

Supplementary Table S1. Gene expression (mRNA relative quantity) of the ABC and SLC transporters in human parotid gland.

gene symbol	mean	SD	CV (%)	median	min	max
<i>ABCB1</i>	0.018	0.016	85.36	0.014	0.002	0.056
<i>ABCC1</i>	0.177	0.127	71.79	0.166	0.020	0.388
<i>ABCC2</i>	0.002	0.001	77.47	0.001	0.000	0.004
<i>ABCC3</i>	0.006	0.008	130.97	0.002	0.001	0.024
<i>ABCC4</i>	0.004	0.002	62.87	0.003	0.001	0.008
<i>ABCG2</i>	0.014	0.015	104.53	0.010	0.003	0.052
<i>SLC10A1</i>	BLQ					
<i>SLC10A2</i>	BLQ					
<i>SLC15A2</i>	0.063	0.064	101.58	0.049	0.009	0.224
<i>SLC22A1</i>	0.002	0.001	38.28	0.002	0.000	0.002
<i>SLC22A3</i>	0.029	0.032	109.22	0.023	0.001	0.106
<i>SLC22A5</i>	0.010	0.004	37.67	0.010	0.002	0.016
<i>SLC22A6</i>	BLQ					
<i>SLC22A7</i>	BLQ					
<i>SLC22A8</i>	BLQ					
<i>SLC47A1</i>	0.000	0.000	59.86	0.000	0.000	0.001
<i>SLCO1A2</i>	0.093	0.145	156.03	0.041	0.001	0.468
<i>SLCO1B1</i>	BLQ					
<i>SLCO1B3</i>	0.000	0.000	142.47	0.000	0.000	0.001
<i>SLCO2B1</i>	0.006	0.004	68.16	0.004	0.002	0.015
<i>ATP1A1</i>	1.575	0.499	31.68	1.534	0.781	2.660

Relative quantity of each transcript is presented, compared to mean expression of reference genes (Δ CT method); SD- standard deviation; CV % - coefficient of variation; BLQ-below limit of quantification.

Supplementary Table S2. Protein abundance of the ABC and SLC transporters in human parotid gland.

protein [pmol/mg]	mean	SD	CV (%)	median	min	max	positive samples
ABCB1	BLQ						
ABCC1	0.329	0.417	126.55	0.230	0.000	1.174	5/9
ABCC2	BLQ						
ABCC3	BLQ						
ABCC4	0.078	0.079	100.87	0.083	0.000	0.183	5/9
ABCG2	0.040	0.042	102.92	0.052	0.000	0.108	5/9
NTCP	BLQ						
ASBT	BLQ						
PEPT2	0.110	0.073	66.24	0.121	0.000	0.207	7/9
OCT1	BLQ						
OCT3	0.451	0.272	60.33	0.385	0.000	0.845	8/9
OCTN2	BLQ						
OAT1	BLQ						
OAT2	BLQ						
OAT3	BLQ						
MATE1	0.048	0.064	133.02	0.000	0.000	0.178	4/9
OATP1A2	BLQ						
OATP1B1	BLQ						
OATP1B3	BLQ						
OATP2B1	BLQ						
Na/K ATPase	7.908	7.030	88.89	8.400	0.575	18.727	9/9

SD- standard deviation; CV % - coefficient of variation; positive samples: number of samples with detectable level of the protein; BLQ-below limit of quantification.

Supplementary Table 3. Correlation between salivary glands transporters protein (Spearman's rank test). Bold fold indicates p value <0.05 .

	ABCC1	ABCC4	ABCG2	PEPT2	OCT3	MATE1	OATP2B1	Na/K ATPase
ABCC1	1.000	-0.773	-0.009	-0.258	0.383	0.229	0.000	0.644
ABCC4		1.000	-0.127	-0.004	-0.052	-0.219	-0.358	-0.957
ABCG2			1.000	0.629	0.461	0.324	-0.358	0.174
PEPT2				1.000	0.042	0.440	0.138	-0.033
OCT3					1.000	0.183	-0.411	0.033
MATE1						1.000	0.300	0.164
OATP2B1							1.000	0.411
Na/K ATPase								1.000

Supplementary Table 4. Overview of used proteospecific peptides and the respective MS parameters.

Protein	Peptide	Q1	Q3.1	Q3.1-CE	Q3.2	Q3.2-CE	Q3.3	Q3.3-CE	DP	EP	CXP
ABCB1	AGAVAEVLAAIR	635.4	971.4	27	430.2	23	900.3	27	80	10	13
	AGAVAEVLAAIR*	639.5	981.4	27	440.2	23	910.3	27	80	10	13
	IATEAIENFR	582.4	749.4	30	565.2	28	678.4	28	70	10	13
	IATEAIENFR*	587.4	759.4	30	575.3	28	688.4	28	70	10	13
ABCC1	DGAFAEFLR	513.2	782.5	20	635.4	23	564.4	23	140	10	13
	DGAFAEFLR*	517.9	792.4	20	645.4	23	574.4	23	140	10	13
ABCC2	LTII PQDPILFSGSLR	885.4	665.3	36	989.3	51	721.7	36	110	10	13
	LTII PQDPILFSGSLR*	890.4	670.2	36	999.3	51	726.8	36	110	10	13
	YLGDDLDLSAIR	698.5	547.3	43	1119.4	33	662.3	36	90	10	13
	YLGDDLDLSAIR*	703.4	557.3	43	1129.4	33	672.3	36	90	10	13
ABCC3	IDGLNVADIGLHDLR	541.0	696.8	20	754.4	20	611.9	20	90	10	13
	IDGLNVADIGLHDLR*	544.3	701.8	20	759.3	20	616.8	20	90	10	13
	HIFDHVIGPEGVLAK	563.9	749.5	27	650.4	29	513.4	37	151	10	13
	HIFDHVIGPEGVLAK*	566.2	749.4	27	650.4	29	513.4	37	151	10	13
ABCC4	SSLISALFR	497.2	706.4	22	593.3	23	401.3	17	90	10	13
	SSLISALFR*	501.9	716.4	22	603.4	23	401.3	17	90	10	13
ABCG2	SSLLDVLAAR	522.8	644.3	23	757.3	23	430.3	22	80	10	13
	SSLLDVLAAR*	527.9	654.3	23	767.3	23	440.3	22	80	10	13
	VIQELGLDK	507.3	802.5	20	674.5	23	545.5	30	120	10	13
	VIQELGLDK*	511.3	810.6	20	682.5	23	553.5	30	120	10	13
ASBT	ENGTEPESSFYK	694.3	857.2	29	986.2	28	631.2	38	140	10	13
	ENGTEPESSFYK*	698.2	865.2	29	994.1	28	639.1	38	140	10	13
	AEIPESK	387.0	573.4	16	702.4	16	460.3	17	78	10	13
	AEIPESK*	391.1	581.4	16	710.4	16	468.2	17	78	10	13
	QEEPLPEHPQDGAK	525.7	594.9	21	615.4	31	650.6	24	140	10	13

MATE1	QEEPLPEHPQDGAK*	528.1	599.0	21	623.4	31	654.5	24	140	10	13
	GGPEATLEVR	514.94	457.9	23	617.3	23	688.4	30	65	10	13
	GGPEATLEVR*	519.9	462.8	23	627.3	23	698.4	30	65	10	13
Na/K-ATPase	LSLDELHR	328.3	435.2	15	391.7	14	669.3	15	100	10	13
	LSLDELHR*	331.5	440.3	15	396.8	14	679.4	15	100	10	13
NTCP	GIYDGDLC	440.7	710.4	18	547.2	19	432.2	25	60	10	13
	GIYDGDLC*	444.7	718.4	18	555.3	19	440.2	25	60	10	13
OAT1	TSLAVLGK	394.3	600.5	18	687.6	19	416.4	22	40	10	13
	TSLAVLGK*	398.3	608.5	18	695.6	19	424.3	22	40	10	13
OAT2	NVALLALPR	483.2	753.5	20	569.4	20	682.6	21	80	10	13
	NVALLALPR*	488.2	763.6	20	579.4	20	692.5	21	80	10	13
OAT3	VAVFNGK	367.3	564.3	15	635.3	17	465.4	18	60	10	13
	VAVFNGK*	371.2	572.4	15	643.5	17	473.3	18	60	10	13
OATP1A2	EGLETNADIIC	601.8	774.4	25	673.4	25	903.3	25	130	10	13
	EGLETNADIIC*	605.6	782.3	25	681.3	25	911.3	25	130	10	13
	YIYGLPAALR	625.4	697.5	27	527.4	27	810.7	29	140	10	13
	YIYGLPAALR*	630.3	707.6	27	537.4	27	820.5	29	140	10	13
OATP1B1	NVTGFFQSFK	587.9	961.4	24	860.4	24	656.4	27	70	10	13
	NVTGFFQSFK*	591.8	969.5	24	868.4	24	664.3	27	70	10	13
	SSIIHIER	477.8	554.3	26	667.4	26	417.2	30	80	10	13
	SSIIHIER*	482.8	564.3	26	677.4	26	427.2	30	80	10	13
OATP1B3	ISTIQIER	479.9	545.3	24	417.2	23	304.2	21	100	10	13
	ISTIQIER*	484.7	555.3	24	427.3	23	314.3	21	100	10	13
	NVTGFFQSLK	570.8	927.5	24	826.4	26	347.2	37	65	10	13
	NVTGFFQSLK*	574.9	935.5	24	834.5	26	355.2	37	65	10	13

OATP2B1	SSPAVEQQLLVSGPGK	798.8	711.9	33	445.2	35	1155.2	35	170	10	13
	SSPAVEQQLLVSGPGK*	803.7	716.7	33	453.1	35	1165.3	35	170	10	13
	YYNNDLLR	535.4	907.5	27	744.6	25	327.0	22	150	10	13
	YYNNDLLR*	540.2	917.6	27	754.5	25	327.0	22	150	10	13
OCT1	ENTIYLK	440.7	423.2	17	637.4	17	536.3	17	80	10	13
	ENTIYLK*	444.7	431.0	17	645.4	17	544.3	17	80	10	13
	LPPADLK	376.7	640.6	17	543.4	17	494.3	14	50	10	13
	LPPADLK*	380.9	648.4	17	551.4	17	494.3	14	50	10	13
OCT3	GIALPETVDDVEK	693.3	1031.3	25	516.2	28	805.2	38	120	10	13
	GIALPETVDDVEK*	697.3	1039.3	25	520.3	28	813.3	38	120	10	13
OCTN2	FEEAEVIIR	552.9	829.4	26	700.5	27	629.4	26	160	10	13
	FEEAEVIIR*	558.1	839.6	26	710.5	27	639.5	26	160	10	13
PEPT2	IEDIPANK	450.3	657.4	19	429.2	27	786.5	20	110	10	13
	IEDIPANK*	454.1	665.4	19	437.3	27	794.6	20	110	10	13

Peptides highlighted in grey were used for quantification (CE, collision energy; DP, declustering potential; EP, entrance potential; CXP, collision cell exit potential; Q, quadrupole).

