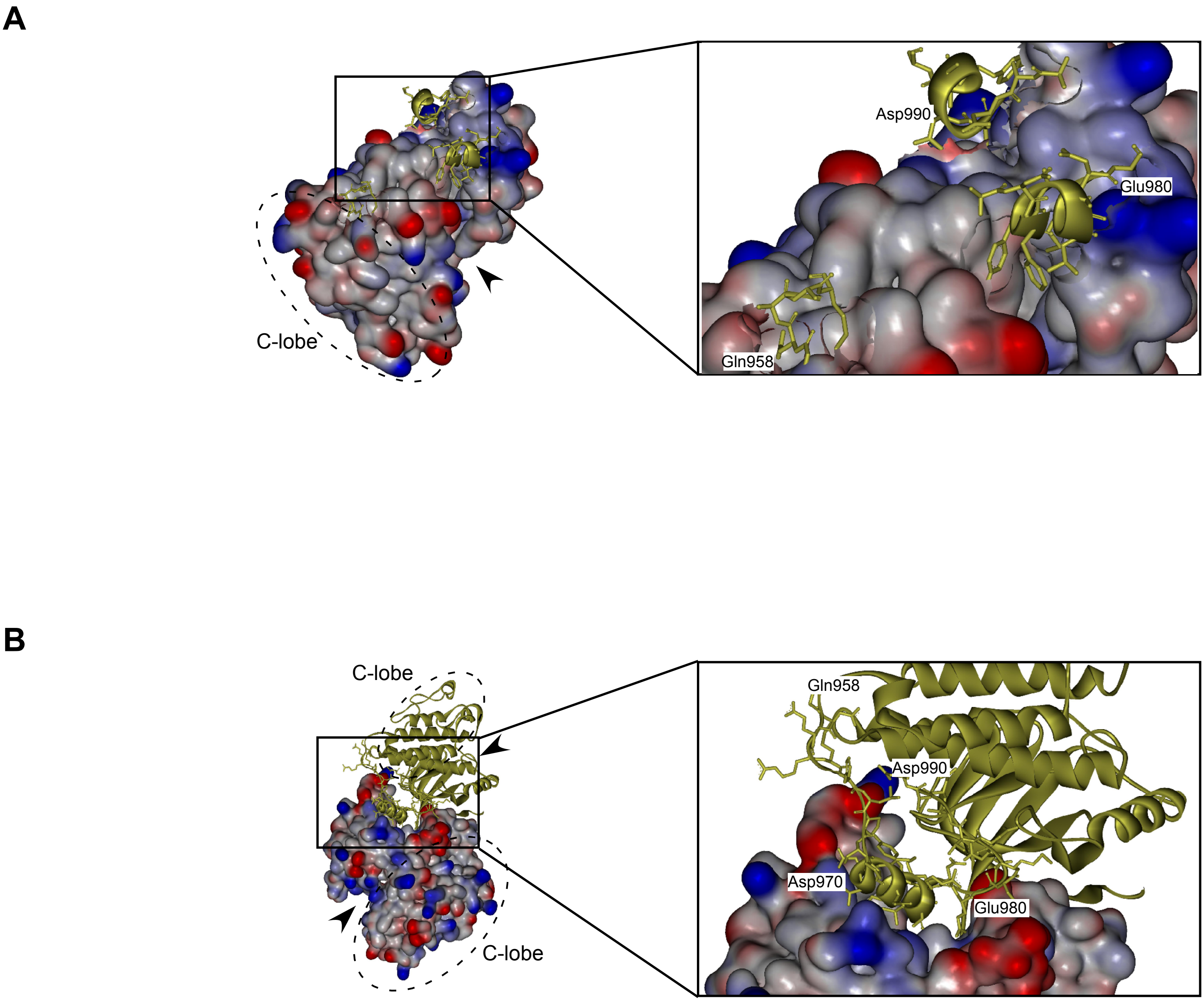
A



B



Supplementary figure 4



Legends to Supplementary figures

Figure S1 EGFRvIVb is constitutively phosphorylated when transiently expressed in kidney cells. HEK-293 cells were transiently transfected with increasing amounts of plasmids encoding either WT-EGFR or EGFRvIVb. Following serum starvation, cells were harvested and protein samples were separated by gel electorpohoresis. Both EGFR and phopho-EGFR levels, along with ERK, were analyzed by immunoblotting (IB), as indicated.

Figure S2 Clustering analysis of tyrosine-phosphorylated sites of EGF-treated mutants of EGFR. Murine fibroblasts ectopically expressing different forms of human EGFR were left untreated or stimulated for 10 min with EGF (10ng/ml). Whole extracts were processed and MS/MS spectra obtained as detailed under Methods. Tyrosine phosphorylation sites and peptide sequence assignments were used to obtain the dendrogram plot, which represents the hierarchy tree distances.

Figure S3 EGFR serves as a client of HSP90. (**A**) NIH-3T3 cells stably expressing either of the indicated EGFR forms were treated with the HSP90 inhibitor 17-AAG (0.1μM) or with DMSO, as solvent control. Following 6 hours of incubation, cells were lysed and proteins were cross-linked using BS^3. Monomers (M) and dimers (D) were detected in whole cell lysates by using antibodies to the phosphorylated form of EGFR's tyrosine 1068. (**B**) NIH-3T3 cells stably expressing EGFRvIVb were incubated for three days with the indicated inhibitors, either alone or in combination, at the indicated concentrations. Shown are typical microscopic fields of each treatment.

Figure S4 Models attributing the transforming activity of the EGFRvIV mutants to inactivation of an auto-inhibitory mechanism mediated by the deleted sequences of the carboxyl tail. (**A**) Partial kinase-tail interface inferred from Protein Data Bank (PDB) ID 1XKK, which contains the full kinase domain bound to a quinazoline inhibitor, and 40 distal amino acids of the C-tail (Wood *et al.*, 2004). The surface topology and charge (blue: positive; red: negative) of the kinase domain are presented. The C-lobe and activation loop (arrowhead) are marked for orientation. The yellow ribbons indicate the partially structured carboxyl-terminus of EGFR that folds *in cis* over the kinase domain of the inactive monomer. Due to poor electron density, amino acids corresponding to segments 964-970 and 980-930 are not included. For orientation, the first amino acid of the C-tail, along with other amino acids, are indicated in the enlarged structure. The structure shows packing of a short alpha helix comprising residues 971-980 against a hinge region connecting the two lobes of the kinase. This short helix partially blocks the front of the ATP-binding cleft. Another inhibitory helical segment (residues 983-990) extends along the N-lobe of the kinase. Note that the corresponding segments are deleted in the EGFRvIV mutants (residues 958 through 1030 or 1043). (**B**) The full kinase-tail interface inferred from PDB ID 3GT8, which depicts the structure of an inactive EGFR kinase domain variant (in complex with AMP-PNP) engaged in a symmetrical dimer (Jura *et al.*, 2009). The surface and charges of one kinase are shown, and the other kinase is modeled in yellow ribbons. The C-lobes and activation loops (arrowheads) are marked for orientation. Note that the proximal segment of the carboxyl terminus of the upper kinase (ribbon; residues 953-990) maintains inhibitory interactions with the lower kinase, possibly by displacing a stimulatory juxtamembrane latch, which forms asymmetrical dimers of active kinases. The inhibitory interfaces include an extended segment (983-990) that runs along the C-lobe of the other kinase, a charged turn (979-983) that binds to the alphaC-beta4 loop, and a helical region termed the AP-2 site (976-978) that binds *in trans* to the N-lobe.

References

Jura N, Endres NF, Engel K, Deindl S, Das R, Lamers MH *et al* (2009). Mechanism for activation of the EGF receptor catalytic domain by the juxtamembrane segment. *Cell* **137:** 1293-307.

Wood ER, Truesdale AT, McDonald OB, Yuan D, Hassell A, Dickerson SH *et al* (2004). A unique structure for epidermal growth factor receptor bound to GW572016 (Lapatinib): relationships among protein conformation, inhibitor off-rate, and receptor activity in tumor cells. *Cancer Res* **64:** 6652-9.

