

Data table 1a. Genes differentially regulated in hVISA/VISA compared to matched VSSA, up-regulated.

ORF ID ^a	Gene	TIGR description ^b	Isolate Pair				
			1	2	3	4	5
Amino acid biosynthesis:							
<i>Aspartate family</i>							
SACOL1362	<i>hom</i>	homoserine dehydrogenase	1.15	1.66*	1.90*	0.70*	1.35
SACOL1428	<i>lysC</i>	aspartokinase, alpha and beta subunits	2.20*	2.49*	5.12*	1.34*	2.21*
SACOL1429	<i>asd</i>	aspartate-semialdehyde dehydrogenase	2.22*	2.56*	3.52*	0.87	1.86*
SACOL1430	<i>dapA</i>	dihydrodipicolinate synthase	2.25*	2.51*	3.03*	0.72*	1.77*
SACOL1431	<i>dapB</i>	dihydrodipicolinate reductase	1.92*	2.35*	3.36*	0.69*	1.72*
SACOL1432	<i>dapD</i>	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	2.18*	2.10*	2.83*	0.65*	1.61*
<i>Glutamate family</i>							
SACOL0514	<i>gltB</i>	glutamate synthase, large subunit	1.23	1.79*	1.69*	1.19	1.13
<i>Pyruvate family</i>							
SACOL0600	<i>ilvE</i>	branched-chain amino acid aminotransferase	1.44	2.06*	2.16*	1.21*	1.24
SACOL2043	<i>ilvB</i>	acetolactate synthase, large subunit, biosynthetic type	1.57	1.95*	1.78*	1.13	1.14
SACOL2045	<i>ilvC</i>	ketol-acid reductoisomerase	1.50	1.82*	1.88*	1.09	1.30
SACOL2046	<i>leuA</i>	2-isopropylmalate synthase	1.75*	1.73	1.85*	1.16	1.19
Biosynthesis of cofactors, prosthetic groups and carriers:							
<i>Glutathione and analogs</i>							
SACOL2641	<i>gpxA2</i>	glutathione peroxidase	3.04*	1.97*	2.12*	1.02	1.45
<i>Heme, porphyrin, and cobalamin</i>							
SACOL2396		uroporphyrinogen III methylase SirB, putative	1.59	1.47	1.87*	1.34*	1.83*
Cellular Processes:							
<i>Adaptions to atypical conditions</i>							
SACOL1759		universal stress protein family	1.11	2.17*	2.54*	1.05	1.79*
SACOL2131		Dps family protein	0.93	2.04	2.76*	1.60*	1.84
<i>Detoxification</i>							
SACOL1368	<i>kataA</i>	catalase	1.08	1.93*	1.46	1.06	1.52*
<i>Pathogenesis</i>							
SACOL0270		staphyloxanthin biosynthesis protein, putative	2.14*	1.06	1.61*	0.75*	1.35
<i>Others</i>							
SACOL1440		xpaC protein, putative	0.99	1.53*	1.37*	1.61*	1.07
Cell envelope:							
<i>Biosynthesis and degradation of murein sacculus and peptidoglycan</i>							
SACOL0248	<i>lrgB</i>	lrgB protein	0.75	1.69*	2.08*	0.73	1.61*
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>							
SACOL0136	<i>cap5A</i>	capsular polysaccharide biosynthesis protein Cap5A	2.13*	2.04*	1.27	2.53*	0.96
SACOL0137	<i>cap5B</i>	capsular polysaccharide biosynthesis protein Cap5B	1.99	2.02*	1.39*	2.91*	0.94
SACOL0139	<i>cap5D</i>	capsular polysaccharide biosynthesis protein Cap5D	1.75	1.82*	1.25	2.05*	0.96
SACOL0140	<i>cap5E</i>	capsular polysaccharide biosynthesis protein Cap5E	2.27	2.06*	1.40*	2.64*	0.80
SACOL0141	<i>cap5F</i>	capsular polysaccharide biosynthesis protein Cap5F	1.94	2.42*	1.62*	2.29*	0.94
<i>Other</i>							
SACOL2539	<i>srtA</i>	sortase	1.20	1.63	1.79*	1.02	1.62*
Central intermediary metabolism:							
<i>Nitrogen metabolism</i>							
SACOL2280	<i>ureA</i>	urease, gamma subunit	3.75*	1.40	1.82*	2.69*	0.73

SACOL2281	<i>ureB</i>	urease, beta subunit	3.65	1.43	1.93*	2.78*	0.67
SACOL2282	<i>ureC</i>	urease, alpha subunit	4.96*	1.36	2.01*	3.14*	0.62*
SACOL2283	<i>ureE</i>	urease accessory protein UreE	2.95*	1.41	1.89*	3.20*	0.78
SACOL2284	<i>ureF</i>	urease accessory protein UreF	4.27*	1.36	1.73*	3.19*	0.66*
SACOL2285	<i>ureG</i>	urease accessory protein UreG	3.71*	1.36	1.63*	2.94*	0.73*
SACOL2286	<i>ureD</i>	urease accessory protein UreD	3.04*	1.51	1.72*	2.85*	0.84
SACOL2394	<i>narH</i>	respiratory nitrate reductase, beta subunit	1.20	1.64	1.97*	1.58*	1.99
SACOL2395	<i>narG</i>	respiratory nitrate reductase, alpha subunit	1.15	1.35*	1.90*	1.44*	1.70*
SACOL2397	<i>nirD</i>	nitrite reductase [NAD(P)H], small subunit	1.45*	1.30	1.79*	1.58*	1.75*
Other							
SACOL1920		D-isomer specific 2-hydroxyacid dehydrogenase family protein	1.08	1.75*	1.57*	1.01	1.30
SACOL2574		D-isomer specific 2-hydroxyacid dehydrogenase family protein	1.31	2.32*	2.23*	1.07	1.56
DNA metabolism:							
Replication, recombination, repair							
SACOL2562	<i>ogt</i>	methylated-DNA--protein-cysteine methyltransferase	1.14	1.58*	1.88*	1.00	1.44
Other							
SACOL0880		Toprim domain protein	1.23	1.53	1.50*	1.05	1.66*
Energy metabolism:							
Fermentation							
SACOL0111		acetoin reductase	1.05	1.80*	2.33*	1.34*	1.53
SACOL1984	<i>aldA2</i>	aldehyde dehydrogenase	1.04	1.77*	1.60*	1.26*	1.21
SACOL2178		alcohol dehydrogenase, zinc-containing	1.59	1.86*	2.09*	1.09	1.34
TCA cycle							
SACOL1449	<i>sucA</i>	2-oxoglutarate dehydrogenase, E1 component	1.81*	0.78	1.07	1.66*	0.89
Fatty acid and phospholipid metabolism:							
Biosynthesis							
SACOL1351	<i>cls1</i>	cardiolipin synthetase	1.24	1.93*	2.01*	1.24	1.65
Protein fate:							
Protein folding and stabilization							
SACOL2385		heat shock protein, Hsp20 family	1.53*	1.53*	1.61*	1.51*	1.32
Protein synthesis:							
Translation factors							
SACOL0815		ribosomal subunit interface protein	1.17	2.53*	2.10*	0.92	1.74*
Ribosomal proteins: synthesis and modification							
SACOL1369	<i>rpmG1</i>	ribosomal protein L33	1.10	2.24*	1.54*	0.88	1.80
tRNA aminoacylation							
SACOL0009	<i>serS</i>	seryl-tRNA synthetase	1.89*	2.42*	2.27*	1.57*	1.34
Purines, pyrimidines, nucleosides and nucleotides:							
2'-Deoxyribonucleotide metabolism							
SACOL0790.1		ribonucleoside-diphosphate reductase 2, NrdH-redoxin, putative	0.55*	1.59*	1.08	1.18*	1.52*
SACOL0792	<i>nrdE</i>	ribonucleoside-diphosphate reductase 2, alpha subunit	0.84	1.58*	1.54*	1.29	1.23
SACOL1622	<i>glyS</i>	glycyl-tRNA synthetase	1.15	1.64*	1.48*	1.72*	1.49*
Regulatory Functions:							
DNA interactions							
SACOL1997		transcriptional regulator, GntR family	1.19	1.02	1.56*	1.91*	0.71
SACOL2193		transcriptional regulator, MerR family	1.13	1.97*	1.86*	1.68*	1.40*
SACOL2517		transcriptional regulator, MerR family	1.67*	2.67*	0.97	1.47*	1.28

Other							
SACOL2585		regulatory protein, putative	0.88	2.60*	1.81*	0.51*	1.67
Signal transduction:							
2-component system							
SACOL1942	<i>vraR</i>	DNA-binding response regulator VraR	1.40	1.83*	0.45*	1.78*	0.77
SACOL1943	<i>vraS</i>	sensor histidine kinase VraS	1.45	2.34*	0.48*	1.82*	0.75*
Transport and binding proteins:							
Anions							
SACOL2386		nitrite extrusion protein	1.32	1.39	1.77*	2.08*	1.59*
Cations and iron carrying compounds							
SACOL0686		Na ⁺ /H ⁺ antiporter, MnhG component, putative	0.85	1.62*	0.99	1.68*	0.93
SACOL2166		iron compound ABC transporter, permease protein	1.05	0.99	1.54*	1.64*	1.03
Unknown substrate							
SACOL0882		ABC transporter, ATP-binding protein	1.49	2.30*	1.97*	1.53*	1.85*
SACOL0883		ABC transporter, permease protein	1.50*	2.24*	1.80*	1.35	1.79*
SACOL0884		ABC transporter, substrate-binding protein	1.35	2.47*	1.72*	1.20	1.81*
SACOL2279		transporter, putative	2.35*	1.74	2.05*	1.65*	0.81
Other							
SACOL2348		drug transporter, putative	0.84	1.46	1.56*	1.04	1.69*
SACOL2619		amino acid permease	1.26	2.82*	1.80*	0.54*	1.58*
Unknown Functions:							
Enzymes of unknown specificity							
SACOL0399		oxidoreductase, putative	1.29	1.61*	1.78*	1.21*	1.32
SACOL0655		oxidoreductase, aldo/keto reductase family	1.22	1.41*	1.66*	0.65*	1.16
SACOL1543		oxidoreductase, aldo/keto reductase family	1.67*	1.70*	1.86*	1.03	1.30
SACOL1772		aminotransferase, class V	1.00	2.58*	1.56*	1.00	1.37
SACOL1774		hydrolase, haloacid dehalogenase-like family	1.25	1.60*	1.56*	1.21	1.25
SACOL2192		oxidoreductase, aldo/keto reductase family	1.53	1.98	1.86*	1.59*	1.38
SACOL2575		aminotransferase, class I	1.45	2.28*	2.08*	1.11	1.58
SACOL2620		aminotransferase, class III	1.08	3.44*	2.63*	0.45*	1.72*
General							
SACOL0089		antigen, 67 kDa	1.42	1.63*	1.54*	1.12	1.11
SACOL0220		flavohepotein, putative	1.25	1.91*	1.97*	0.82*	1.42*
SACOL1553		glyoxalase family protein	0.89	1.64	1.68*	1.51*	1.62*
SACOL2088		sceD protein, putative	2.65*	2.01*	3.70*	2.62*	1.58
SACOL2522		DedA family protein	1.13	1.57*	1.55*	1.37*	1.23
Hypothetical proteins:							
SACOL2344		hypothetical protein	1.23	2.00*	2.02*	1.18*	1.49
SAV2383		assimilatory nitrite reductase [NAD(P)H] small subunit	1.16	1.23	1.64*	1.41*	1.58*
Conserved							
SACOL0467		conserved hypothetical protein	1.42	2.54*	3.65*	1.23*	1.79*
SACOL0597		conserved hypothetical protein	1.08	1.77*	1.47*	0.89*	1.58*
SACOL0669		conserved hypothetical protein	1.05	1.51*	1.12	0.95	1.77*
SACOL1944		conserved hypothetical protein (match to 1942/43)	1.19	2.50*	0.48*	1.70*	0.79
SACOL1956		conserved hypothetical protein	1.17	1.69*	0.42*	1.76*	0.77
SACOL2550		conserved hypothetical protein	1.37	2.36*	2.12*	1.50*	1.36
SACOL2551		conserved hypothetical protein TIGR00051	1.23	2.33*	2.02*	1.86*	1.49
SACOL2710		conserved hypothetical protein	1.42	2.31*	1.66*	0.67*	1.31

Data table 1b. Genes differentially regulated in hVISA/VISA compared to matched VSSA, down-regulated.

ORF ID ^a	Gene	TIGR description ^b	Isolate pair				
			1	2	3	4	5
Biosynthesis of cofactors, prosthetic groups and carriers:							
<i>Pyridoxine</i>							
SACOL0564		pyridoxine biosynthesis protein	0.97	0.50*	0.72*	0.85	0.59*
Cell envelope:							
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>							
SACOL1043		glycosyl transferase, group 1 family protein	0.40*	0.36	0.70*	0.60*	0.96
<i>Other</i>							
SACOL2354		membrane protein, putative	0.69	0.86	0.65*	0.52*	0.95
SACOL2520		membrane protein, putative	0.76	0.68*	0.57	1.12	0.54*
Cellular Processes:							
<i>Pathogenesis</i>							
SACOL0095	<i>spa</i>	immunoglobulin G binding protein A precursor	0.12*	0.08*	0.19*	0.11*	0.98
SACOL2291		staphyloxanthin biosynthesis protein	1.24	0.37*	0.62*	1.40*	0.65
SACOL2418		IgG-binding protein SBI	0.57*	0.31*	0.21*	0.31*	0.41
SACOL2509	<i>fnbB</i>	fibronectin binding protein B	0.47*	0.37*	0.37*	0.84	0.96
SACOL2511	<i>fnbA</i>	fibronectin-binding protein A	0.89	0.66*	0.59*	1.00	0.83
<i>Toxin production and resistance</i>							
SACOL0478		exotoxin 3, putative	0.79	0.83	0.60*	0.66*	0.99
DNA metabolism:							
<i>Replication, recombination, repair</i>							
SACOL0678		integrase/recombinase, phage integrase family	0.69	0.60*	0.48*	1.28*	0.63*
Energy metabolism:							
<i>Amino acids and amines</i>							
SACOL2327	<i>hutG</i>	formiminoglutamase	0.54*	0.85	0.80	0.62*	0.93
<i>ATP-proton motive force interconversion</i>							
SACOL2101	<i>atpB</i>	ATP synthase F0, A subunit	1.27	0.66	0.66*	0.64*	0.75
Protein fate:							
<i>Protein and peptide secretion and trafficking</i>							
SACOL1251		cell division protein FtsY, putative	1.02	0.61*	0.66*	1.69*	0.81
Protein synthesis:							
<i>Ribosomal proteins: synthesis and modification</i>							
SACOL1702	<i>rplU</i>	ribosomal protein L21	0.82	0.59*	0.56*	1.02	0.79
<i>Translation factors</i>							
SACOL1278	<i>frr</i>	ribosome recycling factor	0.75	0.53*	0.62*	0.97	0.66*
<i>tRNA aminoacylation</i>							
SACOL1962	<i>gatC</i>	glutamyl-tRNA(Gln) amidotransferase, C subunit	0.83	0.70	0.39*	0.47*	0.76
<i>tRNA and rRNA base modification</i>							
SACOL1695	<i>queA</i>	S-adenosylmethionine: tRNA ribosyltransferase-isomerase	0.93	0.57*	0.61*	1.48*	0.75

Purines, pyrimidines, nucleosides and nucleotides:***Nucleotide and nucleoside interconversions***

SACOL1277	<i>pyrH</i>	uridylylate kinase	0.68	0.53*	0.46*	0.79*	0.65*
SACOL1371	<i>guaC</i>	GMP reductase	0.41*	0.45*	0.53*	1.16*	0.65
SACOL2111	<i>tdk</i>	thymidine kinase	0.93	0.47*	0.60*	1.17*	0.71

Pyrimidine ribonucleotide biosynthesis

SACOL1214	<i>carA</i>	carbamoyl-phosphate synthase, small subunit	1.35	0.38*	0.62*	0.75	0.55
SACOL1216	<i>pyrF</i>	orotidine 5-phosphate decarboxylase	1.63	0.37*	0.63*	0.73	0.55*

Salvage of nucleosides and nucleotides

SACOL2128	<i>pdp</i>	pyrimidine-nucleoside phosphorylase	0.78	0.59*	0.65*	0.94	0.85
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Regulatory Functions:***DNA interactions***

SACOL2308		phosphosugar-binding transcriptional regulator, RpiR family	0.82	0.60	0.47*	0.53*	0.83
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RNA interactions

SACOL1210	<i>pyrR</i>	pyrimidine operon regulatory protein	0.74	0.46	0.41*	0.43*	0.59
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Other

SACOL1904		transcriptional regulator, putative	0.78	0.82	0.62*	0.52*	0.80
MW1960	<i>agrB</i>	accessory gene regulator B	0.75	0.33*	0.28*	1.27	0.60*
SACOL2023	<i>agrB</i>	accessory gene regulator protein B	0.73	0.53*	0.28*	0.99	0.77
SACOL2026	<i>agrA</i>	accessory gene regulator protein A	0.80	0.34*	0.20*	1.34	0.45*

Transport and binding proteins:***Amino acids, peptides and amines***

SACOL1108		spermidine/putrescine ABC transporter, ATP-binding protein	1.08	0.35*	0.51*	1.12	0.76
SACOL1110		spermidine/putrescine ABC transporter, permease protein	0.86	0.42*	0.42*	0.89	0.86
SACOL2382		proton/sodium-glutamate symport protein	1.07	0.90	0.60*	0.63*	0.81

Carbohydrates, organic alcohols and acids

SACOL0175		PTS system, IIABC components	0.83	0.61*	0.72*	0.51*	0.85
SACOL0454		sodium:dicarboxylate symporter family protein	0.72	0.56*	0.63*	0.82	0.68*

Cations and iron carrying compounds

SACOL0679		Na ⁺ /H ⁺ antiporter, MnhA component, putative	0.71	1.05	0.65*	1.59*	0.66*
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Nucleosides, purines, pyrimidines

SACOL1211	<i>uraA</i>	uracil permease	0.77	0.51	0.58*	0.77	0.59*
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Unknown substrate

SACOL0159		ABC transporter, permease protein	1.31	0.47*	0.59*	0.99	0.52*
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Unknown Functions:***General***

SACOL0507		LysM domain protein	0.81	0.26*	0.46*	0.78*	0.54*
SACOL1164		fibrinogen binding-related protein	0.97	0.82	0.57*	0.64*	1.09
SACOL1168	<i>efb</i>	fibrinogen-binding protein	1.05	0.39	0.30*	0.45*	0.45
SACOL1169		fibrinogen-binding protein precursor-related protein	0.80	0.46	0.42*	0.57*	0.66
SACOL2591		actVA 4 protein	0.88	0.91	0.64*	0.65*	0.82

Hypothetical proteins:

SAV0411		exotoxin homolog	0.85	0.61*	0.69*	0.51*	0.94
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Conserved

SACOL0157		conserved hypothetical protein	1.09	0.38*	0.41*	1.07	0.52*
SACOL0160		conserved hypothetical protein	1.20	0.59*	0.74*	0.87	0.59*
SACOL0199		conserved hypothetical protein	0.73	0.57	0.43*	0.42*	0.61
SACOL0767		conserved hypothetical protein	0.85	0.63	0.39*	1.28*	0.51*
SACOL0802		conserved hypothetical protein	1.07	0.78	0.57*	0.57*	0.71
SACOL1821		conserved hypothetical protein	1.07	0.88	0.60*	0.55*	0.89
SACOL2020		conserved hypothetical protein	0.49	0.85	1.02	0.66	1.00

SACOL2373	conserved hypothetical protein	0.56*	0.66	0.59*	0.47*	0.86
SACOL2461	conserved hypothetical protein	0.83	0.76	0.53*	0.44*	1.03
Domain						
SACOL1847	conserved domain protein, putative	0.80	0.28*	0.63*	0.71*	0.69

Data table 1c. Genes differentially regulated in hVISA/VISA compared to matched VSSA after vancomycin exposure, up-regulated.

ORF ID ^a	Gene	TIGR description ^b	Isolate pair				
			1	2	3	4	5
Amino acid biosynthesis:							
<i>Pyruvate family</i>							
SACOL0600	<i>ilvE</i>	branched-chain amino acid aminotransferase	1.04	2.10*	1.89*	1.07	1.17
Biosynthesis of cofactors, prosthetic groups and carriers:							
<i>Glutathione and analogs</i>							
SACOL2641	<i>gpxA2</i>	glutathione peroxidase	3.19*	1.27	2.17*	1.04	1.06
<i>Other</i>							
SACOL0538	<i>ispE</i>	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	2.75*	0.78	0.76	1.52*	0.87
Cell envelope:							
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>							
SACOL0136	<i>cap5A</i>	capsular polysaccharide biosynthesis protein Cap5A	3.23*	1.37	0.93	3.80*	0.95
SACOL0137	<i>cap5B</i>	capsular polysaccharide biosynthesis protein Cap5B	2.81*	1.21	1.18	3.62*	1.01
SACOL0138	<i>cap5C</i>	capsular polysaccharide biosynthesis protein Cap5C	3.58*	1.54	1.21	4.46*	1.24
SACOL0139	<i>cap5D</i>	capsular polysaccharide biosynthesis protein Cap5D	3.52*	1.26	1.04	4.39*	0.84
SACOL0140	<i>cap5E</i>	capsular polysaccharide biosynthesis protein Cap5E	3.76*	1.50	1.25	4.88*	1.02
SACOL0141	<i>cap5F</i>	capsular polysaccharide biosynthesis protein Cap5F	2.65*	1.32	1.27	3.69*	1.26
SACOL0142	<i>cap5G</i>	capsular polysaccharide biosynthesis protein Cap5G	2.32*	1.39	1.94	3.81*	0.97
SACOL0147	<i>cap5L</i>	capsular polysaccharide biosynthesis protein Cap5L	1.59*	1.54	2.06	1.73*	1.14
SACOL1062	<i>atl</i>	bifunctional autolysin	1.62*	1.49*	1.56*	1.04	1.20
SACOL1522		elastin binding protein, putative	1.54*	1.49*	1.88*	1.10	1.31
<i>Other</i>							
SACOL0466		membrane protein, putative	1.42	1.59*	1.61*	0.92	1.32*
SACOL2676		LPXTG cell wall surface anchor family protein	1.87*	1.17	1.64	1.70*	1.04
Cellular Processes:							
<i>Detoxification</i>							
SACOL1368	<i>kataA</i>	catalase	1.24	1.95*	2.00*	1.36	1.55*
<i>DNA transformation</i>							
SACOL1003		negative regulator of competence MecA, putative	1.10	1.57*	0.99	2.42*	1.21
<i>Pathogenesis</i>							
SACOL0856	<i>clfA</i>	clumping factor A	2.13*	1.48	1.14	1.86*	1.02
<i>Toxin production and resistance</i>							
SACOL0086		drug transporter, putative	1.05	1.54*	0.99	1.57*	1.87
SACOL0672	<i>sarA</i>	staphylococcal accessory regulator A	1.80*	1.81*	1.69*	1.85*	0.95
SACOL2347		drug resistance transporter, EmrB/QacA subfamily	1.17	1.69*	1.93*	0.73	1.99*
SACOL2348		drug transporter, putative	1.11	1.28	1.97*	0.69	1.56*
Central intermediary metabolism:							
<i>Amino sugars</i>							
SACOL2145	<i>glmS</i>	glucosamine--fructose-6-phosphate aminotransferase (isomerizing)	1.89*	1.65	1.33*	1.63*	1.05
<i>Nitrogen metabolism</i>							
SACOL2280	<i>ureA</i>	urease, gamma subunit	3.37*	0.85	1.31	2.48*	0.68
SACOL2281	<i>ureB</i>	urease, beta subunit	2.89*	0.95	1.15	2.12*	0.55
SACOL2282	<i>ureC</i>	urease, alpha subunit	5.32*	0.98	1.10	2.76*	0.75
SACOL2283	<i>ureE</i>	urease accessory protein UreE	3.49*	0.89	1.04	2.61*	0.61*
SACOL2284	<i>ureF</i>	urease accessory protein UreF	4.39*	1.07	1.05	2.85*	0.75
SACOL2285	<i>ureG</i>	urease accessory protein UreG	3.81*	1.05	1.15	2.80*	0.77

SACOL2286	<i>ureD</i>	urease accessory protein UreD	3.19*	1.02	1.18	2.52*	0.72*
SACOL2397	<i>nirD</i>	nitrite reductase [NAD(P)H], small subunit	1.39	1.06	1.10	1.55*	1.68*
Energy metabolism:							
<i>Glycolysis/gluconeogenesis</i>							
SACOL1745	<i>pyk</i>	pyruvate kinase	1.17	1.88*	1.31	1.00	1.54*
<i>Sugars</i>							
SACOL2149	<i>mitD</i>	mannitol-1-phosphate 5-dehydrogenase	1.46	1.70*	1.53*	0.84	1.29*
<i>Other</i>							
SACOL2553		pyruvate oxidase	1.35	2.14*	1.52*	0.76	1.53*
Protein synthesis:							
<i>Ribosomal proteins: synthesis and modification</i>							
SACOL1254	<i>rpsP</i>	ribosomal protein S16	1.12	1.15	2.18*	1.60*	1.03
<i>tRNA aminoacylation</i>							
SACOL0009	<i>serS</i>	seryl-tRNA synthetase	2.10*	1.84*	1.62	1.76*	0.91
Purines, pyrimidines, nucleosides and nucleotides:							
<i>2'-Deoxyribonucleotide metabolism</i>							
SACOL0791	<i>nrdI</i>	nrdI protein	0.89	1.55*	1.59	1.87*	1.29
Regulatory Functions:							
<i>DNA interactions</i>							
SACOL0539	<i>purR</i>	pur operon repressor	3.68*	0.97	0.66	1.65*	0.88
SACOL1374	<i>lexA</i>	LexA repressor	1.02	1.55*	2.09*	1.51*	1.11
SACOL2517		transcriptional regulator, MerR family	1.61*	1.99*	1.23	1.19	1.17
Transcription:							
<i>Transcription factors</i>							
SACOL2113	<i>rho</i>	transcription termination factor Rho	1.96*	1.25	1.75*	1.26	1.29*
Transport and binding proteins:							
<i>Amino acids, peptides and amines</i>							
SACOL2619		amino acid permease	1.10	2.59*	2.04*	0.58*	1.37*
<i>Carbohydrates, organic alcohols and acids</i>							
SACOL2148		PTS system, mannitol-specific IIA component	1.74*	2.14*	1.65*	0.83	1.36*
<i>Unknown substrate</i>							
SACOL0688		ABC transporter, substrate-binding protein	1.18	1.52*	1.22	1.76*	0.97
SACOL0882		ABC transporter, ATP-binding protein	1.20	2.10*	2.04*	1.74*	1.55*
SACOL0883		ABC transporter, permease protein	1.13	1.76*	1.94*	1.64*	1.47*
SACOL0884		ABC transporter, substrate-binding protein	1.10	1.80*	1.87*	1.46*	1.27*
Unknown Functions:							
<i>Enzymes of unknown specificity</i>							
SACOL0399		oxidoreductase, putative	1.49*	1.67*	1.70*	1.00	1.28
SACOL1543		oxidoreductase, aldo/keto reductase family	1.77*	1.69*	1.98*	0.98	1.41*
SACOL2321		oxidoreductase, short chain dehydrogenase/ reductase family	1.35	1.97*	1.67*	1.19	1.25
SACOL2446		epimerase/dehydratase, putative	2.19*	0.83	3.04*	1.02	1.02
SACOL2575		aminotransferase, class I	1.41	1.53*	2.42*	1.37	1.26
SACOL2597		hydrolase, alpha/beta hydrolase fold family	1.25	1.68*	2.00*	0.85	1.47*
SACOL2620		aminotransferase, class III	1.14	2.41*	4.98*	0.46*	1.44*
<i>General</i>							
SACOL0089		antigen, 67 kDa	2.12*	1.75*	1.29	0.88	1.14
SACOL2088		sceD protein, putative	1.91*	0.95	3.66	1.68*	1.33
Hypothetical proteins:							
SAV0058		hypothetical protein	1.30	2.42*	1.57*	0.85	1.41*
SAV0069		hypothetical protein	1.65*	1.28	1.02	2.20*	0.97

SAV0394	hypothetical protein	1.00	1.23	5.19*	0.86	2.74*
SAV0854	hypothetical protein	1.02	1.28	3.93*	1.06	3.11*
SAV0871	hypothetical protein	0.95	1.19	2.49*	0.95	1.54*
SAV0882	hypothetical protein	1.09	1.28	2.84*	1.08	2.94*
SAV0884	hypothetical protein	0.93	1.18	3.28*	1.02	2.40*
SAV0898	hypothetical protein	1.01	1.11	3.89*	1.01	1.76*
<i>Conserved</i>						
SACOL0409	conserved hypothetical protein					
SACOL0467	conserved hypothetical protein	1.50*	1.75*	2.22*	0.86	1.50*
SACOL0511	conserved hypothetical protein	1.38	1.88*	1.43	0.87	1.54*
SACOL2519	conserved hypothetical protein	1.71*	1.15	1.31	1.80*	0.67
SACOL2711	conserved hypothetical protein	1.39	1.61*	1.51*	0.79	1.10
SACOL2723	conserved hypothetical protein	1.72*	1.87*	0.87	0.69*	1.22

Data table 1d. Genes differentially regulated in hVISA/VISA compared to matched VSSA after vancomycin exposure, down-regulated.

ORF ID ^a	Gene	TIGR description ^b	Isolate pair				
			1	2	3	4	5
Amino acid biosynthesis:							
<i>Aspartate family</i>							
SACOL0503		trans-sulfuration enzyme family protein	0.97	0.31*	0.39*	1.65*	0.51*
<i>Glutamate family</i>							
SACOL0963	<i>argH</i>	argininosuccinate lyase	0.88	0.31*	0.35*	0.27*	1.17
SACOL0964	<i>argG</i>	argininosuccinate synthase	1.01	0.51*	0.38	0.41*	1.20
<i>Serine family</i>							
SACOL0502		cysteine synthase/cystathionine beta-synthase family protein	0.91	0.29*	0.45*	1.44*	0.56*
Biosynthesis of cofactors, prosthetic groups, and carriers:							
<i>Pyridoxine</i>							
SACOL0564		pyridoxine biosynthesis protein	0.87	0.65*	0.44*	0.78	0.71*
Cell envelope:							
<i>Biosynthesis and degradation of murein sacculus and peptidoglycan</i>							
SACOL2116	<i>murAB</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	0.81	0.63*	0.57*	0.98	0.73*
<i>Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides</i>							
SACOL1043		glycosyl transferase, group 1 family protein	0.40*	0.51*	0.81	0.49	0.83
SACOL2103		UDP-N-acetylglucosamine 2-epimerase	0.97	0.53	0.09*	1.65	0.35*
<i>Other</i>							
SACOL0479		surface protein, putative	0.94	0.55*	0.91	0.41*	0.80
SACOL1168	<i>efb</i>	fibrinogen-binding protein	0.79	0.44*	0.34*	0.39*	0.63
SACOL2451		amino acid ABC transporter, amino acid-binding protein	0.95	0.62*	0.54*	1.13	0.70
SACOL2520		membrane protein, putative	1.19	0.67*	0.66	1.16	0.58*
SACOL2694	<i>geh</i>	lipase	1.20	0.65*	0.59	1.11	0.44*
Cellular Processes:							
<i>Pathogenesis</i>							
SACOL0095	<i>spa</i>	immunoglobulin G binding protein A precursor	0.07*	0.13*	0.25*	0.08*	1.49
SACOL2418		IgG-binding protein SBI	0.51*	0.32*	0.39*	0.35*	0.56*
<i>Toxin production and resistance</i>							
SACOL0478		exotoxin 3, putative	0.70	0.36*	1.44	0.46*	0.74
SACOL1173	<i>hly</i>	alpha-hemolysin precursor	1.04	0.40*	0.66	0.62*	0.81
SACOL1475		drug transporter, putative	0.49	0.60*	1.15	0.46*	1.38
SACOL2004		leukocidin F subunit precursor, putative	0.77	0.27*	0.38*	0.29*	0.48*
SACOL2006		Aerolysin/Leukocidin family protein	0.88	0.44*	0.76	0.39*	0.70
SACOL2523		drug transporter, putative	1.06	0.75	0.54*	0.66*	0.75*
SACOL2524		transcriptional regulator, MarR family	0.85	0.51*	0.48*	0.68	0.55*
DNA metabolism:							
<i>Replication, recombination, repair</i>							
SACOL0678		integrase/recombinase, phage integrase family	0.70	0.38*	0.54*	1.16	0.46*
Energy metabolism:							
<i>Amino acids and amines</i>							
SACOL1477	<i>ilvA1</i>	threonine dehydratase, catabolic	0.48	0.47*	0.80	0.26*	1.80
SACOL1478	<i>ald1</i>	alanine dehydrogenase	0.49	0.49*	0.71	0.25*	1.26

SACOL1593		glycine cleavage system P protein, subunit 2	0.99	0.59*	0.57*	0.82	0.82
SACOL2654	<i>arcC2</i>	carbamate kinase	1.15	0.66*	0.89	0.48*	0.97
Anaerobic							
SACOL0204	<i>pflB</i>	formate acetyltransferase	0.47	0.28*	0.21*	0.29*	0.71*
SACOL0205	<i>pflA</i>	pyruvate formate-lyase-activating enzyme	0.51	0.28*	0.22*	0.35*	0.63*
ATP-proton motive force interconversion							
SACOL2096	<i>atpG</i>	ATP synthase F1, gamma subunit	0.97	0.58	0.59*	0.58*	0.82
SACOL2097	<i>atpA</i>	ATP synthase F1, alpha subunit	1.08	0.58	0.57*	0.63*	0.91
SACOL2099	<i>atpF</i>	ATP synthase F0, B subunit	1.11	0.58	0.55*	0.64*	0.87
SACOL2100	<i>atpE</i>	ATP synthase F0, C subunit	1.06	0.46*	0.67*	0.65*	0.93
SACOL2101	<i>atpB</i>	ATP synthase F0, A subunit	1.22	0.54	0.54*	0.63*	0.93
Biosynthesis and degradation of polysaccharides							
SACOL2183	<i>lacD</i>	tagatose 1,6-diphosphate aldolase	0.25*	0.47*	0.91	0.92	0.60
Electron transport							
SACOL0494	<i>nuoF</i>	NADH dehydrogenase I, F subunit	0.88	0.50*	0.64	0.51*	0.92
Fermentation							
SACOL0660		alcohol dehydrogenase, zinc-containing	0.70	0.68	0.57*	0.50*	1.02
TCA cycle							
SACOL1159	<i>sdhA</i>	succinate dehydrogenase, flavoprotein subunit	0.90	0.61*	0.48*	0.78	0.65*
SACOL1262	<i>sucC</i>	succinyl-CoA synthase, beta subunit	1.13	0.56*	0.59*	0.85	0.69
SACOL1448	<i>sucB</i>	2-oxoglutarate dehydrogenase, E2 component, dihydroipoamide succinyltransferase	1.39	0.55	0.42*	0.89	0.54*
SACOL1449	<i>sucA</i>	2-oxoglutarate dehydrogenase, E1 component	1.55*	0.60*	0.53*	1.11	0.64
Protein fate:							
Protein folding and stabilization							
SACOL1638	<i>grpE</i>	heat shock protein GrpE	0.81	0.66*	0.76	0.70*	0.57*
SACOL2016	<i>groEL</i>	chaperonin, 60 kDa	0.56*	0.83	0.68*	0.64*	0.70*
SACOL2017	<i>groES</i>	chaperonin, 10 kDa	0.52*	0.61*	0.73	0.70*	0.57*
Protein synthesis:							
tRNA and rRNA base modification							
SACOL1962	<i>gatC</i>	glutamyl-tRNA(Gln) amidotransferase, C subunit	0.63*	0.72	0.89	0.57*	0.89
Translation factors							
SACOL1278	<i>frr</i>	ribosome recycling factor	0.64*	0.54*	0.61*	0.84	0.70*
Purines, pyrimidines, nucleosides and nucleotides:							
Nucleotide and nucleoside interconversions							
SACOL1277	<i>pyrH</i>	uridylate kinase	0.61*	0.61	0.59*	0.74	0.79
Pyrimidine ribonucleotide biosynthesis							
SACOL1212	<i>pyrB</i>	aspartate carbamoyltransferase	0.46*	0.33*	0.94	0.62	0.50*
SACOL1213	<i>pyrC</i>	dihydroorotase	0.46*	0.44*	0.73	0.92	0.65*
SACOL1214	<i>carA</i>	carbamoyl-phosphate synthase, small subunit	0.54*	0.61	0.74	0.84	0.51*
SACOL1215	<i>carB</i>	carbamoyl-phosphate synthase, large subunit	0.59	0.73	0.58*	0.88	0.43*
Salvage of nucleosides and nucleotides							
SACOL2128	<i>pdp</i>	pyrimidine-nucleoside phosphorylase	0.76	0.47*	0.48*	0.66*	0.70
Regulatory Functions:							
DNA interactions							
SACOL0518		transcriptional regulator, GntR family	0.98	1.13	0.65*	0.62*	0.99
SACOL1639	<i>hrcA</i>	heat-inducible transcription repressor HrcA	0.83	0.80	0.64*	0.78	0.58*
RNA interactions							
SACOL1210	<i>pyrR</i>	pyrimidine operon regulatory protein	0.58	0.39*	1.29	0.37*	0.64
Other							
SACOL1398		transcriptional regulator, putative	0.79	1.28	0.51*	0.48*	0.63*
MW1960	<i>agrB</i>	accessory gene regulator B	0.74	0.45*	0.15*	1.20	0.42*
SA1842	<i>agrB</i>	accessory gene regulator B	0.73	0.45*	0.15*	1.22	0.40*
SACOL2023	<i>agrB</i>	accessory gene regulator protein B	0.65*	0.31*	0.10*	1.15	0.29*
SACOL2025	<i>argC2</i>	accessory gene regulator protein C	0.64	0.35*	0.10*	1.12	0.31*

SACOL2026	<i>agrA</i>	accessory gene regulator protein A	0.88	0.49*	0.15*	1.18	0.37*
Signal transduction:							
2-component system							
SACOL0765	<i>saeS</i>	sensor histidine kinase	0.81	0.50*	0.44*	0.90	0.67
SACOL0766	<i>saeR</i>	DNA-binding response regulator	0.80	0.39*	0.37*	0.85	0.60*
Transport and binding proteins:							
Amino acids, peptides and amines							
SACOL1110		spermidine/putrescine ABC transporter, permease protein	0.70	0.46*	0.52*	0.81	1.08
SACOL1111		spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein	0.82	0.57*	0.58*	0.52*	0.85
SACOL1476		amino acid permease	0.43*	0.41*	0.65	0.27*	1.32
SACOL1915		amino acid ABC transporter, ATP-binding protein	0.95	0.50*	0.46	0.37*	1.08
SACOL1916		amino acid ABC transporter, permease/substrate-binding protein	0.82	0.38*	0.38*	0.38*	0.98
SACOL2452		amino acid ABC transporter, permease protein	0.89	0.57*	0.57*	1.02	0.59*
SACOL2453		amino acid ABC transporter, ATP-binding protein	0.85	0.61*	0.60*	0.95	0.63*
Carbohydrates, organic alcohols and acids							
SACOL0175		PTS system, IIABC components	0.85	0.39*	0.43*	0.31*	0.84
SACOL0454		sodium:dicarboxylate symporter family protein	0.55*	0.58*	0.52*	0.61*	0.95
SACOL2181	<i>lacE</i>	PTS system, lactose-specific IIBC components	0.27*	0.63*	0.79	0.86	0.89
SACOL2363		L-lactate permease	0.85	0.78	0.57*	0.40*	0.81
SACOL2376		PTS system, sucrose-specific IIBC components, putative	1.17	0.64*	0.38*	0.62*	0.61*
SACOL2552		PTS system, IIABC components	0.99	0.45*	0.35*	0.41*	0.58*
Cations and iron carrying compounds							
SACOL0946		Na ⁺ /H ⁺ antiporter family protein	0.70	0.48*	0.57	0.45*	0.72
Nucleosides, purines, pyrimidines							
SACOL1211	<i>uraA</i>	uracil permease	0.55*	0.36*	0.73	0.79	0.77
Other							
SACOL0303		acid phosphatase5-nucleotidase, lipoprotein e(P4) family	0.80	0.52*	0.62*	0.39*	0.82
Unknown substrate							
SACOL0158		ABC transporter, ATP-binding protein, authentic frameshift	0.99	0.41*	0.46*	1.21	0.67
SACOL0159		ABC transporter, permease protein	1.10	0.41*	0.26*	1.27	0.53*
SACOL0506		ABC transporter, substrate-binding protein	0.81	0.62*	0.78	0.72*	0.60*
Unknown Functions:							
Enzymes of unknown specificity							
SACOL0569		ATP:guanido phosphotransferase family protein	0.99	0.72	0.81	0.63*	0.61*
General							
SACOL0276	<i>yukA</i>	diarrheal toxin	1.77*	0.58*	0.68	0.56*	0.98
SACOL0507		LysM domain protein	0.72	0.57*	0.51*	0.72	0.87
SACOL0772		exsB protein	0.89	0.63*	1.07	0.54*	1.35
SACOL1164		fibrinogen binding-related protein	0.97	0.63	0.52*	0.55*	0.77
SACOL1169		fibrinogen-binding protein precursor-related protein	0.67	0.43*	0.40*	0.43*	0.64
SACOL2203		ClpA-related protein	0.89	0.64	0.12*	1.56	0.33*
SACOL2484		alkylhydroperoxidase, AhpD family	1.26	0.49*	0.75	0.83	0.52*
SACOL2584	<i>isaA</i>	immunodominant antigen A	0.84	0.36*	0.89	0.56*	0.76
Hypothetical proteins:							
MW1884		hypothetical protein	0.58*	0.63*	0.78	1.25	0.93
MW2407		hypothetical protein	0.05*	0.12*	0.21*	0.05*	1.41
SACOL0272		hypothetical protein	1.43	0.40*	0.64	0.47*	0.82
SACOL1846		hypothetical protein	0.99	0.17*	0.45*	0.40*	0.48*
SAV0411		exotoxin homolog	0.82	0.44*	0.95	0.60*	0.68*

SAV1425	amino acid permease homolog	0.48	0.52*	0.69	0.43*	1.08
Conserved						
SACOL0157	conserved hypothetical protein	1.15	0.24*	0.21*	1.07	0.30*
SACOL0160	conserved hypothetical protein	1.04	0.42*	0.34*	1.12	0.56*
SACOL0271	conserved hypothetical protein	3.37*	0.56	0.65*	0.29*	0.61*
SACOL0495	conserved hypothetical protein	0.74	0.37*	0.47*	0.45*	0.83
SACOL0565	conserved hypothetical protein	0.86	0.68*	0.47*	0.76	0.65*
SACOL0625	conserved hypothetical protein	0.62	1.12	0.52*	0.96	0.56*
SACOL0710	conserved hypothetical protein	0.73	0.75	0.37*	1.42*	0.64*
SACOL0767	conserved hypothetical protein	0.81	0.26*	0.27*	0.81	0.54*
SACOL0768	conserved hypothetical protein	0.76	0.33*	0.34*	0.73	0.38*
SACOL1481	conserved hypothetical protein	0.89	0.62*	1.21	0.45*	1.15
SACOL1847	conserved hypothetical protein, putative	0.91	0.26*	0.54	0.36*	0.51*
SACOL2034	conserved hypothetical protein	0.83	0.49*	0.58*	1.06	0.78
SACOL2464	conserved hypothetical protein	0.61*	0.71	0.87	1.29	0.65*
SAV0040	conserved hypothetical protein	0.77	0.76	0.61*	0.81	0.67*
SAV2510	conserved hypothetical protein	0.49*	0.82	0.93	0.41*	1.19

^aPrefix SACOL, MRSACOL gene ID; SA, N315 gene ID; MW, MW2 gene ID; SAV, Mu50 gene ID.

^bThe Institute for Genomic Research gene function category. Note. *denotes P-value for fold change <0.05