SUPPLEMENTARY MATERIALS

Table S1. Primers used in this study.

Gene	Locus Tag	Forward Primer (5’→3’)	Reverse Primer Sequence (5’→3’)
Complementation:			
aprE and *tolC*	SCBI_3625	CAGGCCATTACGTTCCTTAAAC	CTTGGGTGGCTTCTCGTTAT
gidA	SCBI_4598	CACCGATCATTCACAGCAAAC	GCGAGCAGCGAGTCTTAAT
MCP II	SCBI_0077	GTGTGGGAACACGCTTACTA	GCACTGATTTGGTGGCTTAAA
PIN protein	SCBI_0044	GTCAAGCAGTCTCTCGCTATC	CTGTCTTACGCCACCGTATATC
qRT-PCR:			
l21p	SCBI_0382	GGTGGTAAACAACACCGAGTAA	CGCCATTAGCGATCATCAGAA
*prtA*1	SCBI_0187	CTGTAGACGACCTGTTGCATTA	GGTTTGGTTCTCACGGGTAATA
*prtA*2	SCBI_1952	CCACAGCCTGATGAGCTATTT	GGATCGCCGTGATGTCATT
*prtA*3	SCBI_2172	TCCGCGATAACTTCAGCTTA	TTTGCGTCAGGAAGGAATAGG
*prtA*4	SCBI_3084	CCTCGTATGAAAGTACGCAGAG	CCTCGTATGAAAGTACGCAGAG
Serine protease 1	SCBI_4441	GTGTCGGACTACGGCAATAA	TTCAGCAAGTCGGCAATCT
Serine protease 2	SCBI_4442	AGCATCAGCACCTTCTCTTC	CCTTCAATCACCGAGCTGTAT
yfgC	SCBI_3465	TGCAGTCTTCGCAGGATTAC	CAGCTCTTCATTCAGGCCATA
Metalloprotease	SCBI_3545	GACGAGGCCTACGACTATCT	AGCGGCAGCCCTTTATTATC
ImpD	SCBI_2996	GTTTCGCATGGTGAGCAATAAG	CTGACCCTGGCCTGATTTAC
CcmC	SCBI_3334	CTCGGCTATCTGCTGTTGTT	TCATGACTGACGCTCCTTATTC
Bleomycin resist.	SCBI_1742	TGCCGGATGAGAACGAATG	GGTAGCCATCAGGATCTTCAAA
FliZ	SCBI_2727	GTTCGAACAGACCGAGATGAG	AAACTTGTCTGCCGGGTAAT

Table S2. Protease genes analyzed by qRT-PCR

Gene	**Locus Tag**	**Gene Size (bp)**	**Species Containing Homologues***
*prtA*1	SCBI_0187	1,515	*Serratia* spp.
*prtA*2	SCBI_1952	1,419	*S. marcescens, Photorhabdus* spp., *Xenorhabdus nematophila*
*prtA*3	SCBI_2172	1,617	*Serratia* spp., *Dickeya* spp., *Erwinia* spp.
*prtA*4	SCBI_3084	1,383	*Serratia* spp., *Dickeya* spp.
Serine protease 1	SCBI_4441	3,093	*Serratia* spp., *Cronobacter* spp., *Xenorhabdus* spp., *Pseudomonas* spp.
Serine protease 2	SCBI_4442	3,024	*Serratia* spp., *Cronobacter* spp., *Xenorhabdus* spp., *Pseudomonas* spp.
yfgC	SCBI_3465	1,470	*Serratia* spp., *Yersinia* spp., *Rahnella* spp., *Erwinia* spp., *Edwardsiella* spp., *Citrobacter* spp., *Salmonella enterica*
Metalloprotease	SCBI_3545	1,026	*Serratia* spp., *Rahnella* spp., *Enterobacter* spp., *Cronobacter* spp., *Pantoea* spp., *Salmonella enterica, Klebsiella oxytoca*

*As determined by BlastX, cutoff ≥50% identity.

Table S3. List of all genes significantly up-regulated ≥1.5-fold (p-value <0.05) in mutant 16-D2 compared to wild-type *Serratia* sp. SCBI as determined with RNA-seq.

Locus Tag	**Gene**	**Fold Change**
Defense Mechanisms		
SCBI_2967	ABC-type bacteriocin/antibiotic exporter	4.04
Intracellular Trafficking/Secretion		
SCBI_4445	P pilus assembly/Cpx signaling pathway	1.78
SCBI_0966	Type II secretory pathway, PulC component	5.86
Signal Transduction		
SCBI_2980	Response regulator - CheY-like receiver domain, HTH DNA-binding domain	14.69
SCBI_2906	Colanic acid capsular biosynthesis activation protein A	1.54
Function Unknown		
SCBI_0066	Fic family protein	3.51*
SCBI_2995	Hypothetical	18.38
SCBI_2986	Hypothetical	12.06
SCBI_2996	Hemolysin-coregulated hypothetical protein	10.37
SCBI_2997	Hypothetical	10.17
SCBI_1234	3-Demethylubiquinone-9-3-methyltransferase	9.56
SCBI_2994	Type VI secretion protein	9.26
SCBI_2998	Hypothetical	8.73
SCBI_1189	Hypothetical	7.97
SCBI_1197	Hypothetical	7.87
SCBI_2990	Hypothetical	7.29
SCBI_4194	Hypothetical	7.24
SCBI_2985	Hypothetical	7.13
SCBI_2999	Hypothetical	6.73
SCBI_2620	Hypothetical	6.55
SCBI_2984	Type VI secretion protein IcmF	5.62
SCBI_3391	Hypothetical	4.42
SCBI_0518	Hypothetical	2.62
SCBI_3622	Hypothetical	2.26
SCBI_1730	Acyltransferase	2.10
SCBI_4667	GidA - plasmid	2.05
General Functional Prediction Only		
SCBI_0907	Plasmid maintenance system antidote protein YddM	12.84

SCBI_2974	PhoPQ-activated pathogenicity-related protein	9.82
SCBI_1391	Sulfite oxidase	8.14
SCBI_0049	Putative homoserine kinase type II	5.38
SCBI_2351	6-Phosphogluconolactonase	5.02
SCBI_1806	Amidohydrolase	4.67
SCBI_1310	Plasmid stabilization protein	4.31
SCBI_2273	NADPH-quinone reductase, modulator of drug activity	4.18
SCBI_2260	Oxidoreductase	3.81
SCBI_1734	Periplasmic lipoprotein	3.23
SCBI_2048	Cysteine desufuration protein SufE	3.19
SCBI_0411	Hydrolase	2.78
SCBI_0185	Plasmid stabilization protein	2.12
SCBI_0044	Predicted nucleic acid binding protein, contains PIN domain	1.75
Secondary Metabolite Biosynthesis/Transport/Catabolism		
SCBI_1193	Biotin synthesis protein BioC	5.26
SCBI_2930	Phenylacetic acid degradation protein PaaD	10.65
SCBI_1177	Isochorismatase hydrolase	9.12
SCBI_1289	Isochorismatase hydrolase	3.43
SCBI_3084	Serralysin - PrtA4 homolog	2.32
Inorganic Ion Metabolism/Transport		
SCBI_0727	Adenylylsulfate kinase	10.88
SCBI_2034	Hemin uptake protein	6.46
SCBI_2406	Membrane transporters of cations and cationic drugs	5.52
SCBI_1127	Potassium-transporter ATPase protein	5.04
SCBI_1422	Carbonic anhydrase	4.97
SCBI_0987	Periplasmic solute (metal ion) binding protein/adhesin	3.11
SCBI_0015	ABC-type phosphate transporter system, ATP-binding protein	2.79
Chaperones		
SCBI_2993	Clp ATPase	7.86
SCBI_2044	Cysteine desufuration protein SufB	2.10
Cell Motility		
SCBI_0297	Pilus assembly protein, porin PapC	3.46*
SCBI_2973	P pilus assembly protein, pilin FimA	27.94
SCBI_2971	P pilus assembly protein, porin PapC	6.52
SCBI_2970	P pilus assembly protein, pilin FimA	6.00
SCBI_2972	P pilus assembly protein, chaperone PapD	5.93
SCBI_1959	P pilus assembly protein, porin PapC	3.32
SCBI_0304	Fimbrial protein YfcQ	6.49*