Accession	Names	Protein	Sequence
O54967	tyrosine kinase, non-receptor, 2 [Mus musculus	Ack1	ALPQNDDHpYVMQEHR
gi|1520315	afadin	afadin	EpYFTFPASK
gi|6174396	AHNAK nucleoprotein isoform 1 [Mus musculu	AHNAK	GEpYDVTVPR
gi|6996913	annexin A2 [Mus musculus]	ANXA2	SYSPpYDMLESIKK
Q00993	AXL receptor tyrosine kinase [Mus musculus]	Axl	KIYNGDpYYR
Q00993	AXL receptor tyrosine kinase [Mus musculus]	Axl	pYVLCPSTAPGPTLSADR
Q61140	breast cancer anti-estrogen resistance 1 [Mus	BCAR1	RPGPGTLpYDVPR
gi|1952715	hypothetical protein LOC101314 [Mus musculu	C3orf10	RIEpYIEAR
gi|2170415	caldesmon 1 [Mus musculus]	Cald1	SGRpYEVEETEVVIK
gi|2170415	caldesmon 1 [Mus musculus]	Cald1	LEQpYTNAIEGTK
gi|6680832	calmodulin 2 [Mus musculus]	Calm1	VFDKDGNGpYISAAELR
gi|6680854	caveolin, caveolae protein 1 [Mus musculus]	Cav1	pYVDSEGHLYTVPIR
Q5SNZ0	Girdin; coiled coil domain containing 88A [Mus	Ccdc88a	DSNPpYATLPR
gi|115925	cell division cycle 2 homolog	Cdc2	IGEGTpYGVVYK
gi|6680924	cofilin 1, non-muscle [Mus musculus]	Cfl1	HELQANCpYEEVKDR
GI|1185680	Cobl-like 1 [Mus musculus]	COBLL1	STEGQGPpYHPVVGHIGNED
gi|1662149	Catenin delta-1	CTNND1	FHPEPpYGLEDDQR
gi|1662149	Catenin delta-1	CTNND1	LNGPQDHNHLLpYSTIPR
Q60598	cortactin [Mus musculus]	Cttn	NASTFEEVVQVPSApYQK
P98078	disabled homolog 2 isoform a [Mus musculus]	DAB2	GPLNGDTDpYFGQQFDQLSN
gi|6681137	diazepam binding inhibitor isoform 2 [Mus musc	DBI	TQPTDEEMLFIpYSHFK
gi|1393736	discoidin domain receptor family, member 2 [M	DDR2	NLYSGDpYYR
gi|6753620	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptid	DDX3	GRGDpYDGIGGR
gi|6681159	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 [M	DDX6	SLYVAEpYHSEPAEDEKP
gi|5979785	discs large homolog 1	DLG1	DpYHFVTSR
gi|3198179	docking protein 1 [Mus musculus]	Dok1	GFSSDTALpYSQVQK
gi|3198179	docking protein 1 [Mus musculus]	Dok1	GLpYDLPQEPR
gi|3198179	docking protein 1 [Mus musculus]	Dok1	LTDSKEDPIpYDEPEGLAPAP
gi|3198179	docking protein 1 [Mus musculus]	Dok1	TVPPPVPQDPLGSPPALpYAE
gi|2441893	dual-specificity tyrosine-(Y)-phosphorylation reg	DYRK1A	IYQpYIQSR
gi|2972560	epidermal growth factor receptor isoform a; avi	EGFR	GSHQISLDNPDpYQQDFFPK
gi|2972560	epidermal growth factor receptor isoform a; avi	EGFR	GSTAENAEpYLR
gi|2972560	epidermal growth factor receptor isoform a; avi	EGFR	RPAGSVQNPVpYHNQPLNPA
gi|6264637	PREDICTED: similar to Engulfment and cell m	ELMO2	EVCDGWSLPNPEpYYTLR
gi|1296349	enolase 3, beta muscle [Mus musculus]	ENO1	AAVPSGASTGIpYEALELR
gi|7305031	erythrocyte protein band 4.1-like 3 [Mus muscul	EPB4113	DSVSAAEVGTGQpYATTK
O70318	erythrocyte protein band 4.1-like 2 [Mus muscul	EPB41L2	VDGDNIpYVR
Q03145	Eph receptor A2 [Mus musculus]	EphA2	IApYSLLGLK
Q08509	Epidermal growth factor receptor kinase substr	Eps8	ADPPpYTHTIQK
Q08509	Epidermal growth factor receptor kinase substr	Eps8	STPNHQVDRNpYDAVK
Q80TH2	Protein LAP2 (Erbb2-interacting protein) (Erbin	Erbin	ANTGpYHLQQR
Q80TH2	Protein LAP2 (Erbb2-interacting protein) (Erbin	Erbin	EQLIDpYLMLK
Q80TH2	Protein LAP2 (Erbb2-interacting protein) (Erbin	Erbin	RTEGDpYLSYR
GI|5200148	mitogen activated protein kinase 3 (extracellula	ERK1	IADPEHDHTGFLTEpYVATR
gi|6754632	mitogen activated protein kinase 1 [Mus muscu	ERK2	VADPDHDHTGFLTEpYVATR
P34152	PTK2 protein tyrosine kinase 2 [Mus musculus]	FAK	YMEDSTpYYK
gi|1244872	family with sequence similarity 171, member A1	FAM171A1	HSpYIDLQR
gi|1237912	FAM59a	Fam59a	TEVPpYEELWLEEGKPSR
gi|1185723	Proto-oncogene tyrosine-protein kinase FER (p	Fer	QEDGGVpYSSSGLK
gi|1185723	Proto-oncogene tyrosine-protein kinase FER (p	Fer	VQENDGKEPPPVVNpYEEDA
gi|2924434	fibroblast growth factor receptor substrate 2 [M	FRS2	RPALLNpYENLPSLPPVWEAR

