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Supplementary Table 3. Characterization of hub-genes in the RC-key-module.

KEGG ID	Module Membership	Gene Significance	Related pathway (KEGG)	Protein Name	Length	GO Biological Process (Uniprot)	GO Cellular component (Uniprot)	GO Molecular function (Uniprot)
SMU_286	0,637	0,607	putative ABC transporter, ATP-binding protein	putative ABC transporter, ATP-binding protein ComA	760	single-species submerged biofilm formation [GO:0090609]	integral component of membrane [GO:0016021]	ATPase activity [GO:0016887]; ATPase-coupled bacteriocin transmembrane transporter activity [GO:0043214]; ATP binding [GO:0005524]; cysteine-type peptidase activity [GO:0008234]
SMU_354	0,889	0,636	uncharacterized protein	uncharacterized protein	424	-	-	-
SMU_455 *pbp*2x	0,892	0,720	penicillin binding	putative penicillin-binding protein 2X	749	cell cycle [GO:0007049]; cell division [GO:0051301]; regulation of cell shape [GO:0008360]	integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	penicillin binding [GO:0008658]
SMU_482 *sun*L	0,818	0,655	regulation of transcription	16S rRNA m5C967 methyltransferase	437	regulation of transcription, DNA-templated [GO:0006355]	cytoplasm [GO:0005737]	RNA binding [GO:0003723]; rRNA methyltransferase activity [GO:0008649]
SMU_546	0,805	0,609	putative GTP-binding protein	putative GTP-binding protein	614	translation [GO:0006412]	-	GTPase activity [GO:0003924]; GTP binding [GO:0005525]
SMU_597 *pbp*2b	0,700	0,677	penicillin binding	penicillin-binding protein 2b	692	-	membrane [GO:0016020]	penicillin binding [GO:0008658]
SMU_744 *fts*Y	0,857	0,617	cell division protein	signal recognition particle receptor FtsY	498	SRP-dependent cotranslational protein targeting to	cytoplasm [GO:0005737]; intrinsic	GTPase activity [GO:0003924]; GTP binding [GO:0005525]

						membrane [GO:0006614]	component of plasma membrane - [GO:0031226]	
SMU_821 *dna*G	0,672	0,730	DNA primase	DNA primase	592	-	primosome complex [GO:1990077]	DNA binding [GO:0003677]; DNA primase activity [GO:0003896]; zinc ion binding [GO:0008270]
SMU_1190 *pyk*F	0,650	0,643	carbohydrate degradation	pyruvate kinase	500	-	-	ATP binding [GO:0005524]; kinase activity [GO:0016301]; magnesium ion binding [GO:0000287]; potassium ion binding [GO:0030955]; pyruvate kinase activity [GO:0004743]
SMU_1383 *leu*B	0,906	0,608	amino-acid biosynthesis	3-isopropylmalate dehydrogenase	344	leucine biosynthetic process [GO:0009098]	cytoplasm [GO:0005737]	3-isopropylmalate dehydrogenase activity [GO:0003862]; magnesium ion binding [GO:0000287]; NAD binding [GO:0051287]
SMU_1396 *gbp*C	0,795	0,734	glucan-binding protein C	glucan-binding protein C, *gbp*C	583	-	cell wall [GO:0005618]; extracellular region [GO:0005576]	-
SMU_1692 *act*	0,657	0,611	pyruvate formate-lyase	pyruvate formate-lyase-activating enzyme	263	-	cytoplasm [GO:0005737]	[formate-C-acetyltransferase]-activating enzyme activity [GO:0043365]; 4 iron, 4 sulfur cluster binding [GO:0051539]; metal ion binding [GO:0046872]
SMU_1729c *mlt*G	0,797	0,660	peptidoglycan biosynthetic process	endolytic murein transglycosylase	614	cell wall organization	integral component of	lyase activity [GO:0016829]; lytic endotransglycosylase

						[GO:0071555]; peptidoglycan biosynthetic process [GO:0009252]	plasma membrane [GO:0005887]	activity [GO:0008932]
SMU_1838 *sec*A	0,794	0,665	preprotein translocase subunit *sec*A	protein translocase subunit *sec*A	839	intracellular protein transmembrane transport [GO:0065002]; protein import [GO:0017038]; protein targeting [GO:0006605]	cytoplasm [GO:0005737]; plasma membrane [GO:0005886]	ATP binding [GO:0005524]; metal ion binding [GO:0046872]
SMU_1839 *man*A	0,935	0,629	mannose-6-phosphate isomerase	mannose-6-phosphate isomerase	316	carbohydrate metabolic process [GO:0005975]	-	mannose-6-phosphate isomerase activity [GO:0004476]; zinc ion binding [GO:0008270]
SMU_1978 *ack*A	0,961	0,645	acetate kinase	acetate kinase	399	acetyl-CoA biosynthetic process [GO:0006085]; organic acid metabolic process [GO:0006082]	cytoplasm [GO:0005737]	acetate kinase activity [GO:0008776]; ATP binding [GO:0005524]; magnesium ion binding [GO:0000287]
SMU_2074 *nrd*D	0,643	0,687	putative anaerobic ribonucleoside-triphosphate reductase	putative anaerobic ribonucleoside-triphosphate reductase	734	DNA replication [GO:0006260]	-	ATP binding [GO:0005524]; ribonucleoside-triphosphate reductase activity [GO:0008998]