SCBI_0978	Type VI secretory pathway, prepilin signal peptidase PulO	5.77
Cell Wall/Membrane/Envelope Biogenesis		
SCBI_2365	Cell wall-associated hydrolases (invasion-associated proteins)	5.88
SCBI_2968	Microcin H47 secretion protein	3.88
SCBI_0052	Biotin carboxylase	3.33
SCBI_2056	Cyclopropane fatty acyl phospholipid synthase	1.97
SCBI_0979	Pullalanase-specific type II secretion system outer membrane lipoprotein	5.73
SCBI_3312	OM lipoprotein	3.59
Replication/Repair/Recombination		
SCBI_1954	Hypothetical	8.95
SCBI_2367	Oxidative damage repair enzyme NudI	3.79
SCBI_0474	Transposase IS3/IS911 family	6.63*
SCBI_2789	DNA polymerase II subunit beta	2.20
Transcription		
SCBI_0199	GCN5-like N-acetyltransferase	4.27*
SCBI_1369	Histone acetyltransferase HPA2	5.68
SCBI_0214	LysR family transcriptional regulator	3.79*
SCBI_0517	AraC family transcriptional regulator	42.36
SCBI_2455	Transcriptional regulator	5.12
SCBI_1782	LysR family transcriptional regulator	2.21
SCBI_3467	DNA-binding protein	3.20
Lipid Metabolism/Transport		
SCBI_0509	3-Oxoacid CoA-transferase subunit B	21.10
SCBI_2928	Enoyl-CoA hydratase	3.85
SCBI_2736	ACP phosphodiesterase	3.39
SCBI_2927	Enoyl-CoA hydratase	2.43
Coenzyme Metabolism/Transport		
SCBI_2932	Coenzyme F390 synthetase	2.59
SCBI_4021	3,4-dihydroxy-2-butanone 4-phosphate synthase	2.34
Carbohydrate Metabolism/Transport		
SCBI_2167	Thermophilic glucose-6-phosphate isomerase	4.76
SCBI_1243	Permease of drug/metabolite transporter (DMT) superfamily	9.97
SCBI_0116	Sugar phosphate permease	3.39*
SCBI_0483	Cryptic 6-phosphobetaglucosidase	3.28*

SCBI_0206	ABC-type sugar transport system, periplasmic component - glycerol	2.29*
Amino Acid Metabolism/Transport		
SCBI_0017	ABC transporter substrate-binding protein - amino acid transport	2.96*
SCBI_0795	ABC-type amino acid transport, substrate-binding protein	6.26
SCBI_2224	ABC-type amino acid transport, substrate-binding protein	4.00
SCBI_0725	Sulfate adenylyltransferase subunit 2	12.14
SCBI_0048	Cys/Met metabolism pyridoxal-phosphate-dependent enzyme	11.87*
SCBI_0526	Amino acid transporter system - permease	11.23
SCBI_0801	Putative threonine efflux protein	7.61
SCBI_1506	Putative agmatinase	5.42
SCBI_1272	Threonine efflux protein	5.08
SCBI_2641	Glutathione transferase	4.38
SCBI_0412	Chorismate mutase	3.23
SCBI_1556	ABC-type spermidine/putrescine transport system, permease component	3.12
SCBI_1555	ABC-type spermidine/putrescine transport system, ATP-binding subunit	3.08
SCBI_2935	Amino acid permease	2.29
Cell Cycle Control/Mitosis		
SCBI_1311	Antitoxin - prevent host death family protein	3.97
Entergy Production/Conversion		
SCBI_1662	Acylphosphatase	9.23
SCBI_1951	Citrate carrier protein	4.41
No COG Assigned		
SCBI_0320	Entericidin EcnAB	7.19*
SCBI_0478	Hypothetical	4.19*
SCBI_0306	Hypothetical	4.28*
SCBI_1912	Hypothetical	33.15
SCBI_2979	Hypothetical	15.66
SCBI_2983	Hypothetical	10.72
SCBI_2334	Hypothetical	9.19
SCBI_2988	Hypothetical	8.38
SCBI_1742	Glyoxalase/bleomycin resistance protein/dioxygenase	8.11
SCBI_2969	ABC transporter membrane protein	8.08
SCBI_2975	Hypothetical	7.64
SCBI_1821	Hypothetical	7.47

SCBI_2982	Hypothetical	7.32
SCBI_2976	Hypothetical	7.24
SCBI_2981	Hypothetical	7.05
SCBI_1042	Hypothetical	6.29
SCBI_0844	Hypothetical	5.88
SCBI_0519	Hypothetical	5.57
SCBI_0354	Hypothetical	5.45
SCBI_2754	Hypothetical	4.86
SCBI_0124	Cellulose biosynthesis operon protein BcsF/YhjT	4.50
SCBI_0884	Hypothetical	4.40
SCBI_2755	Hypothetical	3.79
SCBI_1393	Hypothetical	3.73
SCBI_2808	Hypothetical	3.62
SCBI_3526	Hypothetical	3.47
SCBI_3531	Extracellular serine protease	3.45
SCBI_2790	Hypothetical	3.44
SCBI_2753	Hypothetical	3.29
SCBI_3642	Hypothetical	2.93
SCBI_0047	Hypothetical	2.87
SCBI_2286	Hypothetical	2.78
SCBI_0365	Hypothetical	2.37
SCBI_3798	Hypothetical	2.32
SCBI_2305	Transposase IS3 family	1.76

*Original value was infinity.

Table S4. List of all genes significantly down-regulated > -1.5-fold (p-value <0.05) in mutant 16-D2 compared to wild-type *Serratia* sp. SCBI as determined with RNA-seq.

Locus Tag	**Gene**	**Fold Change**
Defense Mechanisms		
SCBI_2137	ABC-type multidrug transport system, ATPase protein	-11.26
Intracellular Trafficking/Secretion		
SCBI_3748	Type II secretory pathway PulJ component	-3.87
Function Unknown		
SCBI_0219	DedA family protein (membrane)	-18.61
SCBI_3343	CsbD family protein	-9.77
SCBI_3000	Membrane protein	-3.88
SCBI_3130	Hypothetical	-1.60
General Function Prediction Only		
SCBI_0440	NADPH-quinone reductase	-11.31
SCBI_1229	Transcriptional regulator ThiJ/PfpI	-10.85
SCBI_0434	Permease	-8.87
SCBI_3231	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	-5.06
SCBI_3045	Permease	-4.56
SCBI_4386	Inositol 2-dehydrogenase	-3.95
SCBI_0043	Permease	-2.17
Secondary Metabolite Biosynthesis/Transport/Catabolism		
SCBI_2339	Isochorimatase hydrolase	-5.52
Inorganic Ion Metabolism/Transport		
SCBI_4319	Nitrite reductase ferredoxin subunit	-2.76
SCBI_0700	ABC-type Fe3+-hydroxamate transport system, periplasmic component	-2.99
Chaperones		
SCBI_3334	Heme exporter protein CcmC	-4.68
SCBI_0414	Peptidase U32	-3.79
SCBI_3332	Cytochrome c-type biogenesis protein CcmE	-3.18
Cell Motility		
SCBI_4404	FimA	-4.00