gi|1438113	Proto-oncogene tyrosine-protein kinase Fyn	FYN	KLDNGGpYYITTR
gi|1438113	Proto-oncogene tyrosine-protein kinase Fyn	FYN	LIEDNEpYTAR
gi|6996917	glucose-6-phosphate dehydrogenase X-linked [	G6PDX	VQPNEAVpYTK
gi|3154287	growth factor receptor bound protein 2-associat	Gab1	SSGSGSSMADERVDpYVVVD
gi|9310241	glycyl-tRNA synthetase [Mus musculus]	GARS	TSpYGWIEIVGCADR
gi|8402926	G protein-coupled receptor 149	GPCR149	DGpYQEEIQLLNK
gi|8402926	G protein-coupled receptor 149	GPCR149	LHANpYQEISR
gi|1340341	glycogen synthase kinase 3 alpha	GSK3A	GEPNVSpYICSR
P01896	histocompatibility 2, D region locus 1 [Mus mus	H2-L	GGDpYALAPGSQSSEMSLR
gi|1588540	homeodomain interacting protein kinase 2 [Mus	HIPK1	AVCSTpYLQSR
Q62120	Janus kinase 2 [Mus musculus]	Jak2	REVGDpYGQLHK
gi|6856551	Keratinocyte-associated transmembrane protei	KCT2	ITNDpYIF
gi|1362831	SH2B adapter protein 3	LNK	AIDNQpYTPLSQLCR
gi|3198229	LIM domain containing preferred translocation	LPP	SEGDTApYGQQVQPNTWK
gi|3198229	LIM domain containing preferred translocation	LPP	YYEPpYYAAGPSYGGR
gi|1338531	mannose-6-phosphate receptor binding protein	M6PRBP1	ENpYPHVR
gi|3359896	myosin heavy chain 10, non-muscle [Mus musc	MYH10	TGLEDPERpYLFVDR
gi|3432818	Non-catalytic region of tyrosine kinase adaptor	Nck1	LpYDLNMPAFVK
gi|4101750	NSFL1 cofactor p47	NSFL1C	LGAAPEEESApYVAGER
Q91YD9	Wiskott-Aldrich syndrome-like [Mus musculus]	N-WASP	VIpYDFIEK
gi|1009259	mitogen activated protein kinase 14 [Mus musc	p38-alpha	HTDDEMTGpYVATR
Q99NH2	partitioning-defective protein 3 homolog isofor	PARD3	ERDpYAEIQDFHR
Q8CI51	PDZ and LIM domain 5 isoform ENH2 [Mus mu	Pdlim5	NTEFpYHIPTHSDASK
Q8K1N2	Pleckstrin homology-like domain family B mem	PHLDB2	ATNESSpYLSILPK
gi|8290525	Peptidyl-prolyl cis-trans isomerase NIMA-intera	PIN4	FGpYHIIMVEGR
Q62077	phospholipase C, gamma 1	PLCG1	IGTAEPDpYGALYEGR
Q62077	phospholipase C, gamma 1	PLCG1	NPGFpYVEANPMPTFK
Q62077	phospholipase C, gamma 1	PLCG1	pYQQPFEDFR
Q61136	PRP4 pre-mRNA processing factor 4 homolog	PRPF4b	LCDFGSASHVADNDITPpYLV
P18052	protein tyrosine phosphatase, receptor type, A [	PTPRA	VVQEYIDAFSDpYANFK
gi|8190212	paxillin isoform alpha [Mus musculus]	PXN	AGEEEHVpYSFPNK
gi|1350762	ankycorbin [Mus musculus]	RAI14	LGLLSQESADGpYSHLR
O89086	RNA binding motif protein 3 [Mus musculus]	RBM3	YDSRPGGYGpYGYGR
gi|2170397	Ras and Rab interactor 1 [Mus musculus]	Rin1	EKPSTDPLpYDTPDTR
Q5SWZ5	Rho interacting protein 3 isoform 2 [Mus muscu	RIP3	VESGpYFSLEK
gi|6671569	acidic ribosomal phosphoprotein P0 [Mus musc	RPP0	IIQLLDDpYPK
Q80U72	PDZ-domain protein scribble [Mus musculus]	Scribble	QKpYFELEVR
gi|1492540	SEC31-like 1 [Mus musculus]	SEC31L1	AQGKPVSGQESSQSPpYER
gi|1346679	septin 2	Sept2	QQPTQFINPETPGpYVGFANL
gi|1185727	hypothetical protein LOC244895 [Mus musculu	SgK269	TTSVISHTpYEEIETESK
gi|1185727	hypothetical protein LOC244895 [Mus musculu	SgK269	VPIVINPNApYDNLAIYK
gi|1185727	hypothetical protein LOC244895 [Mus musculu	SgK269	pYQEVWTSSTSPR
GI|212645	src homology 2 domain-containing transforming	Shc1	ELFDDPSpYVNIQNLDK
gi|6755228	protein tyrosine phosphatase, non-receptor typ	SHP-2	IQNTGDpYYDLYGGEK
gi|6755228	protein tyrosine phosphatase, non-receptor typ	SHP-2	VpYENVGLMQQQR
gi|3154373	solute carrier family 38, member 2 [Mus muscul	SLC38A2	SHpYADVDPENQNFLLESNL
gi|2956808	sorting nexin 9 [Mus musculus]	SNX9	SSSPpYFKDSEPAEAGGIQR
gi|1711553	signal transducer and activator of transcription	STAT3	LLGPGVNpYSGCQITWAK
gi|1711553	signal transducer and activator of transcription	STAT3	YCRPESQEHPEADPGSAAPp
gi|1174465	signal transducer and activator of transcription	STAT5B	AADGpYVKPQIK
gi|1438943	stress-induced phosphoprotein 1 [Mus musculu	STIP1	LApYINPDLALEEK
gi|6678177	syntaxin 4A (placental) [Mus musculus]	STX4	NILSSADpYVER

