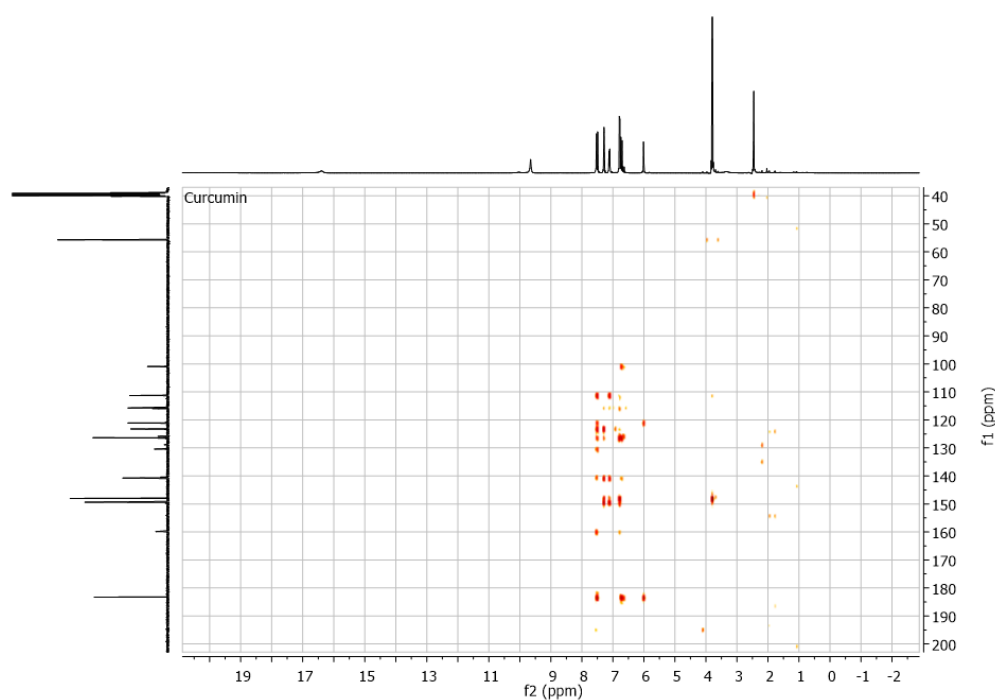


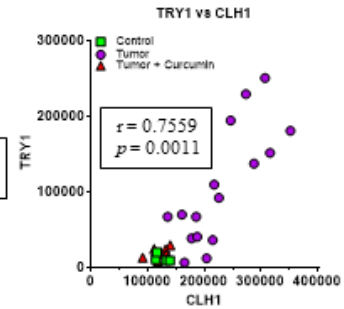
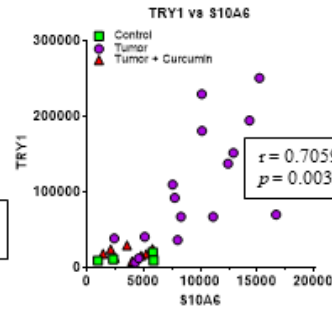
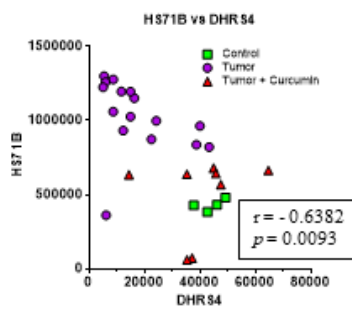
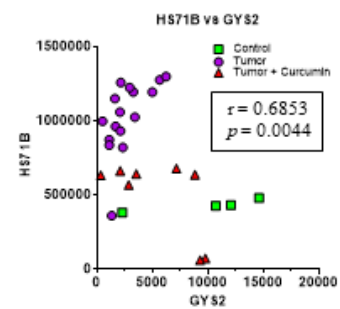
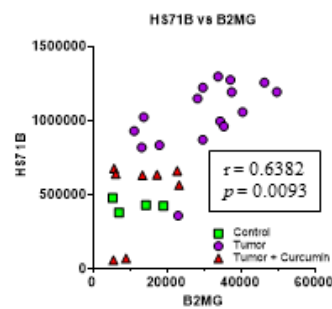
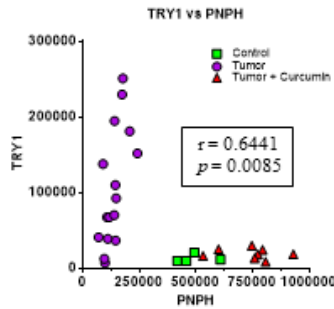
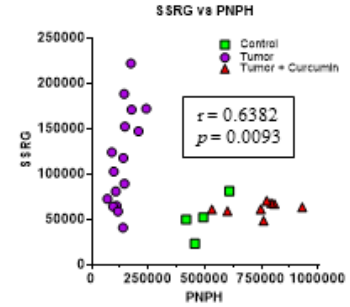
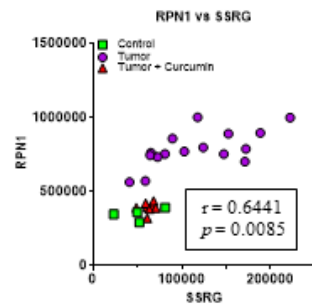
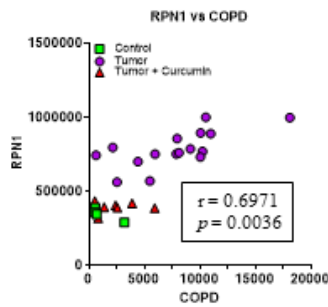
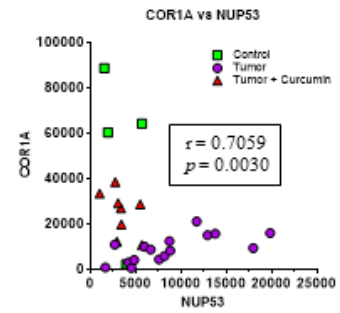
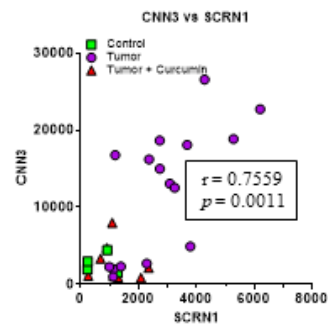
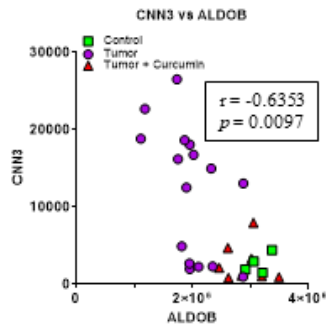
*Supplementary Materials*

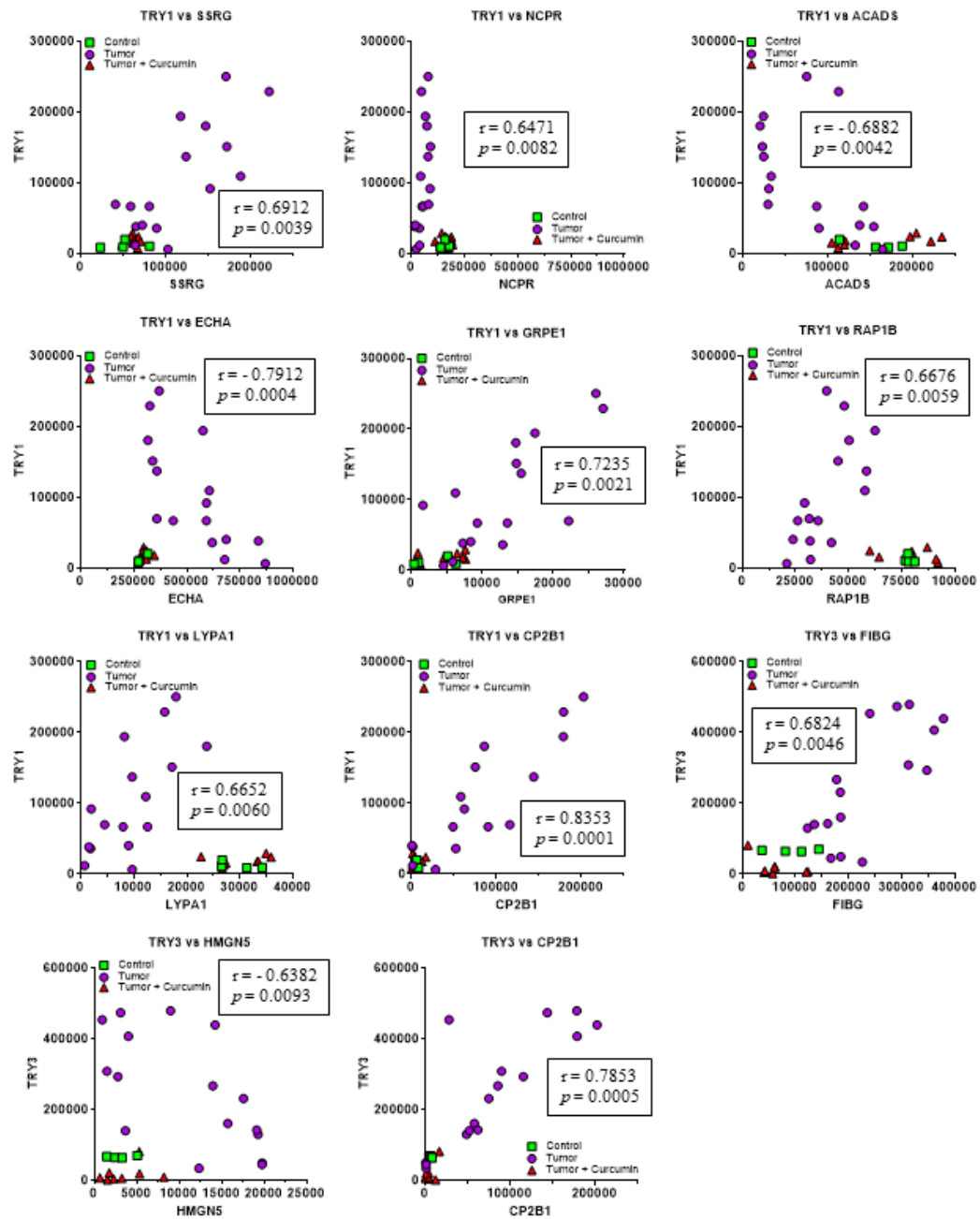
## Curcumin Treatment Identifies Therapeutic Targets within Biomarkers of Liver Colonization by Highly Invasive Mesothelioma Cells – Potential Links with Sarcomas

