SUPPLEMENTARY MATERIAL

Jersin et al. Role of the neutral amino acid transporter SLC7A10 in adipocyte lipid storage, obesity and insulin resistance.

This file includes:

Supplementary Tables:

Supplementary Table 1. Primers used for qPCR.

Supplementary Table 2. Characteristics of donors of liposuction material for human primary adipose stromal cell (hASC) cultures.

Supplementary Table 3. Plasmids for overexpression.

Supplementary Table 4. mRNA expression and correlations for identified candidate genes with differential expression in human adipose tissue (Jersin et al. *Diabetes*)

Supplementary Table 5. mRNA co-expression with SLC7A10/ASC-1 mRNA in human adipocytes from the ADIPO cohort (12 lean, 12 obese) (Jersin et al. *Diabetes*)

Supplementary Figures:

Supplementary Figure 1. Correlations of *SLC7A10* mRNA expression with insulin resistance and adiposity traits in the RIKEN (n=58, panel A) and Sib Pair-Subgroup (n=24, panel B) cohorts.

Supplementary Figure 2. Effects of SLC7A10 inhibition on global gene expression measured by RNA-sequencing in human primary adipocytes.

Supplementary Figure 3. Confirmation of Slc7a10b loss-of-function mutation and outlier detection by RNA-sequencing of zebrafish visceral adipose tissue.

Supplementary Figure 4. Slc7A10b loss-of-function mutation in overfed zebrafish

upregulates genes involved in urate, purine, and lipid metabolic processes.

Supplementary Figure 5. SLC7A10 impairment affects genes related to lipid- and energy metabolism in zebrafish adipose tissue and human primary adipocyte cultures.

Supplementary Figure 6. SLC7A10 inhibition affects mitochondrial respiration in cultured mouse adipocytes.

Supplementary Figure 7. Inhibition of SLC7A10 in human primary and mouse adipocytes regulates adipocyte serine uptake and redox status.

Supplementary References

Supplementary Tables

Gene	Forward primer $(5' \rightarrow 3')$	Reverse primer $(5' \rightarrow 3')$
SLC7A10 Human	CGCCCTCCCAGTCC	CCCGAGCCGATGATGTTC
HPRT* Human	TGACCTTGATTTATTTTGCATACC	CGAGCAAGACGTTCAGTCCT
Slc7a10 Mouse	CTTCTGGATGACACCGTCTG	GATGGCACGAGGTAGGTTCT
Rps13* Mouse	CAGGTCCGTTTTGTGACTG	AGCATCCTTATCCTTTCTGT

Supplementary Table 1. Primers used for qPe	CR.
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* Reference gene

Supplementary Table 2. Characteristics of donors of liposuction material for human primary adipose stromal cell (hASC) cultures.

Donor no.	Figure no.	Age	BMI
1	3C	53	26.4
2	3C	41	32.4
3	3D, 6B	67	26
4	3F, S7B	32	26.9
5	3F, S7B	52	24.3
6	3F, S7C	52	30
7	3F, 6K	52	26.7
8	4B-C, S2A-D, S5A-B, 6D	53	31.5
9*	4B-C, S2A-D, S5A-B, 6D	36	24.3
10	4B-C, S2A-D, S5A-B, 6D	21	29.4
11	4B-C, S2A-D, S5A-B, 6D	58	28
12	4B-C, S2A-D, S5A-B, 6D	45	28.4
13	4B-C, S2A-D, S5A-B, 6D	45	30
14	5A	32	25.5
15	6A, S6A-B	48	27.7
16	6H	46	24.3
17	6H	32	28.4
18	S6B	68	32.8

* Male.

Supplementary Table 3. Plasmids for overexpression.

Vector name	Description	Manufacturer
pCMV6-Kan/Neo	mSlc7a10 (untagged)	Origene
pCMV6-XL4/XL5/XL6	TrueClone TM Empty vector	Origene

	Cohort:	BPD-Fat	: (n=12)		ADIPO (n=12)			SibPair (n=88)						
		OM/SC 1	Post/Pre	0	M mRNA	4	S	C mRNA	4	WHR = α +	$\beta_1 SEX + \beta_2 B$	MI + β3GENI	E EXPRESS	SION + ε
Symbol	Probe ID	mRNA	ratio	Whole	Adipo	SVF	Whole	Adipo	SVF	Probe ID	SC mRNA	R-square*	p-value	pos or neg
Higher in Ol	M vs. SC fat, up-reg	ulated in SC	C fat after	fat loss										
CIDEA	ILMN_2390318	1.70	1.64	1 094	5 627	312	655	2 522	235	221295_at	155	0.520	0.0002	neg
DFNA5	ILMN_1670145	1.77	1.96	920	835	2 344	385	478	1 552	203695_s_at	28.3	0.450	0.122	ns
FLRT2	ILMN_1769615	1.63	1.90	565	255	1 696	313	407	841	204359_at	36.1	0.460	0.048	pos
GAS1	ILMN_2062701	1.73	2.02	1 155	368	2 685	603	256	1 801	204457_s_at	194	0.478	0.010	pos
GPD1L	ILMN_1694106	1.65	1.77	2 049	4 647	2 421	1 193	1 607	1 974	212510_at	95.2	0.590	2.14x10-7	neg
HOXA5	ILMN_1753613	2.38	2.11	1 418	4 692	4 448	800	2 797	2 819	213844_at	50.2	0.469	0.021	neg
SLC7A10	ILMN_1681087	1.83	1.84	1 603	4 986	312	866	2 2 2 5	204	220868_s_at	20.5	0.510	0.001	neg
	M vs. SC fat, down-1	Ĩ		l ,										
ALDH1A2	ILMN_1748538	-1.54	2.48	1 686	464	5 459	505	215	814	207016_s_at	18.0	0.498	0.002	pos
GFPT2	ILMN_1709674	-1.93	1.61	1 153	240	1 225	782	243	1 252	205100_at	12.4	0.443	0.247	ns
PDLIM3	ILMN_2230025	-1.55	1.94	989	487	1 478	513	250	676	209621_s_at	7.9	0.448	0.150	ns
TFPI2	ILMN_2068104	-1.52	1.94	577	221	694	269	178	223	209278_s_at	66.8	0.437	0.542	ns
TMEM158	ILMN_1792455	-1.63	1.67	568	285	964	382	304	445	213338_at	2.8	0.472	0.016	pos
Lower in OM	1 vs. SC fat, up-regu	l lated in SC	fat after j	fat loss										
APOC1	ILMN 1789007	3.21	-1.53	309	259	873	544	536	1 556	204416_x_at	50.0	0.445	0.191	ns
COL6A3	ILMN_2307861	1.67	-1.54	3 342	3 154	15 450	5 519	3 276	23 271	201438_at	569	0.447	0.167	ns
CTHRC1	ILMN_2117508	1.52	-2.01	306	154	378	747	180	1122	225681_at	103	0.465	0.029	pos
CTSG	ILMN_1680424	2.41	-1.64	576	181	2 799	1 135	220	7 428	205653_at	14.4	0.515	0.0003	pos
DCLK1	ILMN_2165354	1.98	-1.56	418	396	1 465	696	471	3 725	229800_at	91.2	0.462	0.041	pos
EMX2	ILMN_2187746	1.63	-1.54	151	175	183	239	443	634	221950_at	12.0	0.489	0.003	pos
FNDC1	ILMN_2163873	3.60	-1.62	205	146	299	322	190	2 152	226930_at	13.6	0.443	0.246	ns
PRRX1	ILMN_1739496	1.76	-2.23	1 112	707	4 367	2 266	1 014	11 052	226695_at	202	0.518	0.0002	pos
SERPINA5	ILMN_1759910	1.52	-3.10	165	163	243	559	202	1925	209443_at	12.6	0.468	0.024	pos

Supplementary Table 4. mRNA expression and correlations for identified candidate genes with differential expression in human adipose tissue (Jersin et al. *Diabetes*)

