

***Salmonella* type III secretion effector SrfJ: a glucosylceramidase affecting the lipidome and the transcriptome of mammalian host cells**

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Supplementary files

Table S1. Lipid species with significantly different levels in the presence of SrfJ

<i>p</i> value	Fold change	Mean (SD) Control	Mean (SD) SrfJ	Mass	Retention time	ID
1.78E-16	11400	1.00 (0.00)	11400 (926)	688.6525	9.33	CE(22:1)
0.0499	6219.7	1.00 (0.00)	6220 (8242)	1025.8927	10.07	Cer(d30:1)
0.0497	0.00015461	6468 (7852)	1.00 (0.00)	1567.1508	7.25	CL(78:2)
0.0104	56672	1.00 (0.00)	56672 (69902)	435.3346	4.97	Heptadecanoyl carnitine
0.0481	2.0913	57908 (64327)	121103 (18838)	1025.2775	8.27	LacCer(d44:1(2OH))
0.0494	0.0000689	14510 (16613)	1.00 (0.00)	531.3772	0.9	LPC(20:1)
0.0101	352400	1.00 (0.00)	352403 (293808)	331.3229	2.36	LPE(2:0)
0.0493	15420	1.00 (0.00)	15420 (17045)	288.3026	0.93	MG(13:0)
0.00825	2.2399	11891 (23780)	26634 (10538)	804.2035	5.88	PA(44:6)
0.0496	17061	1.00 (0.00)	17061 (21850)	987.2195	8.29	PC(52:4)
0.0493	0.0000289	34599 (38083)	1.00 (0.00)	739.5423	7.09	PC(P-34:3)
0.00991	1.6788	9949 (19896)	16702 (4294)	677.5172	7.5	PE(31:0)
0.0495	12368	1.00 (0.00)	12368 (14743)	895.7634	9.89	PE(48:1)
0.0053	0.0000245	40783 (29492)	1.00 (0.00)	751.5478	7.51	PE(O-38:5)
0.0496	11351	1.00 (0.00)	11351 (14087)	762.545	8.88	PE(P-40:2)
0.00529	0.0001619	6177 (4234)	1.00 (0.00)	895.5632	7.77	PS(44:4)
0.0497	0.0000629	15897 (20229)	1.00 (0.00)	786.6563	8.11	SM(d40:1)
0.0494	4330.3	1.00 (0.00)	4330 (4875)	919.2997	9.43	TG(56:0)
0.0103	12072	1.00 (0.00)	12072 (11414)	914.8049	10.09	TG(56:2)
0.0498	11131	1.00 (0.00)	11131 (13860)	931.8561	10.55	TG(58:6)
0.0495	7027.2	1.00 (0.00)	7027 (8339)	1330.2275	10.68	TG(60:6)
0.0495	5873.2	1.00 (0.00)	5873 (6747)	994.3225	9.6	TG(62:4)
0.0102	13767	1.00 (0.00)	13767 (11703)	990.9064	10.39	TG(62:6)
0.006	0.00000441	226910 (277890)	1.00 (0.00)	2422.5576	10.06	Unknown
0.0053	0.00015721	6361 (4490)	1.00 (0.00)	230.0961	0.84	Unknown
0.0056	0.0000355	28193 (27142)	1.00 (0.00)	2466.6545	10.04	Unknown
0.0101	0.00018729	5339 (4204)	1.00 (0.00)	1051.743	0.91	Unknown
0.0102	0.0000609	16423 (13694)	1.00 (0.00)	1757.2122	0.9	Unknown
0.0102	0.0001324	7553 (6332)	1.00 (0.00)	616.4398	0.9	Unknown
0.0192	4.1139	6259 (15329)	25749 (13106)	1218.3748	9.98	Unknown
0.0332	0.30033	32401 (2637)	9731 (15111)	2666.6873	10.87	Unknown
0.0353	22840	1.00 (0.00)	22840 (17718)	2665.6724	10.87	Unknown
0.0353	46351	1.00 (0.00)	46351 (36025)	1963.527	9.51	Unknown