Daniel L. Pouliquen, Alice Boissard, Cécile Henry, Stéphanie Blandin, Pascal Richomme, Olivier Coqueret and Catherine Guette

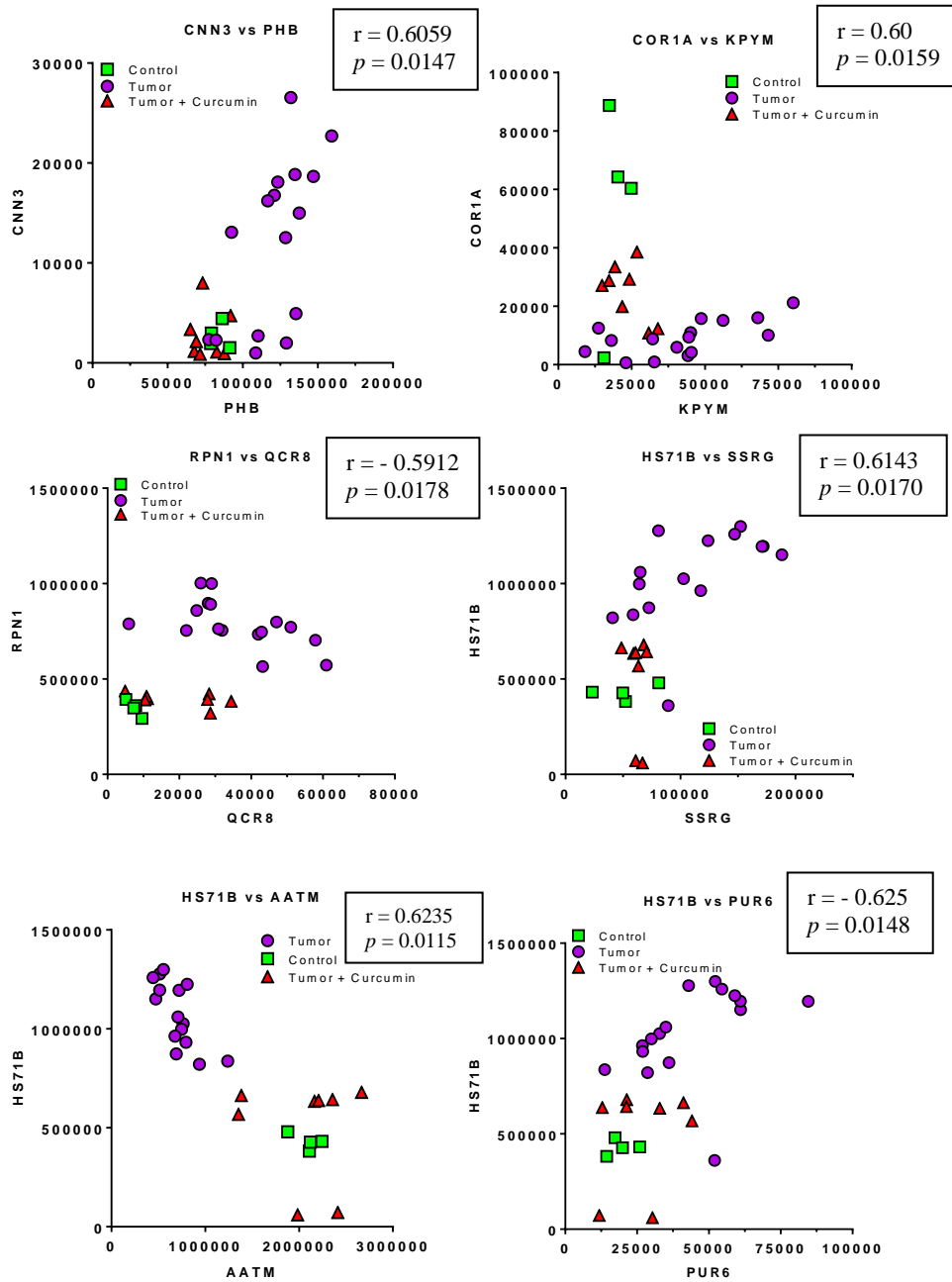


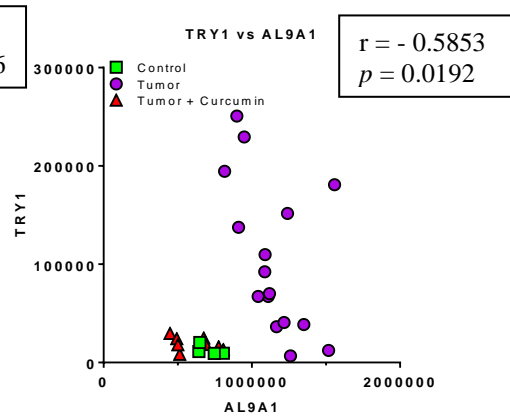
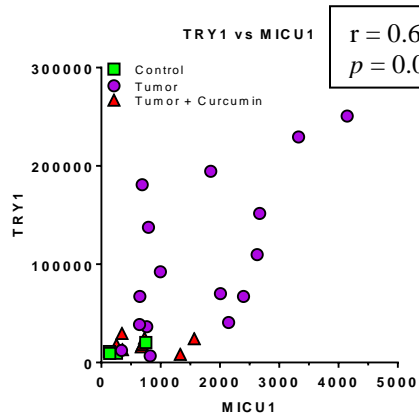
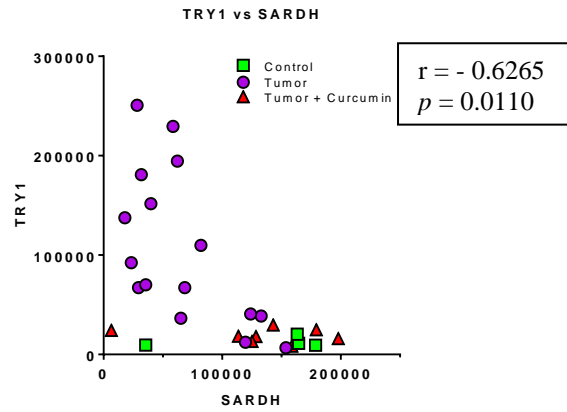
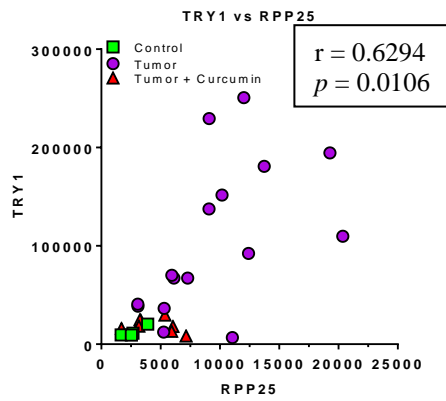
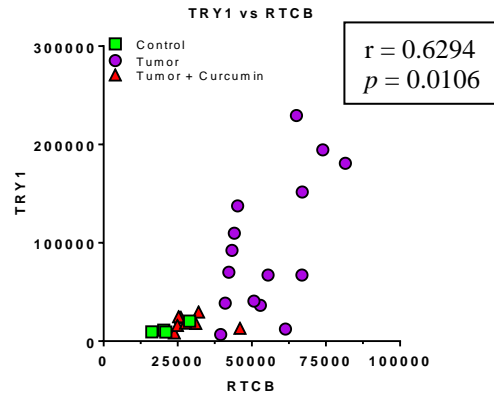
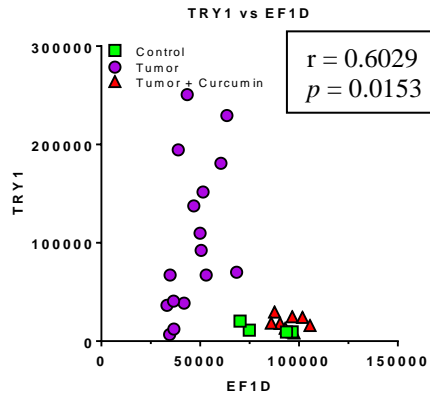
**Figure S1.** NMR spectra of the batch of curcumin used to treat the G3 group of rats. The 2D HMBC (<sup>1</sup>H observed heteronuclear long-range  $J_{HC}$  correlations) was run using the standard JEOL pulse sequence (hmbc.jxp, 32 scans) on a JEOL 400-MHz YH spectrometer at 298 K.