SCBI_0160	Periplasmic lipoprotein	-2.82
Cell Wall/Membrane/Envelope Biogenesis		
SCBI_1720	NodT family RND efflux system OM lipoprotein	-3.04
SCBI_0152	Teichoic acid biosynthesis protein	-2.53
SCBI_1252	D-alanine ligase	-2.00
SCBI_0010	N-acetylglucosamine-1-phosphate uridyltransferase	-1.93
Replication/Repair/Recombination		
SCBI_0021	Hypothetical	-4.18
SCBI_4070	Hypothetical	-5.80
SCBI_2130	DNA replication terminus site-binding protein	-4.23
SCBI_2586	Holliday junction DNA helicase RuvB	-2.45
SCBI_0574	DNA polymerase III subunit psi	-2.26
Transcription		
SCBI_1829	Transcriptional activator DcuR	-6.23
SCBI_3059	Response regulator - citrate/malate metabolism	-4.44
SCBI_1277	Histone acetyltransferase HPA2	-4.93
SCBI_2370	MocR family transcriptional regulator	-3.13
SCBI_0515	AraC-type DNA binding protein	-18.37
SCBI_3185	Transcriptional regulator	-11.05
SCBI_0092	AraC-type DNA binding protein	-10.38
SCBI_1739	Transcriptional regulator ArsR	-8.63
SCBI_2939	LysR family transcriptional regulator	-5.36
SCBI_3459	Transcriptional regulator	-3.22
SCBI_3462	AsnC family transcriptional regulator	-3.19
SCBI_0794	RpiR family transcriptional regulator	-3.10
SCBI_1123	PadR family transcriptional regulator	-2.84
Translation/Ribosomal Structure		
SCBI_0606	rRNA methylase	-2.72
SCBI_0399	Ribosome-binding factor A	-1.80
Lipid Metabolism/Transport		
SCBI_0513	3-Hydroxybutyrate dehydrogenase	-4.20
SCBI_3046	2,3-Dihydroxybenzoate 2,3-dehydrogenase	-3.26
SCBI_2459	Membrane-associated phospholipid phosphatase	-4.55
Coenzyme Metabolism/Transport		
SCBI_3232	2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylic-acid synthase	-4.30
SCBI_2136	Dethiobiotin synthetase	-2.89

SCBI_3230	Dihydroxynaphthoic acid synthase	-2.76
SCBI_3914	Ketopantoate hydroxymethyltransferase	-2.74
SCBI_4524	2-Amino-3-ketobutyrate coenzyme A ligase	-1.86
Carbohydrate Metabolism/Transport		
SCBI_3573	Putative 3-phenylpropionic acid transporter	-3.60
SCBI_1386	Aldolase	-5.72
SCBI_4429	Ribose/xylose/arabinose ABC transport system, ATPase	-3.85
SCBI_3829	Ribose/xylose/arabinose ABC transport system, inner membrane translocator	-3.82
SCBI_1173	Galactosemutarotase	-3.46
SCBI_4394	Xylose isomerase	-3.41
SCBI_3264	Transketolase	-3.16
SCBI_0394	Phosphoglucosamine mutase	-1.85
SCBI_0373	Fructose 1,6-bisphosphatase	-1.67
SCBI_4505	Triosephosphate isomerase	-1.48
Nucleotide Metabolism/Transport		
SCBI_0452	Aspartate carbamoyltransferase catalytic subunit	-3.23
SCBI_4136	Inosine-uridine nucleoside N-ribohydrolase	-2.45
SCBI_0362	2',3'-cyclic-nucleotide 2'-phosphodiesterase	-2.44
SCBI_0451	Aspartate carbamoyltransferase	-2.11
SCBI_3473	Phosphoribosylaminoimidazole (AIR) synthetase	-2.07
SCBI_3474	Phosphoribosylglycin amide formyltransferase	-1.89
SCBI_3451	Phosphoribosylaminoimidazole-succinocarboxamide synthase	-1.65
Amino Acid Metabolism/Transport		
SCBI_0525	Peptidase S58 DmpA	-9.14
SCBI_4462	Acetolactate synthase 2 catalytic subunit	-3.42
SCBI_0630	Carbamoyl phosphate synthase large subunit	-1.75
SCBI_0178	Anaerobic glycerol-3-phosphate dehydrogenase	-17.55
SCBI_2212	Spermidine synthase-like protein	-6.13
SCBI_4387	Acetolactate synthase	-4.85
SCBI_0799	Class V aminotransferase	-3.51
SCBI_1882	Peptidase T	-2.04
SCBI_3574	Glycine/serine hydroxymethyltransferase	-1.55
Energy Production/Conversion		
SCBI_2681	Nitrate reductase molybdenum cofactor assembly chaperone	-14.68
SCBI_3694	Cytochrome C class I	-9.61
SCBI_3196	NAD-dependent aldehyde dehydrogenase	-9.08

SCBI_4392	NAD-dependent aldehyde dehydrogenase	-3.34
SCBI_3029	Nitroreductase	-3.05
SCBI_4339	Phosphoenolpyruvate carboxykinase	-2.27
SCBI_0827	Ubiquinone oxidoreductase subunit NqrD	-1.93
SCBI_0823	Ubiquinone oxidoreductase subunit NqrA	-1.83
SCBI_3155	NapC/NirT cytochrome c protein	-1.82
SCBI_0826	Ubiquinone oxidoreductase subunit NqrC	-1.81
No COG Assigned		
SCBI_4188	Phage shock protein G	-8.14
SCBI_1948	Hypothetical	-6.89
SCBI_1257	Hypothetical	-6.85
SCBI_4134	Hypothetical	-6.80
SCBI_2897	Hypothetical	-5.56
SCBI_4552	Hypothetical	-4.40
SCBI_2644	Hypothetical	-3.81
SCBI_1264	Hypothetical	-3.26
SCBI_3749	Hypothetical	-3.26
SCBI_1377	Adenylate kinase	-3.18
SCBI_4308	Hypothetical	-2.03
SCBI_1887	Colicin-D immunity protein	-1.94
SCBI_2635	Hypothetical	-1.52

Table S5. List of all genes significantly up-regulated $\geq$ 1.5-fold (p-value <0.05) in mutant 22-C7 compared to wild-type *Serratia* sp. SCBI as determined with RNA-seq.

Locus Tag	Gene	Fold Change
Defense Mechanisms		
SCBI_3535	ABC-type bacteriocin/lantibiotic exporter protein	3.00
Signal Transduction		
SCBI_3135	DNA polymerase II subunit beta	4.52
SCBI_2980	Response regulator with CheY domain, HTH DNA-binding domain	2.97
SCBI_3212	Response regulator with CheY domain, HTH DNA-binding domain	1.79
SCBI_0605	Response regulator with CheY domain, winged helix DNA-binding domain	1.57
SCBI_1671	Response regulator - LuxR family	4.30
SCBI_3609	Anti-RNA polymerase sigma factor SigE	2.00
SCBI_3608	Anti-sigma E factor	1.58
SCBI_2382	Fumarate/nitrate reduction transcriptional regulator	1.48
Function Unknown		
SCBI_0448	Hypothetical	3.22*
SCBI_1197	Hypothetical	10.58
SCBI_1296	Hypothetical	10.50
SCBI_1189	Hypothetical	6.87
SCBI_2093	Hypothetical	6.28
SCBI_3391	Hypothetical	5.01
SCBI_2995	Hypothetical	4.48
SCBI_2999	Hypothetical	3.47
SCBI_0601	Inosine/xanthosine triphosphatase	3.24
SCBI_2986	Hypothetical	3.09
SCBI_3637	Hypothetical	2.77
SCBI_2994	Type VI secretion protein	2.76
SCBI_3834	Hypothetical	2.38
SCBI_4566	Hypothetical	2.13
SCBI_0182	Hypothetical	2.12
SCBI_1658	Hypothetical	2.11
SCBI_3835	Hypothetical	1.52
General Function Prediction Only		
SCBI_0907	Plasmid maintenance system antidote protein	10.74