gi|6755690	syntaxin binding protein 3 [Mus musculus]	STXBP3	TNpYLELDR
P26039	talin 1 [Mus musculus]	talin 1	LLGEIAQGNENpYAGIAAR
gi|1193722	C1 domain-containing phosphatase and tensin-	Tenc1	GPLDGSPpYAQVQR
gi|2264375	Tensin 1 [Mus musculus]	tensin 1	AGSLPNpYATINGK
gi|2264375	Tensin 1 [Mus musculus]	tensin 1	HAApYGGYSTPEDR
gi|2014057	Transferrin receptor	TfR	SAFSNLFGGEPLSpYTR
gi|2162461	Transmembrane protein 106B [Mus musculus]	Tmem106b	NGDVSQFPpYVEFTGR
Q99KW3	TRIO and F-actin binding protein isoform 1 [Mu	TRIOFB1	KADGPRPSLDpYVELSPLAPS
Q99KW3	TRIO and F-actin binding protein isoform 1 [Mu	TRIOFB1	YQDVpYVELNHIK
gi|3474033	tubulin, alpha 1B [Mus musculus]	TUBA1B	ApYHEQLSVAEITNACFEPAN
gi|6678469	tubulin, alpha 1C [Mus musculus]	TUBA1C	ApYHEQLTVAEITNACFEPAN
gi|2775414	Vacuolar protein sorting-associated protein VT	VTA1	pYAGSALQYEDVGTAVQNLQ
P39447	tight junction protein 1 [Mus musculus]	ZO1	HEEQPAPApYEVHNR