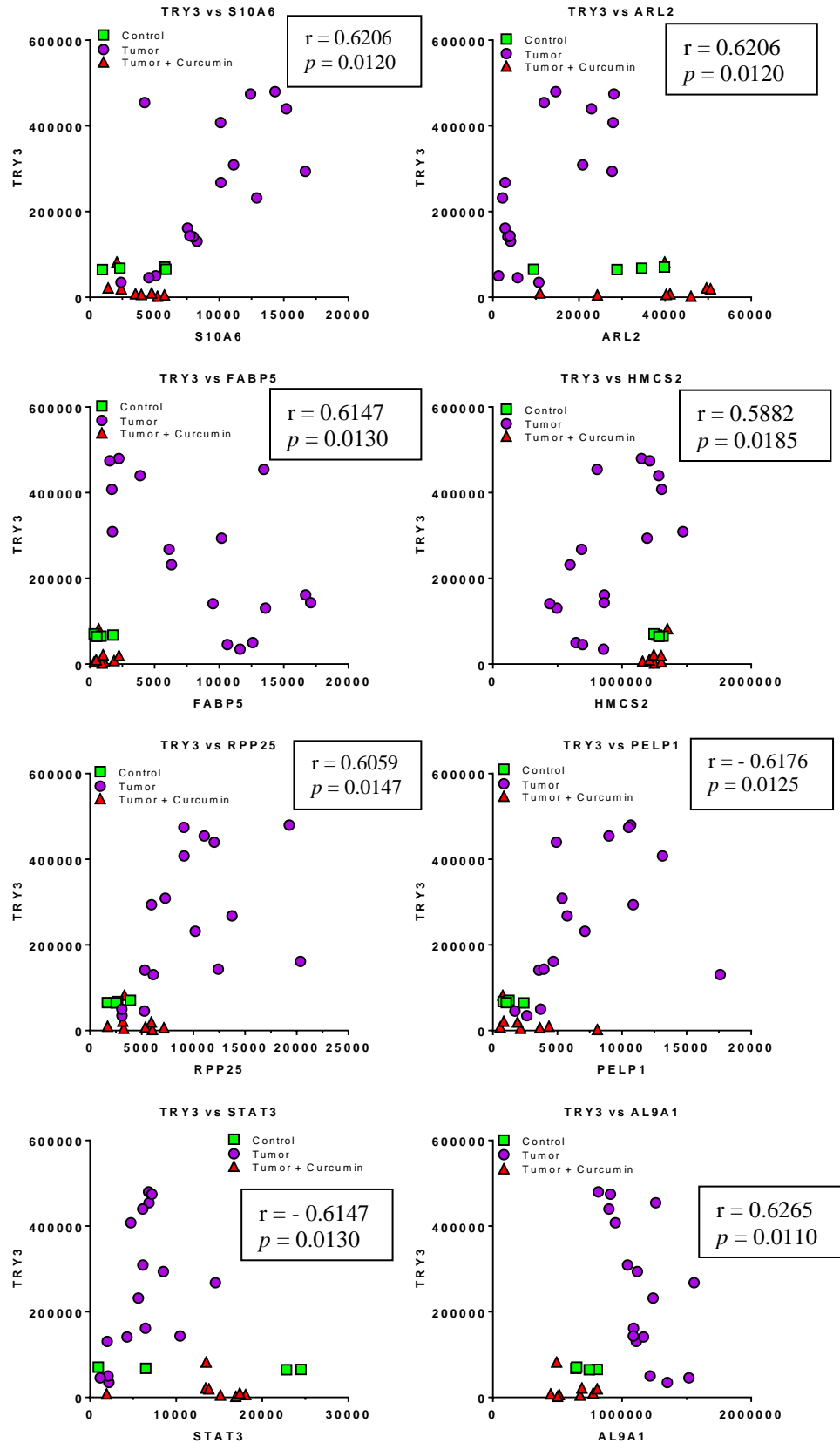




**Figure S2.** Correlation plots,  $p < 0.01$ . Correlations between biomarkers identified in sections 2.2.–2.4. and 2.5.  $p$ - and  $r$ -values obtained for statistical analysis using a Spearman's test (provided only for the group of untreated rats, purple open circles) are indicated in a rectangle in each figure.