Lower in OM	1 vs. SC fat, down-re	egulated in S	SC fat afte	er fat loss										
CCND1	ILMN_1688480	-1.62	-3.23	2 587	4 866	3 457	7 409	18 302	4 661	208712_at	124	0.471	0.017	pos
DARC	ILMN_1723684	-1.65	-1.55	2 191	1 169	2 4 5 6	3 381	666	3 742	208335_s_at	70.5	0.467	0.025	pos
EGFL6	ILMN_2057479	-5.68	-6.95	351	355	711	3 039	15 392	1 146	219454_at	428	0.461	0.045	pos
GPR56	ILMN_1697228	-2.11	-1.64	868	968	1 455	1 347	624	1 959	212070_at	74.7	0.436	0.563	ns
IFIT3	ILMN_1664543	-1.55	-1.53	214	281	255	321	235	293	229450_at	91.5	0.462	0.040	pos
INHBB	ILMN_1685714	-1.80	-1.53	754	1 584	675	1 205	2 511	940	205258_at	75.5	0.478	0.010	pos
ITIH5	ILMN_1731862	-1.60	-1.67	379	515	230	623	1 088	327	219064_at	457	0.486	0.005	pos
MSC	ILMN_1741404	-2.32	-1.72	341	599	274	578	968	312	209928_s_at	3.3	0.470	0.018	pos
NOTCH3	ILMN_1658926	-1.51	-2.58	480	909	888	1 408	3 183	2 143	203238_s_at	16.5	0.479	0.009	pos
PEMT	ILMN_1745806	-1.51	-2.30	1 1 2 9	3 191	798	2 368	10 395	1 665	207621_s_at	138	0.486	0.004	pos
RND3	ILMN_1759513	-3.83	-1.69	2 143	782	1 147	2 996	1 959	1 887	212724_at	83.4	0.469	0.020	pos
SERPINA3	ILMN_1788874	-1.83	-1.66	367	211	624	602	325	1 007	202376_at	4.8	0.457	0.063	ns
SNCG	ILMN_1653161	-2.01	-1.63	566	1 163	327	975	3 253	396	209877_at	18.2	0.440	0.334	ns
SOX7	ILMN_2134056	-3.14	-1.82	495	208	214	764	174	258	228698_at	93.1	0.467	0.024	neg
TNFRSF4	ILMN_2112256	-1.94	-1.55	348	346	470	518	270	541	214228_x_at	6.0	0.454	0.085	ns
TUBB2A	ILMN_2044813	-2.51	-1.82	590	867	325	1 101	2 276	516	204141_at	588	0.492	0.003	pos
UPP1	ILMN_1746837	-2.18	-1.50	1 264	506	772	1 749	640	1 214	203234_at	12.3	0.492	0.003	pos

Adipo, isolated adipocyte fraction; neg, negative correlation; ns, non-significant; OM, omental adipose tissue; pos, positive correlation; Pre, samples obtained before bariatric surgery; Post, samples obtained one year after bariatric surgery; SC, subcutaneous adipose tissue; SVF, stromal vascular fraction; Whole, whole adipose tissue.

Supplementary Table 5. mRNA co-expression with SLC7A10/ASC-1 mRNA in
human adipocytes from the ADIPO cohort (12 lean, 12 obese) (Jersin et al. <i>Diabetes</i>)

SYMBOL	Coeff.	SYMBOL	Coeff.	SYMBOL	Coeff.	SYMBOL	Coeff.
SLC7A10	1	continued	Coen.	continued	coen.	continued	Coen.
UTX	0.909	CCNH	0.766	РНҮН	0.734	DNAJA3	0.715
BCKDHB	0.895	PPP1R16A	0.766	RAPGEF4	0.734	GSDMB	0.715
AK3L1	0.850	ACOT1	0.764	(undefined)	0.733	HIBADH	0.714
TMEM22	0.839	MLYCD	0.763	MED26	0.733	CD40	0.714
RPL34	0.836	TP53I13	0.763	HIGD2A	0.733	TMEM69	0.713
LGALS12	0.830	UBTD1	0.760	C7orf26	0.733	LACTB2	0.713
BRP44L	0.826	CMTM7	0.760	ABCC9	0.732	MRPL46	0.713
COX7C	0.822	CCBL2	0.758	LOC731007	0.731	SOX6	0.713
CHL1	0.822	FAM73B	0.758	POLS	0.731	GSDMB	0.712
MCCC1	0.822	СКВ	0.757	PIGP	0.730	D2HGDH	0.710
DHTKD1	0.821	MRPS11	0.756	C14orf2	0.730	FGFRL1	0.710
AGT	0.820	MOSC2	0.755	DTNA	0.730	PPP1R1B	0.710
SDHB	0.818	PCCA	0.755	LETMD1	0.730	ZFHX4	0.710
ACADM	0.817	COX5A	0.755	TFAM	0.729	RHOT1	0.708
NDUFB5	0.812	RTCD1	0.755	MRPS34	0.729	(undefined)	0.708
MOSC1	0.808	CYC1	0.755	(undefined)	0.729	NAALAD2	0.708
COQ9	0.808	FLJ23834	0.754	CSNK2A1	0.728	TXNDC12	0.707
C7orf30	0.803	AQP7P2	0.754	CICE	0.728	FABP5	0.707
ATL2	0.802	RTN3	0.753	DTNA	0.728	LOC653145	0.707
C6orf66	0.798	LOC648605	0.753	(undefined)	0.727	SNX5	0.706
C17orf95	0.795	ZFPM1	0.753	(undefined)	0.727	PCBD1	0.706
ELOVL3	0.795	(undefined)	0.752	MRPL21	0.725	TSPAN13	0.706
VPS54	0.789	MCAT	0.750	HAX1	0.724	ORMDL3	0.705
ALDH1L1	0.789	LOC652837	0.749	CMC1	0.723	CNIH	0.705
DDT	0.789	CAMK1	0.749	LOC653479	0.723	CCT7	0.704
UBE2W	0.788	GART	0.748	UCKL1	0.723	PATL1	0.703
UQCRFS1	0.788	XRN1	0.748	SLC25A4	0.722	ARIH1	0.703
BTF3L4	0.784	THYN1	0.747	LDHD	0.722	CLPP	0.703
ANO6	0.784	COX5B	0.746	C12orf45	0.722	CASD1	0.702
RDH10	0.783	PXMP2	0.746	DMRT2	0.721	C4orf14	0.702
UQCRH	0.783	POLR1D	0.745	PXMP2	0.720	AUH	0.701
LOC646345	0.780	LOC648695	0.745	SH3GLB1	0.720	BCKDHB	0.701
C7orf44	0.780	AK3L1	0.743	C2orf56	0.719	RFXANK	0.701
PCK1	0.776	FAM18B	0.743	FAM152B	0.718	SCO1	0.701
ATP5F1	0.776	SLC2A1	0.742	PCGF6	0.718	LOC650494	0.701
HSPD1	0.775	HIST1H2BD	0.742	CCNF	0.718	LOC643300	0.700
KIAA1191	0.773	C21orf70	0.741	EXOSC3	0.718	GOT1	0.700
ACAD8	0.772	AK2	0.741	ALKBH1	0.718	SYPL1	0.700
ESRRA	0.771	CDH23	0.739	PCBD1	0.717	DCI	0.699
ABHD3	0.771	CYB5A	0.738	BPHL	0.717	MCCC2	0.699
SLC25A5	0.770	C21orf33	0.738	SLC25A40	0.716	ACOT2	0.699
MRPL41	0.770	CS	0.737	ATP1B3	0.716	(undefined)	0.699
ELK1	0.769	ENDOG	0.737	FBXO21	0.715	STOX1	0.698
TMLHE	0.767	BCKDHB	0.736	MRPS22	0.715	FRMD4A	0.698
C2orf47	0.767	MRPL33	0.735	ZNF280D	0.715	WDR43	0.698
SYMBOL	Coeff.	SYMBOL	Coeff.	SYMBOL	Coeff.	SYMBOL	Coeff.