	Mean						
Site	**WT**	**WT+EGF**	**vIII**	**vIII+EGF**	**vIVa**	**vIVa+EGF**	**vIVb**
Y284	0.85	1	1.16	0.57	0.64	0.89	0.66
Y1230	0.13	1	0.25	0.28	0.18	1.7	0.47
Y835	0.25	1	0.45	0.62	0.5	2.02	0.55
Y238	0.7	1	2.3	2.06	1.75	1.9	3.07
Y696	0.58	1	1.12	1.21	0.78	1.09	1.21
Y860	0.66	1	0.98	1.29	0.54	1.55	1.03
Y391	0.54	1	0.63	0.8	0.58	0.88	0.84
Y63	0.58	1	1.57	1.24	0.69	1.39	1.29
Y154	0.28	1	0.43	0.38	0.33	1.03	0.45
Y419	0.15	1	0.31	0.26	0.23	0.96	0.33
Y100	0.23	1	0.48	0.64	0.18	1.62	0.4
Y6	0.18	1	0.8	0.82	0.58	1.94	0.83
Y1801	0.24	1	0.55	0.56	0.38	1.78	0.6
Y15	1.04	1	1.74	2.07	1.31	1.45	2.68
Y140	0.35	1	1.07	1.09	0.45	0.93	1.11
Y570	0.3	1	0.68	1.1	0.56	1.92	1.6
Y280	0.26	1	0.51	0.46	0.37	1.56	0.77
Y96	0.33	1	0.74	0.81	0.35	1.62	0.68
Y334	0.51	1	0.65	0.59	0.52	1.26	0.77
Y342	0.22	1	0.72	0.61	0.3	0.9	0.65
Y29	0.87	1	1.44	1.46	0.93	1.18	1.57
Y739	0.57	1	0.94	1.24	0.5	1.51	0.75
Y104	0.12	1	0.57	0.32	0.17	0.79	0.22
Y473	0.09	1	0.34	1.26	0.16	0.72	0.23
Y761	0.46	1	2.08	2.54	0.72	1.82	2.68
Y450	0.44	1	0.44	0.7	0.44	1.56	0.58
Y376	0.48	1	1.2	1.09	0.39	1.81	0.88
Y361	0.28	1	0.46	0.64	0.25	1.05	0.69
Y295	0.42	1	1.7	1	0.34	2.25	0.62
Y321	1.09	1	0.93	1.21	0.93	1.08	1.04
Y1172	0.12	1	0.65	0.83	1.16	1.77	2.8
Y1197	0.15	1	0.74	0.72	0.98	1.59	2.26
Y1110	0.14	1	0.79	0.67	0.77	1.23	2.52
Y48	1	1	2.02	1.88	1.1	1	1.53
Y44	1.14	1	1.64	1.68	0.73	1.21	1.13
Y479	0.41	1	0.46	0.5	0.31	1.77	0.61
Y606	0.23	1	0.68	0.43	0.39	2.11	0.84
Y961	0.84	1	0.72	0.74	0.52	0.59	0.71
Y601	0.14	1	0.31	0.55	0.16	1.56	0.64
Y524	0.36	1	0.52	0.82	0.35	1.37	0.76
Y1040	0.3	1	0.36	0.44	0.09	2.09	0.3
Y1283	0.09	1	0.17	0.2	0.12	1.5	0.27
Y1097	0.45	1	0.79	0.81	0.31	1.08	0.72
Y205	0.11	1	0.19	0.18	0.13	0.72	0.24
Y185	0.12	1	0.28	0.16	0.18	0.67	0.26
Y614	0.71	1	0.48	0.56	0.45	0.48	0.59
Y724	0.31	1	0.77	0.43	0.47	1.42	0.8
Y453	0.12	1	0.25	0.33	0.22	0.77	0.29
Y715	0.54	1	0.55	0.53	0.51	0.78	0.58
Y402	0.53	1	0.48	0.7	0.44	0.79	0.57
Y349	0.53	1	0.62	0.83	0.36	1.11	0.45

Y213	0.9	1	1.2	1.52	0.83	0.99	1.05
Y420	0.62	1	1	1.25	0.6	1.03	0.98
Y401	0.66	1	0.93	0.99	0.64	1.07	0.93
Y660	0.18	1	0.28	0.34	0.18	0.84	0.36
Y443	1.15	1	1.34	1.01	0.74	1.5	1.04
Y711	0.37	1	0.81	0.72	0.46	2.42	1.39
Y230	0.67	1	1.06	1.13	0.55	1.38	1.27
Y279	1.02	1	0.88	0.96	0.82	0.94	1.03
Y344	0.47	1	0.61	0.48	0.48	0.81	0.62
Y352	0.82	1	1.11	1.01	1.21	0.88	1.04
Y570	0.66	1	0.78	0.92	0.71	0.97	0.71
Y255	0.51	1	1.11	1.01	0.81	0.99	0.86
Y536	0.25	1	0.53	0.52	0.36	0.91	0.49
Y318	0.38	1	0.48	0.39	0.32	1.37	0.47
Y301	0.25	1	0.53	0.44	0.2	1.31	0.48
Y53	0.13	1	0.38	0.35	0.24	1.72	0.36
Y13	0.23	1	0.34	0.54	0.15	1.47	0.3
Y105	0.67	1	0.81	0.72	0.6	0.99	1.03
Y167	0.4	1	0.52	0.57	0.23	0.93	0.49
Y253	1.47	1	0.74	0.78	1.18	0.96	1.45
Y182	0.63	1	0.51	0.45	0.46	0.74	0.65
Y1076	0.55	1	0.7	0.59	0.41	0.73	0.52
Y251	0.23	1	0.42	0.4	0.36	1.6	0.51
Y563	0.23	1	0.4	0.51	0.38	1.34	0.53
Y122	0.68	1	1.04	1.16	0.74	1.24	0.91
Y771	0.25	1	0.53	0.48	0.31	1.08	0.58
Y783	0.17	1	0.52	0.49	0.26	0.93	0.55
Y1253	0.16	1	0.39	0.35	0.14	0.92	0.37
Y849	0.78	1	1.04	1.3	0.82	1.07	0.93
Y825	0.91	1	0.53	0.83	1.03	0.85	0.8
Y118	1.13	1	0.54	0.67	0.49	0.55	0.76
Y520	0.38	1	0.63	0.71	0.44	1.51	0.84
Y124	0.18	1	0.46	0.45	0.2	1.4	0.35
Y35	0.39	1	0.58	0.63	0.46	0.98	0.85
Y268	0.37	1	0.57	0.71	0.54	1.69	0.8
Y24	0.84	1	0.97	1.15	0.92	1.17	1.19
Y1343	0.17	1	0.39	0.62	0.23	1.97	0.59
Y803	0.35	1	0.81	0.98	0.45	1.13	0.46
Y17	0.15	1	0.76	0.56	0.5	1.24	0.55
Y662	0.38	1	0.71	0.96	0.45	1.44	0.83
Y632	0.39	1	0.54	0.84	0.26	0.81	0.62
Y528	0.34	1	0.61	0.85	0.4	1.05	0.52
Y423	0.11	1	0.14	0.2	0.24	0.6	0.42
Y62	0.63	1	1.79	1.98	0.64	1.38	1.43
Y584	0.41	1	0.47	0.64	0.33	1.08	0.54
Y41	0.66	1	0.8	0.92	0.6	0.98	0.95
Y177	0.08	1	0.27	0.42	0.08	1.17	0.23
Y539	0.14	1	0.29	0.39	0.17	1.86	0.51
Y705	0.4	1	0.55	0.73	0.34	1.12	0.69
Y699	0.08	1	0.64	0.51	0.08	0.99	0.23
Y354	0.27	1	0.43	0.44	0.3	0.83	0.37
Y251	0.35	1	0.65	1.01	0.32	1.44	0.59