0.0356	177150	1.00 (0.00)	177153 (164451)	2398.612	10	Unknown
0.0377	0.36611	21463 (4728)	7858 (12183)	720.7758	7.33	Unknown
0.00397	17689	1.00 (0.00)	17689 (9488)	1156.3372	8.71	Unknown
0.00414	0.17838	34272 (3435)	6114 (14973)	1371.3169	9.3	Unknown
0.0453	3.1572	26471 (32099)	83575 (22538)	742.0622	6.96	Unknown
0.0461	0.46808	43864 (9499)	20532 (24620)	1450.3577	10.01	Unknown
0.0493	0.0000298	33532 (36788)	1.00 (0.00)	613.4736	0.91	Unknown
0.0493	0.0000746	13396 (14707)	1.00 (0.00)	1707.4868	9.83	Unknown
0.0493	0.0000778	12852 (14208)	1.00 (0.00)	1486.4329	9.52	Unknown
0.0493	2465.2	1.00 (0.00)	2465 (2715)	879.1064	0.9	Unknown
0.0493	4264.5	1.00 (0.00)	4264 (4679)	1119.3195	7.75	Unknown
0.0494	0.0000951	10518 (11765)	1.00 (0.00)	896.8426	10.38	Unknown
0.0494	4715.8	1.00 (0.00)	4716 (5287)	1157.9312	7.66	Unknown
0.0494	4817.5	1.00 (0.00)	4818 (5546)	1521.3494	10.29	Unknown
0.0494	5011	1.00 (0.00)	5011 (5749)	2134.552	10.21	Unknown
0.0494	8722.2	1.00 (0.00)	8722 (9979)	1509.02	0.9	Unknown
0.0494	10509	1.00 (0.00)	10509 (11699)	819.5858	0.93	Unknown
0.0494	19412	1.00 (0.00)	19412 (22111)	1039.321	8.48	Unknown
0.0494	21134	1.00 (0.00)	21134 (24081)	1021.2103	7.42	Unknown
0.0494	0.00022753	4395 (4852)	1.00 (0.00)	1489.4008	9.52	Unknown
0.0495	3046.8	1.00 (0.00)	3047 (3624)	942.8744	7.2	Unknown
0.0495	0.00015042	6648 (7733)	1.00 (0.00)	1888.3723	6.97	Unknown
0.0495	31044	1.00 (0.00)	31044 (37135)	405.2786	1.03	Unknown
0.0497	8050	1.00 (0.00)	8050 (10315)	1053.9314	10.24	Unknown
0.0498	15306	1.00 (0.00)	15306 (20090)	1325.2697	10.68	Unknown
0.00528	0.0000292	34290 (22915)	1.00 (0.00)	2578.6462	10.92	Unknown
0.00528	0.0000386	25884 (17526)	1.00 (0.00)	2591.6511	10.85	Unknown
0.00528	0.0000403	24786 (16535)	1.00 (0.00)	2115.4683	10.16	Unknown
0.00528	0.00010753	9300 (6250)	1.00 (0.00)	620.6424	10.5	Unknown
0.00534	0.0000444	22520 (18122)	1.00 (0.00)	1017.2298	7.27	Unknown
0.00536	0.0000104	96483 (80024)	1.00 (0.00)	2105.546	10.18	Unknown

CE: cholesterol ester; Cer: ceramide; CL: cardiolipin; LacCer: lactosylceramide; LPC: lysophosphatidylcholine; LPE: lysophosphatidyletanolamine; MG: monoacylglycerol; PA: phosphatidic acid; PC: phosphatidylcholine; PE: phosphatidyletanolamine; PS: phosphatidylserine; SM: sphingomyelin; TG: triacylglycerol.

Table S2. Differentially expressed genes in HeLa cells transfected with a plasmid expressing SrfJ compared to HeLa cells transfected with an empty vector

Gene symbol	Description	p value	Fold change (linear)
<i>TNFRSF9</i>	Tumor necrosis factor receptor superfamily, member 9	0.0025	-5.76
<i>CREB5</i>	Camp responsive element binding protein 5	0.0006	-5.3
<i>IFIT2</i>	Interferon-induced protein with tetratricopeptide repeats 2	1.19E-05	-5.26
<i>EGR1</i>	Early growth response 1	0.0313	-3.51
<i>IL6</i>	Interleukin 6	0.0022	-3.21
<i>IFIH1</i>	Interferon induced, with helicase C domain 1	3.21E-05	-2.84
<i>CLGN</i>	Calmegin	3.92E-05	-2.64
<i>CCL5</i>	Chemokine (C-C motif) ligand 5	0.0006	-2.61
<i>TNFAIP3</i>	Tumor necrosis factor, alpha-induced protein 3	0.0042	-2.49
<i>CYR61</i>	Cysteine-rich, angiogenic inducer, 61	0.0044	-2.47
<i>CHAC1</i>	Chac glutathione-specific gamma-glutamylcyclotransferase 1	0.0017	-2.34
<i>RELB</i>	V-rel avian reticuloendotheliosis viral oncogene homolog B	8.55E-05	-2.33
<i>CXCL8</i>	Chemokine (C-X-C motif) ligand 8	0.0013	-2.33
<i>ABCC9</i>	Transcript identified by aceview, Entrez Gene ID(s) 10060	0.0004	-2.32
<i>CYP39A1</i>	Cytochrome P450, family 39, subfamily A, polypeptide 1	0.0160	-2.28
<i>CLDN1</i>	Claudin 1	0.0052	-2.26
<i>MAP2K1</i>	Transcript identified by aceview, Entrez Gene ID(s) 5604	0.0472	-2.25
<i>TMEM200A</i>	Transmembrane protein 200A	0.0021	-2.18
<i>F3</i>	Coagulation factor III (thromboplastin, tissue factor)	0.0123	-2.18
<i>ANKRD6</i>	Ankyrin repeat domain 6	0.0036	-2.15
<i>KLF4</i>	Kruppel-like factor 4 (gut)	0.0035	-2.11
<i>OR51B4</i>	Olfactory receptor, family 51, subfamily B, member 4	0.0010	-2.07
<i>NOCT</i>	Nocturnin	0.0007	-2.07
<i>CXCL11</i>	Chemokine (C-X-C motif) ligand 11	0.0014	-2.05
<i>BACH2</i>	Memczak2013 ALT_ACCEPTOR, ALT_DONOR, coding, INTERNAL, intronic best transcript NM_001170794	0.0035	-2.05
<i>DDIT3</i>	DNA-damage-inducible transcript 3	0.0008	-2.04
<i>OR4K5</i>	Olfactory receptor, family 4, subfamily K, member 5	0.0196	-2.03

<i>GBP5</i>	Guanylate binding protein 5	0.0083	-2.02
<i>OIT3</i>	Oncoprotein induced transcript 3	0.0002	-2.02
<i>MMP19</i>	Matrix metalloproteinase 19	0.0039	-2.02
<i>L3MBTL1</i>	L(3)mbt-like 1 (Drosophila)	0.0101	-2
<i>PLD1</i>	Phospholipase D1, phosphatidylcholine-specific	0.0025	2.06
<i>ZKSCAN4</i>	Zinc finger with KRAB and SCAN domains 4	0.0022	2.07
<i>RAB26</i>	RAB26, member RAS oncogene family	0.0100	2.08
<i>VPS35</i>	Retromer complex component	0.0069	2.12
<i>PK4</i>	Pyruvate dehydrogenase kinase, isozyme 4	0.0057	2.13
<i>KPNA7</i>	Karyopherin alpha 7 (importin alpha 8)	0.0116	2.18
<i>HPGD</i>	Hydroxyprostaglandin dehydrogenase 15-(NAD)	0.0024	2.22
<i>TUBGCP3</i>	Memczak2013 ANTISENSE, coding, INTERNAL, intronic best transcript NM_006322	0.0129	2.24
<i>TTL1</i>	Tubulin tyrosine ligase-like family member 1	0.0086	2.25
<i>METTL7A</i>	Methyltransferase like 7A	0.0296	2.25
<i>VIT</i>	Vitrin	0.0126	2.49
<i>ABCA1</i>	ATP binding cassette subfamily A member 1	0.0010	2.56
<i>ELF3</i>	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	0.0017	2.8
<i>CD180</i>	CD180 molecule	0.0054	2.99

Table S3. Differentially expressed genes in RAW264.7 cells infected with wild-type *S. enterica* serovar Typhimurium compared to cells infected with a *srfJ* mutant

Gene symbol	Description	<i>p</i> value	Fold change (linear)
<i>IL1A</i>	Interleukin 1 alpha	2.95E-05	-3.02
<i>XAF1</i>	XIAP associated factor 1	1.50E-05	-2.92
<i>IL1B</i>	Interleukin 1 beta	8.81E-05	-2.65
<i>CD46</i>	CD46 antigen, complement regulatory protein	0.0017	-2.61
<i>SERPINB2</i>	Serine (or cysteine) peptidase inhibitor, clade B, member 2	5.50E-05	-2.56
<i>UPP1</i>	Uridine phosphorylase 1	0.0004	-2.51
<i>IRF7</i>	Interferon regulatory factor 7	0.0010	-2.48
<i>TM4SF1</i>	Transmembrane 4 superfamily member 1	0.0017	-2.46
<i>OLFR391-PS</i>	Olfactory receptor 391, pseudogene	0.0028	-2.43
<i>USP18</i>	Ubiquitin specific peptidase 18	0.0273	-2.38
<i>ISG20</i>	Interferon-stimulated protein	0.0005	-2.35
<i>EFCAB8</i>	EF-hand calcium binding domain 8	0.0421	-2.33
<i>TMED11</i>	Transmembrane emp24 protein transport domain containing	0.0265	-2.26
<i>GBP2</i>	Guanylate binding protein 2	0.0003	-2.26
<i>LRRC18</i>	Leucine rich repeat containing 18	0.0015	-2.25
<i>OLFR1082</i>	Olfactory receptor 1082	0.0165	-2.25
<i>OLFR902</i>	Olfactory receptor 902	0.0445	-2.2
<i>TCF7L2</i>	Transcription factor 7 like 2, T cell specific, HMG box	0.0016	-2.19
<i>GSTP2</i>	Glutathione S-transferase, pi 2	0.0099	-2.16
<i>FAM107B</i>	Family with sequence similarity 107, member B	0.0101	-2.16
<i>GPR55</i>	G protein-coupled receptor 55	0.0018	-2.16
<i>SLY</i>	Sycp3 like Y-linked	0.0347	-2.15
<i>RMDN2</i>	Regulator of microtubule dynamics 2	0.0065	-2.15
<i>CCL5</i>	Chemokine (C-C motif) ligand 5	0.0026	-2.15
<i>CCRL2</i>	Chemokine (C-C motif) receptor-like 2	0.0069	-2.13
<i>MMP8</i>	Matrix metalloproteinase 8	9.71E-05	-2.12
<i>GLT1D1</i>	Glycosyltransferase 1 domain containing 1	0.0413	-2.11
<i>LACC1</i>	Laccase (multicopper oxidoreductase) domain containing 1	0.0442	-2.1
<i>IL12B</i>	Interleukin 12b	0.0268	-2.1
<i>SULT1E1</i>	Sulfotransferase family 1E, member 1	0.0015	-2.1

<i>ZFP936</i>	Zinc finger protein 936	0.0298	-2.09
<i>U90926</i>	Cdna sequence U90926	0.0003	-2.09
<i>CD69</i>	CD69 antigen	0.0076	-2.05
<i>CBLN1</i>	Cerebellin 1 precursor protein	0.0006	-2.05
<i>LRRC16A</i>	Leucine rich repeat containing 16A	0.0071	-2.03
<i>CLEC2D</i>	C-type lectin domain family 2, member d	0.0280	-2.02
<i>MARCO</i>	Macrophage receptor with collagenous structure	0.0010	-2
<i>ABCC2</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	0.0026	2.01
<i>PCYT1B</i>	Phosphate cytidylyltransferase 1, choline, beta isoform	0.0262	2.03
<i>NHLH2</i>	Nescient helix loop helix 2	0.0405	2.04
<i>PRLH</i>	Prolactin releasing hormone	0.0027	2.04
<i>TSPAN6</i>	Tetraspanin 6	0.0095	2.04
<i>CCDC154</i>	Coiled-coil domain containing 154	0.0113	2.04
<i>SERPINA1A</i>	Serine (or cysteine) peptidase inhibitor, clade A, member 1A	0.0120	2.04
<i>OLFR1480</i>	Olfactory receptor 1480	0.0259	2.06
<i>GAL3ST2</i>	Galactose-3-O-sulfotransferase 2	0.0058	2.07
<i>SULT3A1</i>	Sulfotransferase family 3A, member 1	0.0129	2.1
<i>GIMAP3</i>	Gtpase, IMAP family member 3	0.0084	2.11
<i>TTLL11</i>	Tubulin tyrosine ligase-like family, member 11	0.0159	2.11
<i>OLFR259</i>	Olfactory receptor 259	0.0065	2.11
<i>OLFR1026</i>	Olfactory receptor 1026	0.0490	2.13
<i>ATAD5</i>	Atpase family, AAA domain containing 5	0.0316	2.14
<i>SPIN2E</i>	Spindlin family, member 2E	0.0125	2.14
<i>KPTN</i>	Kaptin	0.0480	2.16
<i>OLFR199</i>	Olfactory receptor 199	0.0032	2.18
<i>CNBD1</i>	Cyclic nucleotide binding domain containing 1	0.0339	2.18
<i>OLFR924</i>	Olfactory receptor 924	0.0073	2.19
<i>CHRD1</i>	Chordin-like 1	0.0041	2.26
<i>B3GALT1</i>	UDP-Gal:betaglcnac beta 1,3-galactosyltransferase, polypeptide 1	0.0317	2.27
<i>VCAN</i>	Versican	0.0299	2.29
<i>VMN2R17</i>	Vomer nasal 2, receptor 17	0.0022	2.31
<i>ATP2C2</i>	ATPase, Ca++ transporting, type 2C, member 2	0.0029	2.36

<i>RBBP9</i>	Retinoblastoma binding protein 9	0.0032	2.37
<i>DUSP21</i>	Dual specificity phosphatase 21	0.0292	2.44
<i>VMN1R54</i>	Vomeronasal 1 receptor 54	0.0118	2.53
<i>LCE1C</i>	Late cornified envelope 1C	0.0284	2.58
<i>IPW</i> ; <i>SNORD116</i>	Imprinted gene in the Prader-Willi syndrome region; small nucleolar RNA, C/D box 116 cluster	0.0002	2.97
<i>MUP19</i>	Major urinary protein 19	0.0372	3.05

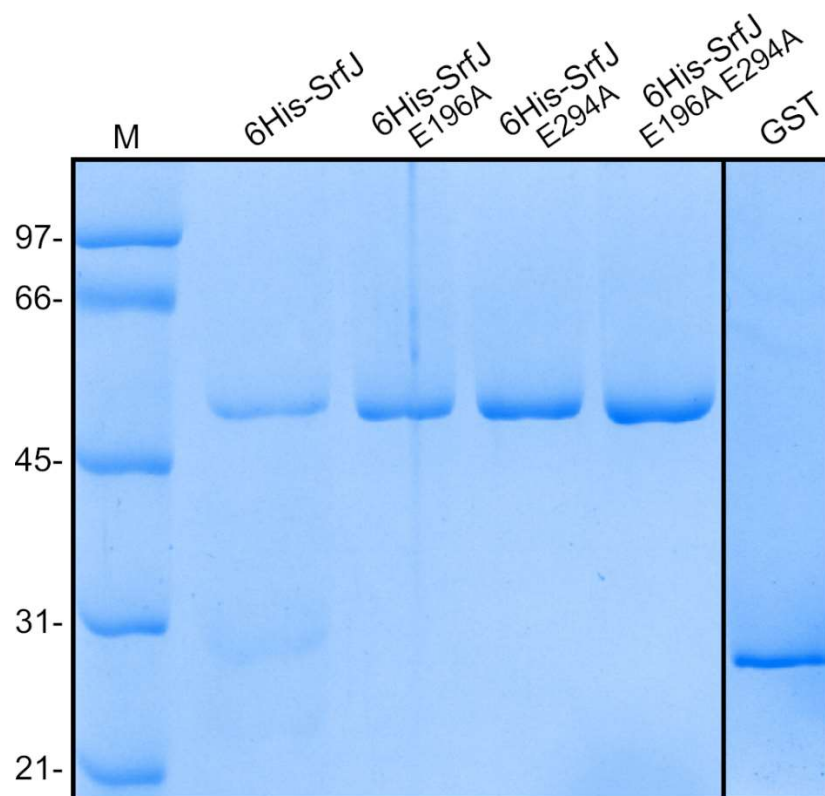


Figure S1. Purified proteins used in the experiment shown in Figure 1. SDS-polyacrylamide gel electrophoresis analysis of purified GST, 6His-SrfJ and derived mutated forms of this protein. The gel was stained with Coomassie blue. M, molecular weight markers in kDa.