

Table S1. Oligopeptide, di-/tripeptide and amino acid transport systems of *L.helveticus* H-9 and *L.paracasei* ABK

Gene	<i>Lb. helveticus</i> H-9	<i>Lb. paracasei</i> ABK	Comment
ABC-type oligopeptide transport system Opp:			
<i>oppA</i>	MBU6033698	MBU6046676	SBP_bac_5, ABC transporter substrate-binding protein
<i>oppA</i>	MBU6033699	MBU6047988	SBP_bac_5, ABC transporter substrate-binding protein
<i>oppA</i>	no*	MBU6048244	SBP_bac_5, ABC transporter substrate-binding protein
<i>oppC5</i>	MBU6033697	no	BPD_transp_1,OppC_N Binding-protein-dependent transport system inner membrane component
<i>oppC</i>	no	MBU6046118	BPD_transp_1,OppC_N Binding-protein-dependent transport system inner membrane component
<i>oppB</i>	MBU6033696	MBU6046119	BPD_transp_1, ABC transporter permease
<i>oppF</i>	MBU6033695	MBU6046120	ABC_tran, oligo_HPY Belongs to the ABC transporter superfamily
<i>oppD</i>	MBU6033694	MBU6046121	ABC_tran, oligo_HPY Belongs to the ABC transporter superfamily
ABC-type di-/tripeptide transport system Dpp:			
<i>Dpp</i>	no	no	
Di-/tripeptide proton-coupled transporter DtpT:			
<i>DtpT</i>	no	MBU6047829	PTR2, amino acid peptide transporter
ABC-type amino acid transport system:			
<i>glnQ</i>	MBU6034061 MBU6034081 MBU6034193 MBU6035110	MBU6046694 MBU6046704 MBU6046753 MBU6047174 MBU6047247	ABC transporter, ATP-binding protein; ABC-type glutamine transport system ATP-binding protein
<i>glnPH2</i>	MBU6034080	MBU6047175	ABC transporter permease glutamine transport system
<i>glnP7</i>	MBU6034194	no	ABC transporter permease glutamine transport system
<i>glnP9</i>	MBU6034195	no	ABC transporter, permease protein
<i>glnP</i>	MBU6035107	MBU6046692 MBU6046693 MBU6047244	ABC transporter permease
<i>glnM</i>	MBU6035108	MBU6047245	ABC transporter permease
<i>glnH</i>	MBU6035109	MBU6047246	ABC transporter substrate-binding protein

<i>proV</i>	no	MBU6046863	ABC transporter, ATP-binding protein; ABC-type proline/glycine betaine transport system ATP-binding protein
<i>metN</i>	MBU6034603	MBU6046651	ABC_tran, NIL, Part of the ABC transporter complex MetNIQ involved in methionine import . Responsible for energy coupling to the transport system
<i>livM</i>	no	MBU6048020	BPD_transp_2, Branched-chain amino acid transport system / permease component Branched chain amino acid ABC transporter permease LivM
Amino acid permease:			
<i>ydaO</i>	no	MBU6046361	Amino acid permease AA_permease_2
<i>yhdG</i>	MBU6033810	MBU6046100	AA_permease_2
--	MBU6033960 MBU6035006	MBU6046991 MBU6047014 MBU6047417 MBU6048255	Amino acid permease
<i>ctrA</i>	MBU6033705	no	AA_permease_2 branched-chain amino acid permease
<i>lysP</i>	no	MBU6047170	AA_permease
<i>steT</i>	MBU6034692	no	AA_permease_2
<i>aapA</i>	MBU6033958	no	Amino acid permease
<i>yagE</i>	no	MBU6047952	Amino acid permease
<i>cycA</i>	MBU6034554	MBU6048008	Amino acid permease
<i>yifK</i>	MBU6033959 MBU6035116	MBU6048142	Amino acid permease
<i>ybeC</i>	no	MBU6048163	AA_permease_2
BCAA transport system carrier II proteins (MFS superfamily):			
<i>brnQ</i>	MBU6035150	MBU6047394 MBU6047892	Branch_AA_trans, Component of the transport system for branched-chain amino acids (BCAAs)
Amino acid exporter:			
<i>thrE</i>	MBU6034728	MBU6048018 MBU6047532	ThrE_2 Threonine/Serine exporter
<i>thrE</i>	MBU6034727	MBU6048017	Putative threonine/serine exporter
<i>thrE</i>	MBU6034897	MBU6047843	Putative threonine/serine exporter, ThrE_2
<i>labL</i>	no	MBU6047531	ThrE, Putative threonine/serine exporter
<i>yqjA</i>	no	MBU6048043	ArAE_1,ArAE_1_C Putative aromatic acid exporter C-terminal domain
<i>cydC</i>	no	MBU6046392	ABC_membrane,ABC_tran ABC transporter, CydDC cysteine exporter (CydDC-E) family,

			permease ATP-binding protein CydD
<i>cydD</i>	no	MBU6046393	ABC transporter, CydDC cysteine exporter (CydDC-E) family, permease ATP-binding protein CydC
Total:	30	43	

no* – not found

Table S2. Carbohydrate transport systems of *L. helveticus* H-9 and *L. paracasei* ABK

Gene	<i>Lb.helveticus</i> H-9	<i>Lb.paracasei</i> ABK	Comment
<i>treB</i>	MBU6034129	MBU6047415 MBU6048282	TreB, the trehalose PTS permease, belongs to the functional superfamily of the phosphoenolpyruvate (PEP)-dependent, sugar transporting phosphotransferase system PTS_EIIA_1, PTS_EIIB, PTS_EIIC
<i>lacE</i>	no*	MBU6048344	PTS_EIIC,PTS_IIB Phosphotransferase system, EIIC
<i>lacF</i>	no	MBU6048346	PTS_IIA PTS system, Lactose/Cellobiose specific IIA subunit
--	no	MBU6047235 MBU6048143 MBU6048257 MBU6048450	PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit
<i>mtIA</i>	no	MBU6047960	PTS_EIIC, PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit
<i>ptcB</i>	no	MBU6046350 MBU6047980	PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit
<i>pts13C</i>	MBU6033953	no	PTS_EIIC The phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), a major carbohydrate active - transport system, cellobiose-specific EIIC component
<i>pts20B</i>	no	MBU6046721	PTS_IIB PTS system, Lactose/Cellobiose specific IIB subunit
<i>pts26BCA</i>	no	MBU6046607	PTS_EIIA_1,PTS_EIIB,PTS_EIIC phosphotransferase system sucrose-specific sucrose PTS system EIIBCA or EIIBC component [EC:2.7.1.211]
<i>pts33BCA</i>	MBU6034053	no	PTS_EIIA_1,PTS_EIIB,PTS_EIIC ko:K02755,ko:K02756,ko:K02757 beta-glucoside PTS system EIICBA component [EC:2.7.1.-] β-glucosides PTS, EIIBCA (EC:2.7.1.69)
<i>pts36A</i>	no	MBU6048451	PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2
<i>pts36C</i>	no	MBU6048449	PTS system sugar-specific permease component EIIC-GAT
<i>ptbA</i>	MBU6034508	no	PTS_EIIA_1 phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1
--	MBU6034560	no	PTS_EIIA_1 phosphoenolpyruvate-

	MBU6035235		dependent sugar phosphotransferase system, EIIA 1
--	MBU6034840	MBU6047236 MBU6048144 MBU6048322	PTS_EIIA_2 Phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 2
<i>chbA</i>	no	MBU6047772	PTS_IIA phosphoenolpyruvate-dependent sugar phosphotransferase system
<i>chbC</i>	MBU6034783	MBU6046722	PTS_EIIC phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS)
<i>fruA</i>	no	MBU6046468	PTS_EIIA_2,PTS_EIIC,PTS_IIB Phosphotransferase System
<i>fruC</i>	no	MBU6048336	PTS_EIIA_2,PTS_EIIC,PTS_IIB
<i>dhaM</i>	no	MBU6046975	EIIA-man PTS system fructose IIA component
--	no	MBU6048173	EIIA-man PTS system fructose IIA component
<i>pfoSR</i>	no	MBU6046559	PTS_EIIC_2 Phosphotransferase system, EIIC
<i>pfoS/R</i>	no	MBU6046913	PTS_EIIC_2 Phosphotransferase system, EIIC
<i>manL</i>	MBU6034559	MBU6046709	EIIA-man, PTSIIB_sorb PTS system sorbose subfamily IIB component
<i>manM</i>	no	MBU6046710	EII-Sor PTS system
<i>manN</i>	MBU6034557	MBU6046711	EIID-AGA PTS system, mannose fructose sorbose family IID component
<i>manR</i>	no	MBU6047616	HTH_11,Mga,PRD,PTS_EIIA_2,PTS_IIB phosphoenolpyruvate-dependent sugar phosphotransferase system
<i>manY</i>	MBU6034558	no	EII-Sor PTS system
<i>celC</i>	no	MBU6046720 MBU6047979	PTS system, Lactose Cellobiose specific IIA subunit
<i>celD</i>	no	MBU6047977	PTS_EIIC phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS)
<i>bglH</i>	no	MBU6048049	PTS_EIIA_1,PTS_EIIB,PTS_EIIC phosphotransferase system
--	no	MBU6047953	protein-N(PI)-phosphohistidine-lactose phosphotransferase system transporter activity
--	no	MBU6048320	PTS_IIB Phosphotransferase system, galactitol-specific IIB component
--	no	MBU6048056 MBU6048169	PTSIIB_sorb PTS system sorbose subfamily IIB component
--	no	MBU6048057 MBU6048171	EIID-AGA PTS system mannose/fructose/sorbose family IID component

<i>XK27_08455</i>	no	MBU6048058	EII-Sor PTS system sorbose-specific IIC component
--	no	MBU6048170	EII-Sor PTS system sorbose-specific IIC component
<i>gatC</i>	no	MBU6047234	EIIC-GAT PTS system sugar-specific permease component
--	no	MBU6048258 MBU6048286 MBU6048321	EIIC-GAT PTS system sugar-specific permease component
<i>srlB</i>	no	MBU6047947	PTSIIA_gutA PTS system glucitol/sorbitol-specific IIA component
<i>ptsI</i>	MBU6035138	MBU6046257	PEP-utilisers_N, PEP-utilizers, PEP- utilizers_C
<i>ptsH</i>	MBU6035139	MBU6046258	PTS-HPr phosphocarrier protein HPR
<i>hprK</i>	MBU6033848	MBU6046810	Hpr_kinase_C,Hpr_kinase_N
Total:	14	50	

no* – not found