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Supplementary Table 1. Characterization of the differential gene expression on SRS and RC samples

KEGG ID	Log2fold change	P adjusted	Related pathway (KEGG)	Protein Name	Length	GO Biological Process (Uniprot)	GO Cellular component (Uniprot)	GO Molecular function (Uniprot)
SMU_1399	-8,373	5,875 E-15	hypothetical protein	Uncharacterized protein	106	-	-	-
SMU_959c	-6,579	1,073 E-14	hypothetical protein	Uncharacterized protein	84	-	-	-
SMU_1032 *tnr*5	-7,613	2,612 E-11	putative transposon integrase	Putative transposon integrase Tn916 ORF3-like	388	DNA recombination [GO:0006310]	-	DNA binding [GO:0003677]; integrase activity [GO:0008907]
SMU_52	-4,039	1,724 E-04	conserved hypothetical protein	Uncharacterized protein	221	-	integral component of membrane [GO:0016021]	-
SMU_1145c	-3,832	1,724 E-04	putative histidine kinase	Histidine kinase	437	-	integral component of membrane [GO:0016021]	phosphorelay sensor kinase activity [GO:0000155]
SMU_1149	-4,085	1,724 E-04	putative transporter, trans-membrane domain bacteriocin immunity protein	Putative transporter, trans-membrane domain bacteriocin immunity protein	246	-	integral component of membrane [GO:0016021]	-
SMU_1404c *cas*1	-4,031	2,012 E-04	hypothetical protein	CRISPR-associated endonuclease Cas1	288	maintenance of CRISPR repeat elements [GO:0043571]	-	DNA binding [GO:0003677]; endodeoxyribonuclease activity [GO:0004520]; metal ion binding [GO:0046872]
SMU_1148	-4,356	3,288 E-04	putative transporter, ATP-binding protein; bacteriocin immunity protein	Putative transporter, ATP-binding protein bacteriocin immunity protein	255	-		ATPase activity [GO:0016887]; ATP binding [GO:0005524]
SMU_1150	-3,997	3,325 E-04	bacteriocin immunity protein	Putative transporter, trans-membrane domain bacteriocin immunity protein	242	-	integral component of membrane [GO:0016021]	-
SMU_1146c	-3,801	4,875 E-04	putative response regulator	Putative response regulator	229	phosphorelay signal transduction system [GO:0000160]; regulation of transcription, DNA-templated [GO:0006355]	-	DNA binding [GO:0003677]
SMU_1490 *lac*G	-2,795	2,642 E-03	6-phospho-beta-galactosidase	6-phospho-beta-galactosidase	468	carbohydrate metabolic process [GO:0005975]; lactose catabolic process	-	6-phospho-beta-galactosidase activity [GO:0033920]

						via tagatose-6-phosphate [GO:0019512]		
SMU_1587c	-3,337	4,627 E-03	hypothetical protein	Uncharacterized protein	212	-		-
SMU_2133c	2,156	1,299 E-02	putative membrane protein	Putative membrane protein	834	-	integral component of membrane [GO:0016021]	-
SMU_35 *pur*N	-2,180	3,221 E-02	phosphoribosylglycinamide formyltransferase	Phosphoribosylglycinamide formyltransferase	184	'de novo' IMP biosynthetic process [GO:0006189]	-	phosphoribosylglycinamide formyltransferase activity [GO:0004644]
SMU_650 *ala*S	1,667	3,221 E-02	putative alanyl-tRNA synthetase (alanine--tRNA ligase)	Alanine--tRNA ligase	872	alanyl-tRNA aminoacylation [GO:0006419]	cytoplasm [GO:0005737]	alanine-tRNA ligase activity [GO:0004813]; ATP binding [GO:0005524]; tRNA binding [GO:0000049]; zinc ion binding [GO:0008270]
SMU_546	1,431	3,277 E-02	putative GTP-binding protein	Putative GTP-binding protein	614	translation [GO:0006412]	-	GTPase activity [GO:0003924]; GTP binding [GO:0005525]
SMU_1184c *mtl*R	-1,845	3,651 E-02	putative transcriptional regulator, antiterminator	Putative transcriptional regulator MtlR [Includes: Putative phosphotransferase enzyme IIA component	650	regulation of transcription, DNA-templated [GO:0006355]	-	kinase activity [GO:0016301]