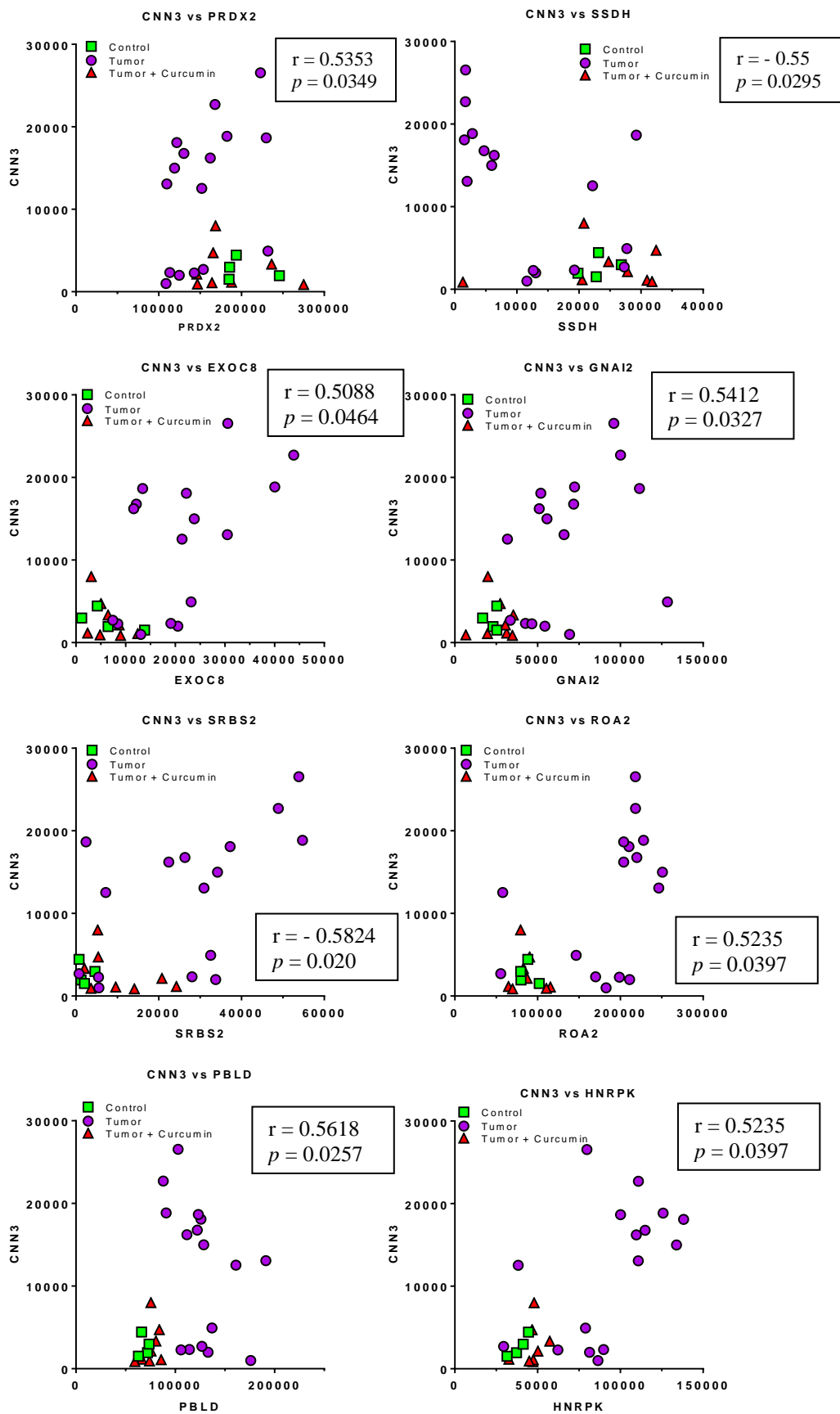




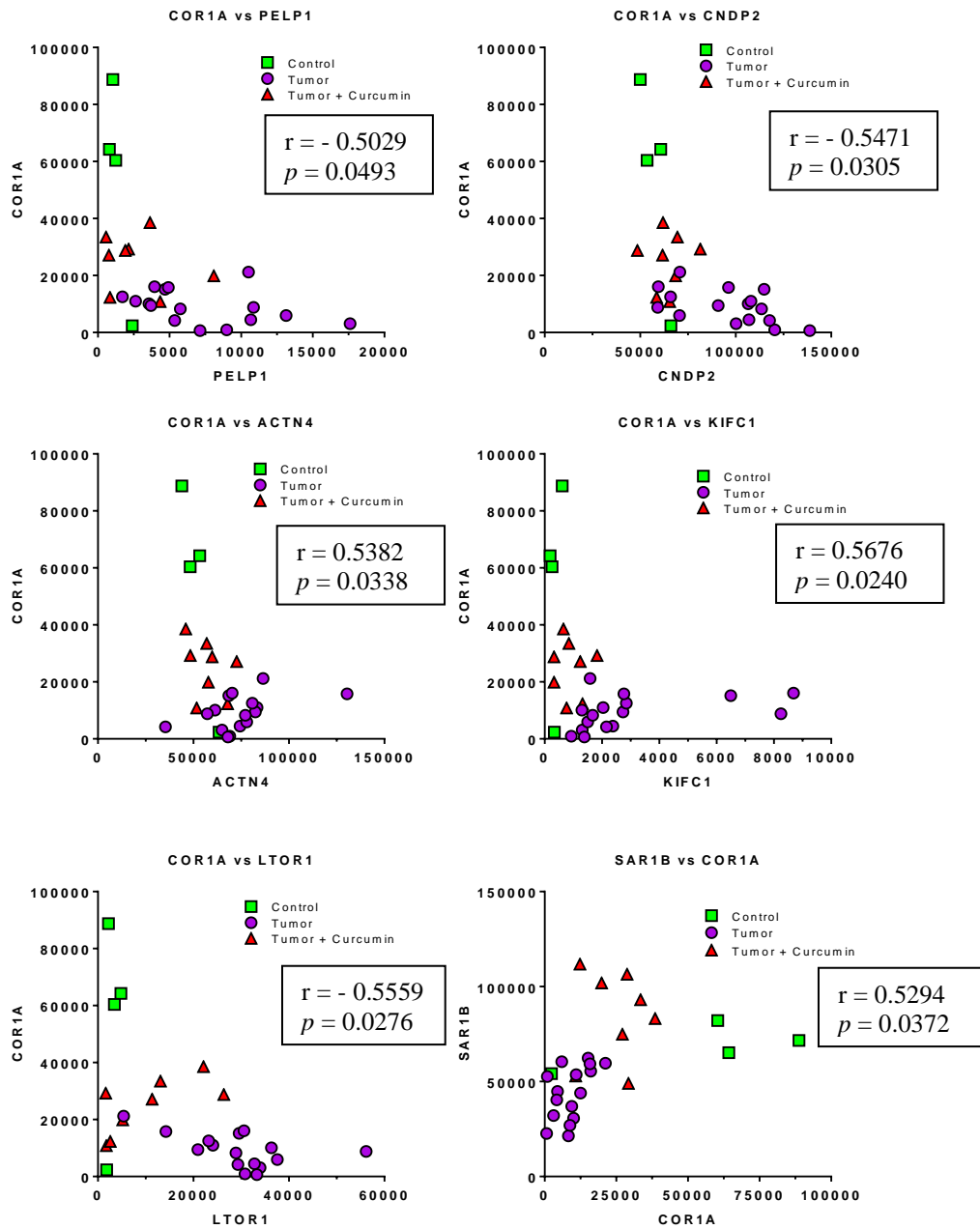


**Figure S3.** Correlation plots,  $0.01 < p < 0.02$ . Correlations between biomarkers identified in sections 2.2.–2.4. and 2.5.  $p$ - and  $r$ -values obtained for statistical analysis using a Spearman's test (provided only for the group of untreated rats, purple open circles) are indicated in a rectangle in each figure.

# (1) Correlations with CNN3

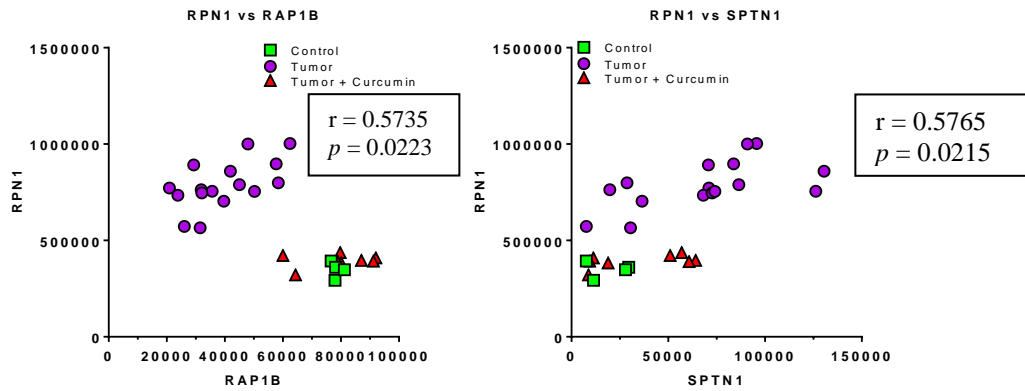


## (2) Correlations with COR1A

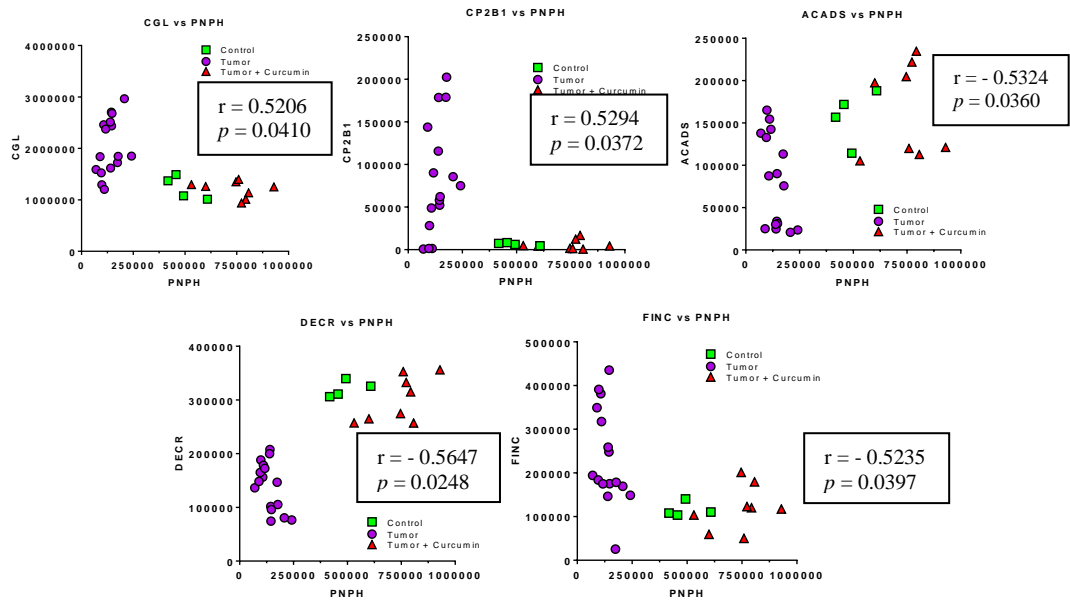




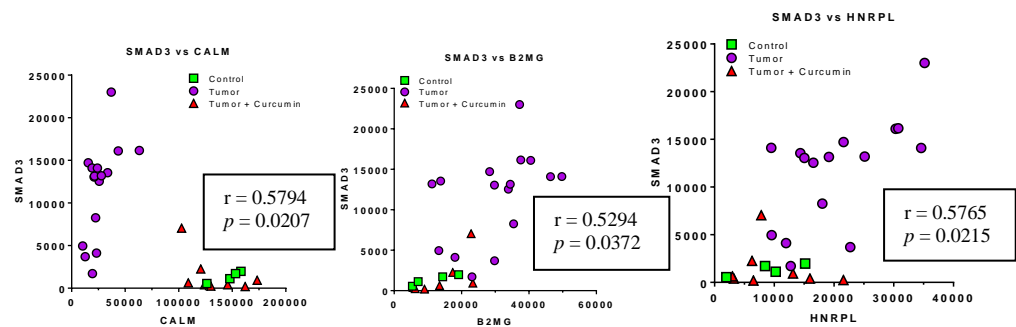
### (3) Correlations with RPN1



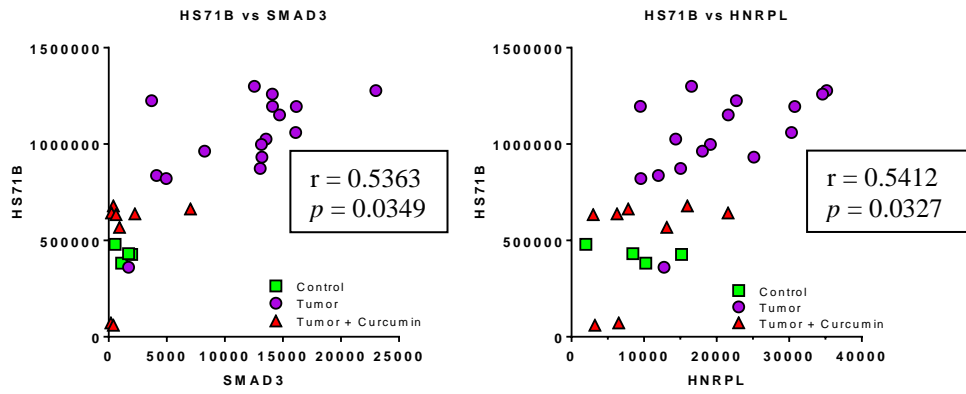
### (4) Correlations with PNPB



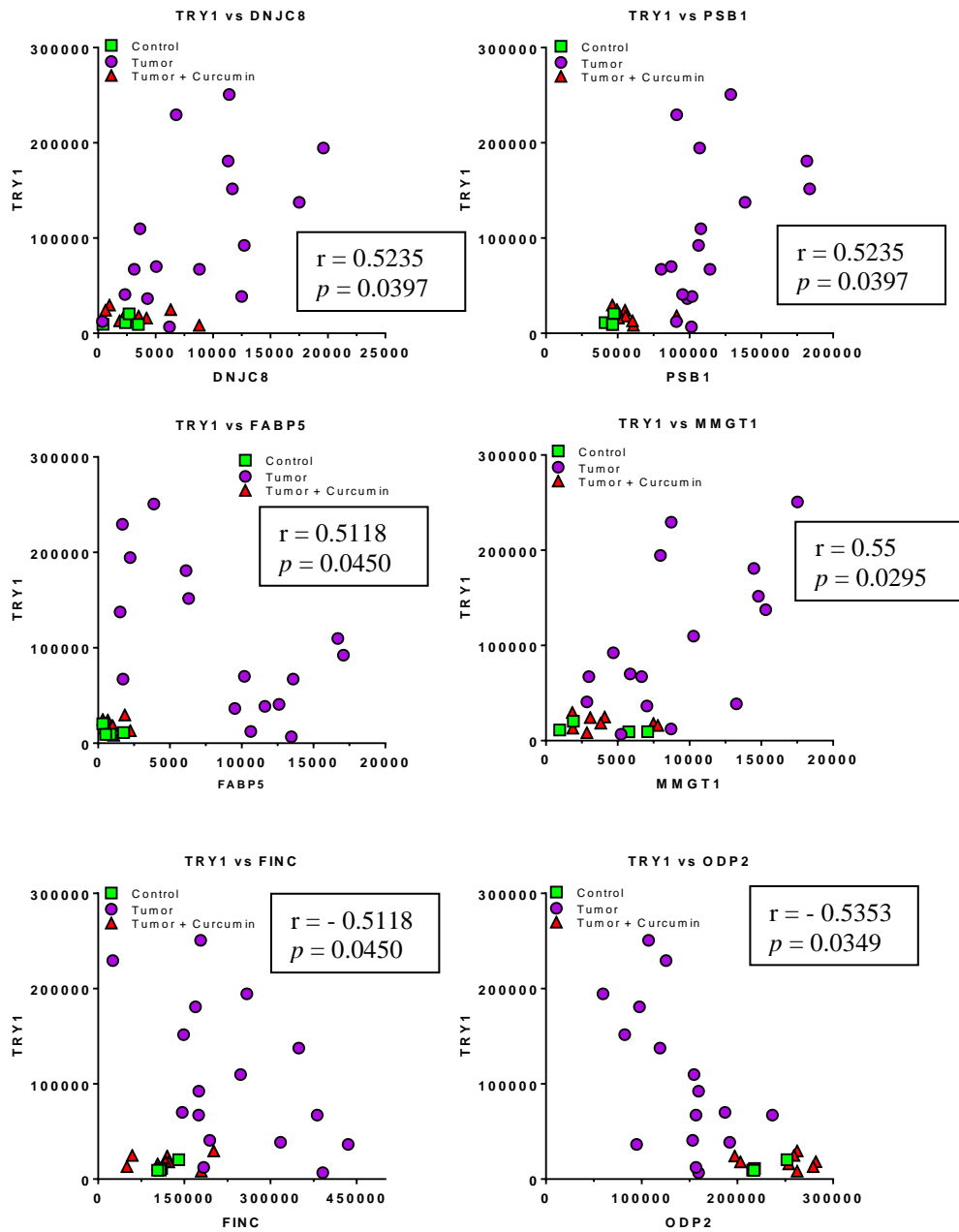
### (5) Correlations with SMAD3

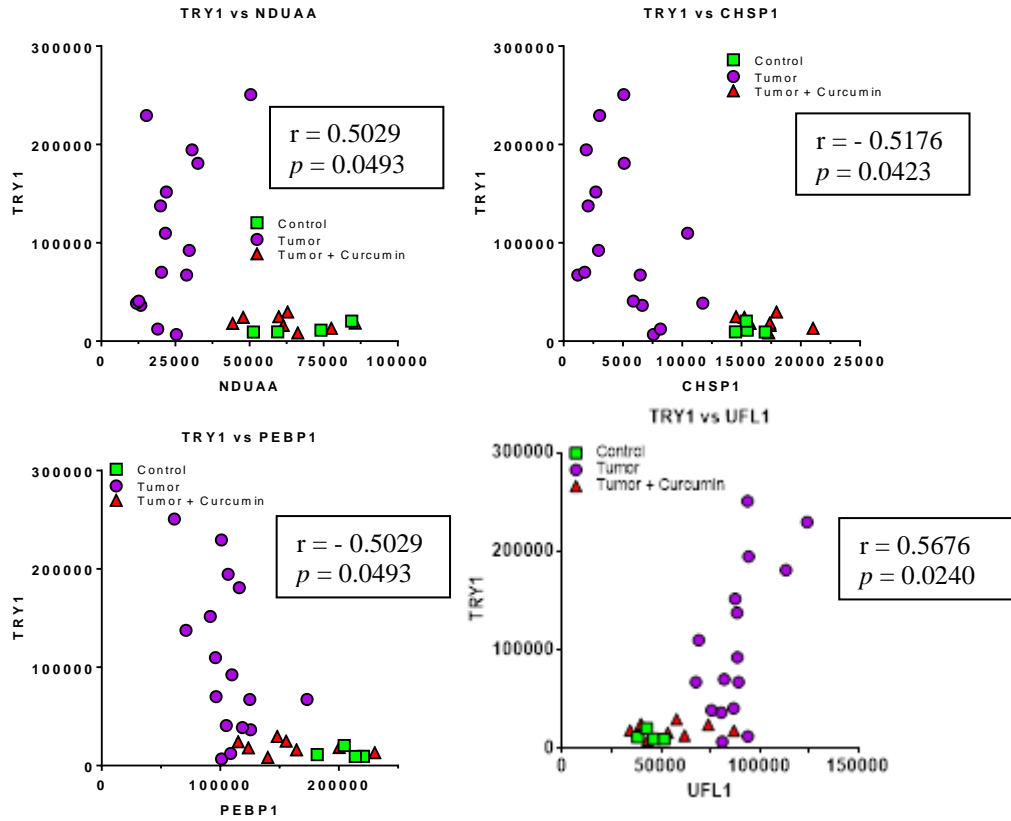


## (6) Correlations with HS71B

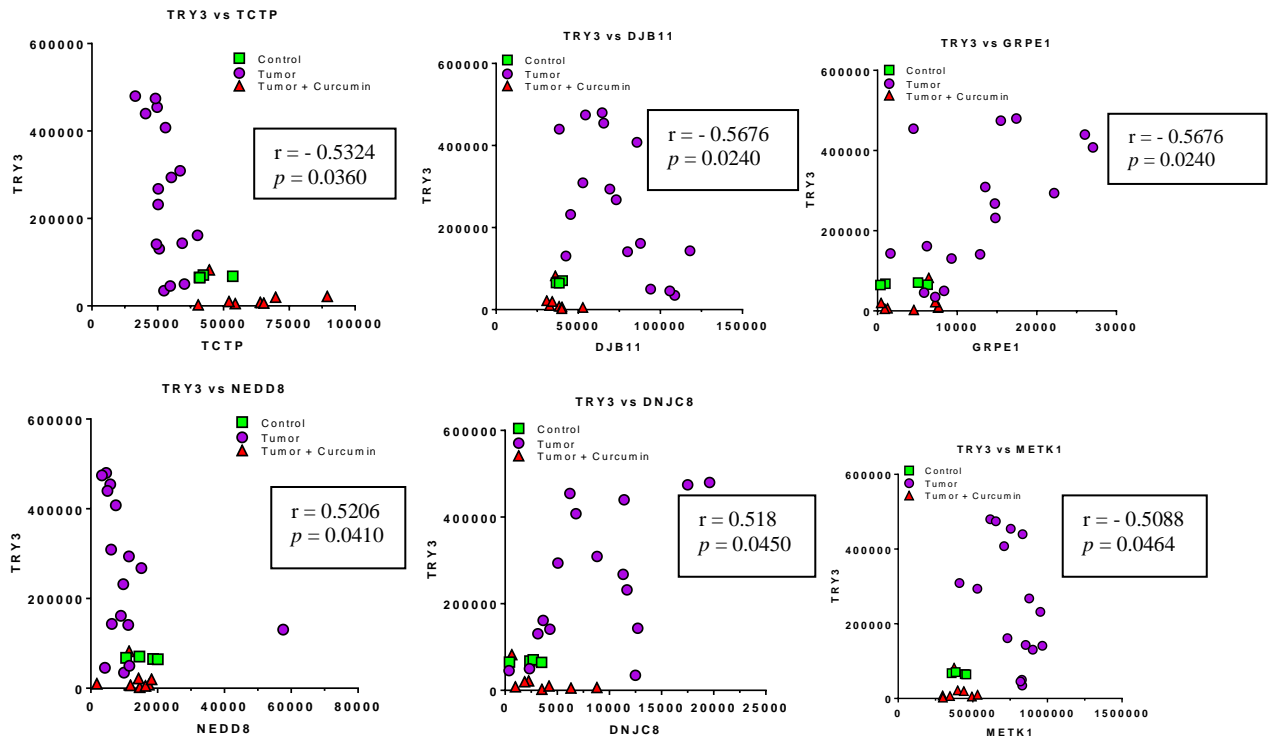


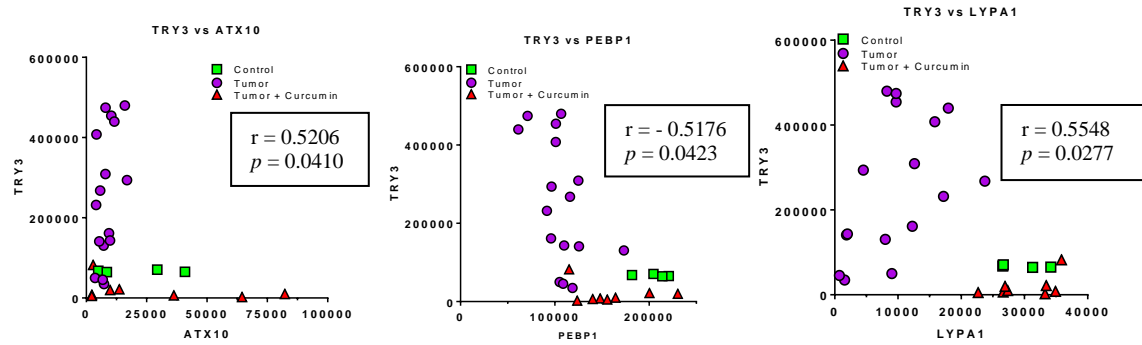
## (7) Correlations with TRY1





# (8) Correlations with TRY3





**Figure S4.** Correlation plots,  $0.02 < p < 0.05$ . Correlation plots between biomarkers identified in sections 2.2.–2.4. and 2.5.  $p$ - and  $r$ -values obtained for statistical analysis using a Spearman's test (provided only for the group of untreated rats, purple open circles) are indicated in a rectangle in each figure.

**Table S1.** Full names of the proteins, listing the 61 biomarkers of interest showing decreased abundance in (G2 vs. G1) and (G3 vs. G2) but not in (G3 vs. G1). The genes encoding the corresponding proteins in *homo sapiens* are provided for convenience.

Code (Rat)	Name	Gene (Human)
AATM	Aspartate aminotransferase, mitochondrial	GOT2
ACADM	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM
ACADS	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADS
ADK	Adenosine kinase	ADK
ADT2	ADT/ATP translocase 2	SLC25A5
ALDOB	Fructose-bisphosphate aldolase B	ALDOB
AMACR	Alpha-methylacyl-CoA racemase	AMACR
AMRP	Alpha-2-macroglobulin receptor-associated protein	LRPAP1
AP2S1	AP-2 complex subunit sigma	AP2S1
ARF6	ADP-ribosylation factor 6	ARF6
ARL2	ADP-ribosylation factor-like protein 2	ARL2
ARPC2	Actin-related protein 2/3 complex subunit 2	ARPC2
ATX10	Ataxin-10	ATXN10
CALM	Calmodulin	CALM1
CES1D	Carboxylesterase 1D	CES1
CHSP1	Calcium-regulated heat stable protein 1	CARHSP1
COL1A2	Collagen alpha-2(I) chain	COL1A2
COPG1	Coatomer subunit gamma-1	COPG1
COR1A	Coronin-1A	CORO1A
DECR	2,4-dienoyl-CoA reductase, mitochondrial	DECR1
DHRS4	Dehydrogenase/reductase SDR family member 4	DHRS4
ECHD3	Enoyl-CoA hydratase domain-containing protein 3, mitochondrial	ECHDC3
EF1D	Elongation factor 1-delta	EEF1D
EXOC4	Exocyst complex component 4	EXOC4
FIS1	Mitochondrial fission 1 protein	FIS1
G6PI	Glucose-6-phosphate isomerase	GPI
GYS2	Glycogen [starch] synthase, liver	GYS2
H2AZ	Histone H2A.Z	H2AZ1/2
HACL1	2-hydroxyacyl-CoA lyase 1	HACL1
HEM6	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	CPOX
HMCS2	Hydroxymethylglutaryl-CoA synthase, mitochondrial	HMGCS2
IDH3A	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A
KIF3C	Kinesin-like protein KIF3C	KIF3C
LYPA1	Acyl-protein thioesterase 1	LYPLA1
MYH10	Myosin-10	MYH10
NCPR	NADPH—cytochrome P450 reductase	POR
NDUAA	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	NDUFA10
NEDD8	NEDD8	NEDD8
