

Table S 1

Microarray study following SYK knockdown in MCF10A

TCGA study of CN/mut altered patient cases

FINAL 55gene ID	FINAL 55gene GENE SYMBOL	Probe set	Description	mean of	mean of	FoldDiff (mRNA) ¹	Num Cases Altered	% Cases Altered	GENE_ID	COMMON	Ave CN gain/loss
				log intensities for collagen control	log intensities for collagen SYK KD						
40	SPRR1A	213796_at	small proline-rich protein 1A	5.3513	1.23999	17.28	89	12.80%	6698	SPRR1A	0.82
40	SPRR1A	214549_x_at	small proline-rich protein 1A	6.63511	3.57669	8.33	89	12.80%	6698	SPRR1A	0.82
4	AMOTL2	203002_at	angiomin like 2	4.05109	2.55416	2.82	10	1.40%	51421	AMOTL2	0.17
29	NEBL	203961_at	nebullette	4.04029	2.61005	2.69	23	3.30%	10529	NEBL	0.18
29	NEBL	203962_s_at	nebullette	4.44726	3.03057	2.67	23	3.30%	10529	NEBL	0.18
35	RHOBTB3	202975_s_at	Rho-related BTB domain containing 3	3.29064	2.05175	2.36	8	1.10%	22836	RHOBTB3	-0.14
32	RAB11FIP1	219681_s_at	RAB11 family interacting protein 1 (class I)	3.33121	2.11184	2.33	104	14.90%	80223	RAB11FIP1	0.20
49	TPM1	206116_s_at	tropomyosin 1 (alpha)	4.9529	3.80533	2.22	7	1.00%	7168	TPM1	-0.22
35	RHOBTB3	202976_s_at	Rho-related BTB domain containing 3	2.96163	1.85266	2.16	8	1.10%	22836	RHOBTB3	-0.14
28	MYL9	201058_s_at	myosin, light chain 9, regulatory	2.44787	1.35916	2.13	19	2.70%	10398	MYL9	0.47
49	TPM1	210987_x_at	tropomyosin 1 (alpha)	5.3621	4.30889	2.08	7	1.00%	7168	TPM1	-0.22
49	TPM1	206117_at	tropomyosin 1 (alpha)	2.714	1.67104	2.06	7	1.00%	7168	TPM1	-0.22
34	RAB25	218186_at	RAB25, member RAS oncogene family	6.18144	5.18108	2.00	85	12.20%	57111	RAB25	0.81
49	TPM1	210986_s_at	tropomyosin 1 (alpha)	6.04476	5.07147	1.96	7	1.00%	7168	TPM1	-0.22

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37	RND3	212724_at	Rho family GTPase 3	3.9234	2.97365	1.93	3	0.40%	390	RND3	-0.17
26	MMP7	204259_at	matrix metalloproteinase 7 (matrilysin, uterine)	1.85931	0.92773	1.91	14	2.00%	4316	MMP7	-0.31
27	MUC1	207847_s_at	mucin 1, cell surface associated	4.6449	3.73202	1.88	94	13.50%	4582	MUC1	0.84
11	CORO1A	209083_at	coronin, actin binding protein, 1A	2.77829	1.86761	1.88	37	5.30%	11151	CORO1A	0.52
46	TIMP2	203167_at	TIMP metalloproteinase inhibitor 2	3.60008	2.69077	1.88	47	6.80%	7077	TIMP2	0.34
27	MUC1	213693_s_at	mucin 1, cell surface associated	5.90508	5.00689	1.86	94	13.50%	4582	MUC1	0.84
36	RHOD	209885_at	ras homolog gene family, member D	5.77086	4.89576	1.83	33	4.70%	29984	RHOD	0.18
52	VILL	209950_s_at	villin-like	1.85609	1.00962	1.80	9	1.30%	50853	VILL	-0.12
5	AP1M2	65517_at	adaptor-related protein complex 1, mu 2 subunit	3.91307	3.08498	1.78	17	2.40%	10053	AP1M2	-0.03
5	AP1M2	218261_at	adaptor-related protein complex 1, mu 2 subunit	4.74543	3.91829	1.77	17	2.40%	10053	AP1M2	-0.03
29	NEBL	207279_s_at	nebulette	2.16513	1.35608	1.75	23	3.30%	10529	NEBL	0.18
9	CHN1	212624_s_at	chimerin (chimaerin) 1	4.32125	3.58034	1.67	6	0.90%	1123	CHN1	-0.13
44	SYK	207540_s_at	spleen tyrosine kinase	2.09222	1.35864	1.66	11	1.60%	6850	SYK	-0.14
36	RHOD	31846_at	ras homolog gene family, member D	6.65006	5.92047	1.66	33	4.70%	29984	RHOD	0.18
50	TRAK2	202124_s_at	trafficking protein, kinesin binding 2	2.90888	2.20315	1.63	12	1.70%	66008	TRAK2	-0.12
42	SPTBN2	205155_s_at	spectrin, beta, non-erythrocytic 2	2.7319	2.06609	1.59	42	6.00%	6712	SPTBN2	0.20

