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Supplementary Table 2. Characterization of hub-genes in the SRS 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_11	0,941	0,696	Uncharacterized protein	Uncharacterized protein	39	-	-	-
SMU_18	0,979	0,641	Uncharacterized protein	Uncharacterized protein	45	-	-	-
SMU_40	0,977	0,707	Uncharacterized protein	Uncharacterized protein	53	-	-	-
SMU_53	0,835	0,712	Uncharacterized protein	Uncharacterized protein	71	-	-	-
SMU_55	0,840	0,673	Uncharacterized protein	Uncharacterized protein	87	-	-	-
SMU_56	0,958	0,788	Uncharacterized protein	Uncharacterized protein	42	-	-	-
SMU_58	0,715	0,646	Uncharacterized protein	Uncharacterized protein	431	-	-	-
SMU_68	0,976	0,714	Uncharacterized protein	Uncharacterized protein	25	-	-	-
SMU_92c	0,990	0,726	Uncharacterized protein	Uncharacterized protein	45	-	-	-
SMU_93c	0,988	0,712	Uncharacterized protein	Uncharacterized protein	36	-	-	-
SMU_94c	0,978	0,759	Uncharacterized protein	Uncharacterized protein	56	-	-	-
SMU_106c	0,908	0,693	Putative transposase	Putative transposase	78	-	-	-
SMU_107	0,981	0,744	Uncharacterized protein	Uncharacterized protein	56	-	-	-
SMU_108	0,979	0,731	DNA binding. Putative transcriptional regulator	Methyltransf_25 domain-containing protein	45	-	-	-
SMU_136c	0,895	0,631	Uncharacterized protein	Putative transcriptional regulator	117	-	-	DNA binding [GO:0003677]
SMU_150	0,988	0,716	Defense response to bacterium	Uncharacterized protein	67	defense response to bacterium [GO:0042742]	-	-
SMU_153	0,957	0,640	Uncharacterized protein	Uncharacterized protein	33	-	-	-
SMU_175	0,959	0,661	Uncharacterized protein	Uncharacterized protein	42	-	-	-
SMU_176	0,981	0,747	Uncharacterized protein	Uncharacterized protein	51	-	-	-
SMU_185	0,954	0,629	Uncharacterized protein	Uncharacterized protein	45	-	-	-
SMU_191c	0,911	0,644	DNA recombination	Putative integrase	387	DNA integration	-	DNA binding

						[GO:0015074]; DNA recombination [GO:0006310]		[GO:0003677]
SMU_197c	0,966	0,658	Uncharacterized protein	Uncharacterized protein	808	-	integral component of membrane [GO:0016021]	-
SMU_198c	0,922	0,702	Putative conjugative transposon protein	Putative conjugative transposon protein	847	-	-	-
SMU_201c	0,989	0,740	integral component of membrane. Putative transposon protein	Putative transposon protein	326	-	integral component of membrane [GO:0016021]	-
SMU_207c	0,871	0,607	DNA replication initiation	Putative transposon protein	410	DNA replication initiation [GO:0006270]	-	DNA binding [GO:0003677]; DNA topoisomerase activity [GO:0003916]
SMU_210c	0,978	0,754	Uncharacterized protein	Uncharacterized protein	103	-	-	-
SMU_211c	0,948	0,634	Uncharacterized protein	Uncharacterized protein	147	-	integral component of membrane [GO:0016021]	-
SMU_216c	0,878	0,614	Uncharacterized protein	Uncharacterized protein	104	-	-	-
SMU_218	0,989	0,739	Putative transcriptional regulator	Putative transcriptional regulator	117	-	-	DNA binding [GO:0003677]
SMU_222c	0,898	0,667	Hypothetical protein possible integrase fragment	Uncharacterized protein	64	-	-	-
SMU_223c	0,977	0,750	Uncharacterized protein	Uncharacterized protein	33	-	-	-
SMU_225c	0,979	0,712	Uncharacterized protein	Uncharacterized protein	37	-	-	-
SMU_276c	0,986	0,666	Uncharacterized protein	Uncharacterized protein	53	-	-	-
SMU_279	0,976	0,711	Uncharacterized protein	Uncharacterized protein	69	-	integral component of membrane [GO:0016021]	-
SMU_378	0,975	0,724	Uncharacterized protein	Uncharacterized protein	79	-	integral component of membrane	-

