Staphylococcus aureus (MRSA), Strain COL, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plates 1-25

Catalog No. NR-19277

Table 1: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 1 (ZSAJA), NR-19497[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1	A01	100	SACOL2693	hypothetical protein	YP_187479.1	3
5	A02	127	SACOL0039	hypothetical protein	YP_184950.1	3
7	A03	127	SACOL0057	hypothetical protein	YP_184963.1	2
10	A04	127	SACOL0393	hypothetical protein	YP_185285.1	-
11	A05	127	SACOL0561	hypothetical protein	YP_185449.1	2.976377953
15	A06	127	SACOL0852	hypothetical protein	-	3.960629921
19	A07	127	SACOL1953	hypothetical protein	YP_186778.1	2.992125984
23	A08	127	SACOL2372	hypothetical protein	YP_187176.1	3
25	A09	127	SACOL2640	hypothetical protein	YP_187428.1	3.992125984
27	A10	130	SACOL1027	hypothetical protein	YP_185893.1	3
29	A11	130	SACOL1156	hypothetical protein	YP_186019.1	2
31	A12	130	SACOL1237	hypothetical protein	-	2.976923077
35	B01	130	SACOL1463	hypothetical protein	-	3.9
37	B02	130	SACOL2200	hypothetical protein	YP_187011.1	4
41	B03	130	SACOL2629	hypothetical protein	YP_187418.1	3
43	B04	130	SACOL2637	hypothetical protein	YP_187425.1	3
45	B05	133	SACOL0226	hypothetical protein	-	4
47	B06	133	SACOL0923	hypothetical protein	-	1.992481203
49	B07	133	SACOL0990	hypothetical protein	YP_185858.1	3
51	B08	133	SACOL1246	hypothetical protein	YP_186106.1	3
53	B09	133	SACOL1379	hypothetical protein	YP_186232.1	1.962406015
55	B10	133	SACOL1391	hypothetical protein	-	3.789473684
58	B11	133	SACOL1559	hypothetical protein	YP_186400.1	2
60	B12	133	SACOL1757	hypothetical protein	YP_186591.1	1.92481203
63	C01	133	SACOL1999	conserved hypothetical protein	YP_186823.1	3
65	C02	133	SACOL2336	hypothetical protein	YP_187143.1	4
67	C03	133	SACOL2406	hypothetical protein	YP_187209.1	3
69	C04	133	SACOL2468	hypothetical protein	-	3.992481203
71	C05	133	SACOL2543	hypothetical protein	YP_187335.1	2
73	C06	136	SACOL0060	hypothetical protein	-	3.977941176
75	C07	136	SACOL0066	conserved domain protein	YP_184971.1	4
77	C08	136	SACOL0174	hypothetical protein	YP_185073.1	-
79	C09	136	SACOL0475	hypothetical protein	YP_185365.1	3.955882353
81	C10	136	SACOL0642	hypothetical protein	YP_185527.1	3
83	C11	136	SACOL1341	hypothetical protein	YP_186195.1	2
85	C12	136	SACOL1713	hypothetical protein	-	3
87	D01	136	SACOL1856	hypothetical protein	-	4
89	D02	136	SACOL2649	conserved hypothetical protein	YP_187437.1	3
91	D03	139	SACOL0133	hypothetical protein	-	2.985611511
96	D04	139	SACOL0817	hypothetical protein	YP_185691.1	2
97	D05	139	SACOL0866	hypothetical protein	YP_185739.1	4
99	D06	139	SACOL1050	hypothetical protein	YP_185915.1	4
101	D07	139	SACOL1336	hypothetical protein	YP_186190.1	2
103	D08	139	SACOL1372	hypothetical protein	YP_186225.1	1.978417266

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Master Clone List for NR-19277

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
105	D09	139	SACOL2414	conserved hypothetical protein	YP_187217.1	3.90647482
107	D10	139	SACOL2417	hypothetical protein	-	3
110	D11	139	SACOL2444	hypothetical protein	-	2
111	D12	142	SACOL0087	hypothetical protein	YP_184992.1	3
113	E01	142	SACOL0661	hypothetical protein	YP_185545.1	3.971830986
115	E02	142	SACOL0819	hypothetical protein	YP_185693.1	2.992957746
118	E03	142	SACOL1037	hypothetical protein	YP_185902.1	1.964788732
119	E04	142	SACOL1165	hypothetical protein	YP_186028.1	3
125	E05	142	SACOL2027	hypothetical protein	-	1.971830986
127	E06	142	SACOL2139	hypothetical protein	YP_186954.1	2.584507042
129	E07	142	SACOL2432	hypothetical protein	-	4
131	E08	142	SACOL2433	hypothetical protein	YP_187234.1	2
133	E09	142	SACOL2595	hypothetical protein	YP_187386.1	2
135	E10	145	SACOL0910	hypothetical protein	YP_185781.1	3
137	E11	145	SACOL0933	hypothetical protein	YP_185803.1	3
139	E12	145	SACOL1061	hypothetical protein	-	2.993103448
142	F01	145	SACOL1334	hypothetical protein	YP_186188.1	2
144	F02	145	SACOL1890	hypothetical protein	YP_186716.1	1.965517241
145	F03	145	SACOL1949	hypothetical protein	YP_186774.1	2
147	F04	145	SACOL2069	K+-transporting ATPase, F subunit	YP_186885.1	5
151	F05	145	SACOL2677	hypothetical protein	YP_187465.1	4
153	F06	148	SACOL0227	hypothetical protein	-	3
157	F07	148	SACOL0878	hypothetical protein	-	3
161	F08	148	SACOL1330	hypothetical protein	-	2.945945946
163	F09	148	SACOL2216	ribosomal protein L36	YP_187026.1	3
165	F10	148	SACOL2331	hypothetical protein	YP_187138.1	2.97972973
168	F11	148	SACOL2642	hypothetical protein	YP_187430.1	1.972972973
169	F12	151	SACOL0500	hypothetical protein	YP_185388.1	5
171	G01	151	SACOL1517	hypothetical protein	-	2
175	G02	151	SACOL1884	hypothetical protein	-	3.947019868
177	G03	151	SACOL2065	hypothetical protein	YP_186881.1	2.98013245
179	G04	151	SACOL2187	hypothetical protein	YP_186998.1	2.947019868
182	G05	151	SACOL2370	hypothetical protein	-	2
185	G06	154	SACOL0729	hypothetical protein	-	1.993506494
187	G07	154	SACOL1527	hypothetical protein	-	2
189	G08	154	SACOL1815	hypothetical protein	YP_186647.1	1.980519481
192	G09	154	SACOL2254	hypothetical protein	-	2
193	G10	154	SACOL2454	hypothetical protein	YP_187253.1	3
197	G11	157	SACOL0094	hypothetical protein	YP_184999.1	3
199	G12	157	SACOL0112	hypothetical protein	YP_185016.1	-
201	H01	157	SACOL0390	lipase precursor, interruption-C	YP_185282.1	2
203	H02	157	SACOL1730	hypothetical protein	-	2
205	H03	157	SACOL1978	hypothetical protein	YP_186802.1	2
207	H04	157	SACOL2380	hypothetical protein	YP_187184.1	-
209	H05	157	SACOL2489	conserved hypothetical protein	YP_187285.1	2
211	H06	157	SACOL2492	hypothetical protein	YP_187287.1	2
213	H07	157	SACOL2510	hypothetical protein	YP_187305.1	2
215	H08	160	SACOL0223	hypothetical protein	YP_185121.1	2
217	H09	160	SACOL1258	hypothetical protein	-	-
221	H10	160	SACOL1508	hypothetical protein	YP_186352.1	-
223	H11	160	SACOL2032	hypothetical protein	-	3
225	H12	160	SACOL2191	hypothetical protein	YP_187002.1	-

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Table 2: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 2 (ZSAJB), NR-19498[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
229	A01	160	SACOL2604	hypothetical protein	-	3
232	A02	163	SACOL0056	hypothetical protein	-	1.969325153
233	A03	163	SACOL0493	hypothetical protein	-	2
235	A04	163	SACOL1684	hypothetical protein	-	2
238	A05	163	SACOL2351	hypothetical protein	YP_187157.1	2
241	A06	166	SACOL1046	hypothetical protein	YP_185911.1	-
246	A07	166	SACOL1469	hypothetical protein	YP_186317.1	2
249	A08	166	SACOL2247	hypothetical protein	YP_187056.1	2.759036145
252	A09	166	SACOL2480	hypothetical protein	YP_187277.1	1.915662651
253	A10	169	SACOL0231	hypothetical protein	YP_185127.1	2
256	A11	169	SACOL0965	hypothetical protein	YP_185834.1	-
257	A12	169	SACOL1087	hypothetical protein	YP_185951.1	2
259	B01	169	SACOL1186	antibacterial protein (phenol soluble modulin)	YP_186048.1	3
261	B02	169	SACOL1187	antibacterial protein (phenol soluble modulin)	YP_186049.1	3
263	B03	169	SACOL1344	hypothetical protein	YP_186197.1	2
265	B04	169	SACOL1863	hypothetical protein	YP_186691.1	-
267	B05	-	SACOL2022	-	YP_186841.1	-
269	B06	169	SACOL2558	hypothetical protein	-	2
271	B07	172	SACOL0471	hypothetical protein	YP_185361.1	1.843023256
273	B08	172	SACOL0919	hypothetical protein	YP_185790.1	-
275	B09	172	SACOL1343	hypothetical protein	-	-
277	B10	172	SACOL2076	conserved hypothetical protein	YP_186892.1	3
280	B11	172	SACOL2740	ribosomal protein L34	YP_187526.1	1.970930233
281	B12	175	SACOL0210	hypothetical protein	YP_185109.1	-
283	C01	175	SACOL1766	hypothetical protein	YP_186600.1	3
285	C02	175	SACOL2024	accessory gene regulator protein D	YP_186843.1	2
287	C03	175	SACOL2455	hypothetical protein	-	2
290	C04	175	SACOL2490	hypothetical protein	-	1.931428571
291	C05	178	SACOL0492	hypothetical protein	-	2
293	C06	178	SACOL1755	hypothetical protein	-	2
295	C07	178	SACOL1878	lantibiotic epidermin precursor EpiA	YP_186705.1	-
297	C08	178	SACOL2005	hypothetical protein	-	2
301	C09	178	SACOL2429	hypothetical protein	YP_187231.1	3
303	C10	181	SACOL0234	conserved hypothetical protein	YP_185130.1	2
307	C11	181	SACOL0850	hypothetical protein	YP_185724.1	2
309	C12	181	SACOL0867	hypothetical protein	-	2
311	D01	181	SACOL0893	pathogenicity island protein	YP_185764.1	3
313	D02	181	SACOL1174	hypothetical protein	YP_186037.1	3
315	D03	181	SACOL1679	conserved hypothetical protein	YP_186519.1	3
317	D04	181	SACOL1959	hypothetical protein	-	2
325	D06	187	SACOL0324	hypothetical protein	YP_185216.1	2
327	D07	187	SACOL0361	conserved hypothetical protein	YP_185253.1	3
329	D08	187	SACOL0465	hypothetical protein	YP_185355.1	2
331	D09	187	SACOL0909	hypothetical protein	YP_185780.1	3
333	D10	187	SACOL0934	conserved hypothetical protein	YP_185804.1	-
335	D11	187	SACOL1911	conserved hypothetical protein	YP_186736.1	2
337	D12	190	SACOL0532	hypothetical protein	YP_185420.1	3
339	E01	190	SACOL0795	hypothetical protein	YP_185668.1	2
345	E02	193	SACOL0378	hypothetical protein	YP_185270.1	2
347	E03	196	SACOL0334	conserved hypothetical protein	YP_185226.1	2
351	E04	196	SACOL1318	hypothetical protein	-	3
353	E05	196	SACOL1934	conserved hypothetical protein	YP_186759.1	2

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
357	E06	199	SACOL0386	conserved hypothetical protein TIGR01669	YP_185278.1	-
359	E07	199	SACOL1487	hypothetical protein	-	1.924623116
361	E08	199	SACOL2250	conserved hypothetical protein	YP_187058.1	2
363	E09	202	SACOL0029	HMG-CoA synthase, truncation	YP_184940.1	-
366	E10	202	SACOL0625	conserved hypothetical protein	YP_185510.1	1.975247525
367	E11	202	SACOL1119	conserved hypothetical protein	YP_185983.1	2
369	E12	202	SACOL1394	hypothetical protein	YP_186246.1	3
371	F01	202	SACOL2568	hypothetical protein	YP_187360.1	2
373	F02	205	SACOL2059	conserved hypothetical protein	YP_186875.1	2
375	F03	205	SACOL2259	hypothetical protein	YP_187066.1	2
377	F04	205	SACOL2457	hypothetical protein	YP_187255.1	2
379	F05	205	SACOL2542	conserved hypothetical protein	YP_187334.1	2
381	F06	208	SACOL0219	hypothetical protein	YP_185118.1	3
383	F07	208	SACOL0304	hypothetical protein	-	1.947115385
385	F08	208	SACOL0601	hypothetical protein	YP_185487.1	3
389	F09	208	SACOL1972	conserved hypothetical protein	YP_186796.1	3
391	F10	208	SACOL1983	hypothetical protein	YP_186807.1	2
393	F11	208	SACOL1987	conserved hypothetical protein	YP_186811.1	3
395	F12	211	SACOL1035	conserved domain protein	YP_185900.1	2
400	G01	211	SACOL1853	hypothetical protein	YP_186683.1	1.687203791
402	G02	211	SACOL1998	conserved hypothetical protein	YP_186822.1	1.976303318
403	G03	214	SACOL0258	hypothetical protein	YP_185153.1	3
407	G04	214	SACOL1556	hypothetical protein	YP_186397.1	3
409	G05	214	SACOL2221	ribosomal protein L30p/L7e	YP_187031.1	2
411	G06	217	SACOL0581	preprotein translocase, SecE subunit	YP_185467.1	3
413	G07	217	SACOL1680	conserved hypothetical protein	YP_186520.1	2
416	G08	220	SACOL0348	conserved hypothetical protein	YP_185240.1	-
417	G09	220	SACOL0986	hypothetical protein	YP_185854.1	2
419	G10	220	SACOL1171	hypothetical protein	YP_186034.1	2
421	G11	220	SACOL1335	hypothetical protein	YP_186189.1	2
425	G12	220	SACOL1852	hypothetical protein	-	3
427	H01	220	SACOL2226	ribosomal protein S14	YP_187036.1	-
429	H02	220	SACOL2311	hypothetical protein	YP_187118.1	3
432	H03	223	SACOL1185	hypothetical protein	YP_186047.1	2
435	H04	226	SACOL0331	hypothetical protein	YP_185223.1	2
437	H05	226	SACOL0436	conserved hypothetical protein	YP_185327.1	2
440	H06	226	SACOL1117	conserved hypothetical protein	YP_185981.1	-
441	H07	226	SACOL1348	conserved hypothetical protein	YP_186201.1	2
443	H08	226	SACOL2312	conserved hypothetical protein	YP_187119.1	3
445	H09	226	SACOL2491	conserved hypothetical protein	YP_187286.1	2
447	H10	226	SACOL2571	conserved hypothetical protein	YP_187363.1	2
449	H11	226	SACOL2726	hypothetical protein	YP_187512.1	2
451	H12	226	SACOL2730	hypothetical protein	YP_187516.1	3

Table 3: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 3 (ZSAJC), NR-19499[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
453	A01	229	SACOL0206	hypothetical protein	YP_185105.1	2
455	A02	229	SACOL0359	hypothetical protein	YP_185251.1	3
457	A03	229	SACOL0912	conserved hypothetical protein	YP_185783.1	3
459	A04	229	SACOL1346	hypothetical protein	YP_186199.1	2

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
462	A05	229	SACOL1467	conserved hypothetical protein	YP_186315.1	2
463	A06	229	SACOL2466	hypothetical protein	YP_187264.1	3
465	A07	229	SACOL2513	hypothetical protein	YP_187307.1	3
467	A08	232	SACOL1175	hypothetical protein	YP_186038.1	2
469	A09	232	SACOL1331	hypothetical protein	YP_186185.1	2
471	A10	232	SACOL1350	conserved hypothetical protein	YP_186203.1	2
473	A11	232	SACOL2447	hypothetical protein	-	3
475	A12	235	SACOL0329	conserved hypothetical protein	YP_185221.1	3
477	B01	235	SACOL0362	conserved hypothetical protein	YP_185254.1	3
481	B02	235	SACOL0911	hypothetical protein	YP_185782.1	2
483	B03	235	SACOL1437	cold shock protein, CSD family	YP_186289.1	3
485	B04	235	SACOL1507	hypothetical protein	YP_186351.1	3
487	B05	235	SACOL1726	ribosomal protein L35	YP_186564.1	-
489	B06	235	SACOL2647	hypothetical protein	YP_187435.1	3
493	B07	238	SACOL0068	hypothetical protein	YP_184973.1	3
495	B08	238	SACOL0131	hypothetical protein	-	3
497	B09	238	SACOL0156	hypothetical protein	YP_185056.1	-
499	B10	238	SACOL0360	hypothetical protein	YP_185252.1	3
502	B11	238	SACOL0420	transcriptional regulator, Cro/CI family	YP_185312.1	1.957983193
503	B12	238	SACOL0434	conserved hypothetical protein	YP_185325.1	3
505	C01	238	SACOL0677	conserved hypothetical protein	YP_185560.1	2
507	C02	238	SACOL1127	hypothetical protein	YP_185991.1	3
509	C03	238	SACOL1446	conserved hypothetical protein	YP_186298.1	2
511	C04	238	SACOL1605	conserved hypothetical protein	YP_186445.1	3
514	C05	238	SACOL2141	site-specific recombinase family protein, degenerate	-	1.983193277
515	C06	238	SACOL2547	hypothetical protein	YP_187339.1	2
518	C07	238	SACOL2586	hypothetical protein	-	1.983193277
520	C08	241	SACOL0352	hypothetical protein	YP_185244.1	1.98340249
521	C09	241	SACOL0358	conserved hypothetical protein	YP_185250.1	-
523	C10	241	SACOL1333	hypothetical protein	YP_186187.1	2
525	C11	241	SACOL1529	hypothetical protein	YP_186371.1	3
528	C12	241	SACOL1938	conserved hypothetical protein	YP_186763.1	1.98340249
529	D01	241	SACOL2573	copper ion binding protein	YP_187365.1	3
533	D02	244	SACOL2077	conserved hypothetical protein	YP_186893.1	2
535	D03	244	SACOL2231	ribosomal protein L29	YP_187041.1	-
537	D04	247	SACOL1218	conserved hypothetical protein	YP_186081.1	-
539	D05	247	SACOL2100	ATP synthase F0, C subunit	YP_186915.1	-
541	D06	247	SACOL2626	conserved hypothetical protein	YP_187415.1	3
543	D07	247	SACOL2695	hypothetical protein	YP_187481.1	3
549	D08	250	SACOL1306	conserved hypothetical protein	YP_186163.1	2
551	D09	253	SACOL0285	conserved hypothetical protein	YP_185180.1	3
554	D10	253	SACOL0322	prophage L54a, Cro-related protein	YP_185214.1	1.806324111
555	D11	253	SACOL0862	hypothetical protein	YP_185735.1	-
557	D12	253	SACOL0903	pathogenicity island protein	YP_185774.1	-
559	E01	253	SACOL1033	hypothetical protein	YP_185898.1	-
561	E02	253	SACOL1099	conserved hypothetical protein	YP_185963.1	2
563	E03	253	SACOL1222	DNA-directed RNA polymerase, omega subunit	YP_186085.1	-
565	E04	253	SACOL1590	conserved hypothetical protein	YP_186430.1	2
567	E05	253	SACOL2217	translation initiation factor IF-1	YP_187027.1	2
569	E06	253	SACOL2556	conserved hypothetical protein	YP_187349.1	2
571	E07	256	SACOL0337	hypothetical protein	YP_185229.1	-
573	E08	256	SACOL0345	hypothetical protein	YP_185237.1	3

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
576	E09	256	SACOL0939	NifU domain protein	YP_185809.1	2
577	E10	256	SACOL1456	conserved hypothetical protein	YP_186307.1	-
579	E11	259	SACOL0326	hypothetical protein	YP_185218.1	2
581	E12	259	SACOL0676	conserved hypothetical protein	YP_185559.1	-
586	F01	259	SACOL1332	hypothetical protein	YP_186186.1	1.965250965
587	F02	259	SACOL1826	conserved hypothetical protein	YP_186658.1	-
589	F03	259	SACOL2033	conserved hypothetical protein	YP_186850.1	-
591	F04	262	SACOL0320	hypothetical protein	YP_185212.1	2
593	F05	262	SACOL1886	hypothetical protein	YP_186712.1	2
595	F06	262	SACOL2565	FeoA domain protein	YP_187357.1	2
599	F07	265	SACOL1567	exodeoxyribonuclease VII, small subunit	YP_186408.1	2
603	F08	265	SACOL2134	conserved hypothetical protein	YP_186949.1	2
605	F09	265	SACOL2589	conserved hypothetical protein	YP_187380.1	2
607	F10	268	SACOL0844	preprotein translocase, SecG subunit	YP_185718.1	2
609	F11	268	SACOL1093	conserved hypothetical protein	YP_185957.1	2
611	F12	268	SACOL1172	hypothetical protein	YP_186035.1	2
613	G01	268	SACOL1247	acyl carrier protein	YP_186107.1	2
615	G02	268	SACOL1324	RNA chaperone Hfq	YP_186179.1	2
617	G03	268	SACOL1375	conserved hypothetical protein	YP_186228.1	-
619	G04	268	SACOL2093	conserved hypothetical protein	YP_186908.1	2
621	G05	268	SACOL2263	molybdopterin converting factor, subunit 1	YP_187070.1	2
623	G06	271	SACOL0356	conserved hypothetical protein	YP_185248.1	-
625	G07	271	SACOL0822	conserved hypothetical protein	YP_185696.1	2
627	G08	271	SACOL0868	conserved hypothetical protein	YP_185740.1	-
631	G09	271	SACOL0942	conserved hypothetical protein	YP_185811.1	-
633	G10	274	SACOL0027	conserved hypothetical protein	YP_184938.1	-
637	G11	274	SACOL2174	conserved hypothetical protein	YP_186985.1	2
639	G12	277	SACOL0274	conserved hypothetical protein	YP_185169.1	2
641	H01	277	SACOL0351	conserved hypothetical protein	YP_185243.1	2
644	H02	277	SACOL0439	ribosomal protein S18	YP_185330.1	2
646	H03	277	SACOL1378	conserved hypothetical protein	YP_186231.1	1.642599278
647	H04	280	SACOL0003	conserved hypothetical protein	YP_184914.1	2
650	H05	280	SACOL0327	hypothetical protein	YP_185219.1	2
653	H06	283	SACOL0530	conserved hypothetical protein	YP_185418.1	2
657	H07	283	SACOL1340	hypothetical protein	YP_186194.1	2
659	H08	283	SACOL1525	ferredoxin	YP_186368.1	-
661	H09	283	SACOL1544	hypothetical protein	YP_186386.1	2
663	H10	286	SACOL0332	conserved hypothetical protein	YP_185224.1	2
665	H11	286	SACOL0446	conserved hypothetical protein	YP_185336.1	2
667	H12	286	SACOL1024	conserved hypothetical protein	YP_185890.1	2

Table 4: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 4 (ZSAJD), NR-19500[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
671	A01	286	SACOL1466	conserved domain protein	YP_186314.1	2
675	A03	286	SACOL2299	conserved hypothetical protein	YP_187106.1	2
677	A04	286	SACOL2405	addiction module antitoxin, Axe family	YP_187208.1	-
679	A05	289	SACOL0590	30S ribosomal protein L7 Ae	YP_185476.1	3.283737024
681	A06	289	SACOL1131	conserved domain protein	YP_185995.1	3.3183391
683	A07	289	SACOL2044	acetolactate synthase, small subunit, truncation	YP_186861.1	3.301038062

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
685	A08	289	SACOL2112	ribosomal protein L31	YP_186927.1	3.294117647
687	A09	292	SACOL0349	conserved hypothetical protein	YP_185241.1	3.301369863
690	A10	292	SACOL0929	conserved hypothetical protein	YP_185799.1	2.609589041
691	A11	292	SACOL1842	conserved hypothetical protein TIGR00278	YP_186673.1	3.260273973
693	A12	292	SACOL2465	addiction module antitoxin, Axe family	YP_187263.1	3.270547945
695	B01	292	SACOL2559	hypothetical protein	YP_187351.1	3.304794521
697	B02	295	SACOL0035	hypothetical protein	YP_184946.1	3.294915254
699	B03	295	SACOL0048	conserved hypothetical protein	YP_184958.1	3.274576271
701	B04	295	SACOL0062	conserved hypothetical protein	YP_184967.1	2.640677966
703	B05	295	SACOL0336	conserved hypothetical protein	YP_185228.1	3.291525424
707	B06	295	SACOL0865	hypothetical protein	YP_185738.1	3.308474576
709	B07	295	SACOL1581	conserved hypothetical protein	YP_186421.1	3.301694915
711	B08	295	SACOL1672	conserved hypothetical protein	YP_186512.1	3.281355932
713	B09	295	SACOL1693	preprotein translocase, YajC subunit	YP_186532.1	3.26779661
717	B10	298	SACOL0333	conserved hypothetical protein	YP_185225.1	3.295302013
719	B11	298	SACOL0445	conserved domain protein	YP_185335.1	3.285234899
722	B12	298	SACOL0537	conserved hypothetical protein	YP_185425.1	2
724	C01	298	SACOL0550	S4 domain protein	YP_185438.1	3.244966443
726	C02	298	SACOL0891	transcriptional regulator, putative	YP_185762.1	3.244966443
727	C03	298	SACOL1076	phosphoribosylformylglycinamidine synthase, PurS protein	YP_185940.1	2.275167785
729	C04	298	SACOL2230	ribosomal protein S17	YP_187040.1	3.238255034
732	C05	301	SACOL0790.1	ribonucleoside-diphosphate reductase 2, NrdH-redoxin, putative	YP_185664.1	2.222591362
733	C06	301	SACOL1091	phosphocarrier protein HPr	YP_185955.1	3.325581395
735	C07	301	SACOL1151	conserved hypothetical protein	YP_186014.1	3.285714286
737	C08	301	SACOL1342	hypothetical protein	YP_186196.1	3.279069767
739	C09		SACOL2404	-	YP_187207.1	
741	C10		SACOL2464	-	YP_187262.1	
743	C11	301	SACOL2502	hypothetical protein	YP_187297.1	3.255813953
745	C12	304	SACOL0508	conserved hypothetical protein	YP_185396.1	3.296052632
747	D01	304	SACOL0624	conserved hypothetical protein	YP_185509.1	3.286184211
749	D02	304	SACOL1292	ribosomal protein S15	YP_186149.1	3.276315789
753	D04	304	SACOL1439	acylphosphatase	YP_186291.1	3.253289474
755	D05	304	SACOL1656	hypothetical protein	YP_186496.1	3.259868421
757	D06	307	SACOL0464	transposase, IS3 family	YP_185354.1	3.247557003
759	D07	307	SACOL0892	pathogenicity island protein	YP_185763.1	3.263843648
761	D08	307	SACOL1513	DNA-binding protein HU	YP_186357.1	3.283387622
763	D09	310	SACOL1106	conserved hypothetical protein	YP_185970.1	3.264516129
766	D10	310	SACOL1121	conserved hypothetical protein	YP_185985.1	3.232258065
767	D11	310	SACOL1254	ribosomal protein S16	YP_186113.1	2.232258065
769	D12	310	SACOL1940	conserved hypothetical protein	YP_186765.1	3.25483871
771	E01	310	SACOL2237	ribosomal protein L23	YP_187047.1	3.270967742
774	E02	310	SACOL2607	hypothetical protein	YP_187397.1	3.251612903
775	E03	313	SACOL0230	PTS system, sorbitol-specific IIB component	YP_185126.1	3.28115016
777	E04	313	SACOL0371	prophage L54a, DNA packaging protein, putative	YP_185263.1	2.658146965
779	E05	313	SACOL0437	ribosomal protein S6	YP_185328.2	3.284345048
781	E06	313	SACOL1067	cytochrome aa3 quinol oxidase, subunit IV	YP_185931.1	3.236421725
785	E07	313	SACOL2235	ribosomal protein S19	YP_187045.1	3.249201278
787	E08	313	SACOL2603	hypothetical protein	YP_187394.1	2.619808307
789	E09	316	SACOL0848	lipoprotein, putative	YP_185722.1	3.262658228
791	E10	319	SACOL0401	conserved hypothetical protein	YP_185293.1	2.282131661

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
793	E11	319	SACOL0863	conserved hypothetical protein	YP_185736.1	3.253918495
796	E12	319	SACOL0899	pathogenicity island protein	YP_185770.1	2.253918495
797	F01	319	SACOL1286	conserved hypothetical protein	YP_186143.1	3.106583072
800	F02	319	SACOL1586	hypothetical protein	YP_186426.1	2.605015674
802	F03	319	SACOL1700	ribosomal protein L27	YP_186539.1	3.269592476
803	F04	319	SACOL1706	hypothetical protein	YP_186545.1	3.206896552
805	F05	319	SACOL2017	chaperonin, 10 kDa	YP_186836.1	3.235109718
808	F06	319	SACOL2532	acetyltransferase, GNAT family	YP_187325.1	3.235109718
811	F08	322	SACOL1042	hypothetical protein	YP_185907.1	3.248447205
813	F09	322	SACOL2494	hypothetical protein	YP_187289.1	3.242236025
815	F10	325	SACOL0382	hypothetical protein	YP_185274.1	3.28
817	F11	325	SACOL1041	hypothetical protein	YP_185906.1	3.218461538
819	F12	325	SACOL1047	conserved domain protein	YP_185912.1	3.246153846
822	G01	325	SACOL1203	YlmG protein	YP_186065.1	3.227692308
823	G02	325	SACOL1345	hypothetical protein	YP_186198.1	3.255384615
825	G03	325	SACOL1651	conserved hypothetical protein TIGR00253	YP_186491.1	3.270769231
827	G04	328	SACOL0271	conserved hypothetical protein	YP_185166.1	3.243902439
829	G05	328	SACOL0450	hypothetical protein	YP_185340.1	2.618902439
831	G06	328	SACOL0950	Na+/H+ antiporter, MnhF component	YP_185819.1	3.265243902
833	G07	328	SACOL1310	conserved hypothetical protein	YP_186167.1	3.286585366
836	G08	328	SACOL2078	conserved hypothetical protein	YP_186894.1	2.625
837	G09	331	SACOL0044	conserved hypothetical protein	YP_184954.1	3.253776435
839	G10	331	SACOL0069	conserved hypothetical protein	YP_184974.1	3.223564955
841	G11	331	SACOL0412	conserved hypothetical protein	YP_185304.1	2.622356495
843	G12	331	SACOL0881	thioredoxin, putative	YP_185752.1	3.241691843
845	H01	331	SACOL1387	conserved hypothetical protein	YP_186240.1	3.250755287
847	H02	331	SACOL1425	IS1272-related, transposase, truncation	YP_186277.1	2.616314199
849	H03	331	SACOL2601	conserved hypothetical protein	YP_187392.1	3.250755287
851	H04	334	SACOL0387	conserved hypothetical protein	YP_185279.1	3.200598802
853	H05	334	SACOL0738	conserved hypothetical protein	YP_185617.1	3.230538922
858	H06	337	SACOL0388	prophage L54a, holin, SPP1 family	YP_185280.1	3.225519288
859	H07	337	SACOL0541	spoVG protein	YP_185429.1	3.216617211
863	H08	337	SACOL1584	hypothetical protein	YP_186424.1	3.231454006
865	H09	337	SACOL1962	glutamyl-tRNA(Gln) amidotransferase, C subunit	YP_186786.1	3.258160237
867	H10	337	SACOL1968	conserved hypothetical protein	YP_186792.1	3.201780415
663	H10	286	SACOL0332	conserved hypothetical protein	YP_185224.1	2
869	H11	337	SACOL2280	urease, gamma subunit	YP_187087.1	2.643916914
665	H11	286	SACOL0446	conserved hypothetical protein	YP_185336.1	2
871	H12	337	SACOL2680	hypothetical protein	YP_187467.1	3.240356083
667	H12	286	SACOL1024	conserved hypothetical protein	YP_185890.1	2

Table 5: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 5 (ZSAJE), NR-19501[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
873	A01	340	SACOL0366	prophage L54a, terminase, small subunit, putative	YP_185258.1	3.232352941
877	A03	343	SACOL0323	hypothetical protein	YP_185215.1	3.227405248
879	A04	343	SACOL0355	conserved hypothetical protein	YP_185247.1	3.262390671
881	A05	343	SACOL0480	hypothetical protein	YP_185370.1	3.253644315
884	A06	343	SACOL0977	conserved hypothetical protein	YP_185845.1	3.253644315

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
886	A07	343	SACOL1438	conserved hypothetical protein	YP_186290.1	3.195335277
887	A08	343	SACOL1670	conserved hypothetical protein	YP_186510.1	3.221574344
889	A09	343	SACOL1702	ribosomal protein L21	YP_186541.1	3.21574344
891	A10	343	SACOL2240	ribosomal protein S10	YP_187050.1	3.27696793
893	A11	343	SACOL2503	hypothetical protein	YP_187298.1	3.247813411
895	A12	346	SACOL0038	conserved hypothetical protein	YP_184949.1	3.251445087
897	B01	346	SACOL1599	comG operon protein 3 precursor	YP_186439.1	3.23699422
899	B02	346	SACOL1794	thioredoxin, putative	YP_186627.1	3.208092486
901	B03	346	SACOL1796	conserved hypothetical protein	YP_186629.1	3.260115607
903	B04	346	SACOL1807	rhodanese-like domain protein	YP_186640.1	3.248554913
907	B05	349	SACOL0278	hypothetical protein	YP_185173.1	3.269340974
910	B06	349	SACOL0365	prophage L54a, HNH endonuclease family protein	YP_185257.1	3.134670487
911	B07	349	SACOL0489	conserved hypothetical protein	YP_185379.1	3.255014327
913	B08	349	SACOL0800	conserved hypothetical protein	YP_185674.1	3.220630372
916	B09	349	SACOL0920	hypothetical protein	YP_185791.1	3.243553009
917	B10	349	SACOL1155	thioredoxin	YP_186018.1	3.249283668
921	B11	349	SACOL1822	arsenical resistance operon repressor	YP_186654.1	2.630372493
923	B12	349	SACOL1930	conserved hypothetical protein	YP_186755.1	3.240687679
925	C01	349	SACOL2305	IS1272-related, transposase, degenerate	-	3.249283668
928	C02	349	SACOL2397	nitrite reductase [NAD(P)H], small subunit	YP_187200.1	3.209169054
932	C03	352	SACOL0335	hypothetical protein	YP_185227.1	3.235795455
933	C04	352	SACOL0521	conserved hypothetical protein TIGR00103	YP_185409.1	3.252840909
935	C05	352	SACOL1071	chitinase-related protein	YP_185935.1	3.230113636
939	C06	352	SACOL1499	conserved hypothetical protein	YP_186343.1	3.221590909
942	C07	352	SACOL2228	ribosomal protein L24	YP_187038.1	3.198863636
944	C08	352	SACOL2251	conserved hypothetical protein	YP_187059.1	3.224431818
945	C09	355	SACOL0804	conserved hypothetical protein	YP_185678.1	3.228169014
947	C10	355	SACOL0875	thioredoxin, putative	YP_185747.1	2.6
949	C11	355	SACOL0895	pathogenicity island protein	YP_185766.1	3.205633803
951	C12	355	SACOL1039	conserved hypothetical protein	YP_185904.1	3.18028169
953	D01	355	SACOL1585	conserved hypothetical protein	YP_186425.1	3.225352113
955	D02	355	SACOL1701	conserved hypothetical protein	YP_186540.1	3.21971831
957	D03	355	SACOL2137	transcriptional regulator CzrA	YP_186952.1	2.622535211
959	D04	358	SACOL0488	hypothetical protein	YP_185378.1	3.223463687
961	D05	358	SACOL0849	hypothetical protein	YP_185723.1	3.223463687
963	D06	358	SACOL0940	conserved hypothetical protein	YP_185810.1	3.248603352
966	D07	358	SACOL1146	conserved hypothetical protein	YP_186009.1	3.203910615
967	D08	361	SACOL0152	conserved hypothetical protein	YP_185052.1	3.1966759
969	D09	361	SACOL1971	hypothetical protein	YP_186795.1	3.229916898
971	D10	361	SACOL2056	anti-anti-sigma factor RsbV	YP_186872.1	2.631578947
973	D11	361	SACOL2288	conserved hypothetical protein	YP_187095.1	3.243767313
975	D12	361	SACOL2333	YnfA family protein	YP_187140.1	3.238227147
977	E01	361	SACOL2495	hypothetical protein	YP_187290.1	3.238227147
979	E02	364	SACOL0011	conserved hypothetical protein	YP_184922.1	2.637362637
981	E03	364	SACOL0525	conserved hypothetical protein	YP_185413.1	3.230769231
983	E04	364	SACOL1055	sspC protein	YP_185920.1	2.21978022
985	E05	364	SACOL1164	fibrinogen binding-related protein	YP_186027.1	2.623626374
987	E06	364	SACOL1603	conserved hypothetical protein TIGR00106	YP_186443.1	3.228021978
989	E07	364	SACOL2307	conserved hypothetical protein	YP_187114.1	3.197802198
993	E09	367	SACOL0395	glycine cleavage system H protein, putative	YP_185287.1	2.621253406
995	E10	367	SACOL0890	transcriptional regulator, Cro/CI family	YP_185761.1	3.182561308
997	E11	367	SACOL1252	conserved hypothetical protein	YP_186111.1	3.234332425

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1000	E12	367	SACOL1482	hypothetical protein	YP_186327.1	3.166212534
1002	F01	370	SACOL2115	conserved hypothetical protein	YP_186930.1	3.186486486
1003	F02	373	SACOL2716	conserved hypothetical protein	YP_187502.1	2.608579088
1005	F03	376	SACOL0639	conserved hypothetical protein	YP_185524.1	2.627659574
1007	F04	376	SACOL0901	pathogenicity island protein	YP_185772.1	3.218085106
1009	F05	376	SACOL0905	pathogenicity island protein	YP_185776.1	3.220744681
1012	F06	376	SACOL0953	Na+/H+ antiporter, MnhC component	YP_185822.1	3.220744681
1013	F07	376	SACOL1347	hypothetical protein	YP_186200.1	3.228723404
1015	F08	376	SACOL1491	conserved hypothetical protein	YP_186335.1	3.175531915
1017	F09	376	SACOL1574	lipoprotein, putative	YP_186414.1	3.244680851
1019	F10	379	SACOL0208	hypothetical protein	YP_185107.1	3.224274406
1021	F11	379	SACOL0681	Na+/H+ antiporter, MnhC component, putative	YP_185564.1	3.224274406
1023	F12	379	SACOL1418	conserved hypothetical protein	YP_186270.1	3.234828496
1025	G01	379	SACOL1484	conserved hypothetical protein	YP_186329.1	3.226912929
1029	G02	379	SACOL1849	hypothetical protein	YP_186680.1	3.171503958
1031	G03	379	SACOL1902	conserved hypothetical protein	YP_186727.1	3.205804749
1033	G04	379	SACOL2550	conserved hypothetical protein	YP_187342.1	3.213720317
1035	G05	382	SACOL0354	conserved hypothetical protein TIGR01671	YP_185246.1	3.219895288
1037	G06	382	SACOL0497	conserved hypothetical protein	YP_185385.1	3.212041885
1039	G07	382	SACOL0528	conserved hypothetical protein	YP_185416.1	3.204188482
1041	G08	382	SACOL1009	conserved hypothetical protein	YP_185877.1	3.212041885
1043	G09	382	SACOL2287	staphylococcal accessory regulator R	YP_187094.1	3.196335079
1045	G10	382	SACOL2739	ribonuclease P protein component	YP_187525.1	3.206806283
1047	G11	385	SACOL0040	conserved hypothetical protein	YP_184951.1	3.21038961
1049	G12	385	SACOL0363	conserved hypothetical protein	YP_185255.1	3.207792208
1052	H01	385	SACOL0377	hypothetical protein	YP_185269.1	2.574025974
1055	H02	385	SACOL1257	ribosomal protein L19	YP_186116.1	3.218181818
1057	H03	385	SACOL1289	ribosome-binding factor A	YP_186146.1	3.207792208
1059	H04	385	SACOL1486	conserved hypothetical protein	YP_186331.1	2.612987013
1061	H05	385	SACOL2127	conserved hypothetical protein	YP_186942.1	3.158441558
1063	H06	385	SACOL2258	staphylococcal accessory regulator V	YP_187065.1	3.218181818
1065	H07	385	SACOL2729	integrase/recombinase, core domain family	YP_187515.1	3.205194805
1067	H08	388	SACOL1648	iojap-related protein	YP_186488.1	3.224226804
1069	H09	388	SACOL1833	crcB family protein	YP_186665.1	3.175257732
1071	H10	388	SACOL2102	conserved hypothetical protein	YP_186917.1	3.211340206
1073	H11	388	SACOL2234	ribosomal protein L22	YP_187044.1	2.167525773
1075	H12	388	SACOL2734	conserved hypothetical protein	YP_187520.1	2.953608247

Table 6: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 6 (ZSAJF), NR-19502[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1077	A01	391	SACOL0218	conserved hypothetical protein	YP_185117.1	3.16112532
1079	A02	391	SACOL0342	hypothetical protein	YP_185234.1	2.606138107
1081	A03	391	SACOL0350	conserved hypothetical protein	YP_185242.1	3.186700767
1084	A04	391	SACOL0876	arsenate reductase, putative	YP_185748.1	3.186700767
1085	A05	391	SACOL0949	Na+/H+ antiporter, MnhG component	YP_185818.1	2
1087	A06	391	SACOL1044	conserved hypothetical protein	YP_185909.1	3.227621483
1089	A07	391	SACOL1725	ribosomal protein L20	YP_186563.1	3.212276215
1091	A08	391	SACOL2310	conserved hypothetical protein	YP_187117.1	2.613810742
1095	A09	391	SACOL2381	conserved hypothetical protein	YP_187185.1	3.21483376
1097	A10	391	SACOL2506	staphylococcal accessory regulator T	YP_187301.1	3.20971867

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Master Clone List for NR-19277

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1101	A11	394	SACOL0466	membrane protein, putative	YP_185356.1	3.210659898
1104	A12	394	SACOL0943	conserved hypothetical protein	YP_185812.1	2.563451777
1106	B01	394	SACOL2061	holo-(acyl-carrier-protein) synthase	YP_186877.1	2.527918782
1108	B02	394	SACOL2223	ribosomal protein L18	YP_187033.1	3.187817259
1109	B03	394	SACOL2681	conserved hypothetical protein	YP_187468.1	3.203045685
1111	B04	397	SACOL0496	conserved hypothetical protein	YP_185384.1	3.201511335
1113	B05	397	SACOL0615	conserved hypothetical protein	YP_185500.1	3.161209068
1115	B06	397	SACOL0709	conserved hypothetical protein	YP_185591.1	3.20906801
1117	B07	397	SACOL0898	pathogenicity island protein	YP_185769.1	3.214105793
1120	B08	397	SACOL1383	large conductance mechanosensitive channel protein	YP_186236.1	3.198992443
1121	B09	397	SACOL1570	conserved hypothetical protein	YP_186411.1	3.214105793
1127	B10	400	SACOL0328	hypothetical protein	YP_185220.1	3.185
1131	B11	400	SACOL0623	conserved hypothetical protein	YP_185508.1	3.2
1133	B12	400	SACOL1007	protozoan/cyanobacterial globin family protein	YP_185875.1	2.61
1137	C01	400	SACOL1895	conserved hypothetical protein	YP_186721.1	3.2075
1139	C02	400	SACOL2215	ribosomal protein S13/S18	YP_187025.1	2.5775
1141	C03	400	SACOL2383	conserved hypothetical protein	YP_187187.1	3.1875
1143	C04	400	SACOL2481	hypothetical protein	YP_187278.1	3.1975
1145	C05	403	SACOL0443	conserved hypothetical protein TIGR01655	YP_185333.1	3.208436725
1147	C06	403	SACOL0586	ribosomal protein L7/L12	YP_185472.1	3.191066998
1149	C07	403	SACOL0629	conserved hypothetical protein	YP_185514.1	3.203473945
1151	C08	403	SACOL1328	glutamine synthetase repressor	YP_186183.1	3.196029777
1154	C09	403	SACOL2212	ribosomal protein L17	YP_187022.1	3.191066998
1155	C10	403	SACOL2229	ribosomal protein L14	YP_187039.1	3.183622829
1159	C12	406	SACOL0989	conserved hypothetical protein	YP_185857.1	3.174876847
1162	D01	406	SACOL1553	glyoxalase family protein	YP_186394.1	2
1163	D02	406	SACOL2408	lipoprotein, putative	YP_187211.1	3.192118227
1165	D03	409	SACOL0299	lipoprotein, putative	YP_185192.1	3.188264059
1167	D04	409	SACOL0672	staphylococcal accessory regulator A	YP_185556.1	3.173594132
1169	D05	409	SACOL0947	ComA2 family protein	YP_185816.1	3.188264059
1171	D06	409	SACOL1239	conserved hypothetical protein	YP_186099.1	2.190709046
1173	D07	412	SACOL0958	general stress protein 13	YP_185827.1	3.174757282
1176	D08	412	SACOL1857	hypothetical protein	YP_186685.1	3.174757282
1178	D09	412	SACOL2590	glyoxalase family protein	YP_187381.1	3.194174757
1179	D10	415	SACOL0330	conserved hypothetical protein	YP_185222.1	3.175903614
1181	D11	415	SACOL0540	endoribonuclease L-PSP, putative	YP_185428.1	3.175903614
1184	D12	415	SACOL0628	conserved hypothetical protein	YP_185513.1	2.56626506
1185	E01	415	SACOL0877	glycine cleavage system H protein	YP_185749.1	2.6
1188	E02	415	SACOL1997	transcriptional regulator, GntR family	YP_186821.1	2.587951807
1189	E03	415	SACOL2733	conserved hypothetical protein	YP_187519.1	3.168674699
1192	E04	418	SACOL0153	conserved hypothetical protein	YP_185053.1	1.564593301
1195	E05	418	SACOL0956	kinase-associated protein B	YP_185825.1	3.157894737
1197	E06	418	SACOL1580	hypothetical protein	YP_186420.1	2.827751196
1200	E07	418	SACOL1854	hypothetical protein	YP_186684.1	2.588516746
1201	E08	418	SACOL2377	conserved hypothetical protein	YP_187181.1	3.153110048
1203	E09	418	SACOL2613	aspartate 1-decarboxylase	YP_187402.1	2.593301435
1205	E10	421	SACOL0880	Toprim domain protein	YP_185751.1	2.586698337
1208	E11	421	SACOL1193	cell division protein FtsL	YP_186055.1	2.596199525
1209	E12	421	SACOL1592	rhodanese-like domain protein	YP_186432.1	3.201900238
1213	F01	421	SACOL2434	membrane protein, putative	YP_187235.1	2.58432304
1215	F02	424	SACOL0385	conserved hypothetical protein	YP_185277.1	3.181603774
1217	F03	424	SACOL0419	hypothetical protein	YP_185311.1	3.188679245

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1219	F04	424	SACOL0974	conserved hypothetical protein	YP_185842.1	3.162735849
1221	F05	424	SACOL1132	conserved hypothetical protein	YP_185996.1	3.183962264
1223	F06	424	SACOL1569	N utilization substance protein B	YP_186410.1	3.179245283
1225	F07	424	SACOL2214	ribosomal protein S11	YP_187024.1	3.176886792
1227	F08	424	SACOL2241	conserved hypothetical protein	YP_187051.1	3.188679245
1229	F09	427	SACOL0259	hypothetical protein	YP_185154.1	3.196721311
1231	F10	427	SACOL0277	hypothetical protein	YP_185172.1	3.194379391
1233	F11	427	SACOL0551	cell-division protein divIC, putative	YP_185439.1	3.170960187
1235	F12	427	SACOL0928	conserved hypothetical protein	YP_185798.1	3.180327869
1237	G01	427	SACOL1301	transcriptional regulator, putative	YP_186158.1	3.175644028
1239	G02	427	SACOL1442	IS1272-related, transposase, degenerate	-	3.196721311
1241	G03	427	SACOL2500	MutT/nudix family protein	YP_187295.1	3.18735363
1243	G04	430	SACOL0374	conserved hypothetical protein	YP_185266.1	3.16744186
1245	G05	430	SACOL0509	MutT/nudix family protein	YP_185397.1	1.579069767
1247	G06	430	SACOL0737	lipoprotein, putative	YP_185616.1	3.193023256
1249	G07	430	SACOL1002	conserved hypothetical protein	YP_185870.1	3.186046512
1251	G08	430	SACOL1824	arsenate reductase (thioredoxin)	YP_186656.1	2.586046512
1253	G09	430	SACOL1909	conserved hypothetical protein	YP_186734.1	2.604651163
1255	G10	430	SACOL2089	single-stranded DNA-binding protein family	YP_186904.1	2.595348837
1257	G11	430	SACOL2554_1	LrgA family protein	YP_187347.1	3.2
1261	G12	433	SACOL0698	glycerol-3-phosphate cytidylyltransferase	YP_185580.1	3.166281755
1263	H01	433	SACOL0791	nrdI protein	YP_185665.1	3.15704388
1265	H02	433	SACOL2206	ribosomal protein S9	YP_187016.1	3.193995381
1267	H03	433	SACOL2225	ribosomal protein S8	YP_187035.1	3.180138568
1269	H04	436	SACOL0353	hypothetical protein	YP_185245.1	3.176605505
1271	H05	436	SACOL0373	conserved hypothetical protein	YP_185265.1	3.199541284
1273	H06	436	SACOL0552	general stress protein 13	YP_185440.1	3.197247706
1275	H07	436	SACOL1166	hypothetical protein	YP_186029.1	3.174311927
1277	H08	436	SACOL1219	conserved hypothetical protein	YP_186082.1	2
1279	H09	436	SACOL1436	hypothetical protein	YP_186288.1	3.174311927
1282	H10	436	SACOL1471	cell wall enzyme EbsB, putative	YP_186318.1	3.160550459
1283	H11	436	SACOL1986	conserved hypothetical protein	YP_186810.1	3.176605505
1285	H12	436	SACOL2368	acetyltransferase, GNAT family	YP_187173.1	3.178899083

Table 7: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 7 (ZSAJG), NR-19503[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1287	A01	439	SACOL0254	ribose transport protein	YP_185150.1	2.587699317
1289	A02	439	SACOL0260	IS1272-related, transposase, degenerate	-	3.182232346
1291	A03	439	SACOL0347	conserved hypothetical protein	YP_185239.1	2.574031891
1293	A04	439	SACOL0577	conserved hypothetical protein	YP_185463.1	3.182232346
1295	A05	439	SACOL1625	cytidine deaminase	YP_186465.1	3.177676538
1299	A06	442	SACOL0109	hypothetical protein	YP_185013.1	3.156108597
1302	A07	442	SACOL0457	conserved hypothetical protein	YP_185347.1	3.171945701
1306	A09	445	SACOL2281	urease, beta subunit	YP_187088.1	2.573033708
1307	A10	445	SACOL2551	conserved hypothetical protein TIGR00051	YP_187343.1	3.188764045
1309	A11	448	SACOL0591	ribosomal protein S12	YP_185477.1	3.142857143
1311	A12	448	SACOL1753	universal stress protein family	YP_186589.1	3.171875
1313	B01	448	SACOL1948	hypothetical protein	YP_186773.1	3.178571429
1315	B02	448	SACOL2132	conserved hypothetical protein	YP_186947.1	2.185267857
1317	B03	451	SACOL2193	transcriptional regulator, MerR family	YP_187004.1	3.175166297

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1319	B04	451	SACOL2621	hypothetical protein	YP_187410.1	3.179600887
1321	B05	454	SACOL0339	prophage L54a, single-stranded DNA binding protein	YP_185231.1	3.174008811
1323	B06	454	SACOL0404	transcriptional regulator, MarR family	YP_185296.1	3.162995595
1325	B07	454	SACOL0771	6-pyruvoyl tetrahydrobiopterin synthase, putative	YP_185648.1	3.178414097
1327	B08	454	SACOL1060	transcriptional regulator, MarR family	YP_185925.1	3.171806167
1329	B09	454	SACOL1113	conserved hypothetical protein	YP_185977.1	3.18722467
1331	B10	454	SACOL2107	phosphotyrosine protein phosphatase	YP_186922.1	3.191629956
1335	B11	454	SACOL2344	hypothetical protein	YP_187150.1	3.174008811
1337	B12	454	SACOL2485	hypothetical protein	YP_187281.1	3.176211454
1341	C01	457	SACOL0753	conserved hypothetical protein	YP_185632.1	3.159737418
1343	C02	457	SACOL0872	OsmC/Ohr family protein	YP_185744.1	3.15536105
1345	C03	457	SACOL1681	Rrf2 family protein	YP_186521.1	3.168490153
1347	C04	457	SACOL1802	conserved hypothetical protein	YP_186635.1	3.166301969
1349	C05	457	SACOL1894	HIT family protein	YP_186720.1	3.177242888
1351	C06	457	SACOL2294	conserved hypothetical protein	YP_187101.1	3.164113786
1353	C07	457	SACOL2379	conserved hypothetical protein	YP_187183.1	3.177242888
1355	C08	457	SACOL2484	alkylhydroperoxidase, AhpD family	YP_187280.1	2.177242888
1357	C09	457	SACOL2487	conserved hypothetical protein	YP_187283.1	3.161925602
1360	C10	460	SACOL0346	prophage L54a, N-6-adenine-methyltransferase	YP_185238.1	3.176086957
1362	C11	460	SACOL0680	Na+/H+ antiporter, MnhB component, putative	YP_185563.1	3.152173913
1363	C12	460	SACOL0726	staphylococcal accessory protein X	YP_185607.1	3.191304348
1365	D01	460	SACOL1339	conserved hypothetical protein	YP_186193.1	3.180434783
1367	D02	460	SACOL2197	surface protein, putative	YP_187008.1	2.173913043
1369	D03	463	SACOL0032	MaoC domain protein	YP_184943.1	3.172786177
1371	D04	463	SACOL0662	conserved hypothetical protein	YP_185546.1	3.177105832
1373	D05	463	SACOL0713	hypothetical protein	YP_185595.1	3.174946004
1375	D06	463	SACOL0954	Na+/H+ antiporter, MnhB component	YP_185823.1	3.172786177
1377	D07	463	SACOL1671	conserved hypothetical protein TIGR00250	YP_186511.1	3.168466523
1379	D08	463	SACOL2186	galactose-6-phosphate isomerase, LacA subunit	YP_186997.1	3.183585313
1381	D09	463	SACOL2385	heat shock protein, Hsp20 family	YP_187189.1	3.146868251
1383	D10	463	SACOL2679	hypothetical protein	-	3.149028078
1385	D11	466	SACOL0583	ribosomal protein L11	YP_185469.1	3.130901288
1388	D12	466	SACOL0888	pathogenicity island, lipoprotein, putative	YP_185759.1	2.587982833
1389	E01	466	SACOL1191	mraZ protein	YP_186053.1	3.173819742
1391	E02	466	SACOL1645	comE operon protein 2	YP_186485.1	3.180257511
1393	E03	466	SACOL2371	conserved hypothetical protein	YP_187175.1	2.587982833
1395	E04	466	SACOL2557	conserved domain protein	YP_187350.1	2.165236052
1398	E05	469	SACOL0930	conserved hypothetical protein	YP_185800.1	1.976545842
1400	E06	469	SACOL0985	surface protein, putative	YP_185853.1	3.153518124
1402	E07	469	SACOL1063	acetyltransferase, GNAT family	YP_185927.1	3.153518124
1403	E08	469	SACOL1129	conserved hypothetical protein	YP_185993.1	3.176972281
1405	E09	469	SACOL2041	conserved hypothetical protein TIGR00150	YP_186858.1	3.172707889
1407	E10	469	SACOL2148	PTS system, mannitol-specific IIA component	YP_186961.1	3.187633262
1409	E11	469	SACOL2232	ribosomal protein L16	YP_187042.1	3.162046908
1411	E12	469	SACOL2531	transcriptional regulator, MarR family	YP_187324.1	3.18336887
1413	F01	472	SACOL0364	prophage L54a, transcriptional regulator, RinA family	YP_185256.1	3.150423729
1415	F02	472	SACOL0686	Na+/H+ antiporter, MnhG component, putative	YP_185568.1	3.167372881
1417	F03	472	SACOL1464	conserved hypothetical protein	YP_186312.1	3.156779661
1420	F04	472	SACOL1558	conserved hypothetical protein	YP_186399.1	2
1421	F05	472	SACOL2013	hypothetical protein	YP_186833.1	3.167372881
1423	F06	472	SACOL2207	ribosomal protein L13	YP_187017.1	2.593220339

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1426	F07	475	SACOL0287	conserved hypothetical protein	YP_185182.2	2
1429	F08	475	SACOL0406	hypothetical protein	YP_185298.1	3.181052632
1433	F10	475	SACOL0768	lipoprotein, putative	YP_185645.1	2.591578947
1435	F11	475	SACOL1189	acetyltransferase, GNAT family	YP_186051.1	3.168421053
1437	F12	475	SACOL2090	ywpF protein	YP_186905.1	3.166315789
1439	G01	475	SACOL2091	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ	YP_186906.1	2.591578947
1441	G02	475	SACOL2220	ribosomal protein L15	YP_187030.1	3.141052632
1443	G03	475	SACOL2256	transcriptional regulator, MarR family	YP_187063.1	3.166315789
1445	G04	478	SACOL0247	holin-like protein LrgA	YP_185143.1	2.569037657
1447	G05	478	SACOL0402	PTS system, IIA component	YP_185294.1	3.158995816
1450	G06	478	SACOL0736	acetyltransferase, GNAT family	YP_185615.1	2.575313808
1451	G07	478	SACOL0746	transcriptional regulator, MarR family	YP_185625.1	3.179916318
1453	G08	478	SACOL1828	conserved hypothetical protein	YP_186660.1	3.165271967
1455	G09	478	SACOL1829	conserved hypothetical protein	YP_186661.1	3.150627615
1457	G10	478	SACOL1832	crcB protein	YP_186664.1	2.569037657
1459	G11	478	SACOL2012	acetyltransferase, GNAT family	YP_186832.1	2.587866109
1463	G12	478	SACOL2360	response regulator-related protein	YP_187165.1	3.133891213
1465	H01	478	SACOL2625	conserved hypothetical protein	YP_187414.1	2.587866109
1467	H02	481	SACOL0015	ribosomal protein L9	YP_184926.1	2.56964657
1469	H03	481	SACOL1598	ComG operon competence protein, putative	YP_186438.1	2.584199584
1471	H04	481	SACOL1771	OsmC/Ohr family protein	YP_186605.1	3.130977131
1473	H05	481	SACOL1919	transcriptional regulator, Fur family	YP_186744.1	2.584199584
1475	H06	481	SACOL2264	molybdenum cofactor biosynthesis protein E	YP_187071.1	3.17047817
1478	H07	481	SACOL2384	staphylococcal accessory protein Z	YP_187188.1	3.180873181
1479	H08	484	SACOL1509	nucleoside diphosphate kinase	YP_186353.1	3.146694215
1481	H09	484	SACOL1541	transcriptional regulator, Fur family	YP_186383.1	3.188016529
1483	H10	484	SACOL1662	acetyl-CoA carboxylase, biotin carboxyl carrier protein, putative	YP_186502.1	2.588842975
1485	H11	484	SACOL2609	conserved hypothetical protein	YP_187399.1	3.181818182
1487	H12	484	SACOL2658	transcriptional regulator, ArgR family	YP_187446.1	3.175619835

Table 8: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 8 (ZSAJH), NR-19504[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1489	A01	487	SACOL0059	conserved hypothetical protein	YP_184965.1	3.13963039
1491	A02	487	SACOL0631	conserved hypothetical protein	YP_185516.1	2
1493	A03	487	SACOL0755	conserved hypothetical protein	YP_185634.1	3.1724846
1495	A04	487	SACOL1565	arginine repressor	YP_186406.1	2.585215606
1497	A05	487	SACOL1688	conserved hypothetical protein TIGR00256	YP_186527.1	3.162217659
1499	A06	487	SACOL2283	urease accessory protein UreE	YP_187090.1	3.170431212
1501	A07	487	SACOL2391	conserved hypothetical protein	YP_187194.1	2.564681725
1504	A08	490	SACOL0376	prophage L54a, major tail protein, putative	YP_185268.1	2
1506	A09	490	SACOL1921	bacterioferritin comigratory protein	YP_186746.1	2
1507	A10	490	SACOL2052	peptidase, SprT family	YP_186868.1	3.165306122
1512	A11	490	SACOL2361	hypothetical protein	YP_187166.1	3.112244898
1513	A12	490	SACOL2467	lipoprotein, putative	YP_187265.1	3.187755102
1516	B01	490	SACOL2650	transcriptional regulator, putative	YP_187438.1	3.13877551
1517	B02	493	SACOL0273	hypothetical protein	YP_185168.1	3.131845842
1519	B03	493	SACOL0741	conserved hypothetical protein	YP_185620.1	2.559837728
1521	B04	493	SACOL0843	conserved hypothetical protein	YP_185717.1	2

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Master Clone List for NR-19277

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1524	B05	493	SACOL0889	pathogenicity island protein	YP_185760.1	2.563894523
1525	B06	493	SACOL1698	ACT domain protein	YP_186537.1	3.172413793
1527	B07	493	SACOL2661	conserved hypothetical protein	YP_187449.1	3.164300203
1529	B08	496	SACOL0071	conserved hypothetical protein	YP_184976.1	3.1875
1531	B09	496	SACOL0567	transcriptional regulator CtsR	YP_185455.1	2.574596774
1533	B10	496	SACOL1126	conserved hypothetical protein	YP_185990.1	3.16733871
1535	B11	499	SACOL0847	SsrA-binding protein	YP_185721.1	3.180360721
1537	B12	499	SACOL0917	NifU domain protein	YP_185788.1	3.154308617
1539	C01	499	SACOL1572	acetyl-CoA carboxylase, biotin carboxyl carrier protein	YP_186413.1	3.160320641
1541	C02	499	SACOL1768	GAF domain protein	YP_186602.1	2.160320641
1544	C03	499	SACOL1817	6,7-dimethyl-8-ribityllumazine synthase	YP_186649.1	2.561122244
1546	C04	499	SACOL1904	transcriptional regulator, putative	YP_186729.1	3.138276553
1549	C05	499	SACOL2039	ribosomal-protein-alanine acetyltransferase, putative	YP_186856.1	3.090180361
1551	C06	499	SACOL2524	transcriptional regulator, MarR family	YP_187318.1	2.561122244
1554	C07	499	SACOL2717	hypothetical protein	YP_187503.1	3.160320641
1555	C08	502	SACOL0229	PTS system, sugar-specific IIA component, putative	YP_185125.1	2.139442231
1557	C09	502	SACOL1284	conserved hypothetical protein	YP_186141.1	3.19123506
1560	C10	502	SACOL1380	conserved hypothetical protein	YP_186233.1	2.577689243
1561	C11	502	SACOL1386	conserved hypothetical protein TIGR00051	YP_186239.1	2.577689243
1563	C12	502	SACOL1627	conserved hypothetical protein TIGR00043	YP_186467.1	2.932270916
1565	D01	502	SACOL2402	conserved hypothetical protein	YP_187205.1	3.157370518
1569	D03	505	SACOL0592	ribosomal protein S7	YP_185478.1	3.138613861
1571	D04	505	SACOL0859	hypothetical protein	YP_185732.1	1.16039604
1573	D05	505	SACOL1064	conserved hypothetical protein	YP_185928.1	2.089108911
1577	D07	505	SACOL1827	RNA polymerase sigma-70 family protein	YP_186659.1	2.17029703
1581	D08	505	SACOL2126	autoinducer-2 production protein LuxS	YP_186941.1	2.411881188
1583	D09	507	SACOL0605	cytidine/deoxycytidylate deaminase family protein, authentic frameshift	-	2.585798817
1586	D10	508	SACOL0092	conserved hypothetical protein	YP_184997.1	3.153543307
1587	D11	508	SACOL0728	conserved hypothetical protein	YP_185609.1	1.580708661
1589	D12	508	SACOL0767	conserved hypothetical protein	YP_185644.1	3.161417323
1593	E02	508	SACOL1705	hypothetical protein	YP_186544.1	2.137795276
1596	E03	508	SACOL2158	conserved hypothetical protein	YP_186970.1	2.582677165
1597	E04	508	SACOL2300	conserved hypothetical protein	YP_187107.1	3.023622047
1599	E05	508	SACOL2438	endopeptidase, putative	YP_187239.1	2.356299213
1601	E06	509	SACOL2015	integrase/recombinase-related protein, authentic frameshift	-	2.561886051
1603	E07	511	SACOL0560	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	YP_185448.1	2.483365949
1605	E08	511	SACOL0657	acetyltransferase, GNAT family, authentic point mutation	-	2.575342466
1607	E09	511	SACOL1325	glutathione peroxidase	YP_186180.1	3.170254403
1609	E10	511	SACOL1665	transcription elongation factor GreA	YP_186505.1	2.753424658
1611	E11	511	SACOL2683	peptide methionine sulfoxide reductase, putative	YP_187470.1	3.154598826
1613	E12	514	SACOL0025	conserved hypothetical protein	YP_184936.1	3.085603113
1615	F01	514	SACOL0951	Na+/H+ antiporter, MnhE component	YP_185820.1	1.968871595
1618	F02	514	SACOL1461	dihydrofolate reductase	YP_186310.1	2
1619	F03	514	SACOL1841	nucleoside triphosphatase YtkD	YP_186672.1	2.426070039
1621	F04	514	SACOL2055	anti-sigma B factor	YP_186871.1	2.453307393

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1623	F05	514	SACOL2064	membrane protein, putative	YP_186880.1	3.147859922
1625	F06	517	SACOL0077	hypothetical protein	YP_184982.1	2.181818182
1628	F07	517	SACOL0684	Na+/H+ antiporter, MnhE component, putative	YP_185566.1	2.574468085
1629	F08	517	SACOL0756	ebsC protein	YP_185635.1	3.145067698
1633	F09	517	SACOL1120	conserved hypothetical protein	YP_185984.1	2.566731141
1635	F10	517	SACOL1134	lipopolysaccharide core biosynthesis protein KdtB	YP_185998.1	2.145067698
1637	F11	517	SACOL1845	lipoprotein, putative	YP_186676.1	3.114119923
1642	F12	520	SACOL0510	acetyltransferase, GNAT family	YP_185398.1	3.015384615
1643	G01	520	SACOL0827	acetyltransferase, putative	YP_185701.1	3.173076923
1647	G02	520	SACOL2265	molybdopterin-guanine dinucleotide biosynthesis protein B	YP_187072.1	3.167307692
1649	G03	520	SACOL2567	hypothetical protein	YP_187359.1	2.823076923
1651	G04	523	SACOL0297	conserved hypothetical protein	YP_185191.1	2.571701721
1654	G05	523	SACOL0734	conserved hypothetical protein	YP_185613.1	2
1655	G06	523	SACOL1227	polypeptide deformylase	YP_186090.1	3.143403442
1657	G07	523	SACOL2519	conserved hypothetical protein	YP_187313.1	3.135755258
1659	G08	523	SACOL2580	hypothetical protein	YP_187372.1	2.585086042
1662	G09	523	SACOL2583	acetyltransferase, GNAT family	YP_187375.1	2
1663	G10	526	SACOL0282	conserved hypothetical protein TIGR01741	YP_185177.1	2.171102662
1666	G11	526	SACOL0289	conserved hypothetical protein	YP_185183.1	2.570342205
1669	G12	526	SACOL1314	conserved hypothetical protein	YP_186170.1	3.153992395
1673	H01	526	SACOL2343	conserved hypothetical protein	YP_187149.1	2.58365019
1675	H02	526	SACOL2541	acetyltransferase, GNAT family	YP_187333.1	3.13878327
1677	H03	529	SACOL0166	conserved hypothetical protein	YP_185065.1	2.514177694
1680	H04	529	SACOL0807	conserved hypothetical protein	YP_185681.1	3.153119093
1682	H05	529	SACOL0871	acetyltransferase, putative	YP_185743.1	-
1683	H06	529	SACOL1762	thiol peroxidase, putative	YP_186596.1	3.15879017
1685	H07	529	SACOL2062	conserved hypothetical protein	YP_186878.1	2.826086957
1687	H08	529	SACOL2267	molybdenum cofactor biosynthesis protein C	YP_187074.1	1.56710775
1690	H09	530	SACOL0288	hypothetical protein, authentic frameshift	-	3.164150943
1691	H10	532	SACOL0172	isochorismatase	YP_185071.1	3.148496241
1693	H11	532	SACOL0710	conserved hypothetical protein	YP_185592.1	2.34962406
1695	H12	532	SACOL1048	acetyltransferase, GNAT family	YP_185913.1	3.152255639

Table 9: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 9 (ZSAJI), NR-19505[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1697	A01	532	SACOL1168	fibrinogen-binding protein	YP_186031.1	3.152255639
1703	A02	532	SACOL2706	hypothetical protein	YP_187492.1	2
1707	A03	535	SACOL0286	conserved hypothetical protein	YP_185181.1	3.145794393
1719	A04	535	SACOL0585	ribosomal protein L10	YP_185471.1	3.14953271
1721	A05	535	SACOL0789	GTP cyclohydrolase I family protein	YP_185662.1	2.730841122
1723	A06	535	SACOL1457	PTS system, IIA component	YP_186308.1	2.568224299
1725	A07	535	SACOL1759	universal stress protein family	YP_186593.1	2.173831776
1727	A08	535	SACOL1812	repressor of toxins	YP_186645.1	2
1729	A09	535	SACOL1952	ferritins family protein	YP_186777.1	3.145794393
1731	A10	535	SACOL2222	ribosomal protein S5	YP_187032.1	3.151401869
1734	A11	535	SACOL2295	staphyloxanthin biosynthesis protein, putative	YP_187102.1	3.145794393
1737	A12	535	SACOL2684	acetyltransferase, GNAT family	YP_187471.1	3.16635514
1740	B01	538	SACOL0438	single-stranded DNA-binding protein	YP_185329.1	3.851301115

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1741	B02	538	SACOL1163	conserved hypothetical protein TIGR00040	YP_186026.1	3.563197026
1743	B03	538	SACOL1255	16S rRNA processing protein RimM	YP_186114.1	3.146840149
1746	B04	538	SACOL1891	RNAIII-activating protein TRAP	YP_186717.1	3.537174721
1747	B05	541	SACOL0037	conserved hypothetical protein	YP_184948.1	4.303142329
1749	B06	541	SACOL0669	conserved hypothetical protein	YP_185553.1	3.534195933
1753	B08	541	SACOL1167	hypothetical protein	YP_186030.1	2.850277264
1755	B09	541	SACOL1539	conserved hypothetical protein	YP_186381.1	3.147874307
1759	B10	541	SACOL2318	conserved hypothetical protein	YP_187125.1	4.329020333
1761	B11	544	SACOL1020	conserved hypothetical protein	YP_185886.1	3.145220588
1763	B12	544	SACOL1397	peptide methionine sulfoxide reductase	YP_186249.1	3.876838235
1765	C01	544	SACOL2173	alkaline shock protein 23	YP_186984.1	2.411764706
1769	C02	547	SACOL0157	conserved hypothetical protein	YP_185057.1	3.548446069
1771	C03	547	SACOL2723	conserved hypothetical protein	YP_187509.1	4.294332724
1773	C04	550	SACOL0984	conserved hypothetical protein TIGR00481	YP_185852.1	2.425454545
1775	C05	550	SACOL1933	ThiJ/PfpI family protein	YP_186758.1	2.401818182
1777	C06	550	SACOL2162	conserved hypothetical protein	YP_186974.1	3.872727273
1779	C07	550	SACOL2185	galactose-6-phosphate isomerase, LacB subunit	YP_186996.1	2.152727273
1781	C08	550	SACOL2366	acetyltransferase, GNAT family	YP_187171.1	3.138181818
1783	C09	550	SACOL2711	conserved hypothetical protein	YP_187497.1	3.14
1785	C10	553	SACOL0802	conserved hypothetical protein	YP_185676.1	4.305605787
1789	C11	553	SACOL1875	epidermin biosynthesis protein EpiD	YP_186703.1	4.323688969
1791	C12	556	SACOL0659	conserved hypothetical protein	YP_185543.1	3.014388489
1793	D01	556	SACOL0854	hypothetical protein	YP_185727.1	4.248201439
1796	D02	556	SACOL1152	colicin V production protein, putative	YP_186015.1	3.115107914
1797	D03	556	SACOL2099	ATP synthase F0, B subunit	YP_186914.1	4.275179856
1800	D04	556	SACOL2118	conserved hypothetical protein	YP_186933.1	2.838129496
1801	D05	556	SACOL2562	methylated-DNA--protein-cysteine methyltransferase	YP_187354.1	3.570143885
1804	D06	559	SACOL0519	acetyltransferase, GNAT family	YP_185407.1	3.148479428
1805	D07	559	SACOL0579	conserved hypothetical protein	YP_185465.1	4.254025045
1807	D08	559	SACOL0968	signal peptidase IA, inactive	YP_185837.1	4.300536673
1809	D09	559	SACOL1596	shikimate kinase	YP_186436.1	3.846153846
1811	D10	559	SACOL1991	conserved hypothetical protein	YP_186815.1	4.230769231
1813	D11	559	SACOL2106	conserved hypothetical protein TIGR01440	YP_186921.1	3.837209302
1816	D12	562	SACOL0904	pathogenicity island protein	YP_185775.1	2.414590747
1818	E01	562	SACOL1210	pyrimidine operon regulatory protein	YP_186073.1	2.8113879
1819	E02	562	SACOL1654	hydrolase, HAD-superfamily, subfamily IIIA	YP_186494.1	4.304270463
1821	E03	562	SACOL1727	translation initiation factor IF-3	YP_186565.1	4.286476868
1823	E04	562	SACOL2660	immunodominant antigen B	YP_187448.1	3.256227758
1825	E05	565	SACOL0855	acetyltransferase, GNAT family	YP_185728.1	3.286725664
1827	E06	565	SACOL1032	ComK family protein	YP_185897.1	4.276106195
1829	E07	565	SACOL1703	rod shape-determining protein MreD, putative	YP_186542.1	4.309734513
1831	E08	565	SACOL1936	cytosolic long-chain acyl-CoA thioester hydrolase family protein	YP_186761.1	4.297345133
1833	E09	565	SACOL1956	conserved hypothetical protein	YP_186781.1	4.251327434
1835	E10	565	SACOL2120	DNA-directed RNA polymerase, delta subunit	YP_186935.1	3.07079646
1837	E11	565	SACOL2315	conserved hypothetical protein	YP_187122.1	3.557522124
1840	E12	568	SACOL0073	conserved hypothetical protein	YP_184978.1	4.278169014
1841	F01	568	SACOL1357	thermonuclease precursor family protein	YP_186210.1	4.105633803
1845	F03	571	SACOL0535	primase-related protein	YP_185423.1	4.250437828
1847	F04	571	SACOL0656	conserved hypothetical protein	YP_185541.1	4.257443082
1849	F05	571	SACOL2224	ribosomal protein L6	YP_187034.1	4.273204904
1851	F06	571	SACOL2400	acetyltransferase, GNAT family	YP_187203.1	4.276707531

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1854	F07	571	SACOL2634	anaerobic ribonucleoside-triphosphate reductase activating protein	YP_187422.1	3.534150613
1857	F08	574	SACOL0554	hypoxanthine phosphoribosyltransferase	YP_185442.1	4.277003484
1859	F09	574	SACOL0874	nitroreductase family protein	YP_185746.1	3.132404181
1861	F10	574	SACOL1107	transcriptional regulator, Cro/CI family	YP_185971.1	4.217770035
1863	F11	574	SACOL1607	5-formyltetrahydrofolate cyclo-ligase family protein	YP_186447.1	3.534843206
1865	F12	574	SACOL1621	CBS domain protein	YP_186461.1	4.266550523
1867	G01	574	SACOL1882	hypothetical protein	YP_186709.1	4.299651568
1869	G02	574	SACOL2098	ATP synthase F1, delta subunit	YP_186913.1	3.548780488
1871	G03	574	SACOL2227	ribosomal protein L5	YP_187037.1	2.412891986
1873	G04	577	SACOL0357	prophage L54a, deoxyuridine 5-triphosphate nucleotidohydrolase	YP_185249.1	4.268630849
1875	G05	577	SACOL0739	acetyltransferase, GNAT family	YP_185618.1	4.253032929
1877	G06	577	SACOL0785	conserved hypothetical protein	YP_185659.1	4.285961872
1879	G07	577	SACOL1090	conserved hypothetical protein	YP_185954.1	4.266897747
1881	G08	577	SACOL1133	conserved hypothetical protein TIGR00095	YP_185997.1	4.251299827
1884	G09	577	SACOL1317	glycerol uptake operon antiterminator regulatory protein	YP_186173.1	2.818024263
1885	G10	577	SACOL1537	segregation and condensation protein B	YP_186379.1	3.559792028
1887	G11	577	SACOL1542	MutT/nudix family protein	YP_186384.1	3.87694974
1889	G12	577	SACOL1925	conserved hypothetical protein	YP_186750.1	4.272097054
1891	H01	580	SACOL0413	ribosomal-protein-serine acetyltransferase, putative	YP_185305.1	4.284482759
1893	H02	580	SACOL1270	heat shock protein HslVU, ATPase subunit HslV	YP_186128.1	4.244827586
1895	H03	580	SACOL1526	conserved hypothetical protein	YP_186369.1	4.251724138
1897	H04	582	SACOL0441	integrase, degenerate	-	3.235395189
1901	H05	583	SACOL0618	SIS domain protein	YP_185503.1	4.171526587
1904	H06	583	SACOL2175	conserved hypothetical protein	YP_186986.1	3.130360206
1905	H07	586	SACOL1100	polypeptide deformylase	YP_185964.1	4.271331058
1908	H08	586	SACOL1850	hypothetical protein	YP_186681.1	3.141638225
1910	H09	586	SACOL2349	transcriptional regulator, TetR family	YP_187155.1	3.109215017
1911	H10	589	SACOL1278	ribosome recycling factor	YP_186135.1	4.259762309
1913	H11	589	SACOL1885	conserved hypothetical protein	YP_186711.1	3.285229202
1915	H12	589	SACOL1954	exonuclease	YP_186779.1	4.264855688

Table 10: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 10 (ZSAJJ), NR-19506[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1917	A01	589	SACOL2275	BioY family protein	YP_187082.1	3.263157895
1920	A02	589	SACOL2709	conserved hypothetical protein	YP_187495.1	3.132427844
1921	A03	592	SACOL0148	capsular polysaccharide biosynthesis galactosyltransferase Cap5M	YP_185048.1	3.136824324
1924	A04	592	SACOL0908	hypothetical protein	YP_185779.1	3.527027027
1925	A05	592	SACOL1136	conserved hypothetical protein	YP_186000.1	3.565878378
1927	A06	592	SACOL1587	translation elongation factor P	YP_186427.1	4.297297297
1929	A07	592	SACOL1896	conserved hypothetical protein	YP_186722.1	3.518581081
1931	A08	592	SACOL1990	conserved hypothetical protein	YP_186814.1	3.22972973
1933	A09	592	SACOL2593	transcriptional regulator, TetR family	YP_187384.1	4.22972973
1938	A10	595	SACOL0678	integrase/recombinase, phage integrase family	YP_185561.1	2.416806723
1939	A11	595	SACOL1711	DNA-3-methyladenine glycosylase	YP_186550.1	4.275630252
1942	A12	595	SACOL1858	hypothetical protein	YP_186686.1	2.803361345

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
1943	B01	595	SACOL1981	isochorismatase family protein	YP_186805.1	4.151260504
1945	B02	595	SACOL2066	K+-transporting ATPase, C subunit	YP_186882.1	4.240336134
1947	B03	595	SACOL2667	isochorismatase family protein	YP_187455.1	4.282352941
1949	B04	595	SACOL2688	intercellular adhesion regulator	YP_187475.1	3.537815126
1951	B05	598	SACOL1202	YlmF protein	YP_186064.1	4.284280936
1953	B06	598	SACOL1485	conserved hypothetical protein	YP_186330.1	3.242474916
1955	B07	598	SACOL1811	conserved hypothetical protein	YP_186644.1	3.558528428
1957	B08	598	SACOL1992	conserved hypothetical protein	YP_186816.1	3.52173913
1959	B09	598	SACOL2630	conserved hypothetical protein	YP_187419.1	3.254180602
1961	B10	601	SACOL0410	FMN reductase-related protein	YP_185302.1	2.803660566
1963	B11	601	SACOL0568	conserved hypothetical protein	YP_185456.1	4.25124792
1965	B12	601	SACOL0607	azoreductase	YP_185492.1	2.108153078
1969	C02	601	SACOL1081	phosphoribosylglycinamide formyltransferase	YP_185945.1	3.269550749
1971	C03	601	SACOL1404	anthranilate synthase, glutamine amidotransferase, component II	YP_186256.1	4.254575707
1974	C04	601	SACOL1870	hypothetical protein	YP_186698.1	3.845257903
1975	C05	604	SACOL0452	alkyl hydroperoxide reductase, C subunit	YP_185342.1	4.286423841
1977	C06	604	SACOL0580	conserved hypothetical protein	YP_185466.1	3.533112583
1979	C07	604	SACOL0864	conserved domain protein	YP_185737.1	4.23013245
1981	C08	604	SACOL0906	phage terminase family protein	YP_185777.1	3.544701987
1983	C09	604	SACOL1650	nicotinate (nicotinamide) nucleotide adenylyltransferase	YP_186490.1	4.248344371
1985	C10	604	SACOL2023	accessory gene regulator protein B	YP_186842.1	3.561258278
1987	C11	604	SACOL2320	conserved hypothetical protein	YP_187127.1	3.627483444
1989	C12	604	SACOL2732	transcriptional regulator, putative	YP_187518.1	3.541390728
1991	D01	607	SACOL0199	conserved hypothetical protein	YP_185098.1	3.507413509
1993	D02	607	SACOL0444	lipoprotein, putative	YP_185334.1	3.504118616
1995	D03	607	SACOL0546	peptidyl-tRNA hydrolase	YP_185434.1	3.850082372
1997	D04	607	SACOL0815	ribosomal subunit interface protein	YP_185689.1	3.532125206
1999	D05	607	SACOL1242	conserved hypothetical protein	YP_186102.1	4.196046129
2001	D06	607	SACOL1512	conserved hypothetical protein	YP_186356.1	2.718286656
2003	D07	607	SACOL2049	3-isopropylmalate dehydratase, small subunit	YP_186866.1	3.538714992
2005	D08	610	SACOL0967	conserved hypothetical protein	YP_185836.1	4.249180328
2007	D09	610	SACOL1086	conserved hypothetical protein	YP_185950.1	3.532786885
2009	D10	610	SACOL1502	conserved hypothetical protein	YP_186346.1	3.109836066
2011	D11	610	SACOL2720	hypothetical protein	YP_187506.1	3.875409836
2014	D12	613	SACOL0191	M23/M37 peptidase domain protein	YP_185090.1	3.518760196
2015	E01	613	SACOL0458	xanthine phosphoribosyltransferase	YP_185348.1	3.525285481
2017	E02	613	SACOL0902	pathogenicity island protein	YP_185773.1	3.543230016
2019	E03	613	SACOL1302	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	YP_186159.1	3.08319739
2021	E04	613	SACOL2699	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	YP_187485.1	4.254486134
2023	E05	613	SACOL2700	imidazoleglycerol-phosphate dehydratase	YP_187486.1	3.831973899
2025	E06	616	SACOL0447	phosphoglycerate mutase family protein	YP_185337.1	3.868506494
2027	E07	616	SACOL1589	lipoprotein, putative	YP_186429.1	3.13474026
2029	E08	619	SACOL0708	DAK2 domain protein	YP_185590.1	3.844911147
2031	E09	619	SACOL0769	conserved hypothetical protein	YP_185646.1	3.523424879
2034	E10	619	SACOL0969	signal peptidase IB	YP_185838.1	3.127625202
2036	E11	619	SACOL1649	conserved hypothetical protein TIGR00488	YP_186489.1	3.11631664
2037	E12	622	SACOL0269	conserved hypothetical protein	YP_185164.1	2.813504823
2039	F01	622	SACOL0833	ATP-dependent Clp protease, proteolytic subunit ClpP	YP_185707.1	3.834405145

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2041	F02	622	SACOL1162	HAM1 protein	YP_186025.1	4.263665595
2044	F03	622	SACOL1501	conserved hypothetical protein	YP_186345.1	3.122186495
2045	F04	622	SACOL2610	transcriptional regulator, TetR family, putative	YP_187400.1	3.136655949
2048	F05	625	SACOL0869	phosphoglycerate mutase family protein	YP_185741.1	3.528
2049	F06	625	SACOL1359	conserved hypothetical protein	YP_186212.1	4.256
2051	F07	625	SACOL1575	hypothetical protein	YP_186415.1	3.5056
2053	F08	625	SACOL1720	GTP-binding protein, putative	YP_186558.1	3.5152
2055	F09	625	SACOL2014	phage terminase family protein	YP_186834.1	3.4416
2057	F10	625	SACOL2393	respiratory nitrate reductase, delta subunit	YP_187196.1	4.0096
2059	F11	628	SACOL0773	para-aminobenzoate synthase, glutamine amidotransferase, component II	YP_185650.1	3.522292994
2061	F12	628	SACOL0957	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	YP_185826.1	3.52388535
2063	G01	628	SACOL1008	conserved hypothetical protein	YP_185876.1	3.845541401
2065	G02	628	SACOL2529	phospholipase/carboxylesterase family protein	YP_187322.1	3.863057325
2067	G03	631	SACOL0082	staphylococcus tandem lipoprotein	YP_184987.1	3.849445325
2069	G04	631	SACOL0522	recombination protein RecR	YP_185410.1	3.507131537
2071	G05	631	SACOL1792	conserved hypothetical protein	YP_186625.1	4.228209192
2073	G06	634	SACOL0118	superoxide dismutase	YP_185022.1	3.829652997
2075	G07	634	SACOL1610	superoxide dismutase	YP_186450.1	3.835962145
2077	G08	634	SACOL1912	glucosamine-6-phosphate isomerase, putative	YP_186737.1	3.544164038
2079	G09	634	SACOL2111	thymidine kinase	YP_186926.1	3.501577287
2081	G10	634	SACOL2201	conserved domain protein, putative	YP_187012.1	2.823343849
2083	G11	634	SACOL2262	molybdopterin-guanine dinucleotide biosynthesis protein A	YP_187069.1	3.110410095
2085	G12	634	SACOL2407	lipoprotein, putative	YP_187210.1	3.522082019
2087	H01	634	SACOL2456	conserved hypothetical protein	YP_187254.1	2.520504732
2089	H02	634	SACOL2570	galactoside O-acetyltransferase	YP_187362.1	3.548895899
2091	H03	637	SACOL0075	hypothetical protein	YP_184980.1	4.263736264
2093	H04	637	SACOL1036	protease, putative	YP_185901.1	3.516483516
2095	H05	637	SACOL1355	DNA-binding response regulator, LuxR family	YP_186207.1	4.20722135
2097	H06	637	SACOL1697	Holliday junction DNA helicase RuvA	YP_186536.1	4.241758242
2099	H07	637	SACOL1769	ribosomal protein S4	YP_186603.1	4.233908948
2101	H08	637	SACOL1973	conserved hypothetical protein	YP_186797.1	3.551020408
2103	H09	637	SACOL2587	conserved hypothetical protein	YP_187378.1	3.535321821
2105	H10	640	SACOL1068	cytochrome aa3 quinol oxidase, subunit III	YP_185932.1	3.7953125
2108	H11	640	SACOL2270	molybdenum ABC transporter, ATP-binding protein ModC	YP_187077.1	3.8375
2109	H12	640	SACOL2638	siroheme synthase, putative	YP_187426.1	4.2359375

Table 11: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 11 (ZSAJK), NR-19507[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2111	A01	643	SACOL0587	conserved hypothetical protein	YP_185473.1	2.821150855
2113	A02	643	SACOL1388	conserved hypothetical protein TIGR00023	YP_186241.1	4.244167963
2115	A03	643	SACOL1724	MutT/nudix family protein	YP_186562.1	3.220839813
2117	A04	643	SACOL2190	conserved hypothetical protein	YP_187001.1	2.799377916
2119	A05	643	SACOL2339	DNA-3-methyladenine glycosylase	YP_187145.1	4.205287714
2121	A06	646	SACOL0284	conserved hypothetical protein	YP_185179.1	4.229102167
2123	A07	646	SACOL1217	orotate phosphoribosyltransferase	YP_186080.1	3.83126935
2126	A08	646	SACOL2522	DedA family protein	YP_187316.1	3.541795666
2129	A09	649	SACOL1115	conserved hypothetical protein	YP_185979.1	3.537750385

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2131	A10	649	SACOL1158	succinate dehydrogenase, cytochrome b558 subunit	YP_186021.1	4.252696456
2133	A11	649	SACOL1452	PAP2 family protein	YP_186304.1	4.238828968
2136	A12	649	SACOL2285	urease accessory protein UreG	YP_187092.1	4.214175655
2137	B01	649	SACOL2703	ATP phosphoribosyltransferase	YP_187489.1	3.223420647
2139	B02	652	SACOL0524	thymidylate kinase	YP_185412.1	2.794478528
2141	B03	652	SACOL0604	deoxynucleoside kinase family protein	YP_185490.1	3.539877301
2143	B04	652	SACOL0646	conserved hypothetical protein	YP_185531.1	3.504601227
2146	B05	652	SACOL0721	conserved hypothetical protein	YP_185602.1	2.711656442
2147	B06	652	SACOL0752	conserved hypothetical protein	YP_185631.1	2.806748466
2151	B07	652	SACOL1205	cell-division initiation protein, putative	YP_186067.1	3.13190184
2154	B08	652	SACOL1776	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	YP_186610.1	3.518404908
2157	B09	655	SACOL2539	sortase	YP_187332.1	3.103816794
2159	B10	658	SACOL0338	conserved hypothetical protein	YP_185230.1	4.212765957
2161	B11	658	SACOL1221	guanylate kinase	YP_186084.1	3.504559271
2163	B12	658	SACOL1374	LexA repressor	YP_186227.1	3.525835866
2165	C01	658	SACOL1602	metallo-beta-lactamase family protein	YP_186442.1	4.218844985
2168	C02	658	SACOL1666	uridine kinase	YP_186506.1	1.720364742
2169	C03	658	SACOL1735	dephospho-CoA kinase	YP_186572.1	3.825227964
2171	C04	658	SACOL1905	DNA-binding response regulator, LuxR family	YP_186730.1	4.255319149
2173	C05	658	SACOL2238	ribosomal protein L4	YP_187048.1	4.243161094
2175	C06	658	SACOL2374	transcriptional regulator, TetR family, putative	YP_187178.1	3.518237082
2178	C07	661	SACOL0110	hypothetical protein	YP_185014.1	4.246596067
2180	C08	661	SACOL0143	capsular polysaccharide biosynthesis protein Cap5H	YP_185043.1	4.232980333
2181	C09	661	SACOL0190	NAD(P)H dehydrogenase (quinone), putative	YP_185089.1	4.242057489
2183	C10	661	SACOL0449	lipoprotein, putative	YP_185339.1	4.243570348
2185	C11	661	SACOL0644	conserved hypothetical protein	YP_185529.1	4.223903177
2187	C12	661	SACOL0654	conserved hypothetical protein	YP_185539.1	3.258698941
2189	D01	661	SACOL1101	lipoprotein, putative	YP_185965.1	4.213313162
2191	D02	661	SACOL1489	recombination protein U	YP_186333.1	4.199697428
2193	D03	661	SACOL1638	heat shock protein GrpE	YP_186478.1	4.231467474
2195	D04	661	SACOL1848	lipoprotein, putative	YP_186679.1	4.21785174
2197	D05	661	SACOL2020	conserved hypothetical protein	YP_186839.1	4.252647504
2199	D06	664	SACOL0424	conserved hypothetical protein	YP_185315.1	3.503012048
2201	D07	664	SACOL0647	conserved hypothetical protein	YP_185532.1	4.231927711
2203	D08	664	SACOL0650	conserved hypothetical protein	YP_185535.1	3.487951807
2205	D09	664	SACOL0651	conserved hypothetical protein	YP_185536.1	4.236445783
2207	D10	664	SACOL0835	conserved hypothetical protein	YP_185709.1	4.22439759
2209	D11	664	SACOL1440	xpaC protein, putative	YP_186292.1	4.246987952
2211	D12	664	SACOL1942	DNA-binding response regulator VraR	YP_186767.1	4.240963855
2213	E01	664	SACOL2104	uracil phosphoribosyltransferase	YP_186919.1	4.227409639
2215	E02	664	SACOL2239	ribosomal protein L3	YP_187049.2	4.251506024
2217	E03	664	SACOL2365	lipoprotein, putative	YP_187170.1	4.225903614
2219	E04	667	SACOL0617	hexulose-6-phosphate synthase, putative	YP_185502.1	4.227886057
2222	E05	667	SACOL1784	acetoin utilization protein AcuA	YP_186617.1	4.236881559
2223	E06	667	SACOL1819	riboflavin synthase, alpha subunit	YP_186651.1	4.256371814
2225	E07	667	SACOL2696	phosphoribosyl-ATP pyrophosphatase/phosphoribosyl-AMP cyclohydrolase	YP_187482.1	3.96101949
2227	E08	670	SACOL0653	conserved hypothetical protein	YP_185538.1	3.508955224
2230	E09	670	SACOL0664	endonuclease III, putative	YP_185548.1	4.244776119

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2231	E10	670	SACOL1010	GTP pyrophosphokinase	YP_185878.1	4.21641791
2235	E11	670	SACOL1830	abortive infection protein family	YP_186662.1	4.234328358
2237	E12	670	SACOL2035	conserved hypothetical protein	YP_186852.1	4.226865672
2239	F01	670	SACOL2313	hydrolase, haloacid dehalogenase-like family	YP_187120.1	4.246268657
2242	F02	670	SACOL2452	amino acid ABC transporter, permease protein	YP_187251.1	3.23880597
2243	F03	670	SACOL2537	ABC transporter, ATP-binding protein	YP_187330.1	4.262686567
2247	F04	673	SACOL2346	conserved hypothetical protein	YP_187152.1	4.222882615
2249	F05	673	SACOL2714	pyrrolidone-carboxylate peptidase	YP_187500.1	4.254086181
2251	F06	676	SACOL0375	prophage L54a, major tail protein, putative	YP_185267.1	4.236686391
2254	F07	676	SACOL0575	serine acetyltransferase	YP_185461.1	4.218934911
2255	F08	676	SACOL0645	conserved hypothetical protein	YP_185530.1	3.5
2257	F09	676	SACOL0649	conserved hypothetical protein	YP_185534.1	4.223372781
2259	F10	676	SACOL0811	conserved hypothetical protein TIGR00257	YP_185685.1	3.525147929
2261	F11	676	SACOL0900	pathogenicity island protein	YP_185771.1	4.229289941
2263	F12	676	SACOL0982	Sua5/YciO/YrdC/YwlC family protein	YP_185850.1	4.232248521
2265	G01	676	SACOL1040	ABC transporter, ATP-binding protein	YP_185905.1	3.834319527
2267	G02	676	SACOL1236	thiamine pyrophosphokinase	YP_186097.1	4.24556213
2269	G03	676	SACOL1420	phosphate transport system protein PhoU, putative	YP_186272.1	4.230769231
2271	G04	676	SACOL1851	hypothetical protein	YP_186682.1	4.263313609
2273	G05	676	SACOL2083	thiamine-phosphate pyrophosphorylase	YP_186899.1	3.50443787
2276	G06	679	SACOL0165	4-phosphopantetheinyl transferase family protein	YP_185064.1	4.215022091
2277	G07	679	SACOL0691	iron-dependent repressor	YP_185573.1	3.197349043
2283	G08	679	SACOL1235	ribulose-phosphate 3-epimerase	YP_186096.1	4.231222386
2285	G09	679	SACOL1798	tRNA (guanine-N(7)-)-methyltransferase	YP_186631.1	4.24005891
2287	G10	682	SACOL2080	HD domain protein	YP_186896.1	4.262463343
2289	G11	682	SACOL2218	adenylate kinase	YP_187028.1	4.24340176
2291	G12	682	SACOL2338	hypothetical protein	YP_187144.1	4.219941349
2293	H01	682	SACOL2348	drug transporter, putative	YP_187154.1	4.218475073
2295	H02	685	SACOL0652	conserved hypothetical protein	YP_185537.1	4.254014599
2297	H03	685	SACOL0821	HD domain protein	YP_185695.1	3.233576642
2299	H04	685	SACOL1846	hypothetical protein	YP_186677.1	2.794160584
2301	H05	688	SACOL0268	hypothetical protein	YP_185163.1	4.203488372
2303	H06	688	SACOL0545	ribosomal Protein L25	YP_185433.1	3.23255814
2305	H07	688	SACOL2233	ribosomal protein S3	YP_187043.1	4.223837209
2307	H08	688	SACOL2330	conserved hypothetical protein	YP_187137.1	3.718023256
2310	H09	688	SACOL2389	transcriptional regulatory protein DegU, putative	YP_187192.1	4.248546512
2311	H10	691	SACOL0417	MttB family protein	YP_185309.1	4.23154848
2313	H11	691	SACOL0619	hydrolase, haloacid dehalogenase-like family	YP_185504.1	4.230101302
2315	H12	691	SACOL0627	uracil-DNA glycosylase	YP_185512.1	3.837916064

Table 12: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 12 (ZSAJL), NR-19508[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2317	A01	691	SACOL2439	lipoprotein, putative	YP_187240.1	3.487698987
2319	A02	694	SACOL0264	ABC transporter, ATP-binding protein	YP_185159.1	4.208933718
2321	A03	694	SACOL0505	ABC transporter, permease protein	YP_185393.1	4.201729107
2323	A04	694	SACOL1451	DNA-binding response regulator ArlR	YP_186303.1	4.182997118
2325	A05	694	SACOL1492	endonuclease III	YP_186336.1	4.239193084
2327	A06	694	SACOL1518	cytidylate kinase	YP_186361.1	4.191642651

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2329	A07	694	SACOL2436	conserved hypothetical protein	YP_187237.1	3.606628242
2331	A08	697	SACOL0123	deoxyribose-phosphate aldolase	YP_185027.1	2.664275466
2335	A09	697	SACOL0603	deoxynucleoside kinase family protein	YP_185489.1	3.044476327
2337	A10	697	SACOL1096	TrkA potassium uptake family protein	YP_185960.1	4.219512195
2340	A11	697	SACOL2040	conserved hypothetical protein	YP_186857.1	4.235294118
2341	A12	697	SACOL2129	deoxyribose-phosphate aldolase	YP_186944.1	3.81348637
2343	B01	697	SACOL2462	ABC transporter, ATP-binding protein	YP_187260.1	4.210903874
2350	B02	700	SACOL2136	conserved hypothetical protein	YP_186951.1	4.208571429
2351	B03	700	SACOL2356	ABC transporter, ATP-binding protein	YP_187161.1	4.235714286
2353	B04	700	SACOL2646	DNA-binding response regulator	YP_187434.1	3.838571429
2355	B05	703	SACOL0136	capsular polysaccharide biosynthesis protein Cap5A	YP_185036.1	2.487908962
2357	B06	703	SACOL0315	N-acetylmannosamine-6-P epimerase, putative	YP_185207.1	4.231863442
2360	B07	703	SACOL0772	exsB protein	YP_185649.1	3.820768137
2361	B08	703	SACOL1675	TPR domain protein	YP_186515.1	3.493598862
2363	B09	703	SACOL1716	uroporphyrinogen-III synthase	YP_186554.1	3.507823613
2365	B10	706	SACOL1077	phosphoribosylformylglycinamidine synthase I	YP_185941.1	3.225212465
2367	B11	706	SACOL2123	conserved hypothetical protein	YP_186938.1	2.804532578
2369	B12	706	SACOL2271	molybdenum ABC transporter, permease protein ModB	YP_187078.1	3.223796034
2371	C01	706	SACOL2534	NAD(P)H-flavin oxidoreductase	YP_187327.1	3.16572238
2373	C02	709	SACOL0028	IS431mec, transposase	YP_184939.1	4.211565585
2375	C03	709	SACOL0244	ScdA protein	YP_185140.1	4.208744711
2377	C04	709	SACOL0279	hypothetical protein	YP_185174.1	2.794076164
2379	C05	709	SACOL0498	PAP2 family protein	YP_185386.1	2.503526093
2383	C06	709	SACOL1201	conserved hypothetical protein TIGR00044	YP_186063.1	4.04090268
2385	C07	709	SACOL2358	DNA-binding response regulator	YP_187163.1	3.878702398
2391	C09	712	SACOL1617	conserved hypothetical protein	YP_186457.1	3.105337079
2393	C10	712	SACOL2392	respiratory nitrate reductase, gamma subunit	YP_187195.1	3.404494382
2397	C12	715	SACOL1995	conserved hypothetical protein	YP_186819.1	4.187412587
2399	D01	715	SACOL2516	gluconate operon transcriptional repressor	YP_187310.1	4.213986014
2401	D02	715	SACOL2545	L-serine dehydratase, iron-sulfur-dependent, beta subunit	YP_187337.1	2.981818182
2403	D03	718	SACOL0283	lipoprotein, putative	YP_185178.1	4.22005571
2405	D04	718	SACOL0290	lipoprotein, putative	YP_185184.1	3.509749304
2409	D06	718	SACOL0602	hydrolase, haloacid dehalogenase-like family	YP_185488.1	3.814763231
2411	D07	718	SACOL0716	DNA-binding response regulator	YP_185598.1	2.791086351
2413	D08	718	SACOL0742	conserved hypothetical protein	YP_185621.1	4.228412256
2415	D09	718	SACOL1141	NPQTN cell wall surface anchor protein	YP_186004.1	3.544568245
2418	D10	718	SACOL2160	hemolysin III, putative	YP_186972.1	4.213091922
2419	D11	721	SACOL0137	capsular polysaccharide biosynthesis protein Cap5B	YP_185037.1	3.490984743
2421	D12	721	SACOL0766	DNA-binding response regulator SaeR	YP_185643.1	4.235783634
2424	E01	721	SACOL0860	thermonuclease precursor	YP_185733.1	3.513176144
2425	E02	721	SACOL1493	DNA replication protein DnaD, putative	YP_186337.1	3.359223301
2427	E03	721	SACOL1646	comE operon protein 1-related protein	YP_186486.1	3.493758669
2429	E04	721	SACOL1655	5-methylthioadenosine/S-adenosylhomocysteine nucleosidase	YP_186495.1	2.485436893
2431	E05	721	SACOL1707	DNA repair protein RadC	YP_186546.1	4.217753121
2433	E06	721	SACOL2329	ribose 5-phosphate isomerase	YP_187136.1	3.53259362
2435	E07	721	SACOL2415	phosphoglycerate mutase	YP_187218.1	3.493758669
2437	E08	721	SACOL2428	dethiobiotin synthase	YP_187230.1	2.338418863
2441	E10	721	SACOL2653	transcriptional regulator, Crp/Fnr family	YP_187441.1	3.833564494
2445	E11	724	SACOL0735	conserved hypothetical protein	YP_185614.1	4.23480663

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2447	E12	724	SACOL2086	transcriptional regulator, TenA family	YP_186902.1	3.490331492
2449	F01	724	SACOL2284	urease accessory protein UreF	YP_187091.1	3.685082873
2451	F02	724	SACOL2554	membrane protein, putative	YP_187346.1	2.809392265
2453	F03	727	SACOL0114	capsular polysaccharide biosynthesis glycosyltransferase, putative	YP_185018.1	3.103163686
2456	F04	727	SACOL0584	ribosomal protein L1	YP_185470.1	4.21045392
2457	F05	727	SACOL1216	orotidine 5-phosphate decarboxylase	YP_186079.1	4.214580468
2459	F06	727	SACOL1873	epidermin immunity protein F	YP_186701.1	2.796423659
2461	F07	727	SACOL1967	geranylgeranylglyceryl phosphate synthase family protein	YP_186791.1	4.074277854
2463	F08	727	SACOL2304	conserved domain protein	YP_187111.1	4.132049519
2465	F09	727	SACOL2424	6-carboxyhexanoate--CoA ligase	YP_187226.1	4.235213205
2467	F10	727	SACOL2518	conserved hypothetical protein	YP_187312.1	4.19394773
2469	F11	727	SACOL2678	conserved hypothetical protein	YP_187466.1	3.526822558
2471	F12	727	SACOL2686	capsular polysaccharide biosynthesis protein Cap1B	YP_187473.1	2.775790922
2473	G01	730	SACOL0010	AzlC family protein	YP_184921.1	3.2
2475	G02	730	SACOL0340	conserved hypothetical protein	YP_185232.1	2.77260274
2480	G04	730	SACOL0883	ABC transporter, permease protein	YP_185754.1	4.226027397
2482	G05	730	SACOL1188	hydrolase, haloacid dehalogenase-like family	YP_186050.1	4.209589041
2484	G06	730	SACOL1803	pseudouridine synthase, family 1	YP_186636.1	4.205479452
2485	G07	730	SACOL2071	DNA-binding response regulator KdpE	YP_186887.1	2.505479452
2487	G08	730	SACOL2088	sceD protein, putative	YP_186903.1	3.493150685
2489	G09	730	SACOL2450	amino acid ABC transporter, permease protein	YP_187249.1	4.197260274
2491	G10	730	SACOL2488	oxidoreductase, short-chain dehydrogenase/reductase family	YP_187284.1	4.197260274
2493	G11	730	SACOL2525	ABC transporter, ATP-binding protein	YP_187319.1	3.482191781
2498	H01	733	SACOL1629	conserved hypothetical protein	YP_186469.1	4.208731241
2500	H02	733	SACOL1871	epidermin immunity protein F	YP_186699.1	4.215552524
2501	H03	736	SACOL0007	YjeF-related protein	YP_184918.1	4.182065217
2504	H04	736	SACOL0019	DNA-binding response regulator YycF	YP_184930.1	4.168478261
2505	H05	736	SACOL0248	lrgB protein	YP_185144.1	4.210597826
2507	H06	736	SACOL1414	peptide ABC transporter, ATP-binding protein	YP_186266.1	4.216032609
2509	H07	736	SACOL1944	conserved hypothetical protein	YP_186769.1	4.201086957
2511	H08	736	SACOL2584	immunodominant antigen A	YP_187376.1	4.201086957
2513	H09	739	SACOL0249	transcriptional regulator, GntR family	YP_185145.1	4.196211096
2516	H10	739	SACOL0463	hypothetical protein	YP_185353.1	4.182679296
2517	H11	739	SACOL1075	phosphoribosylaminoimidazole-succinocarboxamide synthase	YP_185939.1	4.200270636
2519	H12	739	SACOL1299	acetoacetyl-CoA reductase, putative	YP_186156.1	4.202976996

Table 13: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 13 (ZSAJM), NR-19509[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2521	A01	739	SACOL1468	membrane protein, putative	YP_186316.1	3.51014885
2523	A02	739	SACOL1740	alkaline phosphatase synthesis transcriptional regulatory protein PhoP	YP_186577.1	3.48308525
2526	A03	739	SACOL2198	alpha-acetolactate decarboxylase	YP_187009.1	4.201623816
2527	A04	739	SACOL2594	oxidoreductase, short chain dehydrogenase/reductase family	YP_187385.1	4.230040595
2530	A05	739	SACOL2617	alpha-acetolactate decarboxylase	YP_187406.1	4.197564276

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2531	A06	739	SACOL2698	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	YP_187484.1	4.219215156
2533	A07	742	SACOL0121	purine nucleoside phosphorylase	YP_185025.1	4.184636119
2535	A08	742	SACOL1500	conserved hypothetical protein	YP_186344.1	3.785714286
2537	A09	742	SACOL1631	conserved hypothetical protein	YP_186471.1	4.230458221
2539	A10	742	SACOL1708	type III leader peptidase family protein	YP_186547.1	4.21967655
2541	A11	745	SACOL0776	conserved hypothetical protein TIGR00370	YP_185651.1	3.487248322
2543	A12	745	SACOL2130	purine nucleoside phosphorylase	YP_186945.1	4.226845638
2545	B01	747	SACOL1813	IS1272-related, transposase, degenerate	-	4.198125837
2547	B02	748	SACOL0319	hypothetical protein	YP_185211.1	4.209893048
2549	B03	748	SACOL0421	hypothetical protein	YP_185313.1	4.197860963
2551	B04	748	SACOL0770	radical activating enzyme family protein	YP_185647.1	3.834224599
2553	B05	748	SACOL1296	transcriptional regulator, GntR family, putative	YP_186153.1	3.212566845
2557	B06	751	SACOL0236	4-diphosphocytidyl-2C-methyl-D-erythritol synthase, putative	YP_185132.1	4.223701731
2560	B07	751	SACOL0240	4-diphosphocytidyl-2C-methyl-D-erythritol synthase, putative	YP_185136.1	4.190412783
2562	B08	751	SACOL0670	conserved hypothetical protein	YP_185554.1	4.219707057
2563	B09	751	SACOL0727	conserved hypothetical protein TIGR01033	YP_185608.1	3.500665779
2566	B10	751	SACOL0873	3-dehydroquinate dehydratase, type I	YP_185745.1	4.214380826
2570	B12	751	SACOL1647	conserved hypothetical protein	YP_186487.1	3.82023968
2571	C01	751	SACOL1865	serine protease SplE, putative	YP_186693.1	3.501997337
2573	C02	751	SACOL1869	serine protease SplA	YP_186697.1	4.201065246
2575	C03	751	SACOL2026	accessory gene regulator protein A	YP_186844.1	4.218375499
2577	C04	754	SACOL0321	prophage L54a, repressor protein, putative	YP_185213.1	4.188328912
2579	C05	754	SACOL0667	hydrolase, haloacid dehalogenase-like family	YP_185551.1	3.139257294
2581	C06	754	SACOL1003	negative regulator of competence MecA, putative	YP_185871.1	4.226790451
2584	C07	754	SACOL1432	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	YP_186284.1	3.816976127
2585	C08	754	SACOL1864	serine protease SplF, putative	YP_186692.1	4.201591512
2587	C09	754	SACOL1866	serine protease SplD, putative	YP_186694.1	4.185676393
2590	C10	754	SACOL1867	serine protease SplC	YP_186695.1	4.187002653
2591	C11	754	SACOL2736	glucose-inhibited division protein B	YP_187522.1	4.218832891
2593	C12	757	SACOL1277	uridylate kinase	YP_186134.1	3.94319683
2595	D01	757	SACOL1431	dihydrodipicolinate reductase	YP_186283.1	4.220607662
2597	D02	757	SACOL1868	serine protease SplB	YP_186696.1	4.217965654
2599	D03	757	SACOL2608	conserved hypothetical protein	YP_187398.1	4.198150594
2601	D04	760	SACOL0119	cell wall surface anchor family protein	YP_185023.1	4.211842105
2604	D05	760	SACOL0529	conserved hypothetical protein	YP_185417.1	4.203947368
2609	D08	760	SACOL1511	methlytransferase, UbiE/COQ5 family	YP_186355.1	4.215789474
2611	D09	760	SACOL1535	DNA-binding response regulator SrrA	YP_186377.1	4.217105263
2615	D10	763	SACOL0851	lipoprotein, putative	YP_185725.1	4.203145478
2618	D11	763	SACOL1409	tryptophan synthase, alpha subunit	YP_186261.1	4.190039318
2619	D12	763	SACOL1915	amino acid ABC transporter, ATP-binding protein	YP_186740.1	4.178243775
2621	E01	763	SACOL2101	ATP synthase F0, A subunit	YP_186916.1	4.191349934
2623	E02	763	SACOL2411	amino acid ABC transporter, permease protein	YP_187214.1	4.220183486
2625	E03	766	SACOL0049	conserved domain protein	YP_184959.1	4.211488251
2628	E04	766	SACOL1248	ribonuclease III	YP_186108.1	3.490861619
2629	E05	766	SACOL1353	ABC transporter, permease protein, putative	YP_186206.1	4.203655352
2631	E06	766	SACOL1538	segregation and condensation protein A	YP_186380.1	4.212793734
2633	E07	766	SACOL1950	cobyric acid synthase, putative	YP_186775.1	4.202349869
2635	E08	766	SACOL2189	transcriptional regulator, Sir2 family	YP_187000.1	4.2154047
2637	E09	766	SACOL2399	transcriptional regulator NirR	YP_187202.1	4.216710183

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2639	E10	766	SACOL2410	amino acid ABC transporter, ATP-binding protein	YP_187213.1	4.178851175
2641	E11	766	SACOL2538	conserved hypothetical protein	YP_187331.1	4.208877285
2643	E12	769	SACOL0074	conserved domain protein	YP_184979.1	4.191157347
2645	F01	769	SACOL0499	conserved hypothetical protein	YP_185387.1	4.208062419
2647	F02	769	SACOL1145	sortase B	YP_186008.1	4.192457737
2649	F03	769	SACOL1245	3-oxoacyl-(acyl-carrier-protein) reductase	YP_186105.1	3.807542263
2651	F04	769	SACOL1664	conserved hypothetical protein TIGR00370	YP_186504.1	4.22756827
2653	F05	772	SACOL1256	tRNA (guanine-N1)-methyltransferase	YP_186115.1	3.225388601
2655	F06	772	SACOL1536	pseudouridine synthase	YP_186378.1	4.237046632
2657	F07	772	SACOL2306	abortive infection protein family	YP_187113.1	4.212435233
2659	F08	775	SACOL0246	response regulator LytR	YP_185142.1	4.198709677
2661	F09	775	SACOL0845	carboxylesterase	YP_185719.1	4.2
2663	F10	775	SACOL1147	RNA methyltransferase, TrmH family	YP_186010.1	4.232258065
2665	F11	775	SACOL1893	ABC transporter, ATP-binding protein	YP_186719.1	4.190967742
2667	F12	775	SACOL1993	conserved hypothetical protein	YP_186817.1	4.2
2669	G01	775	SACOL2388	transcriptional regulator, MerR family, putative	YP_187191.1	4.214193548
2671	G02	778	SACOL0031	glycerophosphoryl diester phosphodiesterase, putative	YP_184942.1	4.228791774
2673	G03	778	SACOL0690	ABC transporter, ATP-binding protein	YP_185572.1	4.200514139
2677	G04	778	SACOL1770	glycerophosphoryl diester phosphodiesterase, putative	YP_186604.1	4.222365039
2680	G05	778	SACOL2018	abortive infection protein family	YP_186837.1	4.201799486
2684	G06	778	SACOL2507	staphylococcal accessory regulator U	YP_187302.1	4.203084833
2685	G07	781	SACOL0578	RNA methyltransferase, TrmH family	YP_185464.1	3.199743918
2687	G08	784	SACOL2470	hypothetical protein	YP_187267.1	4.218112245
2690	G09	784	SACOL2472	peptide ABC transporter, ATP-binding protein	YP_187269.1	4.209183673
2691	G10	787	SACOL0096	staphylococcal accessory regulator S	YP_185001.1	4.175349428
2693	G11	787	SACOL0427	conserved hypothetical protein	YP_185318.1	4.203303685
2695	G12	787	SACOL0633	conserved hypothetical protein	YP_185518.1	4.212198221
2697	H01	787	SACOL0692	conserved hypothetical protein	YP_185574.1	4.209656925
2699	H02	787	SACOL1623	DNA repair protein RecO family	YP_186463.1	4.214739517
2701	H03	787	SACOL1634	conserved hypothetical protein TIGR00046	YP_186474.1	4.195679797
2703	H04	787	SACOL1660	LamB/YcsF family protein	YP_186500.1	4.191867853
2705	H05	790	SACOL0061	conserved domain protein	YP_184966.1	5.301265823
2707	H06	790	SACOL0120	transcriptional regulator, GntR family	YP_185024.1	5.301265823
2709	H07	790	SACOL0205	pyruvate formate-lyase-activating enzyme	YP_185104.1	4.718987342
2711	H08	790	SACOL0453	NAD(P)H-flavin oxidoreductase, putative	YP_185343.1	5.302531646
2713	H09	790	SACOL1545	oxidoreductase, short-chain dehydrogenase/reductase family	YP_186387.1	5.313924051
2716	H10	790	SACOL2188	lactose phosphotransferase system repressor	YP_186999.1	5.278481013
2717	H11	793	SACOL0201	DNA-binding response regulator, AraC family	YP_185100.1	5.30517024
2719	H12	793	SACOL0616	glucosamine-6-phosphate isomerase	YP_185501.1	4.756620429

Table 14: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 14 (ZSAJN), NR-19510[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2721	A01	793	SACOL1019	conserved hypothetical protein	YP_185885.1	5.296343001
2724	A02	793	SACOL1946	methionine aminopeptidase, type I	YP_186771.1	5.290037831
2725	A03	793	SACOL2697	hisF protein (cyclase)	YP_187483.1	4.287515763
2727	A04	793	SACOL2724	ABC transporter, ATP-binding protein	YP_187510.1	5.297604035
2729	A05	796	SACOL0159	ABC transporter, permease protein	YP_185058.1	5.290201005
2731	A06	796	SACOL0252	conserved hypothetical protein	YP_185148.1	5.301507538

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2734	A07	796	SACOL0718	ABC transporter, ATP-binding protein	YP_185600.1	5.262562814
2735	A08	796	SACOL0798	iron compound ABC transporter, ATP-binding protein, putative	YP_185672.1	5.298994975
2737	A09	796	SACOL0808	membrane protein, putative	YP_185682.1	5.302763819
2739	A10	796	SACOL0840	triosephosphate isomerase	YP_185714.1	4.510050251
2741	A11	796	SACOL0914	FeS assembly ATPase SufC	YP_185785.1	5.293969849
2743	A12	796	SACOL1872	epidermin immunity protein F	YP_186700.1	5.311557789
2745	B01	796	SACOL2651	tributyrin esterase EstA, putative	YP_187439.1	5.300251256
2747	B02	799	SACOL0108	hypothetical protein	YP_185012.1	5.281602003
2749	B03	799	SACOL0138	capsular polysaccharide biosynthesis protein Cap5C	YP_185038.1	5.302878598
2751	B04	799	SACOL0167	acetylglutamate kinase	YP_185066.1	5.312891114
2753	B05	799	SACOL0632	membrane protein, putative	YP_185517.1	5.327909887
2757	B06	799	SACOL0757	transcriptional regulator, DeoR family	YP_185636.1	5.294117647
2759	B07	799	SACOL2255	conserved hypothetical protein	YP_187062.1	3.847309136
2761	B08	799	SACOL2317	phosphosugar-binding transcriptional regulator	YP_187124.1	5.304130163
2763	B09	799	SACOL2517	transcriptional regulator, MerR family	YP_187311.1	5.331664581
2766	B10	799	SACOL2644	ABC transporter, ATP-binding protein	YP_187432.1	5.310387985
2768	B11	802	SACOL0083	staphylococcal tandem lipoprotein	YP_184988.1	5.298004988
2769	B12	802	SACOL1261	ribonuclease HII	YP_186119.1	5.284289277
2771	C01	802	SACOL1412	hydrolase-related protein	YP_186264.1	5.296758105
2773	C02	802	SACOL2581	staphyloxanthin biosynthesis protein	YP_187373.1	5.300498753
2775	C03	802	SACOL2685	capsular polysaccharide biosynthesis protein Cap1C	YP_187472.1	5.306733167
2777	C04	802	SACOL2715	hypothetical protein	YP_187501.1	3.302992519
2780	C05	805	SACOL0079	staphylococcus tandem lipoprotein	YP_184984.1	5.275776398
2781	C06	805	SACOL0080	staphylococcus tandem lipoprotein	YP_184985.1	5.30310559
2783	C07	805	SACOL1016	enoyl-(acyl-carrier-protein) reductase	YP_185882.1	5.30931677
2785	C08	805	SACOL1279	undecaprenyl diphosphate synthase	YP_186136.1	5.283229814
2787	C09	805	SACOL1763	conserved hypothetical protein	YP_186597.1	5.298136646
2789	C10	805	SACOL1840	conserved hypothetical protein	YP_186671.1	5.31552795
2791	C11	805	SACOL2054	RNA polymerase sigma-37 factor	YP_186870.1	5.285714286
2794	C12	805	SACOL2274	acetyltransferase, GNAT family	YP_187081.1	5.272049689
2795	D01	805	SACOL2526	membrane protein, putative, authentic point mutation	-	5.314285714
2798	D02	808	SACOL0127	phosphonate ABC transporter, ATP-binding protein	YP_185031.1	4.727722772
2799	D03	808	SACOL0189	staphylococcus tandem lipoprotein	YP_185088.1	5.288366337
2801	D04	808	SACOL0369	prophage L54a, Clp protease, putative	YP_185261.1	4.292079208
2803	D05	808	SACOL0534	deoxyribonuclease, TatD family	YP_185422.1	5.170792079
2806	D06	808	SACOL1272	transcriptional regulator CodY	YP_186130.1	5.301980198
2807	D07	808	SACOL1415	peptide ABC transporter, ATP-binding protein	YP_186267.1	5.27970297
2809	D08	808	SACOL1683	HesA/MoeB/ThiF family protein	YP_186523.1	5.297029703
2813	D09	811	SACOL0106	HPCH/HPAI aldolase family protein	YP_185010.1	5.302096178
2815	D10	811	SACOL0111	acetoin reductase	YP_185015.1	5.231812577
2818	D11	811	SACOL0483	staphyloccoccus tandem lipoprotein	YP_185373.1	4.754623921
2819	D12	811	SACOL1274	ribosomal protein S2	YP_186131.1	5.289765721
2821	E01	811	SACOL1797	metallo-beta-lactamase family protein	YP_186630.1	5.316892725
2823	E02	811	SACOL2298	N-acetylmuramoyl-L-alanine amidase, family 4	YP_187105.1	4.639950678
2826	E03	811	SACOL2461	conserved hypothetical protein TIGR00245	YP_187259.1	3.96054254
2827	E04	811	SACOL2498	staphylococcus tandem lipoprotein	YP_187293.1	5.295930949
2830	E05	812	SACOL1855	transposase, putative, degenerate	-	4.68226601
2831	E06	814	SACOL0931	hydrolase, haloacid dehalogenase-like family	YP_185801.1	5.245700246

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2834	E07	814	SACOL1204	YlmH protein	YP_186066.1	5.272727273
2835	E08	814	SACOL2412	amino acid ABC transporter, amino acid-binding protein	YP_187215.1	5.27027027
2837	E09	817	SACOL0511	conserved hypothetical protein	YP_185399.1	5.305997552
2839	E10	817	SACOL1280	phosphatidate cytidylyltransferase	YP_186137.1	5.277845777
2841	E11	817	SACOL1406	indole-3-glycerol phosphate synthase	YP_186258.1	5.29130967
2843	E12	817	SACOL2144	ABC transporter, ATP-binding protein	YP_186957.1	5.307221542
2845	F01	817	SACOL2272	molybdenum ABC transporter, molybdenum-binding protein ModA	YP_187079.1	5.279069767
2847	F02	820	SACOL0485	staphylococcus tandem lipoprotein	YP_185375.1	5.267073171
2849	F03	820	SACOL1613	ABC transporter, ATP-binding protein	YP_186453.1	5.264634146
2851	F04	820	SACOL2021	hydrolase, carbon-nitrogen family	YP_186840.1	4.954878049
2853	F05	820	SACOL2497	staphylococcus tandem lipoprotein	YP_187292.1	5.282926829
2855	F06	823	SACOL0022	yycI protein	YP_184933.1	5.260024301
2858	F07	823	SACOL0671	hydrolase, alpha/beta hydrolase fold family	YP_185555.1	4.752126367
2861	F08	826	SACOL0250	PTS system, IIA component	YP_185146.1	4.997578692
2863	F09	826	SACOL0325	prophage L54a, antirepressor, putative	YP_185217.1	4.185230024
2865	F10	826	SACOL0482	staphylococcus tandem lipoprotein	YP_185372.1	4.561743341
2867	F11	826	SACOL1200	conserved hypothetical protein TIGR00726	YP_186062.1	5.268765133
2869	F12	826	SACOL1445	CbbQ/NirQ/NorQ/GpvN family protein	YP_186297.1	4.998789346
2871	G01	826	SACOL1799	conserved hypothetical protein	YP_186632.1	5.279661017
2877	G02	829	SACOL0694	tagH protein, teichoic acid ABC transporter protein, putative	YP_185576.1	5.240048251
2881	G03	829	SACOL2493	staphylococcus tandem lipoprotein	YP_187288.1	5.294330519
2883	G04	829	SACOL2722	N-acetyltransferase family protein	YP_187508.1	5.265379976
2885	G05	832	SACOL0704	iron compound ABC transporter, ATP-binding protein	YP_185586.1	5.263221154
2887	G06	832	SACOL0723	LysM domain protein	YP_185604.1	5.272836538
2889	G07	832	SACOL1109	spermidine/putrescine ABC transporter, permease protein	YP_185973.1	5.271634615
2891	G08	832	SACOL1207	glyoxalase family protein	YP_186069.1	5.268028846
2893	G09	832	SACOL1307	conserved hypothetical protein TIGR00282	YP_186164.1	5.180288462
2895	G10	832	SACOL2273	formate dehydrogenase accessory protein FdhD	YP_187080.1	5.283653846
2897	G11	832	SACOL2303	inositol monophosphatase family protein	YP_187110.1	5.304086538
2899	G12	835	SACOL0023	metallo-beta-lactamase family protein YycJ	YP_184934.1	5.295808383
2901	H01	835	SACOL0126	phosphonate ABC transporter, permease protein	YP_185030.1	5.241916168
2903	H02	835	SACOL0314	conserved hypothetical protein	YP_185206.1	5.2
2905	H03	835	SACOL0341	conserved hypothetical protein	YP_185233.1	5.279041916
2908	H04	835	SACOL0396	conserved domain protein	YP_185288.1	5.286227545
2910	H05	835	SACOL0481	staphylococcus tandem lipoprotein	YP_185371.1	3.725748503
2911	H06	835	SACOL0668	hydrolase, alpha/beta hydrolase fold family	YP_185552.1	5.256287425
2913	H07	835	SACOL1161	glutamate racemase	YP_186024.1	4.936526946
2915	H08	835	SACOL2536	hydrolase, haloacid dehalogenase-like family	YP_187329.1	4.241916168
2917	H09	838	SACOL0527	conserved hypothetical protein	YP_185415.1	4.186157518
2921	H10	838	SACOL1026	conserved hypothetical protein	YP_185892.1	4.708830549
2923	H11	838	SACOL1053	hydrolase, alpha/beta hydrolase fold family	YP_185918.1	5.257756563
2925	H12	838	SACOL1365	hydrolase, haloacid dehalogenase-like family	YP_186218.1	4.933174224

Table 15: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 15 (ZSAJO), NR-19511[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2928	A01	838	SACOL2122	pantothenate kinase, putative	YP_186937.1	5.260143198

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
2929	A02	838	SACOL2208	tRNA pseudouridine synthase A	YP_187018.1	4.737470167
2932	A03	838	SACOL2291	staphyloxanthin biosynthesis protein	YP_187098.1	4.730310263
2933	A04	841	SACOL1006	conserved hypothetical protein	YP_185874.1	5.292508918
2935	A05	841	SACOL1084	cobalt transport family protein	YP_185948.1	5.22235434
2937	A06	841	SACOL1652	shikimate 5-dehydrogenase	YP_186492.1	4.401902497
2939	A07	841	SACOL2209	cobalt transport family protein	YP_187019.1	5.312722949
2941	A08	841	SACOL2440	conserved hypothetical protein	YP_187241.1	5.262782402
2943	A09	841	SACOL2533	glyoxalase family protein	YP_187326.1	5.221165279
2946	A10	844	SACOL1011	conserved hypothetical protein	YP_185879.1	5.302132701
2947	A11	844	SACOL1110	spermidine/putrescine ABC transporter, permease protein	YP_185974.1	5.273696682
2950	A12	844	SACOL1447	conserved hypothetical protein	YP_186299.1	4.71563981
2951	B01	844	SACOL1932	transglycosylase domain protein	YP_186757.1	4.646919431
2953	B02	844	SACOL2153	conserved hypothetical protein TIGR00159	YP_186966.1	5.238151659
2956	B03	844	SACOL2211	ABC transporter, ATP-binding protein	YP_187021.1	5.254739336
2957	B04	844	SACOL2605	conserved hypothetical protein	YP_187395.1	5.16943128
2959	B05	847	SACOL0695	tagG protein, teichoic acid ABC transporter protein, putative	YP_185577.1	5.26918536
2961	B06	850	SACOL0125	phosphonate ABC transporter, permease protein	YP_185029.1	3.281176471
2963	B07	850	SACOL0484	Staphylococcus tandem lipoprotein	YP_185374.1	5.268235294
2965	B08	850	SACOL0486	staphylococcus tandem lipoprotein	YP_185376.1	5.276470588
2967	B09	850	SACOL1160	succinate dehydrogenase, iron-sulfur protein	YP_186023.1	5.275294118
2969	B10	850	SACOL1546	pyrroline-5-carboxylate reductase	YP_186388.1	5.311764706
2971	B11	850	SACOL1718	hemX protein	YP_186556.1	5.212941176
2973	B12	850	SACOL2196	conserved hypothetical protein	YP_187007.1	5.202352941
2975	C01	850	SACOL2473	peptide ABC transporter, ATP-binding protein	YP_187270.1	4.601176471
2977	C02	853	SACOL1319	glycerol uptake facilitator protein	YP_186174.1	4.64126612
2979	C03	853	SACOL1620	conserved hypothetical protein	YP_186460.1	5.223915592
2981	C04	853	SACOL1931	FAD-binding RecX family protein	YP_186756.1	5.264947245
2983	C05	853	SACOL2478	conserved hypothetical protein	YP_187275.1	4.409144197
2985	C06	853	SACOL2482	3-oxoacyl-(acyl carrier protein) reductase, authentic point mutation	-	4.177022274
2987	C07	853	SACOL2615	3-methyl-2-oxobutanoate hydroxymethyltransferase	YP_187404.1	4.822977726
2989	C08	853	SACOL2704	conserved hypothetical protein	YP_187490.1	5.254396249
2992	C09	856	SACOL0884	ABC transporter, substrate-binding protein	YP_185755.1	4.178738318
2993	C10	856	SACOL1054	naphthoate synthase	YP_185919.1	5.23364486
2995	C11	856	SACOL1907	ribosomal large subunit pseudouridine synthase, RluD subfamily	YP_186732.1	4.142523364
2998	C12	856	SACOL1974	NH(3)-dependent NAD+ synthetase	YP_186798.1	5.25817757
2999	D01	856	SACOL2479	conserved hypothetical protein	YP_187276.1	5.162383178
3001	D02	856	SACOL2591	actVA 4 protein	YP_187382.1	5.186915888
3005	D03	859	SACOL0539	pur operon repressor	YP_185427.1	4.279394645
3009	D04	859	SACOL2401	formate/nitrite transporter family protein	YP_187204.1	5.256111758
3011	D05	862	SACOL0391	hypothetical protein	YP_185283.1	4.938515081
3015	D06	862	SACOL1116	inositol monophosphatase family protein	YP_185980.1	4.393271462
3017	D07	862	SACOL1300	ACT domain protein	YP_186157.1	5.257540603
3019	D08	862	SACOL1814	lysophospholipase, putative	YP_186646.1	5.220417633
3021	D09	865	SACOL0626	phosphomethylpyrimidine kinase	YP_185511.1	5.147976879
3023	D10	865	SACOL1416	peptide ABC transporter, permease protein, putative	YP_186268.1	5.169942197
3025	D11	865	SACOL1591	lipoate-protein ligase A family protein	YP_186431.1	5.16416185
3027	D12	865	SACOL2085	phosphomethylpyrimidine kinase	YP_186901.1	5.167630058

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Master Clone List for NR-19277

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3029	E01	865	SACOL2597	hydrolase, alpha/beta hydrolase fold family	YP_187388.1	4.652023121
3032	E02	868	SACOL0703	conserved hypothetical protein	YP_185585.1	4.700460829
3033	E03	868	SACOL1835	oxidoreductase, aldo/keto reductase family	YP_186666.1	5.232718894
3035	E04	868	SACOL2236	ribosomal protein L2	YP_187046.1	5.123271889
3037	E05	868	SACOL2707	cobalt transport family protein	YP_187493.1	4.466589862
3039	E06	871	SACOL0635	lipoate-protein ligase A family protein	YP_185520.1	5.167623421
3041	E07	871	SACOL0689	ABC transporter, permease protein	YP_185571.1	5.213547646
3043	E08	871	SACOL1928	conserved hypothetical protein	YP_186753.1	4.638346728
3046	E09	871	SACOL2109	modification methylase, HemK family	YP_186924.1	4.715269805
3047	E10	871	SACOL2286	urease accessory protein UreD	YP_187093.1	4.34902411
3049	E11	874	SACOL0195	maltose ABC transporter, permease protein	YP_185094.1	5.145308924
3052	E12	874	SACOL0531	tetrapyrrole methylase family protein	YP_185419.1	4.709382151
3053	F01	874	SACOL0763	oxidoreductase, aldo/keto reductase family	YP_185640.1	5.156750572
3056	F02	874	SACOL0820	LysM domain protein	YP_185694.1	5.223112128
3057	F03	874	SACOL0826	prolipoprotein diacylglyceryl transferase	YP_185700.1	5.180778032
3059	F04	874	SACOL1460	degV family protein	YP_186309.1	4.639588101
3061	F05	874	SACOL2735	chromosome partioning protein, ParB family	YP_187521.1	5.171624714
3064	F06	877	SACOL0181	conserved domain protein	YP_185080.1	5.269099202
3065	F07	877	SACOL0422	ABC transporter, ATP-binding protein	YP_185314.1	5.13340935
3067	F08	877	SACOL0506	ABC transporter, substrate-binding protein	YP_185394.1	4.59977195
3071	F09	877	SACOL1989	conserved hypothetical protein	YP_186813.1	4.238312429
3075	F10	880	SACOL0432	spoOJ protein	YP_185323.1	5.181818182
3077	F11	880	SACOL0467	conserved hypothetical protein	YP_185357.1	4.497727273
3079	F12	880	SACOL2009	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative	YP_186829.1	4.646590909
3081	G01	883	SACOL0538	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	YP_185426.1	5.201585504
3083	G02	883	SACOL0924	conserved hypothetical protein	YP_185794.1	5.194790487
3085	G03	883	SACOL0991	oligopeptide ABC transporter, permease protein	YP_185859.1	4.662514156
3087	G04	883	SACOL1800	D-alanine aminotransferase	YP_186633.1	5.193657984
3089	G05	883	SACOL2192	oxidoreductase, aldo/keto reductase family	YP_187003.1	5.204983012
3091	G06	883	SACOL2710	conserved hypothetical protein	YP_187496.1	4.874292186
3093	G07	886	SACOL0913	conserved hypothetical protein	YP_185784.1	4.600451467
3097	G08	886	SACOL1421	phosphate ABC transporter, ATP-binding protein	YP_186273.1	5.14221219
3099	G09	886	SACOL2446	epimerase/dehydratase, putative	YP_187246.1	4.639954853
3101	G10	886	SACOL2614	pantoate--beta-alanine ligase	YP_187403.1	5.22234763
3104	G11	889	SACOL0414	lipoprotein, putative	YP_185306.1	4.721034871
3105	G12	889	SACOL1012	ribosomal large subunit pseudouridine synthases, RluD subfamily	YP_185880.1	5.193475816
3107	H01	889	SACOL1358	conserved hypothetical protein	YP_186211.1	4.143982002
3109	H02	889	SACOL1825	N-acetylmuramoyl-L-alanine amidase, family 4	YP_186657.1	5.187851519
3111	H03	889	SACOL2195	M23/M37 peptidase domain protein	YP_187006.1	4.12935883
3113	H04	892	SACOL1748	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	YP_186584.1	5.161434978
3115	H05	892	SACOL1793	conserved hypothetical protein	YP_186626.1	5.184977578
3120	H06	895	SACOL0313	ROK family protein	YP_185205.1	4.736312849
3121	H07	895	SACOL0408	glyoxalase family protein	YP_185300.1	5.204469274
3123	H08	895	SACOL1072	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	YP_185936.1	4.896089385
3125	H09	895	SACOL2117	fructose-bisphosphate aldolase, class II	YP_186932.1	4.193296089
3127	H10	895	SACOL2121	acetyltransferase, GNAT family	YP_186936.1	4.875977654
3129	H11	895	SACOL2210	ABC transporter, ATP-binding protein	YP_187020.1	5.204469274
3135	H12	898	SACOL1612	ABC transporter, permease protein	YP_186452.1	5.165924276

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Table 16: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 16 (ZSAJP), NR-19512[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3137	A01	898	SACOL2246	sugar transporter, putative	YP_187055.1	5.178173719
3139	A02	898	SACOL2577	dehydrosqualene synthase	YP_187369.1	4.638084633
3141	A03	901	SACOL0731	transcriptional regulator, LysR family	YP_185611.1	5.116537181
3143	A04	901	SACOL0790	integral membrane domain protein	YP_185663.1	5.095449501
3145	A05	901	SACOL0812	degV family protein	YP_185686.1	5.187569367
3147	A06	901	SACOL1309	pyruvate ferredoxin oxidoreductase, beta subunit	YP_186166.1	4.166481687
3149	A07	901	SACOL2096	ATP synthase F1, gamma subunit	YP_186911.1	4.680355161
3151	A08	901	SACOL2416	cation efflux family protein	YP_187219.1	4.639289678
3154	A09	901	SACOL2508	UTP-glucose-1-phosphate uridylyltransferase	YP_187303.1	4.690344062
3155	A10	904	SACOL0606	hydrolase, haloacid dehalogenase-like family	YP_185491.1	4.828539823
3158	A11	904	SACOL0896	pathogenicity island protein	YP_185767.1	5.201327434
3159	A12	904	SACOL0980	transcriptional regulator, LysR family	YP_185848.1	5.202433628
3161	B01	904	SACOL2143	conserved hypothetical protein	YP_186956.1	5.186946903
3164	B02	904	SACOL2179	conserved hypothetical protein	YP_186990.1	4.655973451
3165	B03	904	SACOL2474	peptide ABC transporter, permease protein	YP_187271.1	5.138274336
3167	B04	907	SACOL0090	integral membrane domain protein	YP_184995.1	5.065049614
3169	B05	907	SACOL1266	DNA processing protein DprA, putative	YP_186124.1	5.106945976
3171	B06	907	SACOL1736	formamidopyrimidine-DNA glycosylase	YP_186573.1	5.184123484
3177	B08	907	SACOL2082	lipoprotein, putative	YP_186898.1	3.600882029
3179	B09	907	SACOL2308	phosphosugar-binding transcriptional regulator, RpiR family	YP_187115.1	4.861080485
3181	B10	910	SACOL0179	phosphosugar-binding transcriptional regulator, RpiR family	YP_185078.1	4.004395604
3184	B11	910	SACOL0743	bacitracin resistance protein	YP_185622.1	4.363736264
3185	B12	910	SACOL1234	conserved hypothetical protein TIGR00157	YP_186095.1	5.185714286
3187	C01	910	SACOL1687	N-acetylmuramoyl-L-alanine amidase, family 3	YP_186526.1	4.693406593
3189	C02	913	SACOL0597	conserved hypothetical protein	YP_185483.1	5.040525739
3191	C03	913	SACOL0613	conserved hypothetical protein TIGR00294	YP_185498.1	5.076670318
3194	C04	913	SACOL0803	lipoprotein, putative	YP_185677.1	4.657174151
3195	C05	913	SACOL0879	conserved hypothetical protein	YP_185750.1	4.242059146
3197	C06	913	SACOL1143	iron compound ABC transporter, iron compound-binding protein, putative	YP_186006.1	5.13253012
3199	C07	913	SACOL1479	5-3 exonuclease, putative	YP_186324.1	5.209200438
3201	C08	913	SACOL2691	intercellular adhesion protein B	YP_187478.1	5.127053669
3204	C09	916	SACOL0255	membrane protein, putative	YP_185151.1	5.240174672
3205	C10	916	SACOL0312	N-acetylneuraminate lyase	YP_185204.1	5.159388646
3207	C11	916	SACOL0433	conserved hypothetical protein	YP_185324.1	5.147379913
3209	C12	916	SACOL0556	chaperonin, 33 kDa	YP_185444.1	5.148471616
3211	D01	916	SACOL1000	oligopeptide ABC transporter, permease protein	YP_185868.1	5.128820961
3213	D02	916	SACOL1212	aspartate carbamoyltransferase	YP_186075.1	5.081877729
3215	D03	916	SACOL1276	translation elongation factor Ts	YP_186133.1	4.887554585
3217	D04	916	SACOL1566	geranyltranstransferase	YP_186407.1	5.052401747
3219	D05	916	SACOL2321	oxidoreductase, short chain dehydrogenase/reductase family	YP_187128.1	5.135371179
3221	D06	919	SACOL0513	transcriptional regulatory protein GltC	YP_185401.1	5.168661589
3223	D07	919	SACOL1260	GTP-binding protein, putative	YP_186118.1	4.903155604
3225	D08	919	SACOL2325	transcriptional regulator, LysR family	YP_187132.1	4.253536453
3228	D09	919	SACOL2555	transcriptional regulator, LysR family, putative	YP_187348.1	5.258977149
3229	D10	922	SACOL0149	capsular polysaccharide biosynthesis protein Cap5N	YP_185049.1	5.15835141
3231	D11	922	SACOL0564	pyridoxine biosynthesis protein	YP_185452.1	5.145336226

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Master Clone List for NR-19277

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3233	D12	922	SACOL0665	iron compound ABC transporter, iron compound-binding protein, putative	YP_185549.1	5.112798265
3237	E01	922	SACOL1540	tyrosine recombinase XerD	YP_186382.1	4.527114967
3239	E02	922	SACOL2245	acetyltransferase, GNAT family	YP_187054.1	5.032537961
3241	E03	922	SACOL2645	sensor histidine kinase, putative	YP_187433.1	4.581344902
3245	E04	925	SACOL1614	endonuclease IV	YP_186454.1	3.256216216
3247	E05	925	SACOL2598	cobalamin synthesis protein, putative	YP_187389.1	4.984864865
3251	E07	928	SACOL0132	replication initiation protein, degenerate	-	4.810344828
3253	E08	928	SACOL0270	staphyloxanthin biosynthesis protein, putative	YP_185165.1	4.327586207
3255	E09	928	SACOL0536	dimethyladenosine transferase	YP_185424.1	5.11637931
3261	E11	931	SACOL1269	tyrosine recombinase XerC	YP_186127.1	5.056928034
3263	E12	931	SACOL1996	ABC transporter, ATP-binding protein	YP_186820.1	4.899033298
3265	F01	934	SACOL0177	glucokinase regulator-related protein	YP_185076.1	5.025695931
3268	F02	934	SACOL1128	conserved hypothetical protein	YP_185992.1	5.177730193
3269	F03	934	SACOL1624	GTP-binding protein Era	YP_186464.1	5.132762313
3271	F04	934	SACOL2335	ABC transporter, ATP-binding protein	YP_187142.1	5.128479657
3274	F05	934	SACOL2544	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	YP_187336.1	4.644539615
3275	F06	937	SACOL0834	conserved hypothetical protein TIGR01777	YP_185708.1	5.101387407
3277	F07	937	SACOL0973	fumarylacetoacetate hydrolase family protein	YP_185841.1	5.140875133
3280	F08	937	SACOL1426	conserved hypothetical protein	YP_186278.1	5.178228388
3281	F09	937	SACOL2345	esterase, putative	YP_187151.1	5.071504803
3283	F10	940	SACOL1779	transglycosylase domain protein	YP_186613.1	5.077659574
3286	F11	940	SACOL2279	urea transporter	YP_187086.1	5.172340426
3288	F12	943	SACOL0748	oxidoreductase, aldo/keto reductase family	YP_185627.1	5.152704136
3289	G01	943	SACOL1263	succinyl-CoA synthase, alpha subunit	YP_186121.1	3.890774125
3291	G02	943	SACOL1352	ABC transporter, ATP-binding protein	YP_186205.1	5.098621421
3293	G03	943	SACOL1543	oxidoreductase, aldo/keto reductase family	YP_186385.1	5.138918346
3295	G04	943	SACOL1836	conserved hypothetical protein	YP_186667.1	5.114528102
3297	G05	943	SACOL2154	arginase	YP_186967.1	5.159066808
3299	G06	943	SACOL2248	conserved hypothetical protein	YP_187057.1	3.895015907
3301	G07	943	SACOL2277	iron compound ABC transporter, iron compound-binding protein	YP_187084.1	5.054082715
3303	G08	943	SACOL2719	rarD protein	YP_187505.1	4.688229056
3307	G09	946	SACOL1125	protoheme IX farnesyltransferase	YP_185989.1	5.069767442
3311	G10	949	SACOL0253	ribokinase	YP_185149.1	4.971548999
3313	G11	949	SACOL0502	cysteine synthase/cystathionine beta-synthase family protein	YP_185390.1	5.073761855
3317	G12	949	SACOL1364	homoserine kinase	YP_186217.1	4.798735511
3319	H01	949	SACOL1528	lipoprotein, putative	YP_186370.1	5.126448894
3322	H02	949	SACOL2387	conserved hypothetical protein, authentic point mutation	-	5.220231823
3323	H03	952	SACOL0787	conserved hypothetical protein TIGR00147	YP_185660.1	5.102941176
3325	H04	952	SACOL0927	lipoate synthase	YP_185797.1	5.071428571
3327	H05	952	SACOL1209	ribosomal large subunit pseudouridine synthases, RluD subfamily	YP_186070.1	4.133403361
3331	H07	952	SACOL1422	phosphate ABC transporter, permease protein	YP_186274.1	5.033613445
3333	H08	952	SACOL1531	lipoprotein, putative	YP_186373.1	4.930672269
3335	H09	952	SACOL2314	sodium/bile acid symporter family protein	YP_187121.1	4.969537815
3337	H10	955	SACOL0265	hypothetical protein	YP_185160.1	4.203141361
3339	H11	955	SACOL0636	mevalonate kinase	YP_185521.1	4.22408377
3341	H12	955	SACOL0758	1-phosphofructokinase	YP_185637.1	4.120418848

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Table 17: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 17 (ZSAJQ), NR-19513[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3343	A01	955	SACOL1548	ribonuclease Z	YP_186389.1	5.106806283
3345	A02	955	SACOL1628	PhoH family protein	YP_186468.1	5.036649215
3347	A03	955	SACOL1731	primosomal protein DnaI	YP_186568.1	4.210471204
3349	A04	958	SACOL0013	conserved hypothetical protein	YP_184924.1	4.221294363
3351	A05	958	SACOL0182	hypothetical protein	YP_185081.1	5.086638831
3353	A06	958	SACOL0309	conserved hypothetical protein	YP_185201.1	5.057411273
3355	A07	958	SACOL0715	conserved hypothetical protein	YP_185597.1	5.04697286
3357	A08	958	SACOL0801	UDP-N-acetylenolpyruvoylglucosamine reductase	YP_185675.1	5.001043841
3359	A09	958	SACOL1668	peptidase, U32 family	YP_186508.1	4.659707724
3365	A12	961	SACOL0526	DNA polymerase III, delta prime subunit, putative	YP_185414.1	4.237252862
3367	B01	961	SACOL0747	cobalamin synthesis protein/P47K family protein	YP_185626.1	5.092611863
3370	B02	961	SACOL1130	glycerophosphoryl diester phosphodiesterase, putative	YP_185994.1	5.182101977
3371	B03	961	SACOL1244	malonyl CoA-acyl carrier protein transacylase	YP_186104.1	4.32049948
3373	B04	961	SACOL1423	phosphate ABC transporter, permease protein	YP_186275.1	5.089490114
3375	B05	961	SACOL1717	porphobilinogen deaminase	YP_186555.1	5.097814776
3377	B06	964	SACOL0688	ABC transporter, substrate-binding protein	YP_185570.1	5.044605809
3379	B07	964	SACOL0962	glycerophosphoryl diester phosphodiesterase GlpQ, putative	YP_185831.1	5.039419087
3381	B08	964	SACOL1533	lipoprotein, putative	YP_186375.1	4.985477178
3383	B09	964	SACOL1723	conserved hypothetical protein	YP_186561.1	4.411825726
3385	B10	964	SACOL1982	manganese-dependent inorganic pyrophosphatase	YP_186806.1	5.02593361
3390	B12	967	SACOL0067	conserved hypothetical protein	YP_184972.1	4.613236815
3391	C01	967	SACOL0557	cysteine synthase	YP_185445.1	5.087900724
3393	C02	967	SACOL0825	HPr kinase/phosphatase	YP_185699.1	5.003102378
3395	C03	967	SACOL1182	carbamate kinase	YP_186045.1	4.778697001
3398	C04	967	SACOL2152	conserved hypothetical protein	YP_186965.1	5.127197518
3399	C05	967	SACOL2184	tagatose-6-phosphate kinase	YP_186995.1	5.06204757
3401	C06	970	SACOL0225	inosine-uridine preferring nucleoside hydrolase	YP_185123.1	5.022680412
3403	C07	970	SACOL0829	thioredoxin-disulfide reductase	YP_185703.1	5.024742268
3405	C08	970	SACOL1192	S-adenosyl-methyltransferase MraW	YP_186054.1	5.015463918
3407	C09	970	SACOL1228	methionyl-tRNA formyltransferase	YP_186091.1	4.919587629
3409	C10	970	SACOL1323	tRNA delta(2)-isopentenylpyrophosphate transferase	YP_186178.1	4.977319588
3413	C12	970	SACOL2327	formiminoglutamase	YP_187134.1	5.046391753
3415	D01	970	SACOL2448	2-dehydropantoate 2-reductase, putative	YP_187247.1	5.053608247
3417	D02	970	SACOL2475	peptide ABC transporter, permease protein, putative	YP_187272.1	5.04742268
3419	D03	973	SACOL0440	Abi-like protein	YP_185331.1	4.74717369
3421	D04	973	SACOL0655	oxidoreductase, aldo/keto reductase family	YP_185540.1	5.021582734
3423	D05	973	SACOL1049	1,4-dihydroxy-2-naphthoate octaprenyltransferase	YP_185914.1	5.014388489
3425	D06	973	SACOL1150	ribonuclease HIII	YP_186013.1	5.046248715
3427	D07	973	SACOL1530	lipoprotein, putative	YP_186372.1	5.059609455
3429	D08	973	SACOL1635	ribosomal protein L11 methyltransferase	YP_186475.1	4.976361768
3432	D09	973	SACOL2135	mannose-6-phosphate isomerase, class I	YP_186950.1	4.353545735
3433	D10	973	SACOL2664	mannose-6-phosphate isomerase, class I	YP_187452.1	4.391572456
3435	D11	976	SACOL0987	3-oxoacyl-(acyl-carrier-protein) synthase III	YP_185855.1	4.967213115
3438	D12	976	SACOL0994	oligopeptide ABC transporter, ATP-binding protein	YP_185862.1	5.088114754

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3439	E01	976	SACOL1751	DHH subfamily 1 protein	YP_186587.1	5.024590164
3441	E02	976	SACOL1898	cmp-binding-factor 1	YP_186724.1	5.047131148
3443	E03	976	SACOL2276	inosine-uridine preferring nucleoside hydrolase	YP_187083.1	4.994877049
3445	E04	976	SACOL2451	amino acid ABC transporter, amino acid-binding protein	YP_187250.1	4.983606557
3451	E05	979	SACOL0832	conserved hypothetical protein	YP_185706.1	5.009193054
3453	E06	979	SACOL1747	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit	YP_186583.1	4.072522983
3455	E07	979	SACOL2213	DNA-directed RNA polymerase, alpha subunit	YP_187023.1	4.879468846
3457	E08	979	SACOL2375	transporter, CorA family	YP_187179.1	4.995914198
3459	E09	979	SACOLA0001	replication initiation protein		5
3461	E10	982	SACOL0100	cysteine synthase/cystathionine beta-synthase family protein	YP_185005.1	5.018329939
3465	E12	982	SACOL1761	conserved hypothetical protein	YP_186595.1	3.263747454
3467	F01	982	SACOL1958	conserved hypothetical protein TIGR00147	YP_186783.1	5.00101833
3470	F02	982	SACOL2342	magnesium and cobalt transport protein CorA, putative	YP_187148.1	5.151731161
3473	F04	985	SACOL0666	iron compound ABC transporter, permease protein	YP_185550.1	4.972588832
3475	F05	985	SACOL1920	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_186745.1	4.968527919
3477	F06	985	SACOL2030	sucrose operon repressor	YP_186848.1	4.841624365
3479	F07	988	SACOL0222	L-lactate dehydrogenase	YP_185120.1	4.893724696
3481	F08	988	SACOL1225	lipoprotein, putative	YP_186088.1	4.204453441
3483	F09	988	SACOL1524	conserved hypothetical protein	YP_186367.1	5.003036437
3485	F10	988	SACOL1810	conserved hypothetical protein TIGR01212	YP_186643.1	5.037449393
3487	F11	988	SACOL2296	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_187103.1	5.020242915
3489	F12	988	SACOL2302	transcriptional regulator, putative	YP_187109.1	4.245951417
3494	G01	991	SACOL0455	conserved hypothetical protein	YP_185345.1	5.120080727
3495	G02	991	SACOL0797	iron compound ABC transporter, permease protein	YP_185671.1	4.988900101
3498	G03	991	SACOL1462	thymidylate synthase	YP_186311.1	5.143289606
3499	G04	991	SACOL2713	rhodanese-like domain protein	YP_187499.1	4.98284561
3501	G05	994	SACOL0155	cation efflux family protein	YP_185055.1	4.932595573
3503	G06	994	SACOL0932	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_185802.1	4.870221328
3505	G07	994	SACOL1045	iron compound ABC transporter, iron compound-binding protein	YP_185910.1	4.973843058
3509	G09	994	SACOL1510	polyprenyl synthetase	YP_186354.1	5.021126761
3511	G10	994	SACOL2028	fructokinase, putative	YP_186846.1	4.838028169
3513	G11	994	SACOL2618	L-lactate dehydrogenase	YP_187407.1	5.017102616
3515	G12	994	SACOL2672	accessory secretory protein Asp3, putative	YP_187460.1	5.019114688
3517	H01	997	SACOL0999	oligopeptide ABC transporter, permease protein	YP_185867.1	5.006018054
3519	H02	997	SACOL1897	protein export protein PrsA, putative	YP_186723.1	4.974924774
3521	H03	997	SACOL2548	conserved hypothetical protein	YP_187340.1	4.977933801
3523	H04	1000	SACOL0544	ribose-phosphate pyrophosphokinase	YP_185432.1	4.97
3525	H05	1000	SACOL0599	conserved hypothetical protein	YP_185485.1	4.795
3528	H06	1000	SACOL0707	dihydroxyacetone kinase family protein	YP_185589.1	4.584
3529	H07	1000	SACOL1144	iron compound ABC transporter, permease protein, putative	YP_186007.1	4.954
3531	H08	1000	SACOL1195	phospho-N-acetylmuramoyl-pentapeptide-transferase	YP_186057.1	4.237

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3533	H09	1003	SACOL0198	conserved hypothetical protein	YP_185097.1	5.004985045
3535	H10	1003	SACOL0203	iron compound ABC transporter, iron compound-binding protein, putative	YP_185102.1	4.157527418
3537	H11	1003	SACOL0263	peptidoglycan hydrolase	YP_185158.1	4.058823529
3539	H12	1003	SACOL1519	L-asparaginase	YP_186362.1	4.808574277

Table 18: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 18 (ZSAJR), NR-19514[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3541	A01	1003	SACOL1746	6-phosphofructokinase	YP_186582.1	4.985044865
3547	A02	1003	SACOL2530	conserved hypothetical protein	YP_187323.1	4.957128614
3549	A03	1003	SACOL2549	esterase, putative	YP_187341.1	4.740777667
3551	A04	1006	SACOL0113	NAD-dependent epimerase/ dehydratase family protein	YP_185017.1	4.688866799
3554	A05	1006	SACOL0793	ribonucleoside-diphosphate reductase 2, beta subunit	YP_185667.1	4.505964215
3557	A07	1006	SACOL1291	riboflavin biosynthesis protein RibF	YP_186148.1	4.997017893
3563	A09	1009	SACOL1601	competence protein comGA, putative	YP_186441.1	5.008919723
3565	A10	1009	SACOL1643	DNA polymerase III, delta subunit	YP_186483.1	5.019821606
3567	A11	1009	SACOL1715	delta-aminolevulinic acid dehydratase	YP_186553.1	4.445986125
3570	A12	1012	SACOL0781	osmoprotectant ABC transporter, ATP-binding protein, putative	YP_185656.1	5.08201581
3571	B01	1012	SACOL1103	pyruvate dehydrogenase complex E1 component, beta subunit	YP_185967.1	4.945652174
3574	B02	1012	SACOL1371	GMP reductase	YP_186224.1	5.08201581
3575	B03	1012	SACOL1639	heat-inducible transcription repressor HrcA	YP_186479.1	4.867588933
3577	B04	1012	SACOL1927	conserved hypothetical protein	YP_186752.1	4.893280632
3579	B05	1012	SACOL2396	uroporphyrinogen III methylase SirB, putative	YP_187199.1	4.954545455
3584	B07	1015	SACOL0998	oligopeptide ABC transporter, ATP-binding protein	YP_185866.1	5.078817734
3586	B08	1015	SACOL1557	conserved hypothetical protein	YP_186398.1	5.079802956
3589	B09	1015	SACOL2183	tagatose 1,6-diphosphate aldolase	YP_186994.1	4.95270936
3591	B10	1018	SACOL0637	mevalonate diphosphate decarboxylase	YP_185522.1	4.933202358
3593	B11	1018	SACOL0764	glycosyl transferase, group 2 family protein	YP_185641.1	4.927308448
3595	B12	1018	SACOL1398	transcriptional regulator, putative	YP_186250.1	4.044204322
3597	C01	1018	SACOL1424	phosphate ABC transporter, phosphate-binding protein	YP_186276.1	4.784872299
3599	C02	1018	SACOL1561	2-oxoisovalerate dehydrogenase, E1 component, beta subunit	YP_186402.1	4.847740668
3603	C04	1018	SACOL2167	iron compound ABC transporter, iron compound-binding protein	YP_186979.1	4.919449902
3605	C05	1021	SACOL0034	methicillin-resistance MecR1 regulatory protein	YP_184945.1	4.916748286
3607	C06	1021	SACOL0078	1-phosphatidylinositol phosphodiesterase	YP_184983.1	4.953966699
3609	C07	1021	SACOL0634	phosphate acetyltransferase	YP_185519.1	4.8374143

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Master Clone List for NR-19277

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3611	C08	1021	SACOL0997	oligopeptide ABC transporter, ATP-binding protein	YP_185865.1	4.921645446
3613	C09	1021	SACOL1004	competence protein, putative	YP_185872.1	4.916748286
3615	C10	1021	SACOL1034	lipoate-protein ligase A family protein	YP_185899.1	4.941234084
3618	C11	1021	SACOL1243	fatty acid/phospholipid synthesis protein PlsX	YP_186103.1	5.100881489
3619	C12	1021	SACOL1417	peptide ABC transporter, permease protein	YP_186269.1	4.377081293
3621	D01	1021	SACOL1520	pyridine nucleotide-disulfide oxidoreductase	YP_186363.1	4.861900098
3623	D02	1021	SACOL1604	glucokinase	YP_186444.1	4.860920666
3625	D03	1021	SACOL1947	conserved hypothetical protein	YP_186772.1	4.806072478
3628	D04	1024	SACOL0012	homoserine O-acetyltransferase, putative	YP_184923.1	5.063476563
3629	D05	1024	SACOL1001	tryptophanyl-tRNA synthetase	YP_185869.1	4.876953125
3631	D06	1024	SACOL1429	aspartate-semialdehyde dehydrogenase	YP_186281.1	4.884765625
3633	D07	1024	SACOL1630	conserved hypothetical protein	YP_186470.1	4.870117188
3635	D08	1024	SACOL1786	catabolite control protein A	YP_186619.1	3.827148438
3637	D09	1027	SACOL0099	iron compound ABC transporter, iron compound-binding protein SirA	YP_185004.1	4.934761441
3639	D10	1027	SACOL0262	Ccholoylglycine hydrolase family protein	YP_185157.1	4.102239533
3641	D11	1027	SACOL1562	2-oxoisovalerate dehydrogenase, E1 component, alpha subunit	YP_186403.1	4.911392405
3643	D12	1027	SACOL2003	phospholipase C	YP_186826.1	3.808179163
3645	E01	1027	SACOL2535	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_187328.1	4.842259007
3647	E02	1030	SACOL0098	iron compound ABC transporter, permease protein SirB	YP_185003.1	3.987378641
3650	E03	1030	SACOL0411	membrane protein, putative	YP_185303.1	5.02815534
3651	E04	1030	SACOL0831	conserved hypothetical protein	YP_185705.1	4.894174757
3653	E05	1030	SACOL1847	conserved domain protein, putative	YP_186678.1	4.906796117
3655	E06	1033	SACOL0097	iron compound ABC transporter, permease protein SirC	YP_185002.1	3.818005808
3657	E07	1033	SACOL0101	ornithine cyclodeaminase, putative	YP_185006.1	4.918683446
3659	E08	1033	SACOL0257	ribose operon repressor, putative	YP_185152.1	4.907066796
3661	E09	1033	SACOL1405	anthranilate phosphoribosyltransferase	YP_186257.1	4.878025169
3663	E10	1033	SACOL1514	glycerol-3-phosphate dehydrogenase, NAD-dependent	YP_186358.1	4.896418199
3665	E11	1033	SACOL2574	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_187366.1	4.869312682
3667	E12	1036	SACOL0394	conserved hypothetical protein	YP_185286.1	4.834942085
3669	F01	1036	SACOL1181	ornithine carbamoyltransferase	YP_186044.1	4.857142857
3673	F02	1036	SACOL1843	o-succinylbenzoic acid (OSB) synthetase, putative	YP_186674.1	4.923745174
3675	F03	1036	SACOL2057	sigma factor B regulator protein	YP_186873.1	4.894787645
3679	F04	1036	SACOL2178	alcohol dehydrogenase, zinc-containing	YP_186989.1	4.907335907
3681	F05	1039	SACOL0507	LysM domain protein	YP_185395.1	5.602502406
3683	F06	1039	SACOL0705	iron compound ABC transporter, permease protein	YP_185587.1	5.518768046
3685	F07	1039	SACOL0777	urea amidolyase-related protein	YP_185652.1	5.948026949

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3687	F08	1039	SACOL1696	Holliday junction DNA helicase RuvB	YP_186535.1	5.963426372
3689	F09	1039	SACOL2045	ketol-acid reductoisomerase	YP_186862.1	5.980750722
3692	F10	1039	SACOL2269	molybdopterin biosynthesis MoeB protein, putative	YP_187076.1	5.856592878
3693	F11	1039	SACOL2367	quinone oxidoreductase, YhdH/YhfP family	YP_187172.1	5.235803657
3695	F12	1042	SACOL0569	ATP:guanido phosphotransferase family protein	YP_185457.1	5.850287908
3697	G01	1042	SACOL0722	phosphate transporter family protein	YP_185603.1	5.780230326
3699	G02	1042	SACOL2426	biotin synthetase	YP_187228.1	4.025911708
3701	G03	1045	SACOL0660	alcohol dehydrogenase, zinc-containing	YP_185544.1	5.213397129
3704	G04	1045	SACOL0838	glyceraldehyde 3-phosphate dehydrogenase	YP_185712.1	5.849760766
3705	G05	1045	SACOL1057	V8 Protease	YP_185922.1	5.988516746
3707	G06	1045	SACOL1059	conserved hypothetical protein	YP_185924.1	5.954066986
3710	G07	1045	SACOL1663	urea amidolyase-related protein	YP_186503.1	5.745454545
3711	G08	1045	SACOL2596	conserved hypothetical protein	YP_187387.1	6.004784689
3713	G09	1045	SACOL2656	ornithine carbamoyltransferase	YP_187444.1	5.523444976
3715	G10	1048	SACOL0837	gap transcriptional regulator	YP_185711.1	5.915076336
3717	G11	1048	SACOL1678	bacterial luciferase family protein	YP_186518.1	5.458015267
3719	G12	1048	SACOL2701	histidinol-phosphate aminotransferase, putative	YP_187487.1	5.088740458
3721	H01	1051	SACOL0706	iron compound ABC transporter, permease protein	YP_185588.1	5.893434824
3723	H02	1054	SACOL1095	cytochrome d ubiquinol oxidase, subunit II	YP_185959.1	5.509487666
3725	H03	1054	SACOL1112	conserved hypothetical protein	YP_185976.1	5.95256167
3728	H04	1054	SACOL1552	maltose operon repressor	YP_186393.1	5.714421252
3729	H05	1054	SACOL2332	aldose 1-epimerase	YP_187139.1	5.95256167
3732	H06	1055	SACOL1573	integrase/recombinase, core domain family, authentic frameshift	-	5.545023697
3733	H07	1057	SACOL0398	lipoate-protein ligase A family protein	YP_185290.1	5.947019868
3736	H08	1057	SACOL0858	secretory extracellular matrix and plasma binding protein	YP_185731.1	5.750236518
3739	H09	1060	SACOL0162	formate dehydrogenase, NAD-dependent	YP_185061.1	5.967924528
3741	H10	1060	SACOL0237	alcohol dehydrogenase, zinc-containing	YP_185133.1	5.900943396
3743	H11	1060	SACOL0241	alcohol dehydrogenase, zinc-containing	YP_185137.1	5.833018868
3745	H12	1060	SACOL0399	oxidoreductase, putative	YP_185291.1	5.128301887

Table 19: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 19 (ZSAJS), NR-19515[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3747	A01	1060	SACOL0504	ABC transporter, ATP-binding protein	YP_185392.1	5.947169811
3749	A02	1060	SACOL0882	ABC transporter, ATP-binding protein	YP_185753.1	5.971698113
3752	A03	1060	SACOL1349	conserved hypothetical protein	YP_186202.1	5.399056604
3753	A04	1060	SACOL1695	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	YP_186534.1	5.967924528

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3755	A05	1060	SACOL1734	glyceraldehyde 3-phosphate dehydrogenase	YP_186571.1	5.987735849
3757	A06	1060	SACOL2038	metalloendopeptidase, putative, glycoprotease family	YP_186855.1	5.933962264
3759	A07	1063	SACOL0140	capsular polysaccharide biosynthesis protein Cap5E	YP_185040.1	5.952963311
3761	A08	1063	SACOL0799	transferrin receptor	YP_185673.1	5.466603951
3763	A09	1063	SACOL1080	phosphoribosylformylglycinamidine cyclo-ligase	YP_185944.1	5.939793039
3765	A10	1063	SACOL1985	conserved hypothetical protein	YP_186809.1	5.898400753
3767	A11	1066	SACOL0160	conserved hypothetical protein	YP_185059.1	5.85272045
3769	A12	1066	SACOL0169	N-acetyl-gamma-glutamyl-phosphate reductase	YP_185068.1	5.045028143
3772	B01	1066	SACOL0307	perfringolysin O regulator protein	YP_185199.1	4.695121951
3773	B02	1066	SACOL1402	glutamyl aminopeptidase, putative	YP_186254.1	5.948405253
3775	B03	1066	SACOL2166	iron compound ABC transporter, permease protein	YP_186978.1	5.785178236
3779	B04	1069	SACOL2390	sensory box histidine kinase, putative	YP_187193.1	4.882132834
3781	B05	1072	SACOL1889	uroporphyrinogen decarboxylase	YP_186715.1	5.259328358
3783	B06	1072	SACOL1926	A/G-specific adenine glycosylase	YP_186751.1	5.844216418
3785	B07	1075	SACOL0197	oxidoreductase, Gfo/Idh/MocA family	YP_185096.1	5.909767442
3787	B08	1075	SACOL0717	sensor histidine kinase	YP_185599.1	5.92372093
3789	B09	1075	SACOL0921	CBS domain protein	YP_185792.1	5.586046512
3791	B10	1075	SACOL1477	threonine dehydratase, catabolic	YP_186322.1	5.83627907
3793	B11	1075	SACOL1988	acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase	YP_186812.1	5.844651163
3795	B12	1078	SACOL0235	hexitol dehydrogenase	YP_185131.1	5.866419295
3797	C01	1078	SACOL0712	lipase/esterase	YP_185594.1	5.882189239
3799	C02	1078	SACOL1304	recA protein	YP_186161.1	5.634508349
3801	C03	1078	SACOL1820	riboflavin biosynthesis protein RibD	YP_186652.1	5.907235622
3804	C04	1078	SACOL1943	sensor histidine kinase VraS	YP_186768.1	4.32096475
3805	C05	1078	SACOL2546	perfringolysin O regulator protein, putative	YP_187338.1	5.653988868
3807	C06	1081	SACOL1576	traG protein, putative	YP_186416.1	5.882516189
3809	C07	1081	SACOL2047	3-isopropylmalate dehydrogenase	YP_186864.1	5.452358927
3811	C08	1084	SACOL0305	ABC transporter, permease protein	YP_185197.1	5.885608856
3813	C09	1084	SACOL2341	isopentenyl diphosphate isomerase	YP_187147.1	5.857933579
3815	C10	1086	SACOL2692	intercellular adhesion protein C, authentic frameshift	-	5.821362799
3817	C11	1087	SACOL1140	LPXTG cell wall surface anchor protein	YP_186003.1	5.785648574
3819	C12	1087	SACOL2721	high-affinity nickel-transport protein	YP_187507.1	5.833486661
3821	D01	1090	SACOL0176	conserved hypothetical protein	YP_185075.1	5.851376147
3824	D02	1090	SACOL0233	sorbitol dehydrogenase	YP_185129.1	5.277981651
3825	D03	1090	SACOL0765	sensor histidine kinase SaeS	YP_185642.1	5.634862385
3827	D04	1090	SACOL0810	glycosyl transferase, group 4 family protein	YP_185684.1	4.008256881
3829	D05	1090	SACOL1582	conserved hypothetical protein	YP_186422.1	4.070642202
3831	D06	1090	SACOL1756	proline dipeptidase	YP_186590.1	4.799082569
3835	D08	1090	SACOL2108	Sua5/YciO/YrdC/YwlC family protein	YP_186923.1	5.85412844
3837	D09	1090	SACOL2357	ABC transporter, permease protein	YP_187162.1	5.811926606
3839	D10	1090	SACOL2585	regulatory protein, putative	YP_187377.1	5.040366972
3845	D12	1093	SACOL1148	phenylalanyl-tRNA synthetase, alpha subunit	YP_186011.1	5.628545288
3848	E01	1096	SACOL0409	conserved hypothetical protein	YP_185301.1	5.76459854
3849	E02	1096	SACOL0697	teichoic acid biosynthesis protein X	YP_185579.1	5.823905109
3853	E03	1096	SACOL1588	proline dipeptidase	YP_186428.1	5.011861314
3855	E04	1096	SACOL1917	PTS system, IIC component	YP_186742.1	5.864051095
3858	E05	1099	SACOL1505	3-dehydroquinate synthase	YP_186349.1	5.403093722
3859	E06	1099	SACOL2156	ATP-binding protein, Mrp/Nbp35 family	YP_186968.1	4.98544131

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3861	E07	1099	SACOL2606	dihydroorotate dehydrogenase	YP_187396.1	5.761601456
3863	E08	1100	SACOL0941	NADH dehydrogenase, putative, authentic frameshift	-	4.879090909
3867	E09	1102	SACOL0063	conserved hypothetical protein	YP_184968.1	5.831215971
3870	E10	1102	SACOL0711	conserved hypothetical protein	YP_185593.1	5.323049002
3871	E11	1102	SACOL0922	conserved hypothetical protein	YP_185793.1	5.863883848
3873	E12	1105	SACOL0809	GGDEF domain protein	YP_185683.1	5.865158371
3877	F01	1105	SACOL1124	cytochrome oxidase assembly protein	YP_185988.1	5.012669683
3879	F02	1105	SACOL1453	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	YP_186305.1	5.721266968
3881	F03	1105	SACOL1600	competence protein ComGB, putative	YP_186440.1	5.833484163
3884	F04	1105	SACOL1955	DNA-damage-inducible protein P	YP_186780.1	4.847963801
3885	F05	1105	SACOL2074	D-alanine--D-alanine ligase	YP_186890.1	5.752941176
3887	F06	1105	SACOL2168	conserved hypothetical protein	YP_186980.1	5.753846154
3892	F07	1108	SACOL0573	PIN/TRAM domain protein	YP_185459.1	5.767148014
3894	F08	1108	SACOL1111	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein	YP_185975.1	5.315884477
3895	F09	1108	SACOL1712	abrB protein abrB protein, putative	YP_186551.1	5.873646209
3897	F10	1111	SACOL0196	oxidoreductase, Gfo/Idh/MocA family	YP_185095.1	5.832583258
3899	F11	1111	SACOL0600	branched-chain amino acid aminotransferase	YP_185486.1	5.02520252
3901	F12	1111	SACOL0638	phosphomevalonate kinase	YP_185523.1	5.891989199
3903	G01	1111	SACOL1142	hypothetical protein	YP_186005.1	4.99909991
3907	G02	1111	SACOL1976	nitric-oxide synthase, oxygenase subunit	YP_186800.1	5.815481548
3909	G03	1111	SACOL2110	peptide chain release factor 1	YP_186925.1	5.767776778
3911	G04	1111	SACOL2463	glutamyl-aminopeptidase	YP_187261.1	5.760576058
3913	G05	1114	SACOL2034	conserved hypothetical protein	YP_186851.1	5.831238779
3915	G06	1114	SACOL2528	conserved hypothetical protein	YP_187321.1	5.828545781
3917	G07	1117	SACOL0813	comf operon protein 1, putative	YP_185687.1	5.607878245
3920	G08	1117	SACOL0993	oligopeptide ABC transporter, ATP-binding protein	YP_185861.1	5.794091316
3923	G10	1120	SACOL1017	conserved hypothetical protein	YP_185883.1	5.56875
3925	G11	1120	SACOL1434	alanine racemase family protein	YP_186286.1	5.591964286
3929	G12	1126	SACOL1401	prephenate dehydrogenase	YP_186253.1	5.826820604
3931	H01	1126	SACOL1583	replication initiation factor family protein	YP_186423.1	3.846358792
3934	H02	1126	SACOL1595	glycine cleavage system T protein	YP_186435.1	5.703374778
3935	H03	1126	SACOL1787	chorismate mutase/phospho-2-dehydro-3-deoxyheptonate aldolase	YP_186620.1	5.726465364
3937	H04	1129	SACOL1108	spermidine/putrescine ABC transporter, ATP-binding protein	YP_185972.1	5.748449956
3939	H05	1129	SACOL1230	conserved hypothetical protein TIGR00048	YP_186093.1	5.469441984
3941	H06	1129	SACOL1923	conserved hypothetical protein	YP_186748.1	5.8255093
3943	H07	1132	SACOL0192	maltose ABC transporter, ATP-binding protein, putative	YP_185091.1	4.786219081
3945	H08	1132	SACOL0435	conserved hypothetical protein TIGR00092	YP_185326.1	5.787985866
3947	H09	1132	SACOL1980	conserved hypothetical protein	YP_186804.1	4.465547703
3949	H10	1135	SACOL1070	cytochrome aa3 quinol oxidase, subunit II	YP_185934.1	5.47753304
3951	H11	1135	SACOL1214	carbamoyl-phosphate synthase, small subunit	YP_186077.1	4.727753304
3953	H12	1135	SACOL1616	conserved hypothetical protein TIGR00486	YP_186456.1	4.873127753

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Table 20: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 20 (ZSAJT), NR-19516[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
3955	A01	1135	SACOL1653	GTP-binding protein, putative	YP_186493.1	5.584140969
3957	A02	1138	SACOL0431	trans-sulfuration enzyme family protein	YP_185322.1	5.508787346
3959	A03	1138	SACOL0696	teichoic acid biosynthesis protein B	YP_185578.1	5.681898067
3961	A04	1141	SACOL1618	RNA polymerase sigma factor RpoD	YP_186458.1	5.751971954
3965	A05	1141	SACOL2600	conserved hypothetical protein	YP_187391.1	5.328659071
3967	A06	1144	SACOL0141	capsular polysaccharide biosynthesis protein Cap5F	YP_185041.1	5.659965035
3969	A07	1144	SACOL0144	capsular polysaccharide biosynthesis protein Cap5I	YP_185044.1	5.401223776
3971	A08	1145	SACOL0818	peptide chain release factor 2, programmed frameshift	YP_185692.1	5.681222707
3973	A09	1147	SACOL0004	recF protein	YP_184915.1	5.778552746
3976	A10	1147	SACOL0183	hypothetical protein	YP_185082.1	5.683522232
3977	A11	1147	SACOL0512	conserved hypothetical protein	YP_185400.1	5.780296425
3979	A12	1147	SACOL1102	pyruvate dehydrogenase complex E1 component, alpha subunit	YP_185966.1	5.748038361
3981	B01	1147	SACOL1906	sensor histidine kinase, putative	YP_186731.1	5.683522232
3983	B02	1147	SACOL2496	conserved hypothetical protein	YP_187291.1	5.676547515
3985	B03	1148	SACOL2140	lytic regulatory protein, authentic frameshift	-	5.716898955
3989	B04	1153	SACOL0308	carbohydrate kinase, PfkB family	YP_185200.1	5.753686036
3991	B05	1153	SACOL0983	hypothetical protein	YP_185851.1	5.797918474
3994	B06	1153	SACOL1478	alanine dehydrogenase	YP_186323.1	5.210754553
3996	B07	1153	SACOL1676	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	YP_186516.1	5.147441457
3997	B08	1153	SACOL1758	alanine dehydrogenase	YP_186592.1	5.749349523
3999	B09	1156	SACOL1381	exonuclease SbcD	YP_186234.1	5.711937716
4001	B10	1156	SACOL1742	citrate synthase	YP_186579.1	5.74567474
4003	B11	1156	SACOL2322	peptidase, M20/M25/M40 family	YP_187129.1	5.729238754
4006	B12	1159	SACOL0142	UDP-N-acetylglucosamine 2-epimerase Cap5G	YP_185042.1	5.195858499
4008	C01	1159	SACOL0805	glycerate kinase family protein	YP_185679.1	5.635893011
4009	C02	1159	SACOL1074	phosphoribosylaminoimidazole carboxylase, ATPase subunit	YP_185938.1	5.631578947
4012	C03	1159	SACOL1465	conserved hypothetical protein	YP_186313.1	5.692838654
4014	C04	1159	SACOL1903	conserved hypothetical protein	YP_186728.1	5.705780846
4015	C05	1159	SACOL2297	monooxygenase family protein	YP_187104.1	5.756686799
4018	C06	1159	SACOL2705	lipoprotein, putative	YP_187491.1	5.701466782
4022	C07	1162	SACOL1914	iron-sulfur cluster-binding protein, putative	YP_186739.1	5.688468158
4024	C08	1162	SACOL2103	UDP-N-acetylglucosamine 2-epimerase	YP_186918.1	5.264199656
4026	C09	1165	SACOL1774	hydrolase, haloacid dehalogenase-like family	YP_186608.1	5.298712446
4027	C10	1168	SACOL0002	DNA polymerase III, beta subunit	YP_184913.1	5.52140411
4030	C11	1168	SACOL0425	hypothetical protein	YP_185316.1	5.328767123
4032	C12	1168	SACOL1555	peptidase, M20/M25/M40 family	YP_186396.1	5.530821918
4033	D01	1171	SACOL1441	tellurite resistance protein, putative	YP_186293.1	4.860802733
4035	D02	1171	SACOL2142	SAP domain protein	YP_186955.1	5.489325363
4042	D03	1174	SACOL0622	acetyl-CoA acetyltransferase	YP_185507.1	5.533219762
4043	D04	1174	SACOL1135	conserved hypothetical protein	YP_185999.1	5.322827939
4045	D05	1174	SACOL1636	dnaJ protein	YP_186476.1	5.666950596
4047	D06	1174	SACOL1694	queuine tRNA-ribosyltransferase	YP_186533.1	5.517035775
4049	D07	1174	SACOL1765	aminotransferase, class V	YP_186599.1	5.556218058
4051	D08	1177	SACOL0216	hypothetical protein	YP_185115.1	4.177570093
4053	D09	1177	SACOL0503	trans-sulfuration enzyme family protein	YP_185391.1	5.528462192
4055	D10	1177	SACOL1677	aminotransferase, class V	YP_186517.1	4.733220051

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4057	D11	1177	SACOL2435	glycerate kinase	YP_187236.1	5.573491929
4059	D12	1180	SACOL0220	flavohemoprotein, putative	YP_185119.1	5.520338983
4061	E01	1180	SACOL0981	isopropylmalate synthase-related protein	YP_185849.1	5.528813559
4063	E02	1180	SACOL1483	conserved hypothetical protein	YP_186328.1	5.542372881
4065	E03	1183	SACOL2060	alanine racemase	YP_186876.1	4.775993238
4068	E04	1186	SACOL1264	cell wall hydrolase	YP_186122.1	5.522765599
4069	E05	1186	SACOL1303	competence/damage-inducible protein CinA	YP_186160.1	4.65851602
4071	E06	1186	SACOL1433	peptidase, M20/M25/M40 family	YP_186285.1	4.333895447
4073	E07	1186	SACOL1935	conserved hypothetical protein	YP_186760.1	4.021922428
4079	E08	1189	SACOL1498	glycosyl transferase, group 1 family protein	YP_186342.1	4.991589571
4081	E09	1189	SACOL2278	acyl-CoA dehydrogenase-related protein	YP_187085.1	5.523969722
4085	E10	1192	SACOL1640	oxygen-independent coproporphyrinogen III oxidase, putative	YP_186480.1	5.598993289
4089	E11	1195	SACOL1772	aminotransferase, class V	YP_186606.1	5.272803347
4091	E12	1198	SACOL0186	peptide ABC transporter, permease protein	YP_185085.1	5.535893155
4093	F01	1198	SACOL0370	prophage L54a, major capsid protein, putative	YP_185262.1	5.571786311
4095	F02	1198	SACOL2523	drug transporter, putative	YP_187317.1	5.48163606
4097	F03	1201	SACOL0115	glycosyl transferase, group 1 family protein	YP_185019.1	5.522897585
4099	F04	1201	SACOL0145	capsular polysaccharide biosynthesis protein Cap5J	YP_185045.1	5.538717735
4103	F06	1201	SACOL0754	multi drug resistance protein (norA)	YP_185633.1	5.412156536
4105	F07	1201	SACOL1262	succinyl-CoA synthase, beta subunit	YP_186120.1	5.512905912
4107	F08	1201	SACOL1506	chorismate synthase	YP_186350.1	5.244796003
4109	F09	1201	SACOL1970	cysteine protease precursor SspB	YP_186794.1	5.529558701
4111	F10	1201	SACOL2561	hydroxymethylglutaryl-CoA synthase	YP_187353.1	5.538717735
4114	F11	1204	SACOL0239	TagF domain protein	YP_185135.1	5.431893688
4115	F12	1204	SACOL1785	acetoin utilization protein AcuC	YP_186618.1	5.056478405
4119	G01	1207	SACOL1089	conserved hypothetical protein	YP_185953.1	4.531068766
4121	G02	1207	SACOL1199	cell division protein FtsZ	YP_186061.1	5.507042254
4123	G03	1210	SACOL0151	UDP-N-acetylglucosamine 2-epimerase Cap5P	YP_185051.1	5.574380165
4125	G04	1210	SACOL0595	peptidase, M20/M25/M40 family	YP_185481.1	4.42892562
4127	G05	1210	SACOL0938	DltD protein	YP_185808.1	5.534710744
4129	G06	1210	SACOL1022	ypfP protein	YP_185888.1	5.317355372
4131	G07	1210	SACOL1285	N utilization substance protein A, putative	YP_186142.1	5.482644628
4133	G08	1210	SACOL1516	ribosomal protein S1	YP_186360.1	5.628099174
4135	G09	1213	SACOL0085	peptidase, M20/M25/M40 family	YP_184990.1	5.636438582
4137	G10	1213	SACOL0124	phosphopentomutase	YP_185028.1	5.586974444
4139	G11	1216	SACOL0426	acetyl-CoA acetyltransferase	YP_185317.1	5.606085526
4141	G12	1216	SACOL0761	N-acetylglucosamine-6-phosphate deacetylase	YP_185638.1	5.631578947
4143	H01	1216	SACOL1056	cysteine protease precursor SspB	YP_185921.1	5.547697368
4145	H02	1216	SACOL1809	drug transporter, putative	YP_186642.1	5.601151316
4147	H03	1216	SACOL1818	3,4-dihydroxy-2-butanone-4-phosphate synthase/GTP cyclohydrolase II	YP_186650.1	5.582236842
4149	H04	1219	SACOL0170	ornithine aminotransferase	YP_185069.1	5.49466776
4151	H05	1219	SACOL0211	acetyl-CoA acetyltransferase	YP_185110.1	5.484003281
4154	H06	1219	SACOL0594	translation elongation factor Tu	YP_185480.1	5.471698113
4155	H07	1219	SACOL2125	peptidase, M20/M25/M40 family	YP_186940.1	5.529122231
4157	H08	1222	SACOL0596	aminotransferase, class II	YP_185482.1	5.5400982
4160	H09	1222	SACOL2161	UTP-glucose-1-phosphate uridylyltransferase family protein	YP_186973.1	5.430441899
4161	H10	1222	SACOL2460	drug transporter, putative	YP_187258.1	5.51391162
4163	H11	1225	SACOL0839	phosphoglycerate kinase	YP_185713.1	5.537959184
4167	H12	1225	SACOL1021	membrane protein, putative	YP_185887.1	5.51755102

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Table 21: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 21 (ZSAJU), NR-19517[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4169	A01	1228	SACOL0065	conserved hypothetical protein	YP_184970.1	4.806188925
4171	A02	1228	SACOL0549	tetrapyrrole methylase family protein	YP_185437.1	5.46009772
4173	A03	1228	SACOL1066	fmt protein	YP_185930.1	4.475570033
4176	A04	1228	SACOL1837	S-adenosylmethionine synthetase	YP_186668.1	4.813517915
4177	A05	1228	SACOL2124	conserved hypothetical protein	YP_186939.1	5.258143322
4179	A06	1228	SACOL2170	transporter, putative	YP_186982.1	5.460912052
4182	A07	1228	SACOL2471	transporter, putative	YP_187268.1	4.108306189
4185	A08	1231	SACOL1900	DNA repair exonuclease family protein	YP_186726.1	5.538586515
4187	A09	1234	SACOL0392	NADH-dependent flavin oxidoreductase, Oye family	YP_185284.1	5.576985413
4190	A10	1234	SACOL1861	type I restriction-modification enzyme, S subunit, EcoA family	YP_186689.1	4.691247974
4191	A11	1234	SACOL1964	Staphylococcus aureus sex pheromone	YP_186788.1	5.534846029
4194	A12	1237	SACOL0107	pyridoxal-dependent decarboxylase	YP_185011.1	5.452708165
4195	B01	1237	SACOL0491	cobalamin synthesis protein, putative	YP_185381.1	5.554567502
4198	B02	1237	SACOL1497	polyA polymerase	YP_186341.1	5.444624091
4199	B03	1237	SACOL1760	acetate kinase	YP_186594.1	5.035569927
4201	B04	1237	SACOL2075	cell division protein, FtsW/RodA/SpoVE family	YP_186891.1	5.446240905
4204	B05	1237	SACOL2155	IS1181, transposase, authentic point mutation	N/A	5.423605497
4211	B08	1240	SACOL0964	argininosuccinate synthase	YP_185833.1	5.488709677
4213	B09	1240	SACOL1223	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	YP_186086.1	5.511290323
4215	B10	1240	SACOL1428	aspartokinase, alpha and beta subunits	YP_186280.1	5.467741935
4217	B11	1243	SACOL0944	NADH dehydrogenase, putative	YP_185813.1	5.2614642
4221	B12	1243	SACOL2340	sodium:glutamate symporter	YP_187146.1	5.420756235
4223	C01	1243	SACOL2350	tcaB protein	YP_187156.1	4.66773934
4226	C02	1246	SACOL0213	acyl-CoA dehydrogenase family protein	YP_185112.1	5.376404494
4229	C03	1246	SACOL1051	isochorismate synthase family protein	YP_185916.1	5.504815409
4231	C04	1246	SACOL2257	drug transporter, putative	YP_187064.1	5.128410915
4233	C05	1246	SACOL2437	bicyclomycin resistance protein	YP_187238.1	5.46388443
4236	C06	1246	SACOL2675	SecY/Sec61-alpha family protein	YP_187463.1	5.453451043
4238	C07	1249	SACOL0566	nucleoside permease NupC	YP_185454.1	5.444355484
4239	C08	1249	SACOL0936	DltB protein	YP_185806.1	5.254603683
4241	C09	1249	SACOL1408	tryptophan synthase, beta subunit	YP_186260.1	5.470776621
4243	C10	1249	SACOL2477	conserved hypothetical protein	YP_187274.1	5.496397118
4245	C11	1252	SACOL1065	transcriptional regulator, putative	YP_185929.1	5.39057508
4247	C12	1252	SACOL1941	YihY family protein	YP_186766.1	5.424920128
4250	D01	1255	SACOL0070	permease, putative	YP_184975.1	4.956175299
4251	D02	1255	SACOL0310	nucleoside permease NupC, putative	YP_185202.1	4.706772908
4253	D03	1255	SACOL0733	sugar efflux transporter, putative	YP_185612.1	5.485258964
4255	D04	1255	SACOL0885	pathogenicity island protein, integrase	YP_185756.1	5.50438247
4257	D05	1255	SACOL1658	hypothetical protein	YP_186498.1	4.827091633
4259	D06	1258	SACOL1764	thiamine biosynthesis protein ThiI	YP_186598.1	5.461844197
4262	D07	1258	SACOL1892	membrane protein, putative	YP_186718.1	5.348171701
4266	D08	1261	SACOL0806	peptidase T	YP_185680.1	4.749405234
4267	D09	1261	SACOL1122	cell division protein,FtsW/RodA/SpoVE family	YP_185986.1	5.440126883
4269	D10	1261	SACOL2453	amino acid ABC transporter, ATP-binding protein	YP_187252.1	5.395717684
4271	D11	1264	SACOL0415	Dyp-type peroxidase family protein	YP_185307.1	5.393196203
4273	D12	1264	SACOL0701	nucleoside permease NupC, putative	YP_185583.1	5.484177215
4275	E01	1264	SACOL1659	conserved hypothetical protein	YP_186499.1	5.416139241

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4277	E02	1264	SACOL1749	NADP-dependent malic enzyme, putative	YP_186585.1	5.524525316
4279	E03	1267	SACOL2334	conserved hypothetical protein	YP_187141.1	5.505919495
4281	E04	1270	SACOL2657	arginine deiminase	YP_187445.1	5.446456693
4283	E05	1273	SACOL0116	hypothetical protein	YP_185020.1	5.488609584
4286	E06	1273	SACOL0368	prophage L54a, portal protein, HK97 family	YP_185260.1	5.352710134
4287	E07	1273	SACOL1326	GTP-binding protein, putative	YP_186181.1	5.417910448
4291	E08	1273	SACOL2105	serine hydroxymethyltransferase	YP_186920.1	5.44854674
4293	E09	1273	SACOL2323	imidazolonepropionase	YP_187130.1	5.355852317
4295	E10	1273	SACOL2689	intercellular adhesion protein A	YP_187476.1	5.418695994
4299	E11	1276	SACOL0343	prophage L54a, replicative DNA helicase, putative	YP_185235.1	5.394200627
4301	E12	1276	SACOL0916	cysteine desulfurase, SufS subfamily	YP_185787.1	5.442789969
4303	F01	1276	SACOLA0003	plasmid recombination enzyme		5.45846395
4305	F02	1279	SACOL0961	glutamate dehydrogenase, NAD-specific	YP_185830.1	4.826426896
4307	F03	1279	SACOL0988	3-oxoacyl-(acyl-carrier-protein) synthase II	YP_185856.1	4.709147772
4309	F04	1279	SACOL1265	endopeptidase resistance gene	YP_186123.1	5.451915559
4311	F05	1279	SACOL1503	TPR domain protein	YP_186347.1	5.366692729
4313	F06	1279	SACOL1876	epidermin biosynthesis protein EpiC, authentic point mutation	-	5.388584832
4318	F07	1285	SACOL0163	drug transporter, putative	YP_185062.1	4.572762646
4319	F08	1285	SACOL1251	cell division protein FtsY, putative	YP_186110.1	5.357198444
4321	F09	1285	SACOL2031	ammonium transporter family protein	YP_186849.1	5.33229572
4323	F10	1285	SACOL2409	fmhA protein	YP_187212.1	5.339299611
4325	F11	1291	SACOL0103	drug transporter, putative	YP_185008.1	6.298993029
4327	F12	1291	SACOL1937	aminopeptidase PepS	YP_186762.1	6.336948102
4329	G01	1291	SACOL2702	histidinol dehydrogenase	YP_187488.1	6.355538342
4331	G02	1294	SACOL0232	PTS system, sorbitol-specific IIC component	YP_185128.1	6.390262751
4333	G03	1294	SACOL1411	femB protein	YP_186263.1	6.35316847
4335	G04	1294	SACOL2019	sdrH protein, putative	YP_186838.1	5.5
4337	G05	1294	SACOL2116	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	YP_186931.1	6.343122102
4339	G06	1294	SACOL2266	molybdopterin biosynthesis MoeA protein, putative	YP_187073.1	6.230293663
4343	G07	1297	SACOL0150	capsular polysaccharide biosynthesis protein Cap5O	YP_185050.1	6.240555127
4345	G08	1297	SACOL1400	ImpB/MucB/SamB family protein	YP_186252.1	6.33461835
4347	G09	1297	SACOL1686	histidyl-tRNA synthetase	YP_186525.1	6.117193524
4349	G10	1297	SACOL1721	ATP-dependent Clp protease, ATP-binding subunit ClpX	YP_186559.1	6.064764842
4351	G11	1297	SACOL1778	tyrosyl-tRNA synthetase	YP_186612.1	6.32767926
4353	G12	1300	SACOL1297	conserved hypothetical protein	YP_186154.1	5.268461538
4355	H01	1300	SACOL1435	diaminopimelate decarboxylase	YP_186287.1	6.335384615
4357	H02	1300	SACOL2092	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	YP_186907.1	6.28
4360	H03	1300	SACOL2253	femX protein	YP_187061.1	6.311538462
4361	H04	1303	SACOL0194	maltose ABC transporter, permease protein	YP_185093.1	6.304681504
4363	H05	1303	SACOL0459	xanthine permease	YP_185349.1	6.306983883
4365	H06	1303	SACOL1448	2-oxoglutarate dehydrogenase, E2 component, dihydroipoamide succinyltransferase	YP_186300.1	6.34228703
4368	H07	1303	SACOL1667	peptidase, U32 family	YP_186507.1	6.256331543
4369	H08	1303	SACOL1741	isocitrate dehydrogenase, NADP-dependent	YP_186578.1	6.307751343
4372	H09	1303	SACOL1805	conserved hypothetical protein TIGR00275	YP_186638.1	6.228702993
4374	H10	1303	SACOL2050	threonine dehydratase	YP_186867.1	6.253261704

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4376	H11	1306	SACOL0193	maltose ABC transporter, maltose-binding protein, putative	YP_185092.1	5.797090352
4377	H12	1306	SACOL1709	folylpolyglutamate synthase/dihydrofolate synthase	YP_186548.1	6.30704441

Table 22: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 22 (ZSAJV), NR-19518[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4381	A01	1309	SACOL1560	2-oxoisovalerate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	YP_186401.1	6.28342246
4383	A02	1309	SACOL1682	ATPase, AAA family	YP_186522.1	6.332314744
4385	A03	1309	SACOL1777	serine protease HtrA, putative	YP_186611.1	6.30328495
4387	A04	1312	SACOL2373	conserved hypothetical protein	YP_187177.1	5.598323171
4390	A05	1312	SACOL2382	proton/sodium-glutamate symport protein	YP_187186.1	6.298780488
4391	A06	1312	SACOL2521	transporter, putative	YP_187315.1	5.292682927
4393	A07	1312	SACOL2560	hydroxymethylglutaryl-CoA reductase, degradative	YP_187352.1	5.352896341
4395	A08	1315	SACOL1362	homoserine dehydrogenase	YP_186215.1	6.40608365
4398	A09	1318	SACOL0018	adenylosuccinate synthetase	YP_184929.1	6.3323217
4400	A10	1321	SACOL0009	seryl-tRNA synthetase	YP_184920.1	6.333838002
4401	A11	1321	SACOL1281	membrane-associated zinc metalloprotease, putative	YP_186138.1	5.955336866
4404	A12	1321	SACOL1298	peptidase, M16 family	YP_186155.1	6.305071915
4409	B01	1324	SACOL1922	glutamate-1-semialdehyde-2,1-aminomutase	YP_186747.1	6.019637462
4412	B02	1327	SACOL1104	pyruvate dehydrogenase complex E2 component, dihydrolipoamide acetyltransferase	YP_185968.1	6.010550113
4415	B03	1327	SACOL1699	GTP-binding protein, GTP1/OBG family	YP_186538.1	6.441597589
4421	B04	1327	SACOL2219	preprotein translocase, SecY subunit	YP_187029.1	6.171816127
4423	B05	1330	SACOL0026	conserved hypothetical protein	YP_184937.1	6.515789474
4425	B06	1330	SACOL0553	tRNA(Ile)-lysidine synthetase	YP_185441.1	6.521804511
4429	B07	1330	SACOL0699	penicillin-binding protein 4	YP_185581.1	6.407518797
4431	B08	1330	SACOL1088	conserved hypothetical protein	YP_185952.1	6.166165414
4433	B09	1330	SACOL1969	adenylosuccinate lyase	YP_186793.1	6.354135338
4435	B10	1333	SACOL1504	3-phosphoshikimate 1-carboxyvinyltransferase	YP_186348.1	6.475618905
4439	B11	1336	SACOL1410	femA protein	YP_186262.1	6.504491018
4441	B12	1336	SACOL1722	trigger factor	YP_186560.1	6.221556886
4444	C01	1336	SACOL2128	pyrimidine-nucleoside phosphorylase	YP_186943.1	6.062125749
4445	C02	1339	SACOL0842	enolase	YP_185716.1	6.575056012
4447	C03	1342	SACOL0185	peptide ABC transporter, permease protein	YP_185084.1	6.55290611
4450	C04	1342	SACOL0302	branched-chain amino acid transport system II carrier protein	YP_185195.1	6.347242921
4454	C05	1342	SACOL1211	uracil permease	YP_186074.1	6.342026826
4456	C06	1342	SACOL1229	sun protein	YP_186092.1	6.307004471
4457	C07	1342	SACOL1268	Gid protein	YP_186126.1	6.533532042
4459	C08	1342	SACOL2011	sodium transport family protein	YP_186831.1	6.275707899
4463	C09	1345	SACOL2418	IgG-binding protein SBI	YP_187220.1	6.409665428
4466	C10	1348	SACOL0316	conserved hypothetical protein	YP_185208.1	6.325667656
4467	C11	1348	SACOL1790	UDP-N-acetylmuramate--alanine ligase	YP_186623.1	5.699554896
4470	C12	1348	SACOL1951	Mur ligase family protein	YP_186776.1	6.28041543
4471	D01	1348	SACOL2319	Na+/H+ antiporter family protein	YP_187126.1	6.442136499

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4473	D02	1351	SACOL0946	Na+/H+ antiporter family protein	YP_185815.1	5.948186529
4475	D03	1351	SACOL0975	CoA-disulfide reductase	YP_185843.1	6.116950407
4477	D04	1351	SACOL2113	transcription termination factor Rho	YP_186928.1	5.803849001
4479	D05	1354	SACOL0926	5-nucleotidase family protein	YP_185796.1	6.360413589
4481	D06	1354	SACOL1197	cell division protein	YP_186059.1	5.921713442
4487	D07	1354	SACOL2599	conserved domain protein	YP_187390.1	6.062038405
4490	D08	1357	SACOL0640	pyridine nucleotide-disulfide oxidoreductase	YP_185525.1	6.27266028
4493	D09	1360	SACOL0487	hypothetical protein	YP_185377.1	6.495588235
4495	D10	1363	SACOL0046	metallo-beta-lactamase family protein	YP_184956.1	6.305209098
4497	D11	1366	SACOL0966	glucose-6-phosphate isomerase	YP_185835.1	6.038799414
4499	D12	1369	SACOL0021	yycH protein	YP_184932.1	6.451424397
4501	E01	1369	SACOL0064	metallo-beta-lactamase family protein	YP_184969.1	6.355003652
4503	E02	1369	SACOL0275	conserved hypothetical protein	YP_185170.1	4.877282688
4505	E03	1369	SACOL2242	xanthine/uracil permease family protein	YP_187052.1	6.368882396
4507	E04	1372	SACOL0501	sodium-dependent transporter, putative	YP_185389.1	5.397230321
4515	E07	1375	SACOL1329	glutamine synthetase FemC	YP_186184.1	5.509818182
4519	E09	1378	SACOL1443	branched-chain amino acid transport system II carrier protein	YP_186295.1	4.763425254
4530	E10	1381	SACOL1633	conserved hypothetical protein	YP_186473.1	6.086169442
4531	E11	1381	SACOL1719	glutamyl-tRNA reductase	YP_186557.1	6.332367849
4535	F01	-	SACOL0762	-	YP_185639.1	-
4537	F02	1384	SACOL1196	UDP-N-acetylmuramoylalanine--D-glutamate ligase	YP_186058.1	4.895953757
4539	F03	1387	SACOL0122	tetracycline resistance protein, putative	YP_185026.1	5.434751262
4541	F04	1387	SACOL0543	UDP-N-acetylglucosamine pyrophosphorylase	YP_185431.1	5.044700793
4545	F05	1387	SACOL2459	para-nitrobenzyl esterase	YP_187257.1	5.248017304
4547	F06	1390	SACOL0171	branched-chain amino acid transport system II carrier protein	YP_185070.1	5.948201439
4549	F07	1390	SACOL0405	MATE efflux family protein	YP_185297.1	5.905755396
4552	F08	1390	SACOL1450	sensor histidine kinase ArlS	YP_186302.1	6.2
4553	F09	1390	SACOL1571	acetyl-CoA carboxylase, biotin carboxylase	YP_186412.1	5.103597122
4559	F10	1393	SACOL1030	sodium transport family protein	YP_185895.1	5.601579325
4561	F11	1393	SACOL1578	FtsK/SpoIIIE family protein	YP_186418.1	4.677674085
4564	F12	1393	SACOL2073	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	YP_186889.1	6.137114142
4565	G01	1393	SACOL2427	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	YP_187229.1	6.262024408
4567	G02	1393	SACOL2514	gluconate transporter, permease protein	YP_187308.1	5.155061019
4569	G03	1393	SACOL2669	conserved hypothetical protein	YP_187457.1	5.065326633
4571	G04	1395	SACOL2205	conserved hypothetical protein, degenerate	-	5.665232975
4575	G05	1396	SACOL1094	cytochrome d ubiquinol oxidase, subunit I	YP_185958.1	5.406876791
4577	G06	1396	SACOL1661	acetyl-CoA carboxylase, biotin carboxylase, putative	YP_186501.1	5.783667622
4581	G07	1396	SACOL1957	RNA methyltransferase, TrmA family	YP_186782.1	6.196991404
4583	G08	1399	SACOL0572	DNA repair protein RadA	YP_185458.1	5.165832738
4585	G09	1402	SACOL1253	signal recognition particle protein	YP_186112.1	4.94935806
4587	G10	1405	SACOL2048	3-isopropylmalate dehydratase, large subunit	YP_186865.1	5.592882562
4591	G11	1405	SACOL2636	citrate transporter, permease protein	YP_187424.1	6.250533808
4593	G12	1408	SACOL0751	deoxyribodipyrimidine photolyase, putative	YP_185630.1	6.228693182
4595	H01	1408	SACOL1874	epidermin leader peptide processing serine protease EpiP	YP_186702.1	6.318892045
4597	H02	1408	SACOL2133	conserved hypothetical protein	YP_186948.1	5.573863636
4600	H03	1408	SACOL2359	sensor histidine kinase	YP_187164.1	5.524147727

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4601	H04	1411	SACOL0261	drug transporter, putative	YP_185156.1	6.228915663
4603	H05	1411	SACOL0621	substrate--CoA ligase, putative	YP_185506.1	5.549255847
4606	H06	1414	SACOL0200	phosphoglycerate transporter family protein	YP_185099.1	5.89533239
4607	H07	1414	SACOL0963	argininosuccinate lyase	YP_185832.1	5.445544554
4615	H08	1414	SACOL2738	tRNA modification GTPase TrmE	YP_187524.1	6.084158416
4621	H09	1417	SACOL1360	aspartate kinase	YP_186213.1	4.87791108
4623	H10	1417	SACOL2352	tcaA protein	YP_187158.1	6.141848977
4625	H11	1420	SACOL1013	magnesium transporter	YP_185881.1	6.102816901
4627	H12	1420	SACOL1908	fumarate hydratase, class II	YP_186733.1	6.068309859

Table 23: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 23 (ZSAJW), NR-19519[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4629	A01	1423	SACOL0086	drug transporter, putative	YP_184991.1	5.988756149
4631	A02	1423	SACOL0454	sodium:dicarboxylate symporter family protein	YP_185344.1	5.495432186
4635	A03	1426	SACOL1622	glycyl-tRNA synthetase	YP_186462.1	5.00911641
4637	A04	1432	SACOL0091	transcriptional regulator, GntR family/aminotransferase, class I	YP_184996.1	6.122905028
4639	A05	1432	SACOL0918	FeS assembly protein SufB	YP_185789.1	6.166201117
4643	A06	1435	SACOL0016	replicative DNA helicase	YP_184927.1	5.72543554
4645	A07	1435	SACOL0576	cysteinyl-tRNA synthetase	YP_185462.1	6.059930314
4647	A08	1435	SACOL0620	osmoprotectant proline transporter	YP_185505.1	5.821602787
4653	A09	1435	SACOL1887	protoporphyrinogen oxidase	YP_186713.1	5.505226481
4656	A10	1435	SACOL2292	Na+/H+ antiporter NhaC	YP_187099.1	5.958885017
4657	A11	1435	SACOL2449	drug transporter, putative	YP_187248.1	5.530313589
4662	A12	1441	SACOL1105	pyruvate dehydrogenase complex E3 component, lipoamide dehydrogenase	YP_185969.1	5.879944483
4663	B01	1441	SACOL1403	anthranilate synthase component I	YP_186255.1	6.131158917
4665	B02	1441	SACOL1554	6-phosphogluconate dehydrogenase, decarboxylating	YP_186395.1	6.097154754
4667	B03	1444	SACOL0643	conserved hypothetical protein	YP_185528.1	6.186980609
4669	B04	1444	SACOL1801	peptidase, M20/M25/M40 family	YP_186634.1	6.051939058
4673	B05	1447	SACOL1198	cell division protein FtsA	YP_186060.1	6.111955771
4675	B06	1447	SACOL2095	ATP synthase F1, beta subunit	YP_186910.1	6.089149965
4678	B07	1447	SACOL2180	6-phospho-beta-galactosidase	YP_186991.1	6.00138217
4681	B08	1456	SACOL1368	catalase	YP_186221.1	6.150412088
4683	B09	1456	SACOL1563	2-oxoisovalerate dehydrogenase, E3 component, lipoamide dehydrogenase	YP_186404.1	5.500686813
4688	B10	1462	SACOL0516	PTS system, IIBC components	YP_185404.1	5.924076607
4698	B11	1471	SACOL0251	6-phospho-beta-glucosidase	YP_185147.1	5.90278722
4699	B12	1474	SACOL0828	TPR domain protein	YP_185702.1	5.844640434
4702	C01	1477	SACOL2157	drug resistance transporter, EmrB/QacA subfamily	YP_186969.1	5.86662153
4703	C02	1477	SACOL2376	PTS system, sucrose-specific IIBC components, putative	YP_187180.1	5.72647258
4706	C03	1483	SACOL2619	amino acid permease	YP_187408.1	5.788941335
4707	C04	1489	SACOL0178	PTS system, IIBC components	YP_185077.1	4.934184016
4709	C05	1489	SACOL0389	prophage L54a, amidase, putative	YP_185281.1	5.860980524
4711	C06	1489	SACOL0574	glutamyl-tRNA synthetase	YP_185460.1	5.702484889
4713	C07	1489	SACOL1367	amino acid permease	YP_186220.1	5.77904634
4715	C08	1492	SACOL0897	conserved hypothetical protein	YP_185768.1	4.606568365

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4717	C09	1492	SACOL0935	D-alanine-activating enzyme/D-alanine-D-alanyl carrier protein ligase	YP_185805.1	5.787533512
4719	C10	1492	SACOL1916	amino acid ABC transporter, permease/substrate-binding protein	YP_186741.1	5.237935657
4721	C11	1492	SACOL1961	glutamyl-tRNA(Gln) amidotransferase, A subunit	YP_186785.1	5.693699732
4723	C12	1495	SACOL1522	elastin binding protein, putative	YP_186365.1	5.711036789
4727	D01	1498	SACOL1606	rhomboid family protein	YP_186446.1	5.283044059
4732	D02	1501	SACOL0460	inosine-5-monophosphate dehydrogenase	YP_185350.1	5.818121253
4735	D03	1504	SACOL1975	conserved hypothetical protein	YP_186799.1	5.658244681
4739	D04	1507	SACOL1593	glycine cleavage system P protein, subunit 2	YP_186433.1	5.583941606
4747	D05	1513	SACOL1082	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	YP_185946.1	4.962987442
4749	D06	1513	SACOL1844	O-succinylbenzoic acid--CoA ligase, putative	YP_186675.1	5.776602776
4751	D07	1513	SACOL2362	malate:quinone oxidoreductase	YP_187167.1	5.710508923
4757	D08	1516	SACOL1351	cardiolipin synthetase	YP_186204.1	5.413588391
4759	D09	1519	SACOL0494	NADH dehydrogenase I, F subunit	YP_185382.1	5.60236998
4763	D10	1519	SACOL1079	amidophosphoribosyltransferase	YP_185943.1	5.191573404
4765	D11	1519	SACOL1549	glucose-6-phosphate 1-dehydrogenase	YP_186390.1	5.725477288
4768	D12	1519	SACOL2029	sucrose-6-phosphate hydrolase	YP_186847.1	5.949967084
4771	E01	1522	SACOL0154	aldehyde dehydrogenase	YP_185054.1	5.681997372
4773	E02	1522	SACOL0562	lysyl-tRNA synthetase	YP_185450.1	5.720105125
4775	E03	1522	SACOL1738	hypothetical protein	YP_186575.1	5.229303548
4781	E04	1525	SACOL2628	betaine aldehyde dehydrogenase	YP_187417.1	5.771147541
4783	E05	1528	SACOL1728	amino acid permease	YP_186566.1	5.797120419
4785	E06	1528	SACOL2579	phytoene dehydrogenase	YP_187371.1	5.293848168
4788	E07	1531	SACOL0682	Na+/H+ antiporter, MnhD component, putative	YP_185565.1	6.024167211
4789	E08	1531	SACOL0952	Na+/H+ antiporter, MnhD component	YP_185821.1	5.580666231
4794	E09	1531	SACOL2445	fmtA-like protein	YP_187245.1	6.112998041
4795	E10	1531	SACOL2623	malate:quinone oxidoreductase	YP_187412.1	5.841933377
4797	E11	1537	SACOL1821	conserved hypothetical protein	YP_186653.1	5.895901106
4800	E12	1540	SACOL0214	long-chain-fatty-acid--CoA ligase, putative	YP_185113.1	7.028571429
4802	F01	1540	SACOL0788	proton-dependent oligopeptide transporter family protein	YP_185661.1	6.528571429
4803	F02	1543	SACOL0479	surface protein, putative	YP_185369.1	6.766040181
4807	F03	1543	SACOL2576	dehydrosqualene desaturase	YP_187368.1	6.255994815
4809	F04	1543	SACOL2670	glycosyl transferase, group 1 family protein	YP_187458.1	6.771872975
4811	F05	1546	SACOL0052	glycosyl transferase, group 1 family protein	YP_184962.1	6.678525226
4814	F06	1546	SACOL1031	5 nucleotidase family protein	YP_185896.1	6.045278137
4817	F07	1549	SACOL0783	osmoprotectant ABC transporter, permease protein	YP_185657.1	6.757908328
4819	F08	1552	SACOL0841	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	YP_185715.1	6.716494845
4823	F09	1552	SACOL1929	ABC transporter, ATP-binding protein, putative	YP_186754.1	6.121778351
4825	F10	1555	SACOL2072	ATP-dependent RNA helicase, DEAD/DEAH box family	YP_186888.1	4.594855305
4831	F11	1558	SACOL0451	alkyl hydroperoxide reductase, subunit F	YP_185341.1	6.532092426
4834	F12	1561	SACOL0095	immunoglobulin G binding protein A precursor	YP_185000.1	4.420243434
4835	G01	1561	SACOL0548	polysaccharide biosynthesis protein	YP_185436.1	6.67648943
4837	G02		SACOL0857	-	YP_185730.1	
4839	G03	1564	SACOL0224	PTS system, IIBC components	YP_185122.1	6.46483376
4841	G04	1564	SACOL2046	2-isopropylmalate synthase	YP_186863.1	6.650895141
4843	G05	1564	SACOL2659	zinc metalloproteinase aureolysin	YP_187447.1	6.672634271
4846	G06	1567	SACOL0311	sodium:solute symporter family protein	YP_185203.1	7.09444799

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4853	G07	1573	SACOL2483	transporter, putative	YP_187279.1	6.552447552
4856	G08	1576	SACOL0461	GMP synthase	YP_185351.1	6.860406091
4857	G09	1579	SACOL0129	conserved hypothetical protein	YP_185033.1	6.73780874
4859	G10	1579	SACOL1312	tRNA-i(6)A37 modification enzyme MiaB	YP_186168.1	6.694110196
4861	G11	1579	SACOL2569	delta-1-pyrroline-5-carboxylate dehydrogenase, putative	YP_187361.1	6.724509183
4863	G12	1585	SACOL2403	ABC transporter, substrate-binding protein	YP_187206.1	6.641009464
4865	H01	1588	SACOL0750	anion transporter family protein	YP_185629.1	6.698992443
4867	H02	1588	SACOL2515	gluconokinase	YP_187309.1	6.632871537
4870	H03	1588	SACOL2674	accessory secretory protein Asp1	YP_187462.1	5.921284635
4871	H04	1591	SACOL0202	sensor histidine kinase family protein	YP_185101.1	6.548082967
4879	H06	1594	SACOL1305	HD/HDIG/KH domain protein	YP_186162.1	6.624843162
4883	H07	1597	SACOL1025	peptide chain release factor 3	YP_185891.1	6.629304947
4887	H08	1597	SACOL2176	osmoprotectant transporter, BCCT family	YP_186987.1	6.658108954
4890	H09	1603	SACOL1018	sodium:alanine symporter family protein	YP_185884.1	6.874610106
4891	H10	1603	SACOL2673	accessory secretory protein Asp2	YP_187461.1	6.613225203
4893	H11	1606	SACOL0215	propionate CoA-transferase, putative	YP_185114.1	6.653175592
4895	H12	1606	SACOL1294	metallo-beta-lactamase family protein	YP_186151.1	5.97011208

Table 24: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 24 (ZSAJX), NR-19520[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4899	A01	1612	SACOL2469	glutamate synthase-related protein	YP_187266.1	6.254962779
4901	A02	1618	SACOL0381	conserved hypothetical protein	YP_185273.1	6.640296663
4903	A03	1618	SACOL2063	conserved hypothetical protein	YP_186879.1	6.265142151
4905	A04	1627	SACOL0093	L-lactate permease	YP_184998.1	6.592501537
4912	A05	1633	SACOL2363	L-lactate permease	YP_187168.1	6.545621555
4913	A06	1633	SACOL2476	peptide ABC transporter, peptide-binding protein	YP_187273.1	6.447642376
4915	A07	1633	SACOL2624	acetyl-CoA synthetase, putative	YP_187413.1	5.47458665
4917	A08	1636	SACOL1427	ABC transporter, ATP-binding protein	YP_186279.1	6.375305623
4919	A09	1639	SACOL1773	D-3-phosphoglycerate dehydrogenase	YP_186607.1	5.804148871
4928	A10	1645	SACOL2119	CTP synthase	YP_186934.1	6.193920973
4930	A11	1648	SACOL1190	conserved hypothetical protein	YP_186052.1	6.542475728
4931	A12	1651	SACOL0051	conserved hypothetical protein	YP_184961.1	6.305269534
4933	B01	1651	SACOL2016	chaperonin, 60 kDa	YP_186835.1	5.996365839
4937	B02	1659	SACOL0041	cassette chromosome recombinase B, authentic frameshift	-	6.341772152
4939	B03	1659	SACOL2172	IS1272-related, transposase, degenerate	-	6.167570826
4941	B04	1666	SACOL0744	ABC transporter, ATP-binding protein, MsbA family	YP_185623.1	6.157863145
4943	B05	1672	SACOL0598	L-ribulokinase, putative	YP_185484.1	6.134569378
4945	B06	1672	SACOL2458	amino acid permease	YP_187256.1	6.234449761
4947	B07	1675	SACOL0173	indole-3-pyruvate decarboxylase	YP_185072.1	5.708656716
4951	B08	1681	SACOL1240	DAK2 domain protein	YP_186100.1	5.887566924
4954	B09	1681	SACOL1384	osmoprotectant transporter, BCCT family	YP_186237.1	6.40928019
4958	B10	1686	SACOL1744	IS1272-related, transposase, degenerate	-	6.225385528
4961	B11	1696	SACOL0088	Na/Pi cotransporter family protein	YP_184993.1	6.188679245
4963	B12	1696	SACOL0663	arginyl-tRNA synthetase	YP_185547.1	6.150353774
4965	C01	1696	SACOL1804	polysaccharide biosynthesis protein	YP_186637.1	6.044221698
4967	C02	1696	SACOL2324	urocanate hydratase	YP_187131.1	5.565448113
4969	C03	1699	SACOL1739	sensory box histidine kinase PhoR	YP_186576.1	6.145968217
4971	C04	1699	SACOL2199	acetolactate synthase, catabolic	YP_187010.1	6.092407298

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
4973	C05	1708	SACOL0745	ABC transporter, ATP-binding protein, MsbA family	YP_185624.1	6.120608899
4977	C06	1708	SACOL1321	aerobic glycerol-3-phosphate dehydrogenase	YP_186176.1	6.201405152
4979	C07	1708	SACOL2364	conserved hypothetical protein	YP_187169.1	5.662763466
4982	C08	1711	SACOL2068	K+-transporting ATPase, A subunit	YP_186884.1	6.397428404
4986	C09	1717	SACOL2612	hydrolase, CocE/NonD family	YP_187401.1	6.38905067
4987	C10	1723	SACOL0242	teichoic acid biosynthesis protein, putative	YP_185138.1	6.074869414
4989	C11	1723	SACOL2042	dihydroxy-acid dehydratase	YP_186859.1	6.145095763
4992	C12	1726	SACOL0367	prophage L54a, terminase, large subunit, putative	YP_185259.1	6.275782155
4993	D01	1729	SACOL0238	teichoic acid biosynthesis protein, putative	YP_185134.1	6.152111047
4995	D02	1729	SACOL1767	conserved hypothetical protein	YP_186601.1	6.067090804
4997	D03	1732	SACOL0520	DNA polymerase III, gamma and tau subunits	YP_185408.1	6.113163972
5000	D04	1732	SACOL1098	metallo-beta-lactamase family protein	YP_185962.1	6.252309469
5004	D05	1735	SACOL1782	formate--tetrahydrofolate ligase	YP_186615.2	6.306628242
5006	D06	1738	SACOL1282	prolyl-tRNA synthetase	YP_186139.1	6.144418872
5008	D07	1741	SACOL1783	acetyl-CoA synthetase	YP_186616.1	6.269959793
5012	D08	1747	SACOL0416	conserved domain protein	YP_185308.1	6.237550086
5013	D09	1747	SACOL1153	DNA-dependent DNA polymerase family X	YP_186016.1	6.11219233
5015	D10	1747	SACOL2708	ABC transporter, ATP-binding protein	YP_187494.1	5.557527189
5017	D11	1750	SACOL0996	oligopeptide ABC transporter, oligopeptide-binding protein	YP_185864.1	5.978285714
5019	D12	1750	SACOL2282	urease, alpha subunit	YP_187089.1	5.978285714
5021	E01	1753	SACOL1092	phosphoenolpyruvate-protein phosphotransferase	YP_185956.1	6.144894467
5026	E02	1756	SACOL0243	glycosyl transferase, group 2 family protein	YP_185139.1	6.235193622
5027	E03	1762	SACOL0700	ABC transporter, permease/ATP-binding protein	YP_185582.1	6.026106697
5031	E04	1768	SACOL2430	ABC transporter, permease/ATP-binding protein	YP_187232.1	5.793552036
5035	E05	1771	SACOL1924	toxin exporting ABC transporter, permease/ATP-binding protein, putative	YP_186749.1	5.508187465
5037	E06	1774	SACOL2553	pyruvate oxidase	YP_187345.1	5.708568207
5039	E07	1780	SACOL0058	conserved hypothetical protein	YP_184964.1	5.375842697
5041	E08	1786	SACOL1534	sensor histidine kinase SrrB	YP_186376.1	5.150615901
5044	E09	1789	SACOL0102	siderophore biosynthesis protein, IucC family	YP_185007.1	6.735606484
5045	E10	1789	SACOL0245	sensor histidine kinase LytS	YP_185141.1	5.536053661
5047	E11	1792	SACOL1745	pyruvate kinase	YP_186581.1	5.347098214
5049	E12	1792	SACOL2169	aerobactin biosynthesis protein, IucA/IucC family	YP_186981.1	4.618303571
5051	F01	1794	SACOL0774	para-aminobenzoate synthase, component I, putative, authentic frameshift	-	5.114827202
5053	F02	1795	SACOL1308	pyruvate ferredoxin oxidoreductase, alpha subunit	YP_186165.1	5.643454039
5055	F03	1798	SACOL0207	conserved domain protein	YP_185106.1	6.426028921
5057	F04	1798	SACOL2431	ABC transporter, permease/ATP-binding protein	YP_187233.1	6.166852058
5059	F05	1801	SACOL1159	succinate dehydrogenase, flavoprotein subunit	YP_186022.1	5.494725153
5061	F06	1801	SACOL1685	aspartyl-tRNA synthetase	YP_186524.1	6.540810661
5064	F07	1804	SACOL0043	conserved hypothetical protein	YP_184953.1	6.588137472
5066	F08	1804	SACOL2043	acetolactate synthase, large subunit, biosynthetic type	YP_186860.1	6.697339246
5067	F09	1810	SACOL0089	antigen, 67 kDa	YP_184994.1	6.648618785
5069	F10	1810	SACOL0187	lipoprotein, putative	YP_185086.1	6.346961326
5071	F11	1813	SACOL0105	siderophore biosynthesis protein, IucC family	YP_185009.1	6.484280199
5074	F12	1816	SACOL0780	ATP-dependent DNA helicase RecQ	YP_185655.1	6.188325991
5075	G01	1816	SACOL1157	excinuclease ABC, C subunit	YP_186020.1	6.46530837

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
5077	G02	1834	SACOL1619	DNA primase	YP_186459.1	6.428571429
5081	G03	1843	SACOL1005	oligoendopeptidase F	YP_185873.1	6.33478025
5083	G04	1843	SACOL2501	phosphoglucomutase/phosphomannomutase family protein	YP_187296.1	6.542593597
5087	G05	1849	SACOL0978	membrane protein, putative	YP_185846.1	6.1595457
5089	G06	1849	SACOL1419	oligoendopeptidase F, putative	YP_186271.1	5.996755003
5091	G07	1858	SACOL0139	capsular polysaccharide biosynthesis protein Cap5D	YP_185039.1	6.414962325
5095	G08	1861	SACOL0020	sensory box histidine kinase YycG	YP_184931.1	5.834497582
5097	G09	1864	SACOL2443	membrane protein, putative	YP_187244.1	6.292918455
5100	G10	1867	SACOL1637	dnaK protein	YP_186477.1	6.674343867
5107	G11	1882	SACOL1118	GTP-binding protein TypA	YP_185982.1	6.308714134
5109	G12	1882	SACOL1577	conserved hypothetical protein	YP_186417.1	6.341657811
5113	H01	1894	SACOL2666	N-acetylmuramoyl-L-alanine amidase domain protein	YP_187454.1	6.309398099
5115	H02	1909	SACOL2662	transcriptional antiterminator, BglG family	YP_187450.1	5.118910424
5117	H03	1912	SACOL0779	ABC transporter, ATP-binding protein	YP_185654.1	6.185146444
5119	H04	1912	SACOL2737	glucose inhibited division protein A	YP_187523.1	6.290794979
5122	H05	1915	SACOL2639	sulfite reductase (NADPH) flavoprotein alpha-component	YP_187427.1	6.380678851
5124	H06	1915	SACOL2725	ABC transporter, permease protein	YP_187511.1	6.169190601
5127	H07	1924	SACOL0720	ABC transporter, permease protein	YP_185601.1	6.34043659
5129	H08	1927	SACOL2520	membrane protein, putative	YP_187314.1	5.83601453
5133	H09		SACOL0209	No Clone Available	YP_185108.1	
5136	H10	1945	SACOL0383	conserved hypothetical protein	YP_185275.1	6.311568123
5138	H11	1963	SACOL2036	ABC transporter, ATP-binding protein	YP_186853.1	6.133978604
5139	H12	1966	SACOL2347	drug resistance transporter, EmrB/QacA subfamily	YP_187153.1	6.092573754

Table 25: *Staphylococcus aureus*, Strain COL, Gateway® Clone, Plate 25 (ZSAJY), NR-19521[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
5141	A01	1969	SACOL0005	DNA gyrase, B subunit	YP_184916.1	6.171152869
5143	A02	1969	SACOL0317	lipase precursor, interruption-N	YP_185209.1	5.269680041
5145	A03	1972	SACOL1138	LPXTG cell wall surface anchor protein	YP_186002.1	5.929513185
5147	A04	1972	SACOL1729	threonyl-tRNA synthetase	YP_186567.1	6.116125761
5150	A05	1975	SACOL0778	sulfatase family protein	YP_185653.1	6.143797468
5152	A06	1987	SACOL2663	PTS system, fructose-specific IIABC components	YP_187451.1	6.186713639
5154	A07	1990	SACOL0403	transcriptional antiterminator, BglG family	YP_185295.1	6.142211055
5156	A08	1990	SACOL2290	transcriptional regulator, AraC family	YP_187097.1	6.179396985
5157	A09	1992	SACOL0759	PTS system, fructose-specific IIABC component, authentic frameshift	-	6.175702811
5160	A10	1999	SACOL1038	membrane protein	YP_185903.1	5.793896948
5162	A11	1999	SACOL2527	fructose-1,6-bisphosphatase, putative	YP_187320.1	5.804902451
5163	A12	2002	SACOL0014	DHH subfamily 1 protein	YP_184925.1	5.198801199
5165	B01	2008	SACOL0533	methionyl-tRNA synthetase	YP_185421.1	5.883964143
5167	B02	2011	SACOL2171	aerobactin biosynthesis protein, IucA/IucC family	YP_186983.1	5.711586275
5169	B03	2023	SACOL1069	quinol oxidase, subunit I	YP_185933.1	5.685121107
5172	B04	2023	SACOL1377	transketolase	YP_186230.1	6.152249135
5173	B05	2026	SACOL0823	excinuclease ABC, B subunit	YP_185697.1	6.023198421
5177	B06	2029	SACOL2564	ferrous iron transport protein B	YP_187356.1	6.075406604

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
5179	B07	2032	SACOL1389	DNA topoisomerase IV, B subunit	YP_186242.1	6.082185039
5181	B08	2035	SACOL2643	ABC transporter, permease protein	YP_187431.1	6.230958231
5183	B09	2038	SACOL1965	DNA ligase, NAD-dependent	YP_186789.1	6.390088322
5185	B10	2041	SACOL0033	penicillin-binding protein 2	YP_184944.1	6.9377756
5187	B11	2041	SACOL0188	gamma-glutamyltranspeptidase	YP_185087.1	6.947574718
5189	B12	2044	SACOL1316	DNA mismatch repair protein HexB	YP_186172.1	6.851761252
5193	C01	2077	SACOL0687	Na+/H+ antiporter, putative	YP_185569.1	6.586422725
5195	C02	2077	SACOL2694	lipase	YP_187480.1	6.602311026
5197	C03	2080	SACOL0175	PTS system, IIABC components	YP_185074.1	6.745192308
5201	C04	2090	SACOL2002	map protein, programmed frameshift	YP_186825.1	6.149282297
5203	C05	2095	SACOL1241	ATP-dependent DNA helicase RecG	YP_186101.1	6.811455847
5205	C06	2101	SACOL2552	PTS system, IIABC components	YP_187344.1	6.855782961
5207	C07	2104	SACOL1267	DNA topoisomerase I	YP_186125.1	6.397813688
5211	C08	2113	SACOL2442	Na+/H+ antiporter, putative	YP_187243.1	6.877898722
5213	C09	2116	SACOL0593	translation elongation factor G	YP_185479.1	6.823251418
5215	C10	2128	SACOL0555	cell division protein FtsH, putative	YP_185443.1	6.45018797
5220	C11	2131	SACOL1293	polyribonucleotide nucleotidyltransferase	YP_186150.1	7.392773346
5221	C12	2140	SACOL0792	ribonucleoside-diphosphate reductase, alpha subunit	YP_185666.1	6.828037383
5227	D03	2152	SACOL1288	translation initiation factor IF-2	YP_186145.1	6.281598513
5231	D04	2170	SACOL2243	DNA topoisomerase III	YP_187053.1	5.9
5234	D05	2182	SACOL1644	competence protein ComEC/Rec2, putative	YP_186484.1	7.334555454
5239	D06	2197	SACOL1532	hypothetical protein	YP_186374.1	6.816112881
5241	D07	2218	SACOL1490	penicillin-binding protein 2	YP_186334.1	6.77141569
5243	D08	2224	SACOL1078	phosphoribosylformylglycinamidine synthase II	YP_185942.1	6.208183453
5245	D09	2224	SACOL1689	GTP pyrophosphokinase	YP_186528.1	6.68705036
5247	D10	2227	SACOL1966	ATP-dependent DNA helicase PcrA	YP_186790.1	6.961832061
5250	D11	2233	SACOL0084	transcriptional regulator, AraC family	YP_184989.1	6.426332288
5252	D12	2263	SACOL0428	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	YP_185319.1	7.155103844
5254	E01	2269	SACOL1194	penicillin-binding protein 1	YP_186056.1	7.135301895
5255	E02	2284	SACOL0204	formate acetyltransferase	YP_185103.1	6.356830123
5257	E03	2296	SACOL0212	3-hydroxyacyl-CoA dehydrogenase protein	YP_185111.1	7.632404181
5260	E04	2308	SACOL1691	single-stranded-DNA-specific exonuclease RecJ	YP_186530.1	7.808925477
5264	E05	2344	SACOL1028	serine protease	YP_185894.1	7.663822526
5268	E06	2383	SACOL1154	DNA mismatch repair MutS2 family protein	YP_186017.1	7.582039446
5271	E07	2413	SACOL1295	FtsK/SpoIIIE family protein	YP_186152.1	6.934521343
5273	E08	2425	SACOL2671	secA family protein	YP_187459.1	6.952164948
5276	E09	2437	SACOL0679	Na+/H+ antiporter, MnhA component, putative	YP_185562.1	7.463274518
5277	E10	2437	SACOL1149	phenylalanyl-tRNA synthetase, beta subunit	YP_186012.1	6.96512105
5280	E11	2437	SACOL1390	DNA topoisomerase IV, A subunit	YP_186243.1	7.490356996
5282	E12	2440	SACOL0955	Na+/H+ antiporter, MnhA component	YP_185824.1	7.674180328
5285	F01	2443	SACOL1224	primosomal protein N`	YP_186087.1	7.396234138
5287	F02	2443	SACOL2572	copper-translocating P-type ATPase	YP_187364.1	7.312320917
5289	F03	2452	SACOL1808	leucyl-tRNA synthetase	YP_186641.1	7.356035889
5291	F04	2458	SACOL2194	hyaluronate lyase	YP_187005.1	6.239218877
5295	F05	2512	SACOL1674	helicase, putative, RecD/TraA family	YP_186514.1	5.503582803
5297	F06	2524	SACOL2566	MmpL efflux pump, putative	YP_187358.1	6.69770206
5299	F07	2530	SACOL1579	conserved hypothetical protein	YP_186419.1	6.759683794
5301	F08	2557	SACOL1396	fmtC protein	YP_186248.1	6.926867423
5305	F09	2641	SACOL1259	conserved hypothetical protein	YP_186117.1	7.037864445
5307	F10	2644	SACOL0135	alcohol dehydrogenase, iron-containing	YP_185035.1	7.067322239

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
5309	F11	2644	SACOL0979	ATP-dependent Clp protease, ATP-binding subunit ClpB	YP_185847.1	7.09720121
5313	F12	2665	SACOL1673	alanyl-tRNA synthetase	YP_186513.1	6.637523452
5317	G01	2665	SACOL1737	DNA polymerase I	YP_186574.1	7.012007505
5319	G02	2692	SACOL2070	sensor histidine kinase KdpD	YP_186886.1	7.001485884
5321	G03	2698	SACOL0006	DNA gyrase, A subunit	YP_184917.1	7.055967383
5325	G04	2728	SACOL1495	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG	YP_186339.1	6.890395894
5328	G05	2740	SACOL0495	conserved hypothetical protein	YP_185383.1	5.398175182
5329	G06	2740	SACOL1385	aconitate hydratase	YP_186238.1	6.718978102
5334	G07	2788	SACOL1206	isoleucyl-tRNA synthetase	YP_186068.1	7.175394548
5342	G08	2857	SACOL2509	fibronectin binding protein B	YP_187304.1	6.949947497
5343	G09	2878	SACOL0608	sdrC protein	YP_185493.1	6.550034746
5345	G10	2881	SACOL0824	excinuclease ABC, A subunit	YP_185698.1	6.804928844
5349	G11	2971	SACOL1899	conserved hypothetical protein	YP_186725.1	6.587680916
5353	G12	3016	SACOL2665	phage infection protein, putative	YP_187453.1	5.959880637
5355	H01	3028	SACOL1877	epidermin biosynthesis protein EpiB	YP_186704.1	6.552840159
5358	H02	3064	SACOL0272	hypothetical protein	YP_185167.1	7.157963446
5360	H03	3064	SACOL1382	exonuclease SbcC	YP_186235.1	7.166775457
5361	H04	3085	SACOL1859	hypothetical protein	YP_186687.1	6.645380875
5363	H05	3091	SACOL2511	fibronectin-binding protein A	YP_187306.1	6.730507926
5366	H06	3187	SACOL0076	hypothetical protein	YP_184981.1	6.858487606
5370	H07	3208	SACOL1215	carbamoyl-phosphate synthase, large subunit	YP_186078.1	6.424875312
5371	H08	3232	SACOL1750	DNA polymerase III, alpha subunit	YP_186586.1	7.275680693
5387	H09	3658	SACOL0589	DNA-directed RNA polymerase, beta subunit	YP_185475.1	7.937124112
5397	H10	3859	SACOL1791	FtsK/SpoIIIE family protein	YP_186624.1	6.455558435
5406	H11	4534	SACOL0514	glutamate synthase, large subunit	YP_185402.1	6.973312748
5410	H12	6235	SACOL0379	prophage L54a, tail tape meausure protein, TP901 family	YP_185271.1	7.194707298

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