Table S1. Genes involved in the transcriptomic response of *S. pneumoniae* to treatment with 8 μM seconeolitsine.

spr code	**Protein[a]**	**Gene**	**Cluster**	**Leader/ leading**	**Relative fold variation detected by[b]**				
					RNASeq		**Microarrays**		
					t5	**t15**	**t5**	**t15**	**t30**
0001	Chromosome replication initiation protein	***dnaA***	**1**	→		**2.0**			
0005	Peptidyl-tRNA hydrolase	***pth***	**1**	→	**3.2**	**2.3**			
0006	Transcription-repair coupling factor	***mfd***	**1**	→	**3.0**	**2.2**	**2.9**	**2.8**	
0007	Conserved hypothetical		**1**	→	**2.0**				
0008	Hypothetical		**1**	→	**2.6**	**2.0**			
0009	Conserved hypothetical		**1**	→	**2.7**	**2.2**			
0010	Conserved hypothetical		**1**	→	**2.6**	**2.1**	**2.3**	**2.3**	
0012	ATP-dependent zinc metalloprotease	***ftsH***	**1**	→	**2.0**				
0013	Competence-specific transcription modulator	***comX***	**1**	→			**9.6**	**9.8**	
0014	Transposase		**1**	→	**2.0**		**4.0**	**4.3**	
0016	Transposase		**1**	→	**3.1**	**2.7**			
0017	Degenerate transposase		**1**	←	**5.3**	**4.9**	**3.6**		
0018	Degenerate transposase		**1**	←	**6.5**	**5.4**	**3.7**	**3.7**	*-3.3*
0019	Degenerate transposase		**1**	←	**6.2**	**5.9**	**3.3**	**3.2**	*-2.9*
0022	Conserved hypothetical								*-3.7*
0030	Hypothetical						**2.1**		
0031	Hypothetical						**4.0**		
0032	DNA polymerase I	***polA***			*-4.9*	*-2.9*	*-4.0*	*-3.9*	
0033	Conserved hypothetical				*-4.0*	*-3.6*			
0034	Conserved hypothetical				*-8.9*	*-4.6*			
0043	Competence factor transporting ATP-binding protein	***comA***					**8.3**	**8.2**	
0044	Competence factor transport protein	***comB***					**9.5**		
0045	P-ribosylaminoimidazole-succinocarboxamide synthase	***purC***					**4.5**	**4.3**	
0054	P-ribosyl glucinamide formyltransferase	***purK***			*-2.3*				
0055	Hypothetical				*-2.5*				
0056	Adenylosuccinate lyase	***purB***			*-2.5*				
0059	Beta-galactosidase 3	***bgaC***			*-2.5*				
0068	Conserved hypothetical				*-4.4*	*-2.8*	*-3.9*	*-3.9*	
0069	Hypothetical				*-4.7*		*-4.3*	*-4.2*	
0070	Transporter membrane-spanning protein-K+	***trkH***			*-2.3*				
0071	Transporter NAD+ binding protein-K+	***trkA***			*-2.3*		*-2.7*	*-2.6*	
0076	Response regulator	***rr08***			*-3.9*	*-3.3*	*-3.1*	*-2.9*	
0077	Histidine kinase	***hk08***			*-3.5*	*-2.7*			
0079	Degenerate transposase						**3.9**	**4.2**	
0088	Hypothetical				*-2.7*				
0089	Conserved hypothetical				*-2.5*				
0090	Conserved hypothetical				*-5.4*	*-3.9*		*-4.2*	
0099	ABCT membrane-spanning permease-amino acid						*-2.2*	*-2.1*	
0101	ABCT solute-binding protein-amino acid				*-4.2*	*-3.0*			
0102	Arg-succinate synthase	***argG***			*-5.8*	*-3.8*			

0103	Arg-succinate lyase	***argH***			*-6.5*	*-5.0*			
0104	Hypothetical				*-4.1*				
0105	Transporter, truncation							*-2.1*	
0110	Hypothetical							*-2.1*	
0113	Hypothetical						*-2.1*	*-2.1*	
0121	Surface protein PspA	***pspA***			*-2.4*				
0122	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	***mnmA***			*-3.6*	*-4.0*			
0123	Conserved hypothetical				*-2.4*	*-2.7*			
0124	tRNA uridine 5-carboxymethylaminomethyl modification	***gidA***			*-2.4*	*-2.9*			
0127	Bacteriocin GG peptide	***cibB***			**2.1**				
0128	Bacteriocin GG peptide	***cibA***					**36.3**	**35.6**	
0130	Ribosomal protein Ala acetyltransferase	***rimI***			*-2.2*		*-2.3*	*-2.2*	
0146	ABCT substrate-binding-amino acid				*-2.5*	*-2.1*	*-2.3*	*-2.2*	
0157	Conserved hypothetical				**2.4**	**2.3**			
0158	Hypothetical				**4.7**	**4.7**		**2.0**	
0159	Conserved hypothetical				**4.4**	**3.7**	**3.1**	**3.2**	
0161	Riboflavin synthase beta chain	***ribH***			**5.0**	**4.8**	**2.8**	**2.7**	
0162	Riboflavin biosynthesis; GTP-cyclohydrolase II.	***ribA***			**4.4**	**4.3**	**3.1**	**3.0**	
0163	Riboflavin synthase alpha-chain	***ribC***			**4.2**	**4.1**	**2.6**	**2.6**	
0164	Riboflavin biosynthesis; a deaminase	***ribD***			**3.7**	**3.6**	**2.0**	**2.0**	
0173	Arsenate reductase	***arsC***			**2.1**		**2.2**	**2.2**	
0174	Hypothetical				**3.3**	**2.4**	**2.6**	**2.5**	
0178	Dihydrofolate:folylpoly-Glu synthase	***folC***			**2.9**	**2.5**	**2.3**	**2.3**	
0179	Hypothetical				**2.2**				
0180	Cardiolipin synthase	***cls***			**2.1**				
0181	Hypothetical	***orf47***					**3.5**	**3.4**	
0184	Hypothetical				**2.0**				
0185	Ribonucleoside-tri-P reductase activating protein	***nrdG***			**2.0**				
0186	Hypothetical				**1.9**				
0218	Conserved hypothetical				*-1.9*				
0224	ABCT substrate-binding-iron								**2.2**
0236	Conserved hypothetical				*-3.1*	*-2.6*			
0237	Conserved hypothetical				*-3.3*				
0244	6-P-beta-glucosidase	***bglA***			*1.9*	**2.2**			
0245	L-Gln-D-fructose-6-P-amidotransferase	***glmS***			*-7.6*	*-6.9*			
0247	LPxTG protein. Alkaline amylopullulanase	***spuA***			*-7.4*	*-5.4*			
0251	DNA polymerase III, alpha subunit	***polC***			**1.9**				
0254	Aminopeptidase	***pepS***	**8**	→			*-2.0*	*-2.0*	
0257	Hypothetical		**8**	→	*-3.0*				
0258	Aminopeptidase C	***pepC***	**8**	→	*-4.5*	*-4.3*			
0259	PTS mannose-specific EIID	***manN***	**8**	←	*-3.0*				
0260	PTS mannose-specific EIIC	***manM***	**8**	←	*-3.0*				
0261	PTS mannose-specific EIIAB	***manL***	**8**	←	*-2.7*				
0262	Alcohol DH	***adhP***	**8**	←	*-8.3*	*-3.1*			
0263	Conserved hypothetical		**8**	←	*-4.7*	*-2.5*			
0266	Dihydropteroate synthase	***sulA***	**8**	→	*-2.0*				
0270	Hypothetical				*-7.1*	*-4.5*			

0276	6-P-beta-glucosidase	***bglA***			*-7.2*			
0279	Transcription antiterminator	***bglG***			*-8.3*			
0280	PTS cellobiose transporter subunit IIA	***celC***			*-11.2*			
0281	Hypothetical				*-11.8*	*-10.7*		
0282	PTS cellobiose transporter subunit IIC	***celD***			*-8.3*	*-6.4*		
0283	Hypothetical				*-2.6*	*-2.1*		
0284	Alpha-xylosidase	***xylS***			*-2.0*			
0306	Hypothetical						**3.5**	**3.5**
0309	Hypothetical				*-2.4*	*-2.1*		
0313	Transposase						**3.6**	**3.8**
0314	The type 2 capsule locus	***cps2H***	**9**	→	*-5.0*	*-4.5*		
0315	The type 2 capsule locus	***cps2I***	**9**	→	*-4.4*	*-3.4*		
0316	The type 2 capsule locus	***cps2J***	**9**	→	*-3.9*	*-3.2*	*-2.0*	
0317	The type 2 capsule locus		**9**	→	*-3.5*	*-3.2*		
0318	The type 2 capsule locus	***cps2K***	**9**	→	*-4.6*	*-4.4*	*-3.3*	*-3.0*
0319	The type 2 capsule locus	***cps2P***	**9**	→	*-4.8*	*-3.8*	*-3.3*	*-3.1*
0320	The type 2 capsule locus	***cps2L***	**9**	→	*-3.7*	*-3.9*		*-3.1*
0321	The type 2 capsule locus	***cps2M***	**9**	→	*-3.9*	*-3.8*		
0322	dTDP-glucose-4,6-dehydratase	***cpsN***	**9**	→	*-4.0*	*-3.9*	*-2.7*	*-2.7*
0324	Transposase, truncation		**9**	→				*-2.1*
0325	Hypothetical		**9**	→			*-2.2*	
0327	ABCT substrate-binding protein-oligopeptide	***aliA***	**9**	→	*-5.1*	*-3.8*	*-4.4*	*-4.3*
0331	Conserved hypothetical			→	*-4.3*			
0342	Conserved hypothetical		**2**	→	**3.3**	**2.1**	**3.0**	**2.9**
0343	TCS3: Histidine kinase	***hk03***	**2**	→	**3.4**	**2.2**	**3.3**	**3.2**
0344	TCS3: Response regulator	***rr03***	**2**	→	**3.9**		**3.3**	**3.5**
0345	Hypothetical		**2**	→	**4.4**		**4.0**	**4.0**
0346	Hypothetical		**2**	→	**4.5**	**2.6**	**3.9**	**3.8**
0347	IS861-truncation		**2**	→	**4.9**	**3.0**	**3.6**	
0348	Hypothetical		**2**	→	**3.0**			
0349	Choline binding protein G	***cbpG***	**2**	→	**3.3**	**2.1**	**2.2**	**2.2**
0350	Choline binding protein G		**2**	→	**2.6**		**2.2**	
0351	Choline-binding protein	***pcpC***	**2**	→	**2.3**		**2.0**	**2.0**
0353	Degenerate transposase		**2**	←			**2.5**	**2.5**
0355	Degenerate transposase		**2**	←			**3.8**	
0367	Conserved hypothetical				**1.9**			
0368	DNA mismatch repair	***mutS2***			**2.3**	**2.3**		
0369	D-Ala-Gly permease	***dagA***			**2.6**		**2.9**	**2.9**
0370	Macrophage infectivity potentiator protein	***mip***					**2.8**	**2.8**
0378	Acyl carrier protein	***acpP***			**2.3**			
0379	Enoyl-acyl carrier protein reductase	***fabK***			**2.7**			
0381	3-ketoacyl-acyl carrier protein reductase	***fabG***			**2.3**			
0385	Acetyl-CoA carboxylase subunit	***accC***			**2.3**			
0388	Hypothetical						**3.1**	**3.1**
0389	Hypothetical				**2.5**		**2.8**	
0408	ABCT ATP-binding protein-Gln	***glnQ***				*-2.3*		
0415	Pyruvate formate-lyase	***pfl***			**2.6**			
0421	PTS sugar-specific EII component							*-2.1*

0426	Trk transporter membrane-spanning protein-K+	***trkH***	*-5.4*	*-2.9*			
0427	Trk NAD$^+$ binding protein-K+	***trkA***	*-5.1*	*-3.1*			
0428	Conserved hypothetical		*-2.8*		*-2.6*		
0429	Conserved hypothetical		*-2.7*				
0434	Conserved hypothetical		**1.9**				
0436	Hypothetical		**1.9**				
0437	RNA polymerase delta subunit	***rpoE***	**2.6**	**2.0**			
0439	Conserved hypothetical		*-2.3*				
0445	Type I restriction enzyme	***hsdS***	**2.2**	**2.6**	**2.0**		
0446	Type I restriction enzyme specificity protein	***hsdS***	**2.3**	**2.6**			
0459	ABCT ATP-binding protein						**3.6**
0460	ABCT membrane-spanning permease		*-1.9*				**4.4**
0462	Regulatory protein	***spiR1***	*-2.4*				
0465	Peptide pheromone, bacteriocin-like peptide	***spiP***					**2.7**
0470	Bacteriocine-like	***pncW***				**2.1**	**3.3**
0471	CAAX protease	***pncO***					**3.0**
0472	Immunity protein	***pncQ***					**2.8**
0473	CAAX protease	***pncP***		**2.2**			
0474	ABCT ATP binding protein			**2.5**			**2.9**
0477	Conserved hypothetical		**1.9**				
0479	Conserved hypothetical		**1.8**				
0480	Conserved hypothetical		**2.1**				
0483	Conserved hypothetical		**7.6**				
0484	Hypothetical				**2.3**		
0485	Hypothetical				*-2.0*		
0486	Conserved hypothetical		*-2.2*	*-2.2*			
0489	Hypothetical		*-2.1*				
0490	Conserved hypothetical		*-2.3*				
0491	Hypothetical		*-2.2*	*-2.0*			
0492	Valyl-tRNA synthetase	***valS***	*-2.2*	*-2.1*			
0497	Degenerate transposase				**3.3**	**3.1**	
0498	Degenerate transposase				**4.5**	**4.3**	
0499	Hypothetical		*-3.9*	*-3.3*	*-2.0*		
0502	Hypothetical		*-4.0*				
0503	Hypothetical		*-3.2*		*-2.6*	*-2.8*	
0507	Phe-tRNA synthase alpha chain	***pheS***	*-2.8*	*-1.9*			
0508	Conserved hypothetical		*-2.4*				
0509	Phe-tRNA synthase beta chain	***pheT***	*-2.8*	*-2.0*			
0510	Hypothetical		*-5.5*	*-3.5*	*-4.3*		
0511	Degenerate transposase						*-2.0*
0514	Tetrahydropteroyltri-Glu methyltransferase	***metE***	*-4.0*	*-3.2*			
0515	5,10-methylenetetrahydrofolate reductase	***metF***	*-3.7*				
0524	ABCT membrane-spanning permease-peptide	***vex1***	**2.6**	**2.3**			
0526	ABCT membrane-spanning permease-peptide	***vex3***	**2.6**	**2.3**			
0530	Fructose-bi-P aldolase	***fba***	**2.1**				
0531	Hypothetical		**4.2**	**3.0**	**3.6**	**3.6**	
0532	ABCT membrane-spanning permease-Gln	***glnP***	**4.0**	**3.3**			

0533	ABCT membrane-spanning permease-Gln	***glnP***			**4.4**	**3.4**			
0536	ABCT ATP-binding protein-Gln	***glnH***			**3.1**				
0537	Single-stranded DNA-specific exonuclease	***recJ***				*-1.9*			
0539	Tributyrin esterase	***estA***			**3.0**	**2.9**			
0542	Hypothetical				**2.3**	**2.0**	**2.5**	**2.5**	
0557	ABCT ATP-binding protein				*-2.8*	*-3.0*			
0558	Conserved hypothetical				*-2.7*	*-2.9*			
0559	Conserved hypothetical				*-2.8*	*-2.8*			
0560	Hypothetical				*-2.2*				
0562	PTS sugar-specific EII component				*-2.8*				
0563	Hypothetical				*-2.4*				
0568	Hypothetical				*-2.6*				
0578	Response regulator	***rr09***			*-2.5*	*-2.2*			
0579	Histidine kinase	***hk09***			*-2.4*				
0585	Thymidylate synthase	***thyA***			*-2.8*	*-2.6*			
0599	Hypothetical						*-2.3*	*-2.4*	
0613	Orotidine-5-decarboxylase	***pyrF***			*-3.1*	*-2.3*			
0614	Orotate P-ribosyltransferase	***pyrE***						*-2.4*	
0620	ABCT substrate-binding protein								**2.5**
0621	ABCT substrate-binding protein								**2.4**
0628	Conserved hypothetical		**3**	→	**3.9**				
0629	Hydroxyethylthiazole kinase	***thiM***	**3**	→	**4.2**				
0630	Thiamin-P pyrophosphorylase	***thiE***	**3**	→	**4.8**				
0631	Conserved hypothetical		**3**	→	**6.6**		**2.5**	**2.6**	
0632	ABCT ATP-binding protein		**3**	→	**7.4**	**3.6**	**4.8**	**4.8**	
0633	Conserved hypothetical		**3**	→	**9.4**	**4.9**	**6.6**	**6.3**	
0634	Transcriptional regulator	***tenA***	**3**	→	**13.3**	**5.9**	**6.1**	**6.0**	**2.9**
0635	Hypothetical		**3**	→	**15.1**	**6.9**	**2.6**	**2.7**	
0636	Hydroxyethylthiazole kinase	***thiM***	**3**	→	**9.3**	**4.2**	**4.4**	**4.2**	
0637	Thiamine-P pyrophosphorylase	***thiE***	**3**	→	**12.8**	**5.1**	**3.9**	**4.0**	
0639	COPAB ATPases metal repressor	***copY***	**3**	→		**3.1**			
0645	Hypothetical						**2.2**	**2.2**	
0646	P-beta-gluco or galactosidase	***bgl***			**6.9**				
0652	Conserved hypothetical					*-2.1*			
0653	Conserved hypothetical				*-2.9*				
0655	Uracil P-ribosyltransferase	***upp***			**2.5**				
0665	Peptide chain release factor 2	***prfB***			**1.9**				
0666	ABCT ATP-binding protein	***ftsE***			**2.1**				
0667	Cell division	***ftsX***			**2.3**				
0669	Hypothetical				**2.7**				
0690	Conserved hypothetical						**2.5**	**2.5**	
0692	Glutathione oxidoreductase	***gor***			*-2.4*	*-2.7*			
0697	Conserved hypothetical				**2.9**	**2.9**			
0698	Conserved hypothetical				**3.5**	**3.1**	**2.1**	**2.1**	
0699	Conserved hypothetical				**2.2**	**2.1**		**2.3**	**2.2**
0707	Response regulator, transcriptional regulator	***ciaR***			**3.5**	**3.2**	**2.8**	**2.8**	
0708	Sensor histide kinase CiaH	***ciaH***			**3.5**	**2.8**	**3.1**	**3.0**	
0714	P-glycolate phosphatase	***gph***			**3.2**	**2.8**			

0715	DNA gyrase subunit B	***gyrB***			**2.7**	**2.2**			
0716	Cell division regulator	***ezrA***			**2.3**				
0717	Transposase				**5.4**	**3.9**			
0718	Transposase				**5.2**	**3.8**	**3.1**	**3.1**	
0720	Hypothetical								**2.0**
0721	Conserved hypothetical				**8.5**	**6.7**	**4.7**	**4.6**	
0722	Transposase						**4.2**	**4.5**	
0723	Degenerate transposase							**2.1**	
0725	ATP dependent protease				*-2.3*	*-2.0*			
0728	ABCT ATP-binding protein-Gln	***glnQ***			*-2.0*	*-2.0*			
0744	Pyrimidine nucleoside phosphorylase	***pdp***	**4**	→	**1.9**				
0745	Deoxyribose-phosphate aldolase	***deoC***	**4**	→	**1.9**				
0746	Cytidine deaminase	***cdd***	**4**	→	**2.0**				
0747	Conserved hypothetical		**4**	→	**2.2**				
0748	ABCT ATP-binding-ribose/galactose		**4**	→	**2.4**		**2.1**	**2.1**	
0749	ABCT membrane-spanning permease-ribose/galactose		**4**	→	**2.1**				
0750	ABCT membrane-spanning permease-ribose/galactose		**4**	→	**2.1**				
0751	Degenerate transposase (orf1)		**4**	→	**5.3**	**4.3**	**4.3**	**4.4**	
0752	Degenerate transposase (orf1)		**4**	→	**3.2**		**3.6**	**3.6**	
0753	Degenerate transposase (orf2)		**4**	→	**4.0**	**3.3**	**2.8**	**2.8**	
0754	Degenerate transposase (orf2)		**4**	→	**3.6**		**2.5**	**2.6**	
0765	Degenerate transposase (orf2)				**3.0**				
0766	Degenerate transposase (orf2)				**4.3**	*1.9*			
0767	Transposase (orf1)				**3.6**				
0771	ABCT ATP-binding-unknown substrate				**2.0**				
0773	Conserved hypothetical				**2.2**				
0775	Conserved hypothetical				**2.6**				
0778	Transcriptional repressor of the fructose operon	***fruR***			*-2.9*	*-2.2*			
0779	Fructose-1-P kinase	***fruB***			*-2.7*	*-2.1*			
0780	Fructose specific-P-transferase system IIBC component	***fruA***			*-2.0*				
0782	Hypothetical				*-3.3*	*-3.2*			
0783	Probable pyridoxal-P dependent aminotransferase				*-2.1*	*-2.2*			
0784	Thiamin biosynthesis	***thiI***					*-2.5*	*-2.5*	
0785	Hypothetical								*-2.0*
0788	Hypothetical						*-2.0*	*-2.0*	
0798	Hypothetical						**2.1**	**2.1**	
0812	ABCT ATP-binding-unknown substrate						**2.6**	**2.6**	
0815	Degenerate transposase								*-2.0*
0830	23S rRNA pseudouridine synthase	***rluD***			**1.8**				
0831	Choline binding protein E	***cbpE***			**2.0**				
0839	Conserved hypothetical				**2.3**				
0856	DNA-binding, bind donor DNA	***comEA***					**10.2**	**10.7**	
0857	DNA entry pore	***comEC***					**14.0**	**14.1**	
0858	Hypothetical						**3.2**	**3.2**	
0859	Hypothetical						**3.4**	**3.4**	
0860	Hypothetical						**4.4**	**4.4**	

0865	Dihydroorotate DH electron transfer subunit	***pyrK***					**4.2**
0868	Fibronectin-binding protein-like protein A	***flpA***	*-3.2*	*-2.8*	*-2.8*	*-2.9*	
0869	Conserved hypothetical		*-2.5*	*-2.4*			
0872	Formamidopyrimidine-DNA glycosylase	***mutM***			*-2.1*		
0873	Conserved hypothetical		*-2.1*			*-2.1*	
0881	DNA postentry processing protein	***coiA***			**6.4**	**6.0**	
0886	Degenerate transposase (orf1)		**6.6**		**4.5**	**4.3**	
0898	Degenerative transposase				**2.6**	**2.9**	
0904	Conserved hypothetical			*-2.4*			
0905	Cationic amino acid transporter - APC Superfamily			*-2.0*			
0906	Lipoprotein	***lmb***		*-2.0*			
0909	Hypothetical						*-2.1*
0910	Pneumococcal histidine triad protein E precursor	***phtE***					*-3.2*
0914	Ferrochelatase	***hemH***	*-4.9*	*-3.6*			*-3.7*
0915	Large conductance mechano-sensitive ion channel	***mscL***	*-4.8*	*-4.7*			
0917	Citrulline cluster-linked gene	***ccl***	*-3.1*	*-3.1*	*-2.4*	*-2.3*	
0918	Asp beta-semialdehyde DH	***asd***	*-2.2*	*-2.3*			
0933	Hypothetical		**2.7**				
0934	ABCT substrate-binding-iron	***piaA***		*-2.4*			
0940	Hypothetical		**2.1**				
0943	Hypothetical						*-2.3*
0980	Conserved hypothetical		**2.0**				
0981	Glycosyltransferase	***cpoA***	**2.0**				
0982	Conserved hypothetical		**2.1**	**2.0**			
0983	Hypothetical		**3.1**	**2.8**			
0987	Degenerate transposase		**4.2**				
0988	Transposase		**3.5**				
0993	Degenerate transposase		**3.1**		**2.7**	**2.7**	
0996	DNA repair protein	***radC***			**4.8**	**4.6**	
0997	Conserved hypothetical				**3.1**	**3.0**	
0998	Conserved hypothetical		**2.0**				
0999	Hypothetical		**2.5**		**2.4**	**2.5**	
1017	Riboflavin biosynthesis protein	***mreA***	**2.1**		**3.2**	**3.2**	
1018	Conserved hypothetical				**2.7**	**2.6**	
1023	ABCT membrane-spanning permease		**2.0**	**2.3**			
1026	Hypothetical				*-3.9*	*-4.1*	
1028	Glyceraldehyde-3-P DH	***gapN***	*-3.6*				
1043	Conserved hypothetical		*-2.8*	*-2.3*			
1044	Ribonuclease HII	***rnhB***	*-2.5*				
1045	Conserved hypothetical		*-2.1*	*-2.0*			
1061	Pneumococcal histidine triad protein A	***phtA***	**3.1**	**2.2**	**2.1**	**2.2**	
1064	Glutaredoxin-like protein	***nrdH***	**4.4**		**2.1**	**2.1**	
1065	Ribonucleoside-diphosphate reductase, subunit alpha	***nrdE***	**3.9**		**2.6**	**3.0**	
1066	Ribonucleoside-diP reductase 2, subunit beta	***nrdF***	**4.5**	**2.2**	**3.3**	**3.9**	
1070	PTS system, lactose-specific IIBC component	***lacE***	*-3.9*	*-3.1*			
1071	PTS system, lactose-specific IIA component	***lacF***	*-5.2*				

1072	Antiterminator	***lacT***			*-4.5*	*-3.8*			
1073	Tagatose 1,6-diphosphate aldolase	***lacD***			*-3.3*	*-2.5*			
1074	Tagatose-6-P kinase	***lacC***			*-3.2*				
1075	Galactose-6-P isomerase LacB subunit	***lacB***					*-2.2*	*-2.3*	
1076	Galactose-6-P isomerase LacA subunit	***lacA***			*-3.1*				
1091	Hypothetical				*-3.4*		*-2.5*	*-2.5*	
1094	Conserved hypothetical				*-2.0*				
1098	Sortase	***srtA***			**1.9**				
1109	Formate-tetrahydrofolate ligase	***fhs***			**1.9**	**1.8**			
1120	ABCT membrane spanning permease-Gln	***glnP***			**4.1**	**3.1**			
1121	ABCT ATP-binding-Gln	***glnQ***			**3.0**	**2.6**			
1122	Glucose-6-P-1-DH	***zwf***			**4.0**	**3.1**	**2.2**	**2.5**	
1129	Hypothetical		**10**	←	*-2.8*				
1130	Hypothetical		**10**	←	*-2.7*				
1135	3-isopropylmalate DH	***leuB***	**10**	←	*-2.7*				
1136	2-isopropylmalate synthase	***leuA***	**10**	←	*-3.0*				
1137	2-isopropylmalate synthase	***leuA***	**10**	←	*-2.8*				
1138	Hypothetical		**10**	←	*-2.9*				
1139	Copper sensitivity	***cutC***	**10**	←	*-3.3*	*-2.3*			
1140	Conserved hypothetical		**10**	←	*-2.6*				
1141	DNA topoisomerase I	***topA***	**10**	←	*-6.2*	*-5.4*	*-3.6*	*-3.6*	
1142	Conserved hypothetical		**10**	←	*-2.7*	*-2.5*			
1150	Conserved hypothetical				*-3.1*	*-2.3*			
1151	Required for phosphorylcholine incorporation in teichoic and lipoteichoic acids	***licD1***			*-3.1*	*-2.5*	*-2.3*	*-2.3*	
1152	licD Protein	***licD2***			*-2.6*		*-2.3*	*-2.2*	
1172	CrcB protein	***crcB***			*-2.5*		*-2.0*	*-2.0*	
1173	CrcB protein	***crcB***					*-2.0*		
1176	Conserved hypothetical				*-3.1*				
1182	Hypothetical				*-2.2*	*-2.8*			
1183	ABCT ATP-bindng protein				*-2.6*	*-3.2*			
1194	ABCT substrate-binding protein - oligopeptide	***appA***				*-3.3*			
1195	Conserved hypothetical					*-2.9*			
1197	Degenerate transposase (orf2)				*-2.8*	*-3.1*			
1201	Hypothetical				*-4.7*	*-3.5*			
1202	ABCT ATP-binding protein-unknown substrate				*-5.2*	*-4.7*			
1203	ABCT ATP-binding/membrane spanning protein				*-5.2*	*-4.9*			
1204	Prolyl oligopeptidase	***ptrB***			*-5.1*	*-4.6*	*-2.6*	*-2.7*	
1205	Conserved hypothetical				*-4.3*	*-5.1*	*-2.5*	*-2.5*	
1207	Hypothetical								*-3.1*
1208	Hypothetical								*-3.0*
1237	Hypothetical								*-2.1*
1238	ABCT ATP-binding protein-unknown substrate						*-2.9*		*-4.7*
1250	Conserved hypothetical				*-2.7*				
1251	ABCT substrate-binding-Gln	***glnH***			*-2.6*	*-2.3*			
1252	Phosphate transport system regulatory protein	***phoU***					*-2.2*	*-2.3*	

1253	ABCT ATP-binding-P	***pstB1***			*-2.3*	*-2.1*		*-2.3*	
1254	ABCT ATP-binding-P	***pstB2***			*-2.3*	*-2.2*			
1255	ABCT membrane-spanning permease-P	***pstA***			*-2.3*	*-2.2*	*-3.3*	*-3.5*	
1256	ABCT membrane-spanning permease-P	***pstC***			*-2.6*	*-2.4*			
1257	ABCT substrate-binding-P	***pstS1***			*-2.6*	*-2.3*			
1270	Ser-P kinase/phosphatase	***hprK***			**1.8**				
1292	Conserved hypothetical				*-3.1*	*-2.6*			
1301	Conserved hypothetical						*2.0*	**2.0**	
1310	Peptide deformylase	***fms***			*-2.9*	*-2.8*			
1314	ABCT ATP-binding-Asp/Glu		**11**	←	*-3.6*	*-3.1*	*-3.3*	*-3.3*	
1315	ABCT membrane-spanning permease-Asp/Glu		**11**	←	*-3.3*	*-3.0*	*-3.2*	*-3.3*	
1316	Conserved hypothetical		**11**	←	*-3.1*	*-2.8*			
1317	O6-methylguanine-DNA methyltransferase	***ogt***	**11**	←	*-4.3*	*-3.6*			
1318	Hypothetical		**11**	←	*-3.1*	*-3.1*			
1319	Hypothetical		**11**	→	*-4.0*	*-3.2*			
1320	Conserved hypothetical		**11**	→	*-3.1*		*-2.7*	*-2.6*	
1321	Conserved hypothetical		**11**	←	*-4.5*	*-4.0*	*-2.9*	*-3.0*	
1322	Pyridoxine biosynthesis	***pdx1***	**11**	←	*-4.7*	*-3.9*			
1323	NADH oxidase	***noxA***	**11**	←	*-2.2*	*-2.7*			
1335	Oxidoreductase	***mocA***			*-2.5*			*-2.4*	
1336	DEAD RNA helicase				*-3.0*	*-2.4*			
1337	Degenerate transposase						**3.0**	**3.0**	
1338	Degenerate transposase				**3.5**		**3.2**	**3.1**	
1339	Degenerate transposase				**3.3**		**2.3**	**2.3**	
1340	Degenerate transposase				**4.2**	**3.2**	**2.8**	**2.8**	
1341	Degenerate transposase				**5.8**				
1342	Degenerate transposase						**2.4**	**2.4**	
1346	Hypothetical				*-3.6*				
1353	ABCT substrate-binding protein-Gln	***glnH***	**12**	←	*-3.2*	*-2.7*			
1354	ABCT ATP-binding protein–Gln	***glnQ***	**12**	←	*-3.0*	*-2.5*			
1355	ABCT membrane-spanning permease-Gln	***glnP***	**12**	←	*-2.1*				
1358	Conserved hypothetical		**12**	→				*-2.0*	
1359	Proton-ATPase, F1 sector, epsilon-subunit	***atpe***	**12**	←	*-2.5*	*-2.6*			
1360	Proton-ATPase, F1 sector, beta-subunit	***atpb***	**12**	←	*-3.1*	*-3.2*			
1361	Proton-ATPase, F1 sector, gamma-subunit	***atpg***	**12**	←	*-3.2*	*-3.0*			
1362	Proton-ATPase, F1 sector, alpha-subunit	***atpa***	**12**	←	*-3.5*	*-3.4*	*-3.4*	*-3.5*	
1363	Proton-ATPase, F1 sector, delta-subunit	***atpd***	**12**	←	*-4.0*	*-3.9*	*-2.9*		
1364	Proton-ATPase, F0 sector, subunit b	***atpB***	**12**	←	*-3.6*	*-3.2*			
1365	Proton-ATPase, F0 sector, subunit a	***atpA***	**12**	←	*-3.2*	*-3.1*			
1366	Proton-ATPase, F0 sector, subunit c	***atpC***	**12**	←	*-3.3*	*-3.0*			
1367	Transposase								*-2.1*
1378	ABCT								**2.8**
1383	Polysaccharide transporter				*-2.0*				
1384	UDP-N-acetylmuramoyl-L-Ala-D-Glu-L-Lys ligase	***murE***			*-2.1*				
1386	Hypothetical				**2.6**	**2.1**			
1387	Hypothetical				**2.4**	**2.2**	**2.2**	**2.1**	
1388	Hypothetical				**2.3**	*2.0*			

1389	Manganese-dependent inorganic pyrophosphatase	***ppaC***	**1.9**				
1390	Conserved hypothetical		**2.7**	**2.4**			
1391	Conserved hypothetical		**2.3**	**2.1**			
1392	Conserved hypothetical		**2.7**	**2.6**			
1393	Hypothetical		**2.5**	**2.1**			
1397	Asn-tRNA synthetase	***asnS***	*-2.2*	*-2.0*			
1398	Conserved hypothetical		*-2.1*	*-2.0*			
1399	Asp aminotransferase	***aspB***	*-2.3*	*-2.0*	*-2.0*		
1400	Conserved hypothetical		*-2.6*	*-2.2*	*-2.5*	*-2.5*	
1402	Hypothetical		**4.5**				
1407	Hypothetical		*-2.4*	*-2.1*			
1408	Formylmethionine deformylase	***def***	*-2.9*	*-2.6*			
1420	Hypothetical		**2.6**	**2.4**			
1430	DNA binding, peroxide resistance	***dpr***	*-2.3*	*-2.4*			
1433	Conserved hypothetical		**2.5**	**2.0**			
1434	Homoserine O-succinyltransferase	***metA***	**2.4**				
1435	Adenine P-ribosyltransferase	***apt***	**2.0**				
1436	Conserved hypothetical		**3.1**				
1438	Isochorismatase	***entB***	**1.9**				
1439	Transcriptional pleiotropic repressor	***codY***	**2.0**				
1440	Conserved hypothetical			*-2.3*			
1441	Major facilitator:Oxalate:formate antiporter	***oxlT***	**8.1**	**3.3**			
1446	Degenerate transposase (orf2)				**2.0**	**2.0**	
1447	Degenerate transposase (orf2)				**2.9**	**2.9**	
1448	Degenerate transposase (orf1)				**4.1**	**4.3**	
1452	Hypothetical				**3.5**	**3.5**	
1453	Major facilitator superfamily transporter		**2.2**				
1466	Hypothetical		*-3.7*	*-3.2*	*-4.3*	*-4.1*	
1470	Hypothetical		*-3.4*		*-2.3*		
1471	Hypothetical		*-4.3*	*-2.9*			
1472	Thr-tRNA synthetase 1	***thrS***	*-2.5*				
1477	Conserved hypothetical		**2.5**				
1478	Hypothetical		**2.8**				
1479	Conserved hypothetical		**2.2**				
1480	Iron-dependent transcriptional regulator	***marR***	**2.2**				
1481	Hypothetical		**2.6**			*2.0*	
1482	Hypothetical		**3.5**	**2.5**			
1483	Hypothetical		**3.0**				
1484	Hypothetical		**2.0**				**2.0**
1486	Conserved hypothetical		*-2.8*				
1487	GTP pyrophosphokinase	***relA***	*-2.4*	*-2.1*			
1490	Conserved hypothetical		*-4.4*	*-2.6*	*-2.8*	*-2.7*	
1491	Endopeptidase O	***pepO***	*-3.7*	*-2.5*			
1495	Thioredoxin-linked thiol peroxidase	***tpxD***		*-3.3*			
1501	Hypothetical					**2.2**	
1518	Conserved hypothetical		*-2.6*	*-2.8*			
1531	Neuraminidase B	***nanB***					*-2.1*
1536	Neuraminidase A	***nanA***	**3.4**				

1537	Hypothetical		**5.5**	**4.2**		
1539	ATP-dependent DNA helicase	***recG***	**2.1**	**2.1**		
1540	Ala racemase	***alr***	**2.1**	**2.0**		
1549	Hypothetical				*-2.2*	
1558	Conserved hypothetical		**2.4**			
1559	ABCT ATP-binding		**3.6**	**2.4**		**3.3**
1560	Hypothetical		**5.2**	**3.2**	**4.5**	**4.9**
1561	LPxTG protein. Sialidase A precursor	***natB***			**2.9**	**2.8**
1563	Degenerate transposase		**3.9**		**3.3**	**3.0**
1585	Conserved hypothetical				**2.9**	**2.6**
1598	Ser/Thr transporter	***dctA***	*-3.8*	*-3.1*	*-2.3*	*-2.3*
1599	Conserved hypothetical		*-2.5*	*-2.0*		
1602	Thioredoxin reductase	***trxA***	**2.1**			
1603	Conserved hypothetical		**2.9**			
1612	Conserved hypothetical		*-2.4*		*-2.3*	*-2.3*
1620	ABCT substrate-binding-sugar		*-2.1*	*-2.2*		
1621	Sucrose operon repressor	***scrR***	*-2.0*	*-2.2*		
1624	Conserved hypothetical		**1.9**			
1627	Conserved hypothetical				**2.1**	**2.1**
1628	Peptidase-Mtase, process CglC, CglD, CglF	***cclA***			**7.1**	**6.8**
1629	Conserved hypothetical		**2.0**		**5.7**	**5.7**
1630	Hypothetical		**2.0**		**5.9**	**6.0**
1631	Trp synthase alpha chain	***trpA***	*-3.1*			
1632	Trp synthase beta chain	***trpB***	*-2.9*			
1633	P-ribosylanthranilate isomerase.	***trpF***	*-4.1*			
1634	Indole-3-glycerol-P synthase	***trpC***	*-2.9*			
1635	Anthranilate P-ribosyltransferase	***trpD***	*-4.1*			
1636	Anthranilate synthase component II	***trpG***	*-3.0*			
1637	Anthranilate synthase component I	***trpE***	*-3.4*			
1638	Hypothetical		*-3.8*	*-3.7*		
1640	Hypothetical			**4.1**		
1654	Conserved hypothetical		*-2.7*	*-2.1*		
1655	Conserved hypothetical		*-3.1*	*-2.3*		
1656	ABCT ATP-binding/membrane spanning		*-2.7*	*-2.2*		
1657	ABCT ATP-binding/membrane spanning		*-3.3*	*-2.6*	*-2.4*	*-2.4*
1658	Conserved hypothetical		*-3.0*	*-2.4*		
1659	Hypothetical		*-2.8*			
1664	Restriction system	***dpnD***		*-3.0*		
1665	Type II restriction enzyme DpnI	***dpnC***	*-3.5*	*-3.3*	*-3.0*	*-3.0*
1666	Conserved hypothetical		*-7.0*	*-7.5*		
1672	Cation efflux system protein	***czcD***	**16.4**	**7.3**		
1673	Conserved hypothetical		*-3.2*		*-2.0*	
1675	Transposase		**3.5**			
1681	Hypothetical		*-3.1*			
1682	Glu aminopeptidase	***pepA***	*-3.0*	*-2.5*		
1698	Dextran glucosidase	***dexS***	*-6.2*	*-5.3*		
1699	PTS trehalose-specific IIBC component	***treP***	*-5.8*	*-5.2*		
1701	Degenerate transposase		**3.3**			**3.3**

1702	Degenerate transposase				**3.3**		**2.4**	**2.4**	
1716	Degenerate transposase				**8.5**	**4.6**			
1719	Conserved hypothetical					**2.4**			
1721	Degenerate transposase				**5.5**	**3.2**			
1722	Chaperonin GroEL	***groEL***					**3.2**		
1723	Cochaperonin GroES	***groES***			**2.1**				
1729	Conserved hypothetical						*-3.4*	*-3.5*	
1730	Hypothetical				*-4.6*	*-4.5*	*-3.4*	*-3.4*	
1731	Hypothetical				*-5.5*	*-5.3*	*-2.8*	*-2.7*	
1732	Conserved hypothetical				*-3.6*	*-3.5*			
1733	Hypothetical				*-3.6*	*-3.6*			
1734	ABCT ATP-binding				**5.9**	**5.6**	**2.7**	**2.5**	
1735	ABCT ATP-binding				**6.5**				
1736	ABCT ATP-binding				**7.2**	**5.4**	**2.0**		
1737	Conserved hypothetical				**8.7**	**6.6**	**2.8**	**2.4**	
1738	Conserved hypothetical				**2.1**	**2.1**			
1750	Hypothetical		**5**	←	**3.2**			**2.7**	
1751	Hypothetical		**5**	←	**3.5**				
1752	Hypothetical		**5**	←	**3.3**		**2.1**		
1753	Hypothetical		**5**	←	**3.6**				
1755	Hypothetical		**5**	←	**1.8**		**5.3**	**5.5**	
1756	DNA-damage-inducible protein	***dinF***	**5**	←			**4.5**	**4.8**	
1757	DNA recombination/repair	***recA***	**5**	←			**4.3**	**5.0**	
1758	Membrane protein	***cinA***	**5**	←			**5.1**	**6.0**	
1762	Hypothetical		**5**	←			**7.4**		
1763	Transcriptional activator	***plcR***	**5**	←	**5.1**	**4.8**	**3.0**		
1764	Hypothetical		**5**	→	**13.6**	**14.2**			**3.8**
1765	Hypothetical		**5**	→	**14.4**	**12.8**			
1766	Hypothetical		**5**	→	**18.9**	**13.9**			
1767	Bacteriocin formation protein	***cylM***	**5**	→	**26.0**	**15.9**	**5.3**	**5.0**	
1768	Conserved hypothetical		**5**	→	**23.2**	**14.1**			
1769	Hypothetical		**5**	→	**21.7**	**13.3**			
1770	ABCT ATP-binding/membrane-spanning-hemolysin	***cylB***	**5**	→	**21.8**	**12.8**			**2.0**
1771	Subtilisin-like Ser protease	***nisP***	**5**	→	**16.6**	**9.6**			**2.4**
1772	Hypothetical		**5**	→	**4.6**	**2.9**	**4.9**	**4.9**	**2.0**
1773	ABCT ATP-binding		**5**	→	**4.6**	**3.0**			
1774	Hypothetical		**5**	→	**5.4**				
1775	Nucleoside di-P kinase	***ndk***	**5**	←	**4.1**		**3.4**	**3.5**	
1776	RNA polymerase, beta subunit	***rpoC***	**5**	←	**2.3**		**2.0**		
1785	Asp-ammonia ligase	***asnA***			*-2.5*	*-2.2*			
1795	Conserved hypothetical				*-2.2*				
1796	Conserved hypothetical				*-1.9*				
1797	Pentose-5-P-3-epimerase	***rpe***			*-2.1*				
1798	Conserved hypothetical				*-2.3*				
1799	Ribosomal RNA small subunit methyltransferase	***rsmA***			*-2.5*				
1808	Potential aminotransferase	***aspC***			*-4.3*	*-3.5*	*-2.3*	*-2.4*	
1810	Conserved hypothetical				*-3.1*	*-2.6*			

1811	Conserved hypothetical				*-4.3*	*-3.0*		*-3.2*	
1812	L-asparaginase	***asnB***			*-3.2*		*-2.0*	*-2.1*	
1815	Histidine kinase					**2.2**			
1816	Conserved hypothetical				**2.6**	**2.7**			
1817	ABCT ATP binding				**2.7**	**2.6**	**2.2**	**2.2**	
1818	Hypothetical				**4.8**	**3.2**	**3.5**	**3.6**	
1819	Competence-specific transcription modulator	***comX2***					**9.6**	**9.8**	
1826	Conserved hypothetical				**2.2**	**2.4**	**3.1**		
1827	Transposase				**3.1**	**2.7**			
1828	Transposase				**2.0**		**4.0**	**4.3**	
1829	Nicotinate-nucleotide pyrophosphorylase	***nadC***					**3.8**	**3.8**	
1830	Conserved hypothetical						**3.9**	**3.9**	
1837	Alcohol-acetaldehyde DH	***adhE***			*-7.4*				
1838	Hypothetical				*-3.3*	*-2.8*	*-2.8*	*-2.7*	
1839	Conserved hypothetical				*-3.0*	*-2.7*	*-2.6*	*-2.6*	
1840	Conserved hypothetical				*-3.1*	*-2.9*			
1841	Transketolase	***tktA***			*-3.9*	*-4.6*			
1850	Hypothetical								**2.1**
1857	Hypothetical						**17.4**	**16.3**	
1858	Membrane protein, cell wall chanel	***cglG***					**16.1**	**16.2**	
1861	Membrane protein, cell wall chanel	***cglD***					**13.8**	**14.3**	
1862	Membrane protein, cell wall chanel	***cglC***					**16.9**	**17.4**	
1863	ABCT, transport of CglC-CglG	***cglB***					**14.0**	**15.5**	
1864	ABCT, transport of CglC-CglG	***cglA***						**9.3**	
1865	Conserved hypothetical				*-2.4*				
1866	Zinc-containing alcohol DH	***adh***			*-2.5*				
1867	N-acetylglucosamine-6-P deacetylase	***nagA***			*-2.5*		*-3.8*	*-3.8*	
1868	Hypothetical				*-2.1*				
1869	tRNA-guanine transglycosylase	***tgt***			*-4.1*	*-4.1*			
1870	Hypothetical				*-2.5*		*-2.5*	*-2.4*	
1872	Pyrrolidone carboxyl peptidase				*-3.0*				
1873	Conserved hypothetical								*-2.1*
1875	Conserved hypothetical				*-2.2*				
1876	Hypothetical		**6**	←	**3.6**	**2.9**			
1877	Multi antimicrobial extrusion family		**6**	←	**3.7**	**3.1**			
1878	Thr synthase	***thrC***	**6**	←	**2.4**	**2.1**			
1879	Hypothetical		**6**	←	**3.0**	**2.8**	**2.2**	**2.2**	
1883	Hypothetical		**6**	←	**5.4**	**4.9**	**6.4**		
1884	Gln amidotransferase	***guaA***	**6**	←	**6.9**	**6.3**	**6.3**	**5.7**	
1885	ABCT ATP-binding-fluoroquinolones	***patB***	**6**	←	**3.8**	**4.1**			
1886	Degenerate transposase		**6**	→	**3.2**	**3.8**			
1887	ABCT ATP-binding-fluoroquinolones	***patA***	**6**	←	**3.7**	**4.1**	**2.8**	**2.9**	
1888	DNA mismatch repair protein	***hexA***	**6**	←		**2.1**			
1897	ABCT membrane-spanning permease-P	***pstA***					**2.1**	**2.1**	
1898	ABCT ATP-binding-P	***pstB***			**2.8**		**2.1**	**2.2**	
1899	Negative regulator of pho regulon	***phoU***			**3.1**		**2.2**	**2.2**	
1912	Hypothetical				*-2.0*				
1913	rRNA (guanine-N1)-methyltransferase	***rrmA***			*-2.7*				

1915	Hypothetical				*-2.9*	*-2.4*			
1918	ABCT substrate-binding-maltose	***malX***			*-7.4*	*-5.9*			
1919	ABCT membrane-spanning permease-maltose	***malC***			*-4.8*	*-3.2*			
1920	ABCT membrane-spanning permease-maltose	***malD***			*-4.0*				
1921	MalA protein	***malA***			*-4.6*	*-3.4*			
1922	Maltose operon transcriptional repressor	***malR***			*-4.1*	*-3.6*			
1934	Conserved hypothetical								*-2.7*
1935	Dihydroxyacid dehydratase	***ilvD***			*-3.4*	*-2.2*			
1936	Putative transketolase C-terminal section	***tktC***			*-5.0*	*-4.0*			
1937	Putative transketolase N-terminal section	***tktN***			*-4.5*	*-3.7*			
1938	Conserved hypothetical				*-5.7*	*-4.5*			
1939	Hypothetical				*-6.4*	*-5.2*			
1940	Conserved hypothetical				*-8.7*	*-6.2*			
1942	Hypothetical							*-2.0*	
1945	Choline-binding protein				*-5.2*	*-3.1*			
1951	Conserved hypothetical						*-2.2*	*-2.1*	
1953	Conserved hypothetical				*-4.2*	*-3.1*			
1954	Hypothetical						*-2.2*		
1958	Carbamate kinase	***arcC***			**2.2**	**2.3**			
1959	Conserved hypothetical				**2.9**	**3.1**			
1960	Conserved hypothetical				**2.9**	**3.1**			
1962	Conserved hypothetical				*-2.9*	*-3.0*			
1968	PTS sugar-specific EII component						*-2.3*		
1971	Fucose pathway protein						*-2.1*	*-2.0*	
1972	L-fuculose P aldolase	***fucA***					*-2.2*	*-2.2*	
1979	D-Ala transfer from undecaprenol-P to the poly(glycerol-P) chain	***dltD***			*-4.0*	*-2.6*			
1980	D-Ala carrier protein	***dltC***			*-3.2*				
1981	D-Ala transfer from Dcp to undecaprenol-P	***dltB***			*-4.5*	*-2.9*	*-3.3*	*-3.3*	
1982	D-Ala-D-Ala carrier protein ligase	***dltA***			*-4.8*	*-3.7*			
1983	Conserved hypothetical				*-2.8*				
1992	Hypothetical				*-3.2*				
1993	Chaperonin (heat shock protein 33)	***hslO***				*-2.3*			
1994	Conserved hypothetical					*-2.0*			
2002	ABCT ATP-binding protein-anion		**7**	←	**8.5**	**7.1**		**4.4**	
2003	Conserved hypothetical		**7**	←	**7.5**	**6.5**	**7.2**	**7.9**	
2004	ABCT membrane-spanning permease		**7**	←	**7.0**	**6.3**	**3.1**	**3.4**	**2.1**
2005	Conserved hypothetical		**7**	←	**7.7**	**6.7**	**6.8**	**6.7**	**2.5**
2006	Choline binding protein D	***cbpD***	**7**	←	**2.5**	**2.3**	**11.6**	**11.8**	
2007	Conserved hypothetical		**7**	←	**2.3**	**2.9**			
2008	Replicative DNA helicase	***dnaC***	**7**	←	**2.0**	**2.7**			
2009	50S Ribosomal protein subunit L9	***rplI***	**7**	←	**1.9**	**2.4**			
2010	Conserved hypothetical		**7**	←		**2.2**			
2012	Involved in competence	***comFC***	**7**	←			**11.9**	**11.3**	
2013	Involved in competence	***comFA***	**7**	←			**8.1**	**6.9**	
2018	Degenerate transposase				**2.9**		**2.1**	**2.1**	
2021	General stress protein GSP-781					*-2.0*			
2022	Cell-shape determining protein MreD	***mreD***			**2.5**	**2.2**			

2023	Cell shape determining protein MreC	***mreC***			**1.8**			
2025	ABCT ATP-binding-unknown substrate				**2.0**	**1.9**		
2027	P-glycero-P synthase	***pgsA***			**2.0**	**2.0**		
2028	Conserved hypothetical				**1.9**			
2031	Conserved hypothetical				**2.2**	**2.4**		
2032	Recombination protein	***recF***			**2.6**	**2.6**		
2033	Inosine-5-mono-P DH	***imdH***			*-2.1*			
2036	Conserved hypothetical					**2.1**		
2040	Conserved hypothetical		**1**	→			**3.3**	**3.2**
2041	Response regulator	***comE***	**1**	←	**2.1**		**23.5**	**23.0**
2042	Histidine protein kinase	***comD***	**1**	←	**2.0**		**18.9**	**18.9**
2043	Competence stimulating peptide precursor	***comC***	**1**	←			**6.0**	**6.0**

[a] ABCT, ATP-binding cassette transporter; DH, dehydrogenase; P, phospho; PTS, phosphotransferase system.

[b] DEGs included were those showing significant fold variations detected either in microarrays (≥2 and $P < 0.05$) or by RNASeq (P <1E-14).

Table S2. Response of 35 *S. pneumoniae* R6 genes encoding DNA repair proteins

Uniprot code (_STRR6)	**Description**	**Gene**	**R6 locus**	**SCN RESPONSE**	**SCN DOMAIN**	**Length (aa)**
Q8DRQ1	Transcription-repair-coupling factor	*mfd*	spr0006	UP	UP	1,169
Q8DRP0	DNA repair protein	*radA*	spr0025	NR	NR	420
DPO1	DNA polymerase I	*polA*	spr0032	DOWN	NR	877
RECO	DNA repair protein	*recO*	spr0036	NR	NR	256
HEXB	DNA mismatch repair	*hexB*	spr0160	NR	NR	649
RUVA	Holliday junction DNA helicase	*ruvA*	spr0165	NR	NR	197
UVRA	UvrABC system protein A	*uvrA*	spr0171	NR	NR	943
RUVB	Holliday junction DNA helicase	*ruvB*	spr0238	NR	NR	332
RECU	Holliday junction resolvase	*recU*	spr0330	NR	NR	198
DPO4	DNA polymerase IV	*dinB*	spr0414	NR	NR	353
Q8CZ40	Uncharacterized protein		spr0488	NR	NR	131
Q8DQR4	Single-stranded DNA-specific exonuclease	*recJ*	spr0537	DOWN	NR	744
UVRC	UvrABC system protein C	*uvrC*	spr0543	NR	NR	614
Q8DQ41	Competence protein	*celA*	spr0856	UP	NR	216
FPG	Formamidopyrimidine-DNA glycosylase	*mutM*	spr0872	DOWN	NR	274
DNLJ	DNA ligase	*ligA*	spr1024	NR	NR	652
ADDB	ATP-dependent helicase	*rexB*	spr1039	NR	NR	1,091
ADDA	ATP-dependent helicase	*addA*	spr1040	NR	NR	1,216
MUTX	8-oxo-dGTP diphosphatase	*mutX*	spr1054	NR	NR	154
UNG	Uracil-DNA glycosylase	*ung*	spr1055	NR	NR	217
Q8DPN3	DNA repair protein	*recN*	spr1084	NR	NR	555
UVRB	UvrABC system protein B	*uvrB*	spr1118	NR	NR	662
Q8DPH8	Endonuclease III	*nth*	spr1157	NR	NR	209
Q8DP74	O6-methylguanine-DNA methyltransferase	*ogt*	spr1317	DOWN	DOWN	176
SSB	Single-stranded DNA-binding	*ssb*	spr1395	NR	NR	156
RECR	Recombination protein	*recR*	spr1516	NR	NR	198
Q7ZAK6	Branch migration of Holliday junction	*recG*	spr1539	UP	NR	671
EXOA	Exodeoxyribonuclease	*exoA*	spr1660	NR	NR	275
RECX	Regulatory protein	*recX*	spr1718	NR	NR	258
Q8DNH4	Single-stranded DNA-binding	*ssbB*	spr1724	NR	NR	131
RECA	Protein RecA	*recA*	spr1757	UP	UP	388
HEXA	DNA mismatch repair protein HexA	*hexA*	spr1888	UP	UP	844
MALX	Maltose/maltodextrin-binding protein	*malX*	spr1918	NR	NR	423
RECF	DNA replication and repair protein	*recF*	spr2032	NR	NR	365

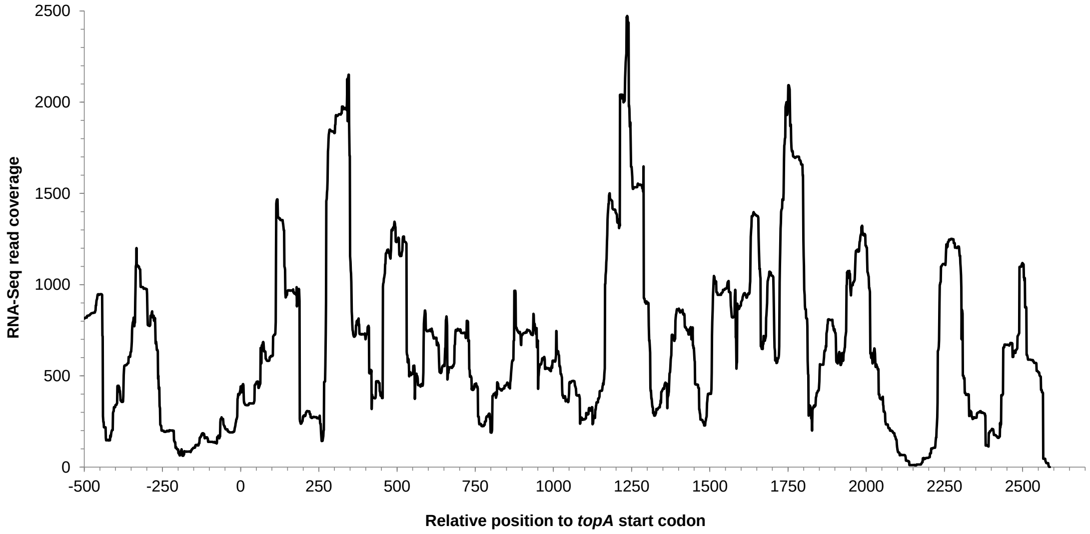

Figure S1. Determination of the start transcription site of *topA* by RNA-Seq. Thirty million reads from the RNA-Seq experiment of R6 strain grown in AGCH containing 0.2% yeast extract and 0.3% sucrose yeast extract to OD_{620nm} of 0.4 (see Methods) were considered. The total of 27,809 reads (roughly 0.1% of reads; in the range of the genome average) fully mapped within the genome section covering from -500 to +500 the *topA* ORF. The lowest read counts (<90 reads were found in the intergenic regions (~-200 and ~+2150 nt) just besides the predicted transcriptional terminators of *topA* and the preceding ORF. However, there were also prominent valleys inside the coding sequence (*e.g.* 143 reads, nt +260). The number of reads upstream *topA* increases just after its well-defined -35 and -10 promoter boxes, in particular from the -24 nucleotide (>190 reads). This nucleotide correspond to an “A” nucleotide, normally involved as transcription starts, surrounded by three (upstream) and two (downstream) less-probable “T” nucleotides. Therefore we propose the -24 position as the most probable start transcription site of *topA* in *S. pneumoniae* R6.