SCBI_0768	Phage-related lysozyme	9.87
SCBI_1391	Sulfite oxidase	7.79
SCBI_1806	Amidohydrolase	7.55
SCBI_1310	Plasmid stabilization protein	6.31
SCBI_0423	Metal-dependent hydrolase of beta-lactamase superfamily	4.39
SCBI_4365	L-ascorbate 6-phosphate lactonase	3.24
SCBI_1919	Gfa-like protein	2.92
SCBI_4048	Plasmid maintenance XRE family antidote protein	2.35
SCBI_3255	5'-nucleotidase	2.03
SCBI_1344	5'-nucleotidase	1.88
SCBI_0339	RNA-binding protein Hfq	1.64
SCBI_0403	Lipoprotein NlpI	1.63
SCBI_1156	Acyl-CoA thioesterase YbgC	1.60
SCBI_1117	Fe2+/Zn2+ uptake protein	1.51
SCBI_0340	GTPase	1.48
Secondary Metabolite Biosynthesis/Transport/Catabolism		
SCBI_1177	Isochorismatase hydrolase	7.33
Inorganic Ion Metabolism/Transport		
SCBI_0500	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	4.76*
SCBI_0985	ABC-type Mn/Zn transport system, ATPAse component	6.81
SCBI_0959	Ammonia permease	6.47
SCBI_0983	Hha toxicity attenuator	1.91
SCBI_0639	CO2+/Mg2+ efflux protein ApaG	1.54
Cell Motility		
SCBI_0301	P pilus assembly protein, pilin FimA	3.04*
SCBI_0297	P pilus assembly protein, porin PapC	3.67*
SCBI_0296	P pilus assembly protein, pilin FimA	8.98*
Cell Wall/Membrane/Envelope Biogenesis		
SCBI_2365	Cell wall-associated hydrolase (invasion-associated protein)	3.80
SCBI_0052	Biotin carboxylase	2.33
SCBI_0783	Membrane-bound lytic murein transglycosylase D	2.31
SCBI_3208	OM protein C	2.15
SCBI_2655	Porin	2.10
SCBI_4160	Lipid A biosynthesis palmitoleoylacyltransferase	2.07
SCBI_1161	OM peptidoglycan-associated protein	1.34
SCBI_3312	OM lipoprotein	3.19

Replication/Repair/Recombination		
SCBI_0930	Exonuclease VII small subunit	3.77
SCBI_4560	Transposase for insertion element IS1669	2.01
SCBI_4660	Hypothetical	1.89
SCBI_4239	DNA topoisomerase type IA zn finger domain protein	1.76
Transcription		
SCBI_0199	Histone acetyltransferase HPA2	3.48*
SCBI_3442	Histone acetyltransferase HPA2	2.39
SCBI_0214	LysR family transcriptional regulator	8.23*
SCBI_0963	DNA-binding winged-HTH domain protein	14.30
SCBI_1334	Transcriptional regulator	3.28
SCBI_3139	Transcriptional regulator	3.25
SCBI_2846	LysR family transcriptional regulator	3.11
SCBI_3467	DNA-binding protein	2.94
SCBI_3610	RNA polymerase sigma factor RpoE	1.90
SCBI_0196	RNA polymerase factor sigma-32	1.89
SCBI_2463	CysB transcriptional regulator	1.71
SCBI_3253	DNA-binding transcriptional repressor LrhA	1.64
Translation/Ribosomal Structure		
SCBI_1585	Translation initiation factor 1	2.42
SCBI_4102	Ribosome hibernation promoting factor HPF	1.92
SCBI_3621	Small protein A (tmRNA-binding protein)	1.92
SCBI_0382	Ribosomal protein L21	1.89
SCBI_0619	Ribosomal protein S20	1.66
Coenzyme Metabolism/Transport		
SCBI_0025	Phosphopantetheinyl transferase	3.71*
SCBI_4583	Molybdopterin-guanine dinucleotide biosynthesis protein MobB	3.50
SCBI_1190	Adenosylmethionine-8-amino-7-oxononanoate aminotransferase	3.10
SCBI_4021	3,4-dihydroxy-2-butanone 4-phosphate synthase	2.99
SCBI_4495	Ribonuclease activity regulator protein RraA	1.83
Carbohydrate Metabolism/Transport		
SCBI_0116	Sugar phosphate permease	2.66*
SCBI_4371	Glycogen phosphorylase	2.31
SCBI_4373	ADP-glucose pyrophosphorylase	2.25
SCBI_2457	N-acetylglucosaminyl transferase	1.87

Amino Acid Metabolism/Transport		
SCBI_3279	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	2.02
SCBI_0048	Cys/Met metabolism pyridoxal-phosphate-dependent enzyme	7.68*
SCBI_0729	ABC-type polar amino acid transport system, ATPase component	12.11
SCBI_2299	Ethanolamine utilization protein	5.16
SCBI_2772	Glycine cleavage system, regulatory protein	4.11
SCBI_4484	5,10-methylenetetrahydrofolate reductase	2.29
SCBI_2505	ABC-type oligopeptide transport system, ATPase component	1.99
SCBI_0313	Aspartate ammonia-lyase	1.69
Cell Cycle Control and Mitosis		
SCBI_2744	Hypothetical	6.08
SCBI_1311	Antitoxin - prevent host-death family protein	3.77
Energy Production/Conversion		
SCBI_0493	Alkanesulfonate monooxygenase	6.04*
SCBI_1951	Citrate carrier protein	8.33
SCBI_1662	Acylphosphatase	8.09
SCBI_2222	NAD-dependent aldehyde dehydrogenase	2.65
SCBI_2549	Glycerol-3-phosphate dehydrogenase	1.79
SCBI_3420	Malic enzyme	1.74
No COG Assigned		
SCBI_0482	Hypothetical	12.51*
SCBI_0435	Hypothetical	14.52*
SCBI_2651	Hypothetical	7.62
SCBI_1547	Phage late control gene	6.51
SCBI_1742	Glyoxalase/bleomycin resistance protein/dioxygenase	6.34
SCBI_0365	Hypothetical	5.82
SCBI_2790	Hypothetical	5.63
SCBI_1821	Hypothetical	5.57
SCBI_2643	Hypothetical	4.77
SCBI_3488	Hypothetical	4.48
SCBI_2388	Hypothetical	4.42
SCBI_2014	Hypothetical	4.36
SCBI_1910	Hypothetical	4.03
SCBI_0124	Cellulose biosynthesis protein BcsF/YhjT	3.79
SCBI_3642	Hypothetical	3.77
SCBI_2084	Hypothetical	3.69

SCBI_3338	Hypothetical	3.67
SCBI_2979	Hypothetical	3.52
SCBI_2637	Hypothetical	3.28
SCBI_2286	Hypothetical	3.19
SCBI_2252	Hypothetical	2.99
SCBI_1545	Phage terminase usbunit GpP	2.98
SCBI_2746	Head DNA stabilization protein	2.90
SCBI_4647	Hypothetical	2.52
SCBI_2390	Hypothetical	2.46
SCBI_3237	Hypothetical	2.41
SCBI_4351	Hypothetical	2.26
SCBI_4608	Hypothetical	2.20
SCBI_2743	Head assembly protein	1.91
SCBI_1757	Biofilm formation regulatory protein BssS	1.90
SCBI_4662	Hypothetical	1.88
SCBI_4607	Hypothetical	1.85
SCBI_0343	Hypothetical	1.82
SCBI_4655	Hypothetical	1.81
SCBI_4673	Hypothetical	1.79
SCBI_2305	IS3 family transposase orfA	1.78
SCBI_4658	Hypothetical	1.59
SCBI_3224	IS3 family transposase orfA	1.58
SCBI_1726	Hypothetical	1.58

*Original value was infinity.

Table S6. List of all genes significantly down-regulated ≥ -1.5-fold (p-value <0.05) in mutant 22-C7 compared to wild-type *Serratia* sp. SCBI as determined with RNA-seq.

Locus Tag	Gene	Fold Change
Defense Mechanisms		
SCBI_3918	ABC-type multidrug transport system, permease component	-2.96
Intracellular Trafficking/Secretion		
SCBI_3604	Signal peptidase I	-2.79
Signal Transduction		
SCBI_4407	Response regulator with CheY domain, HTH DNA-binding domain	-2.88
SCBI_1807	DnaK suppressor protein	-3.83
Function Unknown		
SCBI_3343	CsbD family protein	-7.56
SCBI_3413	Hypothetical	-7.53
SCBI_3295	Hypothetical	-3.53
SCBI_0075	6-N-hydroxylaminopurine resistance protein	-3.44
SCBI_3000	Hypothetical	-2.74
SCBI_2589	Hypothetical	-2.19
SCBI_3325	Hypothetical	-1.63
General Function Prediction Only		
SCBI_0440	NADPH-quinone reductase (modulator of drug activity B)	-19.16
SCBI_3738	Cysteine desulfurase SufE	-8.91
SCBI_4167	Xanthine/uracil/vitamin C permease	-5.50
SCBI_2606	Oxidoreductase	-4.26
SCBI_1789	Collagen-binding surface adhesin SpaP	-2.12
SCBI_1262	Alpha/beta hydrolase superfamily protein	-2.09
SCBI_1788	Periplasmic lipoprotein	-1.88
Secondary Metabolite Biosynthesis/Transport/Catabolism		
SCBI_0289	Isochorismate hydrolase	-6.87
SCBI_1014	Thioesterase - involved in NRP biosynthesis	-2.60
Inorganic Ion Metabolism/Transport		
SCBI_4319	Nitrite reductase small subunit	-6.26
SCBI_0789	Siderophore-interacting protein	-4.64

SCBI_4214	Sodium/hydrogen exchanger	-3.99
SCBI_1103	Alkylphosphonate utilization protein PhnA	-3.68
SCBI_0697	Chloride channel protein EriC	-3.62
SCBI_1278	Sodium/solute symporter protein	-3.32
SCBI_0700	ABC-type Fe3+ hydroxamate transport system, periplasmic component	-3.32
SCBI_0159	Frataxin - iron transport protein	-2.19
Chaperones		
SCBI_1589	Thioredoxin reductase	-1.85
Cell Motility		
SCBI_4404	P pilus assembly protein, pilin FimA	-2.43
SCBI_1526	P pilus assembly protein, pilin FimA	-4.50
SCBI_2824	FlgN family protein	-2.93
SCBI_1518	MrfE fimbrial protein	-7.23
SCBI_2727	Flagella biosynthesis protein FliZ	-9.41
Cell Wall/Membrane/Envelope Biogenesis		
SCBI_1720	OM lipoprotein NodT family	-3.50
SCBI_0152	Teichoic acid biosynthesis protein	-2.95
SCBI_0197	Hypothetical	-2.16
SCBI_3469	Cell envelope integrity inner membrane protein TolA	-1.73
SCBI_1380	OM protein X	-1.61
Replication/Repair/Recombination		
SCBI_1315	NUDIX hydrolase (oxidative damage repair)	-9.15
SCBI_4070	Hypothetical	-3.09
SCBI_2586	Holliday junction DNA helicase RuvB	-2.11
Transcription		
SCBI_3059	Response regulator of citrate/malate metabolism	-3.50
SCBI_1240	Histone acetyltransferase HPA2	-9.03
SCBI_3633	Histone acetyltransferase HPA2	-3.60
SCBI_0625	LysR family transcriptional regulator	-11.97
SCBI_0515	AraC family transcriptional regulator	-7.20
SCBI_1230	AraC family transcriptional regulator	-6.60
SCBI_2058	Transcriptional regulator	-3.87
SCBI_1123	PadR family transcriptional regulator	-3.82
SCBI_4227	Transcriptional repressor IclR	-3.15
SCBI_3459	Transcriptional regulator	-2.20
SCBI_4089	BolA family transcriptional regulator	-1.78

Translation/Ribosomal Structure		
SCBI_1864	Methylase of polypeptide chain release factors	-3.96
SCBI_0989	Ribosomal protein L31	-3.43
SCBI_0399	Ribosome-binding factor A	-2.26
SCBI_4262	Ribosomal protein S14	-2.12
SCBI_4082	30S ribosomal protein S9	-2.10
Lipid Metabolism/Transport		
SCBI_0513	3-Hydroxybutyrate dehydrogenase	-3.45
SCBI_0524	Phospholipase D	-10.18
SCBI_2459	Membrane-associated phospholipidphosphatase	-4.17
SCBI_1860	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	-2.23
SCBI_0734	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	-2.16
Coenzyme Metabolism/Transport		
SCBI_2136	Dethiobiotin synthetase	-2.19
SCBI_3915	Panthothenate synthetase	-2.00
SCBI_4524	2-amino-3-ketobutyrate coenzyme A ligase	-1.77
Carbohydrate Metabolism/Transport		
SCBI_0627	Glycosyl transferase	-3.73
SCBI_4055	Glucuronate isomerase	-5.77
SCBI_4520	Phosphoglyceromutase	-4.82
SCBI_1945	Beta-fructosidase	-4.78
SCBI_1173	Galactose mutarotase	-3.76
SCBI_2118	Phosphotransferase system IIC component	-3.70
SCBI_0394	Phosphoglucosamine mutase	-2.21
SCBI_3852	Ribose 5-phosphate isomerase	-1.95
SCBI_2038	Phosphoenolpyruvate synthase	-1.71
SCBI_4213	Glucose-6-phosphate isomerase	-1.71
SCBI_0709	Enolase	-1.67
SCBI_0373	Fructose-1,6-bisphosphatase	-1.64
Nucleotide Metabolism/Transport		
SCBI_0452	Aspartate carbamoyltransferase, catalytic chain	-3.19
SCBI_2619	Phosphoribosylglycin amide formyltransferase 2	-3.14
SCBI_3451	Phosphoribosylaminoimidazole succinocarboxamide (SAICAR) synthetase	-3.05
SCBI_0271	AICAR transformylase/IMP cyclohydrolase PurH	-2.92
SCBI_3473	Phosphoribosylaminoimidazole (AIR) synthetase	-2.74
SCBI_0362	Phosphodiesterase	-2.45
SCBI_0451	Aspartate carbamoyltransferase	-2.32
SCBI_3590	Phosphoribosylformyl glycinamidine synthase	-2.29

SCBI_4547	Orotate phosphoribosyltransferase	-2.09
SCBI_3281	Amidophosphoribosyltransferase	-1.87
Amino Acid Metabolism/Transport		
SCBI_0630	Carbamoyl phosphate synthase large subunit	-2.01
SCBI_0649	Acetolactate synthase	-22.64
SCBI_0800	Allantoate amidohydrolase	-12.51
SCBI_4595	Asparagine synthetase AsnA	-5.94
SCBI_3419	Homocysteine methyltransferase	-4.51
SCBI_3574	Serine hydroxymethyltransferase	-1.83
Energy Production/Conversion		
SCBI_3196	NAD-dependent aldehyde dehydrogenase	-11.33
SCBI_2103	Electron transport complex protein RnfG	-10.98
SCBI_2106	Electron transport complex protein RnfC	-3.31
SCBI_3029	Nitroreductase	-2.91
SCBI_2450	Pyruvate-formate lyase	-2.19
SCBI_4339	Phosphoenolpyruvate carboxykinase (ATP)	-2.16
SCBI_0006	F0F1 ATP synthase subunit alpha	-1.92
SCBI_0005	F0F1 ATP synthase subunit delta	-1.90
SCBI_0003	F0F1 ATP synthase subunit K	-1.84
SCBI_1143	Succinate dehydrogenase	-1.76
No COG Assigned		
SCBI_4572	Hypothetical	-18.28
SCBI_3042	Hypothetical	-10.20
SCBI_3199	Hypothetical	-4.42
SCBI_4329	Hypothetical	-4.23
SCBI_1705	Hypothetical	-3.54
SCBI_1948	Hypothetical	-3.10
SCBI_3537	Hypothetical	-2.86
SCBI_1297	Peptidase M60 viral enhancin protein	-2.72
SCBI_1377	Adenylate kinase	-2.64
SCBI_1264	Hypothetical	-2.57

Table S7. List of all the genes significantly up-regulated $\geq$ 1.5-fold (p-value <0.05) in mutant 22-F6 compared to wild-type *Serratia* sp. SCBI as determined with RNA-seq.

Locus Tag	**Gene**	**Fold Change**
Signal Transduction		
SCBI_3212	Response regulator with CheY receiver domain, HTH DNA-binding domain	1.66
SCBI_0605	Response regulator with CheY receiver domain, winged-helix DNA-binding domain	1.61
SCBI_1839	Universal stress protein UspA	3.56
SCBI_0569	Diguanylate cyclase	2.64
SCBI_3609	Anti-RNA polymerase sigma factor SigE	1.90
Function Unknown		
SCBI_1296	Hypothetical	13.80
SCBI_1841	Hypothetical	6.48
SCBI_0066	Hypothetical	5.71*
SCBI_0482	Hypothetical	4.69*
SCBI_2148	Hypothetical	4.63
SCBI_2995	Hypothetical	3.83
SCBI_2900	MgtC/SapB transporter	3.15
SCBI_3391	Hypothetical	3.03
SCBI_3012	Hypothetical	2.76
SCBI_4639	Hypothetical	2.31
SCBI_3622	Hypothetical	2.24
SCBI_3834	Hypothetical	2.08
SCBI_1658	Hypothetical	1.87
SCBI_3820	Hypothetical	1.72
SCBI_2534	Hypothetical	1.65
SCBI_0370	Hypothetical	1.61
SCBI_4240	Hypothetical	1.60
SCBI_4133	Hypothetical	2.82
SCBI_2389	Hypothetical	2.18
General Function Prediction Only		
SCBI_3570	Hypothetical	1.92
SCBI_0185	Plasmid stabilization protein	2.30
SCBI_0044	Nucleic-acid binding protein, contains PIN domain	1.98
SCBI_0339	RNA-binding protein Hfq	1.79
SCBI_0293	Hypothetical	1.74

Secondary Metabolite Biosynthesis/Transport/Catabolism		
SCBI_1177	Amidase	7.47
SCBI_2923	Phenylacetate-CoA oxygenase subunit PaaB	6.20
SCBI_1289	Amidase	3.19
Inorganic Ion Metabolism/Transport		
SCBI_3891	Phenylpropionate dioxygenase	2.77
SCBI_0098	Cyanate permease	2.76*
SCBI_3466	Arsenate reductase	2.08
SCBI_0983	Hha toxicity attenuator	2.01
SCBI_4193	Fe2+/Zn2+ uptake regulator	1.66
Cell Motility		
SCBI_2959	P pilus assembly protein, chaperone PapD	6.92
SCBI_0970	Type II secretory pathway, pseudopilin PulG	5.27
SCBI_1666	P pilus assembly protein, pilin FimA	4.29
SCBI_2962	P pilus assembly protein, pilin FimA	3.72
SCBI_2956	MrfF fimbrial protein	2.06
SCBI_2958	Fimbrial protein	3.27
SCBI_1668	P pilus assembly protein, porin PapC	3.11
SCBI_2961	P pilus assembly protein, pilin FimA	3.00
SCBI_0978	Type II secretory pathway, prepilin signal peptidase PulO	6.55
Cell Wall/Membrane/Envelope Biogenesis		
SCBI_2368	D-alanyl-Dalanine carboxypeptidase	3.66
SCBI_2655	Outer membrane porin	2.91
SCBI_3208	Outer membrane porin	2.67
SCBI_2581	Lauroyl/myristoyl acyltransferase	1.94
SCBI_2374	Glycosyltransferase	1.91
SCBI_0783	Murein transglycosylase	1.84
SCBI_1482	UDP-glucose 4-epimerase	1.50
Replication/Repair/Recombination		
SCBI_2623	NUDIX hydrolase (oxidative damage repair enzyme)	4.18
SCBI_1670	DNA-damage-inducible protein J	10.91
SCBI_0962	Methylated DNA-protein cysteine methyltransferase	9.14
SCBI_0930	Exonuclease VII small subunit	4.41
SCBI_4239	DNA topoisomerase type IA zinc finger containing domain	1.98
SCBI_2745	DNA stabilization protein GP10	2.67
Transcription		

SCBI_0199	Histone acetyltransferase HPA2	4.85*
SCBI_0517	AraC family transcriptional regulator	16.38
SCBI_0963	DNA-binding winged-HTH domain protein	11.52
SCBI_1929	DNA-binding transcriptional repressor PuuR	5.84
SCBI_0045	CopG family transcriptional regulator	4.69
SCBI_0495	Transcriptional regulator	4.24*
SCBI_0214	Transcriptional regulator	3.08*
SCBI_2138	MerR family transcriptional regulator	2.93
SCBI_3139	DNA-binding transcriptional repressor PuuR	2.69
SCBI_3467	DNA binding protein	2.68
SCBI_3253	DNA-binding transcriptional repressor LrhA	2.13
SCBI_1012	AraC family transcriptional regulator	2.07
SCBI_0196	RNA polymerase factor sigma-32	2.00
SCBI_3610	RNA polymerase sigma factor RpoE	1.99
SCBI_4641	Hypothetical	1.86
SCBI_2463	Transcriptional regulator CysB	1.81
SCBI_2557	Transcriptional regulator, fatty acid metabolism regulator	1.60
Translation/Ribosomal Structure		
SCBI_0988	Ribosomal protein L36	15.10
SCBI_2937	Endoribonuclease L-PSP	5.92
SCBI_1685	GNAT family acetyltransferase	3.15
SCBI_0338	tRNA delta(2)-isopentenylpyrophosphate transferase	1.98
SCBI_3621	Small protein A (tmRNA-binding protein)	1.77
SCBI_4102	Ribosome-associated protein Y	1.72
SCBI_0774	Ribosome-associated protein Y	1.71
SCBI_0382	Ribosomal protein L21	1.55
Lipid Metabolism/Transport		
SCBI_0508	3-oxoacid CoA-transferase subunit A	33.55
SCBI_2938	Esterase/lipase	2.48
Coenzyme Metabolism/Transport		
SCBI_0025	Phosphopantetheinyl transferase	3.72*
SCBI_4495	Ribonuclease activity regulator protein RraA	1.86
Carbohydrate Metabolism/Transport		
SCBI_2500	Permease	3.78
SCBI_2057	Permease	2.27
SCBI_3267	Phosphotransferase system, galactitol-specific IIB component	3.98
SCBI_1217	Sugar phosphate permease	3.62
SCBI_0117	Chitinase	3.11

SCBI_3153	Mannitol/fructose-specific phosphotransferase system, IIA domain	2.83
SCBI_4313	Phosphotransferase system cellobiose-specific component IIA	2.78
SCBI_2533	Chitinase	2.63
SCBI_4371	Glucan phosphorylase	2.61
SCBI_0483	Beta-glucosidase	2.40*
SCBI_4373	Glucose-1-phosphate adenylyltransferase	2.19
SCBI_4497	MIP family channel protein	2.16
SCBI_1111	Glucosamine-6-phosphate deaminase	2.07
SCBI_2457	N-acetylglucosaminyl transferase	2.05
SCBI_2942	Glycogen synthesis protein	2.14
Nucleotide Metabolism/Transport		
SCBI_2155	dGTP triphosphohydrolase	1.93
Amino Acid Metabolism/Transport		
SCBI_2224	ABC-type amino acid transport, substratebinding protein	4.68
SCBI_3279	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	2.44
SCBI_0120	ABC-type dipeptide/oligopeptide/nickel transport, permease	3.87
SCBI_0801	Threonine efflux protein	10.42
SCBI_1506	Agmatinase	6.02
SCBI_2641	Glutathione transferase	4.05
SCBI_3207	Lactoylglutathione lyase	3.58
SCBI_3276	ABC-type arginine/histidine transporter system, permease	3.09
SCBI_3888	Lactoylglutathione lyase	3.07
SCBI_2505	ABC-type oligopeptide transport system, ATPase component	2.03
SCBI_0313	Aspartate ammonia lyase	2.00
SCBI_1743	Permease	1.67
Cell Cycle Control and Mitosis		
SCBI_2744	Chromosome segregation ATPases	3.55
SCBI_4146	MreB - rod-shape-determining protein	1.58
Energy Production/Conversion		
SCBI_0527	NAD-dependent aldehyde dehydrogenase	14.26
SCBI_1951	Citrate carrier protein	9.07
SCBI_0981	Cytochrome B561	7.61
SCBI_1392	Thiosulfate reductase cytochrome B subunit	5.68

SCBI_1662	Acylphosphatase	5.33
SCBI_2222	Aldehyde dehydrogenase	3.14
SCBI_3352	Cytochrome B561	2.65
SCBI_3275	ABC-type histidine transport system, ATPase component	2.45
SCBI_3279	ABC-type amino acid transport/signal transduction systems, periplasmic component/domain	2.39
SCBI_1114	Porin	2.36
SCBI_0559	Ureidoglycolate lyase	2.25
No COG Assigned		
SCBI_1547	Phage late control gene	13.04
SCBI_1251	Hypothetical	10.83
SCBI_1742	Glyoxalase/bleomycin resistance protein/dioxygenase	8.12
SCBI_1754	Hypothetical	8.09
SCBI_2651	Hypothetical	6.52
SCBI_2004	Hypothetical	6.35
SCBI_0365	Hypothetical	6.14
SCBI_2963	Hypothetical	5.69
SCBI_2388	Hypothetical	5.35
SCBI_2637	Hypothetical	5.25
SCBI_2790	Hypothetical	5.23
SCBI_0306	Hypothetical	4.87*
SCBI_2957	MrfE pilus protein	4.74
SCBI_2782	Hypothetical	4.54
SCBI_2747	Phage protein	3.98
SCBI_2371	Hypothetical	3.85
SCBI_3338	Hypothetical	3.78
SCBI_2286	Hypothetical	3.62
SCBI_2965	Putative secretion protein	3.14
SCBI_2954	Hypothetical	2.92
SCBI_4647	Hypothetical	2.66
SCBI_0472	Transposase IS3/IS911 family protein	2.16
SCBI_1757	Biofilm regulatory protein BssS	2.07
SCBI_4607	Hypothetical	2.02
SCBI_4673	Hypothetical	1.80
SCBI_4655	Hypothetical	1.74
SCBI_4662	Hypothetical	1.67
SCBI_0184	Putative stability determinant	1.66
SCBI_4661	Hypothetical	1.64
SCBI_3692	Hypothetical	1.61
SCBI_4658	Hypothetical	1.60
SCBI_1544	Hypothetical	1.59

*Original value was infinity.

Table S8. List of all the genes significantly down-regulated $\geq$ -1.5-fold (p-value <0.05) in mutant 22-F6 compared to wild-type *Serratia* sp. SCBI as determined with RNA-seq.

Locus Tag	Gene	Fold Change
Defense Mechanisms		
SCBI_1721	ABC-type antimicrobial peptide transport, ATPase	-3.09
Intracellular Trafficking/Secretion		
SCBI_4059	SecD - EnvZ/OmpR regulon moderator	-2.81
Signal Transduction		
SCBI_0114	Response regulator with CheY domain	-5.76*
SCBI_2700	Response regulator with CheY domain	-4.49
Function Unknown		
SCBI_4435	Hypothetical	-6.69
SCBI_3343	Hypothetical	-5.94
SCBI_0699	Hypothetical	-5.83
SCBI_3387	Hypothetical	-3.87
SCBI_2860	Hypothetical	-3.43
SCBI_4456	Hypothetical	-3.12
SCBI_3687	Hypothetical	-2.47
SCBI_3000	Hypothetical	-2.07
SCBI_4325	Hypothetical	-1.70
General Function Prediction Only		
SCBI_0440	Putative NADPH-quinone reductase (modulator of drug activity B)	-11.39*
SCBI_1229	Intracellular protease/amidase	-18.30
SCBI_2218	Hypothetical	-8.30
SCBI_0434	Permease	-4.46
SCBI_3840	Acetyltransferase	-4.11
SCBI_3045	Permease	-3.83
SCBI_0270	Phosphoribosylamine-glycine ligase	-2.69
Inorganic Ion Metabolism/Transport		
SCBI_4319	Nitrite reductase small subunit	-2.79
SCBI_0444	Cation transport ATPase	-8.22*
SCBI_0159	Frataxin - iron transport protein	-3.37
Chaperones		

SCBI_2449	Pyruvate-formate lyase-activating enzyme	-2.70
SCBI_4493	ATP-dependent protease	-2.61
SCBI_0316	Chaperonin GroEL	-1.82
Cell Motility		
SCBI_4403	P pilus assembly protein, chaperone PapD	-7.45
SCBI_2972	P pilus assembly protein, chaperone PapD	-3.40
SCBI_4402	P pilus assembly protein, porin PapC	-2.99
SCBI_1518	MrfE fimbrial protein	-3.42
SCBI_2727	Flagella biosynthesis protein FliZ	-5.17
SCBI_4404	P pilus assembly protein, pilin FimA	-2.26
Cell Wall/Membrane/Envelope Biogenesis		
SCBI_1720	Outer membrane protein	-4.31
SCBI_2689	Glycosyl transferase family protein	-7.45
SCBI_2191	Cell division protein FtsI/penicillin-binding protein 2	-3.91
SCBI_3022	Phosphoglycerol transferase	-3.49
SCBI_4599	16S rRNA methyltransferase GidB	-2.71
SCBI_1473	Mannose-1-phosphate guanylyltransferase	-1.90
SCBI_3469	Cell envelope integrity inner membrane protein TolA	-1.52
Replication/Repair/Recombination		
SCBI_1315	NUDIX hydrolase (oxidative damage repair enzyme)	-15.45
SCBI_1258	Hypothetical	-4.46
SCBI_2115	NUDIX hydrolase (oxidative damage repair enzyme)	-3.72
SCBI_0460	DNA polymerase III, chi subunit	-7.36
SCBI_3746	Prepilin peptidase dependent protein c	-2.91
SCBI_0467	Transposase IS3/IS911 family	-2.25
Transcription		
SCBI_2150	Histone acetyltransferase HPA2	-3.38
SCBI_3633	Histone acetyltransferase HPA2	-3.02
SCBI_1277	Histone acetyltransferase HPA2	-2.61
SCBI_0593	LysR family transcriptional regulator	-7.61
SCBI_3185	Transcriptional regulator	-5.94
SCBI_2939	LysR family transcriptional regulator	-5.29
SCBI_3668	LysR family transcriptional regulator	-4.93
SCBI_1351	AsnC family transcriptional regulator	-3.85
SCBI_4089	BolA family transcriptional regulator	-1.97
SCBI_0924	Transcription antitermination protein NusB	-1.83
Translation/Ribosomal Structure		
SCBI_0989	Ribosomal protein L31	-28.94

SCBI_0399	Ribosome-binding factor A	-2.66
SCBI_0735	tRNA pseudouridine synthase D	-2.35
SCBI_2020	Methionyl-tRNA formyltransferase	-1.81
SCBI_4082	Ribosomal protein S9	-1.70
SCBI_0450	Translation initiation inhibitor, yjgF family	-1.64
SCBI_1766	Ribosomal protein L32	-1.64
Coenzyme Metabolism/Transport		
SCBI_3289	Phosphoglycerate dehydrogenase	-2.35
SCBI_0393	Dihydropteroate synthase	-2.12
Carbohydrate Metabolism/Transport		
SCBI_1013	Permease - Bcr/CflA subfamily drug resistance	-2.44
SCBI_1173	Galactose mutarotase	-4.77
SCBI_4520	Phosphoglyceromutase	-4.10
SCBI_0709	Enolase	-1.98
SCBI_0820	Phosphoheptose isomerase	-1.84
SCBI_2038	Phosphoenolpyruvate synthase	-1.80
SCBI_3852	Ribose 5-phosphate isomerase	-1.67
SCBI_3878	Transketolase	-1.67
Nucleotide Metabolism/Transport		
SCBI_0094	Cytosine deaminase	-8.53
SCBI_1035	Phosphoribosylcarboxylaminoimidazole (NCAIR) mutase	-17.30
SCBI_1034	Phosphoribosylcarboxylaminoimidazole (NCAIR) synthetase	-6.17
SCBI_2619	Phosphoribosylglycin amide formyltransferase 2	-3.61
SCBI_3473	Phosphoribosylaminoimidazole (AIR) synthetase	-3.40
SCBI_0271	AICAR transformylase	-3.00
SCBI_3471	Uracil permease	-2.76
SCBI_0452	Aspartate carbamoyltransferase	-2.55
SCBI_4547	Orotate phosphoribosyltransferase	-2.39
SCBI_0362	2',3'-cyclic-nucleotide 2'-phosphodiesterase	-2.31
SCBI_3540	GMP synthase	-2.21
SCBI_3590	Phosphoribosylformyl glycinamidine synthase	-2.20
SCBI_3451	Phosphoribosylaminoimidazole succinocarboxamide (SAICAR) synthetase	-1.90
SCBI_3474	Phosphoribosylglycin amide formyltransferase	-1.78
SCBI_3281	Amidophosphoribosyl transferase	-1.83
Amino Acid Metabolism/Transport		
SCBI_0630	Carbamoylphosphate synthase large subunit	-2.63
SCBI_0629	Carbamoylphosphate synthase small subunit	-1.80

SCBI_0178	Anaerobic glycerol-3-phosphatedhydrogenase	-11.43
SCBI_2212	Spermidine synthase	-5.26
SCBI_0649	Acetolactase synthase regulatory subunit	-3.95
SCBI_3764	Diaminopimelate decarboxylase	-3.64
SCBI_3843	Glycine cleavage system H protein	-1.99
SCBI_3574	Glycine/serine hydroxymethyltransferase	-1.55
Energy Production/Conversion		
SCBI_2165	Isoquinoline 1-oxidoreductase	-9.92
SCBI_3196	NAD-dependent aldehyde dehydrogenases	-7.34
SCBI_0847	Cytochrome B561	-5.14
SCBI_0104	NADH:flavin oxidoreductase	-5.10
SCBI_0003	F0F1-type ATP synthase subunit C	-2.05
SCBI_4339	Phosphoenolpyruvate carboxykinase	-1.97
SCBI_0005	F0F1-type ATP synthase subunit delta	-1.72
RNA Processing/Modification		
SCBI_0332	Oligoribonuclease	-2.24
No COG Assigned		
SCBI_1948	Hypothetical	-8.15
SCBI_4572	Hypothetical	-7.92
SCBI_4188	Phage shock protein G	-7.74
SCBI_2437	Hypothetical	-7.71
SCBI_2867	Hypothetical	-7.01
SCBI_3537	Hypothetical	-6.78
SCBI_4629	Hypothetical	-6.62
SCBI_3794	Hypothetical	-4.15
SCBI_1297	Peptidase M60 viral enhancin protein	-4.04
SCBI_2866	Hypothetical	-4.01
SCBI_2897	Hypothetical	-3.93
SCBI_1377	Adenylate kinase	-3.45
SCBI_4631	Hypothetical	-3.34
SCBI_1914	Hypothetical	-3.09
SCBI_1264	Hypothetical	-2.08

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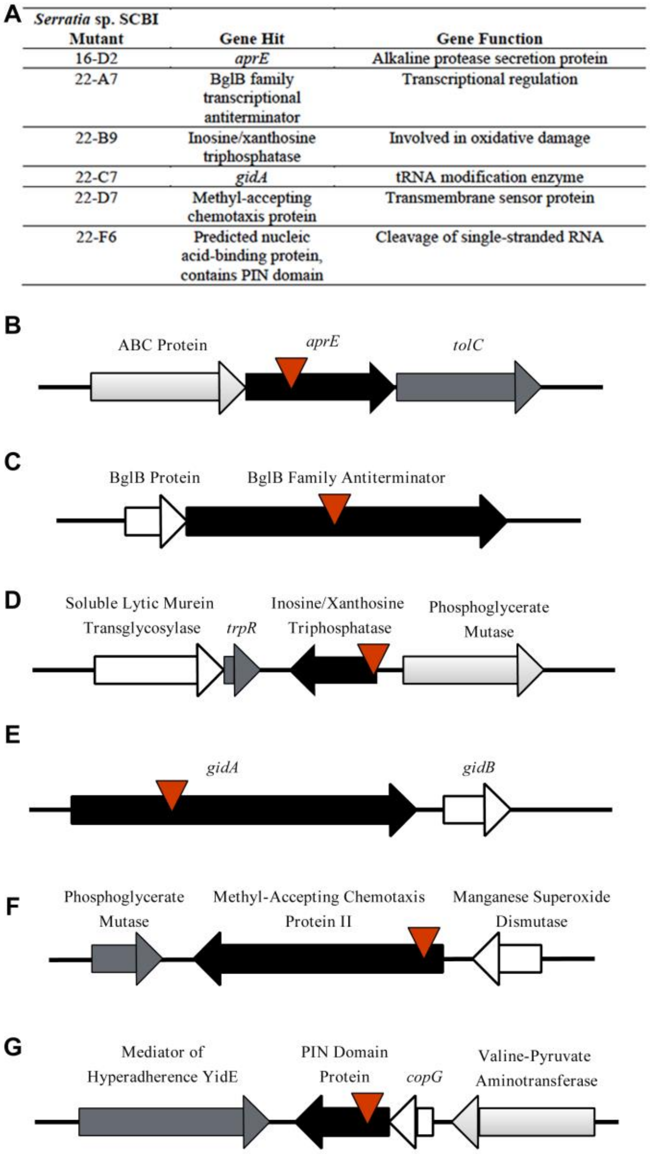
*Original value was infinity.

Table S9. Results of qRT-PCR validation of the expression of 4 randomly selected genes from the protease mutants (16-D2, 22-C7, and 22-F6) as compared to wild-type *Serratia* sp. SCBI.

			Fold Change	
Sample	**Gene**	**Locus Tag**	**RNA-Seq**	**qRT-PCR**
16-D2	Hemolysin co-regulated protein ImpD	SCBI_2996	10.37	8.24
16-D2	Heme exporter protein CcmC	SCBI_3334	-4.68	-5.19
22-C7	Glyoxylase/bleomycin resistance protein	SCBI_1742	6.34	6.91
22-C7	Flagella protein FliZ	SCBI_2727	-9.41	-7.33
22-F6	Glyoxylase/bleomycin resistance protein	SCBI_1742	8.12	5.78
22-F6	Flagella protein FliZ	SCBI_2727	-5.17	-3.64



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Serratia sp. SCBI Mutant	Gene Hit	Gene Function
16-D2	*aprE*	Alkaline protease secretion protein
22-A7	BglB family transcriptional antiterminator	Transcriptional regulation
22-B9	Inosine/xanthosine triphosphatase	Involved in oxidative damage
22-C7	*gidA*	tRNA modification enzyme
22-D7	Methyl-accepting chemotaxis protein	Transmembrane sensor protein
22-F6	Predicted nucleic acid-binding protein, contains PIN domain	Cleavage of single-stranded RNA

Figure S1. Identification of genes inactivated by miniHimar RB1 transposon insertion in the 6 protease mutants. **(A)** The site of transposon insertion was identified using rescue cloning and the genes and their predicted functions are listed. **(B-G)** Diagrams of the miniHimar RB1 transposon insertion site in each of the protease mutants, with the upside-down arrow representing the transposon insertion. **(B)** Mutant 16-D2 had the *aprE* gene inactivated, which lies in the middle of a 3 gene operon coding for a predicted ABC transporter. (**C)** Mutant 22-A7 had a BglB family antiterminator gene hit by the transposon. This gene is the second gene in an operon, in which the first gene is also a BglB family antiterminator. **(D)** Mutant 22-B9 had an inosine/xanthosine triphosphatase gene hit 12 bp downstream of the start codon. **(E)** Mutant 22-C7 had the transposon insertion in *gidA*. **(F)** Mutant 22-D7 had a predicted methyl-accepting chemotaxis protein II inactivated. **(G)** Mutant 22-F6 had the insertion in a predicted nucleic acid-binding protein, which is the second gene in an operon that also contains a predicted CopG family DNA-binding protein.