							[GO:0016021]	
SMU_379	0,979	0,742	Uncharacterized protein	Uncharacterized protein	45	-	integral component of membrane [GO:0016021]	-
SMU_390	0,938	0,647	Uncharacterized protein	Uncharacterized protein	52	-	-	-
SMU_444	0,976	0,709	Uncharacterized protein	Uncharacterized protein	35	-	-	-
SMU_451	0,979	0,748	Uncharacterized protein	Uncharacterized protein	34	-	integral component of membrane [GO:0016021]	-
SMU_457	0,977	0,667	Uncharacterized protein	Uncharacterized protein	55	-	integral component of membrane [GO:0016021]	-
SMU_512c	0,969	0,720	Uncharacterized protein	Uncharacterized protein	151	-	integral component of membrane [GO:0016021]	-
SMU_513	0,937	0,782	Uncharacterized protein	Uncharacterized protein	77	-	integral component of membrane [GO:0016021]	-
SMU_529	0,974	0,745	Uncharacterized protein	Uncharacterized protein	37	-	-	-
SMU_531	0,926	0,643	Chorismate metabolic process. Isomerase	Putative chorismate mutase	103	chorismate metabolic process [GO:0046417]		chorismate mutase activity [GO:0004106]
SMU_545	0,981	0,723	Uncharacterized protein	Uncharacterized protein	46	-	-	-
SMU_571	0,961	0,613	Uncharacterized protein	Uncharacterized protein	50	-	integral component of membrane [GO:0016021]	-
SMU_604	0,954	0,694	Uncharacterized protein	Uncharacterized protein	91	-	-	-
SMU_620	0,932	0,717	Uncharacterized protein	Uncharacterized protein	52	-	-	-
SMU_681	0,990	0,737	Macro domain-containing protein	Macro domain-containing protein	61	-	-	-
SMU_687c	0,966	0,813	Uncharacterized protein	Uncharacterized protein	44	-	-	-
SMU_694c	0,965	0,618	Putative ferredoxin	Putative ferredoxin	64	-	-	-

SMU_722	0,963	0,655	Uncharacterized protein	Uncharacterized protein	59	-	-	-
SMU_750c	0,980	0,742	Uncharacterized protein	Uncharacterized protein	35	-	-	-
SMU_767 ISSmu1	0,963	0,801	Uncharacterized protein	Putative transposase ISSmu1	278	DNA integration [GO:0015074]; DNA recombination [GO:0006310]; transposition [GO:0032196]	-	nucleic acid binding [GO:0003676]
SMU_771c	0,991	0,681	Uncharacterized protein	Uncharacterized protein	44	-	integral component of membrane [GO:0016021]	-
SMU_798c	0,985	0,684	Uncharacterized protein	Uncharacterized protein	42	-	-	-
SMU_812	0,965	0,779	Uncharacterized protein	Uncharacterized protein	37	-	-	-
SMU_875c	0,852	0,657	DNA integration	Putative transposase, IS150-like	205	DNA integration [GO:0015074]	-	nucleic acid binding [GO:0003676]
SMU_891 *hsd*M	0,727	0,698	DNA binding. Site-specific DNA-methyltransferase (adenine-specific) activity	Site-specific DNA-methyltransferase	534	DNA restriction-modification system [GO:0009307]	-	DNA binding [GO:0003677]; N-methyltransferase activity [GO:0008170]; site-specific DNA-methyltransferase (adenine-specific) activity [GO:0009007]
SMU_893	0,957	0,713	Putative anticodon nuclease	Putative anticodon nuclease	381	-	-	-
SMU_895	0,972	0,747	Regulation of transcription	Possible DNA-damage-inducible protein	90	regulation of transcription, DNA-templated [GO:0006355]	-	-
SMU_896	0,951	0,729	Uncharacterized protein	Uncharacterized protein	92	-	-	-
SMU_897	0,767	0,749	Subunit R is required for both nuclease and ATPase activities, but not for modification. DNA	Type I restriction enzyme R Protein	1015	DNA restriction-modification system [GO:0009307]	-	ATP binding [GO:0005524]; DNA binding [GO:0003677];

			restriction-modification system					helicase activity [GO:0004386]; type I site-specific deoxyribonuclease activity [GO:0009035]
SMU_959c	0,907	0,713	Uncharacterized protein	Uncharacterized protein	84	-	-	-
SMU_1000	0,978	0,732	Uncharacterized protein	Uncharacterized protein	41	-	-	-
SMU_1024c	0,983	0,735	Uncharacterized protein			-	-	-
SMU_1025	0,963	0,695	DNA-binding transcription factor activity	Putative transcriptional regulator	141	-	-	DNA-binding transcription factor activity [GO:0003700]
SMU_1026	0,914	0,668	Uncharacterized protein	Uncharacterized protein	126	-	-	-
SMU_1029	0,891	0,778	Uncharacterized protein	Uncharacterized protein	118	-	-	-
SMU_1030	0,943	0,740	Transferase activity	Putative polyribonucleotide nucleotidyltransferase Tn916 ORF8-like	76			transferase activity [GO:0016740]
SMU_1031 *xis*	0,940	0,749	DNA integration	Excisionase	67	DNA integration [GO:0015074]; DNA recombination [GO:0006310]	-	DNA binding [GO:0003677]
SMU_1032 *tnr*5	0,812	0,661	DNA recombination	Putative transposon integrase Tn916 ORF3-like	388	DNA recombination [GO:0006310]	-	DNA binding [GO:0003677]; integrase activity [GO:0008907]
SMU_1047c	0,978	0,740	Uncharacterized protein	Uncharacterized protein	35	-	-	-
SMU_1056	0,978	0,756	Uncharacterized protein	Uncharacterized protein	39	-	-	-
SMU_1087	0,972	0,685	Isomerase activity	Probable tautomerase SMU_1087	61	cellular aromatic compound metabolic process [GO:0006725]	-	isomerase activity [GO:0016853]
SMU_1145c	0,767	0,630	Phosphorelay sensor kinase activity. Histidine Kinase	Histidine kinase	437	-	integral component of membrane	phosphorelay sensor kinase activity

							[GO:0016021]	[GO:0000155]
SMU_1148	0,645	0,604	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_1149	0,684	0,618	Putative transporter, trans-membrane domain bacteriocin immunity protein	Putative transporter, trans-membrane domain bacteriocin immunity protein	246	-	integral component of membrane [GO:0016021]	-
SMU_1154c	0,972	0,725	N-acetyltransferase activity	N-acetyltransferase domain-containing protein	98	-	-	N-acetyltransferase activity [GO:0008080]
SMU_1155	0,921	0,748	Uncharacterized protein	Uncharacterized protein	151	-	-	-
SMU_1156c	0,972	0,669	Uncharacterized protein	Uncharacterized protein	115	-	-	-
SMU_1157c	0,681	0,624	Uncharacterized protein	SIR2_2 domain-containing protein	1061	-	-	-
SMU_1159c	0,974	0,670	Uncharacterized protein	Uncharacterized protein	54	-	-	DNA binding [GO:0003677]; site-specific DNA-methyltransferase (adenine-specific) activity [GO:0009007]
SMU_1205c	0,962	0,670	Uncharacterized protein	Uncharacterized protein	162	-	-	-
SMU_1231c	0,971	0,732	Uncharacterized protein	Uncharacterized protein	31	-	-	-
SMU_1255c	0,975	0,703	Uncharacterized protein	DUF4325 domain-containing protein	85	-	-	-
SMU_1256c	0,955	0,671	Uncharacterized protein	Uncharacterized protein	54	-	-	-
SMU_1259	0,979	0,745	DNA modification	Site-specific DNA-methyltransferase	108	-	-	-
SMU_1261c	0,896	0,667	Histidine biosynthetic process	Phosphoribosyl-ATP diphosphatase	61	histidine biosynthetic process [GO:0000105]	-	ATP binding [GO:0005524]; phosphoribosyl-ATP

								diphosphatase activity [GO:0004636]
SMU_1310	0,986	0,672	Uncharacterized protein	Uncharacterized protein	45	-	-	-
SMU_1330c	0,976	0,739	Putative transposase	Putative transposase	46	-	-	-
SMU_1332c	0,970	0,717	Putative transposase. Mobile and extrachromosomal element functions: Transposon functions	Putative transposase	87	-	-	-
SMU_1349	0,854	0,645	Uncharacterized protein	Uncharacterized protein	191	-	-	-
SMU_1353	0,981	0,745	Putative transposase	Putative transposase	51	DNA integration [GO:0015074]; transposition [GO:0032196]	-	-
SMU_1354c	0,940	0,650	Putative transposase	Putative transposase	86	-	-	-
SMU_1355c	0,932	0,687	Putative transposase fragment	Putative transposase fregment	97	-	-	-
SMU_1356c	0,819	0,666	Putative transposase	Putative transposase	96	-	-	-
SMU_1358	0,947	0,739	Putative transposase	Putative transposase	33	-	-	-
SMU_1359	0,977	0,756	Uncharacterized protein	Uncharacterized protein	36	-	-	-
SMU_1360c	0,948	0,603	Uncharacterized protein	Uncharacterized protein	42	-	-	-
SMU_1365c	0,975	0,724	Uncharacterized protein	Uncharacterized protein	781	-	integral component of membrane [GO:0016021]; plasma membrane [GO:0005886]	-
SMU_1368	0,976	0,768	Uncharacterized protein	Uncharacterized protein	39	-	-	-
SMU_1369	0,977	0,762	Uncharacterized protein	Uncharacterized protein	40	-	-	-
SMU_1372c	0,926	0,652	Uncharacterized protein	Uncharacterized protein	80	-	-	sequence-specific DNA binding [GO:0043565]
SMU_1373c	0,969	0,742	Uncharacterized protein	Uncharacterized protein	60	transposition, DNA-mediated [GO:0006313]	-	sequence-specific DNA binding [GO:0043565];

								transposase activity [GO:0004803]
SMU_1374	0,959	0,625	Uncharacterized protein	Uncharacterized protein	67	-	-	-
SMU_1399	0,841	0,777	Uncharacterized protein	Uncharacterized protein	106	-	-	-
SMU_1505c	0,979	0,653	FDX-ACB domain-containing protein	FDX-ACB domain-containing protein	39	-	-	-
SMU_1575c	0,929	0,709	Uncharacterized protein	Uncharacterized protein	94	-	-	-
SMU_1610 *rpm*G	0,954	0,622	50S ribosomal protein L33. Structural constituent of ribosome	50S ribosomal protein L33	48	translation [GO:0006412]	ribosome [GO:0005840]	structural constituent of ribosome [GO:0003735]
SMU_1638c	0,958	0,740	Uncharacterized protein	Uncharacterized protein	53	-	-	-
SMU_1655c	0,870	0,732	Uncharacterized protein	Uncharacterized protein	46	-	-	-
SMU_1750c	0,978	0,750	Uncharacterized protein	Uncharacterized protein	36	-	-	-
SMU_1752c	0,981	0,746	Uncharacterized protein	Uncharacterized protein	56	-	-	-
SMU_1766c	0,978	0,742	Uncharacterized protein	Uncharacterized protein	50	-	-	-
SMU_1767c	0,981	0,745	Uncharacterized protein	Uncharacterized protein	63	-	-	-
SMU_1768c	0,984	0,651	Uncharacterized protein	Uncharacterized protein	101	-	-	-
SMU_1771c	0,987	0,709	Uncharacterized protein	Uncharacterized protein	102	-	-	-
SMU_1774c	0,832	0,612	Uncharacterized protein	Uncharacterized protein	85	-	-	-
SMU_1775c	0,953	0,750	Uncharacterized protein	Uncharacterized protein	59	-	-	-
SMU_1776c	0,954	0,698	Uncharacterized protein	Uncharacterized protein	81	regulation of transcription, DNA-templated [GO:0006355]	-	-
SMU_1792c	0,928	0,670	Uncharacterized protein	Uncharacterized protein	57	-	-	-
SMU_1804c	0,924	0,681	Uncharacterized protein	Uncharacterized protein	51	-	integral component of membrane [GO:0016021]	-
SMU_1808c	0,963	0,790	Putative integrase	Putative integrase	31	-	-	-
SMU_1813	0,948	0,657	Putative transposase	Putative transposase	36	-	-	-

SMU_1817c	0,966	0,626	Putative maturase-related protein	Putative maturase-related protein	68	-	-	-
SMU_1818c	0,974	0,627	Uncharacterized protein	Uncharacterized protein	57	-	-	-
SMU_1899	0,982	0,657	Putative ABC transporter, ATP-binding and permease protein.	Putative ABC transporter, ATP-binding and permease protein	41	-	-	ATP binding [GO:0005524]
SMU_1902c	0,951	0,690	Uncharacterized protein	Uncharacterized protein	47	-	-	-
SMU_1907	0,993	0,709	Uncharacterized protein	Uncharacterized protein	43	-	-	-
SMU_1908c	0,959	0,617	Uncharacterized protein	Uncharacterized protein	54	-	integral component of membrane [GO:0016021]	-
SMU_1912c	0,907	0,633	Uncharacterized protein	Uncharacterized protein	51	-	-	-
SMU_2048	0,819	0,626	Uncharacterized protein	Uncharacterized protein	50	-	-	-
SMU_2053c	0,929	0,703	Uncharacterized protein	Uncharacterized protein	30	-	integral component of membrane [GO:0016021]	-
SMU_2076c	0,991	0,682	Uncharacterized protein	Uncharacterized protein	42	-	-	-
SMU_2105	0,911	0,615	Uncharacterized protein	Uncharacterized protein	41	-	-	-
SMU_2124	0,978	0,748	Uncharacterized protein	Uncharacterized protein	65	-	-	-
SMU_2131	0,981	0,744	Uncharacterized protein	Uncharacterized protein	54	-	-	-
SMU_2136c	0,981	0,620	Uncharacterized protein	Uncharacterized protein	58	-	-	-