NEUL	Neurolysin, mitochondrial	NLN
ODP2	Dihydrolipoylysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	DLAT
OLA1	Obg-like ATPase 1	OLA1

PEBP1	Phosphatidylethanolamine-binding protein 1	PEBP1
PNPH	Purine nucleoside phosphorylase	PNP
PPAC	Low molecular weight phosphotyrosine protein phosphatase	ACP1
PRDX2	Peroxiredoxin-2	PRDX2
PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial	PRDX3
PRDX5	Peroxiredoxin-5, mitochondrial	PRDX5
PSME2	Proteasome activator complex subunit 2	PSME2
RAB5A	Ras-related protein Rab-5A	RAB5A
RAP1B	Ras-related protein Rap-1b	RAP1B
RINI	Ribonuclease inhibitor	RNH1
S10A8	Protein S100-A8	S100A8
SAR1B	GTP-binding protein SAR1b	SAR1B
SARDH	Sarcosine dehydrogenase, mitochondrial	SARDH
SSDH	Succinate-semialdehyde dehydrogenase, mitochondrial	ALDH5A1
STAT3	STAT3	STAT3
SYFA	Phenylalanine—tRNA ligase alpha subunit	FARSA
TCTP	Translationally-controlled tumor protein	TPT1
TPIS	Triosephosphate isomerase	TP11
UFM1	Ubiquitin-fold modifier 1	UFM1
UGDH	UDP-glucose 6-dehydrogenase	UGDH

**Table S2.** Full names of the proteins, listing the 118 biomarkers of interest showing increased abundance in (G2 vs. G1) and (G3 vs. G2) but not in (G3 vs. G1). The genes encoding the corresponding proteins in *homo sapiens* are provided for convenience.

Code (Rat)	Name	Gene (Human)
AACS	Acetoacetyl-CoA synthetase	AACS
ACADL	Long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADL
ACON	Aconitate hydratase, mitochondrial	ACO2
ACPH	Acylamino-acid-releasing enzyme	APEH
ACTG	Actin, cytoplasmic	ACTG1
ACTN4	Alpha-actinin-4	ACTN4
ADHX	Alcohol dehydrogenase class-3	ADH5
AL1L1	Cytosolic 10-formyltetrahydrofolate dehydrogenase	ALDH1L1
AL9A1	4-trimethylaminobutyraldehyde dehydrogenase	ALDH9A1
AP1B1	AP-1 complex subunit beta-1	AP1B1
ASSY	Argininosuccinate synthase	ASS1
AT1A1	Sodium/potassium-transporting ATPase subunit alpha-1	ATP1A1
B2MG	Beta-2-microglobulin	B2M
CD2AP	CD2-associated protein	CD2AP
CERU	Ceruloplasmin	CP
CGL	Cystathionine gamma-lyase	CTH
CLH1	Clathrin heavy chain 1	CLTC
CNDP2	Cytosolic non-specific dipeptidase	CNDP2
CNN3	Calponin-3	CNN3
CO5A1	Collagen alpha-1(V) chain	COL5A1
COF1	Cofilin-1	CFL1
COPD	Coatomer subunit delta	ARCN1
CP2B1	Cytochrome P450 2B1	/
CSK	Tyrosine-protein kinase CSK	CSK
CTBL1	Beta-catenin-like protein 1	CTNBL1
CTF8A	Chromosome transmission fidelity protein 8 homolog isoform 2	CTF8
DCTN2	Dynactin subunit 2	DCTN2
DDB1	DNA damage-binding protein 1	DDB1
DDX21	Nucleolar RNA helicase 2	DDX21
DHCR7	7-dehydrocholesterol reductase	DHCR7
DHPR	Dihydropteridine reductase	QDPR
DHSO	Sorbitol dehydrogenase	SORD
DJB11	DnaJ homolog subfamily B member 11	DNAJB11
DNJC8	DnaJ homolog subfamily C member 8	DNAJC8
DX39A	ATP-dependent RNA helicase DDX39A	DDX39A
DX39B	Spliceosome RNA helicase Ddx39b	DDX39B
ECHA	Trifunctional enzyme subunit alpha, mitochondrial	HADHA
EF1A1	Elongation factor 1-alpha 1	EEF1A1
EXOC8	Exocyst complex component 8	EXOC8
EZRI	Ezrin	EZR