Y521	0.06	1	0.25	0.4	0.12	0.97	0.39
Y1116	0.77	1	0.94	1.04	0.72	1.01	0.91
Y483	0.78	1	0.67	0.7	0.68	0.78	0.85
Y1558	0.78	1	0.5	0.6	0.43	0.77	0.47
Y1477	0.72	1	0.91	0.92	0.52	0.91	0.51
Y20	0.53	1	0.74	0.91	0.46	0.89	0.71
Y51	0.69	1	0.85	0.83	0.76	0.91	0.73
Y1594	0.11	1	0.24	0.28	0.13	0.94	0.31
Y1974	0.24	1	0.34	0.49	0.17	1.08	0.43
Y282	0.08	1	0.32	0.31	0.19	1.85	0.25
Y282	0.16	1	0.36	0.44	0.27	1.61	0.42
Y280	0.86	1	1.78	1.55	1.03	1.45	1.88
Y1164	0.51	1	0.84	0.72	0.3	0.74	0.83

	Standard Deviation						
vIVb+EGF	**WT**	**WT+EGF**	**vIII**	**vIII+EGF**	**vIVa**	**vIVa+EGF**	**vIVb**
0.77							
2.87	0.04	0	0.02	0.06	0.01	0.01	0.06
2.53							
3.68							
1.65							
1.65							
0.99							
1.93	0.15	0	0.44	0.2	0.08	0.06	0.08
0.95	0.01	0	0.05	0.02	0.03	0.05	0.09
0.87	0.01	0	0.01	0	0.03	0.02	0.03
2.05	0.07	0	0.07	0.05	0.01	0.08	0.02
1.99							
2.47	0.01	0	0.12	0.04	0.01	0	0.01
2.88	0.13	0	0.18	0.29	0.01	0.09	0.16
1.44	0.01	0	0.11	0.25	0.05	0.12	0.06
3.03	0.01	0	0.03	0.05	0.03	0.21	0.18
1.77							
2.03							
1.36							
1.01	0.07	0	0.04	0.1	0.02	0.06	0.27
2.09							
1.46							
1.18							
1.16							
3.43	0.31	0	0	0.46	0.05	0.02	0.13
1.56							
1.67							
1.3	0	0	0.07	0.16	0.02	0.08	0.15
2.71	0.06	0	0.07	0.55	0.25	0.14	0.21
1.19	0.04	0	0.04	0.01	0.09	0.2	0.13
2.27	0.02	0	0.09	0.11	0.07	0.25	0.9
1.76	0.09	0	0.06	0.02	0.07	0.02	0.08
2.42	0.02	0	0.21	0.13	0.02	0.14	0.26
1.6	0.01	0	0	0.1	0.25	0	0.14
1.61	0.02	0	0.17	0.12	0.09	0.29	0.15
1.85	0.03	0	0.13	0.01	0.1	0.01	0.14
1.92							
0.83	0.1	0	0	0.08	0.03	0.03	0.06
3.12							
2.36							
2.78	0.09	0	0.19	0.26	0.06	0.49	0.06
1.49	0.04	0	0.05	0.01	0.06	0.29	0.01
1.27	0.07	0	0.02	0.11	0.06	0.08	0.06
0.75	0.01	0	0.07	0.06	0.05	0.02	0.01
0.76	0.04	0	0.02	0.08	0.04	0.01	0.01
0.53	0.12	0	0.03	0.07	0.11	0.01	0.04
1.64							
0.69							
0.72	0.06	0	0.08	0.15	0.02	0.15	0.05
0.75	0.02	0	0.03	0.24	0.03	0.21	0.07
1.2							

1.25	0.01	0	0.19	0.15	0.04	0.19	0.03
1.24	0.01	0	0.01	0.04	0	0.07	0.04
1.28							
0.87	0.01	0	0.04	0.03	0.04	0.11	0.01
1.61							
4.19							
1.68							
0.97	0.11	0	0	0.08	0.14	0.09	0.1
0.96							
1.28							
0.97	0.06	0	0.09	0.1	0.05	0.1	0.07
1.24	0.07	0	0.06	0.62	0.29	0.16	0.31
1.11							
1.28							
1.57							
2.54	0.01	0	0.18	0.02	0.05	0.75	0.17
1.64							
1.31	0.05	0	0.13	0.06	0.07	0.01	0.27
1.13							
0.96	0.2	0	0.08	0	0.01	0.13	0.37
0.93	0.01	0	0.04	0.21	0.14	0.02	0.07
0.98							
1.37							
1.68							
1.6	0.05	0	0.18	0.01	0.17	0.22	0.28
1.09	0.05	0	0.12	0.14	0.02	0.1	0.04
1.27	0.09	0	0.07	0.11	0.06	0.01	0.09
0.98	0	0	0.03	0.07	0.02	0.15	0.03
1.13	0.04	0	0.15	0.38	0.02	0.02	0.08
0.62	0.05	0	0.09	0.03	0.03	0.21	0.21
0.56	0.15	0	0.01	0.02	0.1	0.1	0.16
2.25	0.01	0	0.06	0.1	0.18	0.11	0.19
1.64	0.01	0	0.03	0.13	0.07	0.26	0.03
1.26							
1.86							
1.23	0	0	0.04	0.14	0.14	0.11	0.05
2.74	0.08	0	0.13	0.07	0.16	0.19	0.22
1.5							
1.54							
1.72							
1.27	0.04	0	0.01	0.07	0.02	0.02	0.04
1.1							
0.54	0.01	0	0.01	0.02	0.06	0.03	0.05
1.97	0	0	0.07	0.19	0.03	0.06	0.18
1.03	0.03	0	0.01	0.26	0.14	0.01	0.01
1.37							
1.35	0.02	0	0.02	0.08	0.05	0.07	0.03
2.13	0.04	0	0.03	0.09	0.1	0.03	0.01
2.13	0.01	0	0.08	0.07	0.09	0.24	0.03
0.96							
1.16							
1.36	0.09	0	0.08	0.1	0.06	0.03	0.04

1.4							
0.9	0.01	0	0.06	0.2	0.06	0.01	0.17
0.96	0.13	0	0.09	0.11	0.04	0.15	0.18
0.79							
0.88	0.14	0	0.15	0.14	0.11	0.17	0.05
1.05							
1.25							
1.03	0.03	0	0	0.04	0	0.04	0.04
1.39	0.08	0	0.04	0.1	0.03	0.13	0.06
2.28	0.05	0	0.03	0.02	0.04	0.18	0.06
2.27							
2.01							
1							

vIVb+EGF
1.2781746
0.0176718
0.0989092
0.0647323
0.1755176
0.0157576
0.000913
0.0753809
0.362315
0.1525322
0.1975143
0.0528626
0.431572
0.1356609
0.3946085
0.3457963
0.1447859
0.0794617
0.1377669
0.1785048
0.0283267
0.3545912
0.0920958
0.1518507
0.0114477
0.0221303
0.0788473
0.11653
0.1904551

0.3270981
0.0088489

0.1207321

0.1565207

0.0446999
0.2693682

0.7435865

0.0913108

0.0864165
0.0679376

0.2509973
0.0665019
0.1495681
0.1363776
0.1043006
0.0222293
0.1679416
0.1343376
0.1025747

0.2332391
0.0796654

0.0846986

0.0232854
0.3208427
0.2154398

0.0445035
0.1592827
0.050532

0.0512477

0.211221
0.3067116

0.1578751

0.0054804
0.179884
0.2175512