Supplemental Material

Supplemental Figures

Figure S1

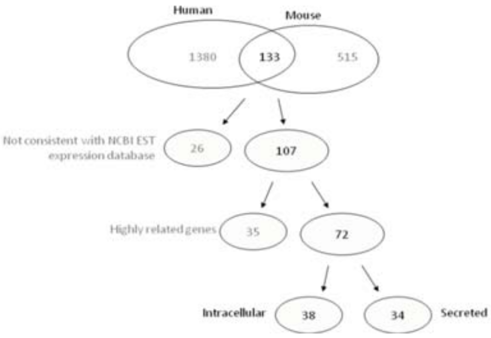


Figure S1. Organ specificity at mRNA level and protein level. Winnowing the liver-specific target list. Of the 133 orthologs common to human and mouse, 26 transcript MPSS expression profiles were not consistent with NCBI EST expression database, while 35 were members of closely-related gene families. Of the remaining 72, 34 are secreted proteins and 38 are intracellular proteins.

Figure S2

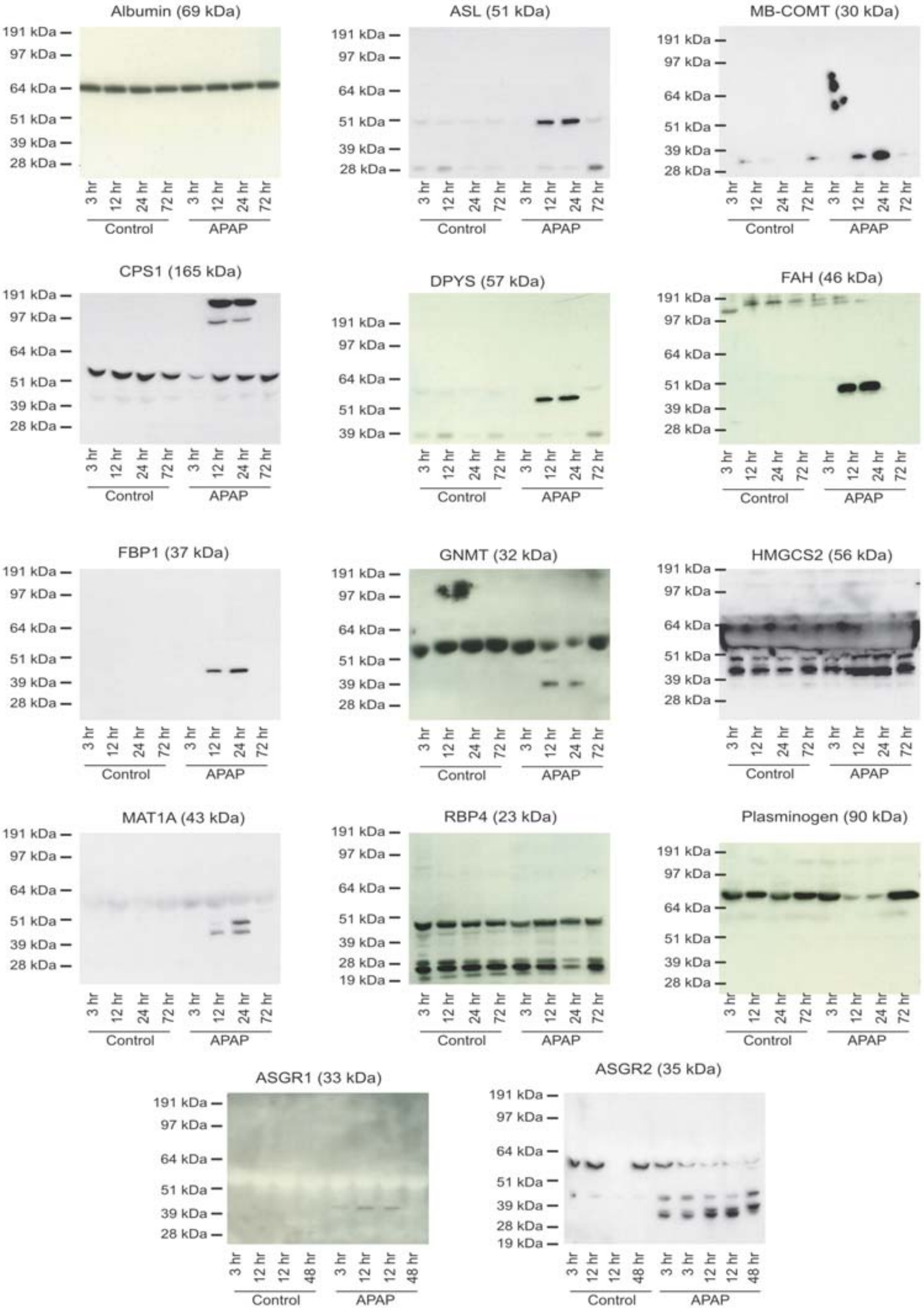


Figure S2. Western blot analyses of mouse plasma at four time points after high-dosage (300 mg/kg) APAP treatment.

Figure S3

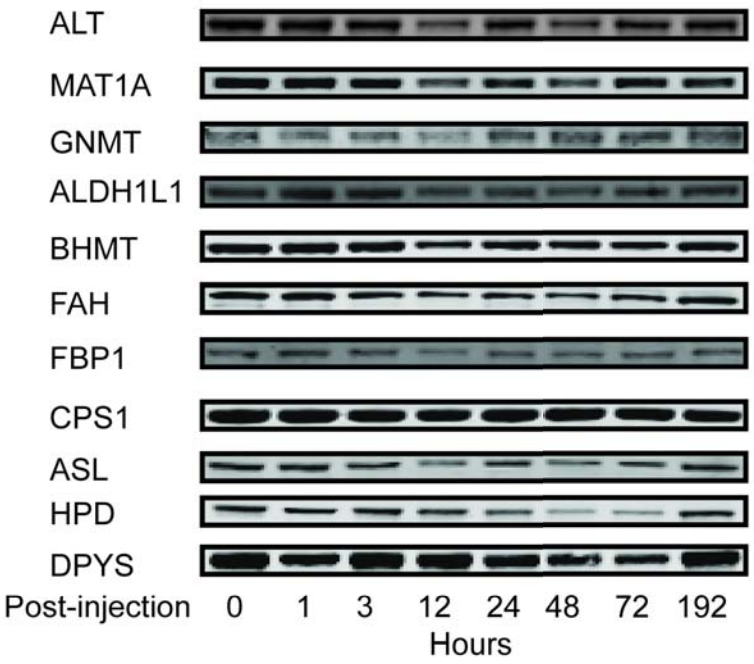


Figure S3. Temporal profiles of liver tissue protein levels. While these protein levels were observed to increase in the blood, Western blot analyses of mouse liver lysates indicate no change or a small decrease in level. The eight time points are taken after high-dosage (300 mg/kg) APAP treatment.

Figure S4

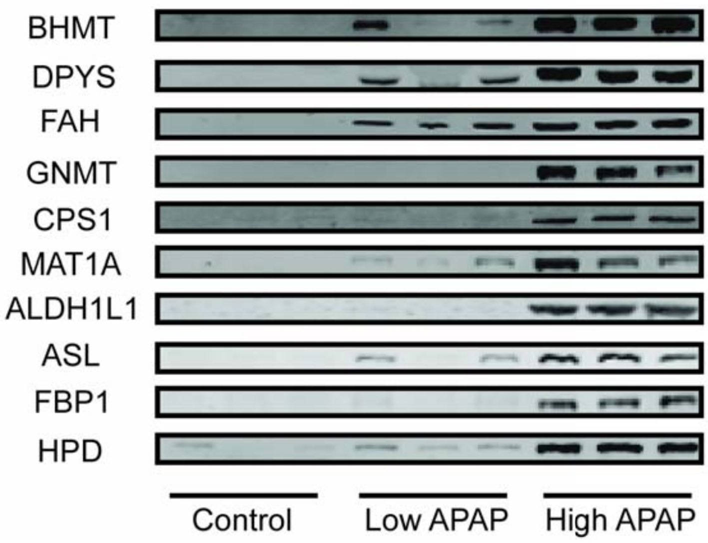


Figure S4. Western blot analyses of mouse plasma at 24 hours post low dosage (150 mg/kg) and high dosage (300 mg/kg) APAP treatment.

Figure S5

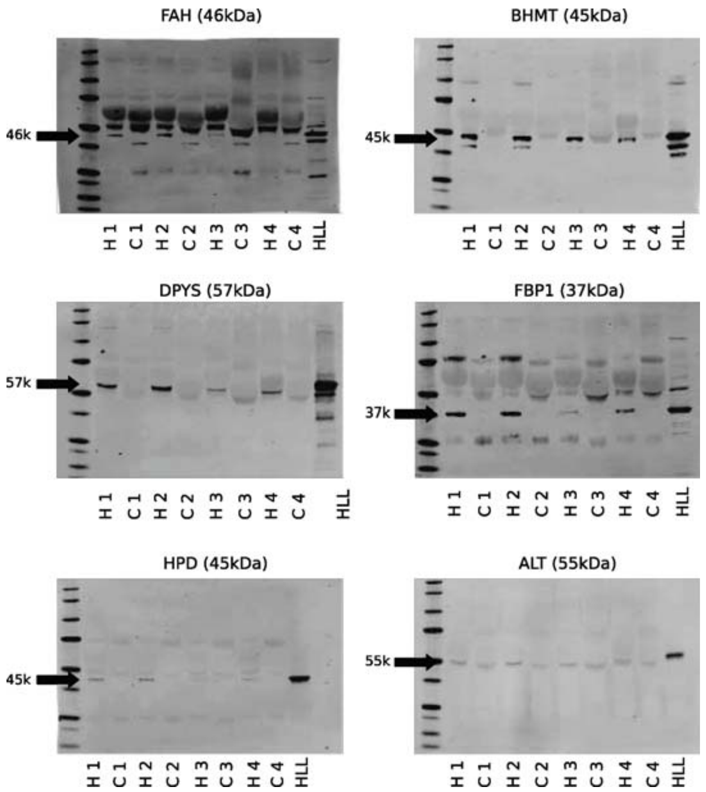


Figure S5. Western blot analysis of human plasma. Each blot contains plasma from four APAP hepatotoxicity patients (H1-H4), four control individuals (C1-C4), and human liver lysate (HLL).

Figure S6

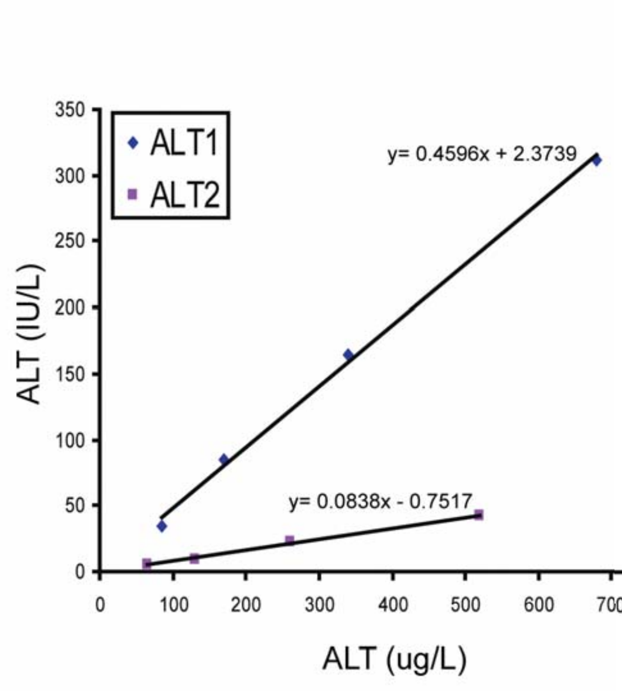


Figure S6. Human ALT1 and ALT2 calibration. Proteins wer eexpressed in 293T cells, purified and quantified by the vendor (Origene, MD). Protein activities were measured by kinetic enzyme assay.

Figure S7

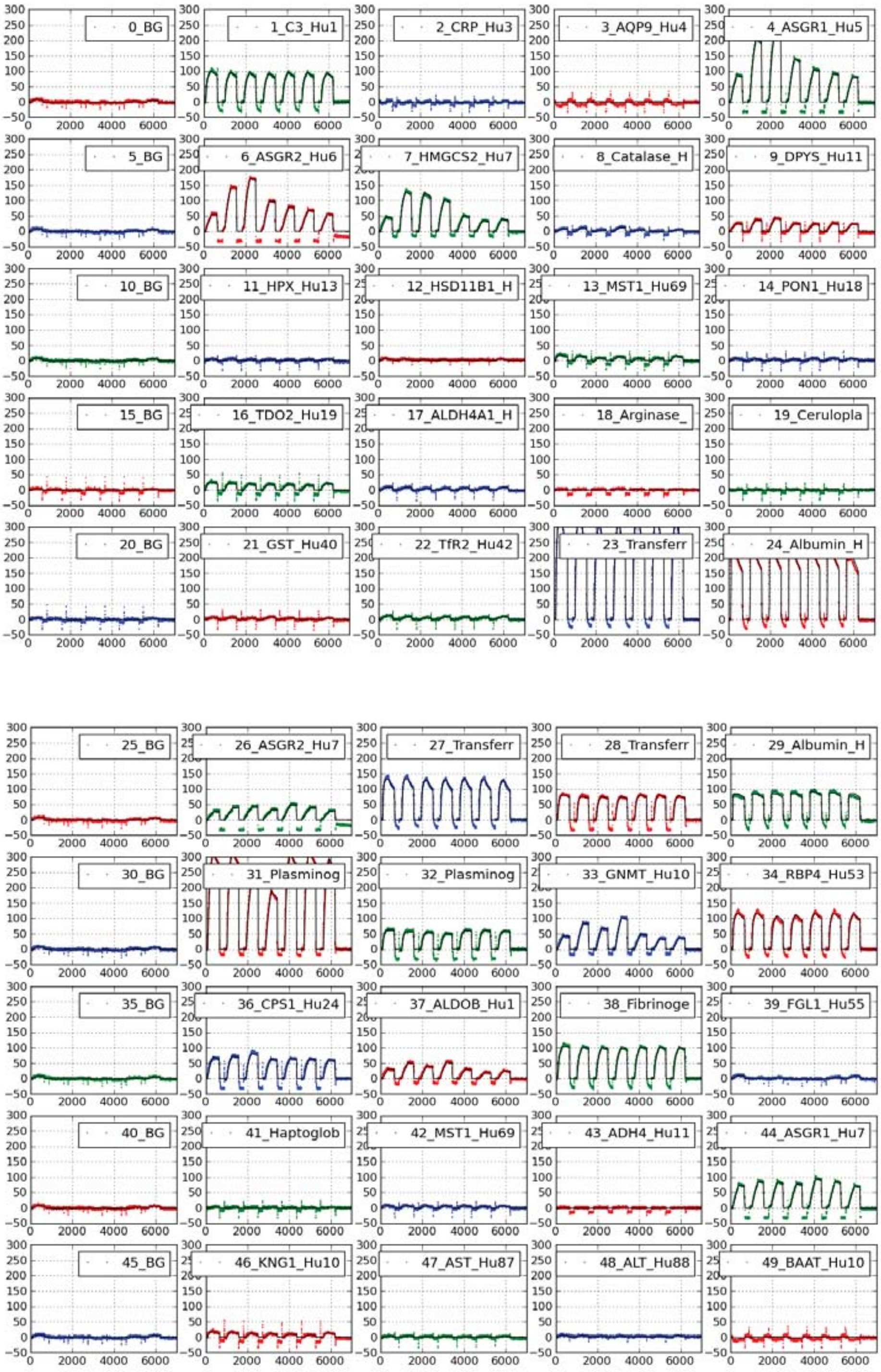
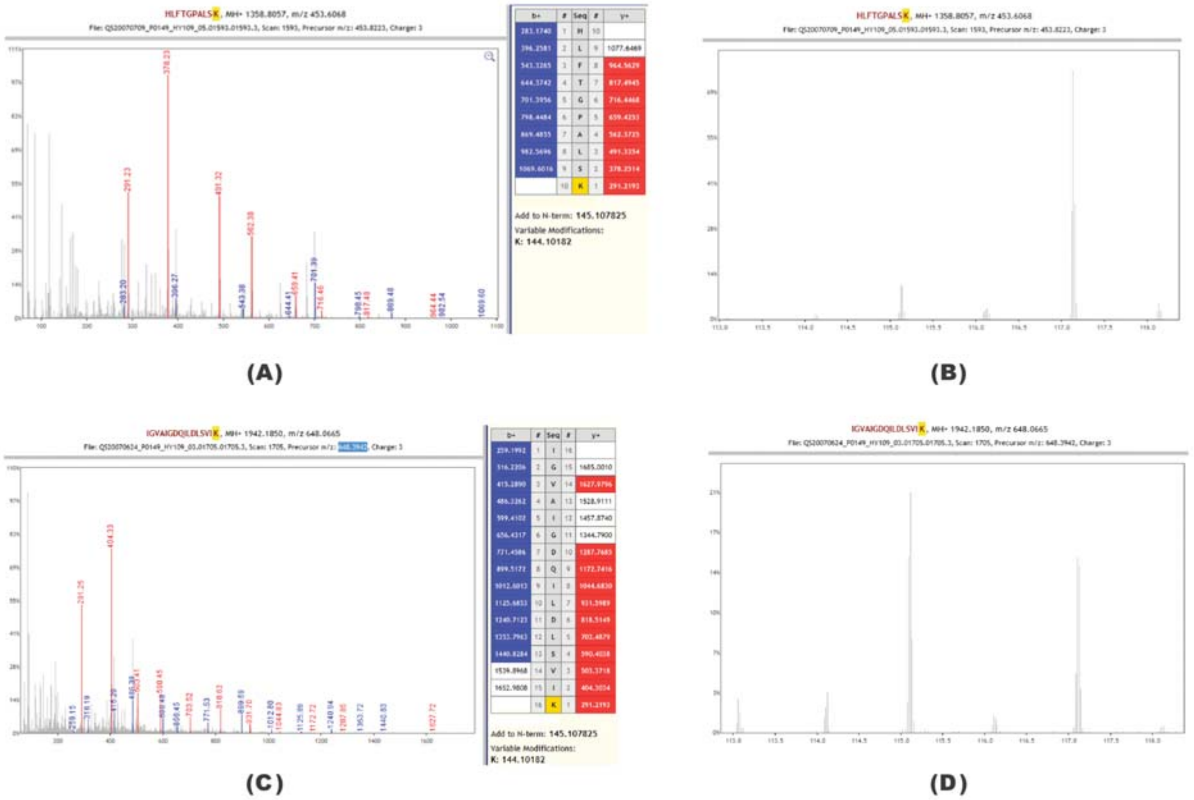


Figure S7. SPRI sensorgrams from seven injections of plasma samples onto a fifty-feature microarray. The sample order was 1, 3, 12, 24, 48, 72 (hours post-treatment), and control. The surface was regenerated after each injection. Black lines are fitted curves.

Figure S8



b+	#	Seq	#	y+
283.1740	1	H	10	
396.2581	2	L	9	1077.6469
543.3265	3	F	8	964.5629
644.3742	4	T	7	817.4945
701.3956	5	G	6	716.4468
798.4484	6	P	5	659.4253
869.4855	7	A	4	562.3725
982.5696	8	L	3	491.3354
1069.6016	9	S	2	378.2514
	10	K	1	291.2193

Add to N-term: 145.107825
Variable Modifications:
K: 144.10182

(A)

(B)

b+	#	Seq	#	y+
259.1992	1	I	16	
316.2206	2	G	15	1685.0010
415.2890	3	V	14	1627.9796
486.3262	4	A	13	1528.9111
599.4102	5	I	12	1457.8740
656.4317	6	G	11	1344.7900
771.4586	7	D	10	1287.7685
899.5172	8	Q	9	1172.7416
1012.6013	9	I	8	1044.6830
1125.6853	10	L	7	931.5989
1240.7123	11	D	6	818.5149
1353.7963	12	L	5	703.4879
1440.8284	13	S	4	590.4038
1539.8968	14	V	3	503.3718
1652.9808	15	I	2	404.3034
	16	K	1	291.2193

Add to N-term: 145.107825
Variable Modifications:
K: 144.10182

(C)

(D)

Figure S8. Example MS2 spectra from target protein FAH in iTRAQ. *(A)* The full mass range MS/MS data for the peptide HLFTGPALSK is shown as an example of high-confidence detection with targeted iTRAQ approach to quantification of FAH in blood plasma samples from mice treated with saline or APAP at 24 hours after treatment (C24 and A24), among three targeted spike-in peptides (ASLQNLLSASQAR, AHEHIFGMVLMNDWSAR, HLFTGPALSK). *(B)* The MS/MS data in (A) for iTRAQ reporter region of m/z = 113 ~ 118. The intensity of m/z=114.1 reporter ion represent the relative level of FAH in saline-treated mouse blood while that of m/z=115.1 represent FAH's relative level in APAP-treated mouse blood. *(C)* An MS/MS data for the peptide IGVAIGDQILDLSVIK is shown as an example of untargeted peptide for FAH, the same parent protein in the same samples as in (A). *(D)* The MS/MS data in (C) for iTRAQ reporter region of m/z = 113 ~ 118. Higher intensities of the target peptide HLFTGPALSK and untargeted peptide IGVAIGDQILDLSVIK in A24 sample relative to C24 sample demonstrates the feasibility and validity of targeted iTRAQ approach against the artificial contribution of peptide backbone fragments from spike-in peptides and the random contribution of iTRAQ reporter ions from co-eluting peptides. If the random contribution of co-eluting peptides was significant, the relative intensities of m/z=114.1 and m/z=115.1 peaks would be approximately 1:1. The peak at m/z=117.1 in (D) represents iTRAQ-117.1 reporter ions of co-eluting byproduct peptides from the mixture of unpurified spike-in peptides as opposed to any spike-in target peptide. Spike-in target peptides show much higher 117.1 peaks in their MS2 data, as seen in (B), relative to untargeted peptides.

Supplemental Tables

Table S1. Organ-specific transcripts

Table S1A. Human MPSS data was obtained from 34 samples representing 28 different organs.

Library ID	Organ Name	Description	Company	Race	Gender	Total signatures seen	Signatures for Unigene sequences	Unigene clusters
HuAG.basl	adrenal gland	none (normal tissue)	Clontech	Caucasian	male/female	53768	33532	14078
HuBl.basl	bladder	none (normal tissue)	Clontech	Caucasian	male/female	45291	28643	12363
HuBM.basl	bone marrow	none (normal tissue)	Clontech	Caucasian	male/female	38421	24079	11265
HuBr.amyg	brain, amygdala	none (normal tissue)	Clontech	Caucasian	male/female	57125	34160	14907
HuBr.CaNu	brain, caudate nucleus	none (normal tissue)	Clontech	Caucasian	male/female	47407	29060	13937
HuBr.cere	brain, cerebellum	none (normal tissue)	Clontech	Caucasian	male/female	46194	26447	12594
HuBr.CoCa	brain, corpus callosum	none (normal tissue)	Clontech	Caucasian	male/female	54926	33771	14572
HuBr.hypo	brain, hypothalamus	none (normal tissue)	Clontech	Caucasian	male/female	47466	29212	13892
HuBr.thal	brain, thalamus	none (normal tissue)	Clontech	Caucasian	male/female	40462	25997	12966
HuColon	colon	•	•	•	•	20540	13836	8558
HuFB.basl	fetal brain, whole	none (normal tissue)	Clontech	Caucasian	male/female	42759	23544	12259
HuHe.basl	heart	none (normal tissue)	Clontech	Caucasian	male	48669	33418	13298
HuKi.basl	kidney	none (normal tissue)	Clontech	Caucasian	male/female	41749	26600	12281
HuLi.norm	liver	none (normal tissue)	•	Asian	male	12018	8595	6161
HuLu.basl	lung	none (normal tissue)	Clontech	Caucasian	male	48020	30963	13522
HuMG.basl	mammary gland	none (normal tissue)	Clontech	Caucasian	female	31735	21556	11606
HuMo.basl	Monocytes	Resting	Lynx, GmbH	•	•	39813	24252	10800
HuOv.cmts	ovary	cancer cell line	•	•	•	23725	17550	9404
HuPB.ctrl	peripheral blood lymphocytes	Healthy control donors	Lynx, GmbH	•	•	26265	17382	9665
HuPG.basl	pituitary gland	none (normal tissue)	Clontech	Caucasian	male/female	46612	29525	13614
HuPl.basl	placenta	none (normal tissue)	Clontech	Caucasian	female	28913	18169	9758
HuPn.basl	pancreas	none (normal tissue)	Clontech	Caucasian	male/female	24410	16121	9327
HuPr.basl	prostate	none (normal tissue)	Clontech	Caucasian	male	42969	26622	12716
HuRe.basl	retina	none (normal tissue)	Clontech	Caucasian	male/female	46450	28997	13988

HuSC.basl	spinal cord	none (normal tissue)	Clontech	Caucasian	male/female	51424	32718	14754
HuSG.basl	salivary gland	none (normal tissue)	Clontech	Caucasian	male/female	27985	18472	10494
HuSI.basl	small intestine	none (normal tissue)	Clontech	Caucasian	male/female	52476	32546	14567
HuSp.basl	spleen	none (normal tissue)	Clontech	Caucasian	male/female	60327	37295	14977
HuSt.basl	stomach	none (normal tissue)	Clontech	Caucasian	male/female	26238	16680	9692
HuTe.basl	testis	none (normal tissue)	Clontech	Caucasian	male	80872	45416	18256
HuTm.basl	thymus	none (normal tissue)	Clontech	Caucasian	male/female	64507	37260	15123
HuTr.basl	trachea	none (normal tissue)	Clontech	Caucasian	male/female	52457	30915	14492
HuTy.basl	thyroid	none (normal tissue)	Clontech	Caucasian	male/female	48125	31134	13865
HuUt.basl	uterus	none (normal tissue)	Clontech	Caucasian	female	66643	39221	15445

Table S1B. Mouse MPSS data was obtained from 84 samples representing 31 different mouse organs.

Accession	Label	Organ	Gender	Library	Total Signatures	Signatures for unigene sequences	Unigene clusters
GSM34293	Adrenal, Female (MoAd.Feml)	adrenal	Female	17MoAdFeml	22866	16235	9546
GSM44327	Adrenal, Male (MoAd.Male)	adrenal	Male	17MoAdMale	27071	20206	10785
GSM44328	Heart:Aorta, Female (MoAo.Feml)	heart / aorta	Female	17MoAoFeml	21894	15786	9407
GSM38489	Heart:Aorta, Male (MoAo.Male)	heart / aorta	Male	17MoAoMale	19910	14341	9176
GSM44329	Brown Fat, Female (MoBF.Feml)	brown fat	Female	17MoBFFeml	21782	16164	9079
GSM44330	Brown Fat, Male (MoBF.Male)	brown fat	Male	17MoBFMale	15077	11839	7644
GSM34294	Bladder, Female (MoBl.Feml)	bladder	Female	17MoBlFeml	21465	14751	9299
GSM27138	Bladder, Male (MoBl.Male)	bladder	Male	17MoBlMale	21880	13436	8522
GSM36603	Bone:Femur, Female (MoBn.FeFm)	bone / femur	Female	17MoBnFeFm	17334	10991	7610
GSM34295	Bone:Femur, Male (MoBn.MaFm)	bone / femur	Male	17MoBnMaFm	14615	11108	7814
GSM44331	Brain:Caudate,Putamen,Accumbens... Female (MoBr.FCPA)	brain (multi parts)	Female	17MoBrFCPA	35685	23749	11958
GSM47338	Brain:Amygdala, Female (MoBr.FeAm)	brain / amygdala	Female	17MoBrFeAm	24660	17228	10042
GSM47339	Brain:Cerebellum, Female (MoBr.FeCb)	brain / cerebellum	Female	17MoBrFeCb	41376	26340	12416
GSM44334	Brain:Cortical mantle, Female (MoBr.FeCM)	brain / cortical mantle	Female	17MoBrFeCM	35759	23079	11797
GSM47340	Brain:Hippocampus, Female (MoBr.FeHi)	brain / hippocampus	Female	17MoBrFeHi	35456	22550	11535
GSM44335	Brain:Midbrain, Female (MoBr.FeMb)	brain / midbrain	Female	17MoBrFeMb	29522	19660	11195
GSM36604	Brain:Olfactory Bulb, Female (MoBr.FeOB)	brain / olfactory bulb	Female	17MoBrFeOB	32890	21735	11375
GSM32353	Brain:Thalamus, Female (MoBr.FeTh)	brain / thalamus	Female	17MoBrFeTh	37011	25820	12521
GSM38490	Brain:Hypothalamus/preoptic area, Female (MoBr.FHyP)	brain / hypothalamus, preoptic	Female	17MoBrFHyP	25935	17962	10313
GSM36721	Brain:OlfactoryTubercle,Prefrontal... Female (MoBr.FTCS)	brain (multi parts)	Female	17MoBrFTCS	29697	20175	11035
GSM34297	Brain:Amygdala, Male (MoBr.MaAm)	brain / amygdala	Male	17MoBrMaAm	25075	15980	9481
GSM32354	Brain:Cerebellum, Male (MoBr.MaCb)	brain / cerebellum	Male	17MoBrMaCb	36637	24684	11927
GSM44336	Brain:Cortical mantle, Male (MoBr.MaCM)	brain / cortical mantle	Male	17MoBrMaCM	33034	23166	11724
GSM32355	Brain:Hippocampus, Male (MoBr.MaHi)	brain / hippocampus	Male	17MoBrMaHi	31883	22390	11760
GSM32356	Brain:Midbrain, Male (MoBr.MaMb)	brain / midbrain	Male	17MoBrMaMb	27641	19783	10937

GSM44337	Brain:Olfactory Bulb, Male (MoBr.MaOB)	brain / olfactory bulb	Male	17MoBrMaOB	46513	28851	12948
GSM38491	Brain:Thalamus, Male (MoBr.MaTh)	brain / thalamus	Male	17MoBrMaTh	27922	19466	10852
GSM36605	Brain:Caudate,Putamen,Accumbens... Male (MoBr.MCPA)	brain (multi parts)	Male	17MoBrMCPA	30007	20702	11286
GSM34296	Brain:Hypothalamus/preoptic area, Male (MoBr.MHyP)	brain / hypothalamus, preoptic	Male	17MoBrMHyp	28836	20476	10917
GSM40111	Brain:OlfactoryTubercle,PrefrontalCortex... Male (MoBr.MTCS)	brain (multi parts)	Male	17MoBrMTCS	25119	16060	9732
GSM40113	Cartilage:Xiphoid, Female (MoCg.FeXi)	cartilage	Female	17MoCgFeXi	28448	15480	9282
GSM38492	Cartilage:Xiphoid, Male (MoCg.MaXi)	cartilage	Male	17MoCgMaXi	20582	14895	9166
GSM40112	Cervix and vagina, Female (MoCV.Feml)	cervix / vagina	Female	17MoCVFeml	14178	11078	7701
GSM35331	Esophagus, Female (MoEs.Feml)	esophagus	Female	17MoEsFeml	15739	12315	8289
GSM27139	Esophagus, Male (MoEs.Male)	esophagus	Male	17MoEsMale	12190	7999	5878
GSM38493	Eye, Female (MoEy.Feml)	eye	Female	17MoEyFeml	31363	22430	11966
GSM36606	Eye, Male (MoEy.Male)	eye	Male	17MoEyMale	32041	19753	11152
GSM40115	Heart: atria, Female (MoHe.FeAt)	heart / atria	Female	17MoHeFeAt	10827	6819	5319
GSM27140	Heart:Ventricles and Septum, Female (MoHe.FeVS)	heart / ventricles, septum	Female	17MoHeFeVS	12316	8299	5874
GSM40116	Heart: atria, Male (MoHe.MaAt)	heart / atria	Male	17MoHeMaAt	21133	14541	8990
GSM36722	Heart:Ventricles and Septum, Male (MoHe.MaVS)	heart / ventricles, septum	Male	17MoHeMaVS	16475	11697	7651
GSM34298	Kidney:Cortex, Female (MoKi.FeCr)	kidney / cortex	Female	17MoKiFeCr	17349	12996	8517
GSM27141	Kidney:Medulla, Female (MoKi.FeMd)	kidney / medulla	Female	17MoKiFeMd	15814	9836	6809
GSM27142	Kidney:Cortex, Male (MoKi.MaCr)	kidney / cortex	Male	17MoKiMaCr	19361	13328	8073
GSM27143	Kidney:Medulla, Male (MoKi.MaMd)	kidney / medulla	Male	17MoKiMaMd	16444	11423	7180
GSM40117	Large intestine, Female (MoLI.Feml)	large intestine	Female	17MoLIFeml	19057	13474	8711
GSM47341	Liver:right lobe, Female (MoLi.FeRL)	liver / right lobe	Female	17MoLiFeRL	11657	8654	6030
GSM36723	Large intestine, Male (MoLI.Male)	large intestine	Male	17MoLIMale	11146	7821	5919
GSM32357	Liver:left lobe, Male (MoLi.MaLL)	liver / left lobe	Male	17MoLiMaLL	13583	10227	6790
GSM36724	Liver:right lobe, Male (MoLi.MaRL)	liver / right lobe	Male	17MoLiMaRL	10891	8177	5746
GSM44332	Lymph nodes: mesenteric, Female (MoLN.FeMs)	lymph nodes	Female	17MoLNFeMs	17248	12776	8396

GSM38494	Lymph nodes: mesenteric, Male (MoLN.MaMs)	lymph nodes	Male	17MoLNMaMs	21904	14691	8935
GSM40118	Lung, Female (MoLu.Feml)	lung	Female	17MoLuFeml	26627	18700	10152
GSM40119	Lung, Male (MoLu.Male)	lung	Male	17MoLuMale	21377	15902	9429
GSM80478	Brain:Medulla, Female (MoMe.Feml)	brain / medulla	Female	17MoMefeml	30870	20296	11268
GSM80479	Brain:Medulla, Male (MoMe.Male)	brain / medulla	Male	17MoMemale	33405	23716	12139
GSM35332	Mammary gland, Female (MoMG.Feml)	mammary gland	Female	17MoMGFeml	22535	17007	9886
GSM34299	Ovary, Female (MoOv.Feml)	ovary	Female	17MoOvFeml	32838	23364	12004
GSM38495	Pituitary, Female (MoPi.Feml)	pituitary	Female	17MoPiFeml	16972	12180	8114
GSM38496	Pituitary, Male (MoPi.Male)	pituitary	Male	17MoPiMale	14397	9959	7149
GSM44333	Placenta - E18, Female (MoPl.FE18)	placenta / E18	Female	17MoPlFE18	22725	16773	9788
GSM80480	Brain:Pons, Female (MoPo.Feml)	brain / pons	Female	17MoPofeml	24186	17750	10434
GSM80481	Brain:Pons, Male (MoPo.Male)	brain / pons	Male	17MoPomale	30896	19257	10848
GSM47342	Prostate, Male (MoPr.Male)	prostate	Male	17MoPrMale	11993	8458	6240
GSM35333	Spinal cord:entire, Female (MoSC.FeEn)	spinal cord / entire	Female	17MoSCFeEn	66524	28512	13695
GSM38497	Spinal cord:entire, Male (MoSC.MaEn)	spinal cord / entire	Male	17MoSCMaEn	28813	19698	11243
GSM40120	Small intestine, Female (MoSI.Feml)	small intestine	Female	17MoSIFeml	22649	16371	9606
GSM47343	Small intestine, Male (MoSI.Male)	small intestine	Male	17MoSIMale	23397	17529	9958
GSM32358	Skin:hairy, from back, Female (MoSk.FeHB)	skin / hairy from back	Female	17MoSkFeHB	22175	15665	9788
GSM36607	Skin:hairy, from back, Male (MoSk.MaHB)	skin / hairy from back	Male	17MoSkMaHB	30215	17440	10754
GSM47344	SkeletalMuscle:Thigh, Female (MoSM.FeTh)	skeletal muscle / thigh	Female	17MoSMFeTh	11925	9411	6318
GSM47345	SkeletalMuscle:Thigh, Male (MoSM.MaTh)	skeletal muscle / thigh	Male	17MoSMMaTh	12372	10045	6721
GSM36608	Spleen, Female (MoSp.Feml)	spleen	Female	17MoSpFeml	22363	15861	9491
GSM47346	Spleen, Male (MoSp.Male)	spleen	Male	17MoSpMale	16483	11743	7823
GSM35328	Stomach, Female (MoSt.Feml)	stomach	Female	17MoStFeml	18033	13731	8835
GSM40121	Testis, Male (MoTe.Male)	testis	Male	17MoTeMale	24033	15349	9666
GSM38498	Thymus, Female (MoTh.Feml)	thymus	Female	17MoThFeml	28015	19943	10852
GSM36725	Thymus, Male (MoTh.Male)	thymus	Male	17MoThMale	22860	15426	9176
GSM36609	Thyroid/parathyroid, Female (MoTp.Feml)	thyroid + parathyroid	Female	17MoTpFeml	20849	15307	9482
GSM38499	Thyroid/parathyroid, Male (MoTp.Male)	thyroid + parathyroid	Male	17MoTpMale	20391	15304	9553
GSM35330	Uterus, Female (MoUt.Feml)	uterus	Female	17MoUtFeml	16494	12085	8260
GSM35329	Uterus:Pregnant E18, Female (MoUt.FP18)	uterus (pregnant)	Female	17MoUtFP18	22103	17068	9999

GSM27144	White fat, Female (MoWF.FeAb)	white fat / abdomen	Female	17MoWFFeAb	13861	10215	7085
GSM32359	White fat, Male (MoWF.MaAb)	white fat / abdomen	Male	17MoWFMaAb	23369	16437	9903

Table S2. Liver-specific targets

Table S2A. Liver-specific targets were selected based on relative gene expression levels in both human and mouse tissues. Gene names, symbols, identification numbers, and logarithmic ratios of liver expression versus expression in other tissues are given here.

Description	Gene symbol	Human gene	Log-ratio (liver / sum of all)	Log-ratio (liver / next highest)	Liver expression (tpm)	Mouse gene	Log-ratio (liver / sum of all)	Log-ratio (liver / next highest)	Liver expression (tpm)
Alpha-1-B glycoprotein	A1BG	Hs.529161	7.01	289.50	1158	Mm.291499	8.41	340.00	340
ATP-binding cassette, sub-family C (CFTR/MRP), member 6	ABCC6	Hs.442182	8.60	388.00	388	Mm.63514	1.53	3.69	354
A disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 13	ADAMTS13	Hs.131433	3.46	13.00	65	Mm.330084	4.25	18.00	18
Alcohol dehydrogenase 4 (class II), pi polypeptide	ADH4	Hs.1219	4.70	38.75	155	Mm.158750	5.67	50.00	50
Afamin	AFM	Hs.168718	8.08	270.00	270	Mm.348786	3.70	12.00	12
Alanine-glyoxylate aminotransferase	AGXT	Hs.144567	8.27	336.36	3700	Mm.7457	7.52	182.00	182
S-adenosylhomocysteine hydrolase	AHCY	Hs.388004	0.95	5.95	113	Mm.330692	2.81	17.00	34
Alpha-2-HS-glycoprotein	AHSG	Hs.324746	5.75	53.00	53	Mm.197554	8.96	497.00	497
Aldo-keto reductase family 1, member C6	AKR1C6	Hs.567245	6.01	128.75	515	Mm.196666	9.83	1824.00	1824
Albumin 1	ALB	Hs.418167	10.27	1236.00	1236	Mm.16773	12.51	5839.00	5839
Aldehyde dehydrogenase 1 family, member L1	ALDH1L1	Hs.434435	4.64	24.00	24	Mm.30035	3.17	17.75	71
Aldolase 2, B isoform	ALDOB	Hs.530274	6.26	82.69	1075	Mm.218862	4.52	22.00	22
Alpha 1 microglobulin/bikunin	AMBP	Hs.436911	14.06	17110.00	17110	Mm.2197	10.43	1382.00	1382
Angiopoietin-like 3	ANGPTL3	Hs.209153	5.70	51.00	51	Mm.28341	5.64	49.00	49
Apolipoprotein A-V	APOA5	Hs.283923	9.31	635.00	635	Mm.29738	3.81	13.00	13
Apolipoprotein B	APOB	Hs.120759	5.78	54.00	54	Mm.221239	6.55	93.00	93
Apolipoprotein C-I	APOC1	Hs.110675	7.64	198.00	198	Mm.182440	1.46	10.16	5771
Apolipoprotein H	APOH	Hs.445358	9.12	835.50	1671	Mm.2266	9.50	724.00	724
Aquaporin 9	AQP9	Hs.104624	1.89	11.00	1133	Mm.335570	5.52	45.00	45
Arginase	ARG1	Hs.440934	7.28	154.00	154	Mm.154144	•	0.00	0
Asialoglycoprotein receptor 1	ASGR1	Hs.12056	6.45	146.00	876	Mm.6559	1.67	4.93	1272
Asialoglycoprotein receptor 2	ASGR2	Hs.567238	2.75	23.28	745	Mm.1357	4.09	28.90	289
Argininosuccinate lyase	ASL	Hs.632015	•	•	•	Mm.23869	5.88	58.00	58
Argininosuccinate synthetase 1	ASS1	Hs.160786	2.40	11.14	5314	Mm.3217	6.75	107.00	107

Bile acid-Coenzyme A: amino acid N-acyltransferase	BAAT	Hs.284712	4.80	53.00	530	Mm.2859	5.21	36.00	36
Betaine-homocysteine methyltransferase	BHMT	Hs.80756	1.70	3.38	2876	Mm.329582	9.95	986.00	986
Complement component 1, r subcomponent-like	C1RL	Hs.567497	3.64	14.80	74	Mm.132974	3.88	25.50	102
Complement component 3	C3	Hs.529053	8.40	337.00	337	Mm.19131	5.61	48.00	48
Complement component 8, beta subunit	C8B	Hs.391835	7.84	275.60	1378	Mm.87072	2.11	130.00	130
Complement factor B	CFB	Hs.69771	8.10	308.00	2464	Mm.653	5.25	37.00	37
Complement component factor h	CFH	Hs.363396	4.78	82.00	246	Mm.8655	0.18	3.00	63
Procollagen, type XVIII, alpha 1	COL18A1	Hs.517356	7.78	219.00	219	Mm.4352	3.91	14.00	14
Catechol-O-methyltransferase	COMT	Hs.370408	5.78	165.00	1155	Mm.100940	4.64	24.00	24
Ceruloplasmin	CP	Hs.558314	2.77	17.43	244	Mm.13787	7.04	131.00	131
Carboxypeptidase B2 (plasma)	CPB2	Hs.512937	3.76	19.06	610	Mm.24242	3.86	15.14	318
Carboxypeptidase N, polypeptide 2	CPN2	Hs.528368	3.80	21.75	348	Mm.290614	4.46	21.00	21
Carbamoyl-phosphate synthetase 1	CPS1	Hs.149252	6.11	68.00	68	Mm.343942	3.81	13.00	13
Cytochrome P450, family 27, subfamily a, polypeptide 1	CYP27A1	Hs.516700	0.52	8.39	1343	Mm.85083	2.88	13.42	161
Cytochrome P450, family 3, subfamily a, polypeptide 25	CYP3A25	Hs.306220	3.59	20.00	180	Mm.301900	3.37	10.53	453
Cytochrome P450, family 4, subfamily a, polypeptide 10	CYP4A10	Hs.1645	7.81	224.00	224	Mm.10742	5.49	44.00	44
Cytochrome P450, family 8, subfamily b, polypeptide 1	CYP8B1	Hs.447793	8.30	314.00	314	Mm.20889	6.77	108.00	108
Dihydropyrimidinase	DPYS	Hs.443161	5.86	57.00	57	Mm.275974	4.25	37.00	37
Enoyl coenzyme A hydratase 1, peroxisomal	ECH1	Hs.196176	9.51	730.00	730	Mm.291776	4.86	28.00	28
Coagulation factor XI	F11	Hs.1430	4.99	36.83	221	Mm.33326	5.17	35.00	35
Coagulation factor XII (Hageman factor)	F12	Hs.1321	6.69	102.00	102	Mm.42224	6.09	67.00	67
Fumarylacetoacetate hydrolase	FAH	Hs.73875	3.19	27.17	163	Mm.3798	5.00	31.00	31
Fructose bisphosphatase 1	FBP1	Hs.494496	1.31	3.58	455	Mm.423078	5.93	60.00	60
Fibrinogen, alpha polypeptide	FGA	Hs.351593	7.85	230.00	230	Mm.88793	4.95	30.00	30
Fibrinogen, B beta polypeptide	FGB	Hs.300774	5.12	59.87	6406	Mm.30063	7.02	129.00	129
Fibrinogen, gamma polypeptide	FGG	Hs.546255	8.27	308.00	308	Mm.16422	3.87	14.95	598

Fibrinogen-like protein 1	FGL1	Hs.491143	3.49	15.19	1656	Mm.277955	6.48	88.00	88
Fibronectin 1	FN1	Hs.203717	2.77	11.17	67	Mm.193099	2.42	7.50	15
Formiminotransferase cyclodeaminase	FTCD	Hs.415846	7.73	593.80	2969	Mm.36278	6.82	112.00	112
Glucose-6-phosphatase, catalytic	G6PC	Hs.212293	5.78	54.00	54	Mm.18064	4.17	17.00	17
Group specific component	GC	Hs.418497	6.07	66.00	66	Mm.196595	7.35	407.50	815
Glutaryl-Coenzyme A dehydrogenase	GCDH	Hs.532699	0.57	10.11	384	Mm.2475	4.81	27.00	27
Gap junction membrane channel protein beta 1	GJB1	Hs.333303	4.23	43.78	394	Mm.21198	-0.21	2.76	593
Glutaminase 2 (liver, mitochondrial)	GLS2	Hs.212606	7.99	254.00	254	Mm.30102	4.58	23.00	23
Glycine N-methyltransferase	GNMT	Hs.144914	7.60	322.33	967	Mm.29395	5.32	39.00	39
G protein-coupled receptor 146	GPR146	Hs.20961	5.00	31.00	31	Mm.270003	1.48	7.33	88
3-hydroxyanthranilate 3,4-dioxygenase	HAAO	Hs.368805	9.32	636.00	636	Mm.30100	4.32	19.00	19
Histidine ammonia-lyase	HAL	Hs.190783	3.37	15.00	30	Mm.13000	0.59	3.86	135
3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	HMGCS2	Hs.59889	6.04	65.00	65	Mm.289131	6.11	68.00	68
Haptoglobin	HP	Hs.513711	6.54	92.00	92	Mm.26730	0.09	2.61	300
4-hydroxyphenylpyruvic acid dioxygenase	HPD	Hs.2899	11.68	3278.00	3278	Mm.6584	3.41	13.02	4269
Hemopexin	HPX	Hs.426485	8.92	482.00	482	Mm.3485	5.90	122.58	7968
Histidine-rich glycoprotein	HRG	Hs.1498	7.27	153.00	153	Mm.358794	8.79	664.50	1329
Inter-alpha trypsin inhibitor, heavy chain 1	ITIH1	Hs.420257	10.04	1051.00	1051	Mm.3227	1.93	4.50	18
Inter-alpha trypsin inhibitor, heavy chain 2	ITIH2	Hs.75285	6.54	92.00	92	Mm.182043	5.75	53.00	53
Inter-alpha trypsin inhibitor, heavy chain 3	ITIH3	Hs.76716	9.03	522.00	522	Mm.4517	2.17	8.50	17
Ketohexokinase	KHK	Hs.567297	5.59	85.61	1541	Mm.22451	4.52	22.00	22
Kininogen 1	KNG1	Hs.77741	6.92	120.00	120	Mm.2160	2.81	10.00	20
Mannan-binding lectin serine peptidase 1	MASP1	Hs.89983	4.82	37.33	112	Mm.1213	4.17	17.00	17
Methionine adenosyltransferase I, alpha	MAT1A	Hs.282670	7.48	177.00	177	Mm.14064	10.95	3947.00	3947
Mannoside acetylglucosaminyltransferase 4, isoenzyme B	MGAT4B	Hs.567419	5.95	61.00	61	Mm.86759	•	0.00	0
Macrophage stimulating 1 (hepatocyte growth factor-like)	MST1	Hs.349110	1.75	12.34	469	Mm.8369	1.67	12.20	305
Nuclear receptor subfamily 0, group B, member 2	NR0B2	Hs.427055	1.19	7.18	79	Mm.346759	1.57	3.62	275

Plasminogen	PLG	Hs.143436	4.93	40.33	121	Mm.971	9.51	726.00	726
Paraoxonase 1	PON1	Hs.370995	5.10	137.43	962	Mm.237657	3.43	51.07	1532
Retinol binding protein 4, plasma	RBP4	Hs.50223	9.70	830.00	830	Mm.2605	2.23	16.75	201
Ras homolog gene family, member B	RHOB	Hs.502876	2.30	29.18	496	Mm.687	2.00	5.50	11
Serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10	SERPINA10	Hs.118620	7.20	146.00	146	Mm.29094	0.06	3.16	269
Serine (or cysteine) peptidase inhibitor, clade A, member 1a	SERPINA1A	Hs.525557	11.01	2056.00	2056	Mm.312593	1.02	26.47	11751
Serine (or cysteine) peptidase inhibitor, clade A, member 6	SERPINA6	Hs.532635	1.86	5.90	496	Mm.290079	9.53	736.00	736
Serine (or cysteine) peptidase inhibitor, clade C (antithrombin), member 1	SERPINC1	Hs.75599	7.81	223.00	223	Mm.260770	7.68	247.63	4705
Serine (or cysteine) peptidase inhibitor, clade D, member 1	SERPIND1	Hs.474270	10.90	1911.00	1911	Mm.6609	2.13	9.00	648
Serine (or cysteine) peptidase inhibitor, clade F, member 2	SERPINF2	Hs.159509	4.70	25.00	25	Mm.279733	5.98	62.00	62
Serine (or cysteine) peptidase inhibitor, clade G, member 1	SERPING1	Hs.384598	1.39	11.35	4382	Mm.38888	1.46	5.38	43
Solute carrier family 22 (organic cation transporter), member 1	SLC22A1	Hs.117367	7.56	269.57	1887	Mm.594	0.05	1.11	340
Solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	SLC25A15	Hs.442781	6.00	63.00	63	Mm.200907	4.70	25.00	25
Solute carrier family 27 (fatty acid transporter), member 5	SLC27A5	Hs.309583	2.09	28.56	1571	Mm.10984	8.09	545.00	545
Solute carrier family 2 (facilitated glucose transporter), member 2	SLC2A2	Hs.167584	9.43	689.00	689	Mm.18443	2.42	5.69	74
Solute carrier family 38, member 3	SLC38A3	Hs.76460	9.62	785.00	785	Mm.296560	1.12	3.02	136
Solute carrier organic anion transporter family, member 2b1	SLCO2B1	Hs.7884	2.44	9.38	75	Mm.11249	5.49	44.00	44
Spermatogenesis associated 13	SPATA13	Hs.131017	3.51	18.83	113	Mm.149776	3.12	12.50	25
Tryptophan 2,3-dioxygenase	TDO2	Hs.183671	3.58	11.00	11	Mm.258622	5.49	67.00	134
Transferrin receptor 2	TFR2	Hs.544932	6.13	69.00	69	Mm.21757	4.70	25.00	25
Transmembrane 4 superfamily member 4	TM4SF4	Hs.133527	6.38	82.00	82	Mm.26618	2.90	7.82	133

Transmembrane serine protease 6	TMPRSS6	Hs.370885	6.41	84.00	84	Mm.34056	4.91	29.00	29
Transferrin	TF	Hs.518267	2.72	7.22	65	Mm.37214	4.86	28.00	28
Thioredoxin domain containing 11	TXNDC11	Hs.313847	1.58	3.50	14	Mm.291015	-1.62	0.24	16
UDP glucuronosyltransferase 2 family, polypeptide B1	UGT2B1	Hs.285887	8.03	260.00	260	Mm.26741	4.09	16.00	16
UDP glucuronosyltransferase 2 family, polypeptide B36	UGT2B36	Hs.150207	3.94	16.89	152	Mm.291575	2.58	381.00	381
Ureidopropionase, beta	UPB1	Hs.474388	6.12	103.50	207	Mm.441195	•	•	•
Zinc finger, A20 domain containing 2	ZA20D2	Hs.406096	1.86	17.12	137	Mm.292405	1.44	4.50	18
Zinc finger, CCCH-type with G patch domain	ZGPAT	Hs.11900	10.06	1070.00	1070	Mm.272712	0.43	4.67	56

Table S2B. Liver-specific targets were categorized by into two highly-valued groups: intracellular/membrane and secreted. Antibodies advertised as validated for western blotting were purchased from the listed vendors.

Gene symbol	UniGene	Category	Antibody source	Cat. No.
ADH4	Mm.158750	intracellular or membrane	Aviva Systems Biology	ARP43573_T100
AFM	Mm.348786	intracellular or membrane	Aviva Systems Biology	ARP33804_P50
AGXT	Mm.7457	intracellular or membrane	Abcam	ab91074
AHCY	Mm.330692	intracellular or membrane	Abcam	ab56146
AHSG	Mm.197554	secreted	Aviva Systems Biology	ARP33815_P50
ALDH1L1	Mm.30035	intracellular or membrane	abcam	ab56777
ALDOB	Mm.218862	intracellular or membrane	Abnova	H00000229-A01
AMBP	Mm.2197	secreted	Novus	H00000259-M01
AQP9	Mm.335570	intracellular or membrane	ADI	AQP91-A
ARG1	Mm.154144	intracellular or membrane	Aviva Systems Biology	ARP45673_T100/ARP45672_T100
ASGR1	Mm.6559	intracellular or membrane	Santa Cruz Biotechnology, Inc.	sc-13467
ASGR2	Mm.1357	intracellular or membrane	Santa Cruz Biotechnology, Inc.	sc-13471
ASL	Mm.23869	intracellular or membrane	Aviva Systems Biology	ARP41667_T100
ASS1	Mm.3217	intracellular or membrane	Aviva Systems Biology	ARP41367_T100
BAAT	Mm.2859	intracellular or membrane	Novus	H00000570-M02
BHMT	Mm.329582	intracellular or membrane	Aviva Systems Biology	ARP41474_T100
COMT	Mm.100940	intracellular or membrane	Santa Cruz Biotechnology, Inc.	sc-28116
CP	Mm.13787	secreted	abcam	ab8813
CPS1	Mm.343942	intracellular or membrane	Abnova	H00001373-M01
DPYS	Mm.275974	intracellular or membrane	ISB	ISB005-2
ECH1	Mm.291776	intracellular or membrane	Abnova	H00001892-M01
FAH	Mm.3798	intracellular or membrane	Aviva Systems Biology	ARP_41681_T100
FBP1	Mm.423078	intracellular or membrane	Aviva Systems Biology	H00002203-A01/ARP41406_T100
FGA	Mm.88793	secreted	Genway	15-288-22856
FGL1	Mm.277955	intracellular or membrane	Novus	H00002267-M01
FTCD	Mm.36278	intracellular or membrane	abcam	ab5820
GCDH	Mm.2475	intracellular or membrane	Aviva Systems Biology	ARP_43559_T100
GJB1	Mm.21198	intracellular or membrane	Aviva Systems Biology	ARP36600_T200
GLS2	Mm.30102	intracellular or membrane	Aviva Systems Biology	ARP_43562_T100
GNMT	Mm.29395	intracellular or membrane	ISB	ISB011-1
HAAO	Mm.30100	intracellular or membrane	Abcam	ab77220
HAL	Mm.13000	intracellular or membrane	Aviva Systems Biology	ARP45694_T100
HMGCS2	Mm.289131	intracellular or membrane	ISB	ISB003 2E11, 3A4, 5D9,6B4,7C12
HP	Mm.26730	secreted	Genway	15-288-20080F
HPD	Mm.6584	intracellular or membrane	ISB	ISB021-2
HPX	Mm.3485	secreted	Novus	H00003263-A01
KHK	Mm.22451	intracellular or membrane	Novus	H00003795-M01
KNG1	Mm.2160	intracellular or membrane	Aviva Systems Biology	ARP45680_P050

MAT1A	Mm.14064	intracellular or membrane	Aviva Systems Biology	ARP41399_T100/ISB029-1
MST1	Mm.8369	intracellular or membrane	Novus	H00004485-M01
PLG	Mm.971	secreted	innovative research	IASMPLG-GF-1.0mg
PON1	Mm.389078	secreted	Novus	H00005444-A01
RBP4	Mm.2605	secreted	Novus/Axxora	H00005950-M01/ALX-210/437-C100
TDO2	Mm.258622	intracellular or membrane	Novus	H00006999-A01
TF	Mm.37214	secreted	Genway	15-288-2009F
TFR2	Mm.21757	intracellular or membrane	HyCult	HM2135
UPB1	Mm.441195	intracellular or membrane	Aviva Systems Biology	ARP_42467_T100

Table S3. SPRI of antibody arrays

Table S3A. Map of SPRI microarray Set A containing 792 printed features.

The position of each feature on the microarray is given as a row number and column number. A value of one in the "Sec." column indicates a secreted, liver-specific protein. A value of one in the "Intra." column indicates an intracellular, liver-specific protein.