FABP5	Fatty acid-binding protein, epidermal	<i>FABP5</i>
FIBA	Fibrinogen alpha chain	<i>FGA</i>
FIBG	Fibrinogen gamma chain	<i>FGG</i>
FINC	Fibronectin	<i>FN1</i>
FUBP1	Far upstream element-binding protein 1	<i>FUBP1</i>
GNAI2	Guanine nucleotide-binding protein G(i) subunit alpha-2	<i>GNAI2</i>
GRB2	Growth factor receptor-bound protein 2	<i>GRB2</i>
GRPE1	GrpE protein homolog 1, mitochondrial	<i>GRPEL1</i>
GUAD	Guanine deaminase	<i>GDA</i>
H2A2A	Histone H2A type 2-A	<i>H2AC18</i>
H2AJ	Histone H2A.J	<i>H2AJ</i>
HMG5	High mobility group nucleosome-binding domain-containing protein 5	<i>HMG5</i>
HNRPC	Heterogeneous nuclear ribonucleoprotein C	<i>HNRNPC</i>
HNRPD	Heterogeneous nuclear ribonucleoprotein D0	<i>HNRNPD</i>
HNRPK	Heterogeneous nuclear ribonucleoprotein K	<i>HNRNPK</i>
HNRPL	Heterogeneous nuclear ribonucleoprotein L	<i>HNRNPL</i>
HS71B	Heat shock 70kDa protein 1B	<i>HSPA1B</i>
HSP7C	Heat shock cognate 71kDa protein	<i>HSPA8</i>
KIFC1	Kinesin-like protein KIFC1	<i>KIFC1</i>
KPYM	Pyruvate kinase PKM	<i>PKM</i>
LASP1	LIM and SH3 domain protein 1	<i>LASP1</i>
LTOR1	Ragulator complex protein LAMTOR1	<i>LAMTOR1</i>
MECP2	Methyl-CpG-binding protein 2	<i>MECP2</i>
METK1	S-adenosylmethionine synthase isoform type-1	<i>MAT1A</i>
MGST1	Microsomal glutathione S-transferase 1	<i>MGST1</i>
MICU1	Calcium uptake protein 1, mitochondrial	<i>MICU1</i>
ML12B	Myosin regulatory light chain 12B	<i>MYL12B</i>
MLEC	Malectin	<i>MLEC</i>
MMGT1	Membrane magnesium transporter 1	<i>MMGT1</i>
MSH2	DNA mismatch repair protein Msh2	<i>MSH2</i>
MVP	Major vault protein	<i>MVP</i>
NONO	Non-POU domain-containing octamer-binding protein	<i>NONO</i>
NSF1C	NSFL1 cofactor p47	<i>NSFL1C</i>
NUCL	Nucleolin	<i>NCL</i>
NUP53	Nucleoporin NUP53	<i>NUP35</i>
NUP93	Nuclear pore complex protein Nup93	<i>NUP93</i>
ODO1	2-oxoglutarate dehydrogenase, mitochondrial	<i>OGDH</i>
OPLA	5-oxoprolinase	<i>OPLAH</i>
PA2G4	Proliferation-associated protein 2G4	<i>PA2G4</i>
PBLD	Phenazine biosynthesis-like domain-containing protein	<i>PBLD</i>
PDL1	PDZ and LIM domain protein 1	<i>PDLIM1</i>
PELP1	Proline-, glutamic acid- and leucine-rich protein 1	<i>PELP1</i>
PGRC1	Membrane-associated progesterone receptor component 1	<i>PGRMC1</i>
PHB	Prohibitin	<i>PHB</i>
PICAL	Phosphatidylinositol-binding clathrin assembly protein	<i>PICALM</i>
PLEC	Plectin	<i>PLEC</i>
PNO1	REVERSED RNA-binding protein PNO1	<i>PNO1</i>
PRS6A	26S protease regulatory subunit 6A	<i>PSMC3</i>
PSA7	Proteasome subunit alpha type-7	<i>PSMA7</i>
PSB1	Proteasome subunit beta type-1	<i>PSMB1</i>
PUR6	Multifunctional protein ADE2	<i>PAICS</i>
QCR8	Cytochrome b-c1 complex subunit 8	<i>UQCRCQ</i>
REEP5	Receptor-expression-enhancing protein 5	<i>REEP5</i>
REEP6	Receptor-expression-enhancing protein 6	<i>REEP6</i>
ROA2	Heterogeneous nuclear ribonucleoproteins A2/B1	<i>HNRNPA2B1</i>
ROA3	Heterogeneous nuclear ribonucleoprotein A3	<i>HNRNPA3</i>
RPN1	Dolichyl-diphosphooligosaccharide – protein glycosyltransferase subunit 1	<i>RPN1</i>
RPP25	Ribonuclease P protein subunit p25	<i>RPP25</i>
RTCB	tRNA-splicing ligase RtcB homolog	<i>RTCB</i>
S10A6	Protein S-100 A6	<i>S100A6</i>
SC31A	Protein transport protein Sec31A	<i>SEC31A</i>
SCRN1	Secernin-1	<i>SCRN1</i>
SMAD3	Mothers against decapentaplegic homolog 3	<i>SMAD3</i>
SND1	Staphylococcal nuclease domain-containing protein 1	<i>SND1</i>
SPRE	Sepiapterin reductase	<i>SPR</i>
SPTN1	Spectrin alpha-chain, non-erythrocytic 1	<i>SPTAN1</i>
SRBS2	Sorbin and SH3 domain-containing protein 2	<i>SORBS2</i>

SRSF2	Serine/arginine-rich splicing factor	SRSF2
SSRG	Translocon-associated protein subunit gamma	SSR3
STIP1	Stress-induced-phosphoprotein 1	STIP1
SYYC	Tyrosine-tRNA ligase, cytoplasmic	YARS1
TMM43	Transmembrane protein 43	TMEM43
TRY1	Anionic trypsin-1	PRSS1
TRY3	Cationic trypsin-3	PRSS3
UBA1	Ubiquitin-like modifier-activating enzyme 1	UBA1
UFL1	E3 UFM1-protein ligase 1	UFL1
VDAC2	Voltage-dependent anion-selective channel protein 2	VDAC2
VIME	Vimentin	VIM
YBOX1	Nuclease-sensitive element-binding protein 1	YBX1

**Table S3.** Changes in liver protein abundances within the G2 group (Advanced vs Initial stages of M5-T1 tumor development).

Protein Code (Rat)	Initial Stage, Median	Advanced Stage, Median	p value
AACS	54067	40564	ns (0.3282)
AATM	622927	757173	ns (0.2345)
ACADL	524220	502495	ns (0.3823)
ACADM	44848	35433	ns (0.7209)
<b>ACADS</b>	<b>111467</b>	<b>27651</b>	<b>0.0379</b>
ACON	168882	160882	ns (0.3823)
ACPH	90423	73123	ns (0.3282)
ACTG	3081679	3240086	ns (0.7984)
ACTN4	69646	75790	ns (0.9591)
<b>ADHX</b>	<b>26754</b>	<b>36789</b>	<b>0.0379</b>
ADK	5405	6606	ns (0.5054)
ADT2	55429	55796	ns (0.5737)
<b>AL1L1</b>	<b>668368</b>	<b>893241</b>	<b>0.0499</b>
AL9A1	1192309	996066	ns (0.1049)
ALDOB	1983863	1876886	ns (0.7209)
AMACR	10162	14510	ns (0.3282)
AMRP	3792	2500	ns (0.8785)
AP1B1	11770	15779	ns (0.2345)
<b>AP2S1</b>	<b>12758</b>	<b>25707</b>	<b>0.0281</b>
APOA4	12433	22665	ns (0.2786)
ARF6	2841	3277	ns (0.7984)
<b>ARL2</b>	<b>4038</b>	<b>21901</b>	<b>0.0499</b>
ARPC2	28296	33716	ns (0.2345)
ASSY	57872	97565	ns (0.1049)
AT1A1	129314	128039	ns (>0.9999)
ATX10	7233	7960	ns (0.5737)
B2MG	31821	32615	ns (0.8785)
CALM	23562	22814	ns (0.5737)
CD2AP	33603	27689	ns (0.5054)
CERU	177331	209497	ns (0.6454)
CES1D	204844	275233	ns (0.1049)
CGL	2013692	1848823	ns (0.5737)
CH60	311063	238775	ns (0.2786)
<b>CHSP1</b>	<b>7101</b>	<b>2880</b>	<b>0.0499</b>
CLH1	195514	280420	ns (0.1049)
CNDP2	103366	101595	ns (0.9591)
CNN3	15879	12804	ns (0.8785)
CO1A2	30129	18045	ns (0.3282)
COF1	134527	118344	ns (0.1949)
COPD	9097	5741	ns (0.4418)
COPG1	9050	10730	ns (0.9591)
COR1A	10541	7114	ns (0.5054)
CSK	49268	28186	ns (0.3823)
CTBL1	6017	10129	ns (0.1949)
CTF8A	8446	9105	ns (0.9591)
DCTN2	46494	48093	ns (0.5054)
DDB1	11408	15120	ns (0.7984)
DDX21	20668	19167	ns (0.8785)
DECR	146429	147510	ns (0.7984)
DHCR7	130389	116207	ns (0.2786)
DHPR	215100	280203	0.0650
DHRS4	11940	13738	ns (0.5737)
DHSO	1650070	1924315	ns (0.2345)
<b>DJB11</b>	<b>91021</b>	<b>59473</b>	<b>0.0281</b>
<b>DNJC8</b>	<b>3970</b>	<b>11361</b>	<b>0.0499</b>
<b>DX39A</b>	<b>14813</b>	<b>35155</b>	<b>0.0207</b>
DX39B	57970	61151	ns (0.7209)

<b>ECHA</b>	<b>648835</b>	<b>358761</b>	<b>0.0002</b>
ECHD3	174101	149514	ns (0.3823)
EF1A1	3235568	2920253	ns (0.3823)
EF1D	39285	49138	ns (0.1304)
EXOC4	1582	5741	ns (0.1049)
EXOC8	21379	17401	ns (0.5737)
EZRI	39159	37765	ns (0.7209)
<b>FABP5</b>	<b>13027</b>	<b>3054</b>	<b>0.0003</b>
<b>FETUA</b>	<b>60527</b>	<b>102185</b>	<b>0.0148</b>
FIBA	200601	314166	ns (0.2345)
<b>FIBG</b>	<b>175924</b>	<b>313436</b>	<b>0.0104</b>
<b>FINC</b>	<b>282832</b>	<b>172271</b>	<b>0.0207</b>
FIS1	13323	8000	ns (0.3282)
FUBP1	13730	19747	0.0830
G6PI	36406	34066	ns (0.8785)
GNAI2	55029	67654	ns (0.7984)
GRB2	11393	11318	ns (0.6454)
GUAD	167200	146823	ns (0.1949)
GYS2	1828	2223	ns (0.6454)
H2A2A	9164	10380	ns (0.2345)
<b>H2AJ</b>	<b>66357</b>	<b>29515</b>	<b>0.0499</b>
H2AZ	14744	14851	ns (0.3823)
HA12	40113	16492	0.0830
HACL1	24953	12628	ns (0.7984)
HEM6	18652	11635	ns (0.5737)
<b>HMCS2</b>	<b>751183</b>	<b>1204017</b>	<b>0.0281</b>
HMGN5	17418	6496	ns (0.1304)
HNRPC	159042	138998	ns (0.2345)
HNRPD	55780	54977	ns (>0.9999)
<b>HNRPK</b>	<b>112930</b>	<b>83132</b>	<b>0.0499</b>
HNRPL	17842	20386	ns (0.8785)
HS71B	1043077	1078850	ns (0.8785)
HSP7C	499867	478945	ns (0.4418)
ICAM1	10653	15469	ns (0.1949)
<b>IDH3A</b>	<b>6822</b>	<b>19339</b>	<b>00.0281</b>
IL6RB	12089	22008	ns (0.1605)
<b>IRGM</b>	<b>3728</b>	<b>6088</b>	<b>0.0148</b>
KIF3C	3502	5543	ns (>0.9999)
KIFC1	2386	1914	ns (>0.9999)
KPYM	44799	36281	ns (0.3823)
LASP1	63529	54398	ns (0.1605)
LTOR1	30081	31053	ns (0.8785)
<b>LYPA1</b>	<b>4995</b>	<b>14210</b>	<b>0.0115</b>
MECP2	3153	2773	ns (0.6454)
METK1	829946	681863	ns (0.1605)
MGST1	17786	8320	ns (>0.9999)
MICU1	909	1928	ns (0.3823)
MIF	312747	450410	ns (0.5054)
ML12B	175875	135185	ns (0.1605)
MLEC	52041	58759	ns (0.4418)
<b>MMGT1</b>	<b>6133</b>	<b>11601</b>	<b>0.0499</b>
MSH2	4342	7815	ns (0.3282)
MVP	72490	43848	ns (0.1605)
MYH10	8826	7906	ns (0.6454)
<b>NCPR</b>	<b>37874</b>	<b>75296</b>	<b>0.0104</b>
NDUAA	20313	25286	ns (0.1605)
NEDD8	7644	6770	ns (0.7984)
NEUL	7502	6908	ns (0.8785)
NONO	70718	68258	ns (0.4418)
NSF1C	107595	103870	ns (0.7984)
NUCL	48934	51716	ns (0.8785)
NUP53	10692	7854	ns (0.6454)
NUP93	29848	23947	ns (0.4418)
ODO1	120449	100847	ns (0.5242)
ODP2	156743	113127	ns (0.1949)
OLA1	11061	12810	ns (0.8785)
OPLA	34623	30264	ns (0.9591)
<b>PA2G4</b>	<b>88770</b>	<b>65574</b>	<b>0.0281</b>
PBLD	118238	131904	ns (0.1049)
<b>PDLI1</b>	<b>30453</b>	<b>74575</b>	<b>0.0499</b>
PEBP1	109333	98742	ns (0.1049)
<b>PELP1</b>	<b>3825</b>	<b>8821</b>	<b>0.0379</b>
PHB	126195	122604	ns (0.8785)
<b>PICAL</b>	<b>62476</b>	<b>30687</b>	<b>0.0070</b>
PLEC	63708	48306	ns (0.2786)
PN01	956	2024	ns (0.2345)
PNPH	108669	156942	ns (0.1049)



<b>PPAC</b>	<b>27304</b>	<b>40260</b>	<b>0.0499</b>
PRDX2	127612	158085	<i>ns (0.3282)</i>
PRDX3	36289	36075	<i>ns (0.9591)</i>
PRDX5	223549	252387	<i>ns (0.7209)</i>
PRS6A	57537	47312	<i>ns (0.1605)</i>
PSA7	22612	18462	<i>ns (0.7984)</i>
PSB1	101503	117910	<i>ns (0.5054)</i>
PSME2	7986	10174	0.0830
PUR6	39544	41576	<i>ns (0.7984)</i>
QCR8	31395	36071	<i>ns (0.8785)</i>
RAB5A	18042	20896	<i>ns (0.2345)</i>
RAP1B	31999	46501	<i>ns (0.1049)</i>
REEP5	1230	1403	<i>ns (0.6454)</i>
REEP6	255248	264586	<i>ns (0.1949)</i>
RIN1	8313	13660	<i>ns (0.2786)</i>
ROA2	214734	193410	<i>ns (0.1049)</i>
ROA3	64200	68160	<i>ns (0.6454)</i>
RPN1	767581	771925	<i>ns (0.7209)</i>
RPP25	5711	9637	<i>ns (0.2345)</i>
<b>RTCB</b>	<b>47414</b>	<b>66022</b>	<b>0.0499</b>
S10A4	19119	12580	<i>ns (0.3823)</i>
S10A8	3316	3791	<i>ns (0.2906)</i>
S10AB	6536	11120	0.0650
SAR1B	48285	42590	<i>ns (0.7209)</i>
SC22B	110489	96745	<i>ns (0.7209)</i>
SC31A	70981	74238	<i>ns (0.5737)</i>
SCRN1	2061	2904	<i>ns (0.7984)</i>
SMAD3	13351	10730	<i>ns (0.5054)</i>
SND1	432306	443993	<i>ns (0.6454)</i>
SPRE	188791	161003	<i>ns (0.5737)</i>
SPTN1	71821	55255	<i>ns (0.5737)</i>
SRBS2	33983	14806	<i>ns (0.1049)</i>
<b>SRSF2</b>	<b>96083</b>	<b>59908</b>	<b>0.0499</b>
SSDH	5317	16903	<i>ns (0.1605)</i>
SSRG	85094	123978	<i>ns (0.6943)</i>
STAT3	3245	6471	<i>ns (0.1049)</i>
STIP1	71664	65649	<i>ns (0.3282)</i>
SYFA	22306	15545	0.0830
SYYC	37680	38234	<i>ns (0.7209)</i>
TAP2	3806	8174	<i>ns (0.1949)</i>
TCTP	28580	25202	<i>ns (0.1605)</i>
TMM43	12055	20745	<i>ns (0.1949)</i>
TPIS	59558	34512	<i>ns (0.1304)</i>
UBA1	147682	132338	<i>ns (0.2786)</i>
UFL1	83963	91275	<i>ns (0.1949)</i>
UFM1	4832	6985	<i>ns (0.3282)</i>
UGDH	103446	99347	<i>ns (0.7209)</i>
VDAC2	109319	115990	<i>ns (0.5737)</i>
<b>VIME</b>	<b>610917</b>	<b>225269</b>	<b>0.0104</b>
YBOX1	6932	6409	<i>ns (0.8785)</i>

The list includes all proteins (in alphabetical order of their code). described in Figures 2 to 7, full names being indicated in the text or Tables S1 and S2. Mann-Whitney statistical test. For all non-significant difference (*ns*), medians and *p* values are indicated in italics. Significant differences are indicated in bold type, and tendencies in normal type. Proteins showing more pronounced decrease or increase in link with tumor progression are additionally highlighted in yellow.



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