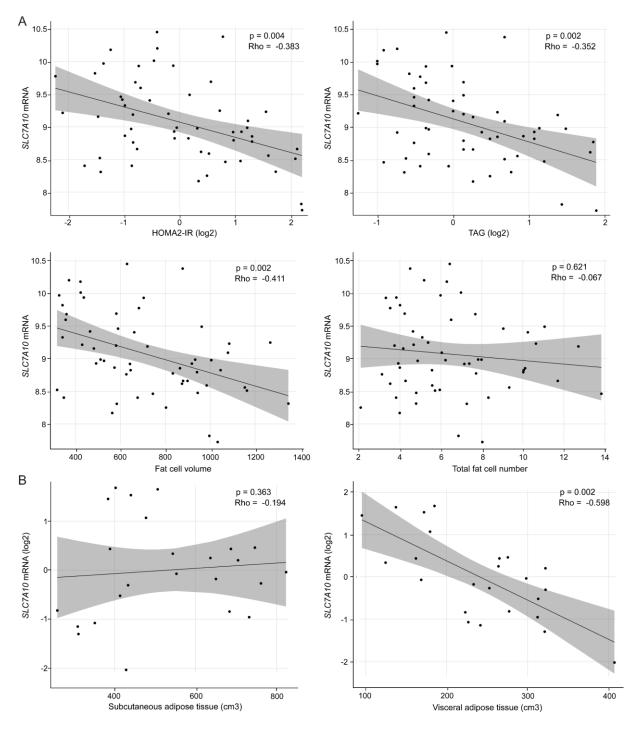
continued		continued		continued		continued	
RPAIN	0.698	CALML4	0.687	TMCO6	0.674	MACROD1	0.660
MTFMT	0.698	RDH14	0.687	SEC24B	0.674	CA2	0.659
SLC4A4	0.698	TAF1L	0.686	(undefined)	0.674	GTF2IRD1	0.659
DTNA	0.698	DDX47	0.685	PRIM1	0.674	C17orf61	0.658
ANKRD11	0.697	CDKN2C	0.685	LETMD1	0.673	FBXO46	0.658
QPCT	0.697	THYN1	0.684	GBE1	0.673	HSCB	0.658
FGFRL1	0.696	SDHA	0.682	TYSND1	0.673	NDUFV2	0.658
MRPL39	0.696	SNORD100	0.682	EBAG9	0.672	LOC643466	0.657
VPS26B	0.696	SUMO2	0.682		0.671		0.656
	0.696	KLF15	0.682	MRPS23 TMLHE	0.671	NDUFB11 MGC70857	0.656
KIAA0261 GCHFR	0.695	HSD17B10	0.682 0.681	MESP1	0.671		0.656
C1orf66						(undefined)	0.655
SPTB	0.695 0.695	GNAQ CMTM7	0.681 0.681		0.671 0.670	NDUFV3 PMPCB	0.655
				MKNK2 (undefined)			
STRADB	0.695	RABGGTB	0.681	(undefined)	0.670	(undefined)	0.655
VPRBP	0.694	GGCT	0.681	ALDH6A1	0.670	VPS35	0.655
PLAGL2	0.694	SLC3A2	0.681	FBXO28	0.669	LPIN1	0.655
SLC16A7	0.694	CNBP	0.680	C2orf56	0.669	AASDHPPT	0.655
ACADL	0.694	RSBN1	0.680	AGPAT2	0.669	LOC642335	0.655
NDUFB6	0.694	RBMS2	0.680	PPARG	0.669	NPC1	0.654
CRLS1	0.694	SCP2	0.680	PIGP	0.668	SLC2A4	0.654
BDH1	0.693	(undefined)	0.680	STK35	0.668	RAVER1	0.654
SPRYD4	0.693	LOC284023	0.679	MAD2L1BP	0.668	DAP3	0.654
ACADM	0.693	(undefined)	0.679	CMTM7	0.667	L2HGDH	0.653
ACP1	0.693	ALKBH1	0.679	INTS6	0.667	MAZ	0.653
NCOR2	0.693	ZNF280D	0.679	SOSTDC1	0.666	FMO5	0.653
COX6A1	0.693	SCN3A	0.678	LIX1L	0.665	EIF3M	0.653
MRPS2	0.692	C17orf95	0.678	PIK3CB	0.665	SEC11A	0.653
C9orf72	0.692	(undefined)	0.678	CS	0.664	(undefined)	0.653
GFPT1	0.692	CNIH	0.678	AQP7	0.664	PCNX	0.652
MLX	0.692	CA2	0.678	ANKRD9 PDZD7	0.664	YPEL5	0.652
SNURF	0.692	SEPHS1	0.678		0.664	NDFIP2	0.652
BLOC1S1 PAXIP1	0.691	ESRRAP2	0.677	ATAD2	0.663	NAT5 (undefined)	0.652
	0.691	LOC729317	0.677	SFXN2	0.663	(undefined)	0.652
UTP18	0.691	(undefined)	0.677	MEIS2	0.663 0.663	HYLS1	0.652
C18orf8	0.690	NET1	0.677	GTPBP3		RPL35A STOX1	0.652
GLRX2	0.690	MCM7	0.677	RAB40C	0.663		0.651
LOC652545	0.690	DUSP4	0.677	TBP	0.663	STAMBP	0.651
GRPEL1	0.690	ICAM3	0.676	CLK2	0.663	DHPS	0.651
CCNC	0.689	DNAH1	0.676	SEC24B	0.662	STBD1	0.650
TRPT1	0.689	CSNK2A2	0.676	NDUFAF2	0.662	FBXO44	0.650
PATZ1	0.689	LOC285074	0.676	HINT3	0.662	OXA1L	0.650
SLC25A22	0.689	C16orf14	0.676	LOC645436	0.662	(undefined)	0.650
PC	0.689	RPL9	0.675	PPP2R2D	0.662	ACY1	0.650
SMARCD1	0.688	(undefined)	0.675	(undefined)	0.661		
UBQLN1	0.688	KIAA0367	0.675	PLCXD1	0.660		
CASZ1	0.688	C1QL2	0.675	TCF12	0.660		
LDLRAD1	0.688	PCCB	0.675	ZNF512B	0.660		
CXorf15	0.687	POLE	0.674	MIA3	0.660	CVMAD O'	0
	Coeff.	SYMBOL	Coeff.	SYMBOL	Coeff.	SYMBOL	Coeff.

SYMBOL

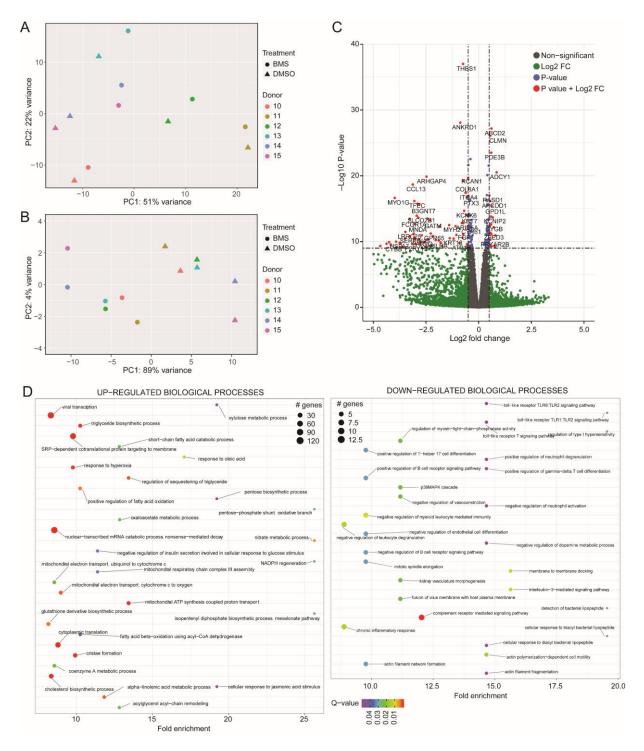
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OLFML1 -0.651 ITGA11 -0.676 DAB2 -0.704 CCNVL1 -0.769 TFP -0.652 CPD -0.677 ZYX -0.705 RAP2.0 -0.771 CSorfs -0.653 ANXA11 -0.677 SUX -0.705 RUF3 -0.781 COL6A2 -0.653 ANXA11 -0.677 C10rf51 -0.707 IQSEC2 -0.787 CUC6A2 -0.654 AP152 -0.678 ZUrof51 -0.709 PTG2 -0.787 HABP4 -0.655 RHB22 -0.678 CUL4A -0.711 MGP -0.845 LOC648470 -0.655 RHB2A -0.678 CUL4A -0.711 RANB3L -0.845 LOC648470 -0.657 SLC7A2 -0.679 RNASEL -0.711 RANB3L -0.845 LOC648470 -0.657 SLC7A2 -0.681 STX2 -0.714 -0.657 SLC7A2 -0.681 SLX2 -0.716 LUC648470 -0.657 SL0	(undefined)	-0.650	continued		continued		continued	
TFPI.0.652CPD.0.677ZYX.0.705RAP2A.0.771CSorfs.0.652LAPTMS.0.677SDX4.0.705FBLN2.0.775STS.0.653ANX11.0.677C10rf51.0.705RUS2.0.781CCU6A2.0.653FAM129A.0.677.C10rf51.0.705RUS2.0.781HABP4.0.655.THBS2.0.678.C10451.0.707IQSEC2.0.787HABP4.0.655.RH6AP28.0.678.C014A5.0.711MGP.0.845LOC648407.0.655.SLC7A2.0.678.0.111MGP.0.845LOC648107.0.655.SLC7A2.0.678.0.711MGP.0.845LOC648108.0.657.C10rf24.0.681.0.711	IFT57	-0.651	CANX	-0.676	SETBP1	-0.703	TLN1	-0.769
CSorf5.0.652LAPTMS.0.677SOX4.0.705FBLN2.0.775ST5.0.653ANXA11.0.677EMX2.0.705RUFY3.0.781COL6A2.0.653FAM129A.0.677CACIG.0.700IQSEC2.0.781CCDC25.0.655AFIBS2.0.678COL4A5.0.709PTTG2.0.793HABP4.0.655FBLN5.0.678COL4A5.0.711MGP.0.845LOC64470.0.655FBLN5.0.678PDLM7.0.711RANBP3.0.846PDC13.0.657KICA2.0.681BTX2.0.714(undefined).0.657MTP1.0.681BSAP.0.716KKA1160.0.657CAIM3.0.684RNA18.0.721LOC65102.0.659SPARC.0.681BSAP.0.716TMEM119.0.661CAIM3.0.684RN14.0.720LUM.0.661CAIM3.0.685SPON2.0.723LUM.0.661CAPES.0.688SL2A12.0.726LOC30905.0.611.0.683SAP18.0.727LUM.0.662REEPS.0.681SANSE.0.732LOC30905.0.611.0.633.0.629 </td <td>OLFML1</td> <td>-0.651</td> <td>ITGA11</td> <td>-0.676</td> <td>DAB2</td> <td>-0.704</td> <td>CCNYL1</td> <td>-0.769</td>	OLFML1	-0.651	ITGA11	-0.676	DAB2	-0.704	CCNYL1	-0.769
STS-0.653ANXA11-0.677EMX2-0.705RUFY3-0.781COLGA2-0.653FAM129A-0.677C21orf51-0.705TMSB10-0.786CCD25-0.654ATHS2-0.678CACTG1-0.707IQSC2-0.787HABP4-0.655THBS2-0.678CDL4A5-0.711MGP-0.787LOC648470-0.655ARHGAP28-0.678CDL4A5-0.711MGP-0.845LOC648470-0.657MY018-0.667RNASEL-0.711RANBP3L-0.846PDC13-0.657MY018-0.661STX2-0.714(undefined)-0.657C1orf24-0.681STX2-0.714KKD11-0.659CALM3-0.684RNK1-0.715LUM-0.659SPARC-0.681SNX0-0.712ILM-0.661ACT8-0.684DKK3-0.716LUM-0.661ACT8-0.685SPON2-0.723ILM-0.661ACT8-0.685SPON2-0.723<	TFPI	-0.652	CPD	-0.677	ZYX	-0.705	RAP2A	-0.771
COLGA2-0.653FAM129A-0.677C21orf51-0.705TMSB10-0.786CCDC25-0.654AP152-0.677ACTG1-0.707IQ5C2-0.787HAB4-0.655THBS2-0.678CNIP1-0.710MGP-0.793CILP-0.655ARHGAP28-0.678COL4A5-0.711MGP-0.793LOC648470-0.655ARHGAP28-0.679RNASEL-0.711RANBP3L-0.845PDCL3-0.657MY01B-0.667RNASEL-0.711RANBP3L-0.846KIAA1100-0.657MY01B-0.681STX2-0.714-0.611-0.611LOC651302-0.659SPARC-0.681PANP-0.716	C5orf5	-0.652	LAPTM5	-0.677	SOX4	-0.705	FBLN2	-0.775
CCDC25.0.654AP1S2.0.677ACTG1.0.707IQSEC2.0.787HABP4.0.655THBS2.0.678ZNF219.0.709PTTG2.0.793CLP.0.655ARHGAP28.0.678COLAA5.0.711MGP.0.845LOC648470.0.655FBIN5.0.678PDLIM7.0.711RANBP3L.0.846PDC13.0.657SLC7A2.0.679RNASL.0.711RANBP3L.0.846(undefined).0.657C10rf24.0.681STX2.0.714	ST5	-0.653	ANXA11	-0.677	EMX2	-0.705	RUFY3	-0.781
HABP4.0.655THBS2.0.678ZNF219.0.709PTTG2.0.793CILP.0.655ARHGAP28.0.678COL4A5.0.711MGP.0.845LOCG48470.0.657FBLN5.0.678PDLIM7.0.711RANBP3L.0.846PDCL3.0.657SIC7A2.0.679RNASEL.0.711.0.817.0.846VIL014.0.657MY01B.0.680MAP1B.0.713	COL6A2	-0.653	FAM129A	-0.677	C21orf51	-0.705	TMSB10	-0.786
CILP.0.655ARHGAP28.0.678COL4A5.0.711MGP.0.845LOC648470.0.655FBLN5.0.678PDLIM7.0.711RANBP3L.0.846POC13.0.657SLC7A2.0.679RNASEL.0.711RANBP3L.0.846POC14.0.657SLC7A2.0.679RNASEL.0.711	CCDC25	-0.654	AP1S2	-0.677	ACTG1	-0.707	IQSEC2	-0.787
LOC648470.0.655FBLN5.0.678PDLIM7.0.711RANBP3L.0.846PDCL3.0.657SLC7A2.0.679RNASEL.0.711(undefined).0.657C10rf24.0.680MAP1B.0.713KIAA1160.0.657C10rf24.0.681STX2.0.714KTD12.0.658MTP.0.681PSAP.0.716LOC651302.0.659SPARC.0.681ANKS1B.0.717TMEM19.0.669CLM13.0.684DKS.0.719LUM.0.661ACTB.0.684DKS1.0.720ITH5.0.661ACTB.0.685SPON2.0.723TRPV2.0.661CAPZB.0.685DGK1.0.724LOC39055.0.661(undefined).0.688SL21A.0.726CLN5.0.662REPS.0.688SAP18.0.727LMOD1.0.663CCD105.0.688SAP18.0.727IMM01.0.663CDC105.0.689RNASEL.0.732IMO11.0.663CDC105.0.689SN3BGRL2.0.741(undefined).0.663SLC39A3.0.689SN3BGRL2.0.741IMU11.0.664CDL45.0.694NTA1.748FL23274.0.666VMA1.0.693KIAA1598.0.742IGL23.0.668IGA1.0.694.743ILU34.0.666VMA1.0.694.748ILU35.0.666VMA1.0.694.748 <tr< td=""><td>HABP4</td><td>-0.655</td><td>THBS2</td><td>-0.678</td><td>ZNF219</td><td>-0.709</td><td>PTTG2</td><td>-0.793</td></tr<>	HABP4	-0.655	THBS2	-0.678	ZNF219	-0.709	PTTG2	-0.793
PDCL3.0.657SLC7A2.0.679RNASEL.0.711(undefined).0.657MYO1B.0.680MAP1B.0.713KIAA1160.0.657C10rf24.0.681STX2.0.714KT012.0.658MTTP.0.681PSAP.0.716LOC651302.0.659SPARC.0.681ANKS1B.0.717TMEM19.0.659CALM3.0.684DKI3.0.719LUM.0.661CDH11.0.684RCN1.0.720ITHS.0.661ACTB.0.685SPON2.0.723TRPV2.0.661CMPEB.0.685CAPNS1.0.726CLN5.0.661LOC38958.0.686SLC2A12.0.726CLN5.0.662LOC38958.0.688RNASEL.0.722IMOD1.0.663CCDC105.0.688RNASEL.0.722IMOD1.0.663CCDC105.0.689RNASEL.0.722IMOD1.0.663SLC3A3.0.689NYO1D.0.733IFTM5.0.664CCBP2.0.690LOZ.0.741Iudefined).0.664CCBP2.0.691MED20.0.742IREX.0.666VMA1.0.694LN1598.0.742INEX.0.666LOAN.0.694ITMEM39.0.743Iudefined).0.668RIA1598.0.742.0.743Iudefined).0.669NIA1.0.694.0.743Iudefined).0.666LOAN.0.694NIA1598.0.743 <t< td=""><td>CILP</td><td>-0.655</td><td>ARHGAP28</td><td>-0.678</td><td>COL4A5</td><td>-0.711</td><td>MGP</td><td>-0.845</td></t<>	CILP	-0.655	ARHGAP28	-0.678	COL4A5	-0.711	MGP	-0.845
(undefined)-0.657MY01B-0.680MAP1B-0.713KIAA1160-0.657C1orf24-0.681STX2-0.714KCTD12-0.658MTTP-0.681PSAP-0.716LOC651302-0.659SPARC-0.681ANKS1B-0.717TMEM119-0.659CALM3-0.684DKK3-0.719LUM-0.660CDH11-0.684RCN1-0.723TTRP2-0.661CAP2B-0.685SPON2-0.724LOC390956-0.661(undefined)-0.685CAPN3-0.726CLN5-0.662LOC389958-0.686SLC2A12-0.726ACTN4-0.662REEP5-0.688RNASEL-0.732(undefined)-0.663CCDC105-0.689RNASEL-0.732(undefined)-0.663SLC39A3-0.689NYA1D-0.735(Indefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.663SLC39A3-0.690CDC26-0.741FL22374-0.666COL4A5-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.743CLC3B-0.668IPAR1-0.694DPT-0.748(undefined)-0.668IPAR1-0.694MGP-0.748(undefined)-0.669IPAR1-0.698MGP-0.748(LC3B-0.669IPAR1-0.698MGP-0.748(LC4SB-0.669IPAR1 </td <td>LOC648470</td> <td>-0.655</td> <td>FBLN5</td> <td>-0.678</td> <td>PDLIM7</td> <td>-0.711</td> <td>RANBP3L</td> <td>-0.846</td>	LOC648470	-0.655	FBLN5	-0.678	PDLIM7	-0.711	RANBP3L	-0.846
KIAA1160.0.657C10rf24.0.681STX2.0.714KCTD12.0.658MTTP.0.681PSAP.0.716LOC651302.0.659SPARC.0.681ANKS1B.0.717TMEM119.0.659CALM3.0.684DKK3.0.719LUM.0.660CDH11.0.684RCN1.0.720ITIH5.0.661ACTB.0.685SPON2.0.723TRP20.0.661CAPZB.0.685DGK1.0.724LOC390956.0.661(undefined).0.685CAPNS1.0.726CLN5.0.662REEP5.0.688SLC2A12.0.726CLN6.0.663CCDC105.0.688RNASEL.0.732IMOD1.0.663CCDC105.0.688RNASEL.0.732IMOD1.0.663CCDC105.0.689NYO1D.0.738(undefined).0.663SLC3A12.0.724.0.735IFITM5.0.663SLC3A3.0.689NYO1D.0.738(undefined).0.663SLC3A3.0.689NYO1D.0.738(undefined).0.664CCBP2.0.691MED20.0.742FL2374.0.665RNA1.0.693KIAA1598.0.742NEXN.0.666CUAA5.0.694TMEM98.0.743(undefined).0.668IPAR1.0.694DPT.0.748(undefined).0.668CN33.0.694DPT.0.748(Undefined).0.666CUAA5.0.694IMEM	PDCL3	-0.657	SLC7A2	-0.679	RNASEL	-0.711		
KCTD12.0.658MTTP.0.681PSAP.0.716LOC651302.0.659SPARC.0.681ANKS1B.0.717TMEM119.0.659CALM3.0.684DKK3.0.719LUM.0.660CDH11.0.684RCN1.0.720ITH5.0.661ACTB.0.685SPON2.0.723TRPV2.0.661CAPZB.0.685CAPNS1.0.726LOC39095.0.661(undefined).0.685CAPNS1.0.726CLN5.0.662LOC389958.0.686SLC2A12.0.726ACTN4.0.662REEP5.0.688SAP18.0.727(undefined).0.663CCDC105.0.688RNASEL.0.735IMD01.0.663CCDC105.0.689LOX.0.735IMD1.0.663SLC39A3.0.689SH3BGRL2.0.741(undefined).0.664CCBP2.0.690CD266.0.741FL22374.0.665ARHGAP21.0.691MED20.0.742BICD2.0.666VWA1.0.693KIAA1598.0.742NEXN.0.666COL4A5.0.694TAX1BP3.0.743CLC338.0.689IDFN.0.748.0.748Gundefined).0.669CNN3.0.696TMEM98.0.748FL23374.0.666CNN3.0.699.0.748GUA2.0.669CNN3.0.699.0.748GUA2.0.669CNN3.0.696MGP.0.748GUA3 <t< td=""><td>(undefined)</td><td>-0.657</td><td>MYO1B</td><td>-0.680</td><td>MAP1B</td><td>-0.713</td><td></td><td></td></t<>	(undefined)	-0.657	MYO1B	-0.680	MAP1B	-0.713		
LOC651302.0.659SPARC.0.681ANKS1B.0.717TMEM119.0.659CALM3.0.684DKK3.0.719LUM.0.660CDH11.0.684RCN1.0.720ITIH5.0.661ACTB.0.685SPON2.0.723TRPV2.0.661CAPZB.0.685DGK1.0.726LOC390956.0.661(undefined).0.685CAPNS1.0.726CLN5.0.662LOC389958.0.686SLC2A12.0.726ACTN4.0.662REP5.0.688SAP18.0.732(undefined).0.663CCDC105.0.688RNASEL.0.732IMD01.0.663CDC105.0.689MY01D.0.738(undefined).0.663DAAM2.0.691MY01D.0.738(undefined).0.663SLC39A3.0.689SH3BGRL2.0.741(undefined).0.666CDL45.0.691MED20.0.742BICD2.0.666VWA1.0.693KIAA1598.0.743CLEC3B.0.668LPAR1.0.694DPT.0.748(undefined).0.668CNN3.0.694MEM98.0.748SRI.0.669DCTN1.0.693MBD4.0.756PON2.0.691DCTN1.0.694MEM98.0.754CLC391013.0.673CCND2.0.701DRAM.0.756LOC391013.0.675CAMK1D.0.701ITGA11.0.757CANX.0.675CAMK1D.0.702<	KIAA1160	-0.657	C1orf24	-0.681	STX2	-0.714		
TMEM119.0.659CALM3.0.684DKK3.0.719LUM.0.660CDH11.0.684RCN1.0.720ITIH5.0.661ACTB.0.685SPON2.0.723TRPV2.0.661CAPZB.0.685DGK1.0.724LOC390956.0.661(undefined).0.685CAPNS1.0.726CLN5.0.662LOC389958.0.686SLC2A12.0.726ACTN4.0.662REP5.0.688SAP18.0.732(undefined).0.663CCDC105.0.688RNASEL.0.732IMD1.0.663ACTB.0.689MY01D.0.738(undefined).0.663SLC3A3.0.689SH3BGRL2.0.741(undefined).0.666CCBP2.0.691MY01D.0.738(undefined).0.666CCBP2.0.691MED20.0.742BICD2.0.666VWA1.0.691MED20.0.742NEXN.0.666COLA3.0.694TAX1BP3.0.743CLEC3B.0.668LPAR1.0.694DPT.0.748(undefined).0.669INHBB.0.694MEM98.0.748SRI.0.669NN3.0.695MEM94.0.754PON2.0.691NHBB.0.694MEM94.0.754CLC391013.0.673CCND2.0.701NAM.0.756LOC391013.0.675CAMK1D.0.702(undefined).0.756	KCTD12	-0.658	MTTP	-0.681	PSAP	-0.716		
LUM.0.660CDH11.0.684RCN1.0.720ITIH5.0.661ACTB.0.685SPON2.0.723TRPV2.0.661CAP2B.0.685DGK1.0.724LOC390956.0.661(undefined).0.685CAPNS1.0.726CLN5.0.662LOC389958.0.686SLC2A12.0.726ACTN4.0.662REEP5.0.688SAP18.0.727(undefined).0.663CCDC105.0.688RNASEL.0.732IMOD1.0.663CCDC105.0.689IDX.0.735IFITM5.0.663DAAM2.0.689MY01D.0.738(undefined).0.663SLC39A3.0.690CD226.0.741(undefined).0.664CCBP2.0.691MED20.0.742BICD2.0.666COL4A5.0.694TAX1BP3.0.743CLEC3B.0.668LPAR1.0.694DPT.0.748(undefined).0.668CNN3.0.695MGP.0.748PON2.0.669INHBB.0.698MGP.0.748SRI.0.669DCTN1.0.699EMX2.0.751PON2.0.671CCND2.0.701BRAM.0.756PON2.0.673CCND2.0.701DRAM.0.756ICC391013.0.673FKP.0.701ITGA11.0.757CANX.0.675CAMK1D.0.702(undefined).0.766	LOC651302	-0.659	SPARC	-0.681	ANKS1B	-0.717		
ITIH5-0.661ACTB-0.685SPON2-0.723TRPV2-0.661CAPZB-0.685DGK1-0.724LOC390956-0.661(undefined)-0.685CAPNS1-0.726CLN5-0.662LOC389958-0.686SLC2A12-0.726ACTN4-0.662REEP5-0.688SAP18-0.732(undefined)-0.663CCDC105-0.688RNASEL-0.732IMOD1-0.663CCDC105-0.689MYO1D-0.738(undefined)-0.663DAAM2-0.699MYO1D-0.738(undefined)-0.663SLC39A3-0.699CDC26-0.741(undefined)-0.664CCBP2-0.690CDC26-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742MEXN-0.666COL4A5-0.694TAX1BP3-0.743(undefined)-0.668CNN3-0.696TMEM98-0.748(undefined)-0.669INHBB-0.699BMZ2-0.741PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754PON2-0.673CCND2-0.701DRAM-0.756LOC391013-0.673FKP-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	TMEM119	-0.659	CALM3	-0.684	DKK3	-0.719		
TRPV2-0.661CAP2B-0.685DGKI-0.724LOC390956-0.661(undefined)-0.685CAPNS1-0.726CLN5-0.662LOC389958-0.686SLC2A12-0.726ACTN4-0.662REEP5-0.688SAP18-0.727(undefined)-0.663CCDC105-0.688RNASEL-0.732LMO1-0.663ACTB-0.689LOX-0.735IFITM5-0.663DAAM2-0.689MY01D-0.738(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.690CDC26-0.741FL22374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.749PON2-0.669DCTN1-0.699MGP-0.749PON2-0.671CXC12-0.700ABHD4-0.754CTN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.673CAMK1D-0.702(undefined)-0.766	LUM	-0.660	CDH11	-0.684	RCN1	-0.720		
LOC390956-0.661(undefined)-0.685CAPNS1-0.726CLN5-0.662LOC389958-0.686SLC2A12-0.726(undefined)-0.662REP5-0.688SAP18-0.727(undefined)-0.663CCDC105-0.688RNASEL-0.732LMOD1-0.663ACTB-0.689LOX-0.735IFITM5-0.663DAAM2-0.689MY01D-0.738(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.690CDC26-0.741(undefined)-0.666CCBP2-0.691MED20-0.742FL22374-0.666VWA1-0.693KIAA1598-0.742BICD2-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXL12-0.700ABHD4-0.754ICT391013-0.673CCND2-0.701ITGA11-0.757CANX-0.673CAMK1D-0.702(undefined)-0.766	ITIH5	-0.661	ACTB	-0.685	SPON2	-0.723		
CLNS-0.662LOC389958-0.686SLC2A12-0.726ACTN4-0.662REEP5-0.688SAP18-0.727(undefined)-0.663CCDC105-0.688RNASEL-0.732LMOD1-0.663ACTB-0.689LOX-0.735IFITM5-0.663DAAM2-0.689MYO1D-0.738(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.690CDC26-0.741FL122374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.669INHBB-0.696TMEM98-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754CYLN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.673FKP-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	TRPV2	-0.661	CAPZB	-0.685	DGKI	-0.724		
ACTN4-0.662REEP5-0.688SAP18-0.727(undefined)-0.663CCDC105-0.688RNASEL-0.732LMOD1-0.663ACTB-0.689LOX-0.735IFITM5-0.663DAAM2-0.689MY01D-0.738(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.691MED20-0.742FL22374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748Gundefined)-0.669INHB8-0.696TMEM98-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.673CCND2-0.701BRAM-0.756LOC391013-0.673PFKP-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	LOC390956	-0.661	(undefined)	-0.685	CAPNS1	-0.726		
(undefined)-0.663CCDC105-0.688RNASEL-0.732LMOD1-0.663ACTB-0.689LOX-0.735IFITM5-0.663DAAM2-0.689MYO1D-0.738(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.690CDC26-0.741FL122374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.669CNN3-0.696TMEM98-0.743SRI-0.669DCTN1-0.699EMX2-0.751PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.673FKP-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	CLN5	-0.662	LOC389958	-0.686	SLC2A12	-0.726		
LMOD1-0.663ACTB-0.689LOX-0.735IFITM5-0.663DAAM2-0.689MYO1D-0.738(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.690CDC26-0.741FL122374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.749PON2-0.669INHBB-0.693MGP-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754CETN2-0.673CCND2-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	ACTN4	-0.662	REEP5	-0.688	SAP18	-0.727		
IFITM5-0.663DAAM2-0.689MYO1D-0.738(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.690CDC26-0.741FL122374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.749PON2-0.669INHBB-0.698MGP-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754LOC391013-0.673CCND2-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	(undefined)	-0.663	CCDC105	-0.688	RNASEL	-0.732		
(undefined)-0.663SLC39A3-0.689SH3BGRL2-0.741(undefined)-0.664CCBP2-0.690CDC26-0.741FL122374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.749PON2-0.669INHBB-0.699MGP-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.701ABHD4-0.754LOC391013-0.673CCND2-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	LMOD1	-0.663	ACTB	-0.689	LOX	-0.735		
(undefined)-0.664CCBP2-0.690CDC26-0.741FL122374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.748SRI-0.669INHBB-0.698MGP-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.673CCMD2-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	IFITM5	-0.663	DAAM2	-0.689	MYO1D	-0.738		
FLJ22374-0.665ARHGAP21-0.691MED20-0.742BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.749SRI-0.669INHBB-0.699EMX2-0.751PON2-0.671CXCL12-0.700ABHD4-0.754CETN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.675CAMK1D-0.702(undefined)-0.766	(undefined)	-0.663	SLC39A3	-0.689	SH3BGRL2	-0.741		
BICD2-0.666VWA1-0.693KIAA1598-0.742NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.748SRI-0.669INHBB-0.699MGP-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.701DRAM-0.756LOC391013-0.673PFKP-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	(undefined)	-0.664	CCBP2	-0.690	CDC26	-0.741		
NEXN-0.666COL4A5-0.694TAX1BP3-0.743CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.748SRI-0.669INHBB-0.698MGP-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754CETN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.675CAMK1D-0.702(undefined)-0.766	FLJ22374	-0.665	ARHGAP21	-0.691	MED20	-0.742		
CLEC3B-0.668LPAR1-0.694DPT-0.748(undefined)-0.668CNN3-0.696TMEM98-0.748SRI-0.669INHBB-0.698MGP-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754CETN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.675CAMK1D-0.702(undefined)-0.766	BICD2	-0.666	VWA1	-0.693	KIAA1598	-0.742		
(undefined)-0.668CNN3-0.696TMEM98-0.748SRI-0.669INHBB-0.698MGP-0.749PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754CETN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.675CAMK1D-0.702(undefined)-0.766	NEXN	-0.666	COL4A5	-0.694	TAX1BP3	-0.743		
SRI -0.669 INHBB -0.698 MGP -0.749 PON2 -0.669 DCTN1 -0.699 EMX2 -0.751 CYLN2 -0.671 CXCL12 -0.700 ABHD4 -0.754 CETN2 -0.673 CCND2 -0.701 DRAM -0.756 LOC391013 -0.675 PFKP -0.702 ITGA11 -0.757 CANX -0.675 CAMK1D -0.702 (undefined) -0.766	CLEC3B	-0.668	LPAR1	-0.694	DPT	-0.748		
PON2-0.669DCTN1-0.699EMX2-0.751CYLN2-0.671CXCL12-0.700ABHD4-0.754CETN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.673PFKP-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	(undefined)	-0.668	CNN3	-0.696	TMEM98	-0.748		
CYLN2-0.671CXCL12-0.700ABHD4-0.754CETN2-0.673CCND2-0.701DRAM-0.756LOC391013-0.673PFKP-0.701ITGA11-0.757CANX-0.675CAMK1D-0.702(undefined)-0.766	SRI	-0.669	INHBB	-0.698	MGP	-0.749		
CETN2 -0.673 CCND2 -0.701 DRAM -0.756 LOC391013 -0.673 PFKP -0.701 ITGA11 -0.757 CANX -0.675 CAMK1D -0.702 (undefined) -0.766	PON2	-0.669	DCTN1	-0.699	EMX2	-0.751		
LOC391013 -0.673 PFKP -0.701 ITGA11 -0.757 CANX -0.675 CAMK1D -0.702 (undefined) -0.766	CYLN2	-0.671	CXCL12	-0.700	ABHD4	-0.754		
CANX -0.675 CAMK1D -0.702 (undefined) -0.766	CETN2	-0.673	CCND2	-0.701	DRAM	-0.756		
	LOC391013	-0.673	PFKP	-0.701	ITGA11	-0.757		
ITGB5 -0.675 ASCC3 -0.702 ITGB1 -0.768	CANX	-0.675	CAMK1D	-0.702	(undefined)	-0.766		
	ITGB5	-0.675	ASCC3	-0.702	ITGB1	-0.768		

Coeff., Pearson's correlation coefficient; SYMBOL, Gene name.

Supplementary Figures



Supplementary Figure 1. Correlations of *SLC7A10* mRNA expression with insulin resistance and adiposity traits in the RIKEN (n=58, panel A) and Sib Pair-Subgroup (n=24, panel B) cohorts. SLC7A10 mRNA expression was retrieved from microarray expression analyses (Affymetrix) and Spearman correlations were calculated.



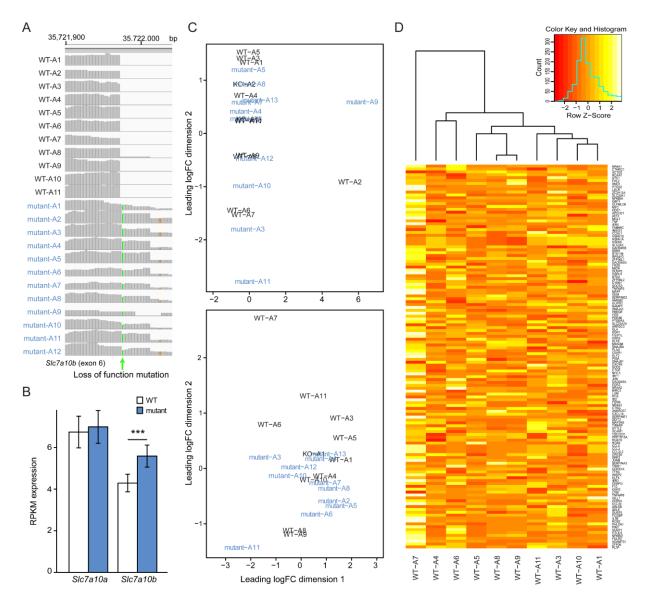
Supplementary Figure 2. Effects of SLC7A10 inhibition on global gene expression measured by RNA-sequencing in human primary adipocytes.

Human adipose stromal cell (hASC) cultures were obtained from abdominal subcutaneous adipose tissue (n=6), differentiated for 8 days, and treated with DMSO or SLC7A10 inhibitor 1 for 24 hours from day 7-8. Global gene expression was measured by RNA-seq, where sample reads were mapped against the Human genome (GrCH38) using HiSat (Version 2.1.0), with options –t "exon" and –g "gene_id" to summarize count values from individual exons into genes, resulting in a matrix of raw counts. Aligned reads were then put into featureCounts (Version 1.5.2) with default options, resulting in a matrix of raw counts. Data were normalized and differential expression analysis was performed utilizing DESeq2 (Version 1.22.2). Pathway analysis of RNA sequencing data was performed using PANTHER classification system (PANTHER v.14.0). Differentially expressed genes identified with a FDR cut-off (p<0.05) were used as input and Fischer's exact test was used to identify statistically over/under represented pathways with a FDR cut-off (p<0.05) (1). Significant ontologies were visualized using ggplot2 package (Version 3.1.0).

(A-B) Principal component (PC) analysis of samples in DMSO and SLC7A10 inhibitor 1 treated groups are shown in (A) unadjusted and (B) adjusted for patient.

(C) Volcano plot of differentially expressed genes between DMSO and SLC7A10 inhibitor 1 treatments. x-axis corresponds to log2 fold change (log2FC) and y-axis corresponds to -log10 (P-value). Red dots represent the transcripts with an absolute log2FC > 0.5 and P-value < 10E-10; green dots represent the transcripts with an absolute log2FC > 0.5; blue dots represent transcripts with P-value < 10E-10; grey dots represent transcripts which do not pass above thresholds.

(**D**) Enrichment plot representing up-regulated and down-regulated biological processes between DMSO and SLC7A10 inhibitor treatments. Top 30 biological processes with an FDR-corrected P-value < 0.05 and fold enrichment \geq 8 (arbitrary threshold for the sake of visual representation) are reported here. Gene Ontology (GO) terms was analyzed by PANTHER (www.pantherdb.org).



Supplementary Figure 3. Confirmation of Slc7a10b loss-of-function mutation and outlier detection by RNA-sequencing of zebrafish visceral adipose tissue.

Mature (four-month old) wildtype (WT) and Slc7a10b mutant male zebrafish were fed 50-100% more than their regular feed for eight weeks. Visceral adipose tissue from three zebrafish housed in the same tank during the overfeeding was pooled. RNA was isolated and RNA-seq was performed. Sample reads were mapped against the

Zebrafish genome (GRCz10) using HiSat (Version 2.05), matrixed in featureCounts (Version 1.5.2) and analyzed using DESeq2 (version 1.22.1).

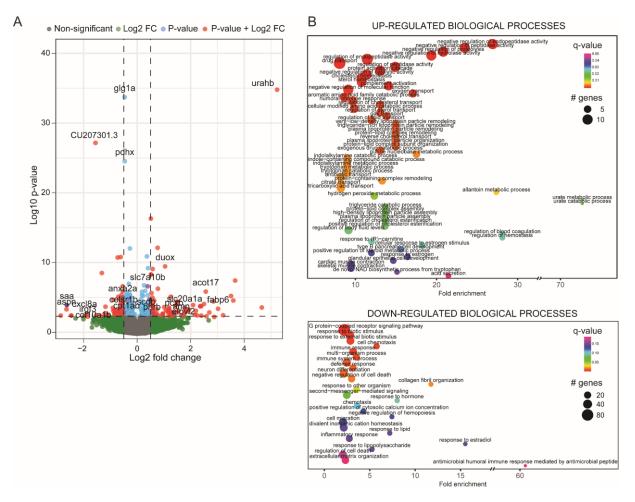
(A) Integrative genomics viewer (IGV) read visualization of each Zebrafish sample at the target site, with the $A \rightarrow T$ splice site mutation sa15382 highlighted in green.

(B) Visualized expression values (RPKM) of average *Slc7a10a* and *Slc7a10b* expression in both WTs and mutants.

(C) Outlier removal of anomalous RNA-Seq sequence reads (by sample) was performed by generating multidimensional scaling plots of distances between digital gene expression profiles. The samples mutant-A9 and WT-A2 were visually identified in the top graph as being erroneous due to their spread from the main cluster in the first dimension. The lower graph displays the distances after the removal of the first two outliers, showing WT-A7 spreading from the main cluster.

(**D**) The differential expression in WT-A7 was further investigated by utilizing the ontology gene expression profiles of the WT samples, and we observed that this sample differed significantly from other wild-types in the expression profile of stress-induced genes identified in human adipose tissue, warranting removal of WT-A7 from further downstream analysis. The stress-induced genes were identified by microarray analysis of omental human adipose tissue biopsies of non-obese patients. Omental biopsies from four patients were either frozen immediately or ~1 hour after surgical excision. The 1-hour delayed freezing induced a large array of immediate-early stress-responsive genes including IL8 (induced already after 10 minutes) [24], largely recapitulating differences we previously observed between lean and extremely obese patients [153] (data not shown). We concluded that the WT-A7 sample was acutely stressed either *in vivo* or *ex vivo*, and that its inclusion in our initial analysis was entirely responsible for an apparent down-regulation of stress-responsive/inflammatory genes in the mutant compared to WT zebrafish. WT-A7 was therefore removed from further analysis, to avoid a dominating artefactual impact on gene ontology terms.

***, p<0.001.

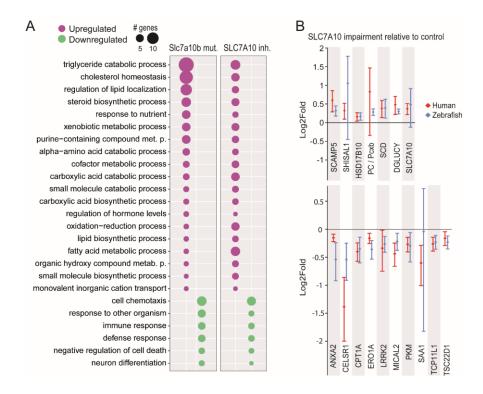


Supplementary Figure 4. Slc7A10b loss-of-function mutation in overfed zebrafish upregulates genes involved in urate, purine, and lipid metabolic processes.

Mature (four-month old) wildtype (WT) and Slc7a10b loss-of-function male zebrafish were fed 50-100% more than their regular feed for eight weeks. Visceral adipose tissue from three zebrafish housed in the same tank during the overfeeding was pooled. RNA was isolated and RNA-seq was performed. Sample reads were mapped against the Zebrafish genome (GRCz10) using HiSat (Version 2.05), matrixed in featureCounts (Version 1.5.2) and analyzed using DESeq2 (version 1.22.1).

(A) Volcano plot of differentially expressed genes between WT and Slc7a10b loss-of-function zebrafish. x-axis corresponds to log2 fold change (log2FC) and y-axis corresponds to -log10 (P-value). The red dots represent the transcripts with an absolute log2FC > 0.5 and P-value < 10E-10; green dots represent the transcripts with an absolute log2FC > 0.5; blue dots represent transcripts with P-value < 10E-10; grey dots represent transcripts which do not pass above thresholds.

(B) Combined differentially expressed genes between Slc7a10b zebrafish WT and mutant into a single ranked list based on fold change, and gene ontology (GO) terms were analyzed using GOrilla (2). Enrichment plot representing up-regulated biological processes between WT and Slc7a10b loss-of-function zebrafish was visualized using the R package ggplot2. Biological processes with a P-value < 0.05 and fold enrichment ≥ 8 (arbitrary threshold for the sake of visual representation) are reported here.

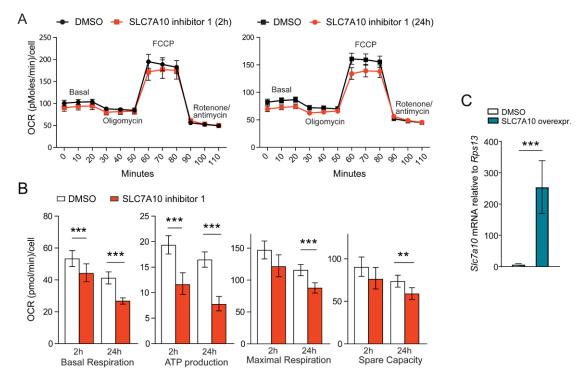


Supplementary Figure 5. SLC7A10 impairment affects genes related to lipid- and energy metabolism in zebrafish adipose tissue and human primary adipocyte cultures.

RNA-sequencing was performed as described in Supplementary Figures 2 and 4. For each dataset, genes were sorted based on fold change into a single ranked list, and analyzed using GOrilla to identify enriched ontologies (2). Significant ontologies were summarized for plotting utilizing the REViGO web package, which clusters representative ontologies via semantic similarity (3). RPKM values for gene expression visualizations were generated using edgeR (Version 3.16.5). Overlapping ontologies between zebrafish adipose tissue and human adipose cultures were plotted using ggplot2 (Version 3.1.0).

(A) Gene ontologies enriched with differentially expressed genes identified in RNA-seq from both zebrafish mutant and SLC7A10 inhibitor treated human adipocytes compared to control. Differentially expressed genes were combined into a single ranked list based on fold change using GOrilla analysis (2). Enriched ontologies in both the zebrafish mutant and SLC7A10 inhibitor 1 RNA-seq were aggregated, filtered by enrichment and significance, and plotted by relative enrichment. Overlapping ontologies between Zebrafish and SLC7A10 inhibitor 1 RNA-seq were visualized using the R package ggplot2 (Version 3.1.0).

(B) Fold changes for up- and down-regulated genes in RNA-seq from both zebrafish mutant and SLC7A10 inhibitor 1 treated (10 μ M) human adipocytes compared to control. Outliers were removed using Whiskers Tukey outlier test. Data are presented as mean \pm SD.



Supplementary Figure 6. SLC7A10 inhibition affects mitochondrial respiration in cultured mouse adipocytes.

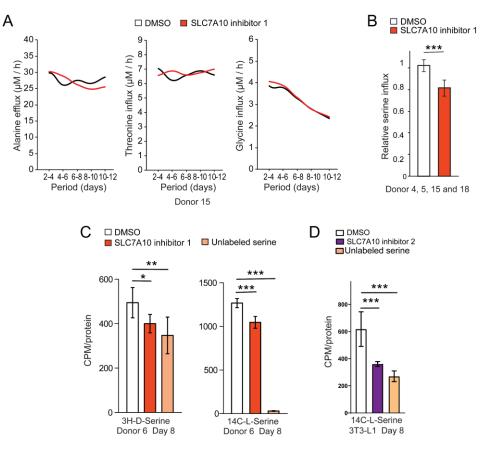
3T3-L1s were differentiated and treated with SLC7A10 inhibitor 1 for either 2 or 24 hours, or Slc7a10 was overexpressed every second day from day 2-8.

(A) OCR was measured at day 8 of differentiation under basal conditions and after sequential addition of the following compounds at indicated final concentrations; oligomycin (3 μ M); FCCP (1.5 μ M); rotenone (1 μ M) and antimycin A (1 μ M).

(**B**) Outliers were removed based on a Whisker Tukey test of the OCR data for each time point in each well, before calculation of basal respiration, ATP production, maximal respiration and spare respiratory capacity according to the manufacturer's protocol. Results are presented as geometric mean \pm 95% confidence interval (n=22-24 replicate wells in a 96-well plate).

(C) 3T3-L1 preadipocytes were induced to differentiate and transfected with Slc7a10 expression plasmid or empty vector on every second day of differentiation (days 2, 4 and 6) and mRNA was collected on day 8. Slc7a10 expression was quantified by qPCR relative to Rsp13 expression (n=3)

, p<0.01. *, p<0.001.



Supplementary Figure 7. Inhibition of SLC7A10 in human primary and mouse adipocytes regulates adipocyte serine uptake and redox status.

(A) Changes in alanine, threonine and glycine flux was not alter for hASCs treated with SLC7A10 inhibitor 1 throughout differentiation. Amino acid flux was calculated based on the amino acid concentrations in unconditioned medium and change in concentrations upon cell culture during 48-hour periods. Data for two replicate wells for a representative experiment are shown.

(**B**) The average reduction in serine influx due to SLC7A10 inhibition was calculated (as in A) for fully differentiated hASCs (day 10-12), for replicate experiments in cells from four different people.

(C) hASCs were treated with SLC7A10 inhibitor 1 for 30 minutes at day 8 of differentiation. Thereafter, radiolabeled 3H-D-serine (1 μ M) or 14C-L-serine (1 μ M) was added for 30 minutes and cellular uptake of the radiolabeled amino acids was measured in cell lysate. Unlabeled D-serine and L-serine (100 mM) were used as positive control of uptake inhibition. Data are presented as mean ± SD (n=3-6).

(**D**) 3T3-L1s were treated with SLC7A10 inhibitor 2 for 30 minutes at day 8 of differentiation. Thereafter, radiolabeled 14C-L-serine (1 μ M) was added for 30 minutes and cellular uptake of the radiolabeled amino acids was measured in cell lysate. Unlabeled L-serine (100 mM) were used as positive control of uptake inhibition. Data are presented as mean \pm SD (n=6).

*, p<0.05, **, p<0.01. ***, p<0.001.

Supplementary References

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