No.	Antibody target	Source plate	Column	Row	Sec.	Intra.
1	Apln	A22	1	1	0	0
2	Nef3	B20	2	1	0	0
3	GCDFP 15	C18	3	1	0	0
4	v-Snare vit 1p (D-19)	D16	4	1	0	0
5	YWHAF	E14	5	1	0	0
6	HAGH	F12	6	1	0	0
7	GPC6	G10	7	1	0	0
8	PN18	H8	8	1	0	0
9	CD4	I6	9	1	0	0
10	TCR2	J4	10	1	0	0
11	IkB alpha	K2	11	1	0	0
12	IL1 alpha capture	K24	12	1	0	0
13	TNF alpha detection	L22	13	1	0	0
14	ALDOB	M20	14	1	0	1
15	haptoglobin	N18	15	1	1	0
16	RBP4	O16	16	1	1	0
17	ASGRP1/2(FL)	P14	17	1	0	1
18	Empty	Empty	18	1	0	0
19	Apln	A22	19	1	0	0
20	Nef3	B20	20	1	0	0
21	GCDFP 15	C18	21	1	0	0
22	v-Snare vit 1p (D-19)	D16	22	1	0	0
23	YWHAF	E14	23	1	0	0
24	HAGH	F12	24	1	0	0
25	GPC6	G10	25	1	0	0
26	PN18	H8	26	1	0	0
27	CD4	I6	27	1	0	0
28	TCR2	J4	28	1	0	0
29	IkB alpha	K2	29	1	0	0
30	IL1 alpha capture	K24	30	1	0	0
31	TNF alpha detection	L22	31	1	0	0
32	ALDOB	M20	32	1	0	1
33	haptoglobin	N18	33	1	1	0
34	RBP4	O16	34	1	1	0

35	ASGRP1/2(FL)	P14	35	1	0	1
36	Empty	Empty	36	1	0	0
37	Rgs4	A20	1	2	0	0
38	Plat	B18	2	2	0	0
39	Eolase	C16	3	2	0	0
40	PSA (A67-B/E3)	D14	4	2	0	0
41	MRE11A	E12	5	2	0	0
42	cyclophilin	F10	6	2	0	0
43	E2A	G8	7	2	0	0
44	PN16	H6	8	2	0	0
45	CD11c	I4	9	2	0	0
46	Dendritic	J2	10	2	0	0
47	TCR (GL3)	J24	11	2	0	0
48	IL1B capture	K22	12	2	0	0
49	TNF capture	L20	13	2	0	0
50	catalase	M18	14	2	0	1
51	ASGPR	N16	15	2	0	1
52	ASGPR2	O14	16	2	0	1
53	AG	P12	17	2	0	1
54	Empty	Empty	18	2	0	0
55	Rgs4	A20	19	2	0	0
56	Plat	B18	20	2	0	0
57	Eolase	C16	21	2	0	0
58	PSA (A67-B/E3)	D14	22	2	0	0
59	MRE11A	E12	23	2	0	0
60	cyclophilin	F10	24	2	0	0
61	E2A	G8	25	2	0	0
62	PN16	H6	26	2	0	0
63	CD11c	I4	27	2	0	0
64	Dendritic	J2	28	2	0	0
65	TCR (GL3)	J24	29	2	0	0
66	IL1B capture	K22	30	2	0	0
67	TNF capture	L20	31	2	0	0
68	catalase	M18	32	2	0	1
69	ASGPR	N16	33	2	0	1
70	ASGPR2	O14	34	2	0	1
71	AG	P12	35	2	0	1
72	Empty	Empty	36	2	0	0
73	Msr2	A18	1	3	0	0
74	Isgf3g	B16	2	3	0	0
75	PSA	C14	3	3	0	0
76	Plasma Kallikrein	D12	4	3	0	0
77	PTPRK	E10	5	3	0	0

78	NORG1	F8	6	3	0	0
79	C/EBP?	G6	7	3	0	0
80	PN14	H4	8	3	0	0
81	CD11b	I2	9	3	0	0
82	IL8	I24	10	3	0	0
83	CD16/CD32	J22	11	3	0	0
84	IL6 detection	K20	12	3	0	0
85	KC capture	L18	13	3	0	0
86	ASGPR2	M16	14	3	0	1
87	LCAT	N14	15	3	1	0
88	ASGPR1	O12	16	3	0	1
89	AG	P10	17	3	0	1
90	Empty	Empty	18	3	0	0
91	Msr2	A18	19	3	0	0
92	Isgf3g	B16	20	3	0	0
93	PSA	C14	21	3	0	0
94	Plasma Kallikrein	D12	22	3	0	0
95	PTPRK	E10	23	3	0	0
96	NORG1	F8	24	3	0	0
97	C/EBP?	G6	25	3	0	0
98	PN14	H4	26	3	0	0
99	CD11b	I2	27	3	0	0
100	IL8	I24	28	3	0	0
101	CD16/CD32	J22	29	3	0	0
102	IL6 detection	K20	30	3	0	0
103	KC capture	L18	31	3	0	0
104	ASGPR2	M16	32	3	0	1
105	LCAT	N14	33	3	1	0
106	ASGPR1	O12	34	3	0	1
107	AG	P10	35	3	0	1
108	Empty	Empty	36	3	0	0
109	Gc	A16	1	4	1	0
110	Rgs4	B14	2	4	0	0
111	ATP 6E	C12	3	4	0	0
112	Asb-3	D10	4	4	0	0
113	Lamin A/C	E8	5	4	0	0
114	NERPVR	F6	6	4	0	0
115	blm	G4	7	4	0	0
116	PN12	H2	8	4	0	0
117	Ly-6G	H24	9	4	0	0
118	G1	I22	10	4	0	0
119	CD3 (T cells)	J20	11	4	0	0
120	Isc 15	K18	12	4	0	0

121	I-TAC capture	L16	13	4	0	0
122	AQP9	M14	14	4	0	1
123	properdin, B factor	N12	15	4	1	0
124	plasminogen	O10	16	4	1	0
125	Transferrin	P8	17	4	1	0
126	Empty	Empty	18	4	0	0
127	Gc	A16	19	4	1	0
128	Rgs4	B14	20	4	0	0
129	ATP 6E	C12	21	4	0	0
130	Asb-3	D10	22	4	0	0
131	Lamin A/C	E8	23	4	0	0
132	NERPVR	F6	24	4	0	0
133	blm	G4	25	4	0	0
134	PN12	H2	26	4	0	0
135	Ly-6G	H24	27	4	0	0
136	G1	I22	28	4	0	0
137	CD3 (T cells)	J20	29	4	0	0
138	Isc 15	K18	30	4	0	0
139	I-TAC capture	L16	31	4	0	0
140	AQP9	M14	32	4	0	1
141	properdin, B factor	N12	33	4	1	0
142	plasminogen	O10	34	4	1	0
143	Transferrin	P8	35	4	1	0
144	Empty	Empty	36	4	0	0
145	Tln1	A14	1	5	0	0
146	B2m	B12	2	5	0	0
147	Neuron Specific Enolase	C10	3	5	0	0
148	Odf 2	D8	4	5	0	0
149	JAK 3 (C-21)	E6	5	5	0	0
150	TKTL	F4	6	5	0	0
151	APC	G2	7	5	0	0
152	?-catenin	G24	8	5	0	0
153	CD14	H22	9	5	0	0
154	LAMP1	I20	10	5	0	0
155	CD45R/B cell	J18	11	5	0	0
156	human lactoferrin	K16	12	5	0	0
157	IFN-r detection	L14	13	5	0	0
158	C3	M12	14	5	1	0
159	CPS1	N10	15	5	0	1
160	ANGPTL3	O8	16	5	0	1
161	A1BG	P6	17	5	1	0
162	Empty	Empty	18	5	0	0
163	Tln1	A14	19	5	0	0

164	B2m	B12	20	5	0	0
165	Neuron Specific Enolase	C10	21	5	0	0
166	Odf 2	D8	22	5	0	0
167	JAK 3 (C-21)	E6	23	5	0	0
168	TKTL	F4	24	5	0	0
169	APC	G2	25	5	0	0
170	?-catenin	G24	26	5	0	0
171	CD14	H22	27	5	0	0
172	LAMP1	I20	28	5	0	0
173	CD45R/B cell	J18	29	5	0	0
174	human lactoferrin	K16	30	5	0	0
175	IFN-r detection	L14	31	5	0	0
176	C3	M12	32	5	1	0
177	CPS1	N10	33	5	0	1
178	ANGPTL3	O8	34	5	0	1
179	A1BG	P6	35	5	1	0
180	Empty	Empty	36	5	0	0
181	Apod	A12	1	6	0	0
182	Ncoa2	B10	2	6	0	0
183	Syntenin	C8	3	6	0	0
184	TSG 101	D6	4	6	0	0
185	Tenascin-R	E4	5	6	0	0
186	NGEPS	F2	6	6	0	0
187	PN10	F24	7	6	0	0
188	PTEN(26H9)	G22	8	6	0	0
189	CD4	H20	9	6	0	0
190	CD8a	I18	10	6	0	0
191	CD45-2	J16	11	6	0	0
192	PKB	K14	12	6	0	0
193	mJE detection	L12	13	6	0	0
194	MIP-2 capture	M10	14	6	0	0
195	ALDH4A1	N8	15	6	0	1
196	albumin	O6	16	6	1	0
197	GJB1	P4	17	6	0	1
198	Empty	Empty	18	6	0	0
199	Apod	A12	19	6	0	0
200	Ncoa2	B10	20	6	0	0
201	Syntenin	C8	21	6	0	0
202	TSG 101	D6	22	6	0	0
203	Tenascin-R	E4	23	6	0	0
204	NGEPS	F2	24	6	0	0
205	PN10	F24	25	6	0	0
206	PTEN(26H9)	G22	26	6	0	0

207	CD4	H20	27	6	0	0
208	CD8a	I18	28	6	0	0
209	CD45-2	J16	29	6	0	0
210	PKB	K14	30	6	0	0
211	mJE detection	L12	31	6	0	0
212	MIP-2 capture	M10	32	6	0	0
213	ALDH4A1	N8	33	6	0	1
214	albumin	O6	34	6	1	0
215	GJB1	P4	35	6	0	1
216	Empty	Empty	36	6	0	0
217	Apob	A10	1	7	1	0
218	Apob alt	B8	2	7	1	0
219	Ubiquitin	C6	3	7	0	0
220	Sortilin	D4	4	7	0	0
221	a-VASP	E2	5	7	0	0
222	STPAP2	E24	6	7	0	0
223	PN8	F22	7	7	0	0
224	Oct3/4	G20	8	7	0	0
225	CD117 (c-kit)	H18	9	7	0	0
226	IL6	I16	10	7	0	0
227	CD49e	J14	11	7	0	0
228	Dyn2	K12	12	7	0	0
229	IFN-r capture	L10	13	7	0	0
230	MCP-5 captrue	M8	14	7	0	0
231	TDO2	N6	15	7	0	1
232	TfR2	O4	16	7	0	1
233	NF1C	P2	17	7	0	0
234	C3 (from chicken)	P24	18	7	1	0
235	Apob	A10	19	7	1	0
236	Apob alt	B8	20	7	1	0
237	Ubiquitin	C6	21	7	0	0
238	Sortilin	D4	22	7	0	0
239	a-VASP	E2	23	7	0	0
240	STPAP2	E24	24	7	0	0
241	PN8	F22	25	7	0	0
242	Oct3/4	G20	26	7	0	0
243	CD117 (c-kit)	H18	27	7	0	0
244	IL6	I16	28	7	0	0
245	CD49e	J14	29	7	0	0
246	Dyn2	K12	30	7	0	0
247	IFN-r capture	L10	31	7	0	0
248	MCP-5 captrue	M8	32	7	0	0
249	TDO2	N6	33	7	0	1

250	TfR2	O4	34	7	0	1
251	NF1C	P2	35	7	0	0
252	C3 (from chicken)	P24	36	7	1	0
253	B2m	A8	1	8	0	0
254	Nek6	B6	2	8	0	0
255	ARGBP2 (NT)	C4	3	8	0	0
256	URP1	D2	4	8	0	0
257	ZAG (H-21)	D24	5	8	0	0
258	IGFBP6	E22	6	8	0	0
259	PN6	F20	7	8	0	0
260	Nanog	G18	8	8	0	0
261	CD152 (CTLA-4)	H16	9	8	0	0
262	B7-1	I14	10	8	0	0
263	CD32	J12	11	8	0	0
264	TCR9	K10	12	8	0	0
265	IL10 detection	L8	13	8	0	0
266	GM-CSF detection	M6	14	8	0	0
267	PON1	N4	15	8	1	0
268	GST	O2	16	8	0	0
269	ASGR2	O24	17	8	0	1
270	C3 (from chicken)	P22	18	8	1	0
271	B2m	A8	19	8	0	0
272	Nek6	B6	20	8	0	0
273	ARGBP2 (NT)	C4	21	8	0	0
274	URP1	D2	22	8	0	0
275	ZAG (H-21)	D24	23	8	0	0
276	IGFBP6	E22	24	8	0	0
277	PN6	F20	25	8	0	0
278	Nanog	G18	26	8	0	0
279	CD152 (CTLA-4)	H16	27	8	0	0
280	B7-1	I14	28	8	0	0
281	CD32	J12	29	8	0	0
282	TCR9	K10	30	8	0	0
283	IL10 detection	L8	31	8	0	0
284	GM-CSF detection	M6	32	8	0	0
285	PON1	N4	33	8	1	0
286	GST	O2	34	8	0	0
287	ASGR2	O24	35	8	0	1
288	C3 (from chicken)	P22	36	8	1	0
289	Gusb	A6	1	9	0	0
290	Cldn11	B4	2	9	0	0
291	Hist 3H2A	C2	3	9	0	0
292	Zip	C24	4	9	0	0

293	Glial Filament Protein	D22	5	9	0	0
294	WNK4	E20	6	9	0	0
295	PN4	F18	7	9	0	0
296	LRP-5/6	G16	8	9	0	0
297	CD45R/B220	H14	9	9	0	0
298	Ly-6G	I12	10	9	0	0
299	Cd49b	J10	11	9	0	0
300	talin	K8	12	9	0	0
301	IL15 detection	L6	13	9	0	0
302	TGF-beta1 detection	M4	14	9	0	0
303	HSD11B2	N2	15	9	0	1
304	ceruloplasmin	N24	16	9	1	0
305	AMBP	O22	17	9	1	0
306	C3 (from chicken)	P20	18	9	1	0
307	Gusb	A6	19	9	0	0
308	Cldn11	B4	20	9	0	0
309	Hist 3H2A	C2	21	9	0	0
310	Zip	C24	22	9	0	0
311	Glial Filament Protein	D22	23	9	0	0
312	WNK4	E20	24	9	0	0
313	PN4	F18	25	9	0	0
314	LRP-5/6	G16	26	9	0	0
315	CD45R/B220	H14	27	9	0	0
316	Ly-6G	I12	28	9	0	0
317	Cd49b	J10	29	9	0	0
318	talin	K8	30	9	0	0
319	IL15 detection	L6	31	9	0	0
320	TGF-beta1 detection	M4	32	9	0	0
321	HSD11B2	N2	33	9	0	1
322	ceruloplasmin	N24	34	9	1	0
323	AMBP	O22	35	9	1	0
324	C3 (from chicken)	P20	36	9	1	0
325	Cd83	A4	1	10	0	0
326	Ctsc	B2	2	10	0	0
327	ubiqitin	B24	3	10	0	0
328	MTLR4	C22	4	10	0	0
329	Integrin alpha 3	D20	5	10	0	0
330	ADRM1	E18	6	10	0	0
331	PN2	F16	7	10	0	0
332	Laminin Receptor	G14	8	10	0	0
333	IFN-r	H12	9	10	0	0
334	F4/80	I10	10	10	0	0
335	m-r	J8	11	10	0	0

336	MyD 88	K6	12	10	0	0
337	IL1 alpha detection	L4	13	10	0	0
338	MIG detection	M2	14	10	0	0
339	HPX	M24	15	10	1	0
340	fibrinogen	N22	16	10	1	0
341	BAAT	O20	17	10	0	1
342	albumin detection Ab	P18	18	10	1	0
343	Cd83	A4	19	10	0	0
344	Ctsc	B2	20	10	0	0
345	ubiqitin	B24	21	10	0	0
346	MTLR4	C22	22	10	0	0
347	Integrin alpha 3	D20	23	10	0	0
348	ADRM1	E18	24	10	0	0
349	PN2	F16	25	10	0	0
350	Laminin Receptor	G14	26	10	0	0
351	IFN-r	H12	27	10	0	0
352	F4/80	I10	28	10	0	0
353	m-r	J8	29	10	0	0
354	MyD 88	K6	30	10	0	0
355	IL1 alpha detection	L4	31	10	0	0
356	MIG detection	M2	32	10	0	0
357	HPX	M24	33	10	1	0
358	fibrinogen	N22	34	10	1	0
359	BAAT	O20	35	10	0	1
360	albumin detection Ab	P18	36	10	1	0
361	C1qc	A2	1	11	0	0
362	Gfap	A24	2	11	0	0
363	Atp1b2	B22	3	11	0	0
364	Proteasome Inhibitor Subunit 1 P13	C20	4	11	0	0
365	AR (441)	D18	5	11	0	0
366	AK2 (N-term)	E16	6	11	0	0
367	HMGCS2	F14	7	11	0	1
368	HDGF	G12	8	11	0	0
369	PN20	H10	9	11	0	0
370	CD86	I8	10	11	0	0
371	CD16/CD32	J6	11	11	0	0
372	IRAK-1	K4	12	11	0	0
373	IL-15 capture	L2	13	11	0	0
374	TGF-beta1 capture	L24	14	11	0	0
375	DPYS	M22	15	11	0	1
376	ferritin heavy chain	N20	16	11	1	0
377	FGL1	O18	17	11	0	1

378	ASGPR1 (8D7)	P16	18	11	0	1
379	C1qc	A2	19	11	0	0
380	Gfap	A24	20	11	0	0
381	Atp1b2	B22	21	11	0	0
382	Proteasome Inhibitor Subunit 1 P13	C20	22	11	0	0
383	AR (441)	D18	23	11	0	0
384	AK2 (N-term)	E16	24	11	0	0
385	HMGCS2	F14	25	11	0	1
386	HDGF	G12	26	11	0	0
387	PN20	H10	27	11	0	0
388	CD86	I8	28	11	0	0
389	CD16/CD32	J6	29	11	0	0
390	IRAK-1	K4	30	11	0	0
391	IL-15 capture	L2	31	11	0	0
392	TGF-beta1 capture	L24	32	11	0	0
393	DPYS	M22	33	11	0	1
394	ferritin heavy chain	N20	34	11	1	0
395	FGL1	O18	35	11	0	1
396	ASGPR1 (8D7)	P16	36	11	0	1
397	Cfh	A21	1	12	1	0
398	Lamp1	B19	2	12	0	0
399	Rho D	C17	3	12	0	0
400	Anti-GST	D15	4	12	0	0
401	GADPH probe dye FAM-MGB	E13	5	12	0	0
402	PMCA	F11	6	12	0	0
403	FGF4	G9	7	12	0	0
404	PN17	H7	8	12	0	0
405	CD3e	I5	9	12	0	0
406	I-Ab	J3	10	12	0	0
407	NF-kB	K1	11	12	0	0
408	IL10 capture	K23	12	12	0	0
409	MIP2 detection	L21	13	12	0	0
410	catalase	M19	14	12	0	0
411	transferrin	N17	15	12	1	0
412	RBP4	O15	16	12	1	0
413	ASGRP1	P13	17	12	0	1
414	Empty	Empty	18	12	0	0
415	Cfh	A21	19	12	1	0
416	Lamp1	B19	20	12	0	0
417	Rho D	C17	21	12	0	0
418	Anti-GST	D15	22	12	0	0
419	GADPH probe dye FAM-MGB	E13	23	12	0	0

420	PMCA	F11	24	12	0	0
421	FGF4	G9	25	12	0	0
422	PN17	H7	26	12	0	0
423	CD3e	I5	27	12	0	0
424	I-Ab	J3	28	12	0	0
425	NF-kB	K1	29	12	0	0
426	IL10 capture	K23	30	12	0	0
427	MIP2 detection	L21	31	12	0	0
428	catalase	M19	32	12	0	0
429	transferrin	N17	33	12	1	0
430	RBP4	O15	34	12	1	0
431	ASGRP1	P13	35	12	0	1
432	Empty	Empty	36	12	0	0
433	Ptprz1	A19	1	13	0	0
434	Ramp3	B17	2	13	0	0
435	GDF15	C15	3	13	0	0
436	Trp-p8	D13	4	13	0	0
437	Kanadaptin	E11	5	13	0	0
438	PYPIV	F9	6	13	0	0
439	casein kinase 1?	G7	7	13	0	0
440	PN15	H5	8	13	0	0
441	CD69	I3	9	13	0	0
442	M8D10.E10	J1	10	13	0	0
443	CD40	J23	11	13	0	0
444	IL4 detection	K21	12	13	0	0
445	KC detection	L19	13	13	0	0
446	HMGCS2	M17	14	13	0	1
447	ApoB	N15	15	13	1	0
448	ASL	O13	16	13	0	1
449	AG	P11	17	13	0	1
450	Empty	Empty	18	13	0	0
451	Ptprz1	A19	19	13	0	0
452	Ramp3	B17	20	13	0	0
453	GDF15	C15	21	13	0	0
454	Trp-p8	D13	22	13	0	0
455	Kanadaptin	E11	23	13	0	0
456	PYPIV	F9	24	13	0	0
457	casein kinase 1?	G7	25	13	0	0
458	PN15	H5	26	13	0	0
459	CD69	I3	27	13	0	0
460	M8D10.E10	J1	28	13	0	0
461	CD40	J23	29	13	0	0
462	IL4 detection	K21	30	13	0	0

463	KC detection	L19	31	13	0	0
464	HMGCS2	M17	32	13	0	1
465	ApoB	N15	33	13	1	0
466	ASL	O13	34	13	0	1
467	AG	P11	35	13	0	1
468	Empty	Empty	36	13	0	0
469	Ncoa2	A17	1	14	0	0
470	Psap	B15	2	14	0	0
471	PERK	C13	3	14	0	0
472	Spectrin beta-1	D11	4	14	0	0
473	Sortilin	E9	5	14	0	0
474	RFP2	F7	6	14	0	0
475	C/EBP?	G5	7	14	0	0
476	PN13	H3	8	14	0	0
477	CD1.1, Ly-38	I1	9	14	0	0
478	Cd33/OAV1D	I23	10	14	0	0
479	4-1 BB (TKS-1)	J21	11	14	0	0
480	IL12 detection	K19	12	14	0	0
481	IP10 capture	L17	13	14	0	0
482	ASGPR1	M15	14	14	0	1
483	C4	N13	15	14	1	0
484	ferritin heavy chain	O11	16	14	1	0
485	transferrin detection Ab alt	P9	17	14	1	0
486	Empty	Empty	18	14	0	0
487	Ncoa2	A17	19	14	0	0
488	Psap	B15	20	14	0	0
489	PERK	C13	21	14	0	0
490	Spectrin beta-1	D11	22	14	0	0
491	Sortilin	E9	23	14	0	0
492	RFP2	F7	24	14	0	0
493	C/EBP?	G5	25	14	0	0
494	PN13	H3	26	14	0	0
495	CD1.1, Ly-38	I1	27	14	0	0
496	Cd33/OAV1D	I23	28	14	0	0
497	4-1 BB (TKS-1)	J21	29	14	0	0
498	IL12 detection	K19	30	14	0	0
499	IP10 capture	L17	31	14	0	0
500	ASGPR1	M15	32	14	0	1
501	C4	N13	33	14	1	0
502	ferritin heavy chain	O11	34	14	1	0
503	transferrin detection Ab alt	P9	35	14	1	0
504	Empty	Empty	36	14	0	0
505	Psap	A15	1	15	0	0

506	Trem2	B13	2	15	0	0
507	PHD4	C11	3	15	0	0
508	ROS N-term	D9	4	15	0	0
509	IRE alpha	E7	5	15	0	0
510	FSTL1	F5	6	15	0	0
511	Axin	G3	7	15	0	0
512	PN11	H1	8	15	0	0
513	TNF	H23	9	15	0	0
514	Cd40	I21	10	15	0	0
515	CD4	J19	11	15	0	0
516	flagellin	K17	12	15	0	0
517	I-TAC detection	L15	13	15	0	0
518	CRP	M13	14	15	1	0
519	ceruloplasmin	N11	15	15	1	0
520	AFP	O9	16	15	1	0
521	MST1	P7	17	15	0	1
522	Empty	Empty	18	15	0	0
523	Psap	A15	19	15	0	0
524	Trem2	B13	20	15	0	0
525	PHD4	C11	21	15	0	0
526	ROS N-term	D9	22	15	0	0
527	IRE alpha	E7	23	15	0	0
528	FSTL1	F5	24	15	0	0
529	Axin	G3	25	15	0	0
530	PN11	H1	26	15	0	0
531	TNF	H23	27	15	0	0
532	Cd40	I21	28	15	0	0
533	CD4	J19	29	15	0	0
534	flagellin	K17	30	15	0	0
535	I-TAC detection	L15	31	15	0	0
536	CRP	M13	32	15	1	0
537	ceruloplasmin	N11	33	15	1	0
538	AFP	O9	34	15	1	0
539	MST1	P7	35	15	0	1
540	Empty	Empty	36	15	0	0
541	Scarb2	A13	1	16	0	0
542	Csf1r	B11	2	16	0	0
543	Guk 1	C9	3	16	0	0
544	RPL 26	D7	4	16	0	0
545	Integrin alpha 5	E5	5	16	0	0
546	LEMD2	F3	6	16	0	0
547	14-3-3?	G1	7	16	0	0
548	YB-1	G23	8	16	0	0

549	IL-6	H21	9	16	0	0
550	CD3c	I19	10	16	0	0
551	CD16/CD32	J17	11	16	0	0
552	CDC42	K15	12	16	0	0
553	JE capture	L13	13	16	0	0
554	C3	M11	14	16	1	0
555	ALDH4A1	N9	15	16	0	1
556	albumin	O7	16	16	1	0
557	SEC14L2	P5	17	16	0	0
558	Empty	Empty	18	16	0	0
559	Scarb2	A13	19	16	0	0
560	Csf1r	B11	20	16	0	0
561	Guk 1	C9	21	16	0	0
562	RPL 26	D7	22	16	0	0
563	Integrin alpha 5	E5	23	16	0	0
564	LEMD2	F3	24	16	0	0
565	14-3-3?	G1	25	16	0	0
566	YB-1	G23	26	16	0	0
567	IL-6	H21	27	16	0	0
568	CD3c	I19	28	16	0	0
569	CD16/CD32	J17	29	16	0	0
570	CDC42	K15	30	16	0	0
571	JE capture	L13	31	16	0	0
572	C3	M11	32	16	1	0
573	ALDH4A1	N9	33	16	0	1
574	albumin	O7	34	16	1	0
575	SEC14L2	P5	35	16	0	0
576	Empty	Empty	36	16	0	0
577	Csf1r	A11	1	17	0	0
578	C4	B9	2	17	0	0
579	Myeloperoxidase	C7	3	17	0	0
580	Nuclear Receptor Corepressor	D5	4	17	0	0
581	ZAG	E3	5	17	0	0
582	PTD	F1	6	17	0	0
583	PN9	F23	7	17	0	0
584	Presenilin 1	G21	8	17	0	0
585	IL-12	H19	9	17	0	0
586	Cd11b	I17	10	17	0	0
587	CD32A	J15	11	17	0	0
588	TGN38	K13	12	17	0	0
589	IP10 detection	L11	13	17	0	0
590	RANTES detection	M9	14	17	0	0
591	AGT	N7	15	17	1	0

592	transferrin	O5	16	17	1	0
593	AHSG	P3	17	17	1	0
594	Empty	Empty	18	17	0	0
595	Csf1r	A11	19	17	0	0
596	C4	B9	20	17	1	0
597	Myeloperoxidase	C7	21	17	0	0
598	Nuclear Receptor Corepressor	D5	22	17	0	0
599	ZAG	E3	23	17	0	0
600	PTD	F1	24	17	0	0
601	PN9	F23	25	17	0	0
602	Presenilin 1	G21	26	17	0	0
603	IL-12	H19	27	17	0	0
604	Cd11b	I17	28	17	0	0
605	CD32A	J15	29	17	0	0
606	TGN38	K13	30	17	0	0
607	IP10 detection	L11	31	17	0	0
608	RANTES detection	M9	32	17	0	0
609	AGT	N7	15	17	1	0
610	transferrin	O5	16	17	1	0
611	AHSG	P3	17	17	1	0
612	Empty	Empty	18	17	0	0
613	Csf1r	A11	19	17	0	0
614	C4	B9	20	17	1	0
615	MGST3	C5	3	18	0	0
616	Intersectin/ESE-1	D3	4	18	0	0
617	Zyxin (C-19)	E1	5	18	0	0
618	FOXA1	E23	6	18	0	0
619	PN7	F21	7	18	0	0
620	Nucleoporin p62	G19	8	18	0	0
621	IL-10	H17	9	18	0	0
622	IL10	I15	10	18	0	0
623	CD8a	J13	11	18	0	0
624	Rab5	K11	12	18	0	0
625	RANTES capture	L9	13	18	0	0
626	MCP-5 capture	M7	14	18	0	0
627	TDO2	N5	15	18	0	1
628	TfR2	O3	16	18	0	1
629	Afm	P1	17	18	0	1
630	C3 (from chicken)	P23	18	18	1	0
631	C4	A9	19	18	1	0
632	Apod	B7	20	18	1	0
633	MGST3	C5	21	18	0	0
634	Intersectin/ESE-1	D3	22	18	0	0

635	Zyxin (C-19)	E1	23	18	0	0
636	FOXA1	E23	24	18	0	0
637	PN7	F21	25	18	0	0
638	Nucleoporin p62	G19	26	18	0	0
639	IL-10	H17	27	18	0	0
640	IL10	I15	28	18	0	0
641	CD8a	J13	29	18	0	0
642	Rab5	K11	30	18	0	0
643	RANTES capture	L9	31	18	0	0
644	MCP-5 capture	M7	32	18	0	0
645	TDO2	N5	33	18	0	1
646	TfR2	O3	34	18	0	1
647	Afm	P1	35	18	0	1
648	C3 (from chicken)	P23	36	18	1	0
649	C1qc	A7	1	19	0	0
650	Shox2	B5	2	19	0	0
651	Emilin-1 (Y-13)	C3	3	19	0	0
652	Tenascin C	D1	4	19	0	0
653	PrxV	D23	5	19	0	0
654	LEMDZ	E21	6	19	0	0
655	PN5	F19	7	19	0	0
656	Muiti Uqbiquitin	G17	8	19	0	0
657	Pir-A/B	H15	9	19	0	0
658	FceR1 alpha	I13	10	19	0	0
659	CD54	J11	11	19	0	0
660	fibronctin	K9	12	19	0	0
661	IL12 capture	L7	13	19	0	0
662	GM-CSF capture	M5	14	19	0	0
663	MST1	N3	15	19	0	1
664	GST	O1	16	19	0	0
665	ASGR1	O23	17	19	0	1
666	C3 (from chicken)	P21	18	19	1	0
667	C1qc	A7	19	19	0	0
668	Shox2	B5	20	19	0	0
669	Emilin-1 (Y-13)	C3	21	19	0	0
670	Tenascin C	D1	22	19	0	0
671	PrxV	D23	23	19	0	0
672	LEMDZ	E21	24	19	0	0
673	PN5	F19	25	19	0	0
674	Muiti Uqbiquitin	G17	26	19	0	0
675	Pir-A/B	H15	27	19	0	0
676	FceR1 alpha	I13	28	19	0	0
677	CD54	J11	29	19	0	0

678	fibronctin	K9	30	19	0	0
679	IL12 capture	L7	31	19	0	0
680	GM-CSF capture	M5	32	19	0	0
681	MST1	N3	33	19	0	1
682	GST	O1	34	19	0	0
683	ASGR1	O23	35	19	0	1
684	C3 (from chicken)	P21	36	19	1	0
685	Ntng1	A5	1	20	0	0
686	Grm1	B3	2	20	0	0
687	DEFA1	C1	3	20	0	0
688	Map2K2	C23	4	20	0	0
689	DJ-1	D21	5	20	0	0
690	Ninein	E19	6	20	0	0
691	PN3	F17	7	20	0	0
692	LEDGF	G15	8	20	0	0
693	IL-12	H13	9	20	0	0
694	NK1.1	I11	10	20	0	0
695	TLR2	J9	11	20	0	0
696	tubulin	K7	12	20	0	0
697	IL 1 beta detection	L5	13	20	0	0
698	TNF alpha detection	M3	14	20	0	0
699	HSD11B1	N1	15	20	0	1
700	arginase I	N23	16	20	0	1
701	transferrin coat Ab	O21	17	20	1	0
702	CRP	P19	18	20	1	0
703	Ntng1	A5	19	20	0	0
704	Grm1	B3	20	20	0	0
705	DEFA1	C1	21	20	0	0
706	Map2K2	C23	22	20	0	0
707	DJ-1	D21	23	20	0	0
708	Ninein	E19	24	20	0	0
709	PN3	F17	25	20	0	0
710	LEDGF	G15	26	20	0	0
711	IL-12	H13	27	20	0	0
712	NK1.1	I11	28	20	0	0
713	TLR2	J9	29	20	0	0
714	tubulin	K7	30	20	0	0
715	IL 1 beta detection	L5	31	20	0	0
716	TNF alpha detection	M3	32	20	0	0
717	HSD11B1	N1	33	20	0	0
718	arginase I	N23	34	20	0	1
719	transferrin coat Ab	O21	35	20	1	0
720	CRP	P19	36	20	1	0

721	Gc	A3	1	21	1	0
722	Trem2	B1	2	21	0	0
723	ubiqitin	B23	3	21	0	0
724	Ube2N	C21	4	21	0	0
725	CD 63	D19	5	21	0	0
726	FAAH	E17	6	21	0	0
727	PN1	F15	7	21	0	0
728	KAP-1	G13	8	21	0	0
729	H-2k	H11	9	21	0	0
730	I-Ab	I9	10	21	0	0
731	m-r	J7	11	21	0	0
732	caspase-1	K5	12	21	0	0
733	IL4 capture	L3	13	21	0	0
734	MIG capture	M1	14	21	0	0
735	HPX	M23	15	21	1	0
736	antitrypsin	N21	16	21	1	0
737	BAAT	O19	17	21	0	1
738	albumin coat Ab	P17	18	21	1	0
739	Gc	A3	19	21	1	0
740	Trem2	B1	20	21	0	0
741	ubiqitin	B23	21	21	0	0
742	Ube2N	C21	22	21	0	0
743	CD 63	D19	23	21	0	0
744	FAAH	E17	24	21	0	0
745	PN1	F15	25	21	0	0
746	KAP-1	G13	26	21	0	0
747	H-2k	H11	27	21	0	0
748	I-Ab	I9	28	21	0	0
749	m-r	J7	29	21	0	0
750	caspase-1	K5	30	21	0	0
751	IL4 capture	L3	31	21	0	0
752	MIG capture	M1	32	21	0	0
753	HPX	M23	33	21	1	0
754	antitrypsin	N21	34	21	1	0
755	BAAT	O19	35	21	0	1
756	albumin coat Ab	P17	36	21	1	0
757	Cst3	A1	1	22	0	0
758	Apoa2	A23	2	22	1	0
759	Aldoc	B21	3	22	0	1
760	L- Plastin (E-17)	C19	4	22	0	0
761	Zyxin	D17	5	22	0	0
762	TSTA3	E15	6	22	0	0
763	NSE	F13	7	22	0	0

764	HAI-1	G11	8	22	0	0
765	PN19	H9	9	22	0	0
766	CD14 (monocyte)	I7	10	22	0	0
767	CD3e	J5	11	22	0	0
768	Actin	K3	12	22	0	0
769	IL6 MP 520F3	L1	13	22	0	0
770	MIP2 capture	L23	14	22	0	0
771	DPYS	M21	15	22	0	1
772	serum amyloid A	N19	16	22	0	0
773	FGL1	O17	17	22	0	1
774	ASGPR2	P15	18	22	0	1
775	Cst3	A1	19	22	0	0
776	Apoa2	A23	20	22	1	0
777	Aldoc	B21	21	22	0	1
778	L- Plastin (E-17)	C19	22	22	0	0
779	Zyxin	D17	23	22	0	0
780	TSTA3	E15	24	22	0	0
781	NSE	F13	25	22	0	0
782	HAI-1	G11	26	22	0	0
783	PN19	H9	27	22	0	0
784	CD14 (monocyte)	I7	28	22	0	0
785	CD3e	J5	29	22	0	0
786	Actin	K3	30	22	0	0
787	IL6 MP 520F3	L1	31	22	0	0
788	MIP2 capture	L23	32	22	0	0
789	DPYS	M21	33	22	0	1
790	serum amyloid A	N19	34	22	0	0
791	FGL1	O17	35	22	0	1
792	ASGPR2	P15	36	22	0	1
793	Background	Background1	0	0	0	0
794	Background	Background2	0	0	0	0
795	Background	Background3	0	0	0	0
796	Background	Background4	0	0	0	0
797	Background	Background5	0	0	0	0
798	Background	Background6	0	0	0	0

Table S3B. Description of SPRI microarray Set B containing 50 printed features. NCBI UniGene numbers are provided for the human form of the target protein. The types of antigen recognized by the antibody is given in the "Antigen" column using the abbreviations H, M, R, and P for human, mouse, rat, and pig, respectively, and based on data from the manufacturers. The "Host" column indicates the host used to raise the antibody.

Position	Antibody target	UniGene ID	Internal ID	Clonality	Host	Antigen	Vendor	Catalog
0	Background	NA	BG	NA	NA	NA	NA	NA
1	C3	Mm.19131	Hu1	Poly	Goat	M	Immun. Consult. Lab.	GC3-90A
2	CRP	Mm.260770	Hu3	Mono	Mouse	H,M,P	R&D systems	MAB1707
3	AQP9	Mm.335570	Hu4	Poly	Rabbit	R,M,H	ADI	AQP91-A
4	ASGR1	Mm.6559	Hu5	Poly	Goat	H,M,R	Santa Cruz Bio.	sc-13467
5	Background	NA	BG	NA	NA	NA	NA	NA
6	ASGR2	Mm.1357	Hu6	Poly	Goat	M,R,H	Santa Cruz Bio.	sc-13471
7	HMGCS2	Mm.289131	Hu7	Poly	Chicken	H,M,R	Genway	15-288-22653
8	CAT (Catalase)	Mm.2605	Hu8	Poly	Rabbit	H,M	Calbiochem	219010
9	DPYS	Mm.275974	Hu11	NA	NA	NA	NA	NA
10	Background	NA	BG	NA	NA	NA	NA	NA
11	HPX	Mm.3485	Hu13	Poly	Mouse	H	Novus	H00001807-A01
12	HSD11B1	Mm.13000	Hu15	Poly	Mouse	H	Novus	H00003290-A01
13	MST1	Mm.8369	Hu69	NA	NA	NA	NA	NA
14	PON1	Mm.389078	Hu18	Poly	Mouse	H	Novus	H00005444-A01
15	Background	NA	BG	NA	NA	NA	NA	NA
16	TDO2	Mm.258622	Hu19	Poly	Mouse	H	Novus	H00006999-A01
17	ALDH4A1	Mm.4517	Hu22	Poly	Mouse	H	Abnova	H00008659-A01
18	ARG1 (Arginase)	Mm.154144	Hu37	Mono	Mouse	M,R	BD	610708
19	CP (Ceruloplasmin)	Mm.13787	Hu38	Mono	Mouse	H,M,R	BD	611488
20	Background	NA	BG	NA	NA	NA	NA	NA
21	GST	Mm.37214	Hu40	Mono	Mouse	ALL	Cell Signaling	2624
22	TFR2	Mm.21757	Hu42	Poly	Rabbit	M	ADI	TFR21-A
23	TF (Transferrin)	Mm.37214	Hu31	Poly	Chicken	H,R,M	Genway	15-288-20009F
24	ALB (Albumin)	Mm.16773	Hu45	Poly	Goat	M	Immun. Consult. Lab.	GAL-90A
25	Background	NA	BG	NA	NA	NA	NA	NA
26	ASGR2	Mm.1357	Hu77	Poly	Goat	H	Santa Cruz Bio.	sc-13472
27	TF (Transferrin)	Mm.37214	Hu43	Poly	Goat	M	Immun. Consult. Lab.	GTX-90A
28	TF (Transferrin)	Mm.37214	Hu81	Mono	Mouse	H	AbD Serotec	9100-1055

29	ALB (Albumin)	Mm.16773	HuAAC	NA	NA	NA	NA	NA
30	Background	NA	BG	NA	NA	NA	NA	NA
31	PLG (Plasminogen)	Mm.971	Hu48	Poly	Rabbit	M	Innovative Research	IASMPLG-GF
32	PLG (Plasminogen)	Mm.971	Hu131	Mono	Rat	M	R&D Systems	MAB742
33	GNMT	Mm.29395	Hu101	Poly	Rabbit	H	Abgent	AP1076a
34	RBP4	Mm.2605	Hu53	Mono	Mouse	H	Novus	H00005950-M01
35	Background	NA	BG	NA	NA	NA	NA	NA
36	CPS1	Mm.343942	Hu24	Mono	Mouse	H	Abnova	H00001373-M01
37	ALDOB	Mm.218862	Hu10	Mono	Mouse	H	Novus	H00000229-M01
38	FGA (Fibrinogen)	Mm.88793	Hu36	Poly	Chicken	H,R,M	Genway	15-288-22856
39	FGL1	Mm.277955	Hu55	Mono	Mouse	H	Novus	H00002267-M01
40	Background	NA	BG	NA	NA	NA	NA	NA
41	HP (Haptoglobin)	Mm.26730	Hu32	Poly	Chicken	H,R,M	Genway	15-288-20080F
42	MST1	Mm.8369	Hu69	Mono	Mouse	H	Novus	H00004485-M01
43	ADH4	Mm.158750	Hu112	Mono	Mouse	H	Novus	H00000127-M01
44	ASGR1	Mm.6559	Hu75	Poly	Goat	M,R	Santa Cruz Bio.	sc-13469
45	Background	NA	BG	NA	NA	NA	NA	NA
46	KNG1	Mm.2160	Hu106	Poly	Rabbit	H	Atlas Antibodies	HPA001616
47	AST (GOT1)	Mm.423078	Hu87	Poly	sheep	P	ABR	PA1-23063
48	ALT (GPT1)	Mm.30130	Hu88	Mono	Mouse	H	Novus	H00002875-M03
49	BAAT	Mm.2859	Hu104	Poly	Rabbit	H	Bethyl Lab.	A300-727A

Table S3C. Profiling the time course with SPRI. Relative concentrations of the targeted proteins were determined by curve-fitting the binding reponses of six mouse plasma samples. Concentrations c0-c5 correspond to samples taken 1, 3, 12, 24, 48, and 72 hours after treatment with APAP. Rmax, kon, and koff indicate the calculated maximal SPR response, kinetic on-rate and kinetic off-rate, respectively. The Rmax parameter floor was set to 20; values of 20 indicate no binding was detected.

Position	Antibody target	c0	c1	c2	c3	c4	c5	Rmax	kon	koff
0	Background	1.56e-06	4.9e-08	2.27e-07	1.02e-12	1e-12	3.94e-07	20	1820	0.00114
1	C3	1.47e-06	1.04e-06	9.87e-07	9.22e-07	1.06e-06	1.08e-06	103	10400	0.000514
2	CRP	1.28e-06	1.53e-12	3.42e-07	1.07e-12	1.5e-12	8.37e-07	420	10	1e-05
3	AQP9	1.19e-11	1.49e-11	1.56e-11	1.56e-11	1.52e-11	1.68e-11	20	10	0.1
4	ASGR1	1.1e-06	3.55e-06	4.65e-06	1.92e-06	1.3e-06	1.12e-06	289	1180	0.000116
5	Background	1.42e-06	7.45e-09	1.24e-07	1e-12	1e-12	5.6e-07	20	1590	0.0014
6	ASGR2	1.07e-06	3.38e-06	4.88e-06	1.92e-06	1.43e-06	1.17e-06	216	982	1e-05
7	HMGCS2	1.23e-06	6.67e-06	6.35e-06	3.78e-06	1.34e-06	8.61e-07	148	1200	0.000336
8	CAT	1.62e-06	2.52e-06	9.51e-07	2.73e-06	9.16e-07	4.88e-09	1660	10	1e-05
9	DPYS	1.1e-06	1.99e-06	2.2e-06	1.12e-06	9.74e-07	1.12e-06	90.3	1150	0.000307
10	Background	1.51e-06	1e-12	1.44e-07	1e-12	1e-12	4.94e-07	20	2160	0.00132
11	HPX	1.18e-06	9.82e-07	9.39e-07	5.69e-07	8.56e-07	9.43e-07	20	1210	0.00119
12	HSD11B1	1.3e-06	9.8e-07	5.6e-07	4.66e-07	3.91e-07	7.42e-07	20	2170	0.00577
13	MST1	2.92e-06	1.29e-06	5.82e-07	5.36e-07	3.27e-07	3.48e-07	20	8810	0.00153
14	PON1	1.28e-06	1.42e-06	7.07e-07	8.07e-07	5.87e-07	9.76e-07	60	573	0.00267
15	Background	1.78e-06	1.38e-06	5.41e-07	2.27e-12	2.36e-12	3.17e-12	20	489	0.00209
16	TDO2	1.8e-06	1.79e-06	8.25e-07	7.37e-07	5.31e-07	6.17e-07	27.6	6540	0.000677
17	ALDH4A1	1.18e-06	9.11e-07	7.46e-07	9.01e-07	7.59e-07	1.01e-06	20	2110	0.000353
18	ARG1	1.42e-06	2.4e-06	1.03e-06	6.02e-07	1e-12	4.39e-07	20	344	0.00182
19	CP	1.34e-11	1.74e-11	1.5e-11	2.27e-11	1.02e-11	6.3e-12	20	10	0.1
20	Background	1.64e-06	8.08e-07	7.64e-07	1e-12	1e-12	1.24e-07	20	819	0.00188
21	GST	1.44e-06	1.79e-06	1.06e-06	2.09e-06	8.18e-07	3.63e-07	1100	10	1e-05
22	TFR2	1.29e-06	1.22e-06	8.23e-07	1.09e-06	9.8e-07	6.72e-07	3000	10	1e-05
23	TF	1.39e-06	1.34e-06	8.49e-07	8.9e-07	1.32e-06	1.28e-06	363	14200	0.00163
24	ALB	1.82e-06	2.17e-06	2.24e-06	2.64e-06	2.26e-06	2.24e-06	211	100000	0.000992
25	Background	1.56e-06	1.76e-07	2.61e-07	1.08e-12	1e-12	3.74e-07	20	1650	0.00123
26	ASGR2	1.06e-06	1.06e-06	1.12e-06	9.01e-07	1.58e-06	1.17e-06	151	679	1e-05
27	TF	1.53e-06	1.47e-06	1.06e-06	1e-06	1.16e-06	1.3e-06	136	21200	0.0011
28	TF	1.43e-06	1.42e-06	8.82e-07	8.07e-07	1.17e-06	1.31e-06	80.6	13600	0.000312
29	ALB	1.53e-06	2.04e-06	2.39e-06	2.96e-06	2.7e-06	2.86e-06	84.2	100000	0.000535
30	Background	1.51e-06	5.55e-08	1.43e-07	1.05e-12	1e-12	4.63e-07	20	1970	0.0014
31	PLG	1.23e-06	1.32e-06	5.26e-07	3.82e-07	1.27e-06	1.4e-06	341	8510	0.000489
32	PLG	1.42e-06	1.45e-06	7.26e-07	5.77e-07	1.1e-06	1.32e-06	61.2	12000	0.000122
33	GNMT	1.2e-06	2.8e-06	2.14e-06	3.69e-06	1.35e-06	9.06e-07	177	849	0.000145
34	RBP4	1.51e-06	1.45e-06	6.86e-07	7.88e-07	1.16e-06	1.31e-06	119	16900	0.000612
35	Background	1.4e-06	8.12e-08	1.17e-07	1e-12	1.01e-12	5.92e-07	20	1530	0.0011

36	CPS1	1.17e-06	1.72e-06	2.23e-06	1.14e-06	1.13e-06	1.21e-06	87	4660	0.000284
37	ALDOB	1.3e-06	2.64e-06	1.95e-06	2.83e-06	1.29e-06	7.44e-07	82.6	1400	0.000302
38	FGA	1.45e-06	1.02e-06	1.01e-06	9.83e-07	1.06e-06	1.11e-06	108	9400	0.000124
39	FGL1	1.38e-06	3.74e-07	4.05e-07	1e-12	1.36e-09	6.59e-07	20	2070	0.000874
40	Background	1.45e-06	3.33e-08	1.49e-07	1e-12	1e-12	5.3e-07	20	1790	0.00142
41	HP	3.77e-06	6.91e-06	2.86e-06	1.61e-07	2.05e-12	1.85e-12	144	10	1e-05
42	MST1	1.46e-06	2.04e-06	1.58e-06	1.58e-06	9.82e-07	5.15e-07	20	2290	0.00515
43	ADH4	2.22e-06	7.56e-07	1.35e-12	7.45e-08	1e-12	1e-12	20	523	0.00308
44	ASGR1	1.08e-06	1.2e-06	1.15e-06	1.05e-06	1.37e-06	1.15e-06	269	1070	8.4e-05
45	Background	1.48e-06	1e-12	1.9e-07	1e-12	1e-12	4.91e-07	20	1730	0.00137
46	KNG1	2.4e-06	1.88e-06	7.72e-07	7.79e-07	2.9e-07	3.82e-07	20	7670	0.00166
47	AST	1.36e-06	6.81e-07	1.58e-07	1e-06	7.78e-07	6.09e-07	20	1050	0.00194
48	ALT	1.39e-06	9.18e-07	6.24e-07	9.57e-07	5.28e-07	5.89e-07	20	1690	0.00394
49	BAAT	2.18e-12	2.46e-12	1.88e-12	1.85e-12	2e-12	1.21e-12	20	10	0.1

Table S4. iTRAQ

Table S4A. Peptides designed for iTRAQ analysis. Three peptides were designed for each liver-specific target. Of the 85 peptides, 69 were successfully detected by MS.

Gene Symbol	UniGene ID	Peptide Sequence	Detected in MS		Gene Symbol	UniGene ID	Peptide Sequence	Detected in MS
ADH4	Mm.158750	VDEMTIPTVDVILGR	YES		CRP	Mm.260770	AQGDVFIKPQLWS	YES
ADH4	Mm.158750	SINGTFFGGWK	YES		CRP	Mm.260770	AFVFPK	no
ADH4	Mm.158750	VDDEANLER	YES		FAH	Mm.3798	ASLQNLLSASQAR	YES
ALDOB	Mm.218862	ELSEIAQR	YES		FAH	Mm.3798	AHEHIFGMVLMNDWSAR	YES
ALDOB	Mm.218862	LSFSYGR	YES		FAH	Mm.3798	HLFTGPALSK	YES
ALDOB	Mm.218862	DSQGNLFR	no		FGA	Mm.88793	EINLQDYEGHQK	YES
APOA1	Mm.26743	VAPLGAELQESAR	YES		FGA	Mm.88793	LEVDIDIK	YES
APOA1	Mm.26743	TQLAPHSEQMR	YES		FGA	Mm.88793	MELERPGK	no
APOA1	Mm.26743	LSPVAEEFR	YES		FGG	Mm.16422	YEALLLTHETSIR	YES
AQP9	Mm.335570	AEPAENNLEK	YES		FGG	Mm.16422	DSVQIHDTTGK	YES
AQP9	Mm.335570	HELSVIM	YES		FGG	Mm.16422	TLEDILFR	YES
AQP9	Mm.335570	NLGVPR	no		FTCD	Mm.36278	TASQLIDMSK	YES
ASGR1	Mm.6559	DEQNFLQR	YES		FTCD	Mm.36278	LFVLEEEHR	YES
ASGR1	Mm.6559	SLSCQMAAFR	YES		FTCD	Mm.36278	AGEYEALPEK	YES
ASGR1	Mm.6559	WNDDVCR	no		GCDH	Mm.2475	ATPEMVSMLK	YES
ASGR2	Mm.1357	ADHSTLLFHLK	YES		GCDH	Mm.2475	IQFGVPLAR	YES
ASGR2	Mm.1357	IENPHWK	YES		GCDH	Mm.2475	DILGGNGISDEYHVIR	YES
ASGR2	Mm.1357	HFPMDLR	no		GCHFR	Mm.86373	SVLGNNFYEYYVNDPPR	YES
ASL	Mm.23869	AEMQQILQGLDK	YES		GCHFR	Mm.86373	VLSMTGVGQTLVWCLHK	YES
ASL	Mm.23869	VAEEWAQGTFK	YES		GCHFR	Mm.86373	MPYLLISTQIR	no
ASL	Mm.23869	ELIGEAAGK	YES		GNMT	Mm.29395	AHMVTLDYTVQVPGTGR	YES
ASS1	Mm.3217	YLLGTSLARPCIAR	YES		GNMT	Mm.29395	VWQLYIGDTR	YES
ASS1	Mm.3217	FAELVYTGFWHSPECEFVR	no		GNMT	Mm.29395	LSYYPHCLASFTELVR	no
ASS1	Mm.3217	MPEFYNR	no		GPT1 (ALT)	Mm.30130	LTEQVFNEAPGIR	YES
AZGP1	Mm.30061	AYLEEECPEMLK	YES		GPT1 (ALT)	Mm.30130	ALELEQELR	YES
AZGP1	Mm.30061	GFSQSLSVQWDR	YES		GPT1 (ALT)	Mm.30130	GGYVEVVNMDAEVQK	no
AZGP1	Mm.30061	DENNVVAQPQ	YES		HPD	Mm.6584	DIAFEVEDCDHIVQK	YES
C3	Mm.19131	ACEPGVDYVYK	YES		HPD	Mm.6584	FLHFHSVTFWVGNAK	no
C3	Mm.19131	DLELLASGVDR	YES		HPD	Mm.6584	EMGDHLVK	no
C3	Mm.19131	EYVLPSFEVR	YES		PCYT2	Mm.21439	ELAFLEATK	YES
CAT	Mm.2605	LCENIAGHLK	YES		PCYT2	Mm.21439	AMGDYLIVGVHTDEEIAK	YES
CAT	Mm.2605	LFAYPDTHR	YES		PCYT2	Mm.21439	MLLVTK	no
CAT	Mm.2605	HMNGYGSHTFK	no		PEMT	Mm.2731	SHCFTQAMMSQPK	YES
CFB	Mm.653	DLEIEEVLFHPK	YES		PLG	Mm.971	VILGAHEEYIR	YES

CFB	Mm.653	LNQISYEDHK	YES		PLG	Mm.971	GTVSVTVSGK	YES
CFB	Mm.653	LEDIVTYHCSR	YES		PLG	Mm.971	WEYCDIPR	YES
CP	Mm.13787	DTANLFPHK	YES		PON1	Mm.389078	LLIGTVFHK	YES
CP	Mm.13787	IYTFHAHGVTYTK	no		PON1	Mm.389078	IQNILSEDPK	YES
CP	Mm.13787	IYHSHVDAPK	no		PON1	Mm.389078	ILLMDLNK	YES
CPS1	Mm.343942	VLGTSVESIMATEDR	YES		TF	Mm.37214	KPVDQYEDCYLAR	YES
CPS1	Mm.343942	FLGVAEQLHNEGFK	YES		TF	Mm.37214	IPSHAVVAR	YES
CPS1	Mm.343942	SIFSAVLDELK	YES		TF	Mm.37214	HTTIFEVLPEK	YES
CRP	Mm.260770	ESDTSYVSLEAESK	YES					

Table S4B. Peptides identification scores.

The precursor charge, mass/charge ratio, and PeptideProphet probability score for each peptide sequence assigned is tabulated.

PeptideProphet probability	spectrum	precursor charge	m/z	peptide sequence	target peptide	gene symbol
0.3927	QS20070624_P0149_HY109_01.01265.01265.2	2	521.5353	AGAEPAPER	no	KNG1
0.9253	QS20070624_P0149_HY109_01.01318.01318.2	2	482.991	ASETLTAQ	no	APOA1
0.9538	QS20070624_P0149_HY109_01.01319.01319.2	2	629.6321	DENNVVAQPQ	YES	AZGP1
0.8769	QS20070624_P0149_HY109_01.01373.01373.2	2	545.5778	ELSEIAQR	YES	ALDOB
0.9752	QS20070624_P0149_HY109_01.01393.01393.2	2	597.6117	DEQNFLQR	YES	ASGR1
0.998	QS20070624_P0149_HY109_01.01401.01401.2	2	716.2396	VNADEVGGEALGR	no	HBB-B1
0.996	QS20070624_P0149_HY109_01.01466.01466.2	2	792.8734	APQVSTPTLVEAAR	no	ALB
0.9946	QS20070624_P0149_HY109_01.01489.01489.2	2	725.7626	QLEQQVEEFR	no	APOA4
1	QS20070624_P0149_HY109_01.01493.01493.2	2	743.3071	VAPLGAELQESAR	YES	APOA1
0.9967	QS20070624_P0149_HY109_01.01513.01513.2	2	716.7537	ATIDQNLEDLR	no	APOA4
0.8798	QS20070624_P0149_HY109_01.01543.01543.2	2	743.3071	VAPLGAELQESAR	YES	APOA1
0.9989	QS20070624_P0149_HY109_01.01633.01633.2	2	865.9026	DTCFSTEGPNLVTR	no	ALB
0.9976	QS20070624_P0149_HY109_01.01749.01749.2	2	556.0868	VNSILGCSQ	no	HPXN
0.9826	QS20070624_P0149_HY109_02.00389.00389.2	2	610.6294	EATTEQQLR	no	BHMT
0.9587	QS20070624_P0149_HY109_02.00394.00394.2	2	609.1291	DGGQTAPASIR	no	GSN
0.1402	QS20070624_P0149_HY109_02.00407.00407.2	2	536.106	RVAPLVK	no	FADS3
0.6058	QS20070624_P0149_HY109_02.00409.00409.2	2	529.0875	RLNSPIGR	no	POLR2B
0.9936	QS20070624_P0149_HY109_02.00413.00413.2	2	629.6321	DENNVVAQPQ	YES	AZGP1
0.2177	QS20070624_P0149_HY109_02.00415.00415.2	2	524.0234	GSAPANETR	no	1700084C01RIK
0.9935	QS20070624_P0149_HY109_02.00417.00417.2	2	603.1004	VDDEANLER	YES	ADH4
0.9746	QS20070624_P0149_HY109_02.00418.00418.2	2	628.6691	LQDQPNIQR	no	PZP
0.887	QS20070624_P0149_HY109_02.00422.00422.2	2	482.991	ASETLTAQ	no	APOA1
0.6357	QS20070624_P0149_HY109_02.00442.00442.2	2	494.5328	LQELQGR	no	APOA1
0.9903	QS20070624_P0149_HY109_02.00447.00447.2	2	777.8169	FSTSQSLPASQTR	no	MUG1
0.9181	QS20070624_P0149_HY109_02.00453.00453.2	2	545.5778	ELSEIAQR	YES	ALDOB
0.9594	QS20070624_P0149_HY109_02.00471.00471.2	2	534.5527	EDVELYR	no	APOA1
0.9935	QS20070624_P0149_HY109_02.00478.00478.2	2	597.6117	DEQNFLQR	YES	ASGR1
0.4854	QS20070624_P0149_HY109_02.00479.00479.2	2	555.6162	QLYTAITR	no	LBA1
1	QS20070624_P0149_HY109_02.00481.00481.2	2	716.2396	VNADEVGGEALGR	no	HBB-B1
0.3073	QS20070624_P0149_HY109_02.00491.00491.2	2	597.6117	DEQNFLQR	YES	ASGR1
0.1807	QS20070624_P0149_HY109_02.00494.00494.2	2	636.133	LNSANGHEER	no	RBM39
0.9716	QS20070624_P0149_HY109_02.00517.00517.2	2	679.243	FNPVTGEVPPR	no	HPXN
0.2136	QS20070624_P0149_HY109_02.00537.00537.2	2	532.56	EVSAWATR	no	NUP155
0.9974	QS20070624_P0149_HY109_02.00541.00541.2	2	792.8734	APQVSTPTLVEAAR	no	ALB
0.2941	QS20070624_P0149_HY109_02.00542.00542.2	2	815.9079	DQTGGVLVVELSLR	no	TECTB
1	QS20070624_P0149_HY109_02.00565.00565.2	2	743.3071	VAPLGAELQESAR	YES	APOA1
0.9944	QS20070624_P0149_HY109_02.00566.00566.2	2	725.7626	QLEQQVEEFR	no	APOA4
0.182	QS20070624_P0149_HY109_02.00575.00575.3	3	585.929	GDATVSYEDLPTAK	no	EG665146
0.9937	QS20070624_P0149_HY109_02.00583.00583.2	2	596.6456	LSPVAEEFR	YES	APOA1
0.8837	QS20070624_P0149_HY109_02.00587.00587.2	2	679.243	FNPVTGEVPPR	no	HPXN
0.9978	QS20070624_P0149_HY109_02.00590.00590.2	2	716.7537	ATIDQNLEDLR	no	APOA4
0.4675	QS20070624_P0149_HY109_02.00593.00593.2	2	884.4833	VLTGSELAPAVFFK	no	SCML2
0.9848	QS20070624_P0149_HY109_02.00607.00607.2	2	651.1658	CCTLPEDQR	no	ALB

0.1032	QS20070624_P0149_HY109_02.00610.00610.2	2	644.1978	ALINSVQQNR	no	2410003A14RIK
1	QS20070624_P0149_HY109_02.00613.00613.2	2	743.3071	VAPLGAELQESAR	YES	APOA1
0.9958	QS20070624_P0149_HY109_02.00615.00615.2	2	887.9819	MQQVEASLQPETLR	no	SERPINA3C
0.9891	QS20070624_P0149_HY109_02.00623.00623.2	2	623.1761	ALELEQELR	YES	GPT1
0.3116	QS20070624_P0149_HY109_02.00626.00626.2	2	635.6822	SGVFPSNYVR	no	ITSN1
0.2225	QS20070624_P0149_HY109_02.00651.00651.3	3	625.7054	LCLMSGEIIQMSSK	no	DNAHC3
1	QS20070624_P0149_HY109_02.00657.00657.2	2	809.882	LTEQVFNEAPGIR	YES	GPT1
0.9389	QS20070624_P0149_HY109_02.00662.00662.2	2	617.6436	DYFVSCPGR	no	HPXN
1	QS20070624_P0149_HY109_02.00673.00673.2	2	865.9026	DTCFSTEGPNLVTR	no	ALB
0.1955	QS20070624_P0149_HY109_02.00674.00674.2	2	809.882	LTEQVFNEAPGIR	YES	GPT1
0.9976	QS20070624_P0149_HY109_02.00685.00685.2	2	777.8181	GFSQSLSVQWDR	YES	AZGP1
0.9986	QS20070624_P0149_HY109_02.00694.00694.2	2	752.3163	ASLQNLLSASQAR	YES	FAH
0.1577	QS20070624_P0149_HY109_02.00695.00695.2	2	730.7682	AQFGGQVLHSK	no	C79407
0.9838	QS20070624_P0149_HY109_02.00698.00698.2	2	809.882	LTEQVFNEAPGIR	YES	GPT1
0.9835	QS20070624_P0149_HY109_02.00699.00699.2	2	672.7439	DAGTIAGLNVLR	no	HSPA8
0.988	QS20070624_P0149_HY109_02.00701.00701.2	2	666.7152	DLELLASGVDR	YES	C3
0.8871	QS20070624_P0149_HY109_02.00723.00723.2	2	573.162	IQFGVPLAR	YES	GCDH
0.9998	QS20070624_P0149_HY109_02.00733.00733.3	3	829.2358	TSCPPPPQIPNTQVIETTVK	no	CFH
0.9211	QS20070624_P0149_HY109_02.00754.00754.2	2	752.3163	ASLQNLLSASQAR	YES	FAH
0.2151	QS20070624_P0149_HY109_02.00802.00802.2	2	735.8227	GLPAPGPYSTPLR	no	RARA
0.1888	QS20070624_P0149_HY109_02.00807.00807.2	2	741.79	LWFGLSVDEK	no	DYSF
0.9383	QS20070624_P0149_HY109_02.00813.00813.2	2	692.2604	EYVLPSFEVR	YES	C3
0.2099	QS20070624_P0149_HY109_02.00814.00814.2	2	843.9107	LGFATSSDVIEMK	no	SKIV2L2
0.9989	QS20070624_P0149_HY109_02.00841.00841.2	2	876.9557	VLGTSVESIMATEDR	YES	CPS1
1	QS20070624_P0149_HY109_02.00853.00853.2	2	931.471	GECQSEGVLFFQGNR	no	HPXN
0.5679	QS20070624_P0149_HY109_02.00867.00867.2	2	867.4261	DNLSPPLGQCLTER	no	F2
0.9917	QS20070624_P0149_HY109_02.00889.00889.2	2	666.7152	DLELLASGVDR	YES	C3
1	QS20070624_P0149_HY109_02.00922.00922.3	3	731.4444	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.928	QS20070624_P0149_HY109_02.00933.00933.2	2	463.9891	AVCEFPA	no	MBL1
0.9981	QS20070624_P0149_HY109_02.00947.00947.3	3	711.7682	TVQDALSSVQESDIAVVAR	no	APOC3
0.9999	QS20070624_P0149_HY109_02.00949.00949.3	3	711.7682	TVQDALSSVQESDIAVVAR	no	APOC3
0.9939	QS20070624_P0149_HY109_02.00951.00951.2	2	769.8386	FVEGLPINDFSR	no	MDH1
0.9958	QS20070624_P0149_HY109_02.00971.00971.2	2	945.9888	EYCGVPGDGYEELIR	no	AMBP
1	QS20070624_P0149_HY109_02.00979.00979.3	3	731.4444	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.9998	QS20070624_P0149_HY109_02.01001.01001.3	3	731.4444	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.9977	QS20070624_P0149_HY109_02.01033.01033.2	2	824.9602	LQALSPELLAPVPR	no	LRG1
0.413	QS20070624_P0149_HY109_02.01042.01042.3	3	882.4009	FVALFYTIITPMLNPLIYTLR	no	OLFR1388
1	QS20070624_P0149_HY109_02.01045.01045.3	3	731.4444	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.4539	QS20070624_P0149_HY109_02.01046.01046.3	3	809.8521	DLGSQTPQALTFNDGMSEVK	no	ZFP161
0.9874	QS20070624_P0149_HY109_02.01047.01047.2	2	786.374	VTIGLLSLDDPQR	no	ITIH4
0.9998	QS20070624_P0149_HY109_02.01071.01071.3	3	731.4444	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.6454	QS20070624_P0149_HY109_02.01085.01085.2	2	681.7781	LVLDPYLLK	no	MRPS17
0.1927	QS20070624_P0149_HY109_02.01111.01111.2	2	622.7356	LLTCFMGLR	no	OAS1A
0.1922	QS20070624_P0149_HY109_02.01113.01113.3	3	858.1888	HSQAEELGLEQPEAEETEEK	no	CEP164
1	QS20070624_P0149_HY109_02.01205.01205.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.4385	QS20070624_P0149_HY109_02.01221.01221.3	3	601.3171	NGQYELIIQLHGK	no	OCRL
1	QS20070624_P0149_HY109_02.01273.01273.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9996	QS20070624_P0149_HY109_02.01375.01375.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9998	QS20070624_P0149_HY109_02.01386.01386.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K

0.9629	QS20070624_P0149_HY109_02.01393.01393.2	2	623.6465	ETAFEFLSSA	no	MDH1
0.9818	QS20070624_P0149_HY109_02.01401.01401.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9928	QS20070624_P0149_HY109_02.01433.01433.2	2	783.3514	YVNWIQQTIAAN	no	2210010C04RIK
0.3281	QS20070624_P0149_HY109_02.01493.01493.2	2	783.3514	YVNWIQQTIAAN	no	2210010C04RIK
0.9003	QS20070624_P0149_HY109_02.01498.01498.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9995	QS20070624_P0149_HY109_02.01526.01526.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9994	QS20070624_P0149_HY109_02.01539.01539.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.7647	QS20070624_P0149_HY109_02.01650.01650.3	3	621.3164	GECQSEGVLFFQGNR	no	HPXN
0.9985	QS20070624_P0149_HY109_02.01769.01769.2	2	587.6569	LLDVAELGSL	no	LRG1
0.3794	QS20070624_P0149_HY109_02.01821.01821.3	3	602.6128	NCGYPGISPEDCASR	no	TFF2
1	QS20070624_P0149_HY109_02.01825.01825.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
0.9996	QS20070624_P0149_HY109_02.01857.01857.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
0.6249	QS20070624_P0149_HY109_02.02010.02010.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9896	QS20070624_P0149_HY109_03.00469.00469.3	3	497.1644	DSVQIHDTTGK	YES	FGG
0.2045	QS20070624_P0149_HY109_03.00470.00470.2	2	590.6021	SVTVQETK	no	KNG1
0.9919	QS20070624_P0149_HY109_03.00486.00486.3	3	622.2762	EESQAPEEAGSSGLGK	no	LOC433368
1	QS20070624_P0149_HY109_03.00488.00488.2	2	612.1363	GTVSVTVSGK	YES	PLG
0.3598	QS20070624_P0149_HY109_03.00496.00496.2	2	562.056	VGASTQSGK	no	PITX2
1	QS20070624_P0149_HY109_03.00497.00497.2	2	612.1363	GTVSVTVSGK	YES	PLG
0.9916	QS20070624_P0149_HY109_03.00516.00516.2	2	890.4024	QAEFHVDESTTVK	no	SERPINA1E
0.8775	QS20070624_P0149_HY109_03.00528.00528.2	2	588.6079	ELIGEAAGK	YES	ASL
0.1872	QS20070624_P0149_HY109_03.00529.00529.2	2	834.8956	SQAYLIGSIGVSGK	no	LOC676640
0.9882	QS20070624_P0149_HY109_03.00536.00536.2	2	698.2063	AGEYEALPEK	YES	FTCD
0.6123	QS20070624_P0149_HY109_03.00540.00540.3	3	791.1791	SGHEIWEEFSMSFTPAVK	no	NR1D2
1	QS20070624_P0149_HY109_03.00549.00549.2	2	917.4021	ESDTSYVSLEAESK	YES	CRP
1	QS20070624_P0149_HY109_03.00552.00552.2	2	716.2396	VNADEVGGEALGR	no	HBB-B1
1	QS20070624_P0149_HY109_03.00553.00553.2	2	716.2396	VNADEVGGEALGR	no	HBB-B1
0.9997	QS20070624_P0149_HY109_03.00556.00556.3	3	569.8861	TCVADESAANCDK	no	ALB
1	QS20070624_P0149_HY109_03.00557.00557.2	2	854.3255	TCVADESAANCDK	no	ALB
0.8593	QS20070624_P0149_HY109_03.00558.00558.2	2	938.0545	LCLMSGEIIQMSSK	no	DNAHC3
0.8477	QS20070624_P0149_HY109_03.00565.00565.2	2	750.7849	AAEVWMDDFK	no	GALNT9
0.2813	QS20070624_P0149_HY109_03.00572.00572.2	2	772.8612	ADEEQLLVTLLR	no	LOC672646
0.9986	QS20070624_P0149_HY109_03.00576.00576.2	2	701.2301	DIPVDSPELK	no	KNG1
0.1834	QS20070624_P0149_HY109_03.00577.00577.2	2	775.3355	AFNVELAQAGIK	no	2310030N02RIK
0.6309	QS20070624_P0149_HY109_03.00578.00578.3	3	1137.534	GVFMAGEEDGSLPQDHSSESPQLDTVLFK	no	UNKNOWN
0.9915	QS20070624_P0149_HY109_03.00580.00580.2	2	744.7909	SVIVEPEGIEK	no	PZP
1	QS20070624_P0149_HY109_03.00581.00581.2	2	855.3858	YMCENQATISSK	no	ALB
1	QS20070624_P0149_HY109_03.00584.00584.2	2	888.9442	AISESGVVINTNVGK	no	ES1
0.9987	QS20070624_P0149_HY109_03.00585.00585.2	2	792.8734	APQVSTPTLVEAAR	no	ALB
0.2685	QS20070624_P0149_HY109_03.00586.00586.3	3	614.2982	YFFDFLDEQAEK	no	PLXNB2
0.9131	QS20070624_P0149_HY109_03.00590.00590.2	2	626.6515	VNEAACDIAR	no	BHMT
1	QS20070624_P0149_HY109_03.00592.00592.2	2	691.7378	TASQLIDMSK	YES	FTCD
1	QS20070624_P0149_HY109_03.00593.00593.2	2	792.3223	DFTPAAQAAFQK	no	HBB-B1
1	QS20070624_P0149_HY109_03.00604.00604.2	2	743.3071	VAPLGAELQESAR	YES	APOA1
0.9925	QS20070624_P0149_HY109_03.00605.00605.2	2	725.7626	QLEQQVEEFR	no	APOA4
0.3755	QS20070624_P0149_HY109_03.00608.00608.2	2	773.8568	FPLLLQDQKR	no	UNKNOWN
1	QS20070624_P0149_HY109_03.00609.00609.3	3	645.6703	KPVDQYEDCYLAR	YES	TF
1	QS20070624_P0149_HY109_03.00612.00612.2	2	886.4827	VGQPGAAGPVSPMCPGR	no	AHSG
0.9981	QS20070624_P0149_HY109_03.00613.00613.2	2	596.6456	LSPVAEEFR	YES	APOA1

0.9984	QS20070624_P0149_HY109_03.00616.00616.2	2	765.8327	SLAPLTVGVQEK	no	APOA4
0.8948	QS20070624_P0149_HY109_03.00617.00617.2	2	626.6568	VINDFVEK	no	SPI1-6
0.1051	QS20070624_P0149_HY109_03.00622.00622.2	2	604.6266	INNQFGNTR	no	MAGEE2
0.9813	QS20070624_P0149_HY109_03.00624.00624.2	2	723.2582	IQNILSEDPK	YES	PON1
0.8684	QS20070624_P0149_HY109_03.00629.00629.2	2	723.2582	IQNILSEDPK	YES	PON1
1	QS20070624_P0149_HY109_03.00630.00630.2	2	789.8109	ACEPGVDYVYK	YES	C3
0.9679	QS20070624_P0149_HY109_03.00636.00636.2	2	627.6647	QLTSFIEK	no	GC
0.9982	QS20070624_P0149_HY109_03.00638.00638.2	2	692.2669	ITCPPPPVPK	no	APOH
1	QS20070624_P0149_HY109_03.00644.00644.3	3	754.1109	AADKDTCFSTEGPNLVTR	no	ALB
0.4838	QS20070624_P0149_HY109_03.00645.00645.2	2	716.7537	ATIDQNLEDLR	no	APOA4
0.7108	QS20070624_P0149_HY109_03.00648.00648.2	2	699.7298	LSISGDYNLK	no	SERPINA1B
0.9881	QS20070624_P0149_HY109_03.00649.00649.2	2	661.187	SELLESLNK	no	PZP
1	QS20070624_P0149_HY109_03.00652.00652.2	2	698.288	ATPEMVSMLK	YES	GCDH
0.9915	QS20070624_P0149_HY109_03.00653.00653.2	2	689.7359	YNILPVADGK	no	PZP
0.9916	QS20070624_P0149_HY109_03.00656.00656.2	2	623.1761	ALELEQELR	YES	GPT1
1	QS20070624_P0149_HY109_03.00658.00658.2	2	698.288	ATPEMVSMLK	YES	GCDH
1	QS20070624_P0149_HY109_03.00662.00662.2	2	801.3504	NLAPLVEDVQSK	no	APOA4
1	QS20070624_P0149_HY109_03.00664.00664.2	2	777.8016	VAEEWAQGTFK	YES	ASL
0.1727	QS20070624_P0149_HY109_03.00665.00665.2	2	647.1602	AILTESENK	no	GOLGA4
0.3289	QS20070624_P0149_HY109_03.00668.00668.3	3	632.6725	QWGLLCDLLEQDK	no	EVC
0.996	QS20070624_P0149_HY109_03.00672.00672.2	2	693.2738	VLIVEPEGIK	no	MUG1
0.9952	QS20070624_P0149_HY109_03.00676.00676.2	2	634.6564	VDGALCLDK	no	HPXN
0.9281	QS20070624_P0149_HY109_03.00677.00677.2	2	689.2203	VPDTITEWK	no	PZP
0.1954	QS20070624_P0149_HY109_03.00680.00680.2	2	740.7594	NTLDSISSNIK	no	PROM1
0.9963	QS20070624_P0149_HY109_03.00681.00681.2	2	727.7723	GNLFMDINNK	no	KNG1
0.99	QS20070624_P0149_HY109_03.00682.00682.2	2	753.3074	LPDLPGNYVTK	no	PZP
0.9983	QS20070624_P0149_HY109_03.00685.00685.2	2	668.2183	NPITSVDAAFR	no	HPXN
0.4245	QS20070624_P0149_HY109_03.00688.00688.2	2	848.9516	AEMLEIVQAIYK	no	NCALD
1	QS20070624_P0149_HY109_03.00689.00689.2	2	809.882	LTEQVFNEAPGIR	YES	GPT1
0.8375	QS20070624_P0149_HY109_03.00690.00690.2	2	825.8651	GSQLLSSGSDGLLK	no	TBL3
0.9878	QS20070624_P0149_HY109_03.00693.00693.2	2	617.2229	TLMSPLGITR	no	SPI1-6
1	QS20070624_P0149_HY109_03.00696.00696.2	2	765.2967	DFANVYVDAVK	no	APOA1
1	QS20070624_P0149_HY109_03.00700.00700.2	2	752.3163	ASLQNLLSASQAR	YES	FAH
0.9938	QS20070624_P0149_HY109_03.00701.00701.2	2	617.6436	DYFVSCPGR	no	HPXN
0.868	QS20070624_P0149_HY109_03.00702.00702.2	2	632.684	GPDSVFLIK	no	HPXN
0.994	QS20070624_P0149_HY109_03.00704.00704.2	2	711.2929	MNEETASLLLR	no	ES1
0.9797	QS20070624_P0149_HY109_03.00705.00705.2	2	952.0179	DILGGNGISDEYHVIR	YES	GCDH
0.9894	QS20070624_P0149_HY109_03.00708.00708.2	2	573.162	IQFGVPLAR	YES	GCDH
0.1184	QS20070624_P0149_HY109_03.00710.00710.2	2	1013.563	EVVCTENLTPWKK	no	PIGT
1	QS20070624_P0149_HY109_03.00721.00721.2	2	655.6968	ELAFLEATK	YES	PCYT2
1	QS20070624_P0149_HY109_03.00728.00728.2	2	655.6968	ELAFLEATK	YES	PCYT2
0.2888	QS20070624_P0149_HY109_03.00729.00729.2	2	610.1572	ENLEISLTR	no	CDC25A
0.9984	QS20070624_P0149_HY109_03.00730.00730.2	2	719.7622	LVQEVTDFAK	no	ALB
0.999	QS20070624_P0149_HY109_03.00733.00733.3	3	437.467	ELAFLEATK	YES	PCYT2
0.9913	QS20070624_P0149_HY109_03.00734.00734.2	2	777.8181	GFSQSLSVQWDR	YES	AZGP1
0.9752	QS20070624_P0149_HY109_03.00736.00736.2	2	752.3163	ASLQNLLSASQAR	YES	FAH
0.9998	QS20070624_P0149_HY109_03.00737.00737.3	3	729.7716	DQSPASHEIATNLGDFALR	no	SERPINA1D
0.9973	QS20070624_P0149_HY109_03.00741.00741.2	2	845.3829	ETFTYEWTVPK	no	CP
0.1939	QS20070624_P0149_HY109_03.00742.00742.2	2	660.673	DAEVGSNLVK	no	BCMO1

0.9986	QS20070624_P0149_HY109_03.00744.00744.2	2	952.0013	FSSSTFEQVNQLVK	no	GC
0.9975	QS20070624_P0149_HY109_03.00745.00745.2	2	736.8652	MSLVLPPTVVK	no	MUG2
0.9302	QS20070624_P0149_HY109_03.00748.00748.2	2	732.8105	TLDNDIMLIK	no	TRY10L
0.9954	QS20070624_P0149_HY109_03.00749.00749.2	2	688.7662	ALVQQLEQFR	no	APOA4
0.4194	QS20070624_P0149_HY109_03.00753.00753.2	2	732.8105	TLDNDIMLIK	no	TRY10L
0.9944	QS20070624_P0149_HY109_03.00757.00757.2	2	666.7152	DLELLASGVDR	YES	C3
0.7297	QS20070624_P0149_HY109_03.00758.00758.2	2	648.6798	VSLFGSNGNTR	no	PNLIPRP1
0.9607	QS20070624_P0149_HY109_03.00761.00761.2	2	633.1762	LPECLEVK	no	APOH
0.9927	QS20070624_P0149_HY109_03.00772.00772.3	3	816.8531	ALYQTEAFTADFQQPTEAK	no	SERPINA3K
1	QS20070624_P0149_HY109_03.00776.00776.2	2	1146.706	IFNNGADLSGITEENAPLK	no	SPI1-6
0.9627	QS20070624_P0149_HY109_03.00781.00781.2	2	692.2604	EYVLPSFEVR	YES	C3
1	QS20070624_P0149_HY109_03.00788.00788.2	2	986.0389	LSQTFPNADFAEITK	no	ALB
0.4326	QS20070624_P0149_HY109_03.00789.00789.3	3	930.0032	SMVLDVVFVLEGSDEVGEANFNK	no	VWF
0.9706	QS20070624_P0149_HY109_03.00793.00793.2	2	545.6222	LCAIPNLR	no	ALB
1	QS20070624_P0149_HY109_03.00797.00797.2	2	1133.193	IFNSGADLSGITEENAPLK	no	SERPINA1E
0.8697	QS20070624_P0149_HY109_03.00798.00798.2	2	624.7137	ILLMDLNK	YES	PON1
0.1032	QS20070624_P0149_HY109_03.00800.00800.2	2	956.4397	NSFCCTELNEENK	no	SETD2
0.1691	QS20070624_P0149_HY109_03.00801.00801.2	2	695.6535	SDTGSSGEAYK	no	PARL
1	QS20070624_P0149_HY109_03.00804.00804.2	2	831.9012	AEMQQILQGLDK	YES	ASL
1	QS20070624_P0149_HY109_03.00806.00806.2	2	876.9557	VLGTSVESIMATEDR	YES	CPS1
0.9753	QS20070624_P0149_HY109_03.00808.00808.2	2	678.1751	DFWDNLEK	no	APOA1
1	QS20070624_P0149_HY109_03.00809.00809.2	2	863.8484	ENYGELADCCTK	no	ALB
0.931	QS20070624_P0149_HY109_03.00810.00810.2	2	752.3163	ASLQNLLSASQAR	YES	FAH
0.1436	QS20070624_P0149_HY109_03.00814.00814.3	3	640.3653	SHSGEFALDSILLLK	no	LRRC61
0.9823	QS20070624_P0149_HY109_03.00818.00818.2	2	889.9519	LFVDPSQGLEVTGK	no	ITIH4
1	QS20070624_P0149_HY109_03.00821.00821.2	2	931.471	GECQSEGVLFFQGNR	no	HPXN
0.9983	QS20070624_P0149_HY109_03.00828.00828.2	2	889.4607	AQGDVFIKPQLWS	YES	CRP
0.9985	QS20070624_P0149_HY109_03.00829.00829.2	2	831.4058	LEEDVLPEMGIK	no	SERPINA3K
1	QS20070624_P0149_HY109_03.00830.00830.2	2	851.4332	TVQGAFFGVPVYK	no	PZP
1	QS20070624_P0149_HY109_03.00832.00832.2	2	812.907	LGEYGFQNAILVR	no	ALB
0.9946	QS20070624_P0149_HY109_03.00833.00833.2	2	629.7252	LVVLPFPGK	no	FETUB
1	QS20070624_P0149_HY109_03.00840.00840.2	2	698.2674	VWQLYIGDTR	YES	GNMT
0.6938	QS20070624_P0149_HY109_03.00842.00842.2	2	945.5261	FAPPQPAEPWSFVK	no	ES1
0.6323	QS20070624_P0149_HY109_03.00844.00844.2	2	678.7292	VDQALPQERR	no	DIP2C
1	QS20070624_P0149_HY109_03.00848.00848.2	2	895.4491	AYLEEECPEMLK	YES	AZGP1
1	QS20070624_P0149_HY109_03.00849.00849.2	2	1096.663	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.9302	QS20070624_P0149_HY109_03.00852.00852.2	2	617.1541	LEVDIDIK	YES	FGA
0.9866	QS20070624_P0149_HY109_03.00853.00853.2	2	831.9012	AEMQQILQGLDK	YES	ASL
0.7592	QS20070624_P0149_HY109_03.00857.00857.3	3	1019.423	GEPGKPGPPGLPGSGGSGAISTATYTTVPR	no	C1QL1
0.7348	QS20070624_P0149_HY109_03.00860.00860.2	2	625.1859	ILLMDNNK	no	LRRTM2
0.9941	QS20070624_P0149_HY109_03.00868.00868.3	3	731.4444	SVLGNNFYEYYVNDPPR	YES	GCHFR
1	QS20070624_P0149_HY109_03.00881.00881.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
0.6974	QS20070624_P0149_HY109_03.00882.00882.2	2	764.3104	DFQLFSSPLGK	no	TF
0.272	QS20070624_P0149_HY109_03.00882.00882.3	3	764.8062	IFNNGADLSGITEENAPLK	no	SPI1-6
0.9584	QS20070624_P0149_HY109_03.00884.00884.2	2	889.4607	AQGDVFIKPQLWS	YES	CRP
0.9917	QS20070624_P0149_HY109_03.00885.00885.2	2	666.7152	DLELLASGVDR	YES	C3
1	QS20070624_P0149_HY109_03.00886.00886.2	2	1146.706	IFNNGADLSGITEENAPLK	no	SPI1-6
0.2873	QS20070624_P0149_HY109_03.00888.00888.2	2	945.9888	EYCGVPGDGYEELIR	no	AMBP
0.3588	QS20070624_P0149_HY109_03.00890.00890.3	3	701.3898	GYGGYGYGCCRPSCYGR	no	#N/A

0.8037	QS20070624_P0149_HY109_03.00892.00892.2	2	973.5057	GTVDEFSGAEYIDELR	no	XPNPEP2
0.9802	QS20070624_P0149_HY109_03.00893.00893.2	2	751.7866	SINGTFFGGWK	YES	ADH4
0.9976	QS20070624_P0149_HY109_03.00897.00897.2	2	824.9602	LQALSPELLAPVPR	no	LRG1
0.9744	QS20070624_P0149_HY109_03.00913.00913.2	2	772.8024	DGTIEIPSCFK	no	APOH
0.9672	QS20070624_P0149_HY109_03.00920.00920.2	2	617.1541	LEVDIDIK	YES	FGA
0.9972	QS20070624_P0149_HY109_03.00922.00922.2	2	837.3767	DQYELLCLDNTR	no	TF
1	QS20070624_P0149_HY109_03.00926.00926.2	2	1096.663	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.9875	QS20070624_P0149_HY109_03.00929.00929.3	3	939.6555	DDNPSLPPFERPEAEAMCTSFK	no	ALB
0.9868	QS20070624_P0149_HY109_03.00933.00933.3	3	939.6555	DDNPSLPPFERPEAEAMCTSFK	no	ALB
0.9963	QS20070624_P0149_HY109_03.00938.00938.2	2	857.3874	QEDFELLCPDGTR	no	TF
0.8995	QS20070624_P0149_HY109_03.00942.00942.3	3	729.8079	YMVLVPSQLYTETPEK	no	MUG1
0.4177	QS20070624_P0149_HY109_03.00944.00944.3	3	601.6553	VTDVMLCAGEMGGGK	no	EGFBP2
1	QS20070624_P0149_HY109_03.00973.00973.2	2	1025.05	LSSSDEEDFLYVDIK	no	MUG1
0.9868	QS20070624_P0149_HY109_03.00977.00977.2	2	747.3397	DIPVNPLCIYR	no	SERPINC1
0.9932	QS20070624_P0149_HY109_03.00978.00978.2	2	685.7845	NLQEILIGAVR	no	EGFR
0.5102	QS20070624_P0149_HY109_03.00981.00981.2	2	900.8438	AFEEEEEEEENK	no	ZBTB38
0.9561	QS20070624_P0149_HY109_03.00993.00993.2	2	710.3218	LLVVYPWTQR	no	HBB-B1
0.2829	QS20070624_P0149_HY109_03.01004.01004.2	2	633.1779	VQLFSSAPK	no	CEP164
1	QS20070624_P0149_HY109_03.01005.01005.3	3	757.1474	VPNAMSVNDEVLSVTACGK	no	MUG1
0.9765	QS20070624_P0149_HY109_03.01012.01012.3	3	731.4444	SVLGNNFYEYYVNDPPR	YES	GCHFR
1	QS20070624_P0149_HY109_03.01014.01014.2	2	1096.663	SVLGNNFYEYYVNDPPR	YES	GCHFR
0.9588	QS20070624_P0149_HY109_03.01020.01020.3	3	504.2128	SIFSAVLDELK	YES	CPS1
0.2722	QS20070624_P0149_HY109_03.01024.01024.2	2	794.8878	TLVVLGEDETIVR	no	SMCR8
0.9712	QS20070624_P0149_HY109_03.01025.01025.2	2	824.8732	QFEDFTVYLGER	no	CP
0.9994	QS20070624_P0149_HY109_03.01028.01028.3	3	638.3342	TDVTQQLSTLFQDK	no	APOA4
0.9999	QS20070624_P0149_HY109_03.01033.01033.3	3	757.1474	VPNAMSVNDEVLSVTACGK	no	MUG1
1	QS20070624_P0149_HY109_03.01034.01034.3	3	687.3647	FDEFFSQGCAPGYEK	no	TF
0.9993	QS20070624_P0149_HY109_03.01036.01036.3	3	638.3342	TDVTQQLSTLFQDK	no	APOA4
0.9996	QS20070624_P0149_HY109_03.01037.01037.3	3	666.0605	EIPAWIPLDPAAANTK	no	AZGP1
0.9991	QS20070624_P0149_HY109_03.01052.01052.3	3	1084.494	STCAQLENPSVETLPESTFEPVPIQAK	no	AGT
0.9991	QS20070624_P0149_HY109_03.01056.01056.3	3	560.2889	SLCTELQGTVAIPR	no	MBL1
0.1262	QS20070624_P0149_HY109_03.01062.01062.2	2	822.4287	LEDSLLAPQPFLR	no	LRG1
0.9122	QS20070624_P0149_HY109_03.01078.01078.2	2	734.2827	VPFDPLDTFK	no	SERPINA3N
0.993	QS20070624_P0149_HY109_03.01084.01084.2	2	740.8331	DIFTGLIGPMK	no	CP
0.9985	QS20070624_P0149_HY109_03.01094.01094.2	2	770.3527	FVFGTTPEDILR	no	THBS1
0.8042	QS20070624_P0149_HY109_03.01096.01096.2	2	951.0381	RDIECLQPLTHLK	no	AW456874
0.9999	QS20070624_P0149_HY109_03.01109.01109.3	3	634.7081	AAPQLPMEELVSLSK	no	AFM
0.9984	QS20070624_P0149_HY109_03.01120.01120.2	2	726.2894	TMEEILEGLK	no	SERPINA3K
0.9793	QS20070624_P0149_HY109_03.01128.01128.3	3	706.7529	AEGIPEFYDYDVALVK	no	CFB
0.9391	QS20070624_P0149_HY109_03.01133.01133.2	2	576.141	TLEDILFR	YES	FGG
1	QS20070624_P0149_HY109_03.01136.01136.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
1	QS20070624_P0149_HY109_03.01138.01138.3	3	673.0522	DLAPTNVDFAFNLYK	no	SERPINA6
0.9967	QS20070624_P0149_HY109_03.01154.01154.2	2	890.4607	SPQELLCGASLISDR	no	F2
0.807	QS20070624_P0149_HY109_03.01165.01165.2	2	890.4607	SPQELLCGASLISDR	no	F2
0.2178	QS20070624_P0149_HY109_03.01185.01185.3	3	1173.966	MPGGPGAPSSPAASSGSSRAAPSGIAACPLSPPPLAR	no	OTOP1
0.9999	QS20070624_P0149_HY109_03.01188.01188.3	3	738.4822	LENYPIPELGPNDVLLK	no	SORD
0.1405	QS20070624_P0149_HY109_03.01189.01189.2	2	657.6723	DHVTANQLK	no	NBEA
0.9998	QS20070624_P0149_HY109_03.01194.01194.3	3	638.0005	AEFDTSEIDSEIAALR	no	MBL2
1	QS20070624_P0149_HY109_03.01200.01200.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6

0.1922	QS20070624_P0149_HY109_03.01206.01206.2	2	869.4091	CLDGSTPMHAGASSGR	no	GM1082
0.5358	QS20070624_P0149_HY109_03.01212.01212.3	3	784.8368	HRPGALTTNGINPDTSTEIGR	no	1810044A24RIK
0.8332	QS20070624_P0149_HY109_03.01224.01224.3	3	757.4621	YFDSFGDLSSASAIMGNAK	no	HBB-B1
0.9997	QS20070624_P0149_HY109_03.01228.01228.3	3	869.6125	LFQEEFPGIPYPPDAAVECHR	no	HPXN
0.9972	QS20070624_P0149_HY109_03.01229.01229.3	3	619.3613	TLNLAQNLLTQLPK	no	CPN2
1	QS20070624_P0149_HY109_03.01232.01232.2	2	1135.69	YFDSFGDLSSASAIMGNAK	no	HBB-B1
0.6905	QS20070624_P0149_HY109_03.01234.01234.3	3	869.6125	LFQEEFPGIPYPPDAAVECHR	no	HPXN
0.3343	QS20070624_P0149_HY109_03.01236.01236.2	2	1134.805	FLGISLVTLWFQVAWAK	no	UNKNOWN
0.9935	QS20070624_P0149_HY109_03.01248.01248.3	3	757.4621	YFDSFGDLSSASAIMGNAK	no	HBB-B1
0.9831	QS20070624_P0149_HY109_03.01256.01256.2	2	716.7614	LCENIAGHLK	YES	CAT
0.5562	QS20070624_P0149_HY109_03.01262.01262.3	3	806.2013	GQVASCAPPLEILNGEINGAK	no	CFH
0.8451	QS20070624_P0149_HY109_03.01268.01268.3	3	902.3559	LLSYLDVEGNSINMVQMTFLK	no	COL11A1
0.9996	QS20070624_P0149_HY109_03.01274.01274.3	3	720.7808	ANVGFLPPFPTLDPEEK	no	AFM
0.9531	QS20070624_P0149_HY109_03.01276.01276.3	3	902.3559	LLSYLDVEGNSINMVQMTFLK	no	COL11A1
1	QS20070624_P0149_HY109_03.01280.01280.3	3	720.7808	ANVGFLPPFPTLDPEEK	no	AFM
0.9998	QS20070624_P0149_HY109_03.01281.01281.3	3	693.0996	APFALQVNTLPLNFDK	no	PZP
0.9997	QS20070624_P0149_HY109_03.01312.01312.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9998	QS20070624_P0149_HY109_03.01321.01321.3	3	693.0996	APFALQVNTLPLNFDK	no	PZP
1	QS20070624_P0149_HY109_03.01336.01336.3	3	919.2894	DLSPQDQFNLIEFSGEANQWK	no	ITIH4
1	QS20070624_P0149_HY109_03.01337.01337.3	3	919.2894	DLSPQDQFNLIEFSGEANQWK	no	ITIH4
1	QS20070624_P0149_HY109_03.01340.01340.3	3	919.2894	DLSPQDQFNLIEFSGEANQWK	no	ITIH4
0.3252	QS20070624_P0149_HY109_03.01358.01358.3	3	838.2255	ENPETEEDVGPIVQHIYELR	no	ITGAV
0.9999	QS20070624_P0149_HY109_03.01360.01360.3	3	726.4558	LFDSDPITVVLPEEVSK	no	CLU
0.9981	QS20070624_P0149_HY109_03.01361.01361.2	2	902.029	VDEMTIPTVDVILGR	YES	ADH4
1	QS20070624_P0149_HY109_03.01372.01372.2	2	902.029	VDEMTIPTVDVILGR	YES	ADH4
1	QS20070624_P0149_HY109_03.01374.01374.2	2	902.029	VDEMTIPTVDVILGR	YES	ADH4
0.9958	QS20070624_P0149_HY109_03.01394.01394.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9756	QS20070624_P0149_HY109_03.01402.01402.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9999	QS20070624_P0149_HY109_03.01408.01408.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
0.2704	QS20070624_P0149_HY109_03.01417.01417.2	2	730.7682	AQFGGQVLHSK	no	C79407
0.972	QS20070624_P0149_HY109_03.01425.01425.2	2	783.3514	YVNWIQQTIAAN	no	2210010C04RIK
0.9982	QS20070624_P0149_HY109_03.01436.01436.2	2	902.029	VDEMTIPTVDVILGR	YES	ADH4
0.2749	QS20070624_P0149_HY109_03.01453.01453.2	2	851.8556	TSSSLDNCQSQWR	no	UNKNOWN
0.9993	QS20070624_P0149_HY109_03.01458.01458.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.28	QS20070624_P0149_HY109_03.01460.01460.3	3	771.1504	GDDDVFVNPTNLLEFLSDR	no	B3GNT7
1	QS20070624_P0149_HY109_03.01464.01464.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
1	QS20070624_P0149_HY109_03.01476.01476.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
0.9999	QS20070624_P0149_HY109_03.01481.01481.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
0.9996	QS20070624_P0149_HY109_03.01482.01482.3	3	716.4676	TGLLSGLDIMEVNPTLGK	no	ARG1
0.9995	QS20070624_P0149_HY109_03.01484.01484.3	3	716.4676	TGLLSGLDIMEVNPTLGK	no	ARG1
1	QS20070624_P0149_HY109_03.01496.01496.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
0.1482	QS20070624_P0149_HY109_03.01504.01504.2	2	565.6467	EMVEMLFS	no	KPNA6
0.2479	QS20070624_P0149_HY109_03.01505.01505.3	3	865.0389	IATVMYTVVTPMMNPFIYSLR	no	LOC639450
1	QS20070624_P0149_HY109_03.01529.01529.3	3	772.1855	APVVMGSSEDVQEFLEIYR	no	FBP1
0.2054	QS20070624_P0149_HY109_03.01532.01532.2	2	816.409	DFIFTVTMEDLR	no	4732429D16RIK
0.9998	QS20070624_P0149_HY109_03.01538.01538.3	3	822.1851	LSEDQEDCILYSSWLAEK	no	MUG1
1	QS20070624_P0149_HY109_03.01540.01540.3	3	822.1851	LSEDQEDCILYSSWLAEK	no	MUG1
1	QS20070624_P0149_HY109_03.01545.01545.3	3	798.5211	ISEDCLYLNIYSPADLTK	no	ES1
0.9842	QS20070624_P0149_HY109_03.01570.01570.3	3	655.6969	DLADELALVDVMEDK	no	LDHA

1	QS20070624_P0149_HY109_03.01573.01573.3	3	718.1117	EQLQDMGLIDLFSPEK	no	SERPINC1
0.5553	QS20070624_P0149_HY109_03.01596.01596.2	2	565.6467	EMVEMLFS	no	KPNA6
0.997	QS20070624_P0149_HY109_03.01597.01597.3	3	892.2436	EVVSLTEECCAEGADPTCYDTR	no	GC
0.9999	QS20070624_P0149_HY109_03.01601.01601.3	3	892.2436	EVVSLTEECCAEGADPTCYDTR	no	GC
1	QS20070624_P0149_HY109_03.01605.01605.3	3	833.5254	GGDSGFVADLSFLDLDNPAGNK	no	C7
1	QS20070624_P0149_HY109_03.01608.01608.3	3	833.5254	GGDSGFVADLSFLDLDNPAGNK	no	C7
0.996	QS20070624_P0149_HY109_03.01622.01622.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9988	QS20070624_P0149_HY109_03.01637.01637.3	3	833.5254	GGDSGFVADLSFLDLDNPAGNK	no	C7
0.9164	QS20070624_P0149_HY109_03.01660.01660.3	3	833.5254	GGDSGFVADLSFLDLDNPAGNK	no	C7
1	QS20070624_P0149_HY109_03.01668.01668.3	3	758.1732	IILQGSPVVQMAEDAVDGER	no	C3
0.9976	QS20070624_P0149_HY109_03.01672.01672.3	3	727.1304	DIQQWEYVPLGPFLGK	no	FAH
0.5022	QS20070624_P0149_HY109_03.01674.01674.3	3	742.1432	LNAGEVVIGDGGFVFALEK	no	BHMT
0.9993	QS20070624_P0149_HY109_03.01705.01705.3	3	648.4008	IGVAIGDQILDLSVIK	no	FAH
0.9999	QS20070624_P0149_HY109_03.01709.01709.3	3	760.1569	TDFANWASSLANAPALISQR	no	C9
0.2443	QS20070624_P0149_HY109_03.01710.01710.3	3	826.247	WNQQQLDDLYLIAICHRR	no	DCPS
0.2342	QS20070624_P0149_HY109_03.01712.01712.2	2	783.3514	YVNWIQQTIAAN	no	2210010C04RIK
0.9989	QS20070624_P0149_HY109_03.01713.01713.3	3	801.9083	ALQEGNFQTPVFIVPLTDLR	no	APOB
0.1489	QS20070624_P0149_HY109_03.01730.01730.2	2	689.2726	FLPQLPMDK	no	LOC381255
0.992	QS20070624_P0149_HY109_03.01732.01732.2	2	587.6569	LLDVAELGSL	no	LRG1
0.5857	QS20070624_P0149_HY109_03.01772.01772.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
1	QS20070624_P0149_HY109_03.01776.01776.3	3	775.5463	LSISGNYNLETLMSPLGITR	no	SERPINA1E
1	QS20070624_P0149_HY109_03.01782.01782.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
0.9998	QS20070624_P0149_HY109_03.01784.01784.3	3	810.2006	TANDAIQDMLCDMEGLPQK	no	AFM
1	QS20070624_P0149_HY109_03.01788.01788.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
1	QS20070624_P0149_HY109_03.01789.01789.2	2	1291.88	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
0.2546	QS20070624_P0149_HY109_03.01790.01790.2	2	708.7618	LFIHGGLAGDK	no	RABEPK
1	QS20070624_P0149_HY109_03.01800.01800.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
1	QS20070624_P0149_HY109_03.01810.01810.3	3	810.2006	TANDAIQDMLCDMEGLPQK	no	AFM
1	QS20070624_P0149_HY109_03.01830.01830.3	3	778.8431	IVNDDFSQVADVLVEDGVVR	no	DPYS
1	QS20070624_P0149_HY109_03.01833.01833.3	3	778.8431	IVNDDFSQVADVLVEDGVVR	no	DPYS
0.2137	QS20070624_P0149_HY109_03.01837.01837.3	3	676.0658	DGFPAAATSANLCLATGVR	no	EYA1
0.9992	QS20070624_P0149_HY109_03.01840.01840.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.1907	QS20070624_P0149_HY109_03.01841.01841.3	3	627.6944	AEQQQVVQIPQQALR	no	SP2
1	QS20070624_P0149_HY109_03.01849.01849.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
0.9984	QS20070624_P0149_HY109_03.01852.01852.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9997	QS20070624_P0149_HY109_03.01856.01856.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
0.9994	QS20070624_P0149_HY109_03.01857.01857.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.3117	QS20070624_P0149_HY109_03.01860.01860.3	3	815.9256	EFQPLDPTQELIFPPELMR	no	AOX3
0.9576	QS20070624_P0149_HY109_03.01861.01861.3	3	778.8431	IVNDDFSQVADVLVEDGVVR	no	DPYS
0.9939	QS20070624_P0149_HY109_03.01873.01873.3	3	845.9359	VYIIYGNDLGLPPIDLDLDK	no	GPLD1
0.5771	QS20070624_P0149_HY109_03.01885.01885.2	2	820.4375	RSHFVLIAGEPLR	no	PIR
0.9985	QS20070624_P0149_HY109_03.01898.01898.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.2156	QS20070624_P0149_HY109_03.01901.01901.3	3	818.9088	SSGVALSIAVGLLECTFPNTGAR	no	SEC23A
0.966	QS20070624_P0149_HY109_03.01910.01910.3	3	700.1447	FALEIPVEFSMVPMAK	no	MUG1
0.9998	QS20070624_P0149_HY109_03.01914.01914.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.3161	QS20070624_P0149_HY109_03.01917.01917.2	2	565.6467	EMVEMLFS	no	KPNA6
0.6875	QS20070624_P0149_HY109_03.01924.01924.3	3	669.7458	QGFIDLPEFPFGLEPR	no	BHMT
0.9977	QS20070624_P0149_HY109_03.01933.01933.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
1	QS20070624_P0149_HY109_03.01945.01945.3	3	969.7254	DGGIPADPNNIFLSTGASDAIVTMLK	no	GPT1

0.9998	QS20070624_P0149_HY109_03.01948.01948.3	3	969.7254	DGGIPADPNNIFLSTGASDAIVTMLK	no	GPT1
0.993	QS20070624_P0149_HY109_03.01964.01964.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9985	QS20070624_P0149_HY109_03.01980.01980.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9996	QS20070624_P0149_HY109_03.01985.01985.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9927	QS20070624_P0149_HY109_03.01994.01994.3	3	583.3278	DIASGLIGPLILCK	no	CP
0.9999	QS20070624_P0149_HY109_03.02002.02002.3	3	919.0024	QVLALCVYPNLLSSPDFPEDAK	no	GPT1
0.9996	QS20070624_P0149_HY109_03.02004.02004.3	3	909.9813	LNEDMACSVAGITSDANVLTNELR	no	PSMA4
0.9759	QS20070624_P0149_HY109_03.02034.02034.2	2	684.2363	SIIGYVEELEA	no	LIFR
0.9322	QS20070624_P0149_HY109_03.02050.02050.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9998	QS20070624_P0149_HY109_03.02062.02062.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9969	QS20070624_P0149_HY109_03.02066.02066.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.1855	QS20070624_P0149_HY109_03.02092.02092.2	2	939.5781	VGLLEALLPGQPEAVAR	no	GSS
1	QS20070624_P0149_HY109_03.02093.02093.3	3	835.5554	SDDLQCVFITLLPNENCAK	no	KLK1B26
1	QS20070624_P0149_HY109_03.02104.02104.3	3	835.5554	SDDLQCVFITLLPNENCAK	no	KLK1B26
0.9297	QS20070624_P0149_HY109_03.02128.02128.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9997	QS20070624_P0149_HY109_03.02158.02158.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.2043	QS20070624_P0149_HY109_03.02165.02165.2	2	1266.438	TAALLTTMMSVTGVSFGVLDTDR	no	BC021785
1	QS20070624_P0149_HY109_03.02181.02181.3	3	979.4154	ATGGLGQLIPGGIPGTEALGGLLNLGGDK	no	5430413K10RIK
0.9992	QS20070624_P0149_HY109_03.02196.02196.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9997	QS20070624_P0149_HY109_03.02224.02224.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9973	QS20070624_P0149_HY109_03.02240.02240.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
1	QS20070624_P0149_HY109_03.02253.02253.3	3	867.3237	EPGQDLVVLSLPITPEFIPSFR	no	C3
1	QS20070624_P0149_HY109_03.02256.02256.3	3	867.3237	EPGQDLVVLSLPITPEFIPSFR	no	C3
1	QS20070624_P0149_HY109_03.02261.02261.3	3	867.3237	EPGQDLVVLSLPITPEFIPSFR	no	C3
1	QS20070624_P0149_HY109_03.02269.02269.3	3	867.3237	EPGQDLVVLSLPITPEFIPSFR	no	C3
0.6023	QS20070624_P0149_HY109_03.02272.02272.2	2	755.3299	KSVEFLLLK	no	EG245391
0.9999	QS20070624_P0149_HY109_03.02273.02273.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.2766	QS20070624_P0149_HY109_03.02274.02274.3	3	772.1562	QCEELGAFTESMVVYGCPN	no	C3
0.2752	QS20070624_P0149_HY109_03.02276.02276.2	2	755.3299	KSVEFLLLK	no	EG245391
0.9999	QS20070624_P0149_HY109_03.02317.02317.3	3	974.4349	LTAQPAPSPEDLTLSMSTIMWLTK	no	MUG1
0.9996	QS20070624_P0149_HY109_03.02336.02336.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9999	QS20070624_P0149_HY109_03.02344.02344.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9985	QS20070624_P0149_HY109_03.02368.02368.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.3719	QS20070624_P0149_HY109_03.02376.02376.2	2	667.7217	AISSVETLIEGA	no	CAPN9
1	QS20070624_P0149_HY109_03.02404.02404.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9993	QS20070624_P0149_HY109_03.02413.02413.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9998	QS20070624_P0149_HY109_03.02422.02422.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9994	QS20070624_P0149_HY109_03.02437.02437.3	3	770.1646	IPESGGDNGVFDIFELIGGAR	no	THBS1
1	QS20070624_P0149_HY109_03.02454.02454.3	3	695.1457	LPIICFDYGMVPISAPR	no	MUG1
1	QS20070624_P0149_HY109_03.02474.02474.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9995	QS20070624_P0149_HY109_03.02488.02488.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9971	QS20070624_P0149_HY109_03.02564.02564.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.4956	QS20070624_P0149_HY109_03.02624.02624.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9999	QS20070624_P0149_HY109_03.02633.02633.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9956	QS20070624_P0149_HY109_03.02676.02676.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9958	QS20070624_P0149_HY109_03.02692.02692.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9995	QS20070624_P0149_HY109_03.02716.02716.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.1386	QS20070624_P0149_HY109_03.02749.02749.3	3	911.6707	RDVDNGLSLVIFSDWYNTSVMR	no	MBTPS1
0.9999	QS20070624_P0149_HY109_03.02761.02761.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K

0.341	QS20070624_P0149_HY109_03.02844.02844.3	3	1178.411	FLVLLALAGLLAFLSLSLQFFHLIPVSATK	no	ACPL2
0.9999	QS20070624_P0149_HY109_03.02904.02904.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9999	QS20070624_P0149_HY109_03.03045.03045.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9989	QS20070624_P0149_HY109_03.03225.03225.3	3	941.7088	AQNVPLPVSTLVEFVIAATDCTAK	no	AHSG
0.1807	QS20070624_P0149_HY109_03.03261.03261.2	2	732.8105	TLDNDIMLIK	no	TRY10L
0.9989	QS20070624_P0149_HY109_03.03292.03292.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9997	QS20070624_P0149_HY109_03.03349.03349.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.9944	QS20070624_P0149_HY109_04.01288.01288.3	3	362.0428	VVDPTHK	no	SERPINA1A
1	QS20070624_P0149_HY109_04.01295.01295.3	3	611.9637	VSTVTTHSSDSEVPSR	no	CLU
0.9986	QS20070624_P0149_HY109_04.01304.01304.2	2	702.1962	AEPAENNLEK	YES	AQP9
1	QS20070624_P0149_HY109_04.01315.01315.2	2	612.1363	GTVSVTVSGK	YES	PLG
0.2679	QS20070624_P0149_HY109_04.01317.01317.2	2	562.056	VGASTQSGK	no	PITX2
1	QS20070624_P0149_HY109_04.01323.01323.3	3	512.5215	LNQISYEDHK	YES	CFB
1	QS20070624_P0149_HY109_04.01327.01327.3	3	512.5215	LNQISYEDHK	YES	CFB
0.9999	QS20070624_P0149_HY109_04.01333.01333.3	3	579.5822	LGDASTYADGVHNK	no	APOA4
1	QS20070624_P0149_HY109_04.01337.01337.3	3	593.9373	QAEFHVDESTTVK	no	SERPINA1E
1	QS20070624_P0149_HY109_04.01341.01341.2	2	890.4024	QAEFHVDESTTVK	no	SERPINA1E
0.9916	QS20070624_P0149_HY109_04.01351.01351.2	2	698.2063	AGEYEALPEK	YES	FTCD
1	QS20070624_P0149_HY109_04.01352.01352.2	2	837.8722	IGGHGAEYGAEALER	no	HBA-A1
0.9911	QS20070624_P0149_HY109_04.01355.01355.2	2	931.4537	KDPSSNDPLTETIR	no	MUG1
0.9999	QS20070624_P0149_HY109_04.01356.01356.3	3	444.4606	DTANLFPHK	YES	CP
0.8686	QS20070624_P0149_HY109_04.01357.01357.3	3	429.1324	LSVSQVVHK	no	SERPINA3K
0.9969	QS20070624_P0149_HY109_04.01363.01363.2	2	881.8886	EINLQDYEGHQK	YES	FGA
0.9962	QS20070624_P0149_HY109_04.01364.01364.3	3	508.865	KVINDFVEK	no	SPI1-6
0.8498	QS20070624_P0149_HY109_04.01384.01384.2	2	801.8657	HTTIFEVLPEK	YES	TF
0.9967	QS20070624_P0149_HY109_04.01385.01385.2	2	854.3255	TCVADESAANCDK	no	ALB
0.9621	QS20070624_P0149_HY109_04.01388.01388.2	2	660.6509	TNCDLYEK	no	ALB
1	QS20070624_P0149_HY109_04.01391.01391.2	2	917.4021	ESDTSYVSLEAESK	YES	CRP
1	QS20070624_P0149_HY109_04.01396.01396.3	3	822.4909	KPFDPENTEEAEFHVDK	no	SERPINA1B
0.995	QS20070624_P0149_HY109_04.01405.01405.3	3	422.1225	LFAYPDTHR	YES	CAT
0.89	QS20070624_P0149_HY109_04.01411.01411.3	3	708.7719	SPEGPVSRVGATLPSRPK	no	USP36
0.9992	QS20070624_P0149_HY109_04.01412.01412.3	3	597.9409	TCGDIPELEHGSAK	no	CFH
0.8567	QS20070624_P0149_HY109_04.01413.01413.2	2	855.3858	YMCENQATISSK	no	ALB
0.9997	QS20070624_P0149_HY109_04.01415.01415.3	3	465.851	LTEVPALVHK	no	PZP
1	QS20070624_P0149_HY109_04.01416.01416.3	3	654.7044	AGPWTPEAAVEHPEAVR	no	BHMT
1	QS20070624_P0149_HY109_04.01419.01419.2	2	691.7378	TASQLIDMSK	YES	FTCD
0.1611	QS20070624_P0149_HY109_04.01421.01421.2	2	698.2728	LTEVPALVHK	no	PZP
0.1533	QS20070624_P0149_HY109_04.01423.01423.2	2	952.9689	KAWSSQDEVSSHVR	no	PLEKHG3
0.7437	QS20070624_P0149_HY109_04.01427.01427.2	2	487.5191	LSFSYGR	YES	ALDOB
0.4438	QS20070624_P0149_HY109_04.01432.01432.2	2	608.6352	SASGASEPPLR	no	1110038F14RIK
0.9942	QS20070624_P0149_HY109_04.01439.01439.2	2	487.0546	HELSVIM	YES	AQP9
0.9921	QS20070624_P0149_HY109_04.01441.01441.2	2	596.6456	LSPVAEEFR	YES	APOA1
0.9905	QS20070624_P0149_HY109_04.01444.01444.2	2	631.1824	QTALAELVK	no	ALB
0.5781	QS20070624_P0149_HY109_04.01451.01451.3	3	612.0011	ILGPSKPVCAEIK	no	2810046L04RIK
1	QS20070624_P0149_HY109_04.01452.01452.3	3	701.7221	SGAQATWTEVSWPHEK	no	HPXN
1	QS20070624_P0149_HY109_04.01455.01455.2	2	1130.663	AADKDTCFSTEGPNLVTR	no	ALB
1	QS20070624_P0149_HY109_04.01457.01457.2	2	789.8109	ACEPGVDYVYK	YES	C3
0.9828	QS20070624_P0149_HY109_04.01459.01459.2	2	723.2582	IQNILSEDPK	YES	PON1
0.9889	QS20070624_P0149_HY109_04.01481.01481.2	2	623.1761	ALELEQELR	YES	GPT1

1	QS20070624_P0149_HY109_04.01483.01483.2	2	995.6093	AHMVTLDYTVQVPGTGR	YES	GNMT
0.9985	QS20070624_P0149_HY109_04.01488.01488.2	2	777.8016	VAEEWAQGTFK	YES	ASL
0.4443	QS20070624_P0149_HY109_04.01489.01489.2	2	698.288	ATPEMVSMLK	YES	GCDH
1	QS20070624_P0149_HY109_04.01492.01492.3	3	703.0855	ANLMHNLGGEEVSVACK	no	AHSG
0.2715	QS20070624_P0149_HY109_04.01509.01509.3	3	639.6706	NYISNSAQSNGTLMK	no	NRXN3
0.3338	QS20070624_P0149_HY109_04.01512.01512.2	2	580.1755	GAPPLPPIPR	no	WIPF1
1	QS20070624_P0149_HY109_04.01517.01517.3	3	796.8357	QQLGPNSGEVESHLSFLEK	no	APOA4
0.9994	QS20070624_P0149_HY109_04.01521.01521.3	3	581.5978	GTFASLSELHCDK	no	HBB-B1
1	QS20070624_P0149_HY109_04.01547.01547.3	3	544.5789	DLQILAEFHEK	no	SERPINA3K
0.9811	QS20070624_P0149_HY109_04.01548.01548.2	2	573.162	IQFGVPLAR	YES	GCDH
0.9649	QS20070624_P0149_HY109_04.01549.01549.2	2	652.72	SLSCQMAAFR	YES	ASGR1
0.9875	QS20070624_P0149_HY109_04.01552.01552.2	2	652.72	SLSCQMAAFR	YES	ASGR1
0.9985	QS20070624_P0149_HY109_04.01555.01555.2	2	655.6968	ELAFLEATK	YES	PCYT2
0.9983	QS20070624_P0149_HY109_04.01563.01563.2	2	719.7622	LVQEVTDFAK	no	ALB
0.9947	QS20070624_P0149_HY109_04.01565.01565.2	2	777.8181	GFSQSLSVQWDR	YES	AZGP1
0.8998	QS20070624_P0149_HY109_04.01588.01588.2	2	732.8105	TLDNDIMLIK	no	TRY10L
0.9975	QS20070624_P0149_HY109_04.01591.01591.2	2	674.7812	PYLLISTQIR	no	GCHFR
0.9985	QS20070624_P0149_HY109_04.01597.01597.3	3	621.2863	ECCHGDLLECADDR	no	ALB
0.9273	QS20070624_P0149_HY109_04.01600.01600.2	2	692.2604	EYVLPSFEVR	YES	C3
0.5455	QS20070624_P0149_HY109_04.01611.01611.2	2	749.1865	AEDEGSTEEGGK	no	TCEAL5
0.9735	QS20070624_P0149_HY109_04.01612.01612.2	2	545.6222	LCAIPNLR	no	ALB
1	QS20070624_P0149_HY109_04.01616.01616.3	3	591.6321	CSPDPGLTALLSDHR	no	HPXN
0.9803	QS20070624_P0149_HY109_04.01619.01619.2	2	636.6681	WEYCDIPR	YES	PLG
0.8558	QS20070624_P0149_HY109_04.01620.01620.2	2	624.7137	ILLMDLNK	YES	PON1
1	QS20070624_P0149_HY109_04.01623.01623.2	2	751.7866	SINGTFFGGWK	YES	ADH4
1	QS20070624_P0149_HY109_04.01625.01625.3	3	780.4744	FPSLHGDCVALPNGDDGECR	no	KNG1
0.9218	QS20070624_P0149_HY109_04.01627.01627.2	2	617.1541	LEVDIDIK	YES	FGA
0.9882	QS20070624_P0149_HY109_04.01628.01628.2	2	863.8484	ENYGELADCCTK	no	ALB
1	QS20070624_P0149_HY109_04.01635.01635.2	2	831.9012	AEMQQILQGLDK	YES	ASL
0.9873	QS20070624_P0149_HY109_04.01639.01639.3	3	725.4274	AETFTFHSDICTLPEK	no	ALB
0.3514	QS20070624_P0149_HY109_04.01641.01641.2	2	730.2791	ILSDMFSTEK	no	ES1
0.5323	QS20070624_P0149_HY109_04.01647.01647.2	2	674.7812	PYLLISTQIR	no	GCHFR
0.1013	QS20070624_P0149_HY109_04.01648.01648.2	2	638.1959	LSAVVQELK	no	BICD1
0.9975	QS20070624_P0149_HY109_04.01651.01651.2	2	889.4607	AQGDVFIKPQLWS	YES	CRP
0.9989	QS20070624_P0149_HY109_04.01652.01652.2	2	698.2674	VWQLYIGDTR	YES	GNMT
0.9942	QS20070624_P0149_HY109_04.01653.01653.2	2	666.187	AWFSEAFGK	no	APOC1
0.3302	QS20070624_P0149_HY109_04.01655.01655.2	2	655.7197	FLQPEFIK	no	UNKNOWN
0.9925	QS20070624_P0149_HY109_04.01657.01657.2	2	578.1581	YVIEFIAR	no	KNG1
1	QS20070624_P0149_HY109_04.01663.01663.2	2	812.907	LGEYGFQNAILVR	no	ALB
0.9157	QS20070624_P0149_HY109_04.01665.01665.2	2	629.7252	LVVLPFPGK	no	FETUB
1	QS20070624_P0149_HY109_04.01672.01672.2	2	706.7737	VCNELAMLGK	no	GC
0.9989	QS20070624_P0149_HY109_04.01677.01677.2	2	729.7572	ALSCLESSWK	no	MUG1
1	QS20070624_P0149_HY109_04.01685.01685.3	3	682.7329	VITAFNDGLNHLDSLK	no	HBB-B1
0.9988	QS20070624_P0149_HY109_04.01687.01687.2	2	895.4491	AYLEEECPEMLK	YES	AZGP1
0.5243	QS20070624_P0149_HY109_04.01688.01688.2	2	625.1859	ILLMDNNK	no	LRRTM2
1	QS20070624_P0149_HY109_04.01695.01695.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
0.2655	QS20070624_P0149_HY109_04.01697.01697.2	2	913.4565	GQAGAAVGPGGGGGGGEVAVR	no	C630007C17RIK
0.9997	QS20070624_P0149_HY109_04.01705.01705.3	3	586.6307	DLEIEEVLFHPK	YES	CFB
0.9828	QS20070624_P0149_HY109_04.01716.01716.2	2	686.772	LLWENGNLLR	no	C3

0.9832	QS20070624_P0149_HY109_04.01719.01719.2	2	751.7866	SINGTFFGGWK	YES	ADH4
0.6349	QS20070624_P0149_HY109_04.01729.01729.3	3	514.5653	FLASVSTVLTSK	no	HBA-A1
0.9561	QS20070624_P0149_HY109_04.01736.01736.3	3	829.2089	LGEHNINVLEGNEQFVNAAK	no	UNKNOWN
0.618	QS20070624_P0149_HY109_04.01748.01748.3	3	829.2089	LGEHNINVLEGNEQFVNAAK	no	UNKNOWN
0.9999	QS20070624_P0149_HY109_04.01753.01753.3	3	939.6555	DDNPSLPPFERPEAEAMCTSFK	no	ALB
0.9996	QS20070624_P0149_HY109_04.01759.01759.3	3	939.6555	DDNPSLPPFERPEAEAMCTSFK	no	ALB
0.9981	QS20070624_P0149_HY109_04.01763.01763.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
0.1449	QS20070624_P0149_HY109_04.01767.01767.2	2	662.7101	ILSSCPEIK	no	PROSC
0.5144	QS20070624_P0149_HY109_04.01771.01771.2	2	817.83	ACDMEFCSACK	no	RNF144
0.2786	QS20070624_P0149_HY109_04.01781.01781.2	2	655.1989	SEPCLLDWR	no	LIFR
0.7355	QS20070624_P0149_HY109_04.01783.01783.3	3	598.6271	ENEFFIVTQTCK	no	KNG1
0.9968	QS20070624_P0149_HY109_04.01796.01796.3	3	786.1462	DMQDGFDISHNPWICDK	no	LRG1
0.9999	QS20070624_P0149_HY109_04.01799.01799.3	3	786.1462	DMQDGFDISHNPWICDK	no	LRG1
0.1601	QS20070624_P0149_HY109_04.01813.01813.2	2	590.5832	HSGYNSVK	no	UNKNOWN
0.9952	QS20070624_P0149_HY109_04.01817.01817.2	2	685.7845	NLQEILIGAVR	no	EGFR
0.9864	QS20070624_P0149_HY109_04.01824.01824.2	2	710.3218	LLVVYPWTQR	no	HBB-B1
0.9441	QS20070624_P0149_HY109_04.01825.01825.2	2	747.3397	DIPVNPLCIYR	no	SERPINC1
0.8451	QS20070624_P0149_HY109_04.01832.01832.2	2	850.3778	DEELSCSVLELK	no	SERPINA3K
0.8543	QS20070624_P0149_HY109_04.01841.01841.2	2	633.1779	VQLFSSAPK	no	CEP164
0.9998	QS20070624_P0149_HY109_04.01856.01856.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
0.6557	QS20070624_P0149_HY109_04.01876.01876.2	2	594.1858	LPLPALFK	no	SERPINF2
0.9461	QS20070624_P0149_HY109_04.01884.01884.2	2	734.2827	VPFDPLDTFK	no	SERPINA3N
0.9706	QS20070624_P0149_HY109_04.01891.01891.2	2	689.2803	ELISQFLLNR	no	SERPINA1D
0.841	QS20070624_P0149_HY109_04.01893.01893.2	2	751.7866	SINGTFFGGWK	YES	ADH4
0.1251	QS20070624_P0149_HY109_04.01893.01893.3	3	750.8132	AMGDYLIVGVHTDEEIAK	YES	PCYT2
0.9986	QS20070624_P0149_HY109_04.01903.01903.2	2	726.2894	TMEEILEGLK	no	SERPINA3K
0.9864	QS20070624_P0149_HY109_04.01911.01911.2	2	730.289	TGTWSFLPTCR	no	APOH
0.9358	QS20070624_P0149_HY109_04.01921.01921.2	2	789.4131	MSPIYNLIPLK	no	C9
0.9946	QS20070624_P0149_HY109_04.01928.01928.2	2	895.4491	AYLEEECPEMLK	YES	AZGP1
0.9952	QS20070624_P0149_HY109_04.01936.01936.2	2	812.3108	WTDCFPCQDK	no	C8A
0.9665	QS20070624_P0149_HY109_04.01947.01947.2	2	576.141	TLEDILFR	YES	FGG
1	QS20070624_P0149_HY109_04.01964.01964.3	3	763.1722	AVLDVAETGTEAAAATGVIGGIR	no	SERPINA3K
0.7948	QS20070624_P0149_HY109_04.01973.01973.2	2	726.2894	TMEEILEGLK	no	SERPINA3K
0.3235	QS20070624_P0149_HY109_04.01976.01976.2	2	991.5493	EDLVYLTSDSPNVLK	no	RG9MTD2
1	QS20070624_P0149_HY109_04.01993.01993.3	3	782.1765	EVEPGTLCDVAGWGVVTHAGR	no	CFD
0.9853	QS20070624_P0149_HY109_04.01995.01995.2	2	732.8025	DLTFYYLIK	no	PZP
1	QS20070624_P0149_HY109_04.01999.01999.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.9988	QS20070624_P0149_HY109_04.02000.02000.2	2	895.4491	AYLEEECPEMLK	YES	AZGP1
0.6718	QS20070624_P0149_HY109_04.02011.02011.2	2	696.2359	ETFMDCLEGR	no	F2
0.4197	QS20070624_P0149_HY109_04.02015.02015.3	3	784.8368	HRPGALTTNGINPDTSTEIGR	no	1810044A24RIK
0.6546	QS20070624_P0149_HY109_04.02033.02033.2	2	518.0623	ERPCLAR	no	4632411J06RIK
0.9994	QS20070624_P0149_HY109_04.02043.02043.3	3	750.8132	AMGDYLIVGVHTDEEIAK	YES	PCYT2
0.9999	QS20070624_P0149_HY109_04.02047.02047.3	3	750.8132	AMGDYLIVGVHTDEEIAK	YES	PCYT2
0.9999	QS20070624_P0149_HY109_04.02059.02059.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
1	QS20070624_P0149_HY109_04.02067.02067.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
1	QS20070624_P0149_HY109_04.02071.02071.3	3	869.6125	LFQEEFPGIPYPPDAAVECHR	no	HPXN
0.9995	QS20070624_P0149_HY109_04.02081.02081.3	3	757.4621	YFDSFGDLSSASAIMGNAK	no	HBB-B1
0.9829	QS20070624_P0149_HY109_04.02111.02111.2	2	671.2418	ADYLALVFER	no	QSCN6
1	QS20070624_P0149_HY109_04.02135.02135.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6

0.2562	QS20070624_P0149_HY109_04.02136.02136.3	3	710.7559	TSLAVTASIPSSYTSVEK	no	NUP210
0.9119	QS20070624_P0149_HY109_04.02172.02172.2	2	747.7943	NLFDELVLDK	no	MUG1
0.7817	QS20070624_P0149_HY109_04.02184.02184.3	3	639.3649	YQIPNDLQCVFIK	no	KLK1B27
0.9663	QS20070624_P0149_HY109_04.02187.02187.2	2	794.8886	EEIVYLPCIYR	no	SELENBP1
1	QS20070624_P0149_HY109_04.02204.02204.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.9043	QS20070624_P0149_HY109_04.02207.02207.2	2	902.029	VDEMTIPTVDVILGR	YES	ADH4
0.9979	QS20070624_P0149_HY109_04.02216.02216.3	3	556.6044	EGNTWLTAFVLK	no	MUG1
1	QS20070624_P0149_HY109_04.02220.02220.3	3	966.0324	VLGPDSAANLELINTWVAENTNHK	no	SERPING1
0.9733	QS20070624_P0149_HY109_04.02223.02223.2	2	834.403	EGNTWLTAFVLK	no	MUG1
1	QS20070624_P0149_HY109_04.02227.02227.3	3	966.0324	VLGPDSAANLELINTWVAENTNHK	no	SERPING1
1	QS20070624_P0149_HY109_04.02231.02231.3	3	966.0324	VLGPDSAANLELINTWVAENTNHK	no	SERPING1
0.9979	QS20070624_P0149_HY109_04.02235.02235.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
0.9999	QS20070624_P0149_HY109_04.02243.02243.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.3221	QS20070624_P0149_HY109_04.02253.02253.3	3	795.5332	AEDLAPGDISSFLLTAALYK	no	UNKNOWN
1	QS20070624_P0149_HY109_04.02255.02255.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
1	QS20070624_P0149_HY109_04.02267.02267.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
1	QS20070624_P0149_HY109_04.02271.02271.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.5052	QS20070624_P0149_HY109_04.02272.02272.2	2	783.3514	YVNWIQQTIAAN	no	2210010C04RIK
0.2944	QS20070624_P0149_HY109_04.02287.02287.2	2	820.4375	RSHFVLIAGEPLR	no	PIR
0.3521	QS20070624_P0149_HY109_04.02289.02289.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.997	QS20070624_P0149_HY109_04.02301.02301.2	2	755.8156	SIFSAVLDELK	YES	CPS1
1	QS20070624_P0149_HY109_04.02328.02328.3	3	1117.838	THTTCPDCPSPIDLSNPSALEAATESLAK	no	FETUB
1	QS20070624_P0149_HY109_04.02335.02335.3	3	1117.838	THTTCPDCPSPIDLSNPSALEAATESLAK	no	FETUB
0.8939	QS20070624_P0149_HY109_04.02357.02357.3	3	597.3018	AYLEEECPEMLK	YES	AZGP1
0.9999	QS20070624_P0149_HY109_04.02361.02361.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.9661	QS20070624_P0149_HY109_04.02368.02368.3	3	750.1513	VWDCTWPAPLGVSPGTVK	no	LIFR
0.8674	QS20070624_P0149_HY109_04.02375.02375.3	3	661.0564	GVAWSNPFPECVIVK	no	C4BP
0.9761	QS20070624_P0149_HY109_04.02381.02381.2	2	834.9116	DFLIPVAWYEDR	no	HGD
1	QS20070624_P0149_HY109_04.02403.02403.3	3	798.5211	ISEDCLYLNIYSPADLTK	no	ES1
1	QS20070624_P0149_HY109_04.02407.02407.3	3	798.5211	ISEDCLYLNIYSPADLTK	no	ES1
0.8322	QS20070624_P0149_HY109_04.02424.02424.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.9701	QS20070624_P0149_HY109_04.02435.02435.2	2	802.8508	GNTLEEILEGLK	no	SERPINA3M
0.9832	QS20070624_P0149_HY109_04.02436.02436.3	3	900.6188	LSVLCQDNYLTQDSEEMVCK	no	CFH
0.467	QS20070624_P0149_HY109_04.02443.02443.3	3	799.1664	NGSGELGYGEVISSLEKPGGR	no	SALL2
0.9988	QS20070624_P0149_HY109_04.02503.02503.2	2	877.9569	DVFLGTFLYEYSR	no	ALB
0.9109	QS20070624_P0149_HY109_04.02545.02545.3	3	761.5731	QVLLIFLLLGVVGAGSEPRR	no	PCDHB22
1	QS20070624_P0149_HY109_04.02568.02568.3	3	912.3257	GPDEEHLGILGPVIWAEVGDTIK	no	CP
0.3742	QS20070624_P0149_HY109_04.02569.02569.2	2	1072.096	DFDEFTHDNNDIMLK	no	2700097O09RIK
0.9673	QS20070624_P0149_HY109_04.02571.02571.2	2	877.9569	DVFLGTFLYEYSR	no	ALB
1	QS20070624_P0149_HY109_04.02623.02623.3	3	762.4805	GITWGEDTLMEYLENPK	no	CYCS
1	QS20070624_P0149_HY109_04.02624.02624.2	2	1162.816	LSISGNYNLETLMSPLGITR	no	SERPINA1E
1	QS20070624_P0149_HY109_04.02627.02627.3	3	762.4805	GITWGEDTLMEYLENPK	no	CYCS
0.9994	QS20070624_P0149_HY109_04.02639.02639.3	3	861.5891	ELGSPPGISLETIDAAFSCPGSSR	no	HPXN
0.9334	QS20070624_P0149_HY109_04.02640.02640.2	2	877.9569	DVFLGTFLYEYSR	no	ALB
0.415	QS20070624_P0149_HY109_04.02723.02723.2	2	820.4375	RSHFVLIAGEPLR	no	PIR
0.9967	QS20070624_P0149_HY109_04.02724.02724.3	3	700.1447	FALEIPVEFSMVPMAK	no	MUG1
0.5572	QS20070624_P0149_HY109_04.02756.02756.3	3	832.2229	AEPLYELVTATDFAYSSTVK	no	C8B
0.9968	QS20070624_P0149_HY109_04.02763.02763.3	3	832.2229	AEPLYELVTATDFAYSSTVK	no	C8B
1	QS20070624_P0149_HY109_04.02792.02792.2	2	874.4881	DIASGLIGPLILCK	no	CP

1	QS20070624_P0149_HY109_04.02795.02795.2	2	874.4881	DIASGLIGPLILCK	no	CP
0.9999	QS20070624_P0149_HY109_04.02799.02799.3	3	583.3278	DIASGLIGPLILCK	no	CP
0.9958	QS20070624_P0149_HY109_04.02803.02803.3	3	940.6649	AVLTSQETLFGGSDCTGNFCLFK	no	TF
0.9976	QS20070624_P0149_HY109_04.02824.02824.3	3	744.831	LPAGLPTSLLTLYLDNNK	no	LUM
0.8669	QS20070624_P0149_HY109_04.02847.02847.2	2	855.4799	DLYSGLIGPLIVCR	no	CP
0.9946	QS20070624_P0149_HY109_04.02851.02851.2	2	855.4799	DLYSGLIGPLIVCR	no	CP
0.2318	QS20070624_P0149_HY109_04.02852.02852.3	3	854.2545	EFVEEFIWPAVQSSALYEDR	no	ASS1
1	QS20070624_P0149_HY109_04.02917.02917.2	2	1045.614	DSPVLLDFFEDSELYR	no	HRG
0.9703	QS20070624_P0149_HY109_04.02919.02919.3	3	967.0789	MLIYTILPDGEVIADSVNFEIEK	no	MUG1
0.9998	QS20070624_P0149_HY109_04.02935.02935.3	3	967.0789	MLIYTILPDGEVIADSVNFEIEK	no	MUG1
1	QS20070624_P0149_HY109_04.03069.03069.3	3	1115.881	GFADQFLYEYSSNYGQAPLPLLVAYTK	no	GC
1	QS20070624_P0149_HY109_04.03257.03257.2	2	1154.743	IPESGGDNGVFDIFELIGGAR	no	THBS1
0.9989	QS20070624_P0149_HY109_04.03407.03407.3	3	1054.815	TELTNIELLDDFDEYTMTIQQVIK	no	C3
0.9997	QS20070624_P0149_HY109_06.00504.00504.3	3	524.2332	ADHSTLLFHLK	YES	ASGR2
1	QS20070624_P0149_HY109_06.00507.00507.3	3	554.5859	GATYAFTGSHYWR	no	HPXN
1	QS20070624_P0149_HY109_06.00512.00512.3	3	703.7388	TYFPHFDVSHGSAQVK	no	HBA-A1
0.1596	QS20070624_P0149_HY109_06.00523.00523.2	2	1165.212	IQEITEQLDITTSEYEK	no	HSPD1
0.9848	QS20070624_P0149_HY109_06.00532.00532.3	3	645.6703	KPVDQYEDCYLAR	YES	TF
0.2142	QS20070624_P0149_HY109_06.00533.00533.2	2	1020.572	HFGELEIQATWYEK	no	ANGPTL7
0.9771	QS20070624_P0149_HY109_06.00537.00537.3	3	645.6703	KPVDQYEDCYLAR	YES	TF
0.9989	QS20070624_P0149_HY109_06.00567.00567.2	2	801.8657	HTTIFEVLPEK	YES	TF
0.1662	QS20070624_P0149_HY109_06.00569.00569.2	2	941.9824	AAAGGAGAAGGAGAAEVAGPGAR	no	4931429I11RIK
1	QS20070624_P0149_HY109_06.00575.00575.2	2	716.7614	LCENIAGHLK	YES	CAT
0.9949	QS20070624_P0149_HY109_06.00581.00581.3	3	664.0753	AHMVTLDYTVQVPGTGR	YES	GNMT
0.784	QS20070624_P0149_HY109_06.00587.00587.3	3	825.5363	DSLCASLSMCELSVESSGFK	no	BC021381
1	QS20070624_P0149_HY109_06.00596.00596.3	3	564.2927	YEALLLTHETSIR	YES	FGG
1	QS20070624_P0149_HY109_06.00597.00597.3	3	683.0789	ENPTTFMGHYLHEVAR	no	ALB
0.9826	QS20070624_P0149_HY109_06.00599.00599.2	2	722.8038	HPDYSVSLLLR	no	ALB
0.9971	QS20070624_P0149_HY109_06.00600.00600.2	2	658.745	LLIGTVFHK	YES	PON1
0.9547	QS20070624_P0149_HY109_06.00611.00611.2	2	716.7614	LCENIAGHLK	YES	CAT
1	QS20070624_P0149_HY109_06.00623.00623.3	3	764.135	QLTEHAVEGDCDFHILK	no	AHSG
0.9968	QS20070624_P0149_HY109_06.00625.00625.3	3	509.5433	LEDIVTYHCSR	YES	CFB
0.9989	QS20070624_P0149_HY109_06.00627.00627.2	2	794.9123	HSLMPMLETLK	no	APOA1
0.9938	QS20070624_P0149_HY109_06.00628.00628.3	3	859.2239	AETFTFHSDICTLPEKEK	no	ALB
1	QS20070624_P0149_HY109_06.00632.00632.3	3	721.1099	RPCFSALTVDETYVPK	no	ALB
0.9999	QS20070624_P0149_HY109_06.00635.00635.3	3	544.5789	DLQILAEFHEK	no	SERPINA3K
0.9737	QS20070624_P0149_HY109_06.00637.00637.2	2	777.8181	GFSQSLSVQWDR	YES	AZGP1
1	QS20070624_P0149_HY109_06.00643.00643.2	2	939.4992	FLGVAEQLHNEGFK	YES	CPS1
0.9997	QS20070624_P0149_HY109_06.00647.00647.3	3	626.6685	FLGVAEQLHNEGFK	YES	CPS1
0.9999	QS20070624_P0149_HY109_06.00651.00651.3	3	626.6685	FLGVAEQLHNEGFK	YES	CPS1
0.254	QS20070624_P0149_HY109_06.00652.00652.3	3	491.8736	IIGILEVGQDK	no	EG235580
0.9998	QS20070624_P0149_HY109_06.00653.00653.3	3	575.6616	YLLGTSLARPCIAR	YES	ASS1
0.9457	QS20070624_P0149_HY109_06.00660.00660.2	2	666.7152	DLELLASGVDR	YES	C3
0.9981	QS20070624_P0149_HY109_06.00667.00667.3	3	478.1767	LCENIAGHLK	YES	CAT
0.9946	QS20070624_P0149_HY109_06.00687.00687.2	2	674.7812	PYLLISTQIR	no	GCHFR
1	QS20070624_P0149_HY109_06.00688.00688.3	3	536.2541	FAQLCEEHGILR	no	UNKNOWN
0.997	QS20070624_P0149_HY109_06.00699.00699.3	3	626.6685	FLGVAEQLHNEGFK	YES	CPS1
0.4639	QS20070624_P0149_HY109_06.00719.00719.3	3	954.0075	GLFGSGGAAGGCGVPGAGADGYGYLAPPK	no	FOXL2
0.1949	QS20070624_P0149_HY109_06.00725.00725.2	2	823.3575	AFIDCCNHITK	no	C3

0.6625	QS20070624_P0149_HY109_06.00727.00727.2	2	624.7137	ILLMDLNK	YES	PON1
0.9989	QS20070624_P0149_HY109_06.00728.00728.3	3	549.2407	AFIDCCNHITK	no	C3
0.3208	QS20070624_P0149_HY109_06.00732.00732.3	3	575.6616	YLLGTSLARPCIAR	YES	ASS1
0.9979	QS20070624_P0149_HY109_06.00735.00735.3	3	549.2407	AFIDCCNHITK	no	C3
0.9999	QS20070624_P0149_HY109_06.00737.00737.3	3	720.4764	AHEHIFGMVLMNDWSAR	YES	FAH
0.9999	QS20070624_P0149_HY109_06.00745.00745.3	3	725.4274	AETFTFHSDICTLPEK	no	ALB
0.7764	QS20070624_P0149_HY109_06.00769.00769.3	3	589.6233	KNLFDELVLDK	no	MUG1
0.3747	QS20070624_P0149_HY109_06.00773.00773.3	3	440.8396	NLIPILEAHR	no	C330023D02RIK
1	QS20070624_P0149_HY109_06.00796.00796.3	3	682.7329	VITAFNDGLNHLDSLK	no	HBB-B1
0.9968	QS20070624_P0149_HY109_06.00799.00799.3	3	477.2037	ILLLGEAQVGK	no	RHOT2
0.9598	QS20070624_P0149_HY109_06.00800.00800.3	3	515.8838	KWFWDFATR	no	HPXN
0.999	QS20070624_P0149_HY109_06.00819.00819.3	3	554.2763	GWFEPIVEDMHR	no	APOE
0.2683	QS20070624_P0149_HY109_06.00824.00824.2	2	833.8904	GPQIWTVAGHPSK	no	PARP4
1	QS20070624_P0149_HY109_06.00828.00828.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
0.1902	QS20070624_P0149_HY109_06.00829.00829.3	3	510.2331	LVALCDVLYGK	no	BST1
0.8505	QS20070624_P0149_HY109_06.00848.00848.2	2	751.7866	SINGTFFGGWK	YES	ADH4
1	QS20070624_P0149_HY109_06.00855.00855.3	3	586.6307	DLEIEEVLFHPK	YES	CFB
0.9998	QS20070624_P0149_HY109_06.00883.00883.3	3	583.6597	AHFSVMGDILSSAIR	no	MUG1
0.3699	QS20070624_P0149_HY109_06.00884.00884.3	3	559.2635	RGTTDLSVEALPK	no	2610101J03RIK
1	QS20070624_P0149_HY109_06.00887.00887.3	3	964.3458	HSLGDNDAHSIFQSVGINIFTNSK	no	PZP
0.285	QS20070624_P0149_HY109_06.00888.00888.3	3	723.4124	CYVCDQQTNGVFNPAK	no	RNF113A1
0.9998	QS20070624_P0149_HY109_06.00907.00907.3	3	964.3458	HSLGDNDAHSIFQSVGINIFTNSK	no	PZP
1	QS20070624_P0149_HY109_06.00915.00915.3	3	774.1789	GSIFNLGSHVLSLEQGNMK	no	PZP
0.9034	QS20070624_P0149_HY109_06.00920.00920.3	3	670.7261	KPWNVVSLIYETK	no	C9
1	QS20070624_P0149_HY109_06.00928.00928.3	3	645.058	YTPEQVAMATVTALHR	no	ALDOB
0.9999	QS20070624_P0149_HY109_06.00936.00936.3	3	622.6943	EEHSFTVMEFVLPR	no	MUG1
0.6117	QS20070624_P0149_HY109_06.00941.00941.2	2	850.3778	DEELSCSVLELK	no	SERPINA3K
0.2437	QS20070624_P0149_HY109_06.00943.00943.3	3	583.9806	RVDMQVGQMQAGER	no	ALPK3
0.2578	QS20070624_P0149_HY109_06.00965.00965.3	3	953.3161	GAANLQLIQALSDSEEEHDSAWDGR	no	WDR23
0.2125	QS20070624_P0149_HY109_06.00968.00968.3	3	631.9864	NGNLPEFGDAIATASK	no	TLN1
0.1458	QS20070624_P0149_HY109_06.00976.00976.2	2	633.7136	FLTAISVVK	no	PAXIP1
0.9999	QS20070624_P0149_HY109_06.00992.00992.3	3	789.1913	AVTHVGMDESEIIFVDWK	no	ORM1
1	QS20070624_P0149_HY109_06.01035.01035.3	3	684.0877	LTQLGTFEDHFLSLQR	no	EGFR
1	QS20070624_P0149_HY109_06.01040.01040.3	3	617.027	YEGGVETFAHLIVLR	no	ORM1
0.1794	QS20070624_P0149_HY109_06.01043.01043.3	3	643.6838	SHGSPETLVLTNTRK	no	TREM3
1	QS20070624_P0149_HY109_06.01045.01045.3	3	730.1185	TFGLGEADCGLRPLFEK	no	F2
0.5521	QS20070624_P0149_HY109_06.01056.01056.3	3	1215.7	VAATLQVPVNSLNADLIQVAFFTCSFDLAIK	no	MINPP1
0.9304	QS20070624_P0149_HY109_06.01060.01060.2	2	576.141	TLEDILFR	YES	FGG
1	QS20070624_P0149_HY109_06.01080.01080.3	3	766.1617	YGFCETADQLHILNEVPR	no	C8G
0.806	QS20070624_P0149_HY109_06.01085.01085.2	2	602.1855	IIWELIK	no	IDH1
0.6134	QS20070624_P0149_HY109_06.01088.01088.3	3	751.7811	EYPNLPPTPSSQYCGHK	no	AW554918
0.5723	QS20070624_P0149_HY109_06.01092.01092.3	3	912.369	ILELLTVTRPNAVALVDAFDFK	no	ACOX1
0.3022	QS20070624_P0149_HY109_06.01097.01097.3	3	912.369	ILELLTVTRPNAVALVDAFDFK	no	ACOX1
1	QS20070624_P0149_HY109_06.01101.01101.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.3209	QS20070624_P0149_HY109_06.01107.01107.3	3	713.4523	GELFQAFIDTAQHMLK	no	D2ERTD435E
1	QS20070624_P0149_HY109_06.01116.01116.3	3	1263.703	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	no	SPI1-6
0.2119	QS20070624_P0149_HY109_06.01124.01124.3	3	665.0546	GGMLANDTVIAELKK	no	UNKNOWN
0.9999	QS20070624_P0149_HY109_06.01133.01133.3	3	869.6125	LFQEEFPGIPYPPDAAVECHR	no	HPXN
0.1066	QS20070624_P0149_HY109_06.01145.01145.2	2	1262.818	VEDLSAEWDAMGGKVQDIK	no	FSD1

1	QS20070624_P0149_HY109_06.01176.01176.3	3	1263.703	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	no	SPI1-6
1	QS20070624_P0149_HY109_06.01191.01191.3	3	681.4179	EALIQFLEQVHQGIK	no	CPN1
0.3901	QS20070624_P0149_HY109_06.01212.01212.3	3	595.2957	SNFSVQETQTLLK	no	8430410K20RIK
1	QS20070624_P0149_HY109_06.01225.01225.3	3	1263.703	SFQHLLQTLNRPDSELQLSTGNGLFVNNDLK	no	SPI1-6
0.8813	QS20070624_P0149_HY109_06.01228.01228.3	3	595.2957	SNFSVQETQTLLK	no	8430410K20RIK
0.3122	QS20070624_P0149_HY109_06.01239.01239.3	3	595.2957	SNFSVQETQTLLK	no	8430410K20RIK
0.9996	QS20070624_P0149_HY109_06.01245.01245.3	3	721.4769	KLDILSNDLVINMLK	no	FBP1
0.8487	QS20070624_P0149_HY109_06.01304.01304.3	3	595.2957	SNFSVQETQTLLK	no	8430410K20RIK
0.998	QS20070624_P0149_HY109_06.01307.01307.3	3	728.4742	YCTAISGDLHILPVAFK	no	EGFR
0.9331	QS20070624_P0149_HY109_06.01313.01313.2	2	637.185	WFWDFATR	no	HPXN
1	QS20070624_P0149_HY109_06.01320.01320.3	3	833.8525	ISFDPQDTFESEFYLDEK	no	SERPINA3K
0.6574	QS20070624_P0149_HY109_06.01341.01341.2	2	746.7866	SLEVLNLSSNK	no	OMG
0.9378	QS20070624_P0149_HY109_06.01343.01343.2	2	631.6989	LWWLDLK	no	HPXN
0.2996	QS20070624_P0149_HY109_06.01349.01349.3	3	421.4684	LWWLDLK	no	HPXN
1	QS20070624_P0149_HY109_06.01359.01359.3	3	723.4806	LVPFVVQLSGHLAQETER	no	APOA4
0.9497	QS20070624_P0149_HY109_06.01361.01361.3	3	927.9975	TNCDLYEKLGEYGFQNAILVR	no	ALB
1	QS20070624_P0149_HY109_06.01367.01367.3	3	723.4806	LVPFVVQLSGHLAQETER	no	APOA4
1	QS20070624_P0149_HY109_06.01379.01379.3	3	723.4806	LVPFVVQLSGHLAQETER	no	APOA4
0.7743	QS20070624_P0149_HY109_06.01411.01411.3	3	630.6687	GNLAHCYSAEELVHR	no	HOXA11
1	QS20070624_P0149_HY109_06.01412.01412.3	3	1051.797	VADALANAAGHLDDLPGALSALSDLHAHK	no	HBA-A1
0.4651	QS20070624_P0149_HY109_06.01415.01415.3	3	725.0857	SQCHSITSYFNSAPPAK	no	6030441H18RIK
0.5808	QS20070624_P0149_HY109_06.01423.01423.3	3	630.6687	GNLAHCYSAEELVHR	no	HOXA11
0.9769	QS20070624_P0149_HY109_06.01436.01436.3	3	885.2726	LCAIPNLRENYGELADCCTK	no	ALB
0.993	QS20070624_P0149_HY109_06.01445.01445.3	3	736.5021	VLSMTGVGQTLVWCLHK	YES	GCHFR
0.9973	QS20070624_P0149_HY109_06.01464.01464.2	2	755.8156	SIFSAVLDELK	YES	CPS1
0.9347	QS20070624_P0149_HY109_06.01465.01465.3	3	805.5922	MLRPLNELLPLAYIEDPK	no	MUG1
0.9998	QS20070624_P0149_HY109_06.01467.01467.3	3	805.5922	MLRPLNELLPLAYIEDPK	no	MUG1
0.9989	QS20070624_P0149_HY109_06.01471.01471.3	3	805.5922	MLRPLNELLPLAYIEDPK	no	MUG1
0.9211	QS20070624_P0149_HY109_06.01473.01473.3	3	829.2089	LGEHNINVLEGNEQFVNAAK	no	UNKNOWN
0.4626	QS20070624_P0149_HY109_06.01476.01476.2	2	652.2038	VLWNQLNK	no	DOPEY2
0.1502	QS20070624_P0149_HY109_06.01481.01481.2	2	749.2527	SVEDQFNEIK	no	MYH13
0.9371	QS20070624_P0149_HY109_06.01505.01505.2	2	724.2875	EDLIWEILK	no	TF
0.9641	QS20070624_P0149_HY109_06.01509.01509.3	3	537.9308	ALLAYAFALAGNK	no	PZP
0.8708	QS20070624_P0149_HY109_06.01512.01512.3	3	829.2089	LGEHNINVLEGNEQFVNAAK	no	UNKNOWN
0.7906	QS20070624_P0149_HY109_06.01532.01532.2	2	712.2942	LAFIENLCGPR	no	ECM1
0.3734	QS20070624_P0149_HY109_06.01552.01552.3	3	748.4912	ATLIVVHTDGSIVETTGLK	no	DEAF1
1	QS20070624_P0149_HY109_06.01555.01555.2	2	884.9989	GLVLIAFSQYLQK	no	ALB
0.9991	QS20070624_P0149_HY109_06.01560.01560.3	3	590.335	GLVLIAFSQYLQK	no	ALB
1	QS20070624_P0149_HY109_06.01564.01564.2	2	755.8156	SIFSAVLDELK	YES	CPS1
1	QS20070624_P0149_HY109_06.01565.01565.2	2	839.9527	VCPFAGILENGIVR	no	APOH
0.1499	QS20070624_P0149_HY109_06.01568.01568.3	3	1007.153	FTAICKPLHYFVIMNPRLCVK	no	OLFR42
1	QS20070624_P0149_HY109_06.01592.01592.3	3	1193.296	LCMAALSHQPQEFPTYVEPTNDEICEAFR	no	GC
0.9994	QS20070624_P0149_HY109_06.01605.01605.3	3	839.9419	LILPYVELDLHSYDLGIENR	no	IDH1
0.9995	QS20070624_P0149_HY109_06.01608.01608.3	3	1193.296	LCMAALSHQPQEFPTYVEPTNDEICEAFR	no	GC
1	QS20070624_P0149_HY109_06.01631.01631.2	2	755.8156	SIFSAVLDELK	YES	CPS1
1	QS20070624_P0149_HY109_06.01699.01699.2	2	755.8156	SIFSAVLDELK	YES	CPS1
1	QS20070624_P0149_HY109_06.01740.01740.2	2	755.8156	SIFSAVLDELK	YES	CPS1
1	QS20070624_P0149_HY109_06.01755.01755.3	3	1255.998	AHCLSEVEHDTMPADLPAIAADFVEDQEVCK	no	ALB
0.9966	QS20070624_P0149_HY109_06.01787.01787.2	2	755.8156	SIFSAVLDELK	YES	CPS1

0.9833	QS20070624_P0149_HY109_06.01799.01799.3	3	504.2128	SIFSAVLDELK	YES	CPS1
0.999	QS20070624_P0149_HY109_06.01839.01839.3	3	605.3459	WFFIGAAVLNPDYR	no	ORM2
1	QS20070624_P0149_HY109_06.01868.01868.3	3	986.4065	AYFPCIGCVHAISTDSPDLEPVLK	no	KNG1
0.3945	QS20070624_P0149_HY109_06.01896.01896.3	3	854.2023	ASCQTHNLDHLDLSDNSLGGK	no	UNKNOWN
0.9998	QS20070624_P0149_HY109_06.01928.01928.3	3	830.8936	YNEDLELEDAIHTAILTLK	no	PSMA2
0.2435	QS20070624_P0149_HY109_06.01967.01967.2	2	851.9843	VISLVSQEPVLFAR	no	ABCB9
0.1544	QS20070624_P0149_HY109_06.01973.01973.3	3	835.5554	SDDLQCVFITLLPNENCAK	no	KLK1B26
0.9908	QS20070624_P0149_HY109_06.01977.01977.3	3	835.5554	SDDLQCVFITLLPNENCAK	no	KLK1B26
0.762	QS20070624_P0149_HY109_06.02035.02035.3	3	794.903	YMNSGPVVAMVWEGLNVVK	no	NME2
1	QS20070624_P0149_HY109_06.02041.02041.3	3	695.1457	LPIICFDYGMVPISAPR	no	MUG1
0.9998	QS20070624_P0149_HY109_06.02043.02043.3	3	695.1457	LPIICFDYGMVPISAPR	no	MUG1
0.9913	QS20070624_P0149_HY109_06.02044.02044.3	3	794.903	YMNSGPVVAMVWEGLNVVK	no	NME2
1	QS20070624_P0149_HY109_06.02061.02061.3	3	977.76	AAPLSLCALTAVDQSVLLLKPEAK	no	PZP
0.9888	QS20070624_P0149_HY109_06.02064.02064.2	2	859.4118	VYMDFLEDCCSR	no	AFM
0.9844	QS20070624_P0149_HY109_06.02075.02075.3	3	572.6463	VGEVLNSILLELK	no	AGT
0.3927	QS20070624_P0149_HY109_06.02077.02077.3	3	971.5156	SSNVIVLLLAQIMGMYFVSSVLLIR	no	GPR89
0.9863	QS20070624_P0149_HY109_06.02092.02092.3	3	604.3575	ITFELIYQELLQR	no	ITIH4
0.999	QS20070624_P0149_HY109_06.02225.02225.3	3	584.6573	GLLVGEFLSTVLSK	no	HC
1	QS20070624_P0149_HY109_06.02235.02235.2	2	898.9973	LPCVEDYLSAILNR	no	ALB
1	QS20070624_P0149_HY109_06.02247.02247.2	2	898.9973	LPCVEDYLSAILNR	no	ALB
0.9999	QS20070624_P0149_HY109_06.02272.02272.3	3	795.2506	YNPVVIDFEMQPIYQLLR	no	C8A
0.9999	QS20070624_P0149_HY109_06.02279.02279.3	3	795.2506	YNPVVIDFEMQPIYQLLR	no	C8A
1	QS20070624_P0149_HY109_06.02283.02283.2	2	898.9973	LPCVEDYLSAILNR	no	ALB
0.9998	QS20070624_P0149_HY109_06.02315.02315.3	3	599.6673	LPCVEDYLSAILNR	no	ALB
0.986	QS20070624_P0149_HY109_06.02531.02531.2	2	782.8563	DNIIDDVISFIR	no	C9
0.9999	QS20070624_P0149_HY109_06.02607.02607.3	3	763.8337	ELDQDTVFALANYILFK	no	SERPINA1B
1	QS20070624_P0149_HY109_06.02615.02615.3	3	763.8337	ELDQDTVFALANYILFK	no	SERPINA1B
1	QS20070624_P0149_HY109_06.02627.02627.3	3	720.7952	LDQDTVFALANYILFK	no	SPI1-6
1	QS20070624_P0149_HY109_06.02787.02787.3	3	862.962	VPTANLENVLPLAEDFTEILSR	no	GC
1	QS20070624_P0149_HY109_06.03263.03263.3	3	941.7088	AQNVPLPVSTLVEFVIAATDCTAK	no	AHSG
0.4188	QS20070709_P0149_HY109_05.01427.01427.3	3	360.6844	HSDFASK	no	GC
0.2457	QS20070709_P0149_HY109_05.01434.01434.3	3	447.124	NKPGVYTK	no	TMPRSS13
0.9999	QS20070709_P0149_HY109_05.01437.01437.3	3	429.4462	TPVSEHVTK	no	ALB
0.1924	QS20070709_P0149_HY109_05.01438.01438.3	3	447.8312	GSPAPPVVAPCR	no	HECTD1
0.9999	QS20070709_P0149_HY109_05.01439.01439.3	3	481.5247	TQLAPHSEQMR	YES	APOA1
0.9913	QS20070709_P0149_HY109_05.01443.01443.3	3	397.7323	GPTHEFSK	no	MUG1
0.8866	QS20070709_P0149_HY109_05.01445.01445.3	3	357.7109	LSQAVHK	no	SPI1-6
0.9999	QS20070709_P0149_HY109_05.01449.01449.3	3	492.8433	SNPTLNEYHTR	no	APOA1
0.8111	QS20070709_P0149_HY109_05.01451.01451.3	3	358.3782	SNFEYLR	no	CNOT10
0.3455	QS20070709_P0149_HY109_05.01454.01454.3	3	429.7462	CSYDEHAK	no	ALB
0.9999	QS20070709_P0149_HY109_05.01457.01457.3	3	365.4144	IPSHAVVAR	YES	TF
0.9807	QS20070709_P0149_HY109_05.01459.01459.3	3	401.0776	VHLTDAEK	no	HBB-B2
0.2218	QS20070709_P0149_HY109_05.01461.01461.3	3	507.1874	EPVSLEEWNK	no	TBC1D15
0.8547	QS20070709_P0149_HY109_05.01465.01465.3	3	438.4736	NLKPAPIK	no	PZP
0.9991	QS20070709_P0149_HY109_05.01469.01469.3	3	472.1454	KYEATLEK	no	ALB
0.9397	QS20070709_P0149_HY109_05.01470.01470.3	3	438.4736	NLKPAPIK	no	PZP
0.9848	QS20070709_P0149_HY109_05.01473.01473.3	3	472.1454	KYEATLEK	no	ALB
0.6683	QS20070709_P0149_HY109_05.01475.01475.3	3	503.5029	KPFDPENTK	no	SERPINA1E
0.2402	QS20070709_P0149_HY109_05.01481.01481.3	3	416.7836	MELERPGK	YES	FGA

0.2421	QS20070709_P0149_HY109_05.01497.01497.3	3	419.4629	TVLTGASGHLR	no	C3
0.1696	QS20070709_P0149_HY109_05.01501.01501.3	3	411.7746	KYEHVIR	no	D030022P06RIK
0.9996	QS20070709_P0149_HY109_05.01509.01509.3	3	394.4261	SDAQIHIPR	no	SERPINA1D
0.942	QS20070709_P0149_HY109_05.01513.01513.3	3	404.7538	IENPHWK	YES	ASGR2
0.9414	QS20070709_P0149_HY109_05.01517.01517.3	3	404.7538	IENPHWK	YES	ASGR2
0.9958	QS20070709_P0149_HY109_05.01521.01521.3	3	395.77	ARPALEDLR	no	APOA1
0.9998	QS20070709_P0149_HY109_05.01526.01526.3	3	414.458	RPDITPELR	no	ORM1
0.7361	QS20070709_P0149_HY109_05.01527.01527.3	3	463.1487	YRPSFVSDK	no	ES1
0.9412	QS20070709_P0149_HY109_05.01529.01529.3	3	446.8303	THEQLTPLVR	no	APOA2
0.9998	QS20070709_P0149_HY109_05.01531.01531.3	3	510.8834	MQHLEQTLNK	no	SERPINA1D
0.1788	QS20070709_P0149_HY109_05.01541.01541.3	3	445.1147	VDHAGEYGANR	no	COQ7
0.3413	QS20070709_P0149_HY109_05.01545.01545.3	3	415.8113	MPQLIVQK	no	PCDH11X
0.2418	QS20070709_P0149_HY109_05.01547.01547.3	3	462.8337	FEFPVYAPK	no	GM364
0.9998	QS20070709_P0149_HY109_05.01549.01549.3	3	501.8748	MQHLEQTLSK	no	SPI1-6
1	QS20070709_P0149_HY109_05.01550.01550.3	3	558.9172	IGGHGAEYGAEALER	no	HBA-A1
0.9999	QS20070709_P0149_HY109_05.01561.01561.3	3	429.1324	LSVSQVVHK	no	SERPINA3K
0.9956	QS20070709_P0149_HY109_05.01562.01562.3	3	497.8369	ATFGCHETYK	no	APOH
0.9989	QS20070709_P0149_HY109_05.01565.01565.3	3	429.1324	LSVSQVVHK	no	SERPINA3K
0.3186	QS20070709_P0149_HY109_05.01566.01566.3	3	422.798	AVLVVHPDK	no	DNAJC6
0.1752	QS20070709_P0149_HY109_05.01579.01579.3	3	483.5388	HVPLIQPVEK	no	FETUB
0.9982	QS20070709_P0149_HY109_05.01581.01581.3	3	451.7959	NECFLQHK	no	ALB
0.9909	QS20070709_P0149_HY109_05.01582.01582.3	3	508.865	KVINDFVEK	no	SPI1-6
0.9906	QS20070709_P0149_HY109_05.01587.01587.3	3	451.7959	NECFLQHK	no	ALB
0.9917	QS20070709_P0149_HY109_05.01593.01593.3	3	453.8263	HLFTGPALSK	YES	FAH
0.996	QS20070709_P0149_HY109_05.01597.01597.3	3	453.8263	HLFTGPALSK	YES	FAH
0.9966	QS20070709_P0149_HY109_05.01598.01598.3	3	424.4531	LHVDPENFR	no	HBB-B1
0.9945	QS20070709_P0149_HY109_05.01601.01601.3	3	392.7562	VCLLHEK	no	ALB
0.1592	QS20070709_P0149_HY109_05.01602.01602.3	3	452.4724	SYFLHKK	no	UNKNOWN
0.9971	QS20070709_P0149_HY109_05.01607.01607.3	3	546.8814	WCAVSEHENTK	no	TF
0.9997	QS20070709_P0149_HY109_05.01610.01610.3	3	511.8821	KQTALAELVK	no	ALB
0.9998	QS20070709_P0149_HY109_05.01611.01611.3	3	610.9939	SHCFTQAMMSQPK	YES	PEMT
1	QS20070709_P0149_HY109_05.01613.01613.3	3	482.2049	VILGAHEEYIR	YES	PLG
0.5313	QS20070709_P0149_HY109_05.01619.01619.3	3	531.5336	TNASLEVDAEENR	no	BPI
0.1322	QS20070709_P0149_HY109_05.01621.01621.3	3	417.1029	QCQFDICR	no	ZC3H7A
1	QS20070709_P0149_HY109_05.01622.01622.3	3	482.2049	VILGAHEEYIR	YES	PLG
0.9993	QS20070709_P0149_HY109_05.01625.01625.3	3	422.1225	LFAYPDTHR	YES	CAT
0.2286	QS20070709_P0149_HY109_05.01645.01645.3	3	512.5756	GGLFCSPLPGAGLR	no	4930573I19RIK
0.5883	QS20070709_P0149_HY109_05.01646.01646.3	3	708.7719	SPEGPVSRVGATLPSRPK	no	USP36
0.3789	QS20070709_P0149_HY109_05.01647.01647.3	3	603.6457	SPFSVGVSPSLDLSK	no	FLNA
0.9865	QS20070709_P0149_HY109_05.01653.01653.3	3	436.124	SLHTLFGDK	no	ALB
0.5371	QS20070709_P0149_HY109_05.01657.01657.3	3	509.5333	WKEDVELYR	no	APOA1
0.9428	QS20070709_P0149_HY109_05.01658.01658.3	3	436.124	SLHTLFGDK	no	ALB
0.5609	QS20070709_P0149_HY109_05.01659.01659.3	3	474.8551	HPDLSTPELLR	no	AFM
0.4153	QS20070709_P0149_HY109_05.01670.01670.3	3	465.851	LTEVPALVHK	no	PZP
0.9999	QS20070709_P0149_HY109_05.01673.01673.3	3	593.6388	AFAQAQSHIFIEK	no	PZP
0.9998	QS20070709_P0149_HY109_05.01677.01677.3	3	645.6703	KPVDQYEDCYLAR	YES	TF
0.7171	QS20070709_P0149_HY109_05.01689.01689.3	3	401.7504	LLGLSGXNK	no	SYNJ1
0.7812	QS20070709_P0149_HY109_05.01714.01714.2	2	723.2582	IQNILSEDPK	YES	PON1
1	QS20070709_P0149_HY109_05.01715.01715.3	3	701.7221	SGAQATWTEVSWPHEK	no	HPXN

0.3348	QS20070709_P0149_HY109_05.01718.01718.3	3	634.0412	ANLQLESEELNILIR	no	2610507B11RIK
0.9704	QS20070709_P0149_HY109_05.01725.01725.2	2	487.0546	HELSVIM	YES	AQP9
1	QS20070709_P0149_HY109_05.01730.01730.3	3	465.852	VVAGVAAALAHK	no	HBB-B1
0.9999	QS20070709_P0149_HY109_05.01731.01731.3	3	654.707	TEVNTNHVLIYIEK	no	PZP
0.1718	QS20070709_P0149_HY109_05.01735.01735.3	3	755.8725	QTPLLLLVYMVTTGSGRDR	no	FOLR2
0.9988	QS20070709_P0149_HY109_05.01739.01739.3	3	439.4802	LFVLEEEHR	YES	FTCD
1	QS20070709_P0149_HY109_05.01741.01741.3	3	664.0753	AHMVTLDYTVQVPGTGR	YES	GNMT
0.9657	QS20070709_P0149_HY109_05.01746.01746.2	2	658.7167	LFVLEEEHR	YES	FTCD
0.1603	QS20070709_P0149_HY109_05.01759.01759.3	3	635.0518	ETLQAMILQLQPTK	no	DISC1
0.9801	QS20070709_P0149_HY109_05.01761.01761.3	3	534.9129	HTTIFEVLPEK	YES	TF
1	QS20070709_P0149_HY109_05.01781.01781.3	3	703.0855	ANLMHNLGGEEVSVACK	no	AHSG
1	QS20070709_P0149_HY109_05.01782.01782.3	3	830.1801	NHYQAEVFSVNFAESEEAK	no	SPI1-6
0.2653	QS20070709_P0149_HY109_05.01789.01789.3	3	796.9297	MGPLDVWDLSPLLSLWMNR	no	TYW1
0.1506	QS20070709_P0149_HY109_05.01817.01817.3	3	509.5433	LEDIVTYHCSR	YES	CFB
0.9991	QS20070709_P0149_HY109_05.01821.01821.3	3	509.5433	LEDIVTYHCSR	YES	CFB
0.9997	QS20070709_P0149_HY109_05.01822.01822.3	3	482.2049	HPDYSVSLLLR	no	ALB
1	QS20070709_P0149_HY109_05.01829.01829.3	3	564.2927	YEALLLTHETSIR	YES	FGG
0.9319	QS20070709_P0149_HY109_05.01841.01841.3	3	478.1767	LCENIAGHLK	YES	CAT
0.8507	QS20070709_P0149_HY109_05.01843.01843.3	3	629.3419	INGEWHTIILASDK	no	MUP2
0.9999	QS20070709_P0149_HY109_05.01849.01849.3	3	581.5978	GTFASLSELHCDK	no	HBB-B1
0.2302	QS20070709_P0149_HY109_05.01851.01851.2	2	617.1339	NQVVEDLK	no	DAAM2
0.9784	QS20070709_P0149_HY109_05.01853.01853.2	2	777.8181	GFSQSLSVQWDR	YES	AZGP1
0.9984	QS20070709_P0149_HY109_05.01857.01857.3	3	581.5978	GTFASLSELHCDK	no	HBB-B1
0.7899	QS20070709_P0149_HY109_05.01866.01866.3	3	596.301	LQTCCDKPLLK	no	ALB
0.9933	QS20070709_P0149_HY109_05.01878.01878.3	3	596.301	LQTCCDKPLLK	no	ALB
0.7697	QS20070709_P0149_HY109_05.01882.01882.3	3	596.301	LQTCCDKPLLK	no	ALB
1	QS20070709_P0149_HY109_05.01909.01909.3	3	544.5789	DLQILAEFHEK	no	SERPINA3K
1	QS20070709_P0149_HY109_05.01913.01913.3	3	544.5789	DLQILAEFHEK	no	SERPINA3K
0.9999	QS20070709_P0149_HY109_05.01921.01921.3	3	721.1099	RPCFSALTVDETYVPK	no	ALB
0.999	QS20070709_P0149_HY109_05.01925.01925.3	3	604.9751	IGEGSTGIVCIATEK	no	PAK7
0.4389	QS20070709_P0149_HY109_05.01938.01938.3	3	572.5735	ENYNWSSNSSARR	no	COL17A1
0.9999	QS20070709_P0149_HY109_05.01945.01945.3	3	750.8132	AMGDYLIVGVHTDEEIAK	YES	PCYT2
0.9998	QS20070709_P0149_HY109_05.01949.01949.3	3	621.2863	ECCHGDLLECADDR	no	ALB
1	QS20070709_P0149_HY109_05.01961.01961.3	3	626.6685	FLGVAEQLHNEGFK	YES	CPS1
0.5444	QS20070709_P0149_HY109_05.01999.01999.2	2	727.2492	NQNIINACTK	no	SEMA6A
0.5212	QS20070709_P0149_HY109_05.02011.02011.3	3	481.8553	MEELTAFVSK	no	SHOX2
0.9106	QS20070709_P0149_HY109_05.02018.02018.2	2	674.7812	PYLLISTQIR	no	GCHFR
0.9998	QS20070709_P0149_HY109_05.02025.02025.3	3	626.6685	FLGVAEQLHNEGFK	YES	CPS1
0.6839	QS20070709_P0149_HY109_05.02030.02030.2	2	692.2604	EYVLPSFEVR	YES	C3
0.1414	QS20070709_P0149_HY109_05.02059.02059.2	2	639.1647	AAGHTGPLHK	no	ACE
1	QS20070709_P0149_HY109_05.02083.02083.3	3	591.6321	CSPDPGLTALLSDHR	no	HPXN
0.9925	QS20070709_P0149_HY109_05.02094.02094.3	3	626.6685	FLGVAEQLHNEGFK	YES	CPS1
1	QS20070709_P0149_HY109_05.02095.02095.3	3	658.0642	GVTSVSQIFHSPDLAIR	no	SERPING1
0.9146	QS20070709_P0149_HY109_05.02102.02102.2	2	545.6222	LCAIPNLR	no	ALB
0.9986	QS20070709_P0149_HY109_05.02126.02126.3	3	725.4274	AETFTFHSDICTLPEK	no	ALB
0.9549	QS20070709_P0149_HY109_05.02145.02145.2	2	578.1581	YVIEFIAR	no	KNG1
0.1916	QS20070709_P0149_HY109_05.02169.02169.3	3	810.1805	GCEVTPDVNISGQKFNIK	no	PLEKHC1
1	QS20070709_P0149_HY109_05.02209.02209.3	3	699.3895	DIAFEVEDCDHIVQK	YES	HPD
1	QS20070709_P0149_HY109_05.02210.02210.3	3	682.7329	VITAFNDGLNHLDSLK	no	HBB-B1

0.1847	QS20070709_P0149_HY109_05.02214.02214.2	2	657.7072	FVIDCEIER	no	GRIA4
0.8357	QS20070709_P0149_HY109_05.02253.02253.3	3	705.0868	TDYDNFLMAHLINEK	no	UNKNOWN
1	QS20070709_P0149_HY109_05.02278.02278.3	3	586.6307	DLEIEEVLFHPK	YES	CFB
0.3403	QS20070709_P0149_HY109_05.02309.02309.3	3	525.5763	AVGTQALSGAGLLK	no	SNX1
0.7016	QS20070709_P0149_HY109_05.02319.02319.3	3	567.2543	DEELSCSVLELK	no	SERPINA3K
0.9638	QS20070709_P0149_HY109_05.02322.02322.3	3	567.2543	DEELSCSVLELK	no	SERPINA3K
0.3308	QS20070709_P0149_HY109_05.02330.02330.3	3	595.6657	QDPHASPPLVQVVPR	no	ANGPTL1
0.9898	QS20070709_P0149_HY109_05.02337.02337.3	3	598.6271	ENEFFIVTQTCK	no	KNG1
0.8963	QS20070709_P0149_HY109_05.02338.02338.2	2	614.6838	SGYVFELLR	no	HRG
0.4002	QS20070709_P0149_HY109_05.02365.02365.3	3	852.5859	GLTFSIGGQISIDVFPEGWDK	no	PMM2
0.9999	QS20070709_P0149_HY109_05.02399.02399.3	3	789.1913	AVTHVGMDESEIIFVDWK	no	ORM1
0.2383	QS20070709_P0149_HY109_05.02457.02457.3	3	797.2054	EYQLEGVNWLLFNWYNR	no	CHD8
0.5684	QS20070709_P0149_HY109_05.02470.02470.3	3	592.3296	NSMIVSPSQPPEMGR	no	TMED7
0.9999	QS20070709_P0149_HY109_05.02481.02481.3	3	789.1913	AVTHVGMDESEIIFVDWK	no	ORM1
0.845	QS20070709_P0149_HY109_05.02505.02505.3	3	484.5287	TMEEILEGLK	no	SERPINA3K
0.2976	QS20070709_P0149_HY109_05.02521.02521.3	3	778.1942	ICPKPDDLPFATVVPLK	no	APOH
0.164	QS20070709_P0149_HY109_05.02522.02522.2	2	730.289	TGTWSFLPTCR	no	APOH
0.8203	QS20070709_P0149_HY109_05.02571.02571.3	3	889.921	LEEVPGGQGRPEAGRPASEAADGK	no	MAGI2
1	QS20070709_P0149_HY109_05.02591.02591.3	3	766.1617	YGFCETADQLHILNEVPR	no	C8G
1	QS20070709_P0149_HY109_05.02599.02599.3	3	869.6125	LFQEEFPGIPYPPDAAVECHR	no	HPXN
1	QS20070709_P0149_HY109_05.02601.02601.3	3	869.6125	LFQEEFPGIPYPPDAAVECHR	no	HPXN
0.9999	QS20070709_P0149_HY109_05.02610.02610.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.8853	QS20070709_P0149_HY109_05.02657.02657.3	3	850.9095	DQSPASHEIATNLGDFAISLYR	no	SPI1-6
0.9878	QS20070709_P0149_HY109_05.02758.02758.2	2	689.2595	AYVAFPDFFR	no	MGAM
0.9792	QS20070709_P0149_HY109_05.02841.02841.2	2	753.3735	STMVEDLVVLVR	no	C8B
1	QS20070709_P0149_HY109_05.03017.03017.2	2	877.9569	DVFLGTFLYEYSR	no	ALB
0.95	QS20070709_P0149_HY109_05.03018.03018.2	2	877.9569	DVFLGTFLYEYSR	no	ALB
1	QS20070709_P0149_HY109_05.04169.04169.2	2	1293.939	VPTANLENVLPLAEDFTEILSR	no	GC

Table S5. Summary

Table S5. Liver-injury plasma analysis with three platforms. Plasma protein-level changes 24-hours after liver injury were analyzed by SPR array Set A and Set B, by iTRAQ, and by immunoblotting. SPR p-values are calculated for four technical replicates. Note that albumin (ALB) and transferrin (TF) were depleted from plasma samples before MS analysis. MS p-values are for statistical significance of the fold changes of the target proteins as compared with all of the detected proteins in the pooled serum samples. Both SPR and MS results are $\log_2$ ratios of liver-injury relative to control. Immunoblot results are qualitative values indicating where obvious increases (Up) or decreases (Down) have occurred following liver injury.

Gene symbol	SPR Set A	P-value	SPR Set B	P-value	iTRAQ target	iTRAQ	P-value	Immunoblot
ADH4	...	...	No signal	...	Yes	2	0.0658	No signal
AFM	No change	...	...	...	No	-0.33	0.3335	Off predicted MW
AGXT	...	...	...	...	No	...	...	Up
AHCY	...	...	...	...	No	...	...	Off predicted MW
AHSG	...	...	...	...	No	-1.02	0.1637	Weak signal
ALDH1L1	...	...	...	...	No	...	...	Up
ALDOB	No signal	...	0.96 ± 0.33	0.0101	Yes	1.93	0.0756	Up
AMBP	...	...	...	...	No	1.36	0.1901	Off predicted MW
AQP9	No signal	...	No signal	...	Yes	-0.22	0.3551	No signal
ARG1	No signal	...	No signal	...	No	0.43	0.3894	No signal
ASGR1	2.33 ± 0.80	0.0101	2.22 ± 0.53	0.0036	Yes	-0.23	0.3541	Up
ASGR2	2.89 ± 0.59	0.0022	2.29 ± 0.45	0.002	Yes	1.88	0.0839	Up
ASL	No signal	...	No signal	...	Yes	1.92	0.0773	Up
ASS1	...	...	...	...	Yes	-0.3	0.339	No signal
BAAT	...	...	...	...	No	...	...	Off predicted MW
BHMT	...	...	...	...	No	3.07	0.0039	Up
COMT	...	...	...	...	No	...	...	Up
CP	-0.12 ± 0.23	0.3579	-2.74 ± 2.64	0.1301	Yes	-1.28	0.1748	Down
CPS1	No signal	...	0.19 ± 0.11	0.0442	Yes	-1.77	0.0404	Up
DPYS	No signal	...	1.14 ± 0.2	0.0015	No	0.97	0.2921	Up
ECH1	...	...	...	...	No	...	...	No signal
FAH	...	...	...	...	Yes	1.96	0.0718	Up
FBP1	...	...	...	...	No	1.82	0.0929	Up
FGA	No change	...	0.01 ± 0.36	0.9411	Yes	1.02	0.2778	Off predicted MW
FGL1	No signal	...	No signal	...	No	...	...	Off predicted MW
FTCD	...	...	...	...	Yes	-1.88	0.0308	Weak signal
GCDH	...	...	...	...	Yes	-1.29	0.1057	Off predicted MW
GJB1	...	...	...	...	No	...	...	No signal
GLS2	...	...	...	...	No	...	...	No signal
GNMT	...	...	1.1 ± 0.54	0.0263	Yes	1.12	0.2527	Up
HAAO	...	...	...	...	No	...	...	Off predicted MW
HAL	...	...	...	...	No	...	...	No signal
HMGCS2	1.70 ± 0.68	0.0154	2.67 ± 0.67	0.004	No	...	...	Up

HP	...	...	1.52 ± 1.23	0.0897	No	...	...	No change
HPD	...	...	...	...	Yes	2.37	0.0283	Up
HPX	...	...	No signal	...	No	-1.88	0.031	No signal
KHK	...	...	...	...	No	...	...	No signal
KNG1	...	...	-0.37 ± 0.54	0.2621	No	-0.85	0.2039	Off predicted MW
MAT1A	...	...	...	...	No	...	...	Up
MST1	No signal	...	No signal	...	No	...	...	Off predicted MW
PLG	-0.89 ± 0.43	0.0255	-0.93 ± 0.37	0.0154	Yes	-1.04	0.1574	Down
PON1	No signal	...	No signal	...	Yes	1.66	0.1223	Off predicted MW
RBP4	No signal	...	-0.54 ± 0.33	0.0452	No	...	...	Down
TDO2	...	...	...	...	No	...	...	No signal
TF	-0.34 ± 0.15	0.02	-0.28 ± 0.16	0.0416	Yes	-1.2	0.1234	Down
TFR2	No signal	...	No signal	...	No	...	...	No signal
UPB1	...	...	...	...	No	...	...	Off predicted MW
ALB*	-0.27 ± 0.60	0.4397	0.31 ± 0.78	0.4847	No	...	...	No change
ALT/GPT1*	...	...	No signal	...	No	1.56	0.145	Up
AST/GOT1*	...	...	No signal	...	No	...	...	Up
GLUD1*	...	...		...	No	...	...	Up

*Indicates conventional liver injury biomarkers.

Table S6. Dose response

Table S6. Putative liver injury biomarker concentration in mouse plasma after low dosage and high dosage APAP treatment. Five concentrations are noticeably elevated after the low dosage and eight are elevated after the high dosage. All eight concentrations are significantly correlated to APAP treatment, based on P-values calculated by one-way ANOVA. Concentrations are in units of µg/ml.

Sample	FBP1	GNMT	HPD	MAT1A	ALDH1L1	CPS1	BHMT	FAH
Control	1.7 ± 1.2	1.2 ± 1.0	3.8 ± 3.3	2.1 ± 0.6	1.7 ± 0.8	1.5 ± 1.1	1.3 ± 0.9	1.4 ± 1.2
APAP(150 mg/kg)	1.7 ± 1.3	0.8 ± 0.5	6.0 ± 0.6	7.8 ± 2.4	0.9 ± 0.8	7.8 ± 2.5	15.5 ± 15.9	182.6 ± 17.8
APAP (300 mg/kg)	11.3 ± 0.4	20.7 ± 4.9	20.7 ± 1.0	19.9 ± 6.9	60.4 ± 3.3	194.7 ± 4.2	226.7 ± 55.3	677.7 ± 132.8
P-value	0.00004	0.00060	0.00001	0.00590	0.00000	0.00000	0.00027	0.00010

Table S7. Temporal profile of 11 transcripts in mouse liver lysate after APAP treatment

We performed mouse liver transcriptome analysis by GeneChip® Mouse Gene 2.0 ST Array (Affymetrix, CA). The eight time points were taken after high-dosage (300 mg/kg) APAP treatment. The transcript profile of the 11 candidate markers was similar to the protein profile.

gene_symbol	0hr	1hr	3hr	12hr	24hr	48hr	72hr	120hr
agxt	15272.51	17737.53	19323.57	15198.36	9449.00	5581.28	15988.59	26479.55
aldh1l1	24304.26	23040.66	20000.04	6353.53	9206.66	4265.65	13099.27	23192.66
bhmt	43521.19	32184.41	32841.95	1836.29	6084.21	2012.53	6851.18	16692.66
comt	2558.23	1675.03	1411.80	1336.29	3793.39	3309.40	2274.84	6614.79
cps1	27502.67	29550.03	18448.57	2224.22	13994.92	3678.15	19625.99	12459.06
dpys	4976.22	4293.78	5628.72	793.19	1357.17	250.03	2656.52	2995.94
fah	3888.92	2850.03	3080.92	819.05	2538.29	1212.53	2309.19	3450.86
fbp1	59478.86	59887.53	43000.04	7525.94	28033.19	16687.53	16087.82	52377.09
gnmt	56571.46	54487.53	56305.18	4732.84	24943.90	11459.41	22194.69	44954.96
hpd	21468.28	14943.78	14257.39	1051.81	3433.70	665.65	4480.95	12372.99
mat1a	51791.03	34950.03	43003.71	4353.53	24267.88	14759.41	15194.69	11028.73