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			Rho-related BTB									
35	RHOBTB3	216048_s_at	domain containing 3	1.73529	1.08295	1.57	8	1.10%	22836	RHOBTB3	-0.14	
30	PCDH9	219737_s_at	protocadherin 9	2.30688	1.67923	1.55	18	2.60%	5101	PCDH9	-0.36	
			RAB11A, member RAS									
31	RAB11A	200864_s_at	oncogene family	3.92712	3.3079	1.54	8	1.10%	8766	RAB11A	-0.21	
			actin binding LIM									
1	ABLIM1	200965_s_at	protein 1	4.80373	4.19058	1.53	8	1.10%	3983	ABLIM1	-0.20	
			CDC42 effector									
7	CDC42EP4	214721_x_at	protein (Rho GTPase	2.86751	2.26813	1.52	56	8.00%	23580	CDC42EP4	0.37	
			binding) 4									
50	TRAK2	202125_s_at	trafficking protein,	2.74738	2.15236	1.51	12	1.70%	66008	TRAK2	-0.12	
			kinesin binding 2									
			vesicle-associated									
51	VAMP8	202546_at	membrane protein 8	6.43236	5.84249	1.51	7	1.00%	8673	VAMP8	0.03	
			(endobrevin)									
19	GPER	210640_s_at	G protein-coupled	1.66389	2.24987	0.67	11	1.60%	2852	GPER	0.15	
			estrogen receptor 1									
			ADAM									
			metallopeptidase									
2	ADAM12	213790_at	domain 12 (meltrin	1.01558	1.61077	0.66	17	2.40%	8038	ADAM12	-0.16	
			alpha)									
			kinesin family									
20	KIF20A	218755_at	member 20A	3.93348	4.52913	0.66	4	0.60%	10112	KIF20A	-0.07	
	MARCKSL											
24	1	200644_at	MARCKS-like 1	2.2633	2.87432	0.65	7	1.00%	65108	MARCKSL1	-0.24	
			WAS protein family,									
54	WASF1	204165_at	member 1	2.45494	3.06884	0.65	20	2.90%	8936	WASF1	-0.14	
			epidermal growth									
			factor receptor									
			(erythroblastic									
			leukemia viral (v-erb-									
			b) oncogene homolog,									
17	EGFR	211607_x_at	avian)	2.16901	2.80621	0.64	21	3.00%	1956	EGFR	0.27	

