

Supporting Information for

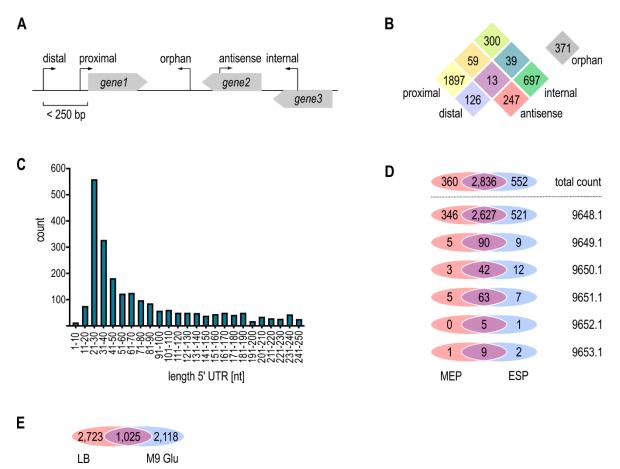
The global RNA-RNA interactome of *Klebsiella pneumoniae* unveils a small RNA regulator of cell division

Eric Ruhland, Malte Siemers, Ruman Gerst, Felix Späth, Laura Nicole Vogt, Marc Thilo Figge, Kai Papenfort, Kathrin Sophie Fröhlich

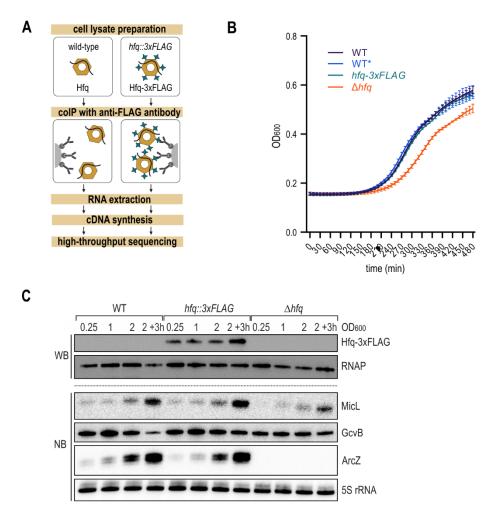
corresponding author: Kathrin Sophie Fröhlich Email: kathrin.froehlich@uni-jena.de

This PDF file includes:

Figures S1 to S12 Supporting Methodology Tables S1 to S5 SI References

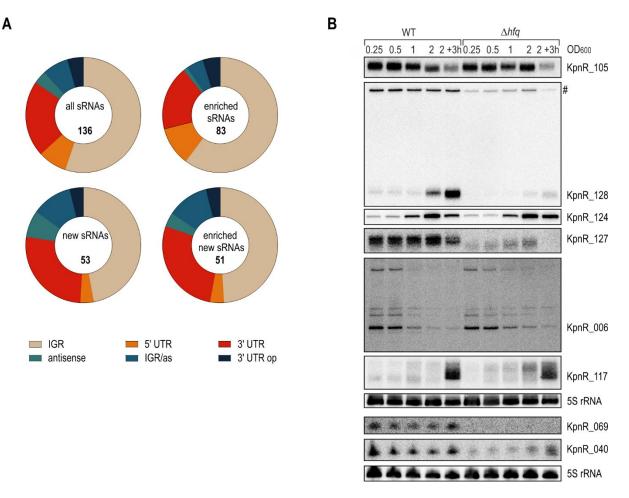


Annotation and classification of transcriptional start sites (TSSs) in *K. pneumoniae* MGH 78578. (A) TSSs were categorized according to their genomic positions. Proximal and distal TSSs are associated with a gene if located ≤ 250 bp upstream of the start codon on the same strand. Antisense TSSs are located on the opposite strand of an annotated gene, internal TSSs within an annotated gene on the sense strand. A TSS not assigned to any of these categories is classified as orphan. (B) Distribution and overlap of classification for 3,748 TSSs identified in this study. (C) Distribution of the lengths of 5' UTRs based on proximal and distal TSSs. (D) Overlap (purple) among TSSs detected in MEP (red) and ESP (blue) distributed between the core genome (9648.1) and the five plasmids (9649.1; 9650.1; 9651.1; 9652.1; 9653.1) in *K. pneumoniae* MGH 78578. (E) Overlap (purple) among TSSs detected in *K. pneumoniae* MGH 78578 in this study for cells grown in LB (red) or in (1) for cells cultivated in minimal M9 medium supplemented with glucose (blue).

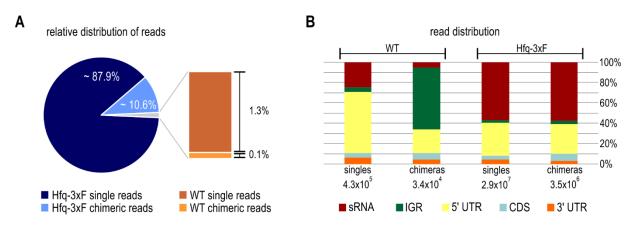


RNA co-immunoprecipitation and expression profiles of *K. pneumoniae*. (A) Strategy to identify Hfq-associated RNA. RNA was co-immunoprecipitated from *K. pneumoniae* (wild-type or chromosomal *hfq::3xFLAG*) using an anti-FLAG antibody. RNA was purified, converted to cDNA, and subjected to high-throughput sequencing. (B) Growth curve of different *K. pneumoniae* strains (wild-type with [WT] or without [WT*] plasmids pKpn4 and pKpn6; chromosomal mutant *hfq::3xFLAG*; chromosomal mutant Δhfq) grown in LB medium. (C) Expression analysis of Hfq-3xFLAG and conserved Hfq-dependent sRNAs. WT and mutant cells (*hfq::3xFLAG* and Δhfq) were grown in LB. Total protein and total RNA samples were collected at indicated optical densities (0.25 to 2 and 3h after cells reached OD₆₀₀ of 2) and subjected to analysis via Western blotting (WB; upper panel) and Northern blotting (NB; lower panel), respectively. RNAP and 5S rRNA served as loading controls.





RIP-seq analysis of Hfq-bound sRNAs and expression profiles of selected sRNA candidates. (A) Relative distribution of different sRNA types annotated in *K. pneumoniae* (left), and distribution of different sRNA types enriched ≥3-fold in the co-IP sample compared to the WT control (right). sRNAs are categorized by their genomic location (IGR: free-standing sRNA gene in intergenic region; 5' UTR: processed from mRNA 5' end; 3' UTR: processed from mRNA 3' end; antisense: antisense to an annotated gene; IGR/as: free-standing sRNA gene in intergenic region extending into an annotated gene; 3' UTR op: free-standing sRNA gene overlapping the 3' end of an annotated gene). (B) Total RNA samples of WT and Δhfq cells were collected at indicated time-points (OD₆₀₀ of 0.25 to 2 and 3h after cells reached OD₆₀₀ of 2) during growth in LB and subjected to Northern blot analysis. KpnR_128 is expressed from its own promoter internal to another transcriptional unit positioned upstream. Both transcripts share the same termination site and the ~300 nt transcript (#) is thus detected by the Kpn_R128 probe. 5S rRNA served as loading control.



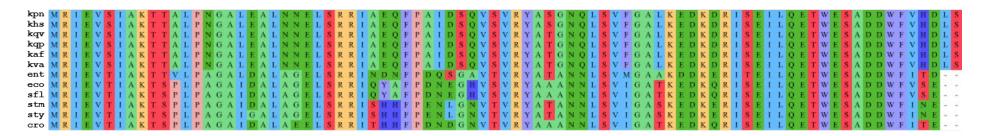
Relative read distribution in the RIL-seq experiment. (A) Distribution of filtered single and chimeric reads in samples recovered from the RIL-seq experiment in *K. pneumoniae* wild-type (WT) or *hfq::3xFLAG* (Hfq-3xF) cells. (B) Distribution of different RNA classes in single and chimeric reads in samples recovered from the RIL-seq experiment in *K. pneumoniae* wild-type or *hfq::3xFLAG* cells.

Α

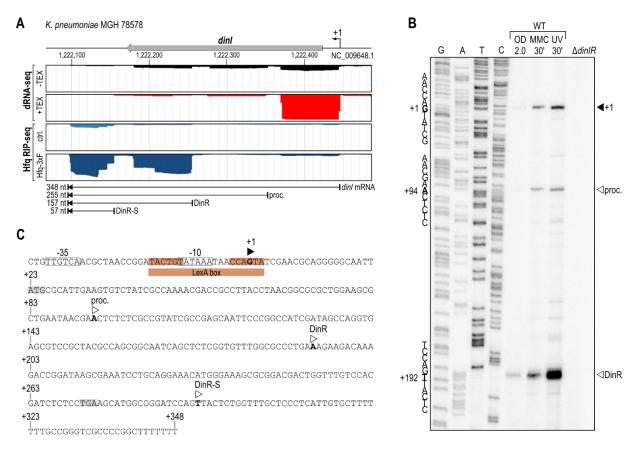
+1 dinl mRNA -35 -10 start kpn kqv khs kqp kaf kva CCTGTTGTCATTAGGTTATTTACCTGTATAAATAACCAGTATATTCAACAGGGGGGCTATTATGCGAATTGAAGTCACCATAGCGAAAACTTCTCCATTGCCAGCTGGGGGCTATTGACGCCCTGGCGGGCCCCTGGCCGGC eco sfl stm sty cro ent LexA box DinR proc. kpn GAACTCTCTCGCCGTATCGCCGAGCAATTCCCCGGCCATCGATAGCCAGGTGAGCGTCCGCTACGCCAGCGGCAATCAGCTCTCGGTGTTTGGCGCCCCTGAAAGAAGAAGAAGACCAGAGACGAGAAAGCCGGAAATCCC kqv khs GAACTCTCTCGCCGTATCGCCGAGCAATTCCCCGGCCATCGATAGCCAGGTGAGCGTCCGCTACGCCACCGGTAATCAGCTCTCGGTGTTTGGCGCCCCTGAAAGAAGAAGAAGACCAGAGACAAAGACCGGATAAGCGAAATCC kqp kaf GAACTCTCTCGCCGTATCGCCGAGCAATTCCCCGGCCATCGATAGCCAGGTGAGCGTCCGCTACGCCACCGGAAACCAGCTCTCGGTGTTTGGCGCCCCTGAAAGAAGAAGAAGACCAGGTGAGCGAAATCC kva GAACTCTCCCGGCGTATCGCCGAGCAATTCCCCGGCCATCGACAGTCAGGTGAGCGTGCGCCTACGCCACCGGCAACCAGCTCTCGGTGTTCGGCGCCCCTGAAAGAAGAAGAAGACAAAGACCAGACAAAGCGAAATCC eco sfl GAACTTTCCCGCCGTATTCAGTATGCGTTTCCTGATAATGAAGGCCACGTATCGGTACGTTATGCCGCAGCGAATAATTTATCGGTTATTGGCGCAACAAAAGAAGATAAACAGCGCATTAGCGAAAATTC GAACTCTCCCGCCGTATTAGCCATCATTTTCCCGAGAAATTTGGGTAACGTCACCGTGCGTTACGCTACCGCCAACAACTTGTCCGTCATTGGCGCATCAAAAGAGGACAAAGAACGACGCATTAGCGAGATTC stm GAACTCTCCCGCCGTATTAGCCATCATTTTCCTGAGAATTTGGGTAACGTCACCGTGCGTTACGCTACCGCCAACAACTTGTCCGTCATTGGCGCGTCAAAAGAGGATAAAGAACGACGATTAGCGAGATTC sty GAACTCTCTCGTCGTATTACCCACCACTTCCCCCGATAACGACGGCAACGTCACCGTGCGTTATGCCGCGGCGAATAATTTGTCCGTCATCGGCGCGACAAAAGAAGAAGAAGACAGCGTATCAGCGAAAATTC cro ent

	stop	terminator
kpn	TGCAGGAAACATGGGAAAGCGCGGACGACTGGTTTGTCCACGATCTCTCCTGAAGCATGGCGGGATCCAGTTACTCTGGTTTGCTCCCTCATTGTGCTTT	TTTT-GCCGGGTCGCCCCGGCTTTTTT
kqv	TGCAGGAAACATGGGAAAGCGCGGACGACTGGTTTGTCCACGATCTCTCCTGAAGCATGGCGGGATCCAGTTACTCTGGTTTGCTCCCTCATTGTGCTTT	TTTT-GCCGGGTCGCCCCGGCTTTTTT
khs	TGCAGGAAACATGGGAAAGCGCGGACGACTGGTTTGTCCACGATCTCTCCTGAAGCATGGCGGGATCCAGTTACTCTGGTTTGCTCCCTCATTGTGCTTT	TTTT-GCCGGGTCGCCCCGGCTTTTTT
kqp	TGCAGGAAACATGGGAAAGCGCGGACGACTGGTTTGTCCACGATCTCTCCTGGAGGCGGGATCCAGTTACTCTGGTTTGCTCCCTCATTGTGCTTT	TTTTT GCCGGGTCGCCCCGGCTTTTTT
kaf	TGCAAGAAACCTGGGAAAGCGCGGACGACTGGTTTGTCCACGATCTCTCCTGGAGCGGGATCCAGTTACTCTGGTTTGCTCCCTCATTGTGCTTT	TTTT-GCCGGGTCGCCCCGGCTTTTTT
kva	TGCAGGAAACCTGGGAAAGCGCGGACGACTGGTTTGTCCACGATCTCTCCTGGAGGCGGGATCCAGTTACTCTGGTTTGCTCCCTCATTGTGCTTT	TCTTTGCCGGGTCGCCCCGGCTTTTTT
eco	TCCAGGAAACGTGGGAAAGCGCCGATGACTGGTTTGTCAGCGAATAATAATATGCAGTGATTTTT-	TTTGCCGGGTCGCCCGGCTTTTTT
sfl	TCCAGGAAACGTGGGAAAGCGCCGATGACTGGTTTGTCAGCGAATAATAATATGCAGTGATTTTTG	TTTTT GCCGGATCGCCCCGGCTTTTTT
stm	TCCAGGAGACCTGGGAGAGCGCTGATGACTGGTTCATCAATGAATAAAAAAATGTAAAAAAATGATATGCAGTGATGATGT-ATG	TTTGCCGGGTCGCCCGGCTTTTTT
sty	TCCAGGAGACCTGGGAGAGCGCTGATGACTGGTTCATCAATGAATAAAAAAATGTAAAAAAATGATATGCAGTGATGATGT-ATG	TTTGCCGGGTCGCCCCGGCTTTTTT
cro	TCCAGGAAACCTGGGAAAGCGCCGATGACTGGTTCATTACAGAATAAAAAGTAAAAAAGCTCTGCCGTTGTGT	TTTGCCGGGTCGCCCCGGCTTTTTT
ent	TCCAGGAAACCTGGGAAAGCGCCGACGACTGGTTTATCACAGATTAATATTAATATTGCTCCTCCTCATTGTTT	TCTTTGCCGGGTCGCCCGGCTTTTTTT

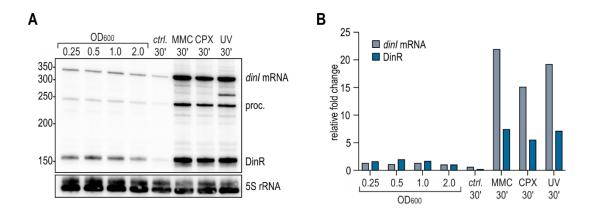




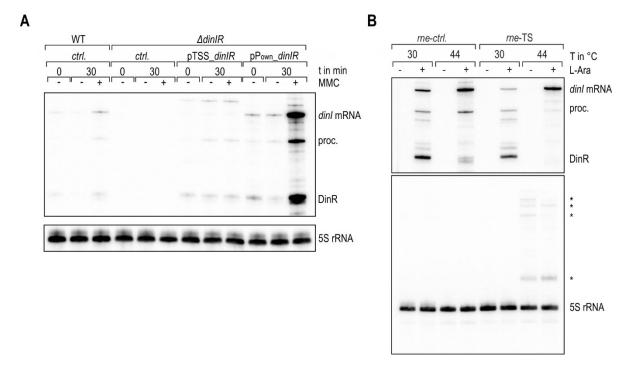
Conservation of *dinl* **in enterobacteria.** (A) Multiple alignment of the *dinl* gene of different enterobacterial species (kpn: *Klebsiella pneumoniae* MGH 78578; kqv: *Klebsiella quasivariicola* 08A119; khs: *Klebsiella pneumoniae* subsp. pneumoniae HS11286; kqp: *Klebsiella quasipneumoniae* KqPF26; kaf: *Klebsiella africana* 200023; kva: *Klebsiella variicola* LEMB11; eco: *Escherichia coli* MG1655; sfl: *Shigella flexneri* 301; stm: *Salmonella* Typhimurium LT2; sty: *Salmonella typhi* CT18; cro: *Citrobacter rodentium* ICC168; ent: *Enterobacter sp.* 638) was calculated using the MultAlin tool (2). Nucleotides are colored regarding their degree of conservation (red: high conservation; blue: partial conservation; black: little or no conservation). The -10 and -35 elements of the *dinl* promoter, as well as the start and stop codons and the Rho-independent terminator are boxed, the transcriptional start site (as determined for *K. pneumoniae*; compare Fig. S6) is indicated by an arrow. The 5' ends of the two most abundant processing intermediates (proc. and DinR) from *dinl* mRNA in *K. pneumoniae* MGH 78578 are indicated by open triangles. The LexA box of *dinl* (as determined for *E. coli* in (3, 4)) is highlighted in orange. (B) Multiple alignment of the Dinl protein of different enterobacterial species (as in (A)) was calculated using the MAFFT tool (5).



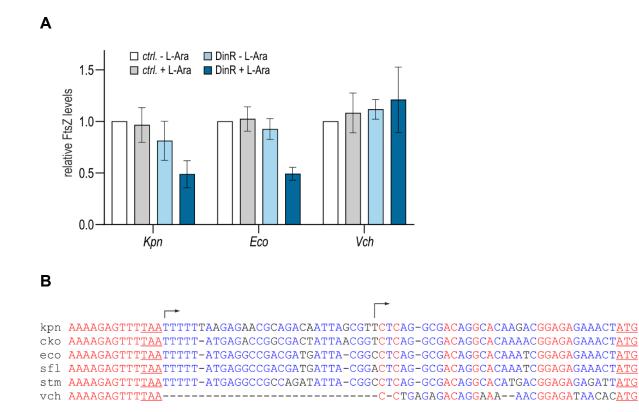
Determination of the 5' ends of dinl mRNA and its major processing products. (A) Readmappings of dRNA-seq (-TEX: black traces; +TEX: red traces) and Hfq RIP-seq (control: light blue traces; Hfq-3xFLAG: dark blue traces) to the dinl locus. The y-axes in individual experiments were set to the same scale. The positions on the K. pneumoniae MGH 78578 genome are indicated above the sequencing traces, and the *dinl* CDS is indicated by a grey arrow. The TSS of *dinl* was determined by analysis of the dRNA-seq dataset, and is marked by a black arrow. Stable processing products were identified from dRNA-seg and Hfg RIP-seg and sizes are below the panels. (B) Primer extension analysis of *dinl* mRNA (using a genespecific primer). RNA was extracted from wild-type cells at OD₆₀₀ of 2.0, and 30 min after DNA damage was induced through mitomycin C (MMC) or ultraviolet light (UV). RNA purified from dinIR mutant cells served as a control. The 5' ends of dinI mRNA (black arrowhead) and its processing products (proc. and DinR; open arrowheads; DinR-S is too close to the 3' end to be resolved in this experiment) were mapped using a sequencing ladder, and correspond to the sites determined by dRNA-seq. (C) Sequence at the dinl locus of K. pneumoniae MGH 78578. The -35 and -10 elements of the *dinl* promoter are boxed, the LexA box is high-lighted in orange. The 5' ends of dinl mRNA (black arrowhead) and its processing products (proc., DinR, DinR-S; open arrowheads) are indicated. Numbering refers to the TSS as position +1.



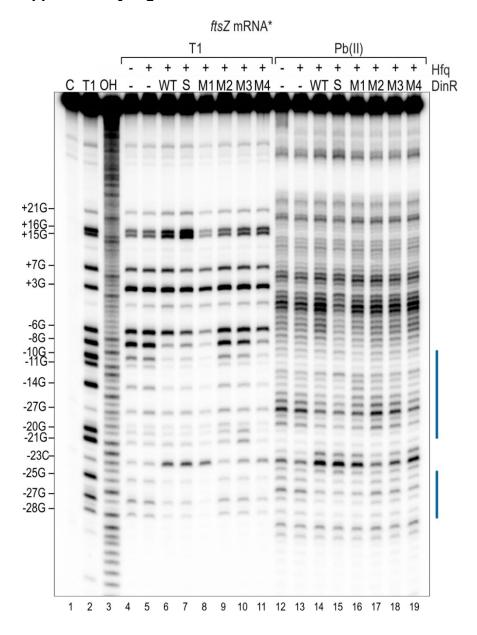
Expression of *dinl* **mRNA and DinR sRNA in** *K. pneumoniae.* (A) RNA samples were collected at different time-points over growth (OD_{600} from 0.25 to 2.0), and 30 min after cells had reached an OD_{600} of 2.0 in the absence (*ctrl.*) or presence of DNA damage induced through mitomycin C (MMC), ciprofloxacin (CPX) or ultraviolet light (UV). Expression of *dinl* mRNA and DinR was assessed by Northern blot analysis; 5S rRNA served as loading control. (B) Quantification of *dinl* mRNA and DinR sRNA signals relative to the expression at OD_{600} of 2.0.



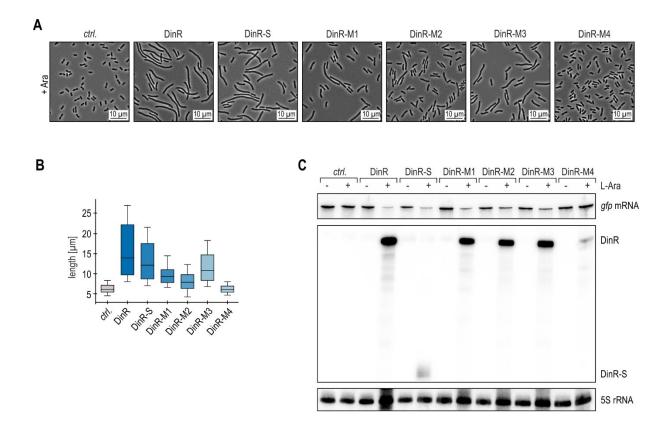
DinR is processed from the *dinl* **mRNA.** (A) *K. pneumoniae* WT or $\Delta dinlR$ cells carrying either an empty control vector (pBAD_{KP}-*ctrl.*) or plasmids harbouring different variants of the *dinl* gene (either starting from the TSS [pTSS_*dinlR*] or 50 bp upstream of the TSS [pPown_*dinlR*]) were grown to OD₆₀₀ of 2.0, when DNA damage was induced by the addition of MMC. DinR and *dinl* mRNA levels were determined by Northern blot analysis of RNA samples collected at the indicated time-points. 5S ribosomal RNA served as a loading control. (B) *Salmonella* Typhimurium expressing a temperature-sensitive RNase E variant (*rne*-TS) or an isogenic control strain (*rne-ctrl.*) were transformed with pBAD_{EC}-*dinlR* and grown to OD₆₀₀ of 0.25 at the non-permissive temperature of 30 °C. Cultures were split and cultivation was continued for 45 min at 30 °C or at 44 °C to inactivate RNase E. RNA samples were collected prior to (-) and 15 min after (+) induction of *dinlR* expression with arabinose. Expression of *dinl* mRNA and DinR were determined by Northern blot analysis. 5S ribosomal RNA served as a loading control was control.



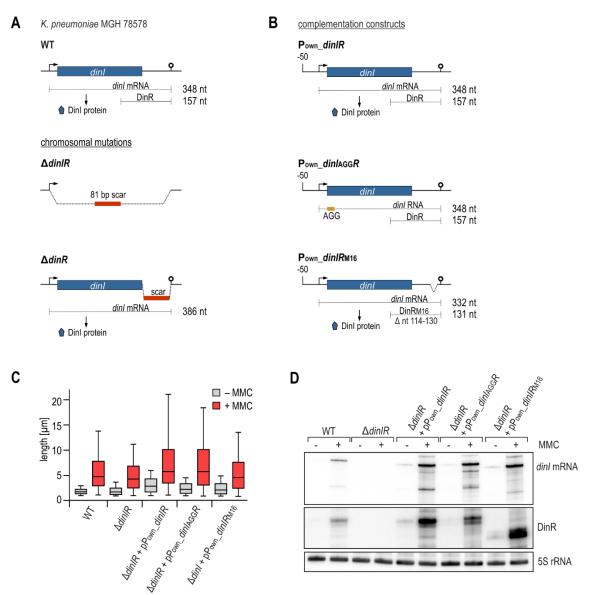
Regulation of *ftsZ* expression and conservation of the 5' UTR. (A) Quantification of FtsZ protein levels. FtsZ expression was determined by Western blot analysis using a FtsZ-specific antiserum in total protein samples collected from K. pneumoniae, E. coli and V. cholerae carrying either an empty control vector (pBAD_{KP}-ctrl., pBAD_{EC}-ctrl., or pBAD_{VC}-ctrl., respectively) or pBAD variants for the expression of DinR (pBAD_{KP}-DinR, pBAD_{EC}-DinR, or pBAD_{VC}-DinR, respectively). Bacteria were diluted from overnight cultures into fresh medium, and sRNA expression was induced by the addition of arabinose for 5 hours. FtsZ levels in the control sample (- L-Ara) was set to 1; error bars denote the standard deviation from five biological replicates. (B) Non-redundant alignment of the ftsZ 5' UTR of different bacterial species (kpn: Klebsiella pneumoniae MGH 78578; cko: Citrobacter koseri ATCC BAA-895; eco: Escherichia coli MG1655; sfl: Shigella flexneri 301; stm: Salmonella Typhimurium LT2; vch: Vibrio cholerae O1 El Tor N16961) was calculated using the Multalign tool (2). The stop codons of the upstream gene ftsA and the start codons of ftsZ are underlined, two transcriptional start sites (as determined by dRNA-seq in K. pneumoniae) are indicated by arrows. All nucleotides are colored with regard to their degree of conservation (red: high conservation; blue: partial conservation; black: little or no conservation).



In vitro analysis of DinR base-pairing on *ftsZ* mRNA. Structure probing of 5' end-labelled *ftsZ* mRNA (TSS at –58 to +60 relative to the start codon; 0.4 pmol) with RNase T1 (lanes 4 to 11) and lead(II) acetate (lanes 12 to 19) in the absence or presence of 2 pmol (5x) Hfq protein and 4 pmol (10x) sRNAs DinR (WT), DinR-S (S), or DinR variants (M1-M4; compare 5(B)). RNase T1 and alkaline ladders of the *ftsZ* transcript were used to map the positions of individual nucleotides. The positions of G residues are indicated relative to the translational start site. Putative DinR binding sites are marked in blue.



DinR overexpression causes cell filamentation. (A) *K. pneumoniae* carrying either an empty control vector (pBAD_{KP}-ctrl.) or pBAD_{KP} variants for the expression of DinR, DinR-S, DinR-M1, DinR-M2, DinR-M3 or DinR-M4 were diluted from overnight cultures into fresh medium, and sRNA expression was induced by the addition of arabinose. Cell morphology was assessed by phase contrast microscopy after 5 hours. (B) Analysis of cell lengths in samples described in (A). The center line indicates the median, boxes represent the 25th and 75th percentiles, and lower and upper whiskers represent the 10th and 90th percentiles, respectively. (C) *E. coli* carrying the post-transcriptional *ftsZ::gfp* reporter and either pBAD_{EC}-ctrl. or pBAD_{EC} variants for the expression of DinR, DinR-S, DinR-M1, DinR-M2, DinR-M3 or DinR-M4 were grown to OD₆₀₀ of 0.5. Total RNA samples were prepared from cells collected prior to (-) or 10 min after the addition of arabinose (+). DinR and *ftsZ::gfp* mRNA levels were determined by Northern blot analysis; 5S ribosomal RNA served as a loading control.



Complementation of the dinIR mutant. (A) Schematic of the dinIR locus of K. pneumoniae in wild-type and mutant cells. In the chromosomal mutant $\Delta din IR$ deletion, a 81 bp scar replaces the sequence from the TSS to the end of the 3' UTR. In the chromosomal mutant $\Delta dinR$, a 81 bp scar replaces the sequence from the stop codon to the beginning of the terminator hairpin (nt 84 to 126 of the sRNA). The size of the *dinl* mRNA increases to 386 nt. (B) Schematic of complementation constructs of dinIR. Plasmid pPown dinIR expresses dinIR under control of its own promoter; Dinl protein is produced. Plasmid pPown dinlAGGR expresses *dinIR* under control of its own promoter; the stop codon of *dinI* is changed from ATG to AGG; Dinl protein is not produced. Plasmid pPown dinIRM16 expresses dinIR under control of its own promoter; nt 114 to 130 of DinR have been deleted; Dinl protein is produced. (C) K. pneumoniae wild-type cells or dinIR mutant cells carrying complementation plasmids (as described in (B)) were diluted from overnight cultures into fresh medium, split and either treated with MMC (1 µg/mL) to induce DNA damage or left untreated. Cell morphology was assessed by phase contrast microscopy after 5 hours and quantified. The center line indicates the median, boxes represent the 25th and 75th percentiles, and lower and upper whiskers represent the 10th and 90th percentiles, respectively. (D) RNA samples prepared from cells treated as described in (C) were analyzed on Northern blot; 5S ribosomal RNA served as a loading control.

SUPPORTING METHODOLOGY

Construction of Bacterial Strains

Klebsiella pneumoniae subsp. pneumoniae MGH 78578, *E. coli* Top10 and *V. cholerae* C6706 are referred to as wild-type strains in this study.

Plasmids were introduced in K. pneumoniae and E. coli by electrotransformation, and into V. cholerae by conjugation via the E. coli S17 helper strain using standard protocols. To construct chromosomal mutations, we followed a published procedure based on the widely-used E. coli one-step inactivation method based on the λ -Red recombinase system (6). Briefly, wild-type cells carrying pACBSR-Hyg (encoding the λ -Red genes under control of the *araBAD* promoter) were transformed with PCR products (obtained by overlap extension PCR) containing the aac(3)/V gene (conferring apramycin resistance) flanked by FRT recombination sites and ~500 bp of sequences homologous to the genomic integration sites. For fragments carrying the aac(3)/V marker gene, pIJ773 (KFO-1407/KFO-1376) or pER15 (KFO-1375/KFO-1376) were amplified and combined with individual flanking regions (Δhfg : KFO-1252/KFO-1408 and KFO-1255/KFO-1378; hfg-3xFLAG: KFO-1252/KFO-1377 and KFO-1255/KFO-1378; ∆sulA: KFO-1798/KFO-1800 and KFO-1799/KFO-1801; *\dinl*: KFO-1792/KFO-1821 and KFO-1905/KFO-1793; ∆dinR: KFO-1792/KFO-2001 and KFO-2000/KFO-1793). Transformants were recovered in the presence of apramycin, and desired mutations were confirmed by colony PCR and sequencing. The temperature-sensitive pACBSR-hyg was lost during growth in LB at 37 °C. To eliminate the *aac(3)/V* cassette, the resulting strain was transformed with pFLP-hyg, and expression of the FLP recombinase was induced with arabinose. Recombination at the FRT site and correct excision of the cassette was confirmed by colony PCR and sequencing, and the helper plasmid was removed by passaging cells at 37 °C. Multiple mutations were introduced by sequentially performing the genomic modifications described above.

Unexpectedly, introduction of the pACBSR-Hyg helper plasmid resulted in selective loss of accessory plasmids pKPN4 and pKPN6, respectively, from a subset of transformed wild-type *K. pneumoniae* MGH 78578, a phenotype that had not been reported in the original protocol. We thus verified that neither loss of the two plasmids nor addition of the epitope to the RNA-binding protein expressed from its native promoter in MGH 78578 impaired bacterial growth under standard conditions when compared to WT cells (Fig S2B). In addition, we performed phenotypic characterization of our results throughout the manuscript using an isogenic WT strain, in which pKPN4 and pKPN6 had been likewise removed.

Bacterial growth conditions

K. pneumoniae, Escherichia coli and *V. cholerae* strains were grown aerobically at 37 °C in LB broth or on LB agar. Where appropriate, media were supplemented with kanamycin (50 μ g/mL), chloramphenicol (20 μ g/mL), ampicillin (100 μ g/mL), hygromycin (100 μ g/mL), or apramycin (50 μ g/mL). Expression from the araBAD promoter was induced with L-arabinose (final concentration: 0.2%). Unless stated otherwise, DNA damage was triggered in *K. pneumoniae* by adding mitomycin C (MMC; 0.5 μ g/mL) or ciprofloxacin (CPX; 4 μ g/mL) to the culture, or by irradiation with UV light (λ =254 nm; 10 mJ/cm²).

Plasmid construction

All plasmids and oligonucleotides used in this study are listed in Tables S4 and S5.

A template plasmid (pER15) for the chromosomal integration of the 3xFLAG epitope tag was constructed via PCR amplification of pIJ773 (KFO-1250/KFO-1251), and self-ligation was carried out as in (7).

The translational GFP reporter fusion of *ftsZ* (pFS7) was constructed via Gibson assembly (GA; NEB #E2611L) as recommended by the manufacturer using a PCR product amplified

from *K. pneumoniae* genomic DNA (KFO-1713/KFO-1714) and the linearized pXG10 vector (KPO-1702/KPO-1703). For the construction of the *ftsZ(M3)::gfp* variant (pER44), plasmid pFS07 was used as a template in PCR amplification with primer set KFO-1851/KFO-1852, and the obtained fragment was self-ligated.

For plasmids expressing DinR from the arabinose-inducible pBAD plasmid, inserts amplified from *K. pneumoniae* genomic DNA were cloned into linearized vectors via GA. For expression in *E. coli*, backbone pKP8-35 was amplified via KPO-0196/KPO-0411 and combined with an insert amplified with KFO-1718/KFO-1716. For expression in *V. cholerae*, backbone pBAD1K was amplified via KPO-0196/KPO-1397 and combined with an insert amplified with KFO-1718/KFO-1397 and combined with an insert amplified with KFO-1718/KFO-1397 and combined with an insert amplified with KFO-1715/KFO-2140. For expression in *K. pneumoniae*, an apramycin resistance cassette (amplified from pIJ773 with KFO-1830/KFO-1831) was introduced into pKP8-35 (linearized with KFO-1832/KFO-1833), and the obtained plasmid (pER41) was amplified via KPO-0196/KPO-0411 and combined with an insert amplified with KFO-1718/KFO-1716 by GA.

For plasmids expressing variants of DinR, pFS1 or pER41 served as a template for PCR amplification with primer pairs KFO-1992/KFO-1993 (pER66 and pER90); KFO-1892/KFO-1893 (pFS51 and pER85); KFO-1849/KFO-1850 (pER43 and pER84); KFO-1990/KFO-1991 (pER65 and pER89), and obtained fragments were self-ligated.

To verify transcriptional control of DinR expression, two variants of *dinl* lacking (KFO-2028/KFO-1716; pER82) or including the annotated promoter (KFO-2029/KFO-1716; pER83) were inserted via GA into linearized pER41 lacking the *araBAD* promoter (amplified by KFO-2027/KPO-0411). Plasmid pER83 served as template for PCR amplification with primer pairs KFO-2719/KFO-2720 to obtain pER156 and with KFO-2721/KFO-2723 to obtain pER158.

T7 transcription and 5' end-labelling of RNA

RNA was in vitro synthesized and 5' end-labelled as described before (8, 9). In short, DNA templates carrying the T7 promotor were amplified by PCR using the oligonucleotides listed in Table S5. In vitro transcription of RNA from template DNA was performed using the AmpliScribe T7-Flash transcription kit (Epicentre). RNA was dephosphorylated using calfphosphatase (NEB), subsequently extracted P:C:I intestinal alkaline with (phenol/chloroform/isoamyl alcohol; 25:24:1) and ethanol precipitated. 5' end labelling was achieved by incubation of dephosphorylated RNA with [32P]- vATP and polynucleotide kinase (NEB) for 1 h at 37 °C. Unincorporated nucleotides were removed using Amersham MicroSpin G-50 columns (Cytiva). Labelled RNA was then purified on a denaturing 6 % PAA / 7 M Urea gel, eluted with RNA elution buffer (0.1 M sodium acetate, 0.1 % SDS, 10 mM EDTA) at 4 °C overnight and recovered by P:C:I extraction.

Riboprobes

The riboprobes to detect DinR, *dinI* and *suIA* mRNAs were synthesized by T7-mediated *in vitro* transcription of ~200 ng of template DNA (amplified on *Klebsiella* gDNA with KFO-1762/KFO-1763; KFO-2554/KFO/2555; KFO-2288/KFO-2260) in the presence of [³²P]- α -UTP with the MAXIscript T7 transcription kit (Invitrogen). Unincorporated nucleotides were removed using MicroSpin G-50 columns (Cytiva).

Primer extension analysis

For primer extension, 5 μ g of RNA were denaturated in the presence of 1 pmol 5' end-labelled primer (KFO-1745) at 70°C for 2 min and adjacently chilled on ice for 5 min. Next, the samples were mixed with the reaction mix (1X first strand buffer, 5 mM DTT, 0.5 mM each dATP, dGTP, dCTP and dTTP) at 42°C, and SuperScript III (100 U; Invitrogen) was added. cDNA synthesis was performed at 50°C for 60 min, followed by incubation at 70°C for 15 min to inactivate the enzyme. Samples were treated with RNase H (2.5 U) for 15 min at 37°C and the reaction was

stopped by the addition of GLII loading buffer. Samples was separated by electrophoresis on a 6% sequencing gel together with a template-specific ladder (prepared using the SequiTherm EXCELII DNA Sequencing Kit).

dRNA sequencing

In brief, RNA samples were fragmented using ultrasound, followed by treatment with polynucleotide kinase (PNK). For the depletion of processed transcripts and the control reaction, equal amounts of RNA were incubated with or without terminator 5'-phosphate-dependent exonuclease (TEX; Lucigen). RNA samples were poly(A)-tailed using poly(A) polymerase and 5'-triphosphates were removed by applying tobacco acid pyrophosphatase (TAP). An RNA adapter was ligated to the 5' end of the RNA prior to cDNA synthesis using an oligo(dT) primer and M-MLV-RNase H- reverse transcriptase. Upon amplification of the cDNA with a high-fidelity polymerase and gel fractionation, the resulting libraries were pooled and sequenced on an Illumina NextSeq 500 system with 1x75 bp read length.

Sequencing reads from the dRNA-seq experiment were processed and analysed according to (10) with minor modifications. Briefly, for every replicate in both conditions, the coverage and based on it, the difference between neighboring nucleotides was computed. Local maxima in the differences were called as TSS if the difference between maximum and minimum coverage in a 7 nt window around the TSS was above 3 TPM, and the ratio between the maximum and the minimum was above 1.3. The set of putative TSS was manually curated and the resulting predictions were used to annotate genes with a 5' UTR within a window of 250 nt upstream of an annotated gene. The most distant TSS was then used to define the 5' UTR of the corresponding gene. 3' UTRs were annotated by extending an area downstream of a gene, up to 150 nt in length unless the next annotation was closer than that window. Custom scripts are available from GitHub (https://github.com/maltesie/KpnInteractomePaper; DOI: 10.5281/zenodo.8409716).

Hfq RIP-seq analysis

Demultiplexed raw reads were imported into the CLC Genomics Workbench (Qiagen) and subjected to quality control and adaptor trimming. The trimmed reads were mapped to the *Klebsiella pneumoniae subsp. pneumoniae* MGH 78578 reference genome (NCBI accession numbers NC_009648.1, NC_009649.1, NC_009651.1, and NC_009653.1) with standard parameter settings. Annotations of sRNAs were added manually. Fold enrichment in samples expressing Hfq-3xFLAG over the untagged control samples was calculated using the CLC "Differential Expression for RNA-Seq" tool.

RIL-seq analysis

Briefly, cells corresponding to 40 OD₆₀₀ units were subjected to UV crosslinking of proteins and RNA followed by cell lysis and co-immunoprecipitation using a monoclonal anti-FLAG antibody (Sigma; #F1804). Recovered RNA was trimmed by RNase A/T1 treatment, and proximal RNAs were ligated. Upon proteinase K treatment, RNA was extracted, fragmented and DNase digested. A previously published protocol (11) was adapted for the strain-specific depletion of ribosomal RNA. Co-immunoprecipitated RNA samples were mixed with an oligonucleotide mix (final concentrations: 5.8 nM for 16S and 23S oligos; 11.6 nM for 5S oligos) in the presence of 1x SSC and 1 mM EDTA. The mixture was denatured, cooled down and incubated with streptavidin beads (ThermoFisher; #65001) in 0.5x SSC at room temperature and 50°C for 5 min each, respectively. Depleted RNA in the supernatant was purified using AMPure XP beads (Beckman-Coulter; #A63881) and subjected to cDNA library preparation. Upon PCR amplification, libraries were sequenced in paired-end mode on an Illumina NextSeq 1000 with 150 bp read-length.

The sequence file was demultiplexed using the split_libs command from RNASeqTools (DOI: 10.5281/zenodo.8388882) and the resulting files were analyzed with ChimericFragments (DOI: 10.5281/zenodo.8376810) used with the default parameters set except for the following: min_seed_length=15, autocomplete_utrs=false, bp_shift_weight=0.0, max_bp_fdr=0.35 and min_reads=5 as described in (12).

Annotation of sRNAs

Complementation of sRNA annotation was based on several criteria. Conserved enterobacterial sRNAs were identified by comparison with published datasets (13-16). Candidate sRNAs in IGRs were selected if a clear TSS, a length ranging from 50 to 350 nts, and a termination site were identified; sequences were scanned for putative ORFs (\geq 20 aa). 5' UTR-derived sRNAs were annotated based on the detection of a processing site or a sharp drop in coverage upstream of the translational start site of the associated mRNA. 3' UTR-derived sRNAs were selected based on the presence of a processing site or a TSS within the 3' end of the associated mRNA and a shared termination site.

Identification of LexA motifs

To identify previously unknown sRNAs contributing to the regulation of the SOS response we examined the Hfq RIP-seq dataset for potentially LexA-controlled transcripts, exploiting our accurate annotation of TSSs by dRNA-seq. We used MEME (17) to compute a LexA position weight matrix based on the sequences of 21 known SOS boxes of *E. coli* (3), and then searched for the obtained motif (WACTGTATATWHAHMCAGTA) within *K. pneumoniae* transcription initiation sites (-70 to +30 relative to the TSS). We identified putative LexA binding sites preceding 71 transcription units (see Table S2).

Chromatin immunoprecipitation (ChIP)

ChIP was performed following the previously published procedures (4, 10) with minor modifications. In brief, *K. pneumoniae* MGH 78578 wild-type cells were grown in two biological replicates in LB medium to a final OD_{600} of 2.0. The culture was split, and incubation was continued for an additional 30 min in the presence or absence of MMC (1 µg/mL).

Formaldehyde was added at a final concentration of 1% to cross-link DNA and proteins, and the reaction was quenched after 20' by the addition of glycine (0.5 M). Cells were washed in 1x TBS, and lysed in lysis buffer (50 mM Hepes-KOH pH=7.0, 150 mM NaCl, 1 mM EDTA, 1% Triton X-100, 0.1% sodium deoxycholate, 0.1% SDS) containing 4 mg/ml lysozyme. DNA was sheared to an average size of ~200 bp using a BioRuptor (5x 30 s pulses). Insoluble material was removed by centrifugation, and a sample of the supernatant was stored as input control. The samples were mixed with protein A magnetic beads (Thermo Fisher #10001D), split and either incubated with anti-LexA antibody (Sigma #06-719; +AB) or no antibody (-AB) at 4°C overnight. Samples were washed twice in lysis buffer, once in modified lysis buffer (500 mM NaCl), once in ChIP wash buffer (10 mM Tris-HCl pH=8.0, 250 mM LiCl, 1 mM EDTA, 0.5% Nonidet-P40, 0.5% sodium deoxycholate), and once in TE. Samples were eluted in elution buffer (50 mM Tris-HCl, 1 mM EDTA, 1% SDS) at 65°C, and cross-linking was reverted by boiling samples (including the input) for 10 min. DNA was purified by P:C:I extraction, and analyzed by quantitative PCR (qPCR) using the GoTaq qPCR Master Mix (Promega #A6002) on a CFX96 Real-Time PCR system (Bio-Rad), with *sgrR* CDS as a control.

Image analysis

The pipeline detects the bacteria and includes a background subtraction, noise removal and automated thresholding. To prevent clustering of cells in close vicinity, a second branch segments the halo around each object and subtracts those from the results of the cell

thresholding. To resolve overlaps and measure cell lengths, the segmented objects are transformed into a graph structure that contains information about the cell's medial axis and diameter. This representation allowed the usage of an algorithm to split overlapping clusters into individual objects by the removal of junction vertices and addition of alternative edges minimize the cell curvature. The length of each graph component and thus the bacterial cell is determined by a JIPipe-provided operation.

A detailed explanation of the workflow and its individual components, all results as well as the utilized software versions, is available through https://asbdata.hki-jena.de/RuhlandEtAl2023_PNAS.

Supplementary Table S1 – sRNAs in *K. pneumoniae* MGH 78578

Number	alternative name	reference genome	left end	right end	strand	classification	reference	enrichment RIP-seq MEP	enrichment RIP-seq ESP	pot. ORF ≥ 20 aa ^(a)
KpnR_001	tpke11	NC_009648.1	15539	15614	+	IGR	(15)	n.d.	n.d.	
KpnR_002	DapZ	NC_009648.1	41908	41977	+	3' UTR	(15)	7.3	6.0	
KpnR_003	SroA	NC_009648.1	79067	79132	-	5' UTR	(15)	0.5	0.3	
KpnR_004	SgrS	NC_009648.1	81037	81261	+	IGR	(15)	n.d.	n.d.	
KpnR_005	KPN_RS00380_5' (sRNA 1)	NC_009648.1	81244	81448	+	5' UTR	(14)	0.4	2.5	
KpnR_006	pdhR_3'	NC_009648.1	137318	137597	+	3' UTR	this study	0.6	3.2	
KpnR_007	tp2	NC_009648.1	137544	137673	-	IGR	(15)	1.8	7.9	
KpnR_008	rpsB_5'	NC_009648.1	215558	215695	+	5' UTR	(15)	0.3	0.2	
KpnR_009	rpsB_3'	NC_009648.1	216411	216509	+	3' UTR	this study	12.0	33.7	
KpnR_010	SraA	NC_009648.1	442430	442486	-	IGR	(15)	n.d.	0.8	
KpnR_011	4.5S_RNA	NC_009648.1	461884	462024	+	IGR	(15)	0.4	0.2	
KpnR_012	ChiX	NC_009648.1	510362	510442	+	IGR	(15)	27.5	15.4	
KpnR_013	KPN_RS02895_5' (sRNA 6)	NC_009648.1	597429	597620	+	IGR	(14)	38.9	56.9	
KpnR_014	SroC	NC_009648.1	769973	770129	-	IGR	(15)	12.7	10.3	
KpnR_015	KPN_RS03910_3915_IGR	NC_009648.1	817664	817879	-	IGR	this study	10.6	3.6	33 aa
KpnR_016	SdhX	NC_009648.1	827990	828076	+	3' UTR	(15)	12.5	20.7	
KpnR_017	KPN_RS04185_AS	NC_009648.1	865729	865826	+	as	this study	1.0	0.3	
KpnR_018	KPN_RS04690_4695_IGR1	NC_009648.1	975650	975775	-	IGR	this study	21.1	10.2	25 aa
KpnR_019	KPN_RS04690_4695_IGR2	NC_009648.1	976289	976417	-	IGR	this study	9.2	3.9	
KpnR_020	RybB	NC_009648.1	984425	984505	-	IGR	(15)	16.6	6.6	
KpnR_021	KPN_RS05160_5165_IGR	NC_009648.1	1089328	1089557	-	IGR	this study	9.1	12.4	39 aa
KpnR_022	KPN_RS05190_3'	NC_009648.1	1097112	1097453	+	3' UTR	this study	16.4	4.8	
KpnR_023	ompA_5'	NC_009648.1	1121359	1121526	-	5' UTR	this study	132.2	12.6	
KpnR_024	KPN_RS31110_KPN_RS31115_IGR	NC_009648.1	1178232	1178539	+	IGR/as	this study	11.2	10.4	33 aa
KpnR_025	phoH_5'	NC_009648.1	1198613	1198845	+	5' UTR	this study	0.8	1.5	
KpnR_026	RtT_RNA_1	NC_009648.1	1200277	1200414	-	IGR	(15)	0.5	2.3	
KpnR_027	RtT_RNA_2	NC_009648.1	1205516	1205645	-	IGR	(15)	3.6	n.d.	
KpnR_028	lpxP_3'	NC_009648.1	1217934	1218011	-	3' UTR	(15)	n.d.	n.d.	
KpnR_029	DinR	NC_009648.1	1222098	1222253	-	3' UTR	this study	4.6	5.3	
KpnR_030	SraB	NC_009648.1	1237475	1237592	+	IGR	(15)	3.3	0.3	
KpnR_031	KPN_RS05910_3'	NC_009648.1	1256448	1256635	+	3' UTR	this study	n.d.	36.1	
KpnR_032	potD_3'	NC_009648.1	1283992	1284057	-	3' UTR	this study	52.5	10.7	
KpnR_033	spy_5'	NC_009648.1	1378348	1378441	+	IGR	this study	19.8	13.1	

KpnR_035	spy3'	NC 009648.1	1379048	1379111	+	3' UTR	(15)	0.1	0.1	
KpnR_036	RyhB2	NC 009648.1	1404504	1404605	_	as	(15)	8.2	11.1	
KpnR_037	FnrS	NC_009648.1	1539850	1539972	+	IGR	(15)	26.2	7.4	
KpnR_038	KPN_RS07525_7530_IGR (sRNA 9)	NC 009648.1	1564287	1564584	+	IGR	(14)	26.7	9.3	
KpnR_039	KPN_RS32550_07555_IGR (sRNA 10)	NC_009648.1	1566904	1567072	+	IGR	(14)	0.8	9.2	
KpnR_040	KPN_RS28800_07710_IGR	NC 009648.1	1595047	1595119	-	IGR	this study	16.8	10.3	
KpnR_041	MicC	NC_009648.1	1603837	1603953	+	IGR	(15)	6.1	42.8	
KpnR_042	KPN_RS08035_8040_IGR (sRNA 12)	NC 009648.1	1668378	1668448	+	IGR	(14)	0.8	1.1	
KpnR_043	fumA 3'	NC 009648.1	1686189	1686371	+	3' UTR	this study	1.7	3.0	
KpnR_044	KPN_RS08415_8430_IGR1	NC_009648.1	1745512	1745772	+	IGR	this study	2.6	9.7	34 aa
KpnR_045	KPN_RS08415_8430_IGR2	NC_009648.1	1745946	1746213	+	IGR/as	this study	9.0	8.7	
KpnR_046	KPN_RS31250_31255_IGR	NC_009648.1	1772623	1772813	-	IGR/as	this study	1.6	5.0	34 aa
KpnR_047	MgrR	NC_009648.1	1792507	1792605	+	IGR	(15)	23.1	17.1	
KpnR_048	marA AS	 NC_009648.1	1805171	1805502	+	as	this study	23.8	9.2	
KpnR_049	 KPN RS09105 9110 IGR	 NC_009648.1	1872673	1872791	+	IGR	this study	0.4	0.8	
KpnR_050	RydB	NC_009648.1	2117929	2118082	-	IGR	(15)	0.9	0.9	
KpnR_051	KPN RS10415 3'	NC 009648.1	2131408	2131492	+	3' UTR op	this study	19.1	8.2	
KpnR_052	KPN_RS11045_30440_IGR (sRNA 14)	NC_009648.1	2246314	2246444	+	IGR	(14)	6.9	11.9	
KpnR_053	KPN_RS11175_AS	NC_009648.1	2271954	2272085	+	as	this study	11.4	8.3	
KpnR_054	KPN_RS11285_11290_IGR	NC_009648.1	2295887	2296029	+	IGR	this study	1.3	0.5	
KpnR_055	RprA	NC_009648.1	2367518	2367625	+	IGR	(15)	13.8	12.1	
KpnR_056	KPN_RS31415_11650_IGR	NC_009648.1	2370293	2370405	-	IGR	this study	24.5	13.3	
KpnR_057	ОррХ	NC_009648.1	2406354	2406535	-	5' UTR	(15)	8.3	5.1	
KpnR_058	dsbB_3'	NC_009648.1	2537931	2538143	+	3' UTR	this study	n.d.	12.6	
KpnR_059	SroD	NC_009648.1	2543260	2543341	-	3' UTR	(15)	1.6	0.0	
KpnR_060	KPN_RS12590_3'	NC_009648.1	2559201	2559318	+	3' UTR	this study	3.2	3.1	
KpnR_061	RydC	NC_009648.1	2580742	2580807	+	IGR	(15)	5.1	2.2	
KpnR_062	RyeA	NC_009648.1	2580911	2581210	+	IGR	(15)	1.5	1.0	
KpnR_063	SdsR	NC_009648.1	2580978	2581082	-	IGR	(15)	6.1	7.1	
KpnR_064	MicL	NC_009648.1	2609852	2610162	-	3' UTR op	(15)	5.8	n.d.	
KpnR_065	3'ETS-leuZ	NC_009648.1	2632966	2633029	-	3' UTR	(15)	9.9	12.5	
KpnR_066	DsrA	NC_009648.1	2645420	2645508	-	IGR	(15)	38.1	4.5	
KpnR_067	ompC_KPN_RS13105_IGR	NC_009648.1	2654265	2654491	+	IGR/as	this study	0.5	1.1	
KpnR_068	JUMPstart_RNA	NC_009648.1	2746038	2746142	-	IGR/as	(15)	1.1	1.0	
KpnR_069	KPN_RS1358_13585_IGR	NC_009648.1	2761160	2761273	+	IGR	this study	12.5	10.1	

KpnR_070	CyaR	NC_009648.1	2775703	2775790	+	IGR	(15)	28.9	23.6	
KpnR_071	MicF	NC_009648.1	2896241	2896333	+	IGR	(15)	18.3	9.4	
KpnR_072	nupC_3'	NC_009648.1	3017927	3018210	+	3' UTR	this study	3.0	3.1	
KpnR_073	STnc250	NC_009648.1	3075394	3075515	-	3' UTR	(15)	n.d.	n.d.	
KpnR_074	SroE	NC_009648.1	3122822	3122897	-	3' UTR	(15)	1.4	2.8	
KpnR_075	sseA_KPN_RS15310_IGR	NC_009648.1	3135762	3135917	-	IGR	this study	0.6	0.2	
KpnR_076	GlmY	NC_009648.1	3166842	3167027	-	IGR	(15)	0.3	0.5	
KpnR_077	RyfD	NC_009648.1	3207437	3207578	-	5' UTR	(15)	0.3	0.5	
KpnR_078	RaiZ	NC_009648.1	3210661	3210819	+	3' UTR	(15)	4.1	104.4	
KpnR_079	tmRNA	NC_009648.1	3231291	3231653	+	IGR	(15)	0.2	0.3	
KpnR_080	KPN_RS16030_3'	NC_009648.1	3290414	3290609	-	3' UTR op	this study	164.0	7.5	
KpnR_081	MicA	NC_009648.1	3318096	3318170	+	IGR	(15)	5.9	5.9	
KpnR_082	sok_AT	NC_009648.1	3394403	3394559	-	5' UTR	(15)	0.0	0.5	
KpnR_083	SokX	NC_009648.1	3394457	3394512	+	IGR	(15)	0.3	0.1	
KpnR_084	CsrB	NC_009648.1	3438471	3438838	-	IGR	(15)	0.5	0.8	
KpnR_085	GcvB	NC_009648.1	3469834	3470041	+	IGR	(15)	15.5	6.7	
KpnR_086	rppH_AS	NC_009648.1	3555242	3555333	+	as	this study	12.7	10.4	
KpnR_087	OmrA	NC_009648.1	3563070	3563157	-	IGR	(15)	12.4	7.1	
KpnR_088	OmrB	NC_009648.1	3563274	3563356	-	IGR	(15)	1.1	5.6	
KpnR_089	ompK26_3'	NC_009648.1	3587787	3587874	-	3' UTR	this study	7.8	4.1	
KpnR_090	6S_RNA	NC_009648.1	3665037	3665220	+	IGR	(15)	0.2	0.2	
KpnR_091	SibC	NC_009648.1	3665896	3666042	+	3' UTR	(15)	2.5	36.2	
KpnR_092	SroG	NC_009648.1	3778913	3779064	-	5' UTR	(15)	0.4	0.3	
KpnR_093	alx_5'	NC_009648.1	3878691	3878875	+	5' UTR	(15)	1.4	0.6	
KpnR_094	RnpB	NC_009648.1	3896359	3896741	-	IGR	(15)	0.3	0.4	
KpnR_095	SraG	NC_009648.1	3934702	3934873	+	IGR	(15)	0.6	0.0	
KpnR_096	ArcZ	NC_009648.1	3973082	3973203	+	IGR/as	(15)	14.2	8.1	
KpnR_097	RyhB	NC_009648.1	4161791	4161886	-	IGR	(15)	12.6	12.0	
KpnR_098	bscO_KPN_RS31745_IGR1 (sRNA 24)	NC_009648.1	4269680	4269841	+	IGR	(14)	3.1	4.0	
KpnR_099	bscO_KPN_RS31745_IGR2	NC_009648.1	4276216	4276497	+	IGR/as	this study	2.0	3.5	28 aa
KpnR_100	RtT_RNA_3	NC_009648.1	4277971	4278104	-	IGR	(15)	0.6	0.5	
KpnR_101	sok_AT	NC_009648.1	4299285	4299435	-	5' UTR	(15)	3.2	24.4	
KpnR_102	KPN_RS21245_21250_IGR (sRNA 25)	NC_009648.1	4314524	4314846	+	IGR/as	(14)	1.1	6.1	
KpnR_103	KPN_RS21430_waa_IGR	NC_009648.1	4355486	4355592	-	IGR/as	this study	1.2	1.5	
KpnR_104	IstR	NC_009648.1	4463773	4463903	-	IGR/as	(15)	0.9	0.4	

KpnR_105	KPN_RS22175_22180_IGR	NC_009648.1	4503473	4503564	+	IGR	this study	0.6	3.1	
KpnR_106	RbsZ	NC_009648.1	4553995	4554205	+	3' UTR op	(15)	n.d.	n.d.	
KpnR_107	Spot_42	NC_009648.1	4571507	4571625	+	IGR	(15)	30.0	17.0	
KpnR_108	CsrC	NC_009648.1	4572621	4572867	+	IGR	(15)	0.3	0.5	
KpnR_109	GlnZ	NC_009648.1	4577815	4577914	-	3' UTR	(15)	13.1	8.7	
KpnR_110	CpxQ	NC_009648.1	4622452	4622509	+	3' UTR	(15)	17.2	6.5	
KpnR_111	OxyS	NC_009648.1	4655076	4655194	-	IGR	(15)	18.7	17.0	
KpnR_112	GlmZ	NC_009648.1	4707421	4707597	+	IGR	(15)	6.6	6.2	
KpnR_113	Pseudomonas_P26	NC_009648.1	4769689	4769817	+	3' UTR op	(15)	0.0	0.2	
KpnR_114	SroH	NC_009648.1	4782709	4782823	-	IGR	(15)	11.0	4.0	
KpnR_115	aceK-int	NC_009648.1	4810817	4810901	+	IGR	(15)	3.1	4.1	
KpnR_116	malM_3'	NC_009648.1	4844452	4844548	+	3' UTR op	(15)	0.0	10.1	
KpnR_117	pspG_KPN_RS23890_IGR	NC_009648.1	4854487	4854571	+	IGR	this study	77.7	8.6	
KpnR_118	KPN_RS23935_23940_IGR (sRNA 27)	NC_009648.1	4866884	4867205	+	IGR	(14)	36.3	12.4	
KpnR_119	KPN_RS23955_KPN_RS23965_IGR (sRNA 28)	NC_009648.1	4872137	4872383	+	IGR	(14)	13.6	5.6	
KpnR_120	SraL	NC_009648.1	4885978	4886125	-	IGR	(15)	0.7	0.6	
KpnR_121	ioID_3'	NC_009648.1	5113801	5113867	+	3' UTR	this study	43.1	92.2	
KpnR_122	iolE_3'	NC_009648.1	5116601	5116790	+	3' UTR	this study	10.7	16.6	
KpnR_123	repA_tap_IGR	NC_009649.1	5598	5684	-	IGR	this study	0.1	0.4	
KpnR_124	KPN_RS30785_KPN_RS26475_IGR	NC_009649.1	50982	51224	-	IGR	this study	3.3	6.5	
KpnR_125	pcoE_3'	NC_009649.1	71349	71428	-	3' UTR	this study	32.8	15.5	
KpnR_126	KPN_RS26860_KPN_RS29675_IGR	NC_009649.1	124376	124473	-	IGR	this study	0.0	0.0	
KpnR_127	KPN_RS32575_KPN_RS26920_IGR1	NC_009649.1	134020	134087	-	IGR	this study	9.1	7.0	
KpnR_128	KPN_RS32575_KPN_RS26920_IGR2	NC_009649.1	134372	134491	+	IGR	this study	6.0	5.3	
KpnR_129	repA_tap_IGR	NC_009650.1	5597	5684	-	IGR	this study	n.d.	n.d.	
KpnR_130	KPN_RS27500_27505_IGR	NC_009650.1	58478	58578	-	IGR	this study	n.d.	n.d.	
KpnR_131	KPN_RS27570_27575_IGR	NC_009650.1	68576	68685	-	IGR	this study	n.d.	n.d.	
KpnR_132	traX_KPN_RS27770_IGR	NC_009650.1	106802	106912	-	IGR	this study	n.d.	n.d.	
KpnR_133	KPN_RS27800_27805_IGR	NC_009651.1	3977	4078	+	IGR	this study	0.3	0.3	
KpnR_134	KPN_RS28310_KPN_RS28295_IGR	NC_009652.1	3747	3848	-	IGR	this study	n.d.	n.d.	
KpnR_135	FadZ	NC_009648.1	4747195	4747235	-	3' UTR	(13)	n.d.	n.d.	
KpnR_136	MalH	NC_009648.1	4836639	4836835	-	3' UTR	(16)	n.d.	n.d.	
KpnR_137	ZbiJ	NC_009648.1	929321	929471	-	3' UTR	(13)	n.d.	n.d.	
(a) determin	ed for newly annotated sRNA can	didatas								

(a) determined for newly annotated sRNA candidates

Supplementary Table S2 – LexA boxes in MGH 78578

reference genome	TSS position	strand	associated gene	alternative name	motif	E. coli LexA regulon	Hfq-RIPseq enrichment MEP	Hfq-RIPseq enrichment ESP
NC_009648.1	69500	-	KPN_RS00315	dinA/polB	ACCTGTATAAAACCCCAGCG	yes	0,5	0,8
NC_009648.1	134256	+	as in KPN_RS00615		TATTGTAGGTCCACTCAGGA	na	na	na
NC_009648.1	279304	+	KPN_RS01315	dinB	TGCTGTATGGGTATACAGTG	yes	0,6	0,9
NC_009648.1	302334	+	KPN_RS01425		TAATTTTTGCACAACCAGCG	no homologue in MG1655	1,0	0,5
NC_009648.1	304001	+	KPN_RS01430		AAATGTTCAATAAATCAGTA	no homologue in MG1655	1,6	0,8
NC_009648.1	495194	-	KPN_RS02385	priC	TAATGGTTAAAATAACAGGT	no	0,5	0,5
NC_009648.1	513937	+	KPN_RS02475	cueR	TCCTGAATAATTTTCCGGTC	no	0,4	0,6
NC_009648.1	898954	+	KPN_RS04345	uvrB	CACTGTTTAAATATCCAGTA	yes	0,5	0,6
NC_009648.1	926126	+	KPN_RS04480	dinG	TAGTGGCTGTTTATACAGTA	yes	0,4	0,6
NC_009648.1	938906	-	KPN_RS04540	rhtA	CCCTGTTTTTTCAACATTA	no	0,4	0,8
NC_009648.1	1032191	+	KPN_RS04965	ftsK	TCCTGTTAATCCATACAGCA	yes	0,4	0,4
NC_009648.1	1122285	-	KPN_RS05300	sulA	TACTGTATATGCATACAGTA	yes	2,8	2,7
NC_009648.1	1222445	-	KPN_RS32185	dinl	TACTGTATAAATAACCAGTA	yes	15,2	7,9
NC_009648.1	1330706	-	KPN_RS06320		CACTGTACATTAATACAGTA	no homologue in MG1655	0,7	0,7
NC_009648.1	1330925	+	KPN_RS06325	ItrA	TACTGTATATATATTCAGTG	no homologue in MG1655	0,5	5,7
NC_009648.1	1392082	-	KPN_RS06630	ydjM	TACTGTATGAATCGACAGTT	yes	0,8	2,1
NC_009648.1	1392082	-	KPN_RS06630	ydjM	CACTGTATAAAAACCCTATA	yes	0,8	2,1
NC_009648.1	1580772	+	KPN_RS07645		TTCTGATTGTAATCACAGGA	no homologue in MG1655	1,9	1,6
NC_009648.1	1602046	-	KPN_RS07740	uspF	GAAGGGATACTTAAACAGGA	no	1,5	0,5
NC_009648.1	1755352	-	KPN_RS08465	dmsD	CAATGGCTACACCACCAGCG	no	0,7	1,9
NC_009648.1	2113961	-	KPN_RS32425		TACTGTTCTTATAATCAATA	no homologue in MG1655	0,7	1,1
NC_009648.1	2116422	-	KPN_RS10330		TACTGTATAAAAAAACAGTA	no homologue in MG1655	0,5	0,8
NC_009648.1	2196973	+	internal in mdtK	mdtK	TACTGGTCAACATTCCGGTG	no	2,1	2,7
NC_009648.1	2366135	+	KPN_RS11635	ydiK	TATTGATATTATTATCAGTA	no	0,7	0,6
NC_009648.1	2445265	-	KPN_RS12010	chaC	AGCTGGATAATATTTCAGCA	no	0,6	0,9
NC_009648.1	2548585	-	KPN_RS12535	dinG	CACTGTCCAAATAACCAGGG	yes	0,4	0,6
NC_009648.1	2556314	-	KPN_RS12575	yoaE	TTCCGTTTAATTACTCAGGA	no	0,6	0,5
NC_009648.1	2602370	-	KPN_RS12815	ruvA	GGCTGGATATCTATCCAGCC	yes	0,4	0,4
NC_009648.1	2619131	-	KPN_RS12900	otsB	CACTGTCTATACTTACATGG	yes	0,6	1,0
NC_009648.1	2689997	-	KPN_RS13305	sbmC	AGCTGTATATTCATACAGTA	yes	0,5	0,4
NC_009648.1	2714275	-	KPN_RS13395		TACTGGTTTTACTAACCGCT	no homologue in MG1655	1,5	1,3
NC_009648.1	2714275	-	KPN_RS13395		TAATGGTTTTATACACTGGA	no homologue in MG1655	1,5	1,3
NC_009648.1	2803617	+	KPN_RS13750		CACTTTTTAAAAATCCAGTG	no	1,1	6,7
NC_009648.1	2867663	-	as in KPN_RS14035		ATCTGGACAATAAAAAAGTT	na	na	na
NC_009648.1	3167027	-	KPN_RS15455	yfhK/glrK	TAATGTCATATATATCAGTA	no	0,8	1,2
NC_009648.1	3327869	-	KPN_RS16255	recA	TACTGTATGACCATACAGTA	yes	0,6	0,4
NC_009648.1	3350324	+	KPN_RS16375		AACTGGTATTTTATCCAGTA	yes	0,5	0,5
NC_009648.1	3350324	+	KPN_RS16375		ACCTGTTTACAATAACTGGT	yes	0,5	0,5
NC_009648.1	3646387	-	KPN_RS17835	yqfA	CACTGGAATCATTCTCAGTT	no	0,5	0,9
NC_009648.1	3803003	-	KPN_RS18625	mug	TGCTGTTTTTATAAACAATG	no	0,4	0,6
NC_009648.1	3829108	-	KPN_RS30150		TACTGTATGTTTATACAGTA	no homologue in MG1655	1,4	1,2
NC_009648.1	3893961	+	KPN_RS19135	yhaK	ATCTGGCTAACAATACAGCG	no	11,7	1,3
NC_009648.1	3904868	-	KPN_RS19195	agaR	AAATGAAAGTTATTCCAGGA	no	1,0	1,3
NC_009648.1	4068128	-	KPN_RS20110	rpsJ	TGATGATTTTCTAAACAGCA	no	1,0	1,9
NC_009648.1	4113170	+	int in KPN_RS20365		TTCTGATATTCCTTACAGCT	na	na	na
NC_009648.1	4121558	-	KPN_RS20400	ompR	AAATGTATACTTAACCTGCT	no	0,5	0,6
NC_009648.1	4170640	-	KPN_RS20610	phd antitoxin	TGTTGTACAATAAAAGAGTA	no	na	na
NC_009648.1	4182892	+	KPN_RS20675	ydcR	TGTCGTTTATTTACACAGGA	no	na	na
NC_009648.1	4275970	-	KPN_RS21060	dppA	CGCTGGATGTAAAACCCGGC	no	na	na

NC_009648.1	4378809	+	KPN_RS21565	rpoZ	GACTGAACCCACATTCAGTA	no	0,7	0,9
NC_009648.1	4416113	-	KPN_RS21735	nlpA	AGATGATTTTATTTCCAGTT	no	1,1	1,9
NC_009648.1	4463983	+	KPN_RS21985	tisB	TACTGTTCATCCATACAGTG	yes	1,3	4,3
NC_009648.1	4508691	+	KPN_RS22205		TGCTGTATAATTAACCAGTT	no homologue in MG1655	2,2	1,7
NC_009648.1	4585490	-	KPN_RS22560	aes	CACTGGATATTAAAACAGTA	no	0,8	1,3
NC_009648.1	4718603	+	KPN_RS23230	uvrD	CTCTGTATATATTAACAGGG	yes	0,8	1,7
NC_009648.1	4726754	-	as in KPN_RS23265	rhtC	ATCTGGTAGCCCATCCAGCA	na	na	na
NC_009648.1	4732717	-	KPN_RS23295	metR	TACTGTATATTCCTCAAGCG	no	0,8	0,9
NC_009648.1	4737198	+	KPN_RS23315	rmuC	AACTGGACGTTTGTACAGCA	yes	0,6	0,5
NC_009648.1	4764396	+	KPN_RS23455	tRNA-Gly	TAATGGCTATTACCTCAGCC	no	na	na
NC_009648.1	4849108	+	KPN_RS23845	lexA	AACTGTATATACACCCAGGG	yes	1,1	3,4
NC_009648.1	4849108	+	KPN_RS23845	lexA	AGCTGTATATACTCACAGCA	yes	1,1	3,4
NC_009648.1	4864335	-	KPN_RS23925	uvrA	TACTGTATATTCATTCAGGT	yes	0,8	0,5
NC_009648.1	4864417	+	KPN_RS23930	ssb1	ACCTGAATGAATATACAGTA	yes	0,6	0,5
NC_009648.1	5137712	-	KPN_RS30735		TGCTGTATAAATATACATTA	no homologue in MG1655	2,4	1,1
NC_009648.1	5137763	+	as in KPN_RS25310		TAATGTATATTTATACAGCA	na	na	na
NC_009648.1	5308814	-	KPN_RS26165	robA	CACTGAATGCTAAAACATCA	no	0,7	0,8
NC_009649.1	109182	+	KPN_RS26790		ACCTGTATCCATAAACAGTG	no homologue in MG1655	1,0	1,2
NC_009650.1	29810	-	KPN_RS27330		CGCTGTAAAACAAAACAGGC	no homologue in MG1655	na	na
NC_009650.1	50040	-	KPN_RS27430	umuD	TACTGTATGCATAACCAGTA	yes	na	na
NC_009651.1	61448	-	KPN_RS28135	umuD	TACTGTATGCATAACCAGTA	yes	0,7	0,9
NC_009653.1	525	+	orphan		TGATGTTTAAACTTATAGTG	na	na	na

Supplementary Table S3 – Bacterial strains

strain	stock name	genotype/relevant markers		source/reference
Klebsiella pneumoniae s	ubsp. pneumoi	niae MGH 78578		
WT	KFKS-031	pKPN3-7	1; 2; 3A/C/D; 4; 6A/B; S1; S2B/C; S3A; S4; S6A; S7; S8A; S9A; S11A/B; S12C/D	(14)
WT	KFKS-245	pKPN3; pKPN5; pKPN7	3E; 6C; S2B; S3B; S6B	this study
∆hfq	KFKS-024	pKPN3; pKPN5; pKPN7; ∆ <i>hfq</i>	3C/E; S2B/C; S3B	this study
hfq::3xFLAG	KFKS-061	pKPN3; pKPN5; pKPN7; <i>hfq::3xFLAG</i>	1; 2; 3A; 4A; S2B/C; S3A; S4; S6A	this study
∆dinlR	KFKS-198	pKPN3; pKPN5; pKPN7; ∆ <i>dinl</i>	6; S6B; S8A; S12C/D	this study
∆dinR	KFKS-199	pKPN3; pKPN5; pKPN7; ∆ <i>dinR</i>	6	this study
∆sulA	KFKS-230	pKPN3; pKPN5; pKPN7; ∆ <i>sulA</i>	6	this study
∆dinIR ∆sulA	KFKS-231	pKPN3; pKPN5; pKPN7; <i>\dinl \sulA</i>	6	this study
∆dinR ∆sulA	KFKS-232	pKPN3; pKPN5; pKPN7; ∆ <i>dinR ∆sulA</i>	6	this study
Escherichia coli				
WT	KFS-0088	TOP10 F- mcrA Δ(mrr-hsdRMS-mcrBC) φ80lacZΔM15 ΔlacX74 nupG recA1 araD139 Δ(ara-leu)7697 galE15 galK16 rpsL(StrR) endA1 λ-	4B/C/D; 5D/E; S9A; S11C	Invitrogen
	KFS-0033	S17 ΔlacU169 (ΦlacZΔM15) recA1 endA1 hsdR17 thi-1 gyrA96 relA1 λpir		New England Biolabs
Vibrio cholerae O1 El To	r C6706			
wт	KPS-0014		4B/C/D; S9A	(18)
Salmonella Typhimuriun	n SL1344			
rne-ctrl.	JVS-6999	[rluC-rne]IG::cat	S6B	(19)
rne-TS	JVS-7000	[rluC-rne]IG::cat rne-3071 (ts)	S6B	(19)

Supplementary Table S4 – Plasmids

trivial name	plasmid ID	description	origin, marker	used in Figure	reference
pBAD _{EC} -ctrl.	pKP8-35	empty vector (used in <i>E. coli</i>)	pBR322, Amp ^R	4B/C/D; 5D/E; S9A; S11C	(9)
pXG10	pXG10-sfGFP	empty vector (used in <i>E. coli</i>)	pSC101*, Cm ^R		(9)
рВАD _{кР} -ctrl.	pER41	empty vector (used in <i>K. pneumoniae</i>)	pBR322, Apm ^R	4B/C/D/E; S8A; S9A; S11A/B	this study
pBAD _{vc} -ctrl.	pBAD1K-ctrl	empty vector (used in V. cholerae)	p15A, Kan ^R	4B/C/D; S9A	(20)
pACBSR-hyg		temperature-sensitive plasmid to express λRED-recombinase system from the arabinose-inducible <i>araBAD</i> promoter	p15A, Hyg ^R		(6)
pFLP-hyg		temperature-sensitive Flp recombinase expression plasmid	p15A, Hyg ^R		(6)
pIJ773		template for apramycin resistance (<i>aac</i> (3)/V) and flanking FRT sites to construct chromosomal deletions in <i>K. pneumoniae</i>	pBR322, Apm ^R		(6)
plJ773-3xFLAG	pER15	template for apramycin resistance (<i>aac</i> (3)/V) and flanking FRT sites to construct chromosomal <i>K. pneumoniae hfq::</i> 3 <i>xFLAG</i>	pBR322, Apm ^R		this study
pBAD _{EC} -DinR	pFS1	expression of DinR under control of the araBAD promoter in E. coli	pBR322, Amp ^R	4B/C/D; 5D/E; S9A; S11C	this study
pBAD _{KP} -DinR	pER45	expression of DinR under control of the araBAD promoter in K. pneumoniae	pBR322, Apm ^R	4B/C/D/E; S9A; S11A/B	this study
pBAD _{vc} -DinR	pER114	expression of DinR under control of the araBAD promoter in V. cholerae	p15A, Kan ^R	4B/C/D; S9A	this study
ftsZ::gfp	pFS7	expression of <i>ftsZ::gfp</i> translational fusion (-62 to /60 of <i>ftsZ</i> relative to the translational start site) under control of the PLtetO-1 promoter	pSC101*, Cm ^R	5D/E	this study
pBAD _{EC} -DinR-M3	pER43	expression of DinR-M3 under control of the araBAD promoter in E. coli	pBR322, Amp ^R	5D/E; S11C	this study
pBAD _{KP} -DinR-M3	pER84	expression of DinR-M3 under control of the araBAD promoter in K. pneumoniae	pBR322, Apm ^R	S11A/B	this study
ftsZ-M3::gfp	pER44	expression of <i>ftsZ-M3::gfp</i> translational fusion (-62 to /60 of <i>ftsZ</i> relative to the translational start site) under control of the PLtetO-1 promoter	pSC101*, Cm ^R	5D/E	this study
pBAD _{EC} -DinR-M2	pFS51	expression of DinR-M2 under control of the araBAD promoter in E. coli	pBR322, Amp ^R	S11C	this study
pBAD _{KP} -DinR-M2	pER85	expression of DinR-M2 under control of the araBAD promoter in K. pneumoniae	pBR322, Apm ^R	S11A/B	this study
pBAD _{EC} -DinR-M4	pER65	expression of DinR-M4 under control of the araBAD promoter in E. coli	pBR322, Amp ^R	S11C	this study
pBAD _{KP} -DinR-M4	pER89	expression of DinR-M4 under control of the araBAD promoter in K. pneumoniae	pBR322, Apm ^R	S11A/B	this study
pBAD _{EC} -DinR-M1	pER66	expression of DinR-M1 under control of the araBAD promoter in E. coli	pBR322, Amp ^R	S11C	this study
pBAD _{KP} -DinR-M1	pER90	expression of DinR-M1 under control of the araBAD promoter in K. pneumoniae	pBR322, Apm ^R	S11A/B	this study
pBAD _{EC} -DinRshort	pFS54	expression of DinRshort under control of the araBAD promoter in E. coli	pBR322, Amp ^R	S11C	this study
pBAD _{KP} -DinRshort	pER95	expression of DinRshort under control of the araBAD promoter in K. pneumoniae	pBR322, Apm ^R	4B/C/D; 5D/E; S9A; S11C	this study
pBAD _{EC-} dinIR	pER37	expression of <i>dinIR</i> under control of the <i>araBAD</i> promoter in <i>E. coli</i>	pBR322, Amp ^R	S11A/B	this study
pTSS_dinIR	pER82	expression of <i>dinIR</i> transcript from TSS (-22 relative to the translational start site) in <i>K. pneumoniae</i>	pBR322, Apm ^R	S8B	this study
pPown_ <i>dinIR</i>	pER83	expression of <i>dinI</i> R transcript -47 from TSS (-69 relative to the translational start site) in <i>K. pneumoniae</i> ; mutation of <i>dinI</i> start codon (ATG to AGG)	pBR322, Apm ^R	S8A	this study
pPown_ <i>dinl</i> AGGR	pER156	expression of <i>dinI</i> R transcript -47 from TSS (-69 relative to the translational start site) in <i>K. pneumoniae</i>	pBR322, Apm ^R	S8A; S12C/D	this study
pPown_ <i>dinIR</i> м16	pER158	expression of <i>dinI</i> R transcript -47 from TSS (-69 relative to the translational start site) in <i>K. pneumoniae;</i> DinR lacks nt 114-130	pBR322, Apm ^R	S12C/D	this study

Supplementary Table S5 – Oligonucleotides

oligo ID	Sequence 5' to 3'	description
	des for construction of plasmids	
KFO-1250	GATCATGACATCGATTACAAGGATGACGATGACAAGTAGTAACTGG AGCTGCTTCGAAGTTC	plasmid construction pER15
KFO-1251	GATGTCATGATCTTTATAATCACCGTCATGGTCTTTGTAGTCCCTAC	plasmid construction pER15
141 0-1201	ACATCGAATTCCTGC	
KPO-1702	ATGCATGTGCTCAGTATCTCTATC	linearization pXG10
KPO-1703	GCTAGCGGATCCGCTGG	linearization pXG10
KPO-0196	GGAGAAACAGTAGAGAGTTGCG	linearization pBAD/pBAD1K
KPO-0411	TTTTTCTAGATTAAATCAGAACGC	linearization pBAD; construction pER82/pER83
KPO-1397	GATCCGGTGATTGATTGAGC	linearization pBAD1K
KFO-1713	GAGATACTGAGCACATGCATTTTTTTAAGAGAACGCAGACAATTAG	plasmid construction pFS7
KFO-1714	GAGCCAGCGGATCCGCTAGCGCCACCGACGCCGATG	plasmid construction pFS7
KPO-1715 KPO-1716	CAACTCTCTACTGTTTCTCCAAGAAGACAAAGACCGGATAAG TCTGATTTAATCTAGAAAAACGATATTGAGCAGAATAATCAGG	plasmid construction pFS1/ER114
KPO-1710		pFS1/pER37/pER82/pER83
KFO-1832	ACTCTTCCTTTTTCAATATTATTGAAG	plasmid construction pER41
KFO-1833	CTGTCAGACCAAGTTTACTC	plasmid construction pER41
KFO-1830	AATATTGAAAAAGGAAGAGTATGTCATCAGCGGTGGAG	plasmid construction pER41
KFO-1831	GAGTAAACTTGGTCTGACAGTCAGCCAATCGACTGGCG	plasmid construction pER41
KFO-1787	CAACTCTCTACTGTTTCTCCGTATCGAACGCAGGGGG	plasmid construction pER37
KFO-2027	GGTAACGAATCAGACAATTGAC	plasmid construction ER82/pER83
KFO-2028	GTCAATTGTCTGATTCGTTACCGTATCGAACGCAGGGGG GTCAATTGTCTGATTCGTTACCCGCAGCCCCCTGTTG	plasmid construction pER82
KFO-2029 KFO-2140	GTCAATGTCTGATTCGTTACCCGCAGCCCCCTGTTG	plasmid construction pER83
	des for mutagenesis	plasmid construction pER114
KFO-1849		plasmid construction pER43
KFO-1850	CAAAAAAACCACAATGAGGGAGCAAACC	plasmid construction pER43
KFO-1851	CGACAGCCACAAGACGGAGAGAAACTATG	plasmid construction pER44
KFO-1852	CTTGTGGCTGTCGCCTGAGAACGC	plasmid construction pER44
KFO-1892	CCTCATTCTGCTTTTTTGCCGGGTCG	plasmid construction pFS51
KFO-1893	AAAAGCAGAATGAGGGAGCAAACCAGAG	plasmid construction pFS51
KFO-1898	CGCAACTCTCTACTGTTTCTCCTTACTCTGGTTTGCTCCCTC	plasmid construction pFS54
KPO-0196	GGAGAAACAGTAGAGAGTTGCG	plasmid construction pFS54
KFO-1990	CTTTTTTTCCCGGGTCGCCCCGGC	plasmid construction pER65
KFO-1991 KFO-1992	CCCGGGAAAAAAGCACAATGAGG	plasmid construction pER65
KFO-1992 KFO-1993	GTTTGCTGCCTCATTGTGCTTTTTTG AATGAGGCAGCAAACCAGAGTAACTG	plasmid construction pER66 plasmid construction pER66
KFO-2719	GCAATTAGGCGCATTGAAGTGTCTATCG	plasmid construction pER156
KFO-2720	CAATGCGCCTAATTGCCCCCTGCGTTCG	plasmid construction pER156
KFO-2721	TTTTTGCCGGGTCGCCC	plasmid construction pER158
KFO-2723	GGGCGACCCGGCAAAAACAAACCAGAGTAACTGGATCC	plasmid construction pER158
oligonucleoti	des for Northern blot probing	
KPO-0009	CTACGGCGTTTCACTTCTGAGTTC	oligoprobe 5S rRNA
KPO-0353	GAATTGGGACAACTCCAGTG	oligoprobe <i>gfp</i>
KFO-0510	GAATACTGCGCCAACACCAG	oligoprobe ArcZ
KFO-0748	GCCCGTCAAAGAGGAATTTC	oligoprobe ChiX
KFO-1297 KFO-1745	CTCGTTCCGGCTCAGGA GGCAAAAAAAGCACAATGAGGGAGCAAACCAG	oligoprobe GcvB oligoprobe DinR
KFO-1745 KFO-1853	AGTTTCTCCCGTCTTGTGC	oligoprobe <i>ftsZ</i>
KFO-1973	AATGAGGGAGCAAACCAGAGTAA	oligoprobe DinR
KFO-2239	AAGCAGGCGAACATCACTGG	oligoprobe KpnR 128
KFO-2394	GTACGGGCAATCATCATATTGG	oligoprobe MicL
KFO-2401	CTAAGGAGGTGGTTCCTGG	oligoprobe CyaR
KFO-2423	CGAAGATCAGATCTAAAGTTTGG	oligoprobe KpnR_105
KFO-2551	GTTCGGCTGTATGTAGGGTAC	oligoprobe KpnR_117
<u> </u>	des for strain construction	
KFO-1407	TGTAGGCTGGAGCTGCTTC	amplification aac(3)IV::FRT
KFO-1376 KFO-1375	CCGGGGATCCGTCGACC GACTACAAAGACCATGACGG	amplification aac(3)IV::FRT amplification
N-0-13/3	GAU I AUAAAGAUGA I GAUGG	amplification aac(3)IV::FRT::3xFLAG
KFO-1252	GATACCGCCAGATGTGGTC	Δhfg and $hfg::3xFLAG$
KFO-1255	AGCGCCGGTCGCTTTAAC	Δhfg and $hfg::3xFLAG$
KFO-1378	GGTCGACGGATCCCCGGGGCCAGTGCTGTTTTTCCAC	Δhfq
KFO-1408	GAAGCAGCTCCAGCCTACAATTCTCTCTTTTCCTTATATGTAT	Δhfq
KFO-1377	CCGTCATGGTCTTTGTAGTCTTCGGCGTCGTCGCTGTC	hfq-3xFLAG
KFO-1378	GGTCGACGGATCCCCGGGGCCAGTGCTGTTTTTCCAC	hfq-3xFLAG
KFO-1798	GGTCGGACCGTTGTTGTTC	∆sulA

KF0-1799 CASEGCCTTCAGATAANTGTTC Asula KF0-1801 GATCGACGGATCCCCGGGTGAAATTAGCG Asula KF0-1801 GATGCACGGATCCCCGGCTGAAATTAGCG Asula KF0-1815 CATCGAATTCCTGCAGCC amplification pU773 KF0-1815 CATCGCATCCTGCTGCAGGC Admin and AdmR KF0-1792 GCAATGCTCCTGCTTCAAGG Admin and AdmR KF0-1793 GCAGGCTCCAGCGATCCCCGGGATCCCCGGCATCCAGGA Admin and AdmR KF0-1792 GCAATGCTCCAGCGATCCCCGGGATCCCCCGCTTCTCTTCTCTCAGAATAG Admin and AdmR KF0-1792 GCAATGCCCAGCGAATCCCCCGGATCCCCCGCCTTCCAGAATAG Admin R KF0-1782 GCAATGCCCAGCGACTCCCCGGCTTCCCCTCTTCGGTCAGCCAGGAATCCCCGAGGACCCCGCCACAAAAAG Inv Riboprobe KF0-1782 GTTTTTTTAATACCACCTCATATAGGCAGAGCCCCGCCTACCCG Inv Riboprobe KF0-2288 GTTTTTTTAATACCACCTCATATAGGCAGAGAAGAAGACGCGGAATA Md In Riboprobe KF0-2289 GTTTTTTTAATACCACTCATATAGGAAGAAGAAGACGCGAATA Md In Riboprobe KF0-2389 GTTTTTTTAATACCACTCATATAGGAAGAAGAAGACGCGAATA Md TT template DinRbin KF0-1990 GTTTTTTTAATACCACTCATATAGGAAGAAGACGCGACAATA Md TT template DinRbin KF0-1991 GCCACCCACGCCCGATG rev TT template DinRbin AG <							Δsu	ΙΔ			
KF0-1810 GAAGCAGCTCCAGCCTAACGATAGTCATGCGCCTTTAG AsulA KF0-1815 CATCGAATTCCTGCAGCC amplification pU773 KF0-1793 GCAATGCTCGTCCAGG Admin and AdmR KF0-1793 GCAAGCTCCTGATGTTCAACG Admin and AdmR KF0-1792 GCAAGGCTCCAGCGCTACATGGTTATTTATACAGTATCGG Admin KF0-1821 GCAAGGCTCCAGCGCATCCCAGGATCCCCGGCTTCTTGTTTAGCAATAG Admin KF0-2020 GCAAGGCAGCTCCCAGCGCATACTAGGGGAAGTCGTGGGCA Admin KF0-1782 GCAAGGCAGCACGCAGCAGTCACTGATGGGGCAGCGTTAACGAG Mcd DinR riboprobe KF0-1783 GCAATGTCAGCGACCACCTACTATAGGCAGCCCGGGCAAAAAAAG Mcd DinR riboprobe KF0-1783 GTMTITTAATCCGACGCACCTATAGGGCAGCGTAACCAGG Mcd DinR riboprobe KF0-1892 GTMTITTAATCCGACGCACCTATAGGCTACCTGGCTATC Mcd din riboprobe KF0-2895 GCATTGAAGTGTTATGGCTAGGGTAACGCGAAAGACCACACT Mcd T1 remplate DinR riboprobe KF0-1890 GTTTTTTTAATCCGACGCCACCTATAGGTTAAGGCAAGACCAAAGACCAGACAATT Mcd T1 remplate DinR riboprobe KF0-1991 GCAACGCGGGCGCACACC rev T1 template DinR riboprobe Mcd T1 remplate DinR riboprobe KF0-1991 GCACGCGGCGCCACG rev T1 template frg2 GCAATGACA	ATT	ATT	TATTC	CTGC	3		_				
KF0-1814 ANTATCAAGCTTATCGATACCG amplification pJJ773 KF0-1815 CATCGAATTCCTCGCAGCC admin and admR KF0-1782 GCAAGCAGCTGCATGCTCCAAGC admin and admR KF0-1805 CGAAGCAGCTCCAAGCCTACATGGTTATTTATCACATATCCGG admin and admR KF0-1805 CGAAGCAGCTCCAGCCTACATCAGGAGAGCATCGTGGGCA admin KF0-1801 GCAGGTCCAGGATCCCCGGGCAACACCTCTTCTTCTGTCAGAAACA admin KF0-1802 GGAGGTCGAGGATCCCCGGGCACCGCGGGCAAAAAAG admin KF0-1782 GTITTTTTATACGAGTCACTATAGGCGGCGCGCGGCGACCTTAC admin Riboprobe KF0-1782 GTITTTTTATACGACTCACTATAGGCTGGCGACCTGGCTACC rev Unin Riboprobe KF0-2828 GTITTTTTATACGACTCACTATAGGACGCTACCTGGCTACC rev Vin Riboprobe KF0-2854 GTITTTTTATACGACTCACTATAGGAAGAAGACGCAGATA fwd in Riboprobe KF0-2899 GTITTTTTATACGACTCACTATAGGAAGAAGACGCAGACAATT fwd in Riboprobe KF0-1991 GCACTAGAAGTGATAGCACACTATAGGAAGAAGACGCAGACAATT fwd in Riboprobe KF0-1992 GTITTTTTATACGACTCACTATAGGAAGAAGACGCAGACAATT fwd in Riboprobe KF0-1991 GCACCGAAGACACTTATAGGAAGAAGACGCAGACAATT fwd in Riboprobe KF0-1992 GTITTTTTT											
KF0-1915 CARTGCCTGCTTCAGG admir and admir KF0-1792 GCAGCCTCCGTCTCAGG Admir and admir KF0-1915 CGAAGCCTCCAGCCTCACAGTGTATTTTATACAGTATCCGG Admir and admir KF0-1915 CGAAGCACCTCCAGCGCACCGCCTTCTCTTTACAGATAGC Admir KF0-1921 GCAAGCACCTCCAGCGCACCGCCCTTTTTGCCGGAATCGTGGAC Admir KF0-1921 GCAAGCTCCACGGATCCCCGGCATTTTTGCCGGGACGCCC Admir oligonucleotides for 17 templates TrittTTTTATATCCGACTCACGAGCGCGCCCGGCAAAAAAAG fwd JinR riboprobe KF0-1763 GATTAAGCGAAATCCTGCATATAGGCGGCGCCCGGCAACCAGCGG rev Dirk Riboprobe fwd Jin Riboprobe KF0-2280 CGAATGGCTCATCCACTATAGGCTGCCCGCCTACCTGGCTATC fwd dirl riboprobe fwd Jin Riboprobe KF0-2585 CGCATTGAAGCTCACTATAGGACTACCTAGTATAGGACGCACACGGGATA fwd Jin template DirkRb KF0-1891 AAAAAAACCCGGGGGCGCC rev T1 template DirkRb KF0-1991 AAAAAAAACCCGGGGGCGCC rev T1 template DirkRb KF0-1991 AGAAAAAACCCGAGCGCACC rev T1 template BrZ KF0-1991 AGAAAAAACCCGAGCGCACC rev T1 template BrZ KF0-1991 CCACTGACGCGCGCACC rev T1 template BrZ									on plJ7	73	
KF0-1793 GCAGCATCTGATGTTCAACC Admin and admR KF0-1995 CGAAGGCACTCCAGCGTCACCGCATGTTTTTTTACAGTATACCG Admin KF0-1991 GCAAGGCAGCTCCAGCGCACCGCTGCCTGTTCAGGAATAG Admin KF0-1921 GCAAGGCAGCCCCAGCGCAATCCCCGGGATCCTGCGC Admin ofigonucleotides for 17 templates FW FW KF0-1783 GATAAGCGAAATCCGCAGGACCCCGGCACCGGCAAAAAAG fwd JinR riboprobe KF0-1783 GATAAGCGAAATCCTGCAGG rev DinR hiboprobe KF0-2280 CGAATGGGTTCATCCGC fwd JinR hiboprobe KF0-2585 CGCATTGAAGTCACTCATATAGGACGCCACCTGCGTACC fwd Jin hiboprobe KF0-1890 GTTTTTTTAATACGACTCACTATAGGACGACACAAGACAAAGACCAGGATA fwd Jin hiboprobe KF0-1891 AAAAAAACCCGGGGGCACC rev T1 template DinRb KF0-1891 AAAAAAACCCGGGGGCACC rev T1 template DinRb KF0-1891 CCAACTTCAATTAGGACAACCAGC primer extension KF0-2726 GCCAACCACTTCAATTAGGACAACCAG primer extension dinR KF0-2727 GTTAGACACTTCAATTAGCGACCACCG qPCR Pani KF0-2728 GTAAAGCCACTTCAATTAGCGACCCC qPCR Pani KF0-2727 GTTAAGCA											
KF0-1995 CGAAGCACCTCCAGCGATCCCCGGATCCCTTTTGTTCAGCAATAG Adim/ KF0-1221 GCAGGTCGACCGGATCCCCGGATCCCCTTTTGTTCGTCAATAG Adim/ KF0-2001 GCAGGTCGACGGATCCCCGGATCCCCTTTTGTTCGTCGAATAG Adim/ KF0-1762 GTITTTTTAATACGACTCACGAGGACCCCGGCAAAAAAG fwd DinR riboprobe KF0-1762 GTITTTTTAATACGACTCACTATAGGCGACCCGGCAAAAAAG fwd DinR riboprobe KF0-1763 GATAAGCCAAATCCTGCAGGA rev DinR riboprobe KF0-2288 GTITTTTTAATACGACTCACTATAGGCTGCCACCGGCAACAAAGA fwd JinBoprobe KF0-2280 GTITTTTTAATACGACTCACTATAGGACGCACCCTGGCTACCCGC fwd JinBoprobe KF0-2584 GTITTTTTAATACGACTCACTATAGGAAGAAGAACAAAGACCGGATA fwd 17 template DinRboin KF0-1999 GTITTTTTAATACGACTCACTATAGGAAGAACAAAGACCGAAAA fwd 17 template DinRboin KF0-1990 GTITTTTTAATACGACTCACTATAGGACAACCAG rev T7 template fisZ GUigonucleatide for primer extension rev T1 template fisZ rev T1 template fisZ GUigonucleatide for primer extension rev T1 template fisZ rev T1 template fisZ KF0-1991 GCCACCGACCCATCACTATAGGGACAACCAG pPCR Preel rev T1 template fisZ KF0-2725 GTGAAAGAACACCAGCCATCAGGGACACCAG <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th>∆dir</th> <th>I and A</th> <th>dinR</th> <th></th> <th></th>							∆dir	I and A	dinR		
KF0-1821 GCAGGTCCACGGATCCCCGGATCCCCGGTTTCTTTGTCAGATAG Adm/n KF0-2000 CGAAGCAGCTCCAGCCTCATCAGGAGAGAGTCGTGGAC Adm/n KF0-1762 GATAGCGAACTCCACGGATCCCCGGGCATCACGAG Adm/n KF0-1763 GATAAGCGAACTCACTGCAGG Ind Dinr hioprobe KF0-1763 GATAAGCGAACTCACTATAGGCGGCGCACCGTTAACGAG Ind Jinborobe KF0-2280 CGAATGGTTCAGTCAGCTCACTATAGGCGGCGCACCGTTACCAGA Ind Jinborobe KF0-2555 CGCATTGAACTCACTATAGGACTCACTATAGGACGTCACCTGGCTATC Ind din liboprobe KF0-2580 CGCATTGAACGTCACTATAGGACGACACAGAGACAAAGACCGGGATA Ind din liboprobe KF0-2585 CGCATTGAACGTCACTATAGGACGACACAGGAGAACAAGACCGGGATA Ind 17 template DinRbin KF0-1990 GTITTTTTAATACGACTCACTATAGGAGAGAAGACAAAGACCGGACATT Ind 17 template DinRbin KF0-1901 GCCACCGACCACTATAGGGAGCAAACCAG primer extension din/n KF0-1912 GCCAACCGCGACAC rev T7 template fizZ GIgonucleatide for primer extension Irrimer extension din/n KF0-2726 GTAAAAAAAGCCACATGAGGGACAACCAG pPCR Prim KF0-27274 GCGAAACAAAGACCACGCCC qPCR Prim KF0-2726 GTAAAGCACTCATACAGCGCTCGCTGAC							∆dir	I and A	dinR		
KF0-2000 CGAAGCAGCTCCAGCCTACATCAGGAGAGATCGTGGGAC AdinR Gilgonucleotides for T7 templates Mod DinR riboprobe Mod DinR riboprobe KF0-1752 GTITITITTAATACGACTGACGAGGCCGGGCAGAGAAAAAG Mod DinR riboprobe KF0-1752 GTITITITTAATACGACTGACGAG Mod DinR riboprobe KF0-2288 GTITITITTAATACGACTGACGAG Mod DinR riboprobe KF0-2584 GTITITITTAATACGACTCACTATAGGAGAGCACCTGGCTAC Mod Ain Roprobe KF0-2584 GTITITITTAATACGACTCACTATAGGAAGAGACAACAAGACGGAGAA Mod T7 template DinR/bin KF0-1599 GTITITITTAATACGACTCACTATAGGATAGAGAAGACGAGAAATT Mod T7 template DinR/Din KF0-1591 AAAAAAGCCGGGGGCGACC rev T7 template DinR/Din KF0-1590 GTITITITTAATACGACTCACTATAGGATAAGAGAACAAAGCGAGAATT Mod T7 template flsZ AG KF0-1591 GCACACGACGCAATGAGGGAGACAAACCAG prime extension din/R Gilgonucleotide for primer extension fwd T7 template flsZ Mod AAAAAGCCGGGGGCGACC KF0-1735 GCGAATAGAACACTCATGAGGCAAAACCAG primer extension din/R Gilgonucleotides for pPCR (ChIP analysis) fwd PR and KF0-2726 GTAAAGACACTGATCATGAGGCACAACCAG pCR PrecA	CAC	ΆΤΑ	ACAGT	TATCO	CGG		∆dir	n/			
KF0-2001 CCAGGTCGACGGATCCCCGGCTTTTTTGCCGGGTCGCC AdliR Oligonucloatides for 77 templates MM DINR riboprobe MM DINR riboprobe KF0-1752 GATTAAGCGAATCCTCCACAGG MM DINR riboprobe KF0-2280 CGAATGGGTTCACTCACCATAGGCTGGGCACGCTTAACCAG MM sulA riboprobe KF0-2280 CGAATGGGTTCACCTCACCATAGGCTGGCCACCTGGCTACC GC rev DinR riboprobe KF0-2585 CGCATTGAAGTGTCACCATATAGGAAGACCACCTGGCTTGCTCCCC Md ri hoprobe KF0-1990 GTTTTTTTTAATACGACTCACTATAGGAAGAAGAACAAAGACCGGAAT Md T7 template DinR bin AG MT 71 template DinR bin Md T7 template DinR bin KF0-1900 GTTTTTTTAATACGACTCACTATAGGTTAAGGAACGCAGACATT Md T7 template DinR bin KF0-1911 AAAAAAGCCGGGGCGACC rev T7 template DinR bin KF0-192 GTTTTTTTAATACGACTCACTATAGGTTAAGGTAACGCAGCACATT Md T7 template DinR bin KF0-1931 CGCCAAAAAAGCACACATGAGGGAGCAAACGAG primer extension KF0-1942 GCGCAAAAAAGAACCACATGAGGGAGCAAACCAG qPCR Pain! KF0-2726 GTGAAGAAATAAAAAGCAGCAGCC qPCR Pain! KF0-2726 GTAAAGCGGTAATCCAAGGTACGTCGGTGGCTATACGGTCAC 235 rRNA depletion #1 235	TGI	TTC	CTGTT	FCAG	ΑΑΤΑΘ	3	∆dir	nl			
oligonucleotides for 17 templates international construction of the second consecond consecond construction of the second construction of the s							∆dir	nR			
KF0-1782 GTTTTTTTAATACGACTCACTATAGGCCACCGCGAAAAAAG fwd DinR riboprobe KF0-1782 GTTTTTTTAATACGACTCACGAG rev DinR riboprobe KF0-2288 GTTTTTTTAATACGACTCACTATAGGCTGGCACGCGTTAACGAG rev DinR riboprobe KF0-2281 GTTTTTTTAATACGACTCACTATAGGACGCTGACCAGGGTTAACGAG rev din/ riboprobe KF0-2555 CGCAATGCAGTGTATGCGC rev din/ riboprobe KF0-1890 GTTTTTTTAATACGACTCACTATAGGAAGAAGAACAAAGACCGGATA fwd T/ template DinRA AG KF0-1691 AAAAAAACCCCGGGGCGACC rev T7 template DinRA KF0-1691 AAAAAAACCCCACACTCACTATAGGTAAGGAAACGCAGACACATT fwd T7 template DinRA KF0-1691 ACAAAAAACCCCACACTCACATGAGGAAACCACA rev T7 template DinRA KF0-1691 ACAAAAAACCCCACACTCACATGAGGAAACCACA rev T7 template fisZ CIGGAAAAAAACCCCACACTCACATGAGGACAAACCAC primer extension rev T7 template fisZ KF0-1725 GTGAAAAAACCACATTGACT qPCR Preal KF0-2726 GTAAACCATTGCATGCT qPCR Preal KF0-2726 GTAAACCATTCAATGCGT qPCR Preal KF0-2726 GTAAACCATTCACTGCTGTTCGCTCCC QPCR Preal KF0-2727 GTAAAGCATTCACTGCTGGTCGCTAC	GGC	3000	GGGT	TCGC	С		∆dir	nR			
KF0-1763 GATAAGCGAAATCCTGCAGT rev SulA riboprobe KF0-2280 CGAATGGGTTCAGTCACCTAAGGCTGGCAGCGTTAACGAG fwