

Table S1. Oligonucleotides used in this study.

<i>Strain construction primers</i>	
01838-usNF-BamHI	TTGGTTGGATCCGGCAACTGGTAACATTAACGAACGC
01838-usNR	CTTTTCTGTCTGTAAAACCTTAACCTCCATTATATGATTTATATATGC
01838-dsCF	GGAGGTTAAGTTTTACAGACAGAAAAGTACATTAAGAGCC
01838-dsCR-Sall	AACCAAGTCGACCGTGACTATGGTAAACACGTCGGC
01761-usNF-BamHI	TTGGTTGGATCCCCCGCACGTGTATTAGTTGAGATTAAATC
01761-usNR	GGAGGCGAACTGAAATTATTGCATAAGAAATATATTTTAGTTATCC
01761-dsCF	CTTATGCAATAATTTCAAGTTCGCTCCAATGTCTTCATC
01761-dsCR-Sall	AACCAAGTCGACCCAGTCTTGTAAGAAGCGGGTTAC
<i>Strain verification primers</i>	
01838 Δ -usNF	TTGGTTCGTATTACCAATTCCGGCAATAATTG
01838 Δ -dsCR	AACCAAGAGACTGGTTAGGACAAATCTCA
01761 Δ -usNF	TTGGTTCGTAGTTCTTTTCATCATAACGATC
01761 Δ -dsCR	AACCAAGAAGGAGTGTGGTTTGATTTTAGGG
<i>qRT-PCR primers</i>	
16SF	GCCTAATACATGCAAGTCGAGCGAACAGACG
16SR	GCGCGGATCCATCTATAAGTGACAGC
00051F	GCACATGCGTCAGATTCGTTGAGT
00051R	AGCCACTATCATGTGAACCCGGTA
00069F	AAATGCTGATCAACGCAATG
00069R	AGGCGCTTTGTTGATCTTTG
00094F	AAATGCGCATGCCGACACAACCTT
00094R	TTGTGCTTGCGTCATTCCTTGTGG
00192F	TTTCGCTAGGCGCATTAGCAGTTG
00192R	CTCCCAGCATTAACTTGTGATTTCCAC
00256F	CAACACGCCAAACAACAATC
00256R	TCGGTATTGCTGGTGTCAA
00300F	CACATGAAGCACAAGCCTCGGAAA
00300R	TTATCGCATTCCCTTGTCTCCCG
00354F	GGAACATACACAGTTGCTGGCAGA
00354R	GGCAAATGTTCTCCCATATACAAGCC
00399F	CAGGGATGATTACAACACTACTGCTCAGCC
00399R	CCTGACTGATTTGTATACTCAAAGAACGG
00427F	CGGGTGAATCAGTGTGGGCAATTT
00427R	TGAGTTCGTTGATGGACGGCTACT
00472F	TTAGCGCAAGAAGTTGCTGA
00472R	GCTGCAGAAGCACGTTTACA
00617F	GTTGGCAAAGCAGTAACACATACGG
00617R	GGTGCTGAGGCAAATTGATAAGTCG
00728F	GTTCTGTCTGTAATGGCGGC
00728R	GTCATCTTCAGATGCTAGCGC
00818F	GTGCTGGCATATGTATGGCAATCGT
00818R	ACCTCTTTGCGTATTGCCCTTTTCG
00897F	CTGCTGGCGCTGAACAAACAATC
00897R	ATGCTTGAAACGTATGCTCGGGTG
00987F	AGCCAAAGCCGATTCACACTCT
00987R	GCTTCGCCAAGTTCATATTTACCAG
00988F	CGTTGCAACTTTGACAACAGCGAC
00994F	CAAGACCCTGCTATTGTCCAACCA
00994R	GTTGACTTTGCAACAGGCTGCGTA
00988R	GGTGTTTGTGTTTGTGCTTACTGC
01114F	GCGAAGGATACGGTCCAAGAGAAA
01114R	GGACGTGCACCATATTCGAATGTACC
01121F	GAACGAAAGGTACCATTGCTGGTCA
01121R	TAAAGGCTGAAGGCCAGGCTAAAC
01125F	TGGCAAAAAGATAACGGTACG
01125R	TGCTGCAGGAGTAACACCAC
01652F	TACAAATCGCACAAGGCTCA
01652R	CAGCCGTATCCAACATTTCC
01761F	CGCAACCCACTAATGATGCC
01761R	CACGCATTGACTCATCTCC

01838F GACCGCCCTTCGATTGGTATTGG
01838R CGGTAACAGTGACTIONGATTACCAGG
01935F GTCGGCACAACAATGGTTGAAGGT
01935R AACTACAAATCCTGTTCCAGCGCC
01936F GGCACAACAGTGGTTGAGGGTATT
01936R CCAGATCCTATCGAAACGACACCA
01938F TCGGCACAACAGTGGTTGATGGTA
01938R TACAAATCCTGTTCCAGCGCCCAT
01939F TACTGCCCATCCAAACGGTGACAA
01939R GTCCACGTTCTGACTGCTTGTCTT
01941F AGTGGGCGATCGTATTACTGCACA
01941R GTCCACGTTCTATTGCACGCTCTT
01942F TGTGGGTGGTACTGGTGTAGTTGT
01942R TAACGTCGTAGTTTCCCTCCGCCTT
01949F TGAGTAATGCATCAGCGTCAGAAG
01949R TCTGTGCCACATGTAATTCCGGT
01954F ACGTTAGTACTTAAGGCAGCCGGA
01954R CCGAAACATTATACTTACCGCCC
01972F GCTGGAGACGTAACAGTTGCAG
01972R CGGCTGTTAAACCTTGCTGTTGAAGGGCC
02127F CCCTATTGCAAACGCTGAGAGCAA
02127R GGTTACCAAGTGTATACGAGGCT
02171F CCAACAGGCCCGTATTTGATGGTA
02171R TATGCTGTCGCATCTAATGCC
02241F TGCCTGTAAGTGTGTCTGAAGGGT
02241R CCCAGAAACCATGGCGATTCCAA
02243F TCAGCAGCAACGACTCAAGCAA
02243R TTCCAATATCATCCGGTGCTG
02260F AGGAAGGAGTATTTCAATGGCAC
02260R GTGAATTTGTTCACTGTGTGATAATCC
02463F TGAGGAACACATGGCTGGACGTTA
02463R TTCGTGCGCTCTTTCTCTGTAGCA
02466F TGCATTACCGAGTCACGAAG
02466R AAGTTGCTGTTTGGGCATTA
02706F TAAAGACAGCAAGAACCCAGACCG
02706R CCCAACTTGTTGGCTTCTATCAGGG
02708F TCGGCCAAGGTGCAGAAATCATCA
02708R GCCTTGATCTTAACAAGTAGGGCA
02709F TCGGTGGTAATTTCCAATCAGCCC
02709R CGAATGAATTCGCTTTGACGCC
02710F GGAAGAGATAGCTTCCACCCAACA
02710R TGGCATTGTTGTTGCGCTATGA
02742F TGTAAGTTTGCCTGGACTAGG
02742R CCCGTTAAATCTGTGCCATT
02798F TGCACCACAGGGTGTAGAAG
02798R TCGGTTATGAGTGACTIONGACGA
02885F CGTACAAGGACAAATACCGG
02885R CTGTCCACTGAGCACAACG
02971F GCAACCGAGTGTGATGGTGTTC
02971R GCTTTGTGCGCTGCGTCATCTTTA
02972F AGCAGCAACATTAGCATTGGGCAC
02972R TTGCTGCCTGTGCCTGTTTACTTG
02979F CCTCGTAATGGCGAAAAGTC
02979R TGGCGAATTTGGTTGCTTAT
03006F CAAGCACAAGCAGCTGAGAAGCAA
03006R GTATGTTGCTGTTGCTCAACACCG

Table S2. List of proteins identified by MudPIT with greater than 10 spectral counts in the absence of arylomycin treatment (0xMIC)

Protein	Spectral Counts ^a				Fold-Decrease vs 0xMIC			p-value ^b
	0xMIC	0.5xMIC	2xMIC	8xMIC	2xMIC	0.5xMIC	8xMIC	
SAOUHSC_00002 - DNA polymerase III, beta subunit [2.7.7.7] {Staphylococcus aureus}	16.5 ± 2	50.5 ± 4	41.8 ± 4	18.3 ± 5	0.3	0.4	0.9	0.379074
SAOUHSC_00006 - DNA gyrase, A subunit [5.99.1.3] {Staphylococcus aureus}	10 ± 5	16.3 ± 5	7.5 ± 3	1 ± 1	0.6	1.3	10.0	0.065498
SAOUHSC_00009 - seryl-tRNA synthetase [6.1.1.11] {Staphylococcus aureus}	21.5 ± 7	49.5 ± 6	48 ± 9	17 ± 4	0.4	0.4	1.3	0.290055
SAOUHSC_00019 - adenylosuccinate synthetase [6.3.4.4] {Staphylococcus aureus}	41.3 ± 9	76.8 ± 15	50.5 ± 7	8.8 ± 1	0.5	0.8	4.7	0.007070
SAOUHSC_00025 - conserved hypothetical protein {Staphylococcus aureus}	76 ± 8	67.8 ± 13	81.5 ± 14	55.3 ± 15	1.1	0.9	1.4	0.140803
SAOUHSC_00051 - 1-phosphatidylinositol phosphodiesterase precursor, putative {Staphylococcus aureus}	591.5 ± 74	70.5 ± 16	125.5 ± 2	76.8 ± 25	8.4	4.7	7.7	0.000282
SAOUHSC_00052 - conserved hypothetical protein {Staphylococcus aureus}	11.8 ± 4	7.3 ± 3	8.5 ± 3	9.3 ± 2	1.6	1.4	1.3	0.303738
SAOUHSC_00069 - protein A {Staphylococcus aureus NCTC 8325} xxxxx	28 ± 5	19.5 ± 5	25.3 ± 9	2.8 ± 2	1.4	1.1	10.2	0.002306
SAOUHSC_00086 - 3-ketoacyl-acyl carrier protein reductase, putative [1.1.1.11] {Staphylococcus aureus}	19.5 ± 7	42.5 ± 6	37.5 ± 8	14.8 ± 5	0.5	0.5	1.3	0.297291
SAOUHSC_00093 - superoxide dismutase, putative {Staphylococcus aureus}	20.3 ± 3	69.3 ± 25	27 ± 2	9 ± 1	0.3	0.8	2.3	0.012559
SAOUHSC_00094 - conserved hypothetical protein {Staphylococcus aureus}	297.8 ± 23	70.3 ± 8	64.5 ± 6	44.3 ± 11	4.2	4.6	6.7	0.000033
SAOUHSC_00101 - phosphopentomutase [5.4.2.7] {Staphylococcus aureus}	10.5 ± 3	33.3 ± 4	26.3 ± 1	10.3 ± 3	0.3	0.4	1.0	0.477449
SAOUHSC_00106 - conserved hypothetical protein {Staphylococcus aureus}	11.5 ± 3	3.3 ± 1	7 ± 1	8 ± 2	3.5	1.6	1.4	0.197371
SAOUHSC_00113 - alcohol dehydrogenase, iron-containing, putative {Staphylococcus aureus}	35.3 ± 5	61 ± 21	42.8 ± 15	5.3 ± 0	0.6	0.8	6.7	0.000578
SAOUHSC_00153 - indolepyruvate decarboxylase, putative {Staphylococcus aureus}	15.3 ± 4	41.3 ± 8	28.8 ± 5	5.8 ± 2	0.4	0.5	2.7	0.034989
SAOUHSC_00187 - formate acetyltransferase [2.3.1.54] {Staphylococcus aureus}	242 ± 36	269.3 ± 90	241.5 ± 72	68 ± 16	0.9	1.0	3.6	0.002243
SAOUHSC_00192 - coagulase {Staphylococcus aureus NCTC 8325} xxxxx	58.3 ± 39	20 ± 13	33 ± 19	6.3 ± 1	2.9	1.8	9.3	0.114781
SAOUHSC_00196 - conserved hypothetical protein {Staphylococcus aureus}	11.3 ± 3	20.3 ± 5	20 ± 6	3 ± 2	0.6	0.6	3.8	0.023285
SAOUHSC_00201 - conserved hypothetical protein {Staphylococcus aureus}	10 ± 3	9.8 ± 2	15.3 ± 1	9.5 ± 2	1.0	0.7	1.1	0.442338
SAOUHSC_00204 - Globin domain protein {Staphylococcus aureus NCTC 8325}	41.3 ± 5	117 ± 16	90 ± 25	15.8 ± 6	0.4	0.5	2.6	0.010546
SAOUHSC_00206 - L-lactate dehydrogenase [1.1.1.27] {Staphylococcus aureus}	55.8 ± 5	104 ± 16	130 ± 41	29 ± 4	0.5	0.4	1.9	0.003149
SAOUHSC_00248 - peptidoglycan hydrolase, putative {Staphylococcus aureus}	28.3 ± 7	28.8 ± 8	65 ± 24	70.8 ± 18	1.0	0.4	0.4	0.035943
SAOUHSC_00253 - conserved hypothetical protein {Staphylococcus aureus}	32 ± 9	23.3 ± 4	34 ± 2	25.8 ± 6	1.4	0.9	1.2	0.298116
SAOUHSC_00256 - conserved hypothetical protein {Staphylococcus aureus}	31.8 ± 4	14.5 ± 7	26.5 ± 12	16 ± 4	2.2	1.2	2.0	0.016119
SAOUHSC_00258 - conserved hypothetical protein {Staphylococcus aureus}	13.3 ± 4	9 ± 2	15 ± 1	30.8 ± 8	1.5	0.9	0.4	0.044870
SAOUHSC_00284 - 5-nucleotidase, lipoprotein e(P4) family {Staphylococcus aureus}	48.5 ± 4	134 ± 73	132.3 ± 90	77 ± 14	0.4	0.4	0.6	0.047008
SAOUHSC_00300 - lipase precursor [3.1.1.3] {Staphylococcus aureus NCTC 8325}	642.3 ± 40	109.3 ± 22	129 ± 44	50.8 ± 16	5.9	5.0	12.7	0.000005
SAOUHSC_00336 - acetyl-CoA acetyltransferase, putative {Staphylococcus aureus}	16 ± 4	32 ± 5	28 ± 3	2.8 ± 1	0.5	0.6	5.8	0.007797
SAOUHSC_00354 - superantigen-like protein	20.5 ± 10	11.8 ± 9	16.5 ± 13	n.d. ^c	1.7	1.2	-	0.040926
SAOUHSC_00364 - alkyl hydroperoxide reductase, subunit F, putative [1.1.1.11] {Staphylococcus aureus}	57.3 ± 12	101.3 ± 27	68.3 ± 16	25 ± 9	0.6	0.8	2.3	0.033407
SAOUHSC_00365 - alkyl hydroperoxide reductase {Staphylococcus aureus}	108.8 ± 24	282.3 ± 106	264.3 ± 128	66.3 ± 23	0.4	0.4	1.6	0.124538
SAOUHSC_00369 - conserved hypothetical protein {Staphylococcus aureus}	10.3 ± 2	16.8 ± 3	19.3 ± 3	8.5 ± 2	0.6	0.5	1.2	0.286741
SAOUHSC_00374 - inosine-5-monophosphate dehydrogenase [1.1.1.205] {Staphylococcus aureus}	107 ± 20	158.8 ± 48	102 ± 12	5 ± 2	0.7	1.0	21.4	0.001145
SAOUHSC_00375 - GMP synthase, putative [6.3.5.2] {Staphylococcus aureus}	37.3 ± 6	77.8 ± 14	50 ± 9	12.5 ± 4	0.5	0.7	3.0	0.005609
SAOUHSC_00399 - superantigen-like protein	24.8 ± 1	7.8 ± 2	11 ± 4	5 ± 2	3.2	2.3	5.0	0.000163
SAOUHSC_00400 - conserved hypothetical protein {Staphylococcus aureus}	74.3 ± 19	24.8 ± 5	43 ± 15	25.5 ± 3	3.0	1.7	2.9	0.020626
SAOUHSC_00401 - conserved hypothetical protein {Staphylococcus aureus}	13 ± 6	51 ± 16	90.3 ± 45	51.8 ± 15	0.3	0.1	0.3	0.028557
SAOUHSC_00405 - conserved hypothetical protein {Staphylococcus aureus}	14.3 ± 2	19.3 ± 3	20.3 ± 3	19.5 ± 4	0.7	0.7	0.7	0.148546
SAOUHSC_00427 - autolysin precursor, putative [3.2.1.-] {Staphylococcus aureus}	250 ± 56	32.5 ± 24	60.5 ± 40	18.8 ± 11	7.7	4.1	13.3	0.003450
SAOUHSC_00461 - methionyl-tRNA synthetase, putative [6.1.1.10] {Staphylococcus aureus}	29.5 ± 7	50.5 ± 9	45 ± 15	6 ± 3	0.6	0.7	4.9	0.010967
SAOUHSC_00472 - ribose-phosphate pyrophosphokinase, putative [2.7.1.1] {Staphylococcus aureus}	14.3 ± 3	8.8 ± 5	4.3 ± 2	n.d. ^c	1.6	3.4	-	0.002683

SAOUHSC_00474 - ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL	46.5 ± 8	130 ± 53	103.5 ± 41	35.8 ± 11	0.4	0.4	1.3	0.226556
SAOUHSC_00488 - conserved hypothetical protein {Staphylococcus aure	45.8 ± 7	67.8 ± 18	48.5 ± 8	17.3 ± 4	0.7	0.9	2.7	0.004761
SAOUHSC_00493 - lysyl-tRNA synthetase [6.1.1.6] {Staphylococcus aur	13.3 ± 4	41.8 ± 15	30.8 ± 9	n.d. ^c	0.3	0.4	-	0.012070
SAOUHSC_00505 - endopeptidase, putative {Staphylococcus aureus NCT	27.8 ± 8	39.5 ± 8	31.5 ± 7	9.5 ± 3	0.7	0.9	2.9	0.044324
SAOUHSC_00509 - glutamyl-tRNA synthetase [6.1.1.17] {Staphylococcu	13.8 ± 4	46.3 ± 10	39.3 ± 7	9 ± 3	0.3	0.4	1.5	0.196135
SAOUHSC_00511 - cysteinyl-tRNA synthetase [6.1.1.16] {Staphylococcu	17 ± 2	48.3 ± 11	35 ± 6	9.3 ± 2	0.4	0.5	1.8	0.025128
SAOUHSC_00518 - ribosomal protein L11 {Staphylococcus aureus NCTC	17.5 ± 4	24 ± 2	37.8 ± 16	9.8 ± 3	0.7	0.5	1.8	0.078533
SAOUHSC_00519 - ribosomal protein L1 {Staphylococcus aureus NCTC 8	21 ± 4	65 ± 26	37.8 ± 13	9.3 ± 3	0.3	0.6	2.3	0.024407
SAOUHSC_00520 - ribosomal protein L10 {Staphylococcus aureus NCTC	14.5 ± 3	23.3 ± 4	24.5 ± 6	9.5 ± 3	0.6	0.6	1.5	0.107422
SAOUHSC_00521 - ribosomal protein L7/L12 {Staphylococcus aureus NC	19 ± 14	187.5 ± 108	127.3 ± 45	21.8 ± 6	0.1	0.1	0.9	0.431944
SAOUHSC_00524 - RNA polymerase beta chain, putative [2.7.7.6] {Stap	37 ± 5	119.5 ± 9	86.5 ± 6	25 ± 7	0.3	0.4	1.5	0.099107
SAOUHSC_00525 - DNA directed RNA polymerase beta-prime chain, put	64.5 ± 1	140 ± 8	124.8 ± 14	30.5 ± 9	0.5	0.5	2.1	0.005679
SAOUHSC_00529 - translation elongation factor G {Staphylococcus aure	191.8 ± 41	485.3 ± 270	256.8 ± 66	83.3 ± 24	0.4	0.7	2.3	0.031007
SAOUHSC_00530 - translation elongation factor Tu {Staphylococcus aure	317.8 ± 66	495 ± 224	476 ± 180	221.8 ± 76	0.6	0.7	1.4	0.188469
SAOUHSC_00532 - conserved hypothetical protein {Staphylococcus aure	21.3 ± 4	52.3 ± 10	40.5 ± 11	14.8 ± 4	0.4	0.5	1.4	0.150931
SAOUHSC_00533 - conserved hypothetical protein {Staphylococcus aure	10.3 ± 5	35.5 ± 9	34 ± 10	7.8 ± 3	0.3	0.3	1.3	0.349180
SAOUHSC_00536 - branched-chain amino acid aminotransferase [2.6.1.4	51 ± 9	83.5 ± 10	72.3 ± 14	27.3 ± 9	0.6	0.7	1.9	0.055677
SAOUHSC_00544 - sdrC protein, putative {Staphylococcus aureus NCTC	66.8 ± 25	63.8 ± 14	90 ± 17	126.3 ± 29	1.0	0.7	0.5	0.086784
SAOUHSC_00545 - sdrD protein, putative {Staphylococcus aureus NCTC	18.5 ± 10	14.3 ± 4	24.3 ± 6	62 ± 21	1.3	0.8	0.3	0.053895
SAOUHSC_00573 - conserved hypothetical protein {Staphylococcus aure	10 ± 3	28.5 ± 7	15.3 ± 3	3.3 ± 1	0.4	0.7	3.1	0.057351
SAOUHSC_00574 - phosphate acetyltransferase [2.3.1.8] {Staphylococc	62.8 ± 11	115 ± 43	130.3 ± 46	19.8 ± 9	0.5	0.5	3.2	0.011185
SAOUHSC_00608 - alcohol dehydrogenase I, putative {Staphylococcus a	186.3 ± 49	297.3 ± 60	192.8 ± 38	50 ± 7	0.6	1.0	3.7	0.017106
SAOUHSC_00611 - arginyl-tRNA synthetase [6.1.1.19] {Staphylococcus	16 ± 5	51 ± 3	33.8 ± 5	12 ± 2	0.3	0.5	1.3	0.237893
SAOUHSC_00617 - conserved hypothetical protein {Staphylococcus aure	393.8 ± 35	248.3 ± 90	293 ± 73	126 ± 17	1.6	1.3	3.1	0.000241
SAOUHSC_00634 - ABC transporter, substrate-binding protein, putative	218.5 ± 28	204.5 ± 17	201.5 ± 50	98.3 ± 20	1.1	1.1	2.2	0.006735
SAOUHSC_00671 - secretory antigen SsaA-like protein {Staphylococcus	282.3 ± 34	284 ± 77	319.8 ± 76	235.5 ± 75	1.0	0.9	1.2	0.296007
SAOUHSC_00707 - fructose 1-phosphate kinase, putative [2.7.1.56] {St	20.3 ± 4	33 ± 7	29.8 ± 4	3 ± 1	0.6	0.7	6.8	0.002919
SAOUHSC_00717 - conserved hypothetical protein {Staphylococcus aure	85 ± 36	53.5 ± 16	78.5 ± 29	31 ± 5	1.6	1.1	2.7	0.092660
SAOUHSC_00728 - lipoteichoic acid synthase	451.8 ± 44	155.8 ± 43	172.3 ± 43	90 ± 22	2.9	2.6	5.0	0.000159
SAOUHSC_00743 - ribonucleotide-disphosphate reductase beta chain, pu	15.8 ± 2	25.5 ± 2	22.5 ± 2	9 ± 2	0.6	0.7	1.8	0.050907
SAOUHSC_00767 - conserved hypothetical protein {Staphylococcus aure	26.5 ± 7	64 ± 11	51.8 ± 9	10 ± 1	0.4	0.5	2.7	0.024495
SAOUHSC_00785 - thioredoxin reductase [1.6.4.5] {Staphylococcus aur	30 ± 9	77.5 ± 18	66 ± 10	21.3 ± 6	0.4	0.5	1.4	0.218755
SAOUHSC_00795 - glyceraldehyde-3-phosphate dehydrogenase, type I [383.5 ± 104	879.3 ± 210	474.8 ± 59	80.3 ± 19	0.4	0.8	4.8	0.014263
SAOUHSC_00796 - phosphoglycerate kinase, putative [2.7.2.3] {Staphy	52 ± 12	152.5 ± 63	71 ± 11	18.5 ± 2	0.3	0.7	2.8	0.017025
SAOUHSC_00797 - triosephosphate isomerase [5.3.1.1] {Staphylococcu:	83.3 ± 25	299.3 ± 83	381.8 ± 96	43.5 ± 14	0.3	0.2	1.9	0.106136
SAOUHSC_00798 - phosphoglycerate mutase, 2,3-bisphosphoglycerate-i	31.8 ± 4	72.3 ± 10	54.5 ± 10	16 ± 3	0.4	0.6	2.0	0.010223
SAOUHSC_00799 - enolase [4.2.1.11] {Staphylococcus aureus NCTC 83:	323 ± 60	787.3 ± 169	534.8 ± 100	98.8 ± 24	0.4	0.6	3.3	0.006472
SAOUHSC_00808 - conserved hypothetical protein {Staphylococcus aure	13 ± 2	32.8 ± 10	39.8 ± 13	12.3 ± 2	0.4	0.3	1.1	0.404925
SAOUHSC_00812 - clumping factor {Staphylococcus aureus NCTC 8325}	12.8 ± 2	9 ± 1	18 ± 5	13 ± 3	1.4	0.7	1.0	0.474354
SAOUHSC_00818 - thermonuclease precursor [3.1.31.1] {Staphylococcu	58.5 ± 14	18.5 ± 5	11.3 ± 2	13 ± 2	3.2	5.2	4.5	0.008202
SAOUHSC_00836 - glycine cleavage system H protein {Staphylococcus a	27 ± 10	144 ± 41	123.8 ± 38	33.8 ± 10	0.2	0.2	0.8	0.327848
SAOUHSC_00847 - ABC transporter, ATP-binding protein, putative {Stap	10 ± 1	26 ± 14	26 ± 9	3.3 ± 1	0.4	0.4	3.1	0.002383
SAOUHSC_00848 - conserved hypothetical protein {Staphylococcus aure	17 ± 2	37.8 ± 5	26 ± 6	2 ± 1	0.5	0.7	8.5	0.000200
SAOUHSC_00849 - aminotransferase, class V superfamily, putative {Sta	12.8 ± 3	25.5 ± 7	25.3 ± 5	0.5 ± 1	0.5	0.5	25.5	0.004096

SAOUHSC_00851 - conserved hypothetical protein {Staphylococcus aure	21 ± 2	36.8 ± 4	32.5 ± 3	4.8 ± 2	0.6	0.6	4.4	0.000834
SAOUHSC_00869 - D-alanine-activating enzyme [6.3.2.-] {Staphylococc	19 ± 4	72.3 ± 15	41.3 ± 4	14.5 ± 4	0.3	0.5	1.3	0.214830
SAOUHSC_00878 - conserved hypothetical protein {Staphylococcus aure	23.3 ± 3	51.3 ± 27	31.8 ± 6	5 ± 2	0.5	0.7	4.7	0.001361
SAOUHSC_00879 - probable cytosol aminopeptidase {Staphylococcus au	13.3 ± 3	23 ± 5	16.3 ± 2	4 ± 1	0.6	0.8	3.3	0.008650
SAOUHSC_00891 - peptidyl-prolyl cis-trans isomerase, cyclophilin-type,	15 ± 3	30.5 ± 4	25 ± 8	3.5 ± 1	0.5	0.6	4.3	0.005538
SAOUHSC_00895 - glutamate dehydrogenase, NAD-specific, putative {S	20 ± 3	32.5 ± 6	26.5 ± 6	7.8 ± 3	0.6	0.8	2.6	0.020647
SAOUHSC_00897 - putative glutamyl endopeptidase precursor	180.3 ± 32	57.8 ± 6	77.8 ± 15	62.5 ± 25	3.1	2.3	2.9	0.013822
SAOUHSC_00900 - glucose-6-phosphate isomerase [5.3.1.9] {Staphyloc	56 ± 8	131.5 ± 34	109.5 ± 34	20.3 ± 4	0.4	0.5	2.8	0.003612
SAOUHSC_00906 - conserved hypothetical protein {Staphylococcus aure	38.3 ± 4	97 ± 38	56.5 ± 4	14.3 ± 4	0.4	0.7	2.7	0.002171
SAOUHSC_00908 - coenzyme A disulfide reductase, putative {Staphyloc	24.8 ± 4	83 ± 12	49.3 ± 10	4.8 ± 1	0.3	0.5	5.2	0.002544
SAOUHSC_00918 - truncated MHC class II analog protein {Staphylococci	194.8 ± 37	339 ± 147	543.5 ± 102	517.3 ± 126	0.6	0.4	0.4	0.024948
SAOUHSC_00920 - conserved hypothetical protein {Staphylococcus aure	37 ± 13	83.5 ± 15	56.5 ± 14	15.8 ± 3	0.4	0.7	2.3	0.081607
SAOUHSC_00921 - 3-oxoacyl- synthase, putative [2.3.1.41] {Staphyloc	55.5 ± 9	166.5 ± 41	141.8 ± 45	19.8 ± 5	0.3	0.4	2.8	0.005791
SAOUHSC_00927 - oligopeptide ABC transporter, substrate-binding prote	10.3 ± 3	7.3 ± 1	12.5 ± 2	9.5 ± 4	1.4	0.8	1.1	0.444272
SAOUHSC_00937 - oligoendopeptidase F [3.4.24.-] {Staphylococcus aur	25.3 ± 10	98.5 ± 13	60.3 ± 12	16.8 ± 3	0.3	0.4	1.5	0.218546
SAOUHSC_00985 - enoyl-CoA hydratase/isomerase family protein, putat	12.3 ± 2	39.3 ± 6	29.8 ± 4	1.8 ± 1	0.3	0.4	7.0	0.001916
SAOUHSC_00987 - cysteine protease precursor, putative {Staphylococcu	637.5 ± 182	123 ± 12	127 ± 45	115 ± 31	5.2	5.0	5.5	0.015083
SAOUHSC_00988 - glutamyl endopeptidase precursor, putative {Staphyli	589 ± 127	191 ± 43	229 ± 100	142.3 ± 43	3.1	2.6	4.1	0.007910
SAOUHSC_00994 - bifunctional autolysin precursor, putative [3.5.1.28] {	1255.5 ± 170	346 ± 113	443 ± 109	322.8 ± 86	3.6	2.8	3.9	0.001373
SAOUHSC_00997 - conserved hypothetical protein {Staphylococcus aure	25.5 ± 1	22.8 ± 4	35 ± 4	38 ± 9	1.1	0.7	0.7	0.102404
SAOUHSC_01002 - quinol oxidase AA3, subunit II, putative [1.9.3.-] {St	13.5 ± 3	19.3 ± 5	20.3 ± 2	8.3 ± 3	0.7	0.7	1.6	0.133892
SAOUHSC_01005 - conserved hypothetical protein {Staphylococcus aure	128 ± 38	254.3 ± 47	609.5 ± 75	585.5 ± 120	0.5	0.2	0.2	0.005406
SAOUHSC_01007 - FoLD bifunctional protein, putative {Staphylococcus a	23.3 ± 4	45.8 ± 11	37.8 ± 9	6.3 ± 1	0.5	0.6	3.7	0.003221
SAOUHSC_01012 - phosphoribosylformylglycinamide synthase I [6.3.5	12 ± 3	31.3 ± 3	31 ± 7	13 ± 4	0.4	0.4	0.9	0.422236
SAOUHSC_01013 - phosphoribosylformylglycinamide synthase II [6.3.!	17.8 ± 3	27.8 ± 6	23.8 ± 6	13.3 ± 4	0.6	0.7	1.3	0.181795
SAOUHSC_01014 - amidophosphoribosyltransferase [2.4.2.14] {Staphyli	11.3 ± 2	25 ± 1	22.8 ± 3	2.3 ± 2	0.5	0.5	5.0	0.012764
SAOUHSC_01015 - phosphoribosylformylglycinamide cyclo-ligase [6.3.	16.8 ± 2	31.5 ± 7	16.3 ± 4	2.5 ± 2	0.5	1.0	6.7	0.001235
SAOUHSC_01017 - phosphoribosylaminoimidazolecarboxamide formyltra	14.3 ± 3	7.3 ± 1	8 ± 3	4.3 ± 3	2.0	1.8	3.4	0.025639
SAOUHSC_01028 - phosphocarrier protein hpr, putative {Staphylococcus	53.3 ± 10	299 ± 110	244.3 ± 64	54.8 ± 17	0.2	0.2	1.0	0.470960
SAOUHSC_01029 - phosphoenolpyruvate-protein phosphotransferase [2.	60.3 ± 4	110 ± 25	91.5 ± 14	21 ± 5	0.5	0.7	2.9	0.000405
SAOUHSC_01035 - conserved hypothetical protein {Staphylococcus aure	10 ± 7	23 ± 11	10.8 ± 5	0.5 ± 1	0.4	0.9	20.0	0.104517
SAOUHSC_01040 - pyruvate dehydrogenase complex, E1 component, alj	54 ± 7	137.5 ± 55	115.5 ± 42	19.5 ± 6	0.4	0.5	2.8	0.005605
SAOUHSC_01041 - pyruvate dehydrogenase complex, E1 component, py	29.5 ± 3	109 ± 16	66 ± 14	27.3 ± 8	0.3	0.4	1.1	0.396672
SAOUHSC_01042 - dihydrolipoamide S-acetyltransferase component of p	27.5 ± 10	84.3 ± 17	58.5 ± 9	14.3 ± 3	0.3	0.5	1.9	0.115985
SAOUHSC_01043 - dihydrolipoamide dehydrogenase [1.8.1.4] {Staphyloc	95 ± 31	159.8 ± 20	89 ± 18	37.3 ± 12	0.6	1.1	2.6	0.067062
SAOUHSC_01064 - pyruvate carboxylase [6.4.1.1] {Staphylococcus aure	109.8 ± 18	158.3 ± 17	143 ± 17	29.5 ± 9	0.7	0.8	3.7	0.003321
SAOUHSC_01081 - conserved hypothetical protein {Staphylococcus aure	34.3 ± 4	29.3 ± 7	35 ± 8	20.8 ± 6	1.2	1.0	1.7	0.061707
SAOUHSC_01093 - phenylalanyl-tRNA synthetase, beta subunit [6.1.1.2]	24.8 ± 8	49.8 ± 8	44.5 ± 12	19.3 ± 7	0.5	0.6	1.3	0.306576
SAOUHSC_01100 - thioredoxin {Staphylococcus aureus NCTC 8325} xxx	19.3 ± 9	36.5 ± 14	59.8 ± 30	17.5 ± 5	0.5	0.3	1.1	0.434586
SAOUHSC_01107 - conserved hypothetical protein {Staphylococcus aure	10.3 ± 1	10.3 ± 2	13 ± 6	6.3 ± 4	1.0	0.8	1.6	0.165373
SAOUHSC_01114 - fibrinogen-binding protein {Staphylococcus aureus N	69.8 ± 31	32.3 ± 10	41.8 ± 11	14.8 ± 5	2.2	1.7	4.7	0.065921
SAOUHSC_01121 - alpha-hemolysin precursor {Staphylococcus aureus N	1683.8 ± 436	400.8 ± 85	673.3 ± 125	269.8 ± 102	4.2	2.5	6.2	0.009854
SAOUHSC_01125 - superantigen-like proten	11.5 ± 2	1.5 ± 1	2.5 ± 1	n.d. ^c	7.7	4.6	-	0.001110
SAOUHSC_01135 - conserved hypothetical protein {Staphylococcus aure	12.3 ± 7	1.5 ± 1	n.d.	0.5 ± 1	8.2	-	24.5	0.070375

SAOUHSC_01145 - penicillin-binding protein 1 {Staphylococcus aureus N	20.5 ± 3	28.8 ± 2	33 ± 5	33.5 ± 10	0.7	0.6	0.6	0.124429
SAOUHSC_01149 - cell division protein, putative {Staphylococcus aureus	20 ± 3	53.8 ± 7	56 ± 9	23 ± 6	0.4	0.4	0.9	0.334638
SAOUHSC_01150 - cell division protein FtsZ {Staphylococcus aureus NC	24 ± 8	50.3 ± 22	31.8 ± 8	21.5 ± 8	0.5	0.8	1.1	0.414766
SAOUHSC_01159 - isoleucyl-tRNA synthetase [6.1.1.5] {Staphylococcus	48.3 ± 8	98.8 ± 27	67.8 ± 8	20.3 ± 6	0.5	0.7	2.4	0.015331
SAOUHSC_01168 - dihydroorotase [3.5.2.3] {Staphylococcus aureus NC	31 ± 7	66.8 ± 4	46.5 ± 10	11.8 ± 3	0.5	0.7	2.6	0.019737
SAOUHSC_01169 - carbamoyl-phosphate synthase, small subunit [6.3.5	10.8 ± 1	13.8 ± 6	6.8 ± 4	n.d. ^c	0.8	1.6	-	0.000035
SAOUHSC_01170 - carbamoyl-phosphate synthase, large subunit [6.3.5.	29.3 ± 6	57.3 ± 12	42 ± 3	7.8 ± 4	0.5	0.7	3.8	0.012275
SAOUHSC_01172 - orotate phosphoribosyltransferase [2.4.2.10] {Staph	16.5 ± 1	20.8 ± 3	19.3 ± 3	2 ± 1	0.8	0.9	8.3	0.000022
SAOUHSC_01180 - conserved hypothetical protein {Staphylococcus aure	10.8 ± 2	11.5 ± 4	20.8 ± 10	11 ± 2	0.9	0.5	1.0	0.469621
SAOUHSC_01193 - conserved hypothetical protein {Staphylococcus aure	11.5 ± 2	22.5 ± 10	15 ± 5	10 ± 5	0.5	0.8	1.2	0.395983
SAOUHSC_01199 - 3-oxoacyl-(acyl-carrier-protein) reductase, putative [45.8 ± 8	87.3 ± 25	74.3 ± 10	17.8 ± 4	0.5	0.6	2.6	0.010019
SAOUHSC_01216 - succinyl-CoA synthetase, beta subunit, putative [6.2.	27.3 ± 7	65 ± 8	48.5 ± 10	18.8 ± 7	0.4	0.6	1.5	0.215009
SAOUHSC_01218 - succinyl-CoA synthetase, alpha subunit, putative [6.2	24 ± 4	45.8 ± 4	32.8 ± 5	11.8 ± 4	0.5	0.7	2.0	0.032301
SAOUHSC_01228 - conserved hypothetical protein {Staphylococcus aure	22.3 ± 5	24 ± 5	28.3 ± 7	1.8 ± 1	0.9	0.8	12.7	0.003118
SAOUHSC_01232 - ribosomal protein S2 {Staphylococcus aureus NCTC 8	18.3 ± 4	45.3 ± 4	30.3 ± 4	n.d. ^c	0.4	0.6	-	0.003334
SAOUHSC_01234 - translation elongation factor Ts {Staphylococcus aure	46.5 ± 11	139 ± 20	129.3 ± 42	28.8 ± 6	0.3	0.4	1.6	0.107001
SAOUHSC_01243 - transcription termination-antitermination factor, puta	27.5 ± 6	39.3 ± 6	33.8 ± 5	24.5 ± 8	0.7	0.8	1.1	0.383231
SAOUHSC_01251 - polyribonucleotide nucleotidyltransferase, putative [2	42 ± 2	90.5 ± 21	75 ± 12	28.3 ± 8	0.5	0.6	1.5	0.073727
SAOUHSC_01278 - conserved hypothetical protein {Staphylococcus aure	20.5 ± 3	50.5 ± 8	37 ± 5	6.5 ± 1	0.4	0.6	3.2	0.001497
SAOUHSC_01287 - glutamine synthetase, type I [6.3.1.2] {Staphylococ	53.3 ± 5	105.8 ± 25	102.3 ± 27	18.5 ± 6	0.5	0.5	2.9	0.001493
SAOUHSC_01327 - catalase [1.11.1.6] {Staphylococcus aureus NCTC 83	32.3 ± 3	66.8 ± 8	46.5 ± 6	17.3 ± 6	0.5	0.7	1.9	0.036733
SAOUHSC_01332 - conserved hypothetical protein {Staphylococcus aure	16.5 ± 3	4.3 ± 2	8.8 ± 6	4.3 ± 3	3.9	1.9	3.9	0.012668
SAOUHSC_01337 - transketolase [2.2.1.1] {Staphylococcus aureus NCTC	92.8 ± 16	273.5 ± 35	196 ± 33	45.5 ± 13	0.3	0.5	2.0	0.032680
SAOUHSC_01347 - aconitate hydratase 1 [4.2.1.3] {Staphylococcus aur	36.3 ± 6	64 ± 4	65.8 ± 6	12.5 ± 4	0.6	0.6	2.9	0.007726
SAOUHSC_01383 - conserved hypothetical protein {Staphylococcus aure	14.5 ± 3	35.8 ± 4	31.5 ± 4	4.5 ± 2	0.4	0.5	3.2	0.023264
SAOUHSC_01403 - cold shock protein, putative {Staphylococcus aureus	158.8 ± 46	538.3 ± 88	379.3 ± 123	166.3 ± 76	0.3	0.4	1.0	0.467806
SAOUHSC_01418 - 2-oxoglutarate dehydrogenase, E1 component [1.2.4	11.8 ± 4	19.3 ± 5	15 ± 2	1.3 ± 1	0.6	0.8	9.4	0.022120
SAOUHSC_01427 - conserved hypothetical protein {Staphylococcus aure	13.8 ± 5	12.3 ± 3	18 ± 3	24.5 ± 7	1.1	0.8	0.6	0.137990
SAOUHSC_01430 - phosphotransferase system enzyme IIA, putative {St	14.5 ± 5	41.5 ± 11	48.3 ± 20	18.5 ± 7	0.3	0.3	0.8	0.329167
SAOUHSC_01451 - threonine dehydratase [4.2.1.16] {Staphylococcus ai	15.8 ± 4	23.3 ± 11	13 ± 3	n.d. ^c	0.7	1.2	-	0.002765
SAOUHSC_01452 - alanine dehydrogenase [1.4.1.1] {Staphylococcus au	14.8 ± 4	28.8 ± 2	26.3 ± 5	6 ± 2	0.5	0.6	2.5	0.036430
SAOUHSC_01467 - penicillin-binding protein 2 {Staphylococcus aureus N	53.8 ± 7	67.5 ± 6	70.5 ± 9	65.3 ± 12	0.8	0.8	0.8	0.225083
SAOUHSC_01471 - asparaginyl-tRNA synthetase, putative [6.1.1.22] {St	14.5 ± 2	35.8 ± 11	16 ± 4	n.d.	0.4	0.9	-	0.000395
SAOUHSC_01490 - DNA-binding protein HU, putative {Staphylococcus ai	16 ± 4	77.3 ± 39	31.8 ± 6	9.5 ± 1	0.2	0.5	1.7	0.099367
SAOUHSC_01493 - 30S ribosomal protein S1, putative {Staphylococcus	43.3 ± 6	124.3 ± 24	89.8 ± 12	48.8 ± 8	0.3	0.5	0.9	0.297095
SAOUHSC_01501 - elastin binding protein {Staphylococcus aureus NCTC	18 ± 3	22 ± 4	28.5 ± 7	19.3 ± 6	0.8	0.6	0.9	0.423883
SAOUHSC_01584 - conserved hypothetical protein {Staphylococcus aure	26.5 ± 6	18 ± 2	16.8 ± 2	5.8 ± 2	1.5	1.6	4.6	0.008901
SAOUHSC_01599 - glucose-6-phosphate 1-dehydrogenase [1.1.1.49] {S	20 ± 2	40.5 ± 5	26.8 ± 6	1.5 ± 1	0.5	0.7	13.3	0.000060
SAOUHSC_01605 - 6-phosphogluconate dehydrogenase, decarboxylating	57.3 ± 5	127.5 ± 18	100.5 ± 22	26.8 ± 12	0.4	0.6	2.1	0.027492
SAOUHSC_01622 - conserved hypothetical protein {Staphylococcus aure	11 ± 6	6.8 ± 4	4.5 ± 1	n.d. ^c	1.6	2.4	-	0.051654
SAOUHSC_01625 - translation elongation factor P {Staphylococcus aure	19.3 ± 5	68.3 ± 22	60.5 ± 10	13.5 ± 5	0.3	0.3	1.4	0.229131
SAOUHSC_01626 - proline dipeptidase, putative [3.4.13.9] {Staphylococ	21.3 ± 4	69.8 ± 16	50.3 ± 10	10.5 ± 2	0.3	0.4	2.0	0.024309
SAOUHSC_01652 - penicillin-binding protein 3 {Staphylococcus aureus N	50.5 ± 5	15.3 ± 1	27 ± 5	23.3 ± 5	3.3	1.9	2.2	0.002851
SAOUHSC_01652 - penicillin-binding protein 3 {Staphylococcus aureus N	50.5 ± 5	15.3 ± 1	27 ± 5	23.3 ± 5	3.3	1.9	2.2	0.002851

SAOUHSC_01653 - superoxide dismutase, Mn, putative [1.15.1.1] {Stap	24.3 ± 4	69.8 ± 26	35.5 ± 4	7 ± 1	0.3	0.7	3.5	0.002413
SAOUHSC_01666 - glycyl-tRNA synthetase [6.1.1.14] {Staphylococcus a	34.3 ± 9	108.5 ± 56	74.3 ± 27	5.8 ± 2	0.3	0.5	6.0	0.009254
SAOUHSC_01683 - DNaK protein, putative {Staphylococcus aureus NCTC	86 ± 21	194 ± 52	118.5 ± 10	73 ± 16	0.4	0.7	1.2	0.319233
SAOUHSC_01722 - alanyl-tRNA synthetase [6.1.1.7] {Staphylococcus au	13 ± 3	31.5 ± 2	23 ± 5	n.d. ^c	0.4	0.6	-	0.001417
SAOUHSC_01737 - aspartyl-tRNA synthetase [6.1.1.12] {Staphylococcu:	13.3 ± 0	25.8 ± 10	16.8 ± 4	n.d. ^c	0.5	0.8	-	0.000000
SAOUHSC_01757 - ribosomal protein L21 {Staphylococcus aureus NCTC	12.5 ± 3	42.3 ± 7	30.3 ± 2	19.5 ± 5	0.3	0.4	0.6	0.129959
SAOUHSC_01759 - rod shape-determining protein MreC {Staphylococcus:	27.8 ± 6	23.8 ± 3	47.8 ± 7	33.3 ± 11	1.2	0.6	0.8	0.335143
SAOUHSC_01767 - valyl-tRNA synthetase [6.1.1.9] {Staphylococcus aur	28 ± 6	63.8 ± 7	50.3 ± 9	10.5 ± 5	0.4	0.6	2.7	0.030432
SAOUHSC_01772 - porphobilinogen synthase [4.2.1.24] {Staphylococcu:	12.3 ± 3	27 ± 5	22.3 ± 6	4.8 ± 4	0.5	0.6	2.6	0.090088
SAOUHSC_01779 - trigger factor [5.2.1.8] {Staphylococcus aureus NCTC	24 ± 2	139.5 ± 37	83.8 ± 16	28.5 ± 4	0.2	0.3	0.8	0.185071
SAOUHSC_01788 - threonyl-tRNA synthetase [6.1.1.3] {Staphylococcus	12.5 ± 3	39.5 ± 17	24.8 ± 11	1.8 ± 2	0.3	0.5	7.1	0.008258
SAOUHSC_01806 - pyruvate kinase [2.7.1.40] {Staphylococcus aureus P	95 ± 4	128.5 ± 26	118.5 ± 24	28.8 ± 10	0.7	0.8	3.3	0.000462
SAOUHSC_01807 - 6-phosphofructokinase, putative [2.7.1.11] {Staphyl	16.8 ± 3	31.3 ± 2	34.3 ± 9	7.5 ± 2	0.5	0.5	2.2	0.014449
SAOUHSC_01810 - NADP-dependent malic enzyme, putative {Staphyloc	29.5 ± 6	57 ± 13	50.5 ± 10	9.5 ± 2	0.5	0.6	3.1	0.012915
SAOUHSC_01816 - conserved hypothetical protein {Staphylococcus aure	15.5 ± 3	25.5 ± 5	22.3 ± 7	n.d. ^c	0.6	0.7	-	0.001381
SAOUHSC_01819 - conserved hypothetical protein {Staphylococcus aure	40.5 ± 11	127 ± 55	58.3 ± 13	20 ± 3	0.3	0.7	2.0	0.067083
SAOUHSC_01820 - acetate kinase [2.7.2.1] {Staphylococcus aureus NC	38.8 ± 3	57.5 ± 39	39.5 ± 22	0.8 ± 1	0.7	1.0	51.7	0.000015
SAOUHSC_01822 - conserved hypothetical protein {Staphylococcus aure	14.3 ± 7	48.8 ± 20	41.3 ± 16	12.8 ± 6	0.3	0.3	1.1	0.438451
SAOUHSC_01839 - tyrosyl-tRNA synthetase [6.1.1.1] {Staphylococcus a	11.3 ± 4	25 ± 5	26.8 ± 5	1 ± 1	0.5	0.4	11.3	0.028621
SAOUHSC_01845 - formate-tetrahydrofolate ligase, putative [6.3.4.3] {	65 ± 8	109.5 ± 16	73.8 ± 12	21.5 ± 5	0.6	0.9	3.0	0.001972
SAOUHSC_01850 - catabolite control protein A {Staphylococcus aureus I	13.8 ± 2	34.3 ± 3	25.5 ± 3	0.8 ± 1	0.4	0.5	18.3	0.000343
SAOUHSC_01858 - conserved hypothetical protein {Staphylococcus aure	10.8 ± 5	18.3 ± 2	16.3 ± 4	8.8 ± 5	0.6	0.7	1.2	0.386756
SAOUHSC_01861 - conserved hypothetical protein {Staphylococcus aure	12 ± 3	29.3 ± 2	21.3 ± 2	3.8 ± 1	0.4	0.6	3.2	0.019725
SAOUHSC_01867 - D-amino acid aminotransferase [2.6.1.21] {Staphylo	15.8 ± 3	33.8 ± 7	25 ± 5	5 ± 3	0.5	0.6	3.2	0.026646
SAOUHSC_01868 - conserved hypothetical protein {Staphylococcus aure	27.3 ± 4	80.8 ± 10	61.8 ± 8	26 ± 4	0.3	0.4	1.0	0.418159
SAOUHSC_01875 - leucyl-tRNA synthetase [6.1.1.4] {Staphylococcus au	26.3 ± 3	48.8 ± 4	44 ± 8	9.3 ± 3	0.5	0.6	2.8	0.003663
SAOUHSC_01895 - conserved hypothetical protein {Staphylococcus aure	12.8 ± 4	10.3 ± 1	9.8 ± 1	5.8 ± 2	1.2	1.3	2.2	0.094348
SAOUHSC_01901 - conserved hypothetical protein {Staphylococcus aure	27 ± 5	113 ± 50	87.5 ± 22	18.8 ± 4	0.2	0.3	1.4	0.121399
SAOUHSC_01910 - phosphoenolpyruvate carboxykinase (ATP) [4.1.1.49]	14 ± 4	41 ± 3	30 ± 5	8.3 ± 3	0.3	0.5	1.7	0.167969
SAOUHSC_01935 - serine protease SplF, putative [3.4.21.19] {Staphylo	342 ± 82	56 ± 5	61.8 ± 9	22 ± 9	6.1	5.5	15.5	0.004060
SAOUHSC_01936 - serine protease SplE [3.4.21.19] {Staphylococcus au	256.8 ± 46	15.8 ± 1	12.3 ± 2	4.3 ± 3	16.3	21.0	60.4	0.000809
SAOUHSC_01938 - serine protease SplD [3.4.21.19] {Staphylococcus au	179.5 ± 39	40 ± 6	42.5 ± 4	19.5 ± 7	4.5	4.2	9.2	0.003508
SAOUHSC_01939 - serine protease SplC {Staphylococcus aureus NCTC 8	98.5 ± 61	18.5 ± 2	17.8 ± 3	10.8 ± 5	5.3	5.5	9.2	0.099803
SAOUHSC_01941 - serine protease SplB {Staphylococcus aureus NCTC 8	257.5 ± 79	54.5 ± 8	50.8 ± 9	30.5 ± 13	4.7	5.1	8.4	0.015220
SAOUHSC_01942 - serine protease SplA [3.4.21.19] {Staphylococcus au	272.3 ± 122	45.8 ± 36	38 ± 24	10 ± 4	6.0	7.2	27.2	0.037866
SAOUHSC_01944 - conserved hypothetical protein {Staphylococcus aure	14.5 ± 8	14.8 ± 8	12 ± 2	7.5 ± 2	1.0	1.2	1.9	0.204410
SAOUHSC_01949 - intracellular serine protease, putative {Staphylococci	11.8 ± 4	n.d. ^c	n.d. ^c	n.d. ^c	-	-	-	0.009645
SAOUHSC_01954 - leukotoxin, LukD {Staphylococcus aureus NCTC 8325	279.3 ± 16	44.8 ± 10	79.5 ± 12	26.8 ± 8	6.2	3.5	10.4	0.000004
SAOUHSC_01964 - conserved hypothetical protein {Staphylococcus aure	11.3 ± 3	29 ± 4	27.3 ± 3	6.8 ± 3	0.4	0.4	1.7	0.182678
SAOUHSC_01972 - protein export protein PrsA, putative {Staphylococcu	17.5 ± 2	80.3 ± 20	80.5 ± 19	137.5 ± 28	0.2	0.2	0.1	0.002662
SAOUHSC_02043 - phage head protein, putative {Staphylococcus aureu:	33.3 ± 2	25.8 ± 7	33 ± 7	27 ± 9	1.3	1.0	1.2	0.255084
SAOUHSC_02071 - single-strand DNA-binding protein, putative {Staphyl	20.3 ± 3	12 ± 2	17 ± 2	13 ± 4	1.7	1.2	1.6	0.098863
SAOUHSC_02092 - aminopeptidase PepS, putative [3.4.11.-] {Staphyloc	20.3 ± 5	48 ± 4	45 ± 4	15.3 ± 4	0.4	0.5	1.3	0.241625
SAOUHSC_02108 - ferritin, putative {Staphylococcus aureus NCTC 8325	10 ± 3	24.3 ± 4	15.8 ± 3	6.8 ± 3	0.4	0.6	1.5	0.225300

SAOUHSC_02116 - glutamyl-tRNA(Gln) amidotransferase, B subunit [6.3	16.3 ± 3	42.3 ± 10	39.5 ± 12	7 ± 2	0.4	0.4	2.3	0.023377
SAOUHSC_02117 - glutamyl-tRNA(Gln) amidotransferase, A subunit [6.3	17.8 ± 1	52.5 ± 21	34.5 ± 6	6.3 ± 1	0.3	0.5	2.8	0.000027
SAOUHSC_02127 - staphopain thiol proteinase [3.4.22.48] {Staphylococ	405.8 ± 104	85 ± 11	114 ± 47	42.3 ± 10	4.8	3.6	9.6	0.006477
SAOUHSC_02133 - nicotinate phosphoribosyltransferase, putative [2.4.2	11.5 ± 5	29.5 ± 3	20.3 ± 7	n.d. ^c	0.4	0.6	-	0.029109
SAOUHSC_02140 - conserved hypothetical protein {Staphylococcus aure	14.8 ± 4	28.3 ± 3	19.3 ± 3	13.3 ± 5	0.5	0.8	1.1	0.411064
SAOUHSC_02161 - MHC class II analog protein {Staphylococcus aureus	23.3 ± 3	163 ± 81	79.8 ± 22	55.5 ± 18	0.1	0.3	0.4	0.067555
SAOUHSC_02163 - conserved hypothetical phage protein {Staphylococci	15.3 ± 2	15 ± 2	34.3 ± 12	17 ± 8	1.0	0.4	0.9	0.415340
SAOUHSC_02167 - conserved hypothetical phage protein {Staphylococci	30.5 ± 11	52 ± 21	50 ± 17	23.5 ± 6	0.6	0.6	1.3	0.299623
SAOUHSC_02169 - conserved hypothetical phage protein {Staphylococci	31.3 ± 2	38.3 ± 6	48 ± 15	15 ± 4	0.8	0.7	2.1	0.003754
SAOUHSC_02171 - staphylokinase precursor, putative {Staphylococcus a	519 ± 29	127.3 ± 17	116 ± 23	79.8 ± 26	4.1	4.5	6.5	0.000014
SAOUHSC_02241 - putative leukocidin F subunit like	1083 ± 162	169.5 ± 26	154.8 ± 44	37.5 ± 9	6.4	7.0	28.9	0.000331
SAOUHSC_02243 - aerolysin/leukocidin family protein	758 ± 432	209 ± 121	143.8 ± 57	53 ± 11	3.6		14.3	0.077032
SAOUHSC_02243 - conserved hypothetical protein {Staphylococcus aure	758 ± 432	209 ± 121	143.8 ± 57	53 ± 11	3.6	5.3	14.3	0.077032
SAOUHSC_02254 - chaperonin, 60 kDa, GrpEL, putative {Staphylococcu	45.5 ± 6	81.5 ± 16	73.3 ± 8	31 ± 6	0.6	0.6	1.5	0.071520
SAOUHSC_02257 - conserved hypothetical protein {Staphylococcus aure	36 ± 3	24 ± 7	31.8 ± 10	36.8 ± 8	1.5	1.1	1.0	0.466694
SAOUHSC_02260 - delta-hemolysin precursor {Staphylococcus aureus N	28.8 ± 8	10.3 ± 2	14 ± 4	9 ± 5	2.8	2.1	3.2	0.039873
SAOUHSC_02333 - sceD protein, putative {Staphylococcus aureus NCTC	34 ± 5	36.3 ± 8	101 ± 38	60.5 ± 21	0.9	0.3	0.6	0.128045
SAOUHSC_02341 - ATP synthase F1, beta subunit [3.6.3.14] {Staphyloc	24.5 ± 6	23.3 ± 1	43.3 ± 9	19.3 ± 7	1.1	0.6	1.3	0.295370
SAOUHSC_02345 - ATP synthase F1, alpha subunit [3.6.3.14] {Staphylo	23.8 ± 7	21.5 ± 3	26.5 ± 3	21.5 ± 10	1.1	0.9	1.1	0.431408
SAOUHSC_02354 - serine hydroxymethyltransferase, putative [2.1.2.1]	17 ± 4	32.5 ± 5	28 ± 5	7 ± 4	0.5	0.6	2.4	0.064974
SAOUHSC_02361 - ribosomal protein L31 {Staphylococcus aureus NCTC	10.8 ± 3	26 ± 5	27.3 ± 10	1.8 ± 2	0.4	0.4	6.1	0.014099
SAOUHSC_02365 - UDP-N-acetylglucosamine 1-carboxyvinyltransferase	15.5 ± 3	30 ± 3	25.5 ± 4	n.d. ^c	0.5	0.6	-	0.000530
SAOUHSC_02366 - conserved hypothetical protein {Staphylococcus aure	54 ± 5	264.8 ± 100	124.5 ± 24	32 ± 7	0.2	0.4	1.7	0.023719
SAOUHSC_02380 - purine nucleoside phosphorylase [2.4.2.1] {Staphylo	32.8 ± 3	55.3 ± 12	50 ± 13	11.5 ± 5	0.6	0.7	2.8	0.004444
SAOUHSC_02383 - conserved hypothetical protein {Staphylococcus aure	10.3 ± 1	17.3 ± 1	8.5 ± 1	n.d. ^c	0.6	1.2	-	0.000018
SAOUHSC_02399 - glucosamine--fructose-6-phosphate aminotransferase	19.3 ± 10	46.5 ± 27	18.5 ± 5	10.5 ± 2	0.4	1.0	1.8	0.222207
SAOUHSC_02405 - phosphoglucosamine mutase [5.4.2.-] {Staphylococci	18 ± 1	36.5 ± 7	29.8 ± 3	8.5 ± 2	0.5	0.6	2.1	0.006197
SAOUHSC_02447 - conserved hypothetical protein {Staphylococcus aure	14.3 ± 0	24.5 ± 6	23.3 ± 1	3.5 ± 2	0.6	0.6	4.1	0.002000
SAOUHSC_02463 - hyaluronate lyase {Staphylococcus aureus NCTC 832	1071.8 ± 94	167.8 ± 31	213.8 ± 26	125.8 ± 23	6.4	5.0	8.5	0.000034
SAOUHSC_02466 - truncated MHC class II analog protein {Staphylococci	47.5 ± 11	28 ± 8	27.5 ± 6	24.8 ± 5	1.7	1.7	1.9	0.055003
SAOUHSC_02468 - acetolactate synthase, putative [4.1.3.18] {Staphylo	10.8 ± 4	24.8 ± 4	29 ± 3	3 ± 2	0.4	0.4	3.6	0.079480
SAOUHSC_02477 - ribosomal protein S9, putative {Staphylococcus aure	17.8 ± 3	57.3 ± 30	16 ± 5	4 ± 1	0.3	1.1	4.4	0.003848
SAOUHSC_02478 - ribosomal protein L13 {Staphylococcus aureus NCTC	17.8 ± 5	25.3 ± 10	17 ± 5	n.d. ^c	0.7	1.0	-	0.007234
SAOUHSC_02485 - DNA-directed RNA polymerase alpha chain, putative	26.3 ± 5	48.3 ± 2	51.8 ± 4	19.3 ± 6	0.5	0.5	1.4	0.198552
SAOUHSC_02490 - adenylate kinase, putative [2.7.4.3] {Staphylococcus	21 ± 5	46.3 ± 9	37 ± 10	11.3 ± 5	0.5	0.6	1.9	0.109364
SAOUHSC_02492 - ribosomal protein L15 {Staphylococcus aureus NCTC	21.3 ± 6	66.5 ± 9	35.5 ± 7	22.8 ± 9	0.3	0.6	0.9	0.445427
SAOUHSC_02493 - ribosomal protein L30 {Staphylococcus aureus NCTC	12.5 ± 2	88.3 ± 25	39.3 ± 10	17.8 ± 2	0.1	0.3	0.7	0.070954
SAOUHSC_02494 - ribosomal protein S5 {Staphylococcus aureus NCTC	23.3 ± 4	27 ± 9	14.8 ± 4	2.3 ± 1	0.9	1.6	10.3	0.001057
SAOUHSC_02496 - ribosomal protein L6, putative {Staphylococcus aurei	25 ± 6	33.8 ± 16	19 ± 7	3 ± 1	0.7	1.3	8.3	0.007539
SAOUHSC_02498 - ribosomal protein S8, putative {Staphylococcus aurei	14.3 ± 10	25.8 ± 8	14.3 ± 3	n.d.	0.6	1.0	-	0.099270
SAOUHSC_02500 - 50S ribosomal protein L5, putative {Staphylococcus i	21 ± 4	36.3 ± 10	26.8 ± 2	3 ± 1	0.6	0.8	7.0	0.002952
SAOUHSC_02501 - ribosomal protein L24 {Staphylococcus aureus NCTC	12.8 ± 4	15.3 ± 3	14.3 ± 1	5.5 ± 2	0.8	0.9	2.3	0.072080
SAOUHSC_02507 - ribosomal protein L22 {Staphylococcus aureus NCTC	15.8 ± 6	18.8 ± 3	10.5 ± 3	1.3 ± 1	0.8	1.5	12.6	0.022276
SAOUHSC_02512 - ribosomal protein L3, putative {Staphylococcus aurei	10.5 ± 2	41.5 ± 13	18.3 ± 4	5 ± 3	0.3	0.6	2.1	0.101045

SAOUHSC_02571 - secretory antigen precursor, putative {Staphylococcus aureus}	632.5 ± 120	582.5 ± 208	894.5 ± 266	526.5 ± 160	1.1	0.7	1.2	0.307420
SAOUHSC_02576 - secretory antigen precursor SsaA, putative {Staphylococcus aureus}	572 ± 161	554.8 ± 138	549 ± 53	673.5 ± 257	1.0	1.0	0.8	0.374692
SAOUHSC_02577 - D-isomer specific 2-hydroxyacid dehydrogenase, NAD-dependent	18 ± 2	44.3 ± 6	37.5 ± 5	5.8 ± 4	0.4	0.5	3.1	0.017754
SAOUHSC_02582 - formate dehydrogenase, alpha subunit, putative {Staphylococcus aureus}	22.8 ± 2	43.3 ± 6	27.3 ± 3	3.8 ± 2	0.5	0.8	6.1	0.000376
SAOUHSC_02583 - transcriptional regulator, putative {Staphylococcus aureus}	37.8 ± 3	40 ± 9	54 ± 10	52.8 ± 16	0.9	0.7	0.7	0.201137
SAOUHSC_02650 - lipoprotein, putative {Staphylococcus aureus NCTC 8325}	21 ± 7	30 ± 16	50.8 ± 19	38.8 ± 11	0.7	0.4	0.5	0.114048
SAOUHSC_02690 - conserved hypothetical protein {Staphylococcus aureus}	10.8 ± 5	9 ± 4	14.5 ± 5	11.8 ± 2	1.2	0.7	0.9	0.427689
SAOUHSC_02699 - conserved hypothetical protein {Staphylococcus aureus}	38.3 ± 10	52 ± 11	78.5 ± 26	56 ± 13	0.7	0.5	0.7	0.162223
SAOUHSC_02703 - phosphoglycerate mutase, putative [5.4.2.1] {Staphylococcus aureus}	32.5 ± 6	165 ± 32	122.5 ± 31	16.8 ± 5	0.2	0.3	1.9	0.048066
SAOUHSC_02706 - immunoglobulin G-binding protein Sbi, putative {Staphylococcus aureus}	143.3 ± 37	58 ± 5	63 ± 15	38.3 ± 10	2.5	2.3	3.7	0.017278
SAOUHSC_02708 - gamma-hemolysin h-gamma-ii subunit, putative {Staphylococcus aureus}	40.8 ± 10	11.8 ± 3	11.8 ± 4	n.d. ^c	3.5	3.5	-	0.003753
SAOUHSC_02709 - leukocidin s subunit precursor, putative {Staphylococcus aureus}	451 ± 116	166.3 ± 112	125.3 ± 83	25.5 ± 8	2.7	3.6	17.7	0.005341
SAOUHSC_02710 - leukocidin f subunit precursor {Staphylococcus aureus}	648.5 ± 52	131.5 ± 19	281.3 ± 53	24.5 ± 10	4.9	2.3	26.5	0.000011
SAOUHSC_02742 - amino acid transporter, putative {Staphylococcus aureus}	11.3 ± 2	2.8 ± 1	5 ± 2	n.d. ^c	4.1	2.3	-	0.000288
SAOUHSC_02767 - peptide ABC transporter, peptide-binding protein, putative	11 ± 3	21.5 ± 3	27 ± 2	17.5 ± 5	0.5	0.4	0.6	0.166870
SAOUHSC_02798 - Surface protein G (sasG)	11.3 ± 2	3.8 ± 2	4.5 ± 1	2.5 ± 1	3.0	2.5	4.5	0.009728
SAOUHSC_02860 - HMG-CoA synthase, putative {Staphylococcus aureus}	22.3 ± 4	66 ± 12	44.5 ± 9	12.8 ± 4	0.3	0.5	1.7	0.071061
SAOUHSC_02862 - ATP-dependent Clp protease, ATP-binding subunit ClpX	11.5 ± 1	36.8 ± 6	30 ± 6	3.5 ± 1	0.3	0.4	3.3	0.001810
SAOUHSC_02869 - delta-1-pyrroline-5-carboxylate dehydrogenase, putative	14.5 ± 5	30 ± 4	29.5 ± 4	8.8 ± 3	0.5	0.5	1.7	0.190439
SAOUHSC_02883 - LysM domain protein [3.5.1.28] {Staphylococcus aureus}	182.8 ± 33	135.8 ± 44	222 ± 93	166 ± 57	1.3	0.8	1.1	0.403257
SAOUHSC_02885 - O-acetyltransferase OatA	35.8 ± 8	10.3 ± 3	11.3 ± 4	10.3 ± 6	3.5	3.2	3.5	0.017941
SAOUHSC_02887 - immunodominant antigen A, putative {Staphylococcus aureus}	1520.8 ± 277	1243.8 ± 287	1852.8 ± 649	1115.8 ± 271	1.2	0.8	1.4	0.168007
SAOUHSC_02922 - L-lactate dehydrogenase [1.1.1.27] {Staphylococcus aureus}	64.5 ± 8	223.3 ± 84	99.3 ± 30	30 ± 7	0.3	0.6	2.2	0.008928
SAOUHSC_02926 - fructose-bisphosphate aldolase class-I, putative [4.1.3.1] {Staphylococcus aureus}	33 ± 5	106 ± 35	62.5 ± 17	31.8 ± 9	0.3	0.5	1.0	0.453858
SAOUHSC_02927 - malate:quinone-oxidoreductase [1.1.99.16] {Staphylococcus aureus}	35 ± 6	63.3 ± 23	44 ± 5	7 ± 3	0.6	0.8	5.0	0.002584
SAOUHSC_02929 - acetyl-CoA synthetase, putative {Staphylococcus aureus}	12.5 ± 2	16.3 ± 6	12.3 ± 4	2.5 ± 2	0.8	1.0	5.0	0.002840
SAOUHSC_02963 - clumping factor B, putative {Staphylococcus aureus}	17.5 ± 2	11 ± 1	21.5 ± 5	9.3 ± 3	1.6	0.8	1.9	0.030973
SAOUHSC_02969 - arginine deiminase [3.5.3.6] {Staphylococcus aureus}	16 ± 5	28.3 ± 3	24.5 ± 7	2.3 ± 1	0.6	0.7	7.1	0.014536
SAOUHSC_02971 - aureolysin, putative {Staphylococcus aureus NCTC 8325}	72.5 ± 3	16.3 ± 4	26.3 ± 7	18 ± 6	4.5	2.8	4.0	0.000114
SAOUHSC_02972 - Immunodominant staphylococcal antigen B	21.8 ± 2	12 ± 1	22.3 ± 9	7.3 ± 3	1.8	1.0	3.0	0.004528
SAOUHSC_02978 - phage infection protein, putative {Staphylococcus aureus}	16.8 ± 3	9.8 ± 1	13.5 ± 3	11 ± 3	1.7	1.2	1.5	0.126738
SAOUHSC_02979 - N-acetylmuramoyl-L-alanine amidase	881.5 ± 76	688.5 ± 87	871.5 ± 192	514.3 ± 140	1.3	1.0	1.7	0.030274
SAOUHSC_02982 - conserved hypothetical protein {Staphylococcus aureus}	36 ± 3	28.5 ± 4	30.3 ± 4	19.8 ± 5	1.3	1.2	1.8	0.018681
SAOUHSC_03006 - lipase [3.1.1.3] {Staphylococcus aureus NCTC 8325}	482.3 ± 127	99.8 ± 14	120 ± 36	65 ± 15	4.8	4.0	7.4	0.008478

^aSpectral counts are the average and SEM of MudPIT data from four independent biological samples.

^bp-values are calculated from the 0xMIC and 8xMIC spectral counts

^cNot detected

Table S3. Fold-change in transcript levels in the presence of arylomycin C₁₆ relative to untreated control.^a

Locus	1 µg/mL	2 µg/mL	8 µg/mL
00051	0.7 ± 0.2	0.8 ± 0	1.2 ± 0.1
00069	1.0 ± 0.02	1.0 ± 0.03	0.7 ± 0.1
00094	1.3 ± 0.2	1.0 ± 0.3	0.8 ± 0.1
00192	1.5 ± 0.1	1.4 ± 0.1	0.8 ± 0.2
00256	1.3 ± 0.1	1.5 ± 0.1	1.1 ± 0.1
00300	0.9 ± 0.3	1.2 ± 0.1	0.9 ± 0
00354	1.4 ± 0.6	0.9 ± 0.4	1.3 ± 0.3
00399	1.5 ± 0.3	1.1 ± 0.1	1.0 ± 0.1
00427	0.6 ± 0.6	1.3 ± 0.04	1.5 ± 0.1
00472	1.7 ± 0.2	1.3 ± 0.1	1.4 ± 0.1
00617	1.1 ± 0.2	1.7 ± 0.2	2.2 ± 0.2
00728	1.5 ± 0.2	1.4 ± 0.1	1.9 ± 0.5
00818	0.6 ± 0.03	0.9 ± 0.1	1.3 ± 0.2
00897	1.2 ± 0.1	1.4 ± 0.1	0.8 ± 0.01
00987	0.9 ± 0.1	1.3 ± 0.2	0.6 ± 0.7
00988	1.8 ± 0.3	1.3 ± 0.3	1.1 ± 0.3
00994	1.5 ± 0.1	1.5 ± 0.2	1.7 ± 0.2
01114	1.2 ± 0.03	1.3 ± 0.04	1.3 ± 0.03
01121	2.2 ± 0.4	2.4 ± 0.3	2.1 ± 0.3
01125	1.7 ± 0.04	1.6 ± 0.2	1.7 ± 0.2
01652	1.9 ± 0.2	2.0 ± 0.1	2.3 ± 0.1
01935	1.2 ± 0.2	0.6 ± 0.1	0.8 ± 0.2
01936	1.0 ± 0.2	0.5 ± 0.1	0.6 ± 0.1
01938	1.2 ± 0.3	0.5 ± 0.1	0.7 ± 0.1
01939	1.0 ± 0.02	1.0 ± 0.01	1.0 ± 0.01
01941	1.0 ± 0.1	1.0 ± 0.1	0.9 ± 0.01
01942	7.8 ± 0.7	4.6 ± 0.3	3.2 ± 0.3
01949	1.0 ± 0.03	0.9 ± 0.02	1.1 ± 0.1
01954	1.1 ± 0.1	0.7 ± 0.1	0.5 ± 0
02127	1.2 ± 0.2	0.9 ± 0.1	0.8 ± 0.1
02171	1.5 ± 0.7	1.5 ± 0.3	1.4 ± 0.4
02241	1.6 ± 0.7	1.1 ± 0.5	0.9 ± 0.4
02243	0.8 ± 0.1	0.5 ± 0	0.5 ± 0.1
02260	1.1 ± 0.4	0.8 ± 0.1	0.9 ± 0.2
02463	1.4 ± 0.03	1.5 ± 0.1	1.5 ± 0.1
02466	1.3 ± 0.2	2.3 ± 0.3	1.6 ± 0.05
02706	1.3 ± 0.3	0.8 ± 0.1	0.4 ± 0.03
02708	1.2 ± 0.02	1.1 ± 0.01	1.1 ± 0.04
02709	1.3 ± 0	0.8 ± 0.1	1.1 ± 0.2
02710	2.0 ± 0.3	1.0 ± 0.1	0.9 ± 0.1
02742	2.6 ± 0.2	3.2 ± 0.3	2.4 ± 0.2
02798	2.4 ± 0.03	1.5 ± 0.1	1.8 ± 0.3
02885	1.9 ± 0.2	1.0 ± 0.3	1.5 ± 0.3
02971	1.0 ± 0.01	1.0 ± 0.02	1.0 ± 0.02
02972	1.6 ± 0.02	1.9 ± 0.3	3.5 ± 0.5
02979	2.7 ± 0.2	2.6 ± 0.1	2.3 ± 0.3
03006	1.1 ± 0.03	2.0 ± 0.1	2.8 ± 0.2
01761	2.8 ± 0.4	3.7 ± 0.4	4.3 ± 0.5
01838	2.3 ± 0.4	2.2 ± 0.4	2.3 ± 0.2
01972	9.6 ± 2.8	16.3 ± 1.0	16.3 ± 0.4

^aValues shown are changes with respect to untreated control samples. See Methods for details.