SUPPLEMENTAL DATA

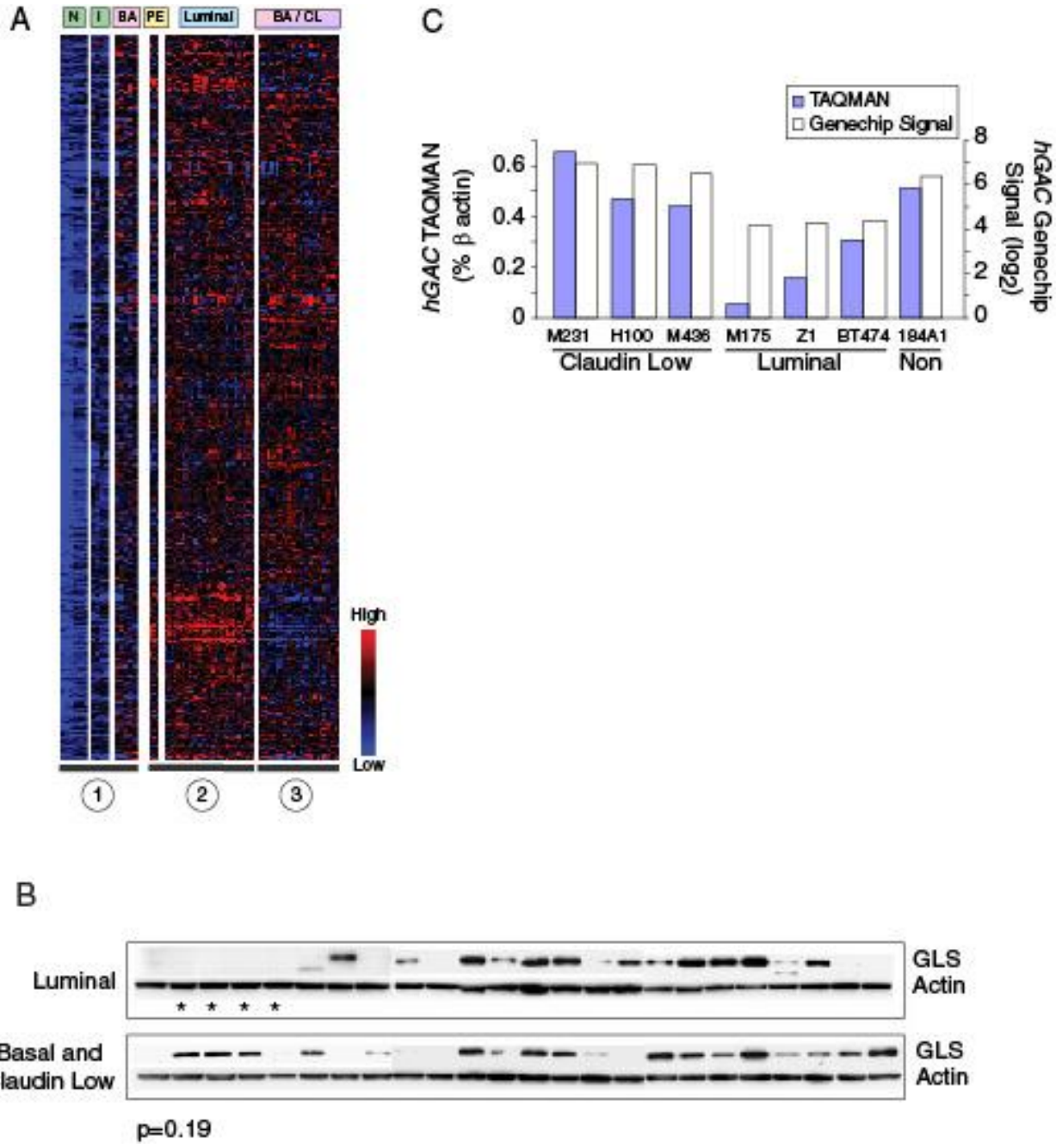

Figure S1, related to Figure 1. Molecular and Phenotypic Characteristics of Our Breast Cell Line Collection

Icon codes in figure keys. (A) Cluster and heatmap of metabolic probeset IDs identified in significance analysis comparing normal samples (1) versus Luminal (2) and Basal/Claudin low cell lines (3). Normal samples: N, purified normal $CD10^+$ and $BerEp4^+$ breast subsets; I, non-

tumorigenic culture-adapted proliferating breast cell lines derived from human mammary epithelial cells (HMECd). Tumorigenic samples: BA, Basal TNBC lines; PE, uncultured purified tumor samples from patient pleural effusions; Luminal, luminal cell lines; BA/CL, Basal and Claudin low TNBC lines. Black underbars denote major clades formed in cluster analysis. (B) Western blot assessing glutaminase expression levels in tumor-derived cell lines; pairs of sibling cell lines (asterisks) are counted as one independent isolate (AU565 and SKBR3, MCF7 and LY2); Luminal and Basal/Claudin Low cell lines do not differentially express total glutaminase protein, p= 0.19 student's t-test. (C) TAQMAN validation of relative *hGAC* Affymetrix genechip signals for representative cells in our panel.

Table S1, Related to Figure 1. Tumorigenic Cell Lines Used in This Study[1]				
Cell Line	**Abbreviated Name**	**Culture Media**	**Molecular Phenotype**	**Glutamine Restriction Group**
BT20	BT20	RPMI / 5% FBS	Basal	C
Du4475	Du4475	RPMI / 5% FBS	Basal	X
HCC1008	H1008	RPMI / 5% FBS	Basal	X
HCC1143	H1143	RPMI / 5% FBS	Basal	X
HCC1187	H1187	RPMI / 5% FBS	Basal	X
HCC1500	H1500	RPMI / 5% FBS	Basal	C
HCC1569	H1569	RPMI / 5% FBS	Basal	B
HCC1599	H1599	RPMI / 5% FBS	Basal	X
HCC1937	H1937	RPMI / 5% FBS	Basal	X
HCC1954	H1954	RPMI / 5% FBS	Basal	A
HCC2157	H2157	RPMI / 5% FBS	Basal	X
HCC3153	H3153	RPMI / 5% FBS	Basal	A
HCC70	H70	RPMI / 5% FBS	Basal	X
MDA-MB-468	M468	DMEM / 5% FBS	Basal	X
600MPE	600MPE	DMEM / 5% FBS	Luminal	X
AU565	AU565	DMEM / 5% FBS	Luminal	X
BT474	B474	RPMI / 5% FBS	Luminal	X
BT483	B483	RPMI / 5% FBS	Luminal	X
CAMA-1	CAMA1	DMEM / 5% FBS	Luminal	X
HCC1007	H1007	RPMI / 5% FBS	Luminal	X
HCC1428	H1428	RPMI / 5% FBS	Luminal	X
HCC202	H202	RPMI / 5% FBS	Luminal	X
HCC2185	H2185	RPMI / 5% FBS	Luminal	X
LY2	LY2	RPMI / 5% FBS	Luminal	A
MCF7	MCF7	RPMI / 5% FBS	Luminal	X
MCF-10A	M10A	RPMI / 5% FBS	Basal	X
MCF12A	M12A	RPMI / 5% FBS	Basal	X
MDA-MB-134VI	M134	DMEM / 5% FBS	Luminal	B
MDA-MB-175-VII	M175	DMEM / 5% FBS	Luminal	A
MDA-MB-361	M361	DMEM / 5% FBS	Luminal	B
MDA-MB-415	M415	DMEM / 5% FBS	Luminal	A
MDA-MB-453	M453	DMEM / 5% FBS	Luminal	X
SKBR3	SKBR3	DMEM / 5% FBS	Luminal	X
T47D	T47D	RPMI / 5% FBS	Luminal	X
UACC812	U812	DMEM / 5% FBS	Luminal	X
ZR-75-1	Z1	RPMI / 5% FBS	Luminal	X
ZR-75-30	Z30	RPMI / 5% FBS	Luminal	X
ZR-75-B	ZB	RPMI / 5% FBS	Luminal	X
BT549	BT549	RPMI / 5% FBS	Claudin Low	B
HBL100	H100	DMEM / 5% FBS	Claudin Low	C
HCC38	H38	RPMI / 5% FBS	Claudin Low	C
HS578t	Hs578t	RPMI / 5% FBS	Claudin Low	B
MDA-MB-157	M157	DMEM / 5% FBS	Claudin Low	B
MDA-MB-231	M231	DMEM / 5% FBS	Claudin Low	C
MDA-MB-435	M435	DMEM / 5% FBS	Claudin Low	C
MDA-MB-436	M436	DMEM / 5% FBS	Claudin Low	C

[1] Cell line name abbreviations used in this study, the normal culture media for each line, the molecular phenotype, and glutamine restriction group membership; X denotes cell lines with smaller proliferative defects in glutamine-free media than the non-tumorigenic cell lines.

Table S2, related to Figure 1. Significant Metabolic Probeset IDs.[2]			
Significant Class Association	**Probeset ID**	**Gene Symbol**	**Score**
Basal CDL	201272_at	AKR1B1	5.98627
Basal CDL	221510_s_at	GLS	5.87002
Basal CDL	202613_at	CTPS	5.75562
Basal CDL	205260_s_at	ACYP1	5.61946
Basal CDL	203909_at	SLC9A6	5.57077
Basal CDL	205996_s_at	AK2	5.44375
Basal CDL	200762_at	DPYSL2	5.26941
Basal CDL	220892_s_at	PSAT1	5.26622
Basal CDL	202026_at	SDHD	5.19516
Basal CDL	205401_at	AGPS	5.15867
Basal CDL	212174_at	AK2	5.11785
Basal CDL	205565_s_at	FXN	5.003
Basal CDL	212604_at	MRPS31	4.92187
Basal CDL	209213_at	CBR1	4.89146
Basal CDL	202589_at	TYMS	4.81951
Basal CDL	201300_s_at	PRNP	4.67459
Basal CDL	219079_at	NCB5OR	4.6724
Basal CDL	217294_s_at	ENO1	4.67206
Basal CDL	211150_s_at	DLAT	4.60905
Basal CDL	219204_s_at	SRR	4.57848
Basal CDL	219698_s_at	METTL4	4.52715
Basal CDL	218558_s_at	MRPL39	4.49672
Basal CDL	215535_s_at	AGPAT1	4.49345
Basal CDL	215707_s_at	PRNP	4.39831
Basal CDL	201012_at	ANXA1	4.37549
Basal CDL	203340_s_at	SLC25A12	4.34122
Basal CDL	221020_s_at	MFTC	4.33304
Basal CDL	205379_at	CBR3	4.33221
Basal CDL	201968_s_at	PGM1	4.30168
Basal CDL	200978_at	MDH1	4.25182
Basal CDL	221437_s_at	MRPS15	4.19826
Basal CDL	201634_s_at	CYB5-M	4.11264
Basal CDL	213133_s_at	GCSH	4.10644
Basal CDL	202502_at	ACADM	4.09831
Basal CDL	219220_x_at	MRPS22	4.0809
Basal CDL	208746_x_at	ATP5L	4.03913
Basal CDL	218982_s_at	MRPS17	3.98973
Basal CDL	202345_s_at	FABP5	3.97897
Basal CDL	214431_at	GMPS	3.96944
Basal CDL	212568_s_at	DLAT	3.95771
Basal CDL	216705_s_at	ADA	3.95428
Basal CDL	200818_at	ATP5O	3.94961
…	…	…	…

[2] Scores for metabolism-associated transcripts positively associated with the sample classes indicated in column 1, for each of three significance analyses. Analyses were: 1. Purified normal samples plus non-tumorigenic, culture adapted cells (N/I) versus carcinoma derived cell lines and uncultured pleural effusions (CDL/PE); 2. Basal carcinomas versus all other samples (Basal CDL); 3. Luminal carcinomas versus all other samples (Luminal CDL). See EXCEL file 'Timmerman Table S2 for full list.

Table S3, related to Figure 1. Class Association Statistics of *hGAC* and *GLS* Probeset IDs in Expression Datasets Derived from Primary Clinical Tumor Samples[3]

Gene Set ID	Total samp no.	Association tested	*p*-values *hGAC* 221510_s_at	*p*-values *GLS* 203157_s_at	*p*-values *GLS* 203158_s_at	*p*-values *GLS* 203159_at	*p*-values *GLS* 211414_at
GSE1561	49	- Apocrine/luminal (32) vs. basal (16) - ER status (22 ER-; 27 ER+)	3.3e-9 (basal) 0.001 (ER-)	0.514 (basal) 0.442 (ER-)	0.011 (basal) 0.015 (ER-)	0.655 (basal) 0.964 (ER-)	0.016 (basal) 0.011 (ER-)
GSE2034	286	- ER status (77 ER-; 209 ER+)	4.2e-11 (ER-)	0.060 (ER-)	3.4e-8 (ER-)	0.002 (ER-)	0.170 (ER-)
GSE20271	177	- ER status (78 ER-; 98 ER+)	1.7e-4 (ER-)	4.4e-5 (ER-)	1.6e-4 (ER-)	0.031 (ER-)	4.6e-4 (ER-)
GSE23988	61	- ER status (29 ER-; 32 ER+)	2.4e-7 (ER-)	0.089 (ER-)	0.010 (ER-)	0.278 (ER-)	0.364 (ER-)
GSE4922	289	- ER status (34 ER-; 211 ER+)	5.3e-10 (ER-)	0.969 (ER-)	0.026 (ER-)	0.527 (ER-)	0.087 (ER-)
GSE1456	159	- Luminal A/B (62) vs basal (25)	1.2e-8 (basal)	0.173 (basal)	0.002 (basal)	0.003 (basal)	0.080 (basal)
GSE7390	198	- ER status (64 ER-; 134 ER+)	1.2e-7 (ER-)	0.060 (ER-)	1.4e-6 (ER-)	0.041 (ER-)	0.003 (ER-)
Chin 2006	118	- ER status (43 ER-; 75 ER+) - Subtype Euclidean-based (66 lumA/B; 28 basal) - Subtype correlation-based (61 lumA/B; 30 basal)	4.5e-8 (ER-) 2.2e-13 (basal) 4.7e-13 (basal)	ND	ND	ND	ND

[3] Datasets were downloaded from NCBI GEO or obtained from Chin et al. (Chin, et al. 2006) and analyzed for gene expression differences between classes based on ER status and molecular subtype (Student's t-test)

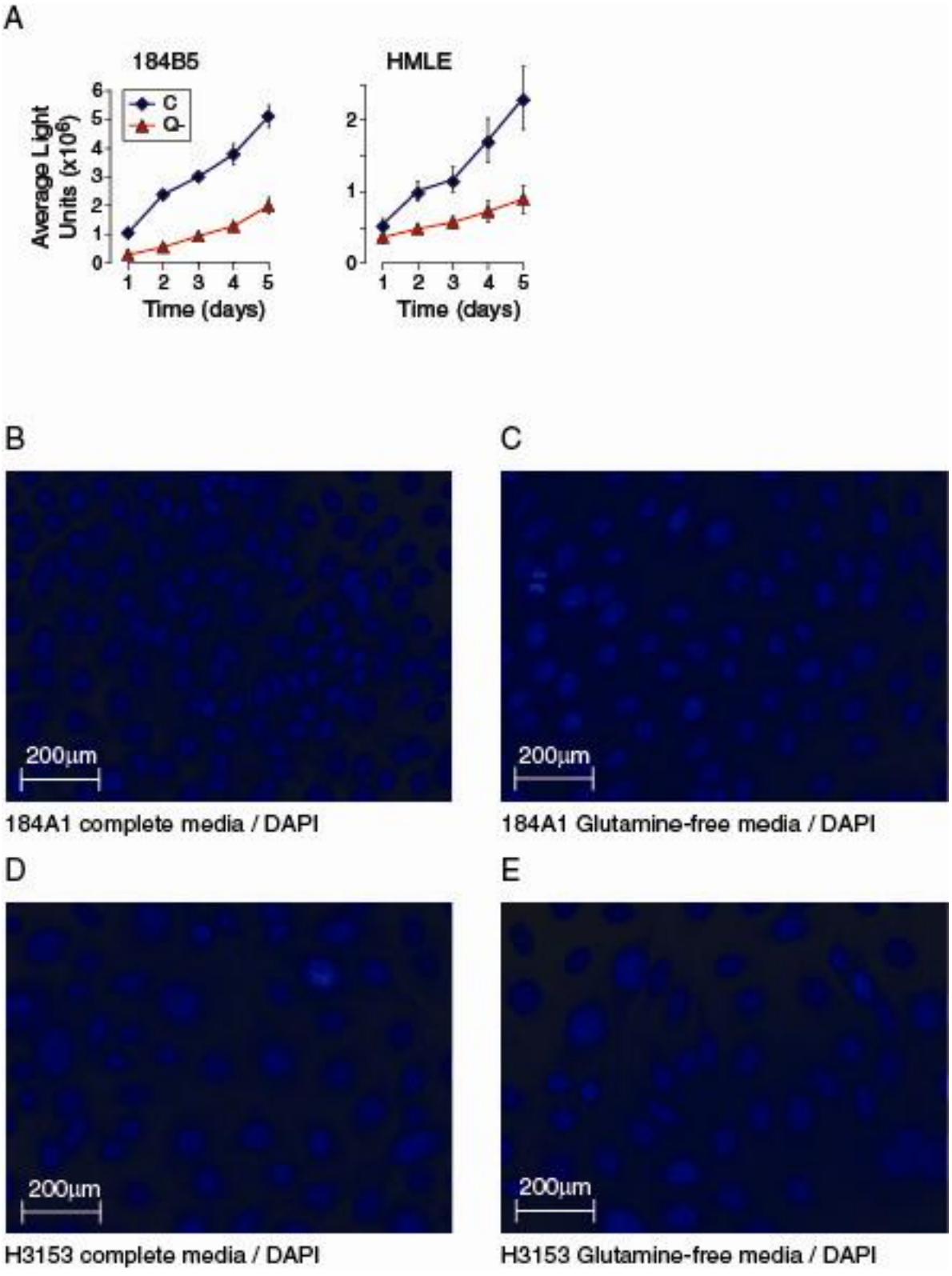

Figure S2, related to Figure 2. Non-Tumorigenic Cells Adapt to Glutamine Restriction by Slowing Culture Expansion

(A) Growth curves of two additional non-tumorigenic cell lines (184B5, HMLE); C, complete media; Q-, glutamine-free media. Icons represent mean values; error bars, standard deviations. (B-E) Regular nuclear morphology of glutamine free and complete media cultures (DAPI stain). (B and C) 184A1 non-tumorigenic cells; (D and E) H3153, a similarly-sensitive TNBC line.

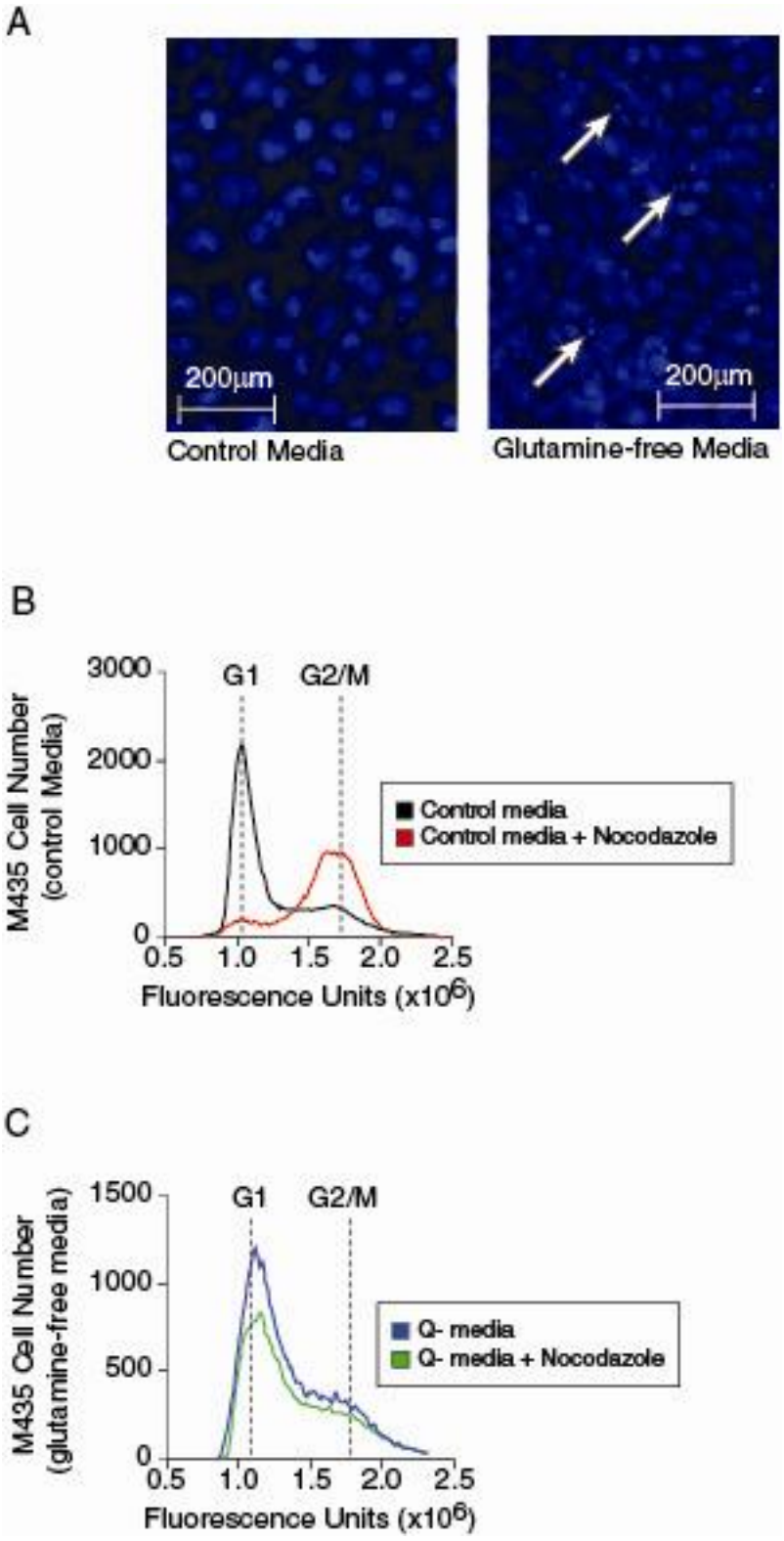

Figure S3, related to Figure 3. Glutamine Restriction Induces S-Phase Stalling and Apoptosis in Group C Carcinomas

Icon codes in figure keys. (A) Nuclear morphology (DAPI stain) of a representative group C TNBC line grown in (left) control media vs. (right) glutamine free media, arrows at apoptotic figures. (B) Example cell cycle profiles of a Group C TNBC line cultured 5 days in complete media with and without 18 hours nocodazole treatment (red vs. black curves); (C) Example cell cycle profiles of a Group C TNBC line cultured 5 days in glutamine-free media without and with 18 hours nocodazole treatment (blue vs green curves)

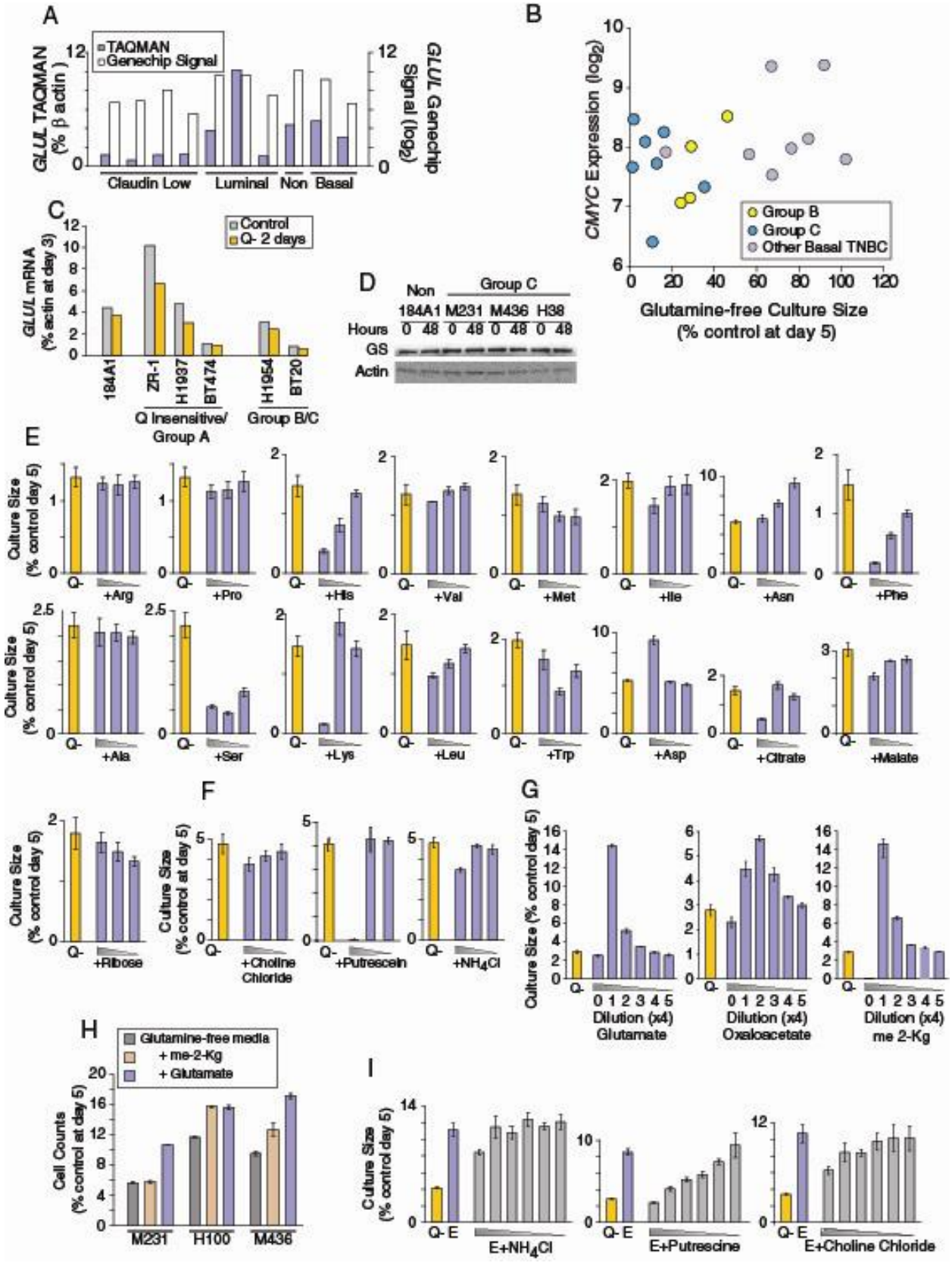

Figure S4, related to Figure 4. Glutamine is an irreplaceable nutrient for some TNBC

Icon codes in figure keys. Icons represent mean values +/-SD. (A) TAQMAN validation of relative *GLUL* Genechip signals for representative cells in our panel. (B) *cMYC* genechip hybridization signal (y-axis) versus glutamine-free culture sizes, derived from Figure 2A. (C) *GLUL* mRNA is not induced upon glutamine restriction; Q insensitive, basal TNBC with smaller glutamine-restricted proliferative defects than the non-tumorigenic cell lines; paired bars represent mRNA measurements (TAQMAN) in individual cell lines; Control, control media; Q-, glutamine-free media (see also Figure 4E). (D) Glutamine synthetase protein levels are not substantially altered in response to 48 hours of glutamine restriction; non, non tumorigenic exemplar 184A1. (E-H) Proliferative analysis of alternate nutrient additions; values normalized to control media population sizes; Icons represent mean values; error bars, standard deviations. (E) Yellow bar, Q-, glutamine free media alone; blue bars, glutamine free media plus 20mM alternate nutrient and 2 serial 4X dilutions shown; standard three letter abbreviations used for amino acids. (F) Titrations of amino group sources does not restore culture expansion, icon codes and conditions per part E. (G, H) Nutrients that marginally increase glutamine-free culture sizes; me 2-KG, dimethyl 2-ketoglutarate. (G) ATP-based cell titer assay using M436; icon codes and conditions per part E. (H) Direct cell counts (Accuri) in 3 Group C cell lines. (I) Glutamate plus titrations of amino group sources do not improve culture expansion over glutamate alone in glutamine-free media; yellow bar, Q-, glutamine free media alone; E, glutamate in glutamine-free media; gray bars, various amino group sources with glutamate in glutamine-free media; dilutions are 4X from 20mM.

Table S4, related to Figure 4. Class Associations of *GLUL* in Expression Datasets Derived from Primary Clinical Tumor Samples[4]				
Gene Set ID	**Association tested**	***GLUL* 200648_s_at**	***GLUL* 217202_s_at**	***GLUL* 215001_s_at**
GSE 1561	ER (ER+) Subtype (Luminal)	0.171 / -1.36 0.828 / -1.10	0.149 / -1.30 0.830 / -1.09	0.741 / 1.04 0.196 / 1.15
GSE 2034	ER (ER+)	0.024 / 1.30	0.024 / 1.16	1.3e-15 / 1.81
GSE 20271	ER (ER+)	2.3e-6 / 2.13	9.4e-5 / 1.65	4.0e-8 / 1.93
GSE 23988	ER (ER+)	2.1e-4 / 2.66	0.004 / 1.92	4.7e-6 / 2.20
GSE 4922	ER (ER+)	9.2e-4 / 1.87	5.7e-4 / 1.92	1.0e-6 / 1.61
GSE 1456	Subtype (Luminal)	1.0e-8 / 4.52	3.9e-7 / 3.64	4.9e-10 / 2.63
GSE 7390	ER (ER+)	5.4e-6 / 1.95	1.8e-6 / 1.99	1.7e-9 / 1.75
Chin 2006	ER (ER+)	0.005 / 2.09	0.004 / 2.44	8.6e-7 / 1.73
Chin 2006	Subtype (eucl) (Luminal)	2.1e-4 / 2.82	8.3e-5 / 3.49	2.7e-10 / 2.36
Chin 2006	Subtype (corr) (Luminal)	2.7e-4 / 2.79	1.3e-4 / 3.47	5.6e-10 / 2.31

[4] Datasets were downloaded from NCBI GEO or obtained from Chin et al. (Chin, et al. 2006) and analyzed for gene expression differences between classes based on ER status or molecular subtype: p value (t-test) / fold change, where ratio of average marker expression in ER+/luminal vs. ER-/basal samples in raw expression data (>1 means up-regulation in ER+/luminal, and <-1 means up-regulation in ER-/basal).

Table S5, related to Figure 4. Myc Association Statistics			
Probeset ID	**Myc Family Member / Transcriptional Target Gene**	**t-test Group C vs all Basal + Claudin low, p =**	**t-test Group B+C vs all Basal + Claudin Low, p =**
202922_at	GCLC, glutamate-cysteine ligase, catalytic subunit	0.680732996	0.285144004
202923_s_at	GCLC, glutamate-cysteine ligase, catalytic subunit	0.930452219	0.232623985
203925_at	GCLM, glutamate-cysteine ligase, modifier subunit	0.744924053	0.992793651
221510_s_at	GLS, glutaminase	0.07184016	0.30721294
203157_s_at	GLS, glutaminase	0.038305794	0.066323391
203158_s_at	GLS, glutaminase	0.158391485	0.482694785
203159_at	GLS, glutaminase	0.114072714	0.225283679
205531_s_at	GLS2, glutaminase 2 (liver, mitochondrial)	0.074431839	0.088951816
200648_s_at	GLUL, glutamate-ammonia ligase (glutamine synthase)	0.259776929	0.026125116
215001_s_at	GLUL, glutamate-ammonia ligase (glutamine synthase)	0.792003217	0.17200119
217202_s_at	GLUL, glutamate-ammonia ligase (glutamine synthase)	0.245547385	0.053102733
200650_s_at	LDHA, lactate dehydrogenase A	0.266049864	0.082323534
208403_x_at	MAX, MYC associated factor X	0.981466482	0.951836406
209331_s_at	MAX, MYC associated factor X	0.249051824	0.604375051
209332_s_at	MAX, MYC associated factor X	0.116828225	0.070735325
210734_x_at	MAX, MYC associated factor X	0.762960743	0.835511118
203159_at	GLS, glutaminase	0.114072714	0.225283679
214108_at	MAX, MYC associated factor X	0.749550292	0.414116063
207824_s_at	MAZ, MYC-associated zinc finger protein (purine-binding transcription factor)	0.003248803	0.000688372
212064_x_at	MAZ, MYC-associated zinc finger protein (purine-binding transcription factor)	0.006013447	0.036746352
213188_s_at	MINA, MYC induced nuclear antigen	0.422365219	0.389165846
213189_at	MINA, MYC induced nuclear antigen	0.272299316	0.347385343
202431_s_at	MYC, v-myc myelocytomatosis viral oncogene homolog (avian)	0.15501392	0.068167919

Table S5 (cont'd). Myc Association Statistics[5]			
Probeset ID	**Myc Family Member / Transcriptional Target Gene**	**t-test Group C vs all Basal + Claudin low, p =**	**t-test Group B+C vs all Basal + Claudin Low, p =**
203359_s_at	MYCBP, c-myc binding protein	0.747532179	0.141452857
203360_s_at	MYCBP, c-myc binding protein	0.459129501	0.181826356
203361_s_at	MYCBP, c-myc binding protein	0.673391404	0.456707435
201959_s_at	MYCBP2, MYC binding protein 2	0.56877653	0.116142118
201960_s_at	MYCBP2, MYC binding protein 2	0.843906145	0.156008882
209757_s_at	MYCN, v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	0.318485559	0.234655027
214787_at	MYCPBP, c-myc promoter binding protein	0.600841503	0.039313472
203964_at	NMI, N-myc (and STAT) interactor	0.586342711	0.199606276
201599_at	OAT, ornithine aminotransferase (gyrate atrophy)	0.324024156	0.233368527
204243_at	RLF, rearranged L-myc fusion sequence	0.673422221	0.199249805
208916_at	SLC1A5, solute carrier family 1 (neutral amino acid transporter), member 5	0.632444253	0.968534998
218237_s_at	SLC38A1, solute carrier family 38, member 1	0.2669149	0.02960135
218041_x_at	SLC38A2, solute carrier family 38, member 2	0.635279484	0.554865205
220924_s_at	SLC38A2, solute carrier family 38, member 2	0.671218493	0.525109732
207528_s_at	SLC7A11, solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	0.072142142	0.016771364
201195_s_at	SLC7A5, solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	0.91245638	0.347283019

[5]A summary of statistical analyses (t-tests) comparing expression levels of MYC, MYC family members, and various Myc transcriptional targets in the auxotrophic samples (Groups B and C) versus other basal and claudin low samples. Expression values from Affymetrix U133A genechip hybridization signals

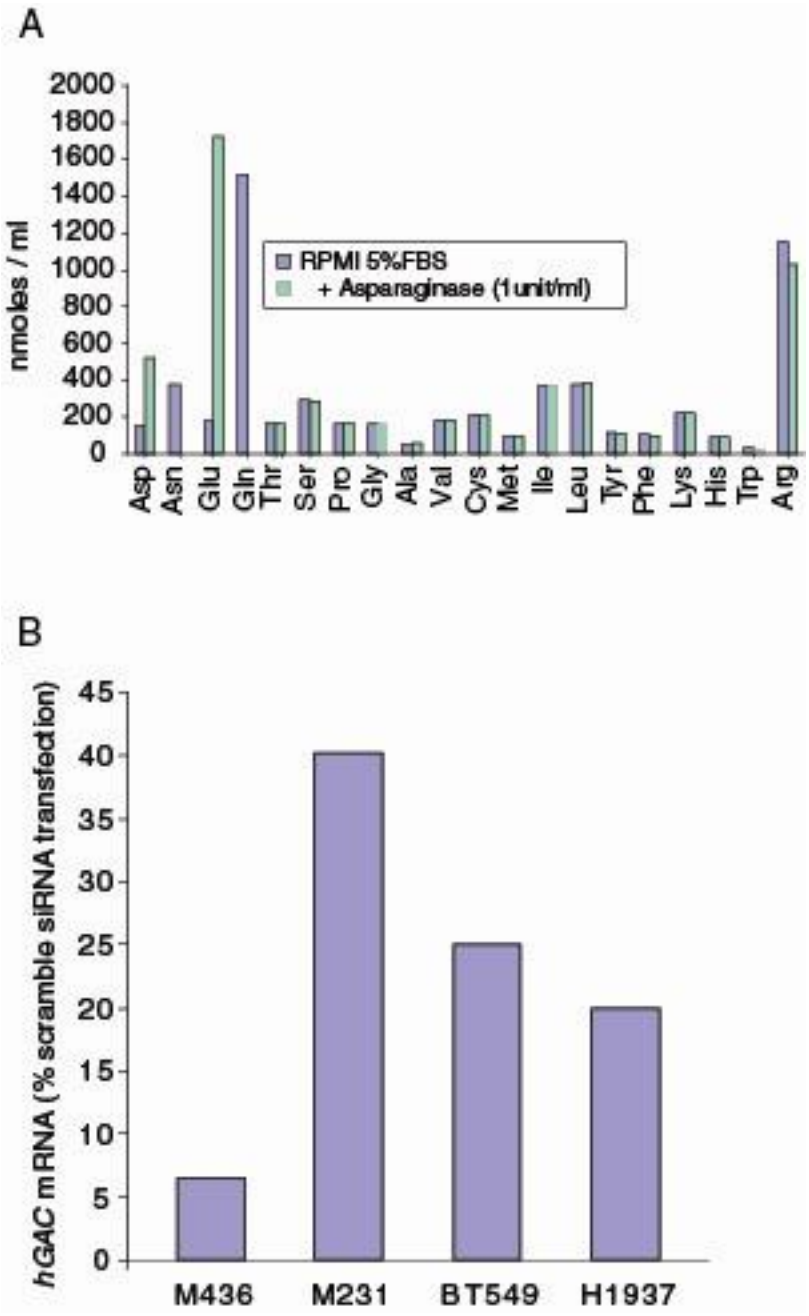

Figure S5, related to Figure 5. Glutamine Auxotrophy Presents Therapeutic Opportunity

(A) Amino acid analysis of RPMI culture media treated with and with out Asparaginase (1u/ml); standard 3-letter amino acid abbreviations used, analysis by HPLC. (B) Efficiency of *hGAC* siRNA-mediated mRNA knockdown in 4 exemplar cell lines, values normalized to *hGAC* message levels in each cell line transfected with a negative control siRNA. Corresponding proliferative defects illustrated in Figure 5H.

Table S6, related to Figure 5. Class Associations of Glutamine Transporter Probeset IDs in Expression Datasets Derived from Primary Clinical Tumor Samples[6]							
Gene Set ID	**Association tested**	***ASCT2* 208916_at**	***SLC38A1* 218237_s_at**	***SLC38A2* 220924_s_at**	***SLC38A2* 218041_x_at**	***SLC7A5* 201195_s_at**	***SLC3A2* 200924_s_at**
GSE1561	ER (ER+)	0.339 / -1.07	0.318 / 1.19	0.051 / 1.27	0.038 / 1.29	4.5e-6 / -2.64	0.765 / -1.00
	Subtype (Luminal)	0.286 / 1.09	0.003 / 2.35	0.014 / 1.37	0.015 / 1.37	3.6e-5 / -2.12	0.407 / 1.18
GSE2034	ER (ER+)	0.016 / -1.16	0.018 / 1.24	0.519 / 1.06	0.551 / 1.06	1.1e-15 / -2.52	0.019 / -1.14
GSE20271	ER (ER+)	0.337 / -1.02	0.006 / 1.56	0.008 / 1.32	0.003 / 1.35	1.6e-4 / -1.64	0.539 / -1.02
GSE23988	ER (ER+)	0.248 / 1.11	2.3e-5 / 2.91	9.6e-6 / 2.05	7.4e-6 / 2.18	0.054 / -1.18	0.480 / 1.12
GSE4922	ER (ER+)	0.267 / -1.05	0.042 / 1.41	0.902 / 1.07	0.937 / 1.05	1.91e-12 / -3.24	0.699 / 1.06
GSE1456	Subtype (Luminal)	0.145 / 1.15	0.013 / 1.91	0.295 / -1.14	0.411 / -1.12	1.7e-5 / -2.84	0.868 / -1.00
GSE7390	ER (ER+)	3.4e-5 / -1.31	0.021 / 1.03	0.695 / -1.02	0.519 / -1.05	1.1e-15 / -3.08	0.005 / -1.15
Chin 2006	ER (ER+)	0.192 / -1.03	0.132 / 1.43	0.180 / 1.21	0.335 / 1.19	1.1e-6 / -2.30	0.175 / 1.12
Chin 2006	Subtype (eucl) (Luminal)	0.556 / 1.05	0.008 / 2.23	0.023 / 1.36	0.036 / 1.34	1.1e-7 / -2.57	0.878 / 1.29
Chin 2006	Subtype (corr) (Luminal)	0.475 / 1.03	0.014 / 2.19	0.052 / 1.30	0.074 / 1.28	1.8e-7 / -2.38	0.769 / 1.30

[6]Datasets were downloaded from NCBI GEO or obtained from Chin et al. (Chin, et al. 2006) and analyzed for gene expression differences between classes based on ER status or molecular subtype: p value (t-test) / fold change, where ratio of average marker expression in ER+/luminal vs. ER-/basal samples in raw expression data (>1 means up-regulation in ER+/luminal, and <-1 means up-regulation in ER-/basal).

Table S7, related to Figure 5. Metabolomics Results[7]							
13C label Source / Time	**Metabolite analyzed (+X denotes number of ^{13}Carbons)**						
	Asp+0	**Asp+1**	**Asp+2**	**Asp+3**	**Asp+4**		
12 hr 13C glutamine	25.1%	10.6%	18.0%	8.2%	38.1%		
12 hr 13C glutamine	25.5%	10.3%	16.0%	9.7%	38.5%		
6 hr 13C glutamine	28.7%	8.7%	15.7%	9.0%	37.8%		
average	**26.5%**	**9.9%**	**16.6%**	**9.0%**	**38.1%**		
standard deviation	**2.0%**	**1.0%**	**1.2%**	**0.8%**	**0.3%**		
	Citrate+0	**Citrate+1**	**Citrate+2**	**Citrate+3**	**Citrate+4**	**Citrate+5**	**Citrate+6**
12 hr 13C glutamine	27.4%	10.6%	18.8%	8.8%	31.8%	2.6%	0%
12 hr 13C glutamine	29.6%	10.8%	18.7%	5.6%	28.9%	6.5%	0%
6 hr 13C glutamine	31.6%	7.3%	14.4%	11.6%	33.1%	2.0%	0%
average	**29.5%**	**9.6%**	**17.3%**	**8.7%**	**31.3%**	**3.7%**	**0.0%**
standard deviation	**2.1%**	**2.0%**	**2.5%**	**3.0%**	**2.2%**	**2.4%**	**0.0%**
	Glu+0	**Glu+1**	**Glu+2**	**Glu+3**	**Glu+4**	**Glu+5**	
12 hr 13C glutamine	31.2%	4.8%	2.4%	16.0%	3.2%	42.3%	
12 hr 13C glutamine	27.0%	4.8%	3.5%	11.6%	7.3%	45.8%	
6 hr 13C glutamine	24.7%	5.3%	4.7%	14.5%	1.9%	48.9%	
average	**27.6%**	**5.0%**	**3.5%**	**14.0%**	**4.1%**	**45.7%**	
standard deviation	**3.3%**	**0.3%**	**1.1%**	**2.3%**	**2.9%**	**3.3%**	
	Gln+0	**Gln+1**	**Gln+2**	**Gln+3**	**Gln+4**	**Gln+5**	
12 hr 13C glutamine	17.8%	5.4%	0.0%	0.0%	4.2%	72.6%	
12 hr 13C glutamine	12.3%	1.5%	0.0%	0.0%	5.0%	81.2%	
6 hr 13C glutamine	10.2%	0.0%	0.1%	0.8%	3.5%	85.3%	
average	**13.4%**	**2.3%**	**0.0%**	**0.3%**	**4.2%**	**79.7%**	
standard deviation	**4.0%**	**2.8%**	**0.1%**	**0.5%**	**0.7%**	**6.5%**	
	Malate+0	**Malate+1**	**Malate+2**	**Malate+3**	**Malate+4**		
12 hr 13C glutamine	26.1%	11.4%	19.9%	6.2%	36.4%		
12 hr 13C glutamine	24.6%	10.5%	19.4%	6.6%	38.8%		
6 hr 13C glutamine	26.0%	9.4%	15.5%	9.5%	39.6%		
average	25.6%	10.4%	18.3%	7.4%	38.3%		
standard deviation	0.8%	1.0%	2.4%	1.8%	1.6%		

[7] Incorporation of ^{13}C-carbon from exposure to ambient ^{13}C-5-glutamine by various metabolites as indicated in gray rows, expressed as percent total metabolite pool analyzed. Columns report percent per number of labeled carbons in each substrate pool.

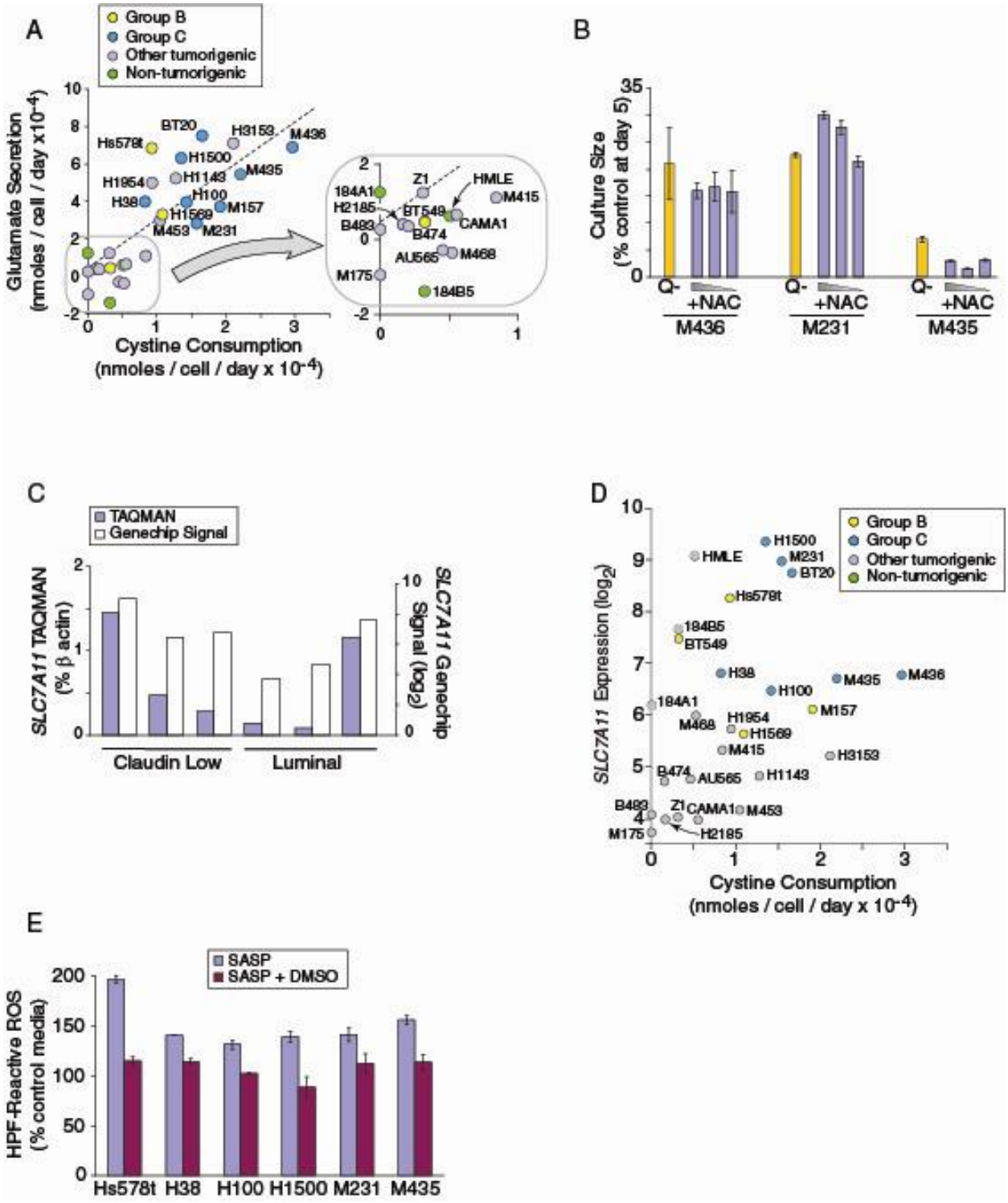

Figure S6, Related to Figure 6. xCT-Mediated Cystine Transport Raises Free Radical Levels in TNBC

Icon codes in figure keys. Icons represent mean values+/-SD. (A) Duplicate of Figure 6A color coded by glutamine restriction group membership illustrating cystine consumption vs. glutamate secretion, derived from HPLC analysis of culture supernatants. (B) N-acetylcystine does not substantially restore culture expansion in the absence of glutamine; 3 exemplar Group C TNBC samples shown; values normalized to parallel cultures in control media; Q-, glutamine free media; NAC, 4-fold titrations of N-acetylcystine from 20mM in glutamine-free media. (C) TAQMAN validation of relative *SLC7A11* Affymetrix genechip signals for representative cells in our panel. (D) Relationship between *SLC7A11* Genechip hybridization signals and cystine consumption, icons coded by glutamine restriction group membership. See figure 6C for coding by molecular subtype. (E) Quantitation of HPF (hydroxyphenylfluorescine) reactivity in response to 300μM SASP treatment, derived from FACS analysis (FL-1 channel detection). Parallel cultures using SASP + 2% DMSO exhibit reduced HPF signal, indicating the specific reduction in hydroxyl radicals (maroon bars).

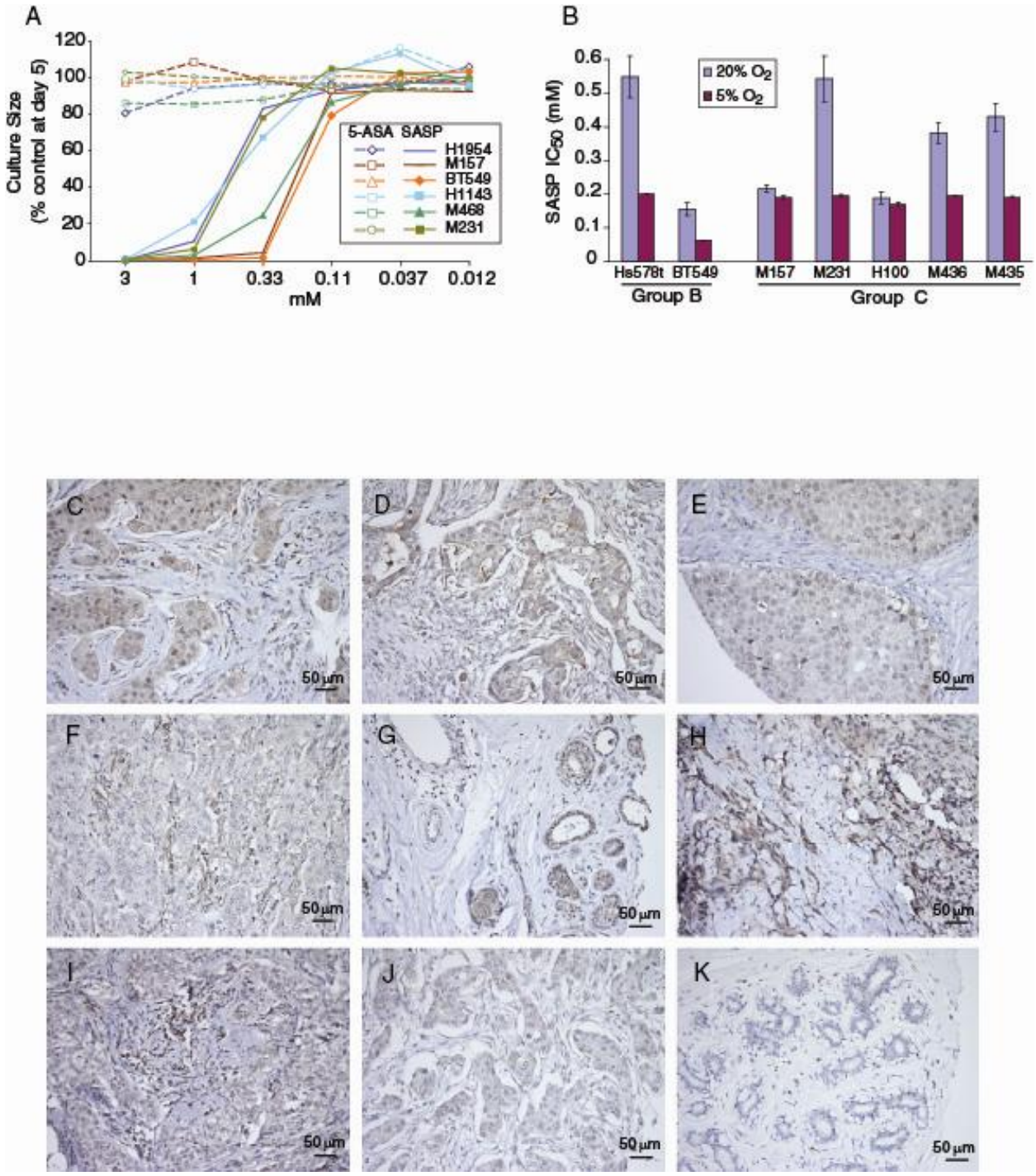

Figure S7, related to Figure 7. The xCT Transporter is Expressed in Breast Tumors *in vivo*, and is Therapeutically Inhibited by Sulfasalazine

Icons represent mean values+/-SD. (A) Comparison of SASP and the anti-inflammatory cleavage product 5-ASA for growth attenuation in 6 exemplar basal and claudin low TNBC. Identical titrations shown, values expressed as % of parallel control media cultures. Open icons

and dotted lines, 5-ASA treatment; closed icons and solid lines, 300μM SASP treatment. B) Comparison of SASP sensitivity in ambient (20%) oxygen (blue bars); vs. tissue normoxia (5% O_2), maroon bars. (C-K) Staining results showing xCT expression in paraffin sections of anonymous TNBC breast tumors; blue, Hematoxylin (nuclei); brown, horseradish peroxidase (specific anti-xCT stain). (C-I) Images of tumors counted as strong xCT staining. (J) Images of tumor counted as light xCT stain. (K) Normal breast section, with infrequent xCT positive stromal cells.

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Purification of Normal Mammary Epithelial Cells

Purified from 3 distinct reduction mammoplasties as previously described, collected under IRB approval (Allinen et al., 2004). Briefly, tissue was minced, digested with collagenase I (Sigma C0130) and hyaluronidase (Sigma H3506) 1-2 hrs/37C, washed, filtered through graded pore sized strainers (Tetko, 03-500-47, 03-250-50 and 03-20-14, Fisher 08-771-19 and 08-771-1) to harvest organoids (filter tops). These were trypsinized (5 min/ 37C), filtered (100μm, 40μm, and 20μm mesh), single cell flow through put on Percoll gradients to remove debris and erythrocytes (Percoll-Pharmacia 17-0891-01). Luminal epithelia were purified via anti-BerEP4-conjugated magnetic bead adherence, basal/myoepithelia by anti-CD10-conjugated beads. Cells were immediately frozen on dry ice. Samples were at least 95% pure by PCR.

Pleural Effusion Tumor Cell Purification and Analysis

Patient permission was obtained under IRB approval. Cells were purified by centrifugation, red blood cells lysed, and remainders frozen in aliquots in 10% DMSO/ 90% FBS/ liquid nitrogen. Tumor abundance, purity, and phenotype were determined by immune fluorescence on cytospin samples using markers of carcinomas, mesothelia, lymphocytes, and endothelia. Cytospins were fixed/permeabilized in 1% paraformaldehyde/ 0.1% Triton-X 100 or 100% methanol. Antibodies: BD Transduction Labs: Cytokeratin 8, CAM 5.2,1:3; MUC1, 555925; CD44, 550392; Moesin, 610401; E-cadherin, 610181; VE-cadherin, 555289. Zymed: Mesothelin,35-4200; Calretinin, 18-0291; OB-cadherin, 32-1700; N-cadherin, 33-3900. Neomarkers: Vimentin, MS-129-PO; P-cadherin, MS-1741-S0; CD10, MS-973-PO; BerEP4, MS-1851-P0. Novocastra Cytokeratin 8, RTU-CK8-TS1; DAKO, Cytokeratin 17, M7046; CHEMICON Cytokeratin 5/14, CBL267; Sigma Smooth Muscle Actin, F3777; Santa Cruz Biotechnology Estrogen Receptor, SC-8002. Samples with large tumor clumps that excluded contaminating cells were re-

suspended in warm DMEM/10% FBS, applied to 30μm MACS Pre-Separation Filters (Milteny Biotech 130-041-407), filter-top material (tumor clumps) washed 5 times with fresh media on the filter, an aliquot methanol fixed to gauge purity, and the remainder re-suspended in lysis buffer (XB, NuGEN), and frozen on dry ice. SUM86PE: 85% tumor cells, 10% medium sized vimentin$^+$ cells, remainder small vimentin positive lymphocytes. SUM87PE: Homogenous large epithelial clumps, 0.7% small vimentin positive lymphocytes. SUM 153 PE: Homogenous tumor clumps, 2.6% lymphocytes.

Dataset Generation

RNA was prepared (PicoPure RNA Isolation Kit 0204, Arcturus) from samples described above, from 4 non-tumorigenic human mammary epithelial cell (HMEC)-derived cell lines: (184A1, 184B5, HMLE, HMLE-PR) (Stampfer, Hallowes et al. 1980; Elenbaas, Spirio et al. 2001), and 10 carcinoma-derived cell lines previously determined by Neve, et. al. (Neve, 2006; "Neve dataset"). Quality was assessed (Agilent Technologies 2100 Bioanalyzer). Labeled cDNA was prepared from 50 ng total RNA (Ovation Biotin RNA Amplification and Labeling System, NuGEN) per manufacturers' instructions, and hybridized to Affymetrix U133A GeneChips using standard procedures developed and performed by the David J. Gladstone Institute Genomics Core, UCSF. Affymetrix image files were normalized (RMA, (Irizarry et al., 2003)), and the resultant $\log_2$ values used to produce the dataset Timmerman_pico. Datasets merge: The mean hybridization signal for each probeset ID across all samples in the Neve dataset (jmean), and the mean hybridization signal for each probeset ID across the 10 breast cancer derived cell lines (CDL) in the Timmerman_pico dataset were determined (lmean). Mean value differences between the Timmerman_pico and Neve datasets were calculated for each probeset ID (jmean-lmean), and added to each sample in the Timmerman_pico dataset. Values for the 10 duplicated CDL in the resulting merged dataset (Timmerman_merge) were examined before all subsequent analyses to verify that signal hybridization alterations in the merged dataset were

not due to sample preparation or dataset normalization. Duplicate samples in the Timmerman_merge dataset derived from the Timmerman_pico source were then removed before all statistical and bioinformatics-based dataset analyses. Cluster and Treeview software were used (Eisen et al., 1998) to visualize group relationships.

Significance Analyses

Several two class unpaired analyses using Significance Analysis for Microarray EXCEL spreadsheet add in (Tusher et al., 2001) were performed. The first contrasted the purified normal and non-tumorigenic, HMEC-derived samples (the N/I class) against the Carcinoma-derived lines (CDL) plus the purified pleural effusion tumors (PE) samples (the CDL/PE class). We identified 2887 significant Probeset IDs with a median of 0.41 Probeset IDs falsely called; 1631 positively associated and 1256 negatively associated with the CDL/PE (ie: positively associated with the N/I class). More than 28.4% versus 8.0% of all transcripts associated with the CDL/PE versus the N/I group encode molecules involved in intracellular metabolism and other mitochondrial-specific functions. To identify CDL subtype-specific metabolic transcripts, all Probeset IDs associated with metabolic GO descriptions were selected from the Timmerman_merge dataset, (2003 Probeset IDs in total) and two additional significance analyses were performed, pitting the luminal CDL/PE (the "LUMINAL analysis") and then the basal/mesenchymal CDL (the "BASAL/MES analysis") against all other samples. About 360/760 metabolic probeset IDs identified in the N/I versus CDL/PE significance analysis were-re identified in these two latter analyses, suggesting that almost half (47%) of transcripts identified as CDL/PE-associated are in fact on this list based on alterations in only a subset of the samples, and further strengthening the impression of strong metabolic differences between the luminal and basal/mesenchymal CDL. At highest stringency, about 202 novel probeset IDs with positive, and 31 with negative luminal CDL/PE expression bias were also identified. Similarly, at highest stringency 142 new Probeset IDs with positive basal/mesenchymal CDL

subset expression bias were uniquely identified. Essentially all probeset IDs negatively associated with the basal/mesenchymal CDL class were also positively associated with the luminal CDL/PE in the luminal analysis above (77/86); three remaining probeset IDs were previously positively associated with the N/I clade, providing 6 unique Probeset IDs negatively associated with the basal/mesenchymal clade. These significance analyses have highlighted about 760 Probeset IDs which identify molecules involved in intracellular metabolic processes and mitochondrial functions that are expressed differentially between these 4 classes of samples: the N/I, the CDL/PE, the luminal CDL/PE, and the basal/mesenchymal CDL.

TP53 Analysis

Using the IARC TP53 Database (http://p53.iarc.fr/CellLines.aspx), we found 36 of our cell lines with reliable information on TP53 status. They include 15 luminal, 13 basal, and 8 claudin low samples, 27 with p53 mutations, and 9 wildtype. Of the mutant alleles, 14 have no assessment as to functionality, while the remaining 19 are deemed nonfunctional by various analyses summarized in the database, including protein structure and the ability to transactivate transcription. Of the 36 cell lines, 10 are glutamine sensitive cells (7 Group C and 3 Group B). We did not identify any correlation between p53 status and glutamine dependency. We have included this result in the text.

	p53 Mutant	Deleterious / Nonfunctional (no information)	p53 WT	Total
Luminal	9	8 (1)	6	15
Basal	11	6 (5)	2	13
Cl. Low	7	5 (2)	1	8
Total	27	19 (14)	9	36

	Mutant vs. WT	Nonfunctional vs. All
t-test Group C vs. All p=	8.31E-01	5.81E-01
t-test GroupC+B vs. All p=	6.71E-01	6.97E-01

DAPI Nuclear Stain

Subconfluent cultures were grown on coverslips, paraformaldehyde fixed (2% / 20 min/room temp), and nuclei stained by standard methods (DAPI, Molecular Probes). Nuclear morphology, mitotic frequency, and apoptotic figure assessment was done by manual cell counts of at least 2000 cells/condition.

Quantitative PCR

RNA samples were prepared (Quiagen RNA Mini Kit) and specific primer/probe mixes used (Assay-on-Demand, Applied Biosystems, or a custom designed IDT PrimeTime Mini qPCR Assay specific for the *hGAC* splice variant) to quantify specific message levels (*Taq*Man, Applied Biosystems PRISM 7900). Exemplar cell lines representing low and high expression were selected for each gene analyzed to validate genechip hybridization variation, or for analysis of expression alterations with glutamine restriction.

For Figures S5B, 4E, 4F, 5H6H: 1.5ug total RNA (NucleoSpin RNAII kit, Macherey-Nagel), was reverse transcribed (iScript, Biorad) per manufacturer's directions. Power SYBR (AB) green PCR reactions performed in triplicate, analyzed with the Step One Plus (AB) sequence detection system. Data quantified against a standard curve, normalized to *TBP* (TATA box binding protein). Primers: *hGAC*: 5' GGGAATTCACTTTTGTCACGATC, 5' CTTTCATAGTCCAATGGTCCAAAG; *GLUL*: 5' AAGGTGTGTGGAAGAGTTGCC, 5' TGCTCACCATGTCCATTATC; *xCT*: 5' TGCTGGGCTGATTTTATCTTCG, 5' GAAAGGGCAACCATGAAGAGG; *TBP*: 5' CCCGAAACGCCGAATATAATCC, 5' GACTGTTCTTCACTCTTGGCTC.

Western Blot

RIPA extracts were prepared by standard techniques in the presence of protease and phosphatase inhibitors. 20 μg of lysates were resolved on 4-20% polyacrylamide gels, transferred to PVDF membrane, blocked in 5% BSA/TBST 30 minutes, exposed to primary

antibodies overnight/4C in blocking buffer. Specific hybridization was visualized with HRP-conjugated secondary and chemiluminescence (Amersham RPN2106). Antibodies: AMPK, p-AMPK T-172, ACC, p-ACC S-79, cleaved PARP, retinoblastoma, and phosphorylated retinoblastoma (Cell Signaling); glutaminase (Abnova H00002744-M01); glutamine synthase (Santa Cruz sc-9067); beta actin (Sigma). Glutaminase assembly, Figure S1E; M231 extracts were included on each of 6 separate blots, to normalize signal intensities for the assembly in Photoshop. Duplicate M231 lanes were removed after assembly. Signal intensities were scored as none=1, light=2, strong=3. Pairs of sibling cell lines (asterisks) are counted as one independent isolate (AU565 and SKBR3, MCF7 and LY2).

Culture Expansion Assays

Assays were performed at least 3 times in triplicate, in 96-well format. Relative cell number determined (Cell Titer Glow, Promega), verified by microscopy. Averages reported +/-SD.96-well format triplicate cultures at 1-4X10^4/ml or, confluent 1-4X10^5 /ml, with control, glutamine deficient,(GIBCO 21870, 11960), or 3 or 4-fold serial drug/ nutrient dilutions for 5 days/37^{o}C/5%$CO_{2,}$. Highest concentrations: Asparaginase 100 units/ml, DON 5mM, Sulfasalazine 3mM, N-acetylcysteine 10 mM, 5-ASA 3mM, Carboplatin 100μg/ml, Doxorubicin 150ng/ml, Paclitaxel 1.7 mg/ml. Cell cycle, direct cell counts, glucose uptake, Annexin V, ROS detection and siRNA used larger format cultures.

Doubling Times

Cell numbers in triplicate cultures determined by particle counter (Coulter), ATP levels (Cell-Titer Glow, Promega), or trypan blue exclusion. Growth curve calculations used standard techniques.

Annexin V / Cell Death Assay

FACSCalibur (Becton Dickinson) or C6 Flow Cytometer (Accuri). 30,000 cells in triplicate analyzed, mean fluorescence values reported. Annexin V-FITC (Southern Biotechnology 10038-02) and TOTO3 (Molecular Probes T3604), or Propidium Iodide (PI; Molecular Probes, P1304MP) used per manufacturer's protocol. Percent Annexin V positive, PI negative reported.

Cell Cycle

Cultures +/- 18 hrs 100-200nM nocodazole were 70% ethanol fixed, propidium iodide and RNAse (5ug/ml) stained using standard techniques. 30,000-100,000 cells were analyzed in triplicate. Cell cycle curve fitting and cell cycle fraction calculations by FLOJO curve fitting software (Tree Star, Inc.).

Cell Counts

Live cell numbers in 30μl determined in triplicate using the C6 Flow Cytometer (Accuri). Manual counts used trypan blue exclusion, in triplicate.

SUPPLEMENTAL REFERENCES

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Elenbaas, B., Spirio, L., Koerner, F., Fleming, M. D., Zimonjic, D. B., Donaher, J. L., Popescu, N. C., Hahn, W. C., and Weinberg, R. A. (2001). Human breast cancer cells generated by oncogenic transformation of primary mammary epithelial cells. Genes Dev 15, 50-65.

Stampfer, M., Hallowes, R. C., and Hackett, A. J. (1980). Growth of normal human mammary cells in culture. In Vitro 16, 415-425.

Table S2: Significant Metabolic Probeset IDs. Probeset IDs and significance scores for metab

Significance analysis classes were:

1) Purified normal samples plus nontumorigenic, culture adapted cells (N/I) versus car
2) Basal carcinomas versus all other samples (Basal CDL).
3) Luminal carcinomas versus all others (Luminal CDL).

Significant Class Association	Probeset ID	Gene Symbol	Score
Basal CDL	201272_at	AKR1B1	5.98627
Basal CDL	221510_s_at	GLS	5.87002
Basal CDL	202613_at	CTPS	5.75562
Basal CDL	205260_s_at	ACYP1	5.61946
Basal CDL	203909_at	SLC9A6	5.57077
Basal CDL	205996_s_at	AK2	5.44375
Basal CDL	200762_at	DPYSL2	5.26941
Basal CDL	220892_s_at	PSAT1	5.26622
Basal CDL	202026_at	SDHD	5.19516
Basal CDL	205401_at	AGPS	5.15867
Basal CDL	212174_at	AK2	5.11785
Basal CDL	205565_s_at	FXN	5.003
Basal CDL	212604_at	MRPS31	4.92187
Basal CDL	209213_at	CBR1	4.89146
Basal CDL	202589_at	TYMS	4.81951
Basal CDL	201300_s_at	PRNP	4.67459
Basal CDL	219079_at	NCB5OR	4.6724
Basal CDL	217294_s_at	ENO1	4.67206
Basal CDL	211150_s_at	DLAT	4.60905
Basal CDL	219204_s_at	SRR	4.57848

Basal CDL	219698_s_at	METTL4	4.52715
Basal CDL	218558_s_at	MRPL39	4.49672
Basal CDL	215535_s_at	AGPAT1	4.49345
Basal CDL	215707_s_at	PRNP	4.39831
Basal CDL	201012_at	ANXA1	4.37549
Basal CDL	203340_s_at	SLC25A12	4.34122
Basal CDL	221020_s_at	MFTC	4.33304
Basal CDL	205379_at	CBR3	4.33221
Basal CDL	201968_s_at	PGM1	4.30168
Basal CDL	200978_at	MDH1	4.25182
Basal CDL	221437_s_at	MRPS15	4.19826
Basal CDL	201634_s_at	CYB5-M	4.11264
Basal CDL	213133_s_at	GCSH	4.10644
Basal CDL	202502_at	ACADM	4.09831
Basal CDL	219220_x_at	MRPS22	4.0809
Basal CDL	208746_x_at	ATP5L	4.03913
Basal CDL	218982_s_at	MRPS17	3.98973
Basal CDL	202345_s_at	FABP5	3.97897
Basal CDL	214431_at	GMPS	3.96944
Basal CDL	212568_s_at	DLAT	3.95771
Basal CDL	216705_s_at	ADA	3.95428
Basal CDL	200818_at	ATP5O	3.94961
Basal CDL	218421_at	CERK	3.94643
Basal CDL	201633_s_at	CYB5-M	3.9291
Basal CDL	201633_s_at	CYB5-M	3.9291
Basal CDL	205633_s_at	ALAS1	3.92187

Basal CDL	218653_at	SLC25A15	3.92135
Basal CDL	218096_at	AGPAT5	3.90334
Basal CDL	202780_at	OXCT1	3.90194
Basal CDL	209080_x_at	TXNL2	3.84647
Basal CDL	202233_s_at	UQCRH	3.8143
Basal CDL	201030_x_at	LDHB	3.78794
Basal CDL	205194_at	PSPH	3.77857
Basal CDL	210453_x_at	ATP5L	3.7778
Basal CDL	201571_s_at	DCTD	3.77634
Basal CDL	203401_at	PRPS2	3.77157
Basal CDL	218357_s_at	TIMM8B	3.74203
Basal CDL	207573_x_at	ATP5L	3.72784
Basal CDL	213564_x_at	LDHB	3.67974
Basal CDL	209773_s_at	RRM2	3.67929
Basal CDL	213302_at	PFAS	3.67311
Basal CDL	203939_at	NT5E	3.64784
Basal CDL	208909_at	UQCRFS1	3.63633
Basal CDL	213149_at	DLAT	3.63593
Basal CDL	204331_s_at	MRPS12	3.62398
Basal CDL	203033_x_at	FH	3.54352
Basal CDL	208864_s_at	TXN	3.51617
Basal CDL	210008_s_at	MRPS12	3.49788
Basal CDL	218194_at	DKFZP566E144	3.49414
Basal CDL	202675_at	SDHB	3.49341
Basal CDL	218304_s_at	OSBPL11	3.48155
Basal CDL	217772_s_at	MTCH2	3.46284

Basal CDL	212603_at	MRPS31	3.41895
Basal CDL	213129_s_at	GCSH	3.41784
Basal CDL	209549_s_at	DGUOK	3.40776
Basal CDL	210145_at	PLA2G4A	3.40674
Basal CDL	209932_s_at	DUT	3.38908
Basal CDL	204639_at	ADA	3.38637
Basal CDL	212348_s_at	AOF2	3.38188
Basal CDL	208847_s_at	ADH5	3.35333
Basal CDL	216685_s_at	MTAP	3.3331
Basal CDL	218398_at	MRPS30	3.29645
Basal CDL	201890_at	RRM2	3.28627
Basal CDL	201231_s_at	ENO1	3.24926
Basal CDL	203095_at	MTIF2	3.24493
Basal CDL	201757_at	NDUFS5	3.24088
Basal CDL	218561_s_at	C6orf149	3.23635
Basal CDL	221311_x_at	DJ122O8.2	3.23277
Basal CDL	32836_at	AGPAT1	3.21939
Basal CDL	214224_s_at	PIN4	3.218
Basal CDL	203816_at	DGUOK	3.21536
Basal CDL	214126_at	MCART1	3.21528
Basal CDL	209397_at	ME2	3.21236
Basal CDL	202715_at	CAD	3.18445
Basal CDL	210137_s_at	DCTD	3.18328
Basal CDL	208956_x_at	DUT	3.18046
Basal CDL	202799_at	CLPP	3.15989
Basal CDL	217869_at	HSD17B12	3.15787

Basal CDL	201251_at	PKM2	3.14074
Basal CDL	204059_s_at	ME1	3.13872
Basal CDL	214170_x_at	FH	3.1328
Basal CDL	201572_x_at	DCTD	3.13114
Basal CDL	209694_at	PTS	3.09748
Basal CDL	201580_s_at	DJ971N18.2	3.09021
Basal CDL	202096_s_at	BZRP	3.07965
Basal CDL	208967_s_at	AK2	3.05353
Basal CDL	202591_s_at	SSBP1	3.04047
Basal CDL	211363_s_at	MTAP	3.03526
Basal CDL	201351_s_at	YME1L1	3.00696
Basal CDL	209003_at	SLC25A11	2.99378
Basal CDL	209003_at	SLC25A11	2.99378
Basal CDL	204172_at	CPOX	2.99128
Basal CDL	212175_s_at	AK2	2.98863
Basal CDL	202325_s_at	ATP5J	2.96828
Basal CDL	202533_s_at	DHFR	2.96259
Basal CDL	218119_at	TIMM23	2.95413
Basal CDL	213011_s_at	TPI1	2.95235
Basal CDL	204646_at	DPYD	2.94968
Basal CDL	205480_s_at	UGP2	2.93815
Basal CDL	219489_s_at	NXN	2.93324
Basal CDL	217989_at	DHRS8	2.92549
Basal CDL	209513_s_at	HSDL2	2.92029
Basal CDL	218118_s_at	TIMM23	2.91867
Basal CDL	203282_at	GBE1	2.9065

Basal CDL	203646_at	FDX1	2.89695
Basal CDL	210154_at	ME2	2.89572
Basal CDL	203465_at	MRPL19	2.89442
Basal CDL	222014_x_at	MTO1	2.88843
Basal CDL	217960_s_at	TOMM22	2.88828
Basal CDL	203339_at	SLC25A12	2.88797
Basal CDL	203093_s_at	TIMM44	2.87839
Basal CDL	219974_x_at	ECHDC1	2.87092
Basal CDL	221692_s_at	MRPL34	2.86268
Basal CDL	205412_at	ACAT1	2.86205
Basal CDL	203925_at	GCLM	2.86029
Basal CDL	209645_s_at	ALDH1B1	2.83086
Basal CDL	219821_s_at	GFOD1	2.80667
Basal CDL	208969_at	NDUFA9	2.80098
Basal CDL	212816_s_at	CBS	2.79961
Basal CDL	216574_s_at	RPE	2.79858
Basal CDL	216304_x_at	YME1L1	2.79574
Basal CDL	203663_s_at	COX5A	2.77514
Basal CDL	203746_s_at	HCCS	2.76862
Basal CDL	218716_x_at	MTO1	2.76261
Basal CDL	202075_s_at	PLTP	2.75648
Basal CDL	200955_at	IMMT	2.75378
Basal CDL	221920_s_at	MSCP	2.75283
Basal CDL	214452_at	BCAT1	2.74809
Basal CDL	221575_at	SCLY	2.74167
Basal CDL	40472_at	LOC254531	2.73999

Basal CDL	200824_at	GSTP1	2.7365
Basal CDL	211755_s_at	ATP5F1	2.71942
Basal CDL	211653_x_at	AKR1C2	2.69955
Basal CDL	205133_s_at	HSPE1	2.69712
Basal CDL	208447_s_at	PRPS1	2.69464
Basal CDL	209512_at	HSDL2	2.69371
Basal CDL	203032_s_at	FH	2.69274
Basal CDL	200822_x_at	TPI1	2.67173
Basal CDL	205100_at	GFPT2	2.66971
Basal CDL	200903_s_at	AHCY	2.66868
Basal CDL	203092_at	TIMM44	2.66665
Basal CDL	216594_x_at	AKR1C1 /// AKR1C2	2.66076
Basal CDL	207088_s_at	SLC25A11	2.65863
Basal CDL	207088_s_at	SLC25A11	2.65863
Basal CDL	202839_s_at	NDUFB7	2.65571
Basal CDL	210153_s_at	ME2	2.65567
Basal CDL	201554_x_at	GYG	2.65484
Basal CDL	221641_s_at	ACATE2	2.64544
Basal CDL	207508_at	ATP5G3	2.64205
Basal CDL	204571_x_at	PIN4	2.63997
Basal CDL	212230_at	PPAP2B	2.62178
CDL/PE	209773_s_at	RRM2	10.8628
CDL/PE	202532_s_at	DHFR	10.654
CDL/PE	201890_at	RRM2	10.6239
CDL/PE	48808_at	DHFR	10.2799
CDL/PE	203800_s_at	MRPS14	9.33279

CDL/PE	207507_s_at	ATP5G3	9.02103
CDL/PE	205711_x_at	ATP5C1	8.74684
CDL/PE	208870_x_at	ATP5C1	8.72223
CDL/PE	201441_at	COX6B1	8.5811
CDL/PE	207508_at	ATP5G3	8.51842
CDL/PE	202534_x_at	DHFR	8.43275
CDL/PE	203621_at	NDUFB5	8.38446
CDL/PE	213366_x_at	ATP5C1	8.36107
CDL/PE	218226_s_at	NDUFB4	8.33941
CDL/PE	218654_s_at	MRPS33	8.31032
CDL/PE	AFFX-HUMGAPDH/M33197_5_at	GAPD	8.16007
CDL/PE	202330_s_at	UNG	7.97723
CDL/PE	210519_s_at	NQO1	7.97362
CDL/PE	208846_s_at	VDAC3	7.93474
CDL/PE	218487_at	ALAD	7.92366
CDL/PE	218281_at	MRPL48	7.88875
CDL/PE	201467_s_at	NQO1	7.87832
CDL/PE	200978_at	MDH1	7.85666
CDL/PE	201619_at	PRDX3	7.84115
CDL/PE	217772_s_at	MTCH2	7.81773
CDL/PE	202589_at	TYMS	7.68481
CDL/PE	217900_at	FLJ10326	7.66872
CDL/PE	202343_x_at	COX5B	7.65156
CDL/PE	218190_s_at	HSPC051	7.54489
CDL/PE	218653_at	SLC25A15	7.53444
CDL/PE	201468_s_at	NQO1	7.48672

CDL/PE	203033_x_at	FH	7.44056
CDL/PE	202004_x_at	SDHC	7.43423
CDL/PE	203115_at	FECH	7.43319
CDL/PE	209389_x_at	DBI	7.39473
CDL/PE	203371_s_at	NDUFB3	7.30297
CDL/PE	209065_at	UQCRB	7.28158
CDL/PE	218123_at	C21orf59	7.23894
CDL/PE	200681_at	GLO1	7.20366
CDL/PE	208955_at	DUT	7.15619
CDL/PE	211025_x_at	COX5B	7.10221
CDL/PE	212510_at	GPD1L	7.06155
CDL/PE	202839_s_at	NDUFB7	7.04311
CDL/PE	201339_s_at	SCP2	7.03262
CDL/PE	209095_at	DLD	7.0322
CDL/PE	215088_s_at	SDHC	6.99589
CDL/PE	201570_at	CGI-51	6.98386
CDL/PE	212694_s_at	PCCB	6.9114
CDL/PE	208758_at	ATIC	6.89689
CDL/PE	219819_s_at	MRPS28	6.89425
CDL/PE	213735_s_at	COX5B	6.85877
CDL/PE	209932_s_at	DUT	6.82652
CDL/PE	211070_x_at	DBI	6.74209
CDL/PE	209224_s_at	NDUFA2	6.72243
CDL/PE	218049_s_at	MRPL13	6.70644
CDL/PE	203189_s_at	NDUFS8	6.6721
CDL/PE	210149_s_at	ATP5H	6.66799

CDL/PE	206790_s_at	NDUFB1	6.53425
CDL/PE	218160_at	NDUFA8	6.51972
CDL/PE	203775_at	SLC25A13	6.48951
CDL/PE	201118_at	PGD	6.47059
CDL/PE	218185_s_at	ARMC1	6.46399
CDL/PE	212581_x_at	GAPD	6.45408
CDL/PE	218538_s_at	MRS2L	6.43773
CDL/PE	202325_s_at	ATP5J	6.42699
CDL/PE	202891_at	NIT1	6.39469
CDL/PE	202233_s_at	UQCRH	6.33703
CDL/PE	217919_s_at	MRPL42	6.31574
CDL/PE	210532_s_at	C14orf2	6.30751
CDL/PE	217398_x_at	GAPD	6.29822
CDL/PE	201135_at	ECHS1	6.29196
CDL/PE	204571_x_at	PIN4	6.26811
CDL/PE	200955_at	IMMT	6.26254
CDL/PE	202309_at	MTHFD1	6.25828
CDL/PE	218569_s_at	KBTBD4	6.23281
CDL/PE	209143_s_at	CLNS1A	6.20854
CDL/PE	209623_at	MCCC2	6.13536
CDL/PE	210296_s_at	PXMP3	6.13316
CDL/PE	218046_s_at	MRPS16	6.11707
CDL/PE	214259_s_at	AKR7A2	6.10598
CDL/PE	213453_x_at	GAPD	6.07241
CDL/PE	201432_at	CAT	6.07066
CDL/PE	201754_at	COX6C	6.05975

CDL/PE	211569_s_at	HADHSC	6.05736
CDL/PE	207573_x_at	ATP5L	6.01631
CDL/PE	202533_s_at	DHFR	6.00827
CDL/PE	201119_s_at	COX8A	5.99026
CDL/PE	214170_x_at	FH	5.99016
CDL/PE	214224_s_at	PIN4	5.98443
CDL/PE	221693_s_at	MRPS18A	5.95308
CDL/PE	201193_at	IDH1	5.94542
CDL/PE	208911_s_at	PDHB	5.92649
CDL/PE	202961_s_at	ATP5J2	5.92101
CDL/PE	209036_s_at	MDH2	5.90577
CDL/PE	209036_s_at	MDH2	5.90577
CDL/PE	205412_at	ACAT1	5.90472
CDL/PE	203560_at	GGH	5.89133
CDL/PE	218970_s_at	CUTC	5.85822
CDL/PE	202428_x_at	DBI	5.84472
CDL/PE	201554_x_at	GYG	5.80668
CDL/PE	218119_at	TIMM23	5.7886
CDL/PE	209916_at	DHTKD1	5.76577
CDL/PE	221770_at	RPE	5.7633
CDL/PE	209003_at	SLC25A11	5.7461
CDL/PE	213133_s_at	GCSH	5.73697
CDL/PE	204587_at	SLC25A14	5.7114
CDL/PE	203606_at	NDUFS6	5.69863
CDL/PE	201563_at	SORD	5.69013
CDL/PE	201740_at	NDUFS3	5.6662

CDL/PE	211023_at	PDHB	5.6576
CDL/PE	208699_x_at	TKT	5.65445
CDL/PE	210453_x_at	ATP5L	5.64774
CDL/PE	200818_at	ATP5O	5.637
CDL/PE	205379_at	CBR3	5.6335
CDL/PE	218270_at	MRPL24	5.62883
CDL/PE	202077_at	NDUFAB1	5.60333
CDL/PE	201568_at	QP-C	5.59701
CDL/PE	210045_at	IDH2	5.57074
CDL/PE	208308_s_at	GPI	5.56375
CDL/PE	219180_s_at	PEX26	5.56363
CDL/PE	208746_x_at	ATP5L	5.56309
CDL/PE	211595_s_at	MRPS11	5.55952
CDL/PE	217140_s_at	VDAC1	5.53691
CDL/PE	217949_s_at	VKORC1	5.53684
CDL/PE	208998_at	UCP2	5.51829
CDL/PE	201966_at	NDUFS2	5.4909
CDL/PE	209066_x_at	UQCRB	5.49073
CDL/PE	202298_at	NDUFA1	5.48698
CDL/PE	217874_at	SUCLG1	5.47869
CDL/PE	203190_at	NDUFS8	5.46842
CDL/PE	221311_x_at	DJ122O8.2	5.4674
CDL/PE	203465_at	MRPL19	5.45744
CDL/PE	202090_s_at	UQCR	5.43746
CDL/PE	213149_at	DLD	5.4196
CDL/PE	211755_s_at	ATP5F1	5.41378

CDL/PE	209512_at	HSDL2	5.4106
CDL/PE	320_at	PEX6	5.40459
CDL/PE	208956_x_at	DUT	5.39313
CDL/PE	204179_at	MB	5.37104
CDL/PE	201134_x_at	COX7C	5.36631
CDL/PE	202929_s_at	DDT	5.34804
CDL/PE	202596_at	ENSA	5.29692
CDL/PE	208972_s_at	ATP5G1	5.27146
CDL/PE	202502_at	ACADM	5.26622
CDL/PE	201035_s_at	HADHSC	5.25843
CDL/PE	203608_at	ALDH5A1	5.2567
CDL/PE	211855_s_at	SLC25A14	5.23562
CDL/PE	218392_x_at	SFXN1	5.22353
CDL/PE	218212_s_at	MOCS2	5.21545
CDL/PE	213846_at	COX7C	5.20715
CDL/PE	217356_s_at	PGK1	5.19513
CDL/PE	204386_s_at	MRP63	5.18829
CDL/PE	218570_at	KBTBD4	5.18628
CDL/PE	201403_s_at	MGST3	5.18033
CDL/PE	201931_at	ETFA	5.17684
CDL/PE	208907_s_at	MRPS18B	5.16993
CDL/PE	201816_s_at	GBAS	5.1694
CDL/PE	222216_s_at	MRPL17	5.12853
CDL/PE	203032_s_at	FH	5.12455
CDL/PE	211733_x_at	SCP2	5.10087
CDL/PE	209513_s_at	HSDL2	5.09824
CDL/PE	216591_s_at	SDHC	5.07941

CDL/PE	219162_s_at	MRPL11	5.05494
CDL/PE	214431_at	GMPS	5.05144
CDL/PE	201612_at	ALDH9A1	5.04746
CDL/PE	208881_x_at	IDI1	5.04267
CDL/PE	201463_s_at	TALDO1	5.04027
CDL/PE	201956_s_at	GNPAT	5.02542
CDL/PE	208745_at	ATP5L	5.022
CDL/PE	201717_at	MRPL49	5.0101
CDL/PE	218536_at	MRS2L	4.99842
CDL/PE	200883_at	UQCRC2	4.99646
CDL/PE	202338_at	TK1	4.96768
CDL/PE	218357_s_at	TIMM8B	4.95827
CDL/PE	208847_s_at	ADH5	4.9487
CDL/PE	218025_s_at	PECI	4.94539
CDL/PE	211576_s_at	SLC19A1	4.93948
CDL/PE	202125_s_at	ALS2CR3	4.92749
CDL/PE	213738_s_at	ATP5A1	4.89749
CDL/PE	212568_s_at	DLAT	4.88132
CDL/PE	200961_at	SEPHS2	4.87968
CDL/PE	201275_at	FDPS	4.8749
CDL/PE	201066_at	CYC1	4.87473
CDL/PE	201036_s_at	HADHSC	4.85339
CDL/PE	201226_at	NDUFB8	4.84149
CDL/PE	217773_s_at	NDUFA4	4.83543
CDL/PE	218111_s_at	CMAS	4.8331
CDL/PE	209608_s_at	ACAT2	4.82997

CDL/PE	219547_at	COX15	4.82312
CDL/PE	200980_s_at	PDHA1	4.82294
CDL/PE	203008_x_at	TXNDC9	4.81456
CDL/PE	202322_s_at	GGPS1	4.79853
CDL/PE	201707_at	PEX19	4.7977
CDL/PE	203633_at	CPT1A	4.79486
CDL/PE	203517_at	MTX2	4.7894
CDL/PE	217980_s_at	MRPL16	4.78651
CDL/PE	211758_x_at	TXNDC9	4.77316
CDL/PE	214864_s_at	GRHPR	4.75199
CDL/PE	203228_at	PAFAH1B3	4.74941
CDL/PE	203458_at	SPR	4.73813
CDL/PE	203039_s_at	NDUFS1	4.73803
CDL/PE	217956_s_at	MASA	4.73069
CDL/PE	218440_at	MCCC1	4.72114
CDL/PE	219553_at	NME7	4.70644
CDL/PE	200982_s_at	ANXA6	4.70606
CDL/PE	210589_s_at	GBA	4.69109
CDL/PE	205849_s_at	UQCRB	4.67962
CDL/PE	218421_at	CERK	4.64475
CDL/PE	208764_s_at	ATP5G2	4.62834
CDL/PE	202735_at	EBP	4.61414
CDL/PE	213787_s_at	EBP	4.60925
CDL/PE	209077_at	TXN2	4.60654
CDL/PE	204615_x_at	IDI1	4.58037
CDL/PE	218168_s_at	CABC1	4.57854

CDL/PE	208717_at	OXA1L	4.57341
CDL/PE	219080_s_at	CTPS2	4.57126
CDL/PE	213129_s_at	GCSH	4.56841
CDL/PE	218890_x_at	MRPL35	4.56196
CDL/PE	216574_s_at	RPE	4.55979
CDL/PE	218988_at	SLC35E3	4.5569
CDL/PE	204160_s_at	ENPP4	4.55661
CDL/PE	202698_x_at	COX4I1	4.53744
CDL/PE	201634_s_at	CYB5-M	4.53312
CDL/PE	217491_x_at	COX7C	4.5318
CDL/PE	200642_at	SOD1	4.52906
CDL/PE	201706_s_at	PEX19	4.52896
CDL/PE	200925_at	COX6A1	4.5264
CDL/PE	201093_x_at	SDHA	4.51236
CDL/PE	209600_s_at	ACOX1	4.51209
CDL/PE	201014_s_at	PAICS	4.50623
CDL/PE	218112_at	MRPS34	4.49778
CDL/PE	202812_at	GAA	4.49139
CDL/PE	212461_at	OAZIN	4.48542
CDL/PE	221909_at	FLJ14627	4.48198
CDL/PE	203031_s_at	UROS	4.48036
CDL/PE	202831_at	GPX2	4.47156
CDL/PE	212145_at	MRPS27	4.46495
CDL/PE	212604_at	MRPS31	4.44918
CDL/PE	218671_s_at	ATPIF1	4.44572
CDL/PE	207335_x_at	ATP5I	4.44359

CDL/PE	218557_at	NIT2	4.43301
CDL/PE	215695_s_at	GYG2	4.43278
CDL/PE	217776_at	RDH11	4.43099
CDL/PE	202144_s_at	ADSL	4.42838
CDL/PE	205012_s_at	HAGH	4.42813
CDL/PE	201569_s_at	CGI-51	4.4147
CDL/PE	218563_at	NDUFA3	4.41184
CDL/PE	214830_at	SLC38A6	4.40571
CDL/PE	202856_s_at	SLC16A3	4.39645
CDL/PE	200657_at	SLC25A5	4.39494
CDL/PE	201347_x_at	GRHPR	4.39393
CDL/PE	218408_at	TIMM10	4.38764
CDL/PE	211658_at	PRDX2	4.38176
CDL/PE	208845_at	VDAC3	4.38026
CDL/PE	203192_at	ABCB6	4.37056
CDL/PE	203832_at	ENO1 /// SNRPF	4.36891
CDL/PE	211727_s_at	COX11	4.36338
CDL/PE	203116_s_at	FECH	4.3561
CDL/PE	210820_x_at	COQ7	4.34379
CDL/PE	201818_at	FLJ12443	4.33402
CDL/PE	202675_at	SDHB	4.31931
CDL/PE	209492_x_at	ATP5I	4.30994
CDL/PE	220741_s_at	PPA2	4.30049
CDL/PE	201923_at	PRDX4	4.28483
CDL/PE	204300_at	PET112L	4.27924
CDL/PE	208700_s_at	TKT	4.27649

CDL/PE	217932_at	MRPS7	4.27467
CDL/PE	208787_at	MRPL3	4.25503
CDL/PE	221589_s_at	ALDH6A1	4.25332
CDL/PE	209836_x_at	LAT1-3TM	4.25134
CDL/PE	204788_s_at	PPOX	4.24924
CDL/PE	212038_s_at	VDAC1	4.23098
CDL/PE	212213_x_at	OPA1	4.22968
CDL/PE	219401_at	XYLT2	4.22299
CDL/PE	216308_x_at	GRHPR	4.21926
CDL/PE	218609_s_at	NUDT2	4.21533
CDL/PE	202053_s_at	ALDH3A2	4.21423
CDL/PE	219055_at	FLJ10379	4.20338
CDL/PE	209078_s_at	TXN2	4.20235
CDL/PE	212198_s_at	TM9SF4	4.20202
CDL/PE	208714_at	NDUFV1	4.196
CDL/PE	202026_at	SDHD	4.19114
CDL/PE	204942_s_at	ALDH3B2	4.17863
CDL/PE	203551_s_at	COX11	4.16862
CDL/PE	209275_s_at	CLN3	4.15634
CDL/PE	202593_s_at	MIR16	4.15356
CDL/PE	217294_s_at	ENO1	4.15326
CDL/PE	209380_s_at	ABCC5	4.1432
CDL/PE	213333_at	MDH2	4.14275
CDL/PE	213333_at	MDH2	4.14275
CDL/PE	208909_at	UQCRFS1	4.13653
CDL/PE	200831_s_at	SCD	4.1262

CDL/PE	212449_s_at	LYPLA1	4.1216
CDL/PE	217942_at	MRPS35	4.10413
CDL/PE	212322_at	SGPL1	4.09203
CDL/PE	201597_at	COX7A2	4.08596
CDL/PE	218118_s_at	TIMM23	4.07447
CDL/PE	218200_s_at	NDUFB2	4.07154
CDL/PE	211594_s_at	MRPL9	4.06981
CDL/PE	211275_s_at	GYG	4.03767
CDL/PE	221024_s_at	SLC2A10	4.01948
CDL/PE	221437_s_at	MRPS15	3.98776
CDL/PE	201576_s_at	GLB1	3.98717
CDL/PE	218547_at	DHDDS	3.98179
CDL/PE	209218_at	SQLE	3.96931
CDL/PE	208817_at	COMT	3.95891
CDL/PE	212083_at	TEX261	3.95125
CDL/PE	203774_at	MTR	3.94506
CDL/PE	202706_s_at	UMPS	3.93836
CDL/PE	202471_s_at	IDH3G	3.93659
CDL/PE	209522_s_at	CRAT	3.93456
CDL/PE	203067_at	PDHX	3.92396
CDL/PE	203880_at	COX17	3.90896
CDL/PE	203663_s_at	COX5A	3.90111
CDL/PE	210250_x_at	ADSL	3.89683
CDL/PE	205851_at	NME6	3.89226
CDL/PE	203478_at	NDUFC1	3.87903
CDL/PE	217408_at	MRPS18B	3.87823

CDL/PE	202054_s_at	ALDH3A2	3.87425
CDL/PE	204067_at	SUOX	3.87375
CDL/PE	201106_at	GPX4	3.86668
CDL/PE	206348_s_at	PDK3	3.86451
CDL/PE	202785_at	NDUFA7	3.84554
CDL/PE	221927_s_at	ABHD11	3.8452
CDL/PE	219076_s_at	PXMP2	3.84026
CDL/PE	218027_at	MRPL15	3.83116
CDL/PE	218101_s_at	NDUFC2	3.82931
CDL/PE	213106_at	ATP8A1	3.82693
CDL/PE	200086_s_at	COX4I1	3.82303
CDL/PE	218316_at	TIMM9	3.81526
CDL/PE	202908_at	WFS1	3.80852
CDL/PE	203040_s_at	HMBS	3.8012
CDL/PE	207332_s_at	TFRC	3.78436
CDL/PE	209094_at	DDAH1	3.76539
CDL/PE	200903_s_at	AHCY	3.76207
CDL/PE	209426_s_at	AMACR	3.74654
CDL/PE	202279_at	C14orf2	3.73983
CDL/PE	33646_g_at	GM2A	3.73729
CDL/PE	208997_s_at	UCP2	3.72751
CDL/PE	204282_s_at	FARS2	3.72055
CDL/PE	217846_at	QARS	3.69998
CDL/PE	218433_at	PANK3	3.69013
CDL/PE	202017_at	EPHX1	3.68973
CDL/PE	218339_at	MRPL22	3.6799

CDL/PE	209609_s_at	MRPL9	3.67951
CDL/PE	221585_at	CACNG4	3.65956
CDL/PE	202024_at	ASNA1	3.64948
CDL/PE	203152_at	MRPL40	3.64715
CDL/PE	201682_at	PMPCB	3.64288
CDL/PE	203974_at	HDHD1A	3.63431
CDL/PE	219220_x_at	MRPS22	3.62761
CDL/PE	209473_at	ENTPD1	3.62065
CDL/PE	211150_s_at	DLAT	3.62002
CDL/PE	202282_at	HADH2	3.61773
CDL/PE	201349_at	SLC9A3R1	3.61423
CDL/PE	208818_s_at	COMT	3.59483
CDL/PE	218773_s_at	MSRB2	3.59282
CDL/PE	203634_s_at	CPT1A	3.5859
CDL/PE	217990_at	GMPR2	3.58535
CDL/PE	202591_s_at	SSBP1	3.58495
CDL/PE	57588_at	SLC24A3	3.57886
CDL/PE	202651_at	LPGAT1	3.57628
CDL/PE	213897_s_at	MRPL23	3.56797
CDL/PE	203095_at	MTIF2	3.56783
CDL/PE	204044_at	QPRT	3.55894
CDL/PE	202382_s_at	GNPDA1	3.55891
CDL/PE	200832_s_at	SCD	3.5362
CDL/PE	201757_at	NDUFS5	3.52544
CDL/PE	209746_s_at	COQ7	3.52506
CDL/PE	218592_s_at	CECR5	3.52321
CDL/PE	204295_at	SURF1	3.52144

CDL/PE	202139_at	AKR7A2	3.51315
CDL/PE	214306_at	OPA1	3.50174
CDL/PE	203433_at	MTHFS	3.49831
CDL/PE	202447_at	DECR1	3.49795
CDL/PE	218320_s_at	NDUFB11	3.48636
CDL/PE	203672_x_at	TPMT	3.48145
CDL/PE	213835_x_at	GTPBP3	3.48008
CDL/PE	203335_at	PHYH	3.47716
CDL/PE	205260_s_at	ACYP1	3.4736
CDL/PE	212814_at	KIAA0828	3.46532
CDL/PE	209279_s_at	NSDHL	3.45276
CDL/PE	211752_s_at	NDUFS7	3.44301
CDL/PE	221692_s_at	MRPL34	3.44045
CDL/PE	202950_at	CRYZ	3.43978
CDL/PE	218558_s_at	MRPL39	3.42189
CDL/PE	201256_at	COX7A2L	3.41696
Luminal CDL	212510_at	GPD1L	-9.0625
Luminal CDL	204942_s_at	ALDH3B2	-8.8636
Luminal CDL	203963_at	CA12	-8.6304
Luminal CDL	204508_s_at	CA12	-8.2544
Luminal CDL	209164_s_at	CYB561	-8.1569
Luminal CDL	209696_at	FBP1	-8.0299
Luminal CDL	215867_x_at	CA12	-7.7363
Luminal CDL	221589_s_at	ALDH6A1	-7.4612
Luminal CDL	214164_x_at	CA12	-7.395
Luminal CDL	221927_s_at	ABHD11	-7.3634

Luminal CDL	204862_s_at	NME3	-7.248
Luminal CDL	204290_s_at	ALDH6A1	-7.2004
Luminal CDL	207522_s_at	ATP2A3	-7.0913
Luminal CDL	217973_at	DCXR	-6.9356
Luminal CDL	209460_at	ABAT	-6.79
Luminal CDL	209163_at	CYB561	-6.6979
Luminal CDL	204067_at	SUOX	-6.6832
Luminal CDL	210859_x_at	CLN3	-6.588
Luminal CDL	209623_at	MCCC2	-6.5573
Luminal CDL	209275_s_at	CLN3	-6.4859
Luminal CDL	210735_s_at	CA12	-6.4327
Luminal CDL	208998_at	UCP2	-6.3503
Luminal CDL	221588_x_at	ALDH6A1	-6.3051
Luminal CDL	208997_s_at	UCP2	-6.1374
Luminal CDL	203773_x_at	BLVRA	-6.0564
Luminal CDL	203633_at	CPT1A	-5.9788
Luminal CDL	211729_x_at	BLVRA	-5.8555
Luminal CDL	215726_s_at	CYB5	-5.7751
Luminal CDL	209366_x_at	CYB5	-5.7671
Luminal CDL	207843_x_at	CYB5	-5.7443
Luminal CDL	214203_s_at	PRODH	-5.7376
Luminal CDL	202752_x_at	SLC7A8	-5.6971
Luminal CDL	216092_s_at	SLC7A8	-5.6288
Luminal CDL	218320_s_at	NDUFB11	-5.5474
Luminal CDL	209459_s_at	ABAT	-5.5374
Luminal CDL	213106_at	ATP8A1	-5.5256

Luminal CDL	204624_at	ATP7B	-5.4122
Luminal CDL	209624_s_at	MCCC2	-5.4102
Luminal CDL	203771_s_at	BLVRA	-5.3645
Luminal CDL	209224_s_at	NDUFA2	-5.3355
Luminal CDL	211552_s_at	ALDH4A1	-5.3171
Luminal CDL	202982_s_at	ZAP128	-5.272
Luminal CDL	220741_s_at	PPA2	-5.2444
Luminal CDL	204607_at	HMGCS2	-5.1335
Luminal CDL	208764_s_at	ATP5G2	-5.1151
Luminal CDL	203478_at	NDUFC1	-4.9587
Luminal CDL	200925_at	COX6A1	-4.9512
Luminal CDL	212053_at	KIAA0251	-4.8791
Luminal CDL	203342_at	TIMM17B	-4.8565
Luminal CDL	203115_at	FECH	-4.8198
Luminal CDL	201754_at	COX6C	-4.791
Luminal CDL	210980_s_at	ASAH1	-4.779
Luminal CDL	203515_s_at	PMVK	-4.7779
Luminal CDL	219080_s_at	CTPS2	-4.7412
Luminal CDL	218021_at	DHRS4	-4.7099
Luminal CDL	212560_at	SORL1	-4.672
Luminal CDL	204941_s_at	ALDH3B2	-4.6423
Luminal CDL	213702_x_at	ASAH1	-4.633
Luminal CDL	203722_at	ALDH4A1	-4.6165
Luminal CDL	203634_s_at	CPT1A	-4.5663
Luminal CDL	208817_at	COMT	-4.5463
Luminal CDL	210045_at	IDH2	-4.5293

Luminal CDL	206043_s_at	KIAA0703	-4.5005
Luminal CDL	208818_s_at	COMT	-4.4787
Luminal CDL	218563_at	NDUFA3	-4.4693
Luminal CDL	218164_at	SSP411	-4.4302
Luminal CDL	213042_s_at	ATP2A3	-4.4241
Luminal CDL	206754_s_at	CYP2B6	-4.4218
Luminal CDL	211569_s_at	HADHSC	-4.4152
Luminal CDL	209600_s_at	ACOX1	-4.3994
Luminal CDL	209919_x_at	GGT1	-4.3172
Luminal CDL	211417_x_at	GGT1	-4.268
Luminal CDL	219429_at	FA2H	-4.2593
Luminal CDL	205770_at	GSR	-4.255
Luminal CDL	205012_s_at	HAGH	-4.2469
Luminal CDL	215603_x_at	GGT1 /// GGTL4	-4.24
Luminal CDL	209522_s_at	CRAT	-4.2225
Luminal CDL	205355_at	ACADSB	-4.2177
Luminal CDL	204231_s_at	FAAH	-4.2064
Luminal CDL	210688_s_at	CPT1A	-4.1697
Luminal CDL	211715_s_at	BDH	-4.1624
Luminal CDL	219664_s_at	DECR2	-4.1619
Luminal CDL	210816_s_at	CYB561	-4.1344
Luminal CDL	209916_at	DHTKD1	-4.1314
Luminal CDL	201525_at	APOD	-4.126
Luminal CDL	204867_at	GCHFR	-4.1136
Luminal CDL	207131_x_at	GGT1	-4.1131
Luminal CDL	205709_s_at	CDS1	-4.1071

Luminal CDL	201036_s_at	HADHSC	-4.0907
Luminal CDL	204295_at	SURF1	-4.0768
Luminal CDL	202712_s_at	CKMT1	-4.0655
Luminal CDL	217491_x_at	COX7C	-4.0479
Luminal CDL	218025_s_at	PECI	-4.0451
Luminal CDL	213501_at	ACOX1	-4.0329
Luminal CDL	205066_s_at	ENPP1	-3.9994
Luminal CDL	200966_x_at	ALDOA	-3.9884
Luminal CDL	222217_s_at	SLC27A3	-3.9593
Luminal CDL	213540_at	HSD17B8	-3.9269
Luminal CDL	218773_s_at	MSRB2	-3.9203
Luminal CDL	208284_x_at	GGT1	-3.9095
Luminal CDL	215695_s_at	GYG2	-3.9086
Luminal CDL	214687_x_at	ALDOA	-3.8994
Luminal CDL	201134_x_at	COX7C	-3.8804
Luminal CDL	216381_x_at	AKR7A3	-3.8267
Luminal CDL	203116_s_at	FECH	-3.8235
Luminal CDL	201612_at	ALDH9A1	-3.8102
Luminal CDL	212062_at	ATP9A	-3.8023
Luminal CDL	205843_x_at	CRAT	-3.7921
Luminal CDL	210272_at	CYP2B6	-3.7806
Luminal CDL	218190_s_at	HSPC051	-3.7694
Luminal CDL	212656_at	TSFM	-3.7556
Luminal CDL	212772_s_at	ABCA2	-3.7402
Luminal CDL	202590_s_at	PDK2	-3.7368
Luminal CDL	215299_x_at	SULT1A1	-3.7017

Luminal CDL	203509_at	SORL1	-3.6966
Luminal CDL	201966_at	NDUFS2	-3.6583
Luminal CDL	210046_s_at	IDH2	-3.6325
Luminal CDL	217942_at	MRPS35	-3.632
Luminal CDL	210010_s_at	SLC25A1	-3.6242
Luminal CDL	218760_at	COQ6	-3.6127
Luminal CDL	213846_at	COX7C	-3.6069
Luminal CDL	203767_s_at	STS	-3.6056
Luminal CDL	216591_s_at	SDHC	-3.593
Luminal CDL	218844_at	FLJ20920	-3.5739
Luminal CDL	201568_at	QP-C	-3.5521
Luminal CDL	203768_s_at	STS	-3.5413
Luminal CDL	204717_s_at	SLC29A2	-3.5405
Luminal CDL	204788_s_at	PPOX	-3.4988
Luminal CDL	202263_at	NQO3A2	-3.4949
Luminal CDL	209531_at	GSTZ1	-3.4903
Luminal CDL	203615_x_at	SULT1A1	-3.4461
Luminal CDL	202862_at	FAH	-3.4457
Luminal CDL	218985_at	SLC2A8	-3.4393
Luminal CDL	219722_s_at	MGC4171	-3.4372
Luminal CDL	209221_s_at	OSBPL2	-3.4265
Luminal CDL	214082_at	CA5B	-3.3894
Luminal CDL	201304_at	NDUFA5	-3.3821
Luminal CDL	206790_s_at	NDUFB1	-3.3787
Luminal CDL	205073_at	CYP2J2	-3.3785
Luminal CDL	218988_at	SLC35E3	-3.3605

Luminal CDL	203769_s_at	STS	-3.3564
Luminal CDL	204305_at	MIPEP	-3.3561
Luminal CDL	202282_at	HADH2	-3.3487
Luminal CDL	203458_at	SPR	-3.3468
Luminal CDL	212322_at	SGPL1	-3.3274
Luminal CDL	201425_at	ALDH2	-3.3148
Luminal CDL	204573_at	CROT	-3.3032
Luminal CDL	218112_at	MRPS34	-3.3029
Luminal CDL	218688_at	DKFZP586B1621	-3.2871
Luminal CDL	207122_x_at	SULT1A2	-3.2835
Luminal CDL	202004_x_at	SDHC	-3.2761
Luminal CDL	201035_s_at	HADHSC	-3.2748
Luminal CDL	218275_at	SLC25A10	-3.2599
Luminal CDL	205759_s_at	SULT2B1	-3.2598
Luminal CDL	216958_s_at	IVD	-3.2472
Luminal CDL	215088_s_at	SDHC	-3.2448
Luminal CDL	36830_at	MIPEP	-3.2433
Luminal CDL	206469_x_at	AKR7A3	-3.2199
Luminal CDL	222275_at	MRPS30	-3.217
Luminal CDL	211385_x_at	SULT1A2	-3.2106
Luminal CDL	214079_at	DHRS2	-3.2039
Luminal CDL	202554_s_at	GSTM3	-3.2011
Luminal CDL	220753_s_at	CRYL1	-3.1957
Luminal CDL	214243_s_at	SERHL /// dJ222E13.1	-3.1893
Luminal CDL	202593_s_at	MIR16	-3.1812
Luminal CDL	203770_s_at	STS	-3.1768

Luminal CDL	221908_at	FLJ14627	-3.154
Luminal CDL	203682_s_at	IVD	-3.1539
Luminal CDL	206463_s_at	DHRS2	-3.1327
Luminal CDL	203576_at	BCAT2	-3.124
Luminal CDL	215794_x_at	GLUD2	-3.106
Luminal CDL	215794_x_at	GLUD2	-3.106
Luminal CDL	207521_s_at	ATP2A3	-3.0957
Luminal CDL	203974_at	HDHD1A	-3.0884
Luminal CDL	209605_at	TST	-3.085
Luminal CDL	217773_s_at	NDUFA4	-3.0848
Luminal CDL	200697_at	HK1	-3.068
Luminal CDL	218570_at	KBTBD4	-3.0645
Luminal CDL	203814_s_at	NQO2	-3.0516
Luminal CDL	200789_at	ECH1	-3.0487
Luminal CDL	218212_s_at	MOCS2	-3.0271
Luminal CDL	201413_at	HSD17B4	-3.0077
Luminal CDL	210149_s_at	ATP5H	-2.9798
Luminal CDL	210246_s_at	ABCC8	-2.961
Luminal CDL	219547_at	COX15	-2.9301
Luminal CDL	201931_at	ETFA	-2.913
Luminal CDL	218569_s_at	KBTBD4	-2.9062
Luminal CDL	218226_s_at	NDUFB4	-2.9061
Luminal CDL	200947_s_at	GLUD1	-2.8894
Luminal CDL	200947_s_at	GLUD1	-2.8894
Luminal CDL	201119_s_at	COX8A	-2.88
Luminal CDL	218840_s_at	NADSYN1	-2.8682

Luminal CDL	202959_at	MUT	-2.8633
Luminal CDL	221909_at	FLJ14627	-2.8473
Luminal CDL	206753_at	RODH-4	-2.8324
Luminal CDL	203800_s_at	MRPS14	-2.8294
Luminal CDL	208972_s_at	ATP5G1	-2.8264
Luminal CDL	201135_at	ECHS1	-2.8262
Luminal CDL	202025_x_at	ACAA1	-2.8199
Luminal CDL	202275_at	G6PD	-2.8065
Luminal CDL	205776_at	FMO5	-2.7864
Luminal CDL	201661_s_at	ACSL3	-2.7824
Luminal CDL	202532_s_at	DHFR	-2.7746
Luminal CDL	205851_at	NME6	-2.766
Luminal CDL	204824_at	ENDOG	-2.7516
Luminal CDL	206527_at	ABAT	-2.7407
Luminal CDL	221139_s_at	CSAD	-2.7278
Luminal CDL	204224_s_at	GCH1	-2.7207
Luminal CDL	207335_x_at	ATP5I	-2.7166
Luminal CDL	201102_s_at	PFKL	-2.7016
Luminal CDL	201339_s_at	SCP2	-2.7014
Luminal CDL	200946_x_at	GLUD1	-2.6974
Luminal CDL	200946_x_at	GLUD1	-2.6974
Luminal CDL	208291_s_at	TH	-2.6938
Luminal CDL	211065_x_at	PFKL	-2.685
Luminal CDL	217801_at	ATP5E	-2.6761
Luminal CDL	213333_at	MDH2	-2.6652
Luminal CDL	213333_at	MDH2	-2.6652

Luminal CDL	201403_s_at	MGST3	-2.6614
Luminal CDL	201919_at	FLJ10618	-2.6539
Luminal CDL	206492_at	FHIT	-2.6512
Luminal CDL	209759_s_at	DCI	-2.6488
Luminal CDL	204509_at	CA12	-2.6442
Luminal CDL	209607_x_at	SULT1A3	-2.641
Luminal CDL	217990_at	GMPR2	-2.6399
Luminal CDL	202365_at	MGC5139	-2.6286
Luminal CDL	203190_at	NDUFS8	-2.6265
Luminal CDL	209492_x_at	ATP5I	-2.6211
Luminal CDL	211177_s_at	TXNRD2	-2.6181
Luminal CDL	201619_at	PRDX3	-2.6047
Luminal CDL	202077_at	NDUFAB1	-2.6005
Luminal CDL	217874_at	SUCLG1	-2.5918
Luminal CDL	201900_s_at	AKR1A1	-2.5874
Luminal CDL	213724_s_at	PDK2	-2.5839
Luminal CDL	218101_s_at	NDUFC2	-2.5736
N/I	220346_at	MTHFD2L	-10.052
N/I	205676_at	CYP27B1	-9.5463
N/I	215078_at	SOD2	-8.8738
N/I	205844_at	VNN1	-7.1319
N/I	204257_at	FADS3	-6.975
N/I	209453_at	SLC9A1	-6.7676
N/I	212741_at	MAOA	-6.7093
N/I	210852_s_at	AASS	-6.4098
N/I	202804_at	ABCC1	-6.406

N/I	219357_at	GTPBP1	-6.3769
N/I	217546_at	MT1K	-6.3576
N/I	204745_x_at	MT1G	-6.2491
N/I	207604_s_at	SLC4A7	-6.2477
N/I	219597_s_at	DUOX1	-6.1868
N/I	216841_s_at	SOD2	-6.0407
N/I	204294_at	AMT	-6.0315
N/I	32091_at	KIAA0446	-5.7938
N/I	202237_at	NNMT	-5.7455
N/I	219181_at	LIPG	-5.5709
N/I	207064_s_at	AOC2	-5.5279
N/I	210876_at	ANXA2	-5.361
N/I	215223_s_at	SOD2	-5.3157
N/I	204570_at	COX7A1	-5.2784
N/I	202235_at	SLC16A1	-5.275
N/I	203234_at	UPP1	-5.2737
N/I	207992_s_at	AMPD3	-5.2548
N/I	202679_at	NPC1	-5.2471
N/I	212110_at	SLC39A14	-5.219
N/I	218717_s_at	LEPREL1	-5.1995
N/I	202422_s_at	ACSL4	-5.192
N/I	220232_at	SCD4	-5.1643
N/I	215082_at	ELOVL5	-5.1485
N/I	212859_x_at	MT1E	-5.1266
N/I	217165_x_at	MT1F	-5.1176
N/I	206461_x_at	MT1H	-5.0682

N/I	203158_s_at	GLS	-5.0599
N/I	213629_x_at	MT1F	-4.9972
N/I	218136_s_at	MSCP	-4.9927
N/I	202800_at	SLC1A3	-4.8789
N/I	218208_at	PQLC1	-4.8398
N/I	202392_s_at	PISD	-4.8308
N/I	220703_at	C10orf110	-4.8087
N/I	208118_x_at	LAT1-3TM /// IMAA /// LOC388221 /// LOC440345	-4.7757
N/I	200924_s_at	SLC3A2	-4.7233
N/I	220528_at	VNN3	-4.7089
N/I	202234_s_at	SLC16A1	-4.6823
N/I	208581_x_at	MT1X	-4.6066
N/I	205234_at	SLC16A4	-4.6057
N/I	204894_s_at	AOC3	-4.4972
N/I	209934_s_at	ATP2C1	-4.4734
N/I	213113_s_at	SLC43A3	-4.4679
N/I	201012_at	ANXA1	-4.4632
N/I	209369_at	ANXA3	-4.4421
N/I	200710_at	ACADVL	-4.4408
N/I	219489_s_at	NXN	-4.4022
N/I	207386_at	CYP7B1	-4.3709
N/I	203074_at	ANXA8	-4.3381
N/I	203157_s_at	GLS	-4.1904
N/I	209674_at	CRY1	-4.1775

N/I	206376_at	SLC6A15	-4.1535
N/I	204154_at	CDO1	-4.1468
N/I	213988_s_at	SAT	-4.119
N/I	219397_at	FLJ13448	-4.1121
N/I	201300_s_at	PRNP	-4.0997
N/I	214829_at	AASS	-4.0819
N/I	214241_at	NDUFB8	-4.0817
N/I	219558_at	ATP13A3	-4.044
N/I	209900_s_at	SLC16A1	-4.0364
N/I	214285_at	FABP3	-4.0128
N/I	213238_at	ATP10D	-4.0126
N/I	221432_s_at	SLC25A28	-3.9987
N/I	36566_at	CTNS	-3.9634
N/I	202854_at	HPRT1	-3.9484
N/I	209935_at	ATP2C1	-3.9398
N/I	203455_s_at	SAT	-3.928
N/I	215607_x_at	KIAA2010	-3.853
N/I	206628_at	SLC5A1	-3.8422
N/I	218739_at	ABHD5	-3.8342
N/I	210592_s_at	SAT	-3.831
N/I	212434_at	GRPEL1	-3.7959
N/I	221992_at	LOC283970	-3.7423
N/I	218552_at	ECHDC2	-3.7317
N/I	219532_at	ELOVL4	-3.6654
N/I	206867_at	"GCKR	-3.658
N/I	204326_x_at	MT1X	-3.6466
N/I	203180_at	ALDH1A3	-3.6241

N/I	204663_at	ME3	-3.6199
N/I	217395_at	MT4	-3.6017

bolism-associated transcripts identified from three significance analyses using the Timmerman_r

cinoma derived cell lines (CDL) and uncultured pleural effusions (PE).

merge dataset: