

## **5 Anhang**

## A.1 $\sigma^S$ -abhängige Gene, die nicht zur Kerngruppe gehören

**Tabelle 12:** 341 RpoS-abhängige Gene, die nicht zur Kerngruppe (siehe Abschnitt 3.1.3) gehören. Einige wenige Gene haben Ratiowerte > 2 in allen drei Experimenten und sind dennoch an dieser Stelle gelistet. Bei diesen Genen erfüllte mindestens ein Wert nicht das Kriterium für statistisch signifikante differentielle Genexpression wie in (Weber et al., 2005) beschrieben. Die Werte stellen den Durchschnitt aus drei biologisch unabhängigen Microarrayanalysen dar. n.d. (nicht detektierbares Signal).

Genname / b-Nummer	Genprodukt	Ratio			
		OD 4	NaCl	pH 5	
<i>acrD</i>	b2470	aminoglycoside/multidrug efflux system	1,60	3,65	1,84
<i>agp</i>	b1002	glucose-1-phosphatase/inositol phosphatase	0,95	4,19	1,54
<i>aldB</i>	b3588	aldehyde dehydrogenase B, NADP-dependent, multi-substrate	4,35	2,59	1,56
<i>appC</i>	b0978	cytochrome bd-II oxidase, subunit I	3,29	1,69	0,89
<i>appY</i>	b0564	DLP12 prophage; DNA-binding transcriptional activator	2,09	0,88	1,95
<i>arcA</i>	b4401	DNA-binding response regulator in two-component regulatory system with ArcB or CpxA	2,74	2,69	1,37
<i>argG</i>	b3172	argininosuccinate synthetase	1,99	2,12	1,86
<i>argH</i>	b3960	argininosuccinate lyase	1,44	2,35	1,15
<i>aroM</i>	b0390	conserved protein	2,47	3,66	1,64
<i>artJ</i>	b0860	arginine transporter subunit -!- periplasmic-binding component of ABC superfamily	1,94	0,90	2,34
<i>artQ</i>	b0862	arginine transporter subunit -!-membrane component of ABC superfamily	2,11	2,42	2,07
<i>b0609</i>	b0609	unknown CDS	0,89	3,67	0,77
<i>basR</i>	b4113	DNA-binding response regulator in two-component regulatory system with BasS	1,69	2,09	1,22
<i>basS</i>	b4112	sensory histidine kinase in two-component regulatory system with BasR	2,41	1,45	1,49
<i>bcsE</i>	b3536	conserved protein	1,89	2,38	1,29
<i>bdm</i>	b1481	biofilm-dependent modulation protein	2,73	4,64	4,10
<i>btuD</i>	b1709	vitamin B12 transporter subunit -!- ATP-binding component of ABC superfamily	1,89	8,37	1,03
<i>btuE</i>	b1710	predicted glutathione peroxidase	2,54	7,26	1,18
<i>cbrA</i>	b3690	predicted oxidoreductase, FAD/NAD(P)-binding domain	2,02	2,58	1,38
<i>cedA</i>	b1731	cell division modulator	n.d.	2,05	n.d.
<i>cfa</i>	b1661	cyclopropane fatty acyl phospholipid synthase (unsaturated-phospholipid methyltransferase)	4,84	3,41	1,46
<i>chaC</i>	b1218	regulatory protein for cation transport	1,58	3,07	1,32
<i>cheA</i>	b1888	fused chemotactic sensory histidine kinase (soluble) in two-component regulatory system with CheB and CheY	2,11	4,18	2,39
<i>cheY</i>	b1882	chemotaxis regulator transmitting signal to flagellar motor component	1,61	3,04	1,24
<i>cheZ</i>	b1881	chemotaxis regulator	1,93	3,49	1,71
<i>chiA</i>	b3338	periplasmic endochitinase	2,05	2,37	1,60
<i>clcA</i>	b0155	chloride channel, voltage-gated	1,15	2,07	0,86
<i>clpX</i>	b0438	ATPase and specificity subunit of ClpX-ClpP ATP-dependent serine protease	1,56	2,15	1,21
<i>cpxP</i>	b3913	periplasmic protein combats stress	0,75	1,06	2,05
<i>cpxR</i>	b3912	DNA-binding response regulator in two-component regulatory system with CpxA	1,79	2,09	1,36
<i>csgB</i>	b1041	curlin nucleator protein, minor subunit in curli complex	1,57	2,62	1,47
<i>csiE</i>	b2535	stationary phase inducible protein	1,46	2,85	1,87
<i>cueR</i>	b0487	DNA-binding transcriptional activator	2,50	1,73	1,56
<i>cutA</i>	b4137	copper binding protein, copper sensitivity	2,01	0,76	0,88
<i>cybC</i>	b4236	cytochrome b562, truncated (pseudogene)	1,76	2,03	1,21
<i>cysH</i>	b2762	3'-phosphoadenosine 5'-phosphosulfate reductase	2,21	0,57	0,15
<i>cysQ</i>	b4214	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosphate nucleotidase	1,61	4,32	1,88
<i>dacC</i>	b0839	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6a)	1,65	3,82	1,83
<i>dbpA</i>	b1343	ATP-dependent 3'--5' RNA helicase specific for 23S rRNA	2,55	3,85	1,24
<i>ddpA</i>	b1487	D-Ala-D-Ala transporter subunit -!- periplasmic-binding component of ABC superfamily	2,15	0,91	1,46
<i>ddpF</i>	b1483	D-Ala-D-Ala transporter subunit -!- ATP-binding component of ABC superfamily	2,01	5,46	1,46
<i>deoA</i>	b4382	thymidine phosphorylase	1,46	2,15	1,58
<i>deoC</i>	b4381	2-deoxyribose-5-phosphate aldolase, NAD(P)-linked	1,96	2,35	1,43
<i>deoD</i>	b4384	purine-nucleoside phosphorylase	1,73	2,28	1,44

Genname / b-Nummer	Genprodukt	Ratio			
		OD 4	NaCl	pH 5	
<i>djlC</i>	b0649	Hsc56 co-chaperone of HscC	0,95	2,25	0,79
<i>dppA</i>	b3544	dipeptide transporter -/- periplasmic-binding component of ABC superfamily	3,46	0,48	1,32
<i>dppB</i>	b3543	dipeptide transporter-/- membrane component of ABC superfamily	2,62	0,39	1,15
<i>dppC</i>	b3542	dipeptide transporter -/- membrane component of ABC superfamily	2,44	0,50	1,18
<i>dppD</i>	b3541	dipeptide transporter -/- ATP-binding component of ABC superfamily	2,51	0,48	1,05
<i>dppF</i>	b3540	dipeptide transporter -/- ATP-binding component of ABC superfamily	2,71	0,55	1,35
<i>dsbG</i>	b0604	periplasmic disulfide isomerase/thiol-disulphide oxidase	2,59	2,86	1,97
<i>dsrB</i>	b1952	predicted protein	2,40	2,26	1,55
<i>exuT</i>	b3093	hexuronate transporter	0,92	2,29	1,14
<i>fhIA</i>	b2731	DNA-binding transcriptional activator	2,75	4,54	1,85
<i>flgC</i>	b1074	flagellar component of cell-proximal portion of basal-body rod	1,50	2,54	1,57
<i>flhE</i>	b1878	conserved protein of flagellar operon	2,23	1,77	1,59
<i>fliJ</i>	b1942	flagellar protein	2,01	1,03	1,24
<i>flxA</i>	b1566	Qin prophage; predicted protein	2,65	2,36	1,11
<i>focA</i>	b0904	formate transporter	1,45	6,31	1,86
<i>frdA</i>	b4154	fumarate reductase (anaerobic) catalytic and NAD/flavoprotein subunit	1,03	3,00	1,15
<i>frlB</i>	b3371	fructoselysine-6-P-deglycase	2,35	3,07	1,13
<i>fruA</i>	b2167	fused fructose-specific PTS enzyme IIB'BC components	2,31	2,68	1,97
<i>fruK</i>	b2168	fructose-1-phosphate kinase	n.d.	4,14	1,87
<i>fsaA</i>	b0825	fructose-6-phosphate aldolase 1	n.d.	4,45	1,05
<i>fucA</i>	b2800	L-fuculose-1-phosphate aldolase	1,06	2,42	1,39
<i>gabT</i>	b2662	4-aminobutyrate aminotransferase, PLP-dependent	2,09	2,04	1,57
<i>gadE</i>	b3512	DNA-binding transcriptional activator	13,06	8,68	1,14
<i>gapC_1</i>	b1417	glyceraldehyde-3-phosphate dehydrogenase C, C-ter fragment (pseudogene)	1,51	2,45	1,82
<i>gapC_2</i>	b1416	glyceraldehyde-3-phosphate dehydrogenase C, N-ter fragment (pseudogene)	0,78	2,17	1,46
<i>garK</i>	b3124	glycerate kinase I	2,10	2,99	1,71
<i>garL</i>	b3126	alpha-dehydro-beta-deoxy-D-glucarate aldolase	1,82	2,92	1,92
<i>gcd</i>	b0124	glucose dehydrogenase	1,20	1,15	2,10
<i>gdhA</i>	b1761	glutamate dehydrogenase, NADP-specific	2,05	1,46	3,06
<i>ggt</i>	b3447	gamma-glutamyltranspeptidase	4,66	5,19	2,02
<i>glcB</i>	b2976	malate synthase G	1,34	2,97	1,59
<i>glgS</i>	b3049	predicted glycogen synthesis protein	1,31	3,93	2,47
<i>gloA</i>	b1651	glyoxalase I, Ni-dependent	1,51	2,17	1,38
<i>hcr</i>	b0872	HCP oxidoreductase, NADH-dependent	2,49	2,98	1,96
<i>hdeA</i>	b3510	stress response protein acid-resistance protein	11,26	9,16	1,65
<i>hdeB</i>	b3509	acid-resistance protein	6,61	4,46	1,28
<i>hdeD</i>	b3511	acid-resistance membrane protein	2,52	2,07	1,27
<i>hemH</i>	b0475	ferrochelataase	1,54	3,11	1,52
<i>hlyE</i>	b1182	hemolysin E	2,79	1,50	n.d.
<i>hscA</i>	b2526	DnaK-like molecular chaperone specific for IscU	2,11	5,49	0,93
<i>hslO</i>	b3401	heat shock protein Hsp33	1,96	2,54	1,40
<i>hyfD</i>	b2484	hydrogenase 4, membrane subunit	1,58	2,75	1,58
<i>idi</i>	b2889	isopentenyl diphosphate isomerase, different from other paralogs	1,49	2,55	1,54
<i>ihfA</i>	b1712	integration host factor (IHF), DNA-binding protein, alpha subunit	1,75	2,60	1,39
<i>ivbL</i>	b3672	ilvB operon leader peptide	2,03	1,42	1,12
<i>ivy</i>	b0220	inhibitor of vertebrate C-lysozyme	2,24	1,54	1,14
<i>kbl</i>	b3617	glycine C-acetyltransferase	0,71	2,29	0,91
<i>kch</i>	b1250	voltage-gated potassium channel	2,55	1,63	1,10
<i>lasT</i>	b4403	predicted rRNA methyltransferase	1,15	2,15	1,10
<i>lsrF</i>	b1517	predicted aldolase	1,21	4,87	2,09
<i>ltaE</i>	b0870	L-allo-threonine aldolase, PLP-dependent	1,13	3,37	2,04
<i>luxS</i>	b2687	S-ribosylhomocysteinase	1,96	2,41	1,48
<i>mak</i>	b0394	manno(fructo)kinase	1,54	2,67	1,47
<i>malP</i>	b3417	maltodextrin phosphorylase	1,48	8,70	5,22
<i>malQ</i>	b3416	4-alpha-glucanotransferase (amylomaltase)	1,24	3,09	1,91
<i>manX</i>	b1817	fused mannose-specific PTS enzyme IIAB components	1,05	2,34	0,82
<i>marC</i>	b1529	predicted transporter	n.d.	2,54	1,86

Genname / b-Nummer	Genprodukt	Ratio		
		OD 4	NaCl	pH 5
<i>mdtE</i>	b3513 multidrug resistance efflux transporter	3,48	1,38	0,99
<i>mdtI</i>	b1599 multidrug efflux system transporter	1,47	2,09	1,25
<i>menD</i>	b2264 bifunctional 2-oxoglutarate decarboxylase -/- SHCHC synthase	1,38	2,29	1,69
<i>mlrA</i>	b2127 DNA-binding transcriptional regulator	7,08	3,02	5,72
<i>mltB</i>	b2701 membrane-bound lytic murein transglycosylase B	1,79	2,94	1,46
<i>mntH</i>	b2392 manganese/divalent cation transporter	2,17	2,38	1,72
<i>mrcA</i>	b3396 fused penicillin-binding protein 1a murein transglycosylase -/- murein transpeptidase	1,41	2,55	0,92
<i>mscS</i>	b2924 mechanosensitive channel	2,73	3,28	1,07
<i>mtlA</i>	b3599 fused mannitol-specific PTS enzyme IIABC components	1,04	2,20	1,49
<i>nagB</i>	b0678 glucosamine-6-phosphate deaminase	1,99	3,32	1,95
<i>nanK</i>	b3222 predicted N-acetylmannosamine kinase	1,93	11,20	1,34
<i>napH</i>	b2204 ferredoxin-type protein essential for electron transfer from ubiquinol to periplasmic nitrate reductase (NapAB)	0,94	2,07	0,83
<i>narI</i>	b1227 nitrate reductase 1, gamma (cytochrome b(NR)) subunit	2,72	2,23	1,32
<i>nfi</i>	b3998 endonuclease V	n.d.	1,00	2,20
<i>nhaA</i>	b0019 sodium-proton antiporter	3,74	3,91	1,64
<i>nlpC</i>	b1708 predicted lipoprotein	1,03	2,15	0,87
<i>norV</i>	b2710 flavorubredoxin oxidoreductase	1,36	2,27	0,96
<i>nrdD</i>	b4238 anaerobic ribonucleoside-triphosphate reductase	1,71	10,18	2,12
<i>nrdE</i>	b2675 ribonucleoside-diphosphate reductase 2, alpha subunit	3,56	1,16	3,84
<i>nudC</i>	b3996 NADH pyrophosphatase	1,21	2,41	2,02
<i>ompA</i>	b0957 outer membrane protein A (3a;II*;G;d)	1,95	2,39	1,31
<i>ompG</i>	b1319 outer membrane porin	n.d.	6,06	n.d.
<i>ompR</i>	b3405 DNA-binding response regulator in two-component regulatory system with EnvZ	1,32	2,09	1,20
<i>ompX</i>	b0814 outer membrane protein	2,15	2,52	1,11
<i>paaX</i>	b1399 DNA-binding transcriptional regulator, aryl-CoA responsive	1,18	2,19	1,77
<i>paaY</i>	b1400 predicted hexapeptide repeat acetyltransferase	1,15	3,20	2,15
<i>pabA</i>	b3360 aminodeoxychorismate synthase, subunit II	1,55	3,04	2,36
<i>pfkA</i>	b3916 6-phosphofruktokinase I	1,50	1,95	2,08
<i>pfkB</i>	b1723 6-phosphofruktokinase II	2,07	2,49	1,71
<i>phnA</i>	b4108 predicted phosphonate metabolizing protein	1,20	0,99	2,20
<i>phnO</i>	b4093 predicted acyltransferase with acyl-CoA N-acyltransferase domain	1,49	2,48	1,32
<i>phr</i>	b0708 deoxyribodipyrimidine photolyase, FAD-binding	1,98	6,44	4,55
<i>pinQ</i>	b1545 Qin prophage; predicted site-specific recombinase	1,26	2,25	n.d.
<i>pinR</i>	b1374 Rac prophage; predicted site-specific recombinase	1,38	2,02	0,97
<i>pitA</i>	b3493 phosphate transporter, low-affinity	1,10	2,16	1,73
<i>polB</i>	b0060 DNA polymerase II	1,96	3,57	1,61
<i>potG</i>	b0855 putrescine transporter subunit -/- ATP-binding component of ABC superfamily	1,94	2,76	1,27
<i>poxA</i>	b4155 predicted lysyl-tRNA synthetase	2,16	2,62	1,78
<i>pphA</i>	b1838 serine/threonine-specific protein phosphatase 1	1,48	2,29	1,34
<i>prlC</i>	b3498 oligopeptidase A	1,65	2,20	1,40
<i>proP</i>	b4111 proline/glycine betaine transporter	4,90	0,79	1,40
<i>ptrB</i>	b1845 protease II	1,51	2,93	2,03
<i>ptsG</i>	b1101 fused glucose-specific PTS enzyme IIBC components	2,25	2,39	1,75
<i>pykA</i>	b1854 pyruvate kinase II	0,89	2,56	0,83
<i>ravA</i>	b3746 fused AAA+ ATPase	2,22	2,70	1,67
<i>rbn</i>	b3886 predicted inner membrane protein, previously thought to be tRNA processing exoribonuclease BN	n.d.	1,01	2,00
<i>rfaS</i>	b3629 lipopolysaccharide core biosynthesis protein	2,71	2,25	1,35
<i>rhlB</i>	b3780 ATP-dependent RNA helicase	2,57	2,30	1,71
<i>RhsC</i>	b0701 part of RhsC protein (b0700) in RhsC element	n.d.	3,08	1,47
<i>rluA</i>	b0058 pseudouridine synthase for 23S rRNA (position 746) and tRNA <sup>phe</sup> (position 32)	1,84	2,43	1,83
<i>rluD</i>	b2594 23S rRNA pseudouridine synthase	1,64	2,59	1,39
<i>rnk</i>	b0610 regulator of nucleoside diphosphate kinase	0,88	2,43	0,65
<i>rtcB</i>	b3421 conserved protein	1,25	2,12	1,48
<i>rutG</i>	b1006 predicted transporter	3,18	2,57	1,57

Genname / b-Nummer	Genprodukt	Ratio			
		OD 4	NaCl	pH 5	
<i>sbmC</i>	b2009	DNA gyrase inhibitor	1,72	3,09	1,50
<i>sfsA</i>	b0146	predicted DNA-binding transcriptional regulator	1,28	3,04	1,41
<i>slp</i>	b3506	outer membrane lipoprotein	3,68	2,79	1,08
<i>sodC</i>	b1646	superoxide dismutase, Cu, Zn	1,88	3,83	2,23
<i>speB</i>	b2937	agmatinase	1,26	1,71	2,34
<i>ssnA</i>	b2879	predicted chlorohydrolase/aminohydrolase	1,45	5,58	n.d.
<i>ssuE</i>	b0937	NAD(P)H-dependent FMN reductase	6,10	1,60	3,42
<i>sufA</i>	b1684	Fe-S cluster assembly protein	10,24	1,14	3,09
<i>sufB</i>	b1683	component of SufBCD complex	13,76	1,06	3,51
<i>sufC</i>	b1682	component of SufBCD complex, ATP-binding component of ABC superfamily	4,18	1,03	3,21
<i>sufD</i>	b1681	component of SufBCD complex	6,23	0,98	3,86
<i>sufE</i>	b1679	sulfur acceptor protein	3,38	1,02	3,42
<i>sufS</i>	b1680	selenocysteine lyase, PLP-dependent	4,76	1,08	4,06
<i>sugE</i>	b4148	multidrug efflux system protein	1,92	2,62	2,75
<i>tdh</i>	b3616	threonine 3-dehydrogenase, NAD(P)-binding, Zn-binding	0,75	2,55	0,97
<i>tesB</i>	b0452	acyl-CoA thioesterase II	1,38	2,20	1,14
<i>thiG</i>	b3991	thiamin biosynthesis ThiGH complex subunit	2,20	1,58	1,12
<i>trmA</i>	b3965	tRNA (uracil-5-)-methyltransferase	1,64	2,13	1,38
<i>udk</i>	b2066	uridine/cytidine kinase	1,96	3,66	1,72
<i>viaA</i>	b3745	predicted von Willibrand factor containing protein	1,67	2,02	1,26
<i>wecH</i>	b3561	predicted O-acetyltransferase	1,53	2,38	2,53
<i>yaaJ</i>	b0007	predicted transporter	1,41	4,00	0,86
<i>yaeJ</i>	b0191	conserved protein	1,53	2,17	1,20
<i>yaeR</i>	b0187	predicted lyase	1,34	2,15	1,68
<i>yafV</i>	b0219	predicted C-N hydrolase family amidase, NAD(P)-binding	1,18	2,61	1,47
<i>ybaA</i>	b0456	conserved protein	4,38	4,62	1,53
<i>ybaL</i>	b0478	predicted transporter with NAD(P)-binding Rossmann-fold domain	1,60	2,81	1,41
<i>ybaW</i>	b0443	conserved protein	2,04	3,30	1,14
<i>ybaZ</i>	b0454	predicted methyltransferase	1,12	2,06	1,17
<i>ybdR</i>	b0608	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	n.d.	10,34	1,22
<i>ybeM</i>	b0626	predicted C-N hydrolase superfamily, NAD(P)-binding amidase/nitrilase	2,10	2,27	1,90
<i>ybhB</i>	b0773	predicted kinase inhibitor	2,31	2,74	1,80
<i>ybhF</i>	b0794	fused predicted transporter subunits -/- ATP-binding components of ABC superfamily	1,63	2,15	0,98
<i>ybhG</i>	b0795	predicted membrane fusion protein (MFP) component of efflux pump, membrane anchor	1,25	2,76	0,99
<i>ybhN</i>	b0788	conserved inner membrane protein	n.d.	3,36	n.d.
<i>ybhO</i>	b0789	cardiolipin synthase 2	5,86	12,20	10,58
<i>ybhR</i>	b0792	predicted transporter subunit -/- membrane component of ABC superfamily	3,01	7,99	10,47
<i>ybiH</i>	b0796	predicted DNA-binding transcriptional regulator	n.d.	3,63	1,06
<i>ybiI</i>	b0803	conserved protein	n.d.	4,05	4,85
<i>ybiM</i>	b0806	predicted protein	2,27	2,67	1,86
<i>ybiN</i>	b0807	predicted SAM-dependent methyltransferase	1,57	3,12	1,90
<i>ybjQ</i>	b0866	conserved protein	1,98	3,06	1,47
<i>ybjR</i>	b0867	predicted amidase and lipoprotein	1,48	2,56	1,56
<i>ybjT</i>	b0869	conserved protein with NAD(P)-binding Rossmann-fold domain	0,93	2,03	1,56
<i>ycaP</i>	b0906	conserved inner membrane protein	4,30	7,59	4,62
<i>ycbB</i>	b0925	predicted carboxypeptidase	2,14	1,96	1,90
<i>ycbK</i>	b0926	conserved protein	1,64	2,28	1,31
<i>yccE</i>	b1001	predicted protein	2,86	2,91	1,80
<i>yccU</i>	b0965	predicted CoA-binding protein with NAD(P)-binding Rossmann-fold domain	n.d.	2,58	2,05
<i>ycfH</i>	b1100	predicted metallodependent hydrolase	2,39	2,50	1,71
<i>ycfM</i>	b1105	predicted outer membrane lipoprotein	1,80	2,39	1,43
<i>ycfR</i>	b1112	predicted protein	1,66	2,24	1,84
<i>ycgG</i>	b1168	conserved inner membrane protein	1,36	2,46	1,55
<i>ycgI</i>	b1173	predicted protein	1,16	2,27	1,34
<i>ychH</i>	b1205	predicted inner membrane protein	0,97	3,62	n.d.

Genname / b-Nummer	Genprodukt	Ratio		
		OD 4	NaCl	pH 5
<i>yciE</i>	b1257 conserved protein	1,90	16,66	n.d.
<i>yciQ</i>	b1268 predicted inner membrane protein	1,39	2,15	n.d.
<i>yciV</i>	b1266 conserved protein	1,79	2,25	1,50
<i>ycjY</i>	b1327 predicted hydrolase	n.d.	2,21	n.d.
<i>ydaN</i>	b1342 predicted Zn(II) transporter	1,83	2,84	1,68
<i>ydbC</i>	b1406 predicted oxidoreductase, NAD(P)-binding	1,13	2,01	0,91
<i>ydbK</i>	b1378 fused predicted Fe-S subunit of pyruvate-flavodoxin oxidoreductase	1,61	2,14	1,41
<i>ydcD</i>	b1457 predicted protein	2,77	1,05	1,08
<i>ydcJ</i>	b1423 conserved protein	7,36	1,74	1,32
<i>ydcK</i>	b1428 predicted enzyme	n.d.	8,32	7,80
<i>ydcT</i>	b1441 predicted spermidine/putrescine transporter subunit -/- ATP-binding component of ABC superfamily	7,71	2,54	1,98
<i>ydcU</i>	b1442 predicted spermidine/putrescine transporter subunit -/- membrane component of ABC superfamily	2,81	1,14	1,15
<i>ydcV</i>	b1443 predicted spermidine/putrescine transporter subunit -/- membrane component of ABC superfamily	11,68	n.d.	2,35
<i>ydcW</i>	b1444 gamma-aminobutyraldehyde dehydrogenase, NAD-dependent	7,01	1,71	1,90
<i>yddV</i>	b1490 predicted diguanylate cyclase	2,01	3,33	1,39
<i>ydeI</i>	b1536 conserved protein	n.d.	26,42	6,38
<i>ydfO</i>	b1549 Qin prophage; predicted protein	1,60	2,19	1,29
<i>ydfX</i>	b1568 Qin prophage; predicted protein	1,79	3,10	n.d.
<i>ydgD</i>	b1598 predicted peptidase	2,61	5,24	1,19
<i>ydhF</i>	b1647 predicted oxidoreductase, NADP-binding	1,36	3,74	1,96
<i>ydhK</i>	b1645 conserved inner membrane protein	1,50	2,15	1,28
<i>ydhL</i>	b1648 conserved protein	n.d.	4,38	2,50
<i>ydhM</i>	b1649 predicted DNA-binding transcriptional regulator	1,65	2,18	1,34
<i>ydhQ</i>	b1664 conserved protein	2,33	2,80	1,06
<i>ydhS</i>	b1668 conserved protein with FAD/NAD(P)-binding domain	2,14	2,34	2,61
<i>ydhW</i>	b1672 predicted protein	1,82	3,02	1,86
<i>ydhY</i>	b1674 predicted 4Fe-4S ferridoxin-type protein	1,30	2,70	1,57
<i>ydiN</i>	b1691 predicted transporter	2,32	1,23	0,97
<i>ydiV</i>	b1707 conserved protein	n.d.	1,04	3,47
<i>ydiZ</i>	b1724 predicted protein	4,89	6,11	1,88
<i>ydjL</i>	b1776 predicted oxidoreductase, Zn-dependent and NAD(P)-binding	2,20	1,10	1,08
<i>ydjN</i>	b1729 predicted transporter	2,63	0,69	0,18
<i>ydjZ</i>	b1752 conserved inner membrane protein	2,20	3,81	1,54
<i>yeaI</i>	b1785 predicted diguanylate cyclase	1,23	2,80	1,17
<i>yeaQ</i>	b1795 conserved inner membrane protein	n.d.	8,73	4,18
<i>yeaW</i>	b1802 predicted 2Fe-2S cluster-containing protein	1,90	3,98	4,25
<i>yebT</i>	b1834 conserved protein	2,12	2,64	1,80
<i>yebV</i>	b1836 predicted protein	3,78	2,49	2,66
<i>yebW</i>	b1837 predicted protein	2,23	3,75	1,94
<i>yedK</i>	b1931 predicted protein	1,90	3,66	3,14
<i>yedP</i>	b1955 conserved protein	1,41	2,62	2,01
<i>yedQ</i>	b1956 predicted diguanylate cyclase	2,42	3,64	1,88
<i>yedR</i>	b1963 predicted inner membrane protein	1,33	2,34	1,51
<i>yedY</i>	b1971 predicted sulfite oxidase, molybdenum containing subunit	3,11	3,45	1,82
<i>yeeF</i>	b2014 predicted amino-acid transporter	n.d.	2,19	1,08
<i>yeeJ</i>	b1978 adhesin	2,35	2,11	1,48
<i>yehE</i>	b2112 predicted protein	n.d.	8,16	5,84
<i>yehX</i>	b2129 predicted transporter subunit -/- ATP-binding component of ABC superfamily	1,95	7,56	1,81
<i>yehY</i>	b2130 predicted transporter subunit -/- membrane component of ABC superfamily	2,10	2,85	1,45
<i>yehZ</i>	b2131 predicted transporter subunit -/- periplasmic-binding component of ABC superfamily	5,61	14,36	2,37
<i>yfbE</i>	b2253 uridine 5'-(beta-1-threo-pentapyranosyl-4-ulose diphosphate) aminotransferase, PLP-dependent	2,73	9,04	1,55
<i>yfbF</i>	b2254 undecaprenyl phosphate-L-Ara4FN transferase	2,02	3,01	1,08

Genname / b-Nummer	Genprodukt	Ratio			
		OD 4	NaCl	pH 5	
<i>yfhB</i>	b2560	conserved protein	1,67	2,15	1,08
<i>yfiH</i>	b2593	conserved protein	1,36	2,04	1,21
<i>ygcF</i>	b2777	conserved protein	1,40	2,58	1,48
<i>ygcJ</i>	b2758	predicted protein	1,74	2,18	1,24
<i>ygcO</i>	b2767	predicted 4Fe-4S cluster-containing protein	1,18	2,44	1,54
<i>ygdI</i>	b2809	predicted protein	2,62	3,76	3,08
<i>ygeN</i>	b2858	predicted protein (pseudogene)	2,61	3,08	3,01
<i>ygfJ</i>	b2877	conserved protein	1,70	3,98	1,63
<i>yghF</i>	b2970	predicted secretion pathway protein, C-type protein	3,89	2,31	1,82
<i>yghK</i>	b2975	glycolate transporter	1,60	2,00	0,70
<i>yghY</i>	b3000	predicted dienlactone hydrolase (pseudogene)	2,51	3,79	1,68
<i>ygiE</i>	b3040	zinc transporter	2,39	3,14	1,73
<i>ygiL</i>	b3043	predicted fimbrial-like adhesin protein	2,88	5,48	0,94
<i>ygiV</i>	b3023	predicted transcriptional regulator	2,64	2,51	1,45
<i>ygiF</i>	b3068	G/U mismatch-specific DNA glycosylase	1,84	2,53	2,03
<i>yhaO</i>	b3110	predicted transporter	n.d.	3,53	n.d.
<i>yhbP</i>	b3154	conserved protein	1,07	2,00	1,36
<i>yhbW</i>	b3160	predicted enzyme	2,31	5,07	1,04
<i>yhcH</i>	b3221	conserved protein	1,53	3,03	1,01
<i>yhcN</i>	b3238	conserved protein	1,52	3,44	1,09
<i>yhdH</i>	b3253	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	1,24	2,93	1,45
<i>yhiM</i>	b3491	conserved inner membrane protein	7,76	2,49	2,37
<i>yhiP</i>	b3496	predicted transporter	1,11	4,84	1,02
<i>yhjQ</i>	b3534	cell division protein (chromosome partitioning ATPase) (pseudogene)	1,70	2,49	1,69
<i>yhjY</i>	b3548	conserved protein	3,27	4,40	1,99
<i>yiaC</i>	b3550	predicted acyltransferase with acyl-CoA N-acyltransferase domain	4,05	2,99	1,21
<i>yiaF</i>	b3554	conserved protein	3,93	3,38	1,30
<i>yibF</i>	b3592	predicted glutathione S-transferase	1,50	2,60	1,03
<i>yibG</i>	b3596	conserved protein	2,40	1,89	1,13
<i>yibI</i>	b3598	predicted inner membrane protein	3,37	3,42	1,56
<i>yieK</i>	b3718	predicted 6-phosphogluconolactonase	1,71	2,68	1,82
<i>yihI</i>	b3866	conserved protein	1,51	2,42	1,65
<i>yiiM</i>	b3910	conserved protein	1,73	2,08	1,74
<i>yjbB</i>	b4020	predicted transporter	1,81	2,15	1,31
<i>yjeE</i>	b4168	ATPase with strong ADP affinity	1,77	2,55	1,30
<i>yjeF</i>	b4167	predicted carbohydrate kinase	3,52	4,89	1,96
<i>yjeS</i>	b4166	predicted Fe-S electron transport protein	3,19	4,45	1,85
<i>yjfN</i>	b4188	predicted protein	1,39	2,42	2,51
<i>yjfO</i>	b4189	conserved protein	1,06	4,88	2,61
<i>yjfY</i>	b4199	predicted protein	3,66	8,62	5,19
<i>yjgA</i>	b4234	conserved protein	2,09	1,67	2,31
<i>yjhS</i>	b4309	conserved protein	2,00	4,51	n.d.
<i>yjiD</i>	b4326	DNA replication/recombination/repair protein	1,26	2,06	1,11
<i>yjiN</i>	b4336	conserved inner membrane protein	n.d.	6,85	3,45
<i>yjiV</i>	b4343	conserved protein (pseudogene)	1,12	2,18	1,31
<i>yjjN</i>	b4358	predicted oxidoreductase, Zn-dependent and NAD(P)-binding	0,88	2,15	0,91
<i>yjjU</i>	b4377	predicted esterase	2,69	1,35	0,78
<i>yjjV</i>	b4378	predicted DNase	2,34	1,14	0,76
<i>yjjY</i>	b4402	predicted protein	2,36	2,59	1,40
<i>ykfB</i>	b0250	CP4-6 prophage; predicted protein	1,15	2,05	1,29
<i>ykff</i>	b0235	conserved protein	1,59	2,04	1,16
<i>ylil</i>	b0837	predicted dehydrogenase	4,71	7,93	4,13
<i>yndC</i>	b1046	predicted group transfer	1,69	2,35	1,77
<i>ymfC</i>	b1135	23S rRNA pseudouridine synthase	1,73	2,05	1,31
<i>ymgB</i>	b1166	predicted protein	3,30	3,84	n.d.
<i>ymgE</i>	b1195	predicted inner membrane protein	n.d.	8,68	5,86
<i>yncC</i>	b1450	predicted DNA-binding transcriptional regulator	2,31	2,98	2,08

Genname / b-Nummer	Genprodukt	Ratio		
		OD 4	NaCl	pH 5
<i>yncD</i>	b1451 predicted iron outer membrane transporter	1,33	3,67	0,88
<i>yneE</i>	b1520 conserved inner membrane protein	2,37	3,05	1,47
<i>ynfC</i>	b1585 predicted protein	1,69	2,83	1,24
<i>ynfD</i>	b1586 predicted protein	2,62	4,33	4,06
<i>yniA</i>	b1725 predicted phosphotransferase/kinase	1,03	4,37	1,63
<i>ynjA</i>	b1753 conserved protein	1,01	3,14	1,58
<i>yoaC</i>	b1810 predicted protein	3,02	3,33	2,72
<i>yodA</i>	b1973 conserved metal-binding protein	n.d.	2,85	n.d.
<i>yohC</i>	b2135 predicted inner membrane protein	2,79	3,17	n.d.
<i>yohD</i>	b2136 conserved inner membrane protein	2,51	3,98	1,47
<i>yojI</i>	b2211 fused microcin transport subunits -/- membrane component and ATP-binding component of ABC superfamily	3,02	0,95	1,06
<i>yopf</i>	b2475 conserved protein	1,88	2,11	1,86
<i>yphG</i>	b2549 conserved protein	2,64	2,51	1,54
<i>yqeB</i>	b2875 conserved protein with NAD(P)-binding Rossmann fold	0,81	2,02	1,03
<i>yqjF</i>	b3101 predicted quinol oxidase subunit	1,18	4,31	1,64
<i>yraR</i>	b3152 predicted nucleoside-diphosphate-sugar epimerase	1,62	2,25	1,78
<i>yrbB</i>	b3446 predicted protein	1,96	2,15	0,00
<i>ytfI</i>	b4215 predicted protein	1,05	2,57	1,78
<i>ytfJ</i>	b4216 predicted transcriptional regulator	1,11	3,27	1,36
<i>ytfK</i>	b4217 conserved protein	2,18	4,55	2,30
<i>zitB</i>	b0752 zinc efflux system	1,59	3,16	1,07

Nicht mehr annotiert sind b0609 und b1005. Neu annotiert wurde b3913 (cpxP) -> b4484 und b4343 (yjiV) -> b4688. Siehe *E. coli* Genome Project (<http://www.genome.wisc.edu/sequencing/updating.htm>) und (Serres et al., 2004).



## A.2 $\sigma^S$ -reprimierte Gene

**Tabelle 13:** 95  $\sigma^S$ -reprimierte Gene (relative Expressionslevel < 0,5). Zur Erläuterung siehe auch Abschnitt 3.1.2. „Circa 10% aller Gene in E. coli sind RpoS-abhängig“ im Ergebnisteil. n.d. (nicht detektierbares Signal). Die Werte stellen den Durchschnitt aus drei biologisch unabhängigen Microarrayanalysen dar.

Genname / b-Nummer	Genprodukt	Ratio			
		OD4	NaCl	pH 5	
acnB	b0118	bifunctional aconitate hydratase 2 -/- 2-methylisocitrate dehydratase	0,71	0,55	0,44
aldA	b1415	aldehyde dehydrogenase A, NAD-linked	0,70	0,41	0,49
aphA	b4055	acid phosphatase/phosphotransferase, class B, non-specific	0,69	0,50	0,64
cirA	b2155	ferric iron-catecholate outer membrane transporter	0,99	0,21	0,89
cpdB	b4213	2':3'-cyclic-nucleotide 2'-phosphodiesterase	0,53	0,47	0,69
cpsB	b2049	mannose-1-phosphate guanyltransferase	0,67	0,41	0,68
cyoB	b0431	cytochrome o ubiquinol oxidase subunit I	0,71	0,48	0,74
cyoE	b0428	protoheme IX farnesyltransferase	0,77	0,50	0,75
cysH	b2762	3'-phosphoadenosine 5'-phosphosulfate reductase	2,21	0,57	0,15
cysK	b2414	cysteine synthase A, O-acetylserine sulfhydrylase A isozyme	1,07	0,67	0,41
cysU	b2424	sulfate/thiosulfate transporter subunit	0,92	0,62	0,15
dnaK	b0014	chaperone Hsp70, co-chaperone with DnaJ	0,77	0,50	0,76
dppA	b3544	dipeptide transporter -/- periplasmic-binding component of ABC superfamily	3,46	0,48	1,32
dppB	b3543	dipeptide transporter -/- membrane component of ABC superfamily	2,62	0,39	1,15
dppC	b3542	dipeptide transporter -/- membrane component of ABC superfamily	2,44	0,50	1,18
dppD	b3541	dipeptide transporter -/- ATP-binding component of ABC superfamily	2,51	0,48	1,05
dut	b3640	deoxyuridinetriphosphatase	0,69	0,50	0,76
entA	b0596	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase, NADH-dependent	0,85	0,48	0,79
entB	b0595	isochorismatase	0,92	0,41	0,86
entC	b0593	isochorismate synthase 1	0,80	0,50	1,12
entE	b0594	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex	0,86	0,40	1,15
fadA	b3845	3-ketoacyl-CoA thiolase (thiolase I)	0,44	1,05	0,76
fadB	b3846	fused 3-hydroxybutyryl-CoA epimerase/delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase/enoyl-CoA hydratase -/- 3-hydroxyacyl-CoA dehydrogenase	0,43	0,73	0,43
fcl	b2052	bifunctional GDP-fucose synthetase: GDP-4-dehydro-6-deoxy-D-mannose epimerase and GDP-4-dehydro-6-L-deoxygalactose reductase	n.d.	0,27	1,13
fepA	b0584	iron-enterobactin outer membrane transporter	1,34	0,35	0,98
fhuE	b1102	ferric-rhodotorulic acid outer membrane transporter	0,96	0,40	0,85
gatA	b2094	galactitol-specific enzyme IIA component of PTS	0,83	0,44	0,60
gatB	b2093	galactitol-specific enzyme IIB component of PTS	0,75	0,29	0,62
gatC	b2092	galactitol-specific enzyme IIC component of PTS	0,66	0,31	0,63
gatY	b2096	D-tagatose 1,6-bisphosphate aldolase 2, subunit	0,83	0,44	0,65
gatZ	b2095	D-tagatose 1,6-bisphosphate aldolase 2, predicted tag6P kinase subunit	0,87	0,42	0,60
glpA	b2243	sn-glycerol-3-phosphate dehydrogenase (anaerobic), small Fe4S subunit	1,27	0,73	0,48
glpQ	b2239	periplasmic glycerophosphodiester phosphodiesterase	0,74	0,96	0,38
glpT	b2240	sn-glycerol-3-phosphate transporter	0,76	0,69	0,33
gltF	b3214	periplasmic protein	1,01	0,43	0,72
glyA	b2551	serine hydroxymethyltransferase	0,67	0,48	0,61
gmd	b2053	GDP-D-mannose dehydratase, NAD(P)-binding domain	1,03	0,25	0,77
groL	b4143	Cpn60 chaperonin GroEL, large subunit of GroESL	0,65	0,44	0,75
groS	b4142	Cpn10 chaperonin GroES, small subunit of GroESL	0,77	0,43	0,71
guaB	b2508	IMP dehydrogenase	0,96	0,49	0,69
guaC	b0104	GMP reductase	0,93	0,43	0,81
icd	b1136	e14 prophage; isocitrate dehydrogenase, specific for NADP+	0,63	0,38	0,60
ilvC	b3774	ketol-acid reductoisomerase, NAD(P)-binding	1,08	0,47	1,06
mgIA	b2149	fused methyl-galactoside transporter subunitsI -/- ATP-binding components of ABC superfamily	0,52	0,85	0,38
mgIC	b2148	methyl-galactoside transporter subunit	0,48	0,94	0,40
mgo	b2210	malate dehydrogenase, FAD/NAD(P)-binding domain	1,32	1,17	0,44
ndk	b2518	multifunctional nucleoside diphosphate kinase -/- apyrimidinic endonuclease -/-	0,40	0,59	0,59

Genname / b-Nummer	Genprodukt	Ratio			
		OD4	NaCl	pH 5	
	3'-phosphodiesterase				
nirD	b3366	nitrite reductase, NAD(P)H-binding, small subunit	0,58	0,46	0,56
ompF	b0929	outer membrane porin 1a (Ia;b;F)	0,25	0,26	0,69
ompT	b0565	DLP12 prophage; outer membrane protease VII (outer membrane protein 3b)	0,61	0,45	0,46
paaA	b1388	multicomponent phenylacetyl-CoA oxygenase subunit	0,47	n.d.	n.d.
paaC	b1390	multicomponent phenylacetyl-CoA oxygenase subunit	0,40	n.d.	n.d.
pntA	b1603	pyridine nucleotide transhydrogenase, alpha subunit	0,67	0,49	0,63
pqqL	b1494	predicted peptidase	n.d.	0,40	n.d.
proW	b2678	glycine betaine transporter subunit	1,14	0,47	0,69
pspE	b1308	thiosulfate:cyanide sulfurtransferase (rhodanese)	0,48	0,97	0,71
pta	b2297	phosphate acetyltransferase	1,00	0,94	0,45
purC	b2476	phosphoribosylaminoimidazole-succinocarboxamide synthetase	0,68	0,47	0,86
purN	b2500	phosphoribosylglycinamide formyltransferase 1	0,74	0,44	0,74
pyrB	b4245	aspartate carbamoyltransferase, catalytic subunit	0,58	0,15	0,86
pyrC	b1062	dihydro-orotase	0,68	0,32	0,75
pyrD	b0945	dihydro-orotate oxidase, FMN-linked	0,86	0,44	0,82
pyrI	b4244	aspartate carbamoyltransferase, regulatory subunit	0,64	0,31	0,85
rhaT	b3907	L-rhamnose:proton symporter	0,49	0,92	0,86
rplW	b3318	50S ribosomal subunit protein L23	0,68	0,74	0,46
rpsJ	b3321	30S ribosomal subunit protein S10	0,71	0,73	0,50
sdhA	b0723	succinate dehydrogenase, flavoprotein subunit	0,61	0,59	0,45
sdhB	b0724	succinate dehydrogenase, FeS subunit	0,65	0,64	0,49
sdhC	b0721	succinate dehydrogenase, membrane subunit, binds cytochrome b556	0,62	0,46	0,45
sdhD	b0722	succinate dehydrogenase, membrane subunit, binds cytochrome b556	0,57	0,77	0,42
shiA	b1981	shikimate transporter	0,95	0,48	0,87
spr	b2175	predicted peptidase, outer membrane lipoprotein	0,50	0,37	0,59
tdcB	b3117	catabolic threonine dehydratase, PLP-dependent	0,47	n.d.	0,61
tiaE	b3553	2-keto-D-gluconate reductase (glyoxalate reductase) (2-ketoaldonate reductase)	0,94	0,50	0,74
tktA	b2935	transketolase 1, thiamin-binding	0,55	0,35	0,50
tnaA	b3708	tryptophanase/L-cysteine desulfhydrase, PLP-dependent	0,57	0,83	0,35
tnaB	b3709	tryptophan transporter of low affinity	0,48	0,95	0,77
ucpA	b2426	predicted oxidoreductase, sulfate metabolism protein, SDR family	0,48	0,89	0,68
ugd	b2028	UDP-glucose 6-dehydrogenase	n.d.	0,27	n.d.
wcaB	b2058	predicted acyl transferase	0,95	0,49	0,83
wcaJ	b2047	predicted UDP-glucose lipid carrier transferase	1,08	0,48	n.d.
wza	b2062	lipoprotein required for capsular polysaccharide translocation through the outer membrane	1,09	0,21	0,91
wzc	b2060	protein-tyrosine kinase	0,97	0,45	n.d.
ycdO	b1018	conserved protein	0,73	0,43	0,64
yciI	b1251	predicted enzyme	0,72	0,42	0,74
yddB	b1495	predicted porin protein	0,92	0,42	0,68
ydjN	b1729	predicted transporter	2,63	0,69	0,18
yeiC	b2166	predicted kinase	0,37	1,21	0,83
yeiN	b2165	conserved protein	0,39	1,23	1,01
yeiT	b2146	predicted oxidoreductase subunit	1,05	n.d.	0,41
ygaH	b2683	predicted inner membrane protein	0,76	0,48	0,88
ygaX	b2680	predicted transporter	1,13	0,45	1,04
yhcA	b3215	predicted periplasmic chaperone protein	0,75	0,44	0,70
yjbF	b4027	predicted lipoprotein	1,01	0,40	0,93
yncE	b1452	conserved protein	0,77	0,50	0,62