

Large (60S) Subunit

RPL3	0.7881	RPL22	0.7905
RPL3L	-0.029	RPL23	0.5934
RPL4	1.1956	RPL23A	0.3506
RPL5	-0.011	RPL24	0.5247
RPL6		RPL26	
RPL7	0.4218	RPL27	0.553
RPL7A	0.3839	RPL27A	0.6294
RPL8	0.6048	RPL28	0.7492
RPL9	0.3425	RPL29	0.4805
RPL10		RPL30	0.4523
RPL10A	1.4562	RPL31	0.4635
RPL11	0.5497	RPL32	0.7939
RPL12	0.6035	RPL34	0.5987
RPL13	0.483	RPL35	1.1237
RPL13A	0.5944	RPL35A	-0.112
RPL14	0.6763	RPL36	0.987
RPL15	0.7026	RPL37	0.4447
RPL17	0.7517	RPL37A	0.4994
RPL18	0.3406	RPL38	0.5965
RPL18A	1.0524	RPL39	0.7767
RPL19	0.4485	UBA52	0.2572
RPL21	0.5102	RPL41	0.1711
		RPL36A	1.4735
RPLP0	1.0036		
RPLP1	0.8381		
RPLP2	0.6903		
MRPL19	0.4568		

Small (40S) Subunit

LAMR1	1.3032	RPS15	0.5672
RPS2	1.0905	RPS15A	0.475
RPS3	0.7106	RPS16	0.4276
RPS3A	0.6919	RPS17	0.9441
RPS4X	0.6236	RPS18	1.1197
RPS4Y	0.3027	RPS19	0.8965
RPS5	0.9744	RPS20	0.6198
RPS6	1.1212	RPS21	0.9272
RPS7	0.8835	RPS23	0.5158
RPS8	0.9723	RPS24	1.2201
RPS9	-0.015	RPS25	0.4863
RPS10	0.6541	RPS26	0.489
RPS11	0.2498	RPS27	0.1954
RPS12	0.7743	RPS27A	0.2573
RPS13	0.4519	RPS28	0.5924
RPS14	0.6301	RPS29	0.4626
		FAU	0.3163

RPS6KB1	0.311
RPS6KB2	-0.355
RPS6KA1	-0.167
RPS6KA2	0.064
RPS6KA3	-0.395
RPS6KA6	0.0048

Legend

	villus, >2x
	villus
	crypt
	crypt, >2x
	No criteria met
	Not found

Supplementary fig 1—expression of genes related to ribosomal proteins.

CARBOHYDRATE METABOLISM

A4GNT 1.5e6	CBGL1	GALGT -1.3e6	HYAL2 -97445	MGAT1 -7.6e6	Q8NCI6 24322	SIAT8E -1.6e6
ABCC8 92280	CHIA 53831	GALK2	HYAL3 -1.2e6	MPI -58543	Q8NFI3 8.0e6	SLC2A2 -5.6e6
ABO	CHIT1 22816	GALNAC-T3 -31707	HYAL4 38141	NAGA -5.7e5	Q8NHT8	SLC2A3 -9.8e6
ABO	CNOT7 -2.2e6	GALNAC-T4	IDH3A	NAGLU -23212	Q8TC30 83449	SLC2A4 -53736
ABO	CTBS	GBA	IDH3B 1.3e6	NEU1 -6.8e6	Q8TC58	SLC2A5 -1.7e6
ABO	DHRS2 30853	GBE1 -99637	IDH3G -1.0e6	NEU2	Q8TDQ7 -1.2e6	SLC2A8 -1.7e6
ADRB3 766572	DJ20N2.5	GCKR 3657.3	IMPA1 3.1e6	NEU3 5294.8	Q8W295 -7135	SLC35A1 -4.7e6
AGL 4.9e6	DJ20N2.5	GFPT1 87001	INSR -1.1e6	NEU4 -6.3e6	Q96AB0 -58543	SLC3A1
AKR1B1 -3.2e6	DKFZP434C1915 -86509	GK -3.4e6	KIAA0089 -6.0e6	NTHL1 4.7e6	Q96C11 26619	SLC3A2 -3.2e6
AKR7A2 -3.7e6	DKFZP451A0519 -1.9e6	GK2 69269	KIAA1128 -1.1e6	O76044	Q96DB1 2.7e6	SLC5A2
ALDH1B1	DKFZP566B1524 -32474	GKP3	KIAA1161	O95210 -1.5e6	Q96DR0 -3.8e6	SMA3
ALDH2 46787	DKFZP762F216 -1.2e6	GLA -3.1e6	KIAA1434	OGG1 -2.1e6	Q96FF8 -6990	SMA4
ALDH3A1 118915	DPM3 5.2e6	GLB1 -8.4e6	KLOTHO 1.9e6	PGLS 2.3e6	Q96M7 1.7e6	SMA5 2.6e6
AMY1A	EPM2A 7325.3	GLB1 -8.4e6	KLOTHO	PGM1 -1.6e6	Q9BPZ4 -1.4e6	SMPD1 1.5e6
AMY2A -1.4e6	EPM2A 7325.3	GLO1 -1.5e5	LCT -1.6e6	PGM3 63738	Q9BS14	SMPDL3A -2.0e6
AMY2B	F-LAMBDA>8	GMD5 245123	LUCA1/HYAL1 -51079	PGM5	Q9BTY2 -3.9e6	SMPDL3B -4.9e6
B3GAT1 1.7e6	FBP1 -1.1e6	GNPDA1 -8.0e6	LUCA-3	PHKA2 3.6e6	Q9BUP6 1.2e6	SMPL_HUMAN
B4GALT3 -1.4e6	FBP2 6.7e6	GPD1 -14904	LYZ 1.3e6	PHKG1	Q9H227	SPAM1 83449
B4GALT4 -1.1e6	FLJ00088	GPI 63102	MAN1A1	PYGB -2.1e5	Q9H8T2 -1.4e6	TALDO1 2.7e6
B4GALT5 -2.5e6	FUCA1 -1.1e6	GUSB -79879	MAN1A2 -4.9e6	PYGL -7.4e5	Q9HC38 -3.8e6	TDG
B4GALT6 -7135	FUT1 1.4e6	H6PD 22638	MAN1B1 97050	PYGM 10931	Q9P0X0 -2.8e6	TFE1 -2.0e6
BA395L14.5	FUT2	HAS3 -4.2e6	MAN1C1 -4.2e6	Q13139	Q9UK23 -4.7e6	TREH -2.2e6
BM32A 1.7e6	FUT3 -1.3e5	HEXA -2.5e6	MAN2A1 -7.6e6	Q16106	Q9UKI5 -95037	UNG 190414
BPGM -5.9e6	FUT4 3.4e6	HEXB -4.8e6	MAN2A2 -5.0e6	Q8N2A7 83168	Q9UM21 -4.9e6	UNG2 2.7e6
C1ORF22 -1.7e6	FUT5 57343	HGNT-IV-H ALT	MAN2B1	Q8N2K4 -95037	Q9UQ53 -1.2e6	
C2/4GNT -7.6e6	FUT9	HUM2DD -1.8e6	MAN2B2 -1.9e6	Q8N5D6 -95037	Q9Y3E8	
C20ORF31 6889.3	G6VTS68545 81,227	HYAL1 -51079	MAN2C1 92727	Q8N5E6 83168	RPE 27336	
C2GNT3 49697	GAA -1.3e6	HYAL1 -51079	MANBA 5.0e6	Q8N909	SI -3.1e6	
CARKL 2.2e6	GALC -1.1e6	HYAL1 -51079	ME1 83546	Q8NAC2 -1.1e6	SIAT8A -1.8e6	
	GALE -67354	HYAL1 -51079	MGAM -1.3e6	Q8NC62 1.6e6	SIAT8B 85417	

FATTY ACID METABOLISM

ABCD2 -53033	FABP1 -2.9e6	ARACHIDONIC ACID METABOLISM	ALOX15B -40237	HAO1 -5431	GGTLA1 -1.6e6	ACO1 -88886
ACAA1 -1.1e6	FABP2	CPLA2 BETA 6.3e6	ALOX5 2.2e6	HAO2	LTA4H 3.5e6	AKR1C3 28760
ACAA2 -7.8e6	FABP7 96217	O75457 -1.3e5	ALOX5AP -3.2e6	ACADM -8.8e6	LTC4S 73298	CYP4F8 -1.9e6
ACADL -1.2e6	FACL1	FATTY ACID BIOSYNTHESIS	ALOXE3 2.0e6	ACADS 68414	MGST2 -3.2e6	HPGD
ACADM -8.8e6	FACL2 -7.1e6	ACACA	GGTLA1 -1.6e6	ACADSVL -4.6e6	PRG3 83010	PTGES 1.2e6
ACADS 68414	FACL3 -1.8e6	ACACB -95052	LT44H 3.5e6	ACADVLL -4.6e6	PROSTAGLANDIN BIOSYNTHESIS	Q8I1V14 -1.9e6
ACADSB -6.6e6	FACL4	DKFZP547D048 211716	LTC4S 73298	ACOX1 -88886	PTGDS 65534	PTGDS 65534
ACADVLL -6.6e6	FACL5 -8.9e6	ELOVL1 -4.5e6	MGST2 -3.2e6	ACOX2 -2.6e6	PTGIS -33404	PTGDS2 -2.6e6
ACOX2 47495	GNPAT 295152	ELOVL2	PRG3 83010	ACOX3 47495	PTGS1	PTGIS -33404
ACOX3 47495	HADHA -6.6e6	ELOVL3 2.8e6	PROSTAGLANDIN BIOSYNTHESIS	CPT1A -1.8e6	PTGS2 -2.4e6	PTGS1
ADIPOR1 -8.1e6	HADHB -3.5e6	ELOVL4 -42178	PTGDS 65534	CPT1B 30503	PTGS2 -2.4e6	PTGS1
ADIPOR2 -8.9e6	HADHSC 4.3e6	FASN	PTGDS2 -2.6e6	CPT2	TBXAS1 2.4e6	PTGS2 -2.4e6
ALOX12 -1.1e6	HSD17B4 -2.8e5	MLYCD 2.8e6	PTGIS -33404	ECH1 4.6e6	LEUKOTRIENE METABOLISM	TBXAS1 2.4e6
ALOX15B -40237	IPLA2 -4.5e6	NDUFAB1 3.4e6	PTGS1	ECHS1 -95681	PROSTAGLANDIN BIOSYNTHESIS	
ASAH1 -5.2e5	LIPE	P60174	PTGS2 -2.4e6	HADHB -3.5e6	CYP4F2 -1.5e6	CYP4F3 2.3e6
CACH1 -27246	LPL 1.4e6	PRKAA1 3.4e6	PTGS2 -2.4e6	Q9UDG6	LTB4DH -1.4e6	PTGDS 65534
CD36 -2.4e6	O00324 4.3e6	PRKAA2 -42278	TBXAS1 2.4e6	FATTY ACID CATABOLISM	PTGDS2 -2.6e6	PTGIS -33404
CPT1A -1.8e6	PCCA 7.1e6	PRKAB1 -29434	PCCB 13610	POSITIVE REGULATION OF FATTY ACID BIOSYNTHESIS	PTGS1	PTGS2 -2.4e6
CPT1B 30503	PECI -2.8e6	PRKAB2 -1.0e6	Q9Y2B3 16406	ICOSANOID METABOLISM	PTGS2 -2.4e6	TBXAS1 2.4e6
CPT2	PPARA	PRKAG1 -2.8e6	FATTY ACID DESATURATION	CYP2J2 -1.2e5	ALOX12 -1.1e6	
CROT	Q7Z4Z9	PRKAG2 -3.8e6	CYB5RP 1.5e6	PLA2G4A 1.8e6	ALOX12B 42206	
CRYL1	RETSRDR1	PRKAG3 83462	FADS2 -71428	LEUKOTRIENE BIOSYNTHESIS	ALOX15 86613	
CYP4A11 1.5e6	SC4MOL	Q9BSN4 211716	O15121 -1.2e6	POSITIVE REGULATION OF FATTY ACID OXIDATION	ALOX15B -40237	
DCI -2.3e6	THEA 1.1e6	Q9H7D1 211716	FATTY ACID OXIDATION	ALOX3 2.0e6	ALOX5 2.2e6	
DKFZP761P18121 -4.5e6	ACYL-COA METABOLISM	Q9NWU1 2.2e6	MACS1 -5062	GGTLA1 -1.6e6	ALOX5AP -3.2e6	
	CES HBR3	SCD -7.7e6	PERC	LTA4H 3.5e6	ALOXE3 2.0e6	
	CRAT -4.4e6	LEUKOTRIENE BIOSYNTHESIS	Q86YN6	LTC4S 73298	ALOX15B -40237	
	MLYCD 2.8e6	ALOX12 -1.1e6	Q8N1N9	MGST2 -3.2e6	ALOX5 2.2e6	
	PTE1 -2.3e6	ALOX12B 42206	Q8TAL0	PRG3 83010	ALOXE3 2.0e6	
	PTE2A -5.3e6	ALOX15 86613	FATTY ACID ALPHA-OXIDATION	PROSTAGLANDIN METABOLISM	ALOXE3 2.0e6	

Legend
 villus, >2x
 villus
 crypt
 crypt, >2x
 No criteria met
 Not found

Supplementary fig 2—expression of metabolism related genes.

VESICULAR FRACTION		CYP2J2 -1.16	G6PC -0.133	SPC21 0.0902	UGT2B7
ALS2 -0.003	CYP39A1 0.0084	HMOX1 -1.987	SPC22 0.3402	UGT8 0.1128	
STEAP 1.9972	CYP3A3 -2.496	HMOX2 -0.414	SPC25 0.7673		
MICROSOME		CYP3A4 -2.496	HSD11B1 0.0788	SQLE 1.1843	
AADAC -0.472	CYP3A43 -0.1	HSD11B2 -0.011	SRD5A1 -0.559	SRD5A2 0.0278	
ALDH3A2 -0.037	CYP3A5 -0.632	HSD17B3 -0.342	SSR3 -0.077	STCH -0.104	
APOB -1.672	CYP3A7 -0.279	KIAA1605 -0.389	STS -0.056	STX16 -0.05	
ATP2A2 0.102	CYP46A1 0.1446	LTC4S 0.0733	TAPBP -0.049	TCL1A -0.12	
COMT 0.417	CYP4A11 0.1643	MGST1 0.0348	TMP21 0.0706	UGT1A1	
CYB5 -0.937	CYP4B1 0.5423	MGST2 -0.318	UGT1A10	UGT1A2	
CYP17A1 0.0407	CYP4F11 -1.103	MGST3 0.0701	UGT1A3	UGT1A4	
CYP19A1	CYP4F12 -0.29	MTP -0.742	UGT1A5	UGT1A6	
CYP1A1 -1.503	CYP4F2 -1.515	O75452 -0.223	UGT1A7	UGT1A8	
CYP1A2 -0.111	CYP4F3 -2.284	OAS2 -0.164	UGT1A9	UGT2A1 0.1226	
CYP1B1 0.1075	CYP4F8 -0.191	OAS3 -0.104	UGT2B10	UGT2B11	
CYP21A2	CYP7A1 0.5002	P78383 -0.719	UGT2B15	UGT2B17	
CYP26A1 -0.043	CYP7B1 0.0706	PGRMC1 -0.808	UGT2B28	UGT2B4	
CYP26A2 -0.024	CYP8B1 -0.016	PGRMC2 -0.888	UGT2B28		
CYP2A13 -0.083	DAD1 -0.744	PIK3C2B -0.382	UGT2B28		
CYP2A6 -0.019	DKFZP762K054 -0.389	Q86U73 0.1765	UGT2B28		
CYP2A7	DNAJC1 -0.434	Q8WUD6 -0.363	UGT2B28		
CYP2B6 -0.389	DPEP1 -1.299	Q9BPW9 -0.117	UGT2B28		
CYP2C10 -1.921	EPHX1 -0.029	Q9Y2P9 -0.117	UGT2B28		
CYP2C18 -1.062	EPIM	RDH -0.117	UGT2B28		
CYP2C19 -0.113	FMO1 0.0159	RNP24 0.1082	UGT2B28		
CYP2C8 -0.829	FMO2 0.1765	SEC63 0.1269	UGT2B28		
CYP2C9 -1.921	FMO3 -0.026	SLC37A4 -0.612	UGT2B28		
CYP2D6	FMO4 -0.327	SLC9A6 -0.544	UGT2B28		
CYP2E1 0.0081	FMO5 -0.679	SPC12 -0.733	UGT2B28		
CYP2F1 -0.02	FMO6	SPC18 0.0104	UGT2B28		
VACUOLE		CTSZ -1.347	LYSAL1 -0.188	TMEM9 0.4852	
DNPEP -0.474	DNASE2 0.1185	DPP7 -0.029	M6PR 0.0122	TOM1L1 -0.709	
DNPEP -0.474	DPP7 -0.029	FUCA1 -1.143	MAN2B1	USP4	
Q9BTY6 -0.474	GAA -0.128	GALC -1.125	MANBA 0.4985	USP5 0.3923	
Q9HAC6 -0.474	GALNS	GALB1 -0.836	MPO -0.103	USP6 0.168	
Q9NV55 -0.474	GBA	GLA -0.308	NAGA -0.574	VAMP4 -0.964	
LYSOSOME		GGH 1.7115	NAGLU -0.023	LYSOSOMAL MEMBRANE	
ABCB9 0.1923	GLB1 -0.836	GLB1 -0.836	NEU1 -0.68	ACP2 -1.07	
ACP5 -0.225	GM2A -0.206	GNS -0.115	NPC1 -0.794	CD63 -0.891	
ADR2 0.0235	GUSB -0.08	GUSB -0.08	O43601 -0.505	CORO1A -0.626	
AGA 0.8048	HEXA -0.251	HEXA -0.251	PCYOX1	CTNS -0.02	
AP3M1 0.0984	HEXB -0.485	HPS1 -0.237	PPGB -1.036	LAMP2 -2.128	
ARSA -0.537	HPS4 0.2951	HYAL2 -0.097	PPT1 0.0943	SCARB2 -0.754	
ARSB 0.0907	IDUA -0.004	IGF2R -0.821	PPT2 0.1707	TSC403 0.2814	
ARSD	IFI30	LAMP1 -0.792	PRCP 0.3285	AZUROPHIL GRANULE	
ASA1 -0.521	IGF2R -0.821	LAMP2 -2.128	PRDX6 -0.391	AZU1 -0.141	
CD68 -0.085	LAMP1 -0.792	LAMP2 -2.128	PRG3 0.083	Q86SR2 -0.141	
CLN2 -0.933	LAPTM5 -1.175	LGMN -1.196	PSAP -0.578	HSP70-DEPENDENT V-TYPE ATPASE COMPLEX	
CLN3 -0.296	LGMN -1.196	LIPA -1.489	Q8N7T4 -0.403	ATP6V0A4 0.0699	
CLN5 -0.965	LIPA -1.489	LIP2 0.0216	Q9BWE2 -0.403	ATP6V0D1 -0.31	
CTBS	LIP2 0.0216	LUCA1/HYAL1 -0.051	RAMP2 0.0596		
CTSB -1.185	LIP2 0.0216		RAMP3 0.028		
CTSC 0.5313	LIP2 0.0216		SFTPB 0.0645		
CTSD	LIP2 0.0216		SGSH 0.1012		
CTSF 0.2113	LIP2 0.0216		SLC30A4 0.0673		
CTSH -0.591	LIP2 0.0216		SMPD1		
CTSK -0.207	LIP2 0.0216		SMPD1 0.1469		
CTSL -1.328	LIP2 0.0216		STS -0.056		
CTSL2 -0.115	LIP2 0.0216		TIAL1		
CTSS -0.232	LIP2 0.0216		TM4SF3 -0.617		

Legend

- villus, >2x
- villus
- crypt
- crypt, >2x
- No criteria met
- Not found

Supplementary fig 3—expression of vesicle/transport related genes