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16	ECT2	219787_s_at	epithelial cell transforming sequence 2 oncogene	3.15335	3.79151	0.64	37	5.30%	1894	ECT2	0.35
21	KIF2C	211519_s_at	kinesin family member 2C	3.04305	3.68307	0.64	10	1.40%	11004	KIF2C	-0.11
17	EGFR	210984_x_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	2.33473	2.9983	0.63	21	3.00%	1956	EGFR	0.27
17	EGFR	201984_s_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog, avian)	2.98141	3.65271	0.63	21	3.00%	1956	EGFR	0.27
21	KIF2C	209408_at	kinesin family member 2C	3.98417	4.68218	0.62	10	1.40%	11004	KIF2C	-0.11
10	CKAP4	200999_s_at	cytoskeleton-associated protein 4	3.94643	4.67124	0.61	4	0.60%	10970	CKAP4	0.01
25	MET	203510_at	met proto-oncogene (hepatocyte growth factor receptor)	4.11472	4.84654	0.60	9	1.30%	4233	MET	0.10
12	CTNNAL1	202468_s_at	catenin (cadherin-associated protein), alpha-like 1	4.07129	4.81079	0.60	8	1.10%	8727	CTNNAL1	-0.16
22	LAMP1	201551_s_at	lysosomal-associated membrane protein 1	3.33078	4.0833	0.59	29	4.20%	3916	LAMP1	-0.19
39	SMTN	209427_at	smoothelin	3.55693	4.31091	0.59	9	1.30%	6525	SMTN	-0.31

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33	RAB20	219622_at	RAB20, member RAS oncogene family related RAS viral (r- ras) oncogene	2.85501	3.63536	0.58	28	4.00%	55647	RAB20	-0.19
38	RRAS	212647_at	homolog chemokine (C-X-C motif) ligand 2	3.32575	4.13953	0.57	18	2.60%	6237	RRAS	0.09
15	CXCL2	209774_x_at	ADAM metallopeptidase domain 15	1.38434	2.20515	0.57	24	3.40%	2920	CXCL2	-0.02
3	ADAM15	217007_s_at	smoothelin	3.50458	4.32974	0.56	94	13.50%	8751	ADAM15	0.84
39	SMTN	207390_s_at		3.02705	3.86486	0.56	9	1.30%	6525	SMTN	-0.31
23	LAMP2	200821_at	lysosomal-associated membrane protein 2 ADAM metallopeptidase domain 12 (meltrin alpha)	2.99777	3.83674	0.56	9	1.30%	3920	LAMP2	-0.03
2	ADAM12	202952_s_at	WAS protein family, member 2	1.31031	2.18956	0.54	17	2.40%	8038	ADAM12	-0.16
55	WASF2	221725_at	epidermal growth factor receptor (erythroblastic leukemia viral (v-erb- b) oncogene homolog, avian)	3.80122	4.70557	0.53	5	0.70%	10163	WASF2	-0.36
17	EGFR	201983_s_at	TIMP metallopeptidase inhibitor 1	4.65262	5.56341	0.53	21	3.00%	1956	EGFR	0.27
45	TIMP1	201666_at	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	6.4029	7.3157	0.53	12	1.70%	7076	TIMP1	0.02
14	CXCL1	204470_at		1.24742	2.16559	0.53	23	3.30%	2919	CXCL1	-0.02

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6	AXL	202686_s_at	AXL receptor tyrosine kinase	3.52507	4.47528	0.52	19	2.70%	558	AXL	0.04
18	FSCN1	201564_s_at	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	4.15038	5.26761	0.46	9	1.30%	6624	FSCN1	0.18
47	TNNT1	213201_s_at	troponin T type 1 (skeletal, slow)	2.15726	3.39845	0.42	23	3.30%	7138	TNNT1	0.14
18	FSCN1	210933_s_at	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	3.91259	5.16952	0.42	9	1.30%	6624	FSCN1	0.18
53	VIM	201426_s_at	vimentin	3.68115	5.4293	0.30	22	3.20%	7431	VIM	0.21

¹ **>=1.5 down-regulated genes; <= 0.67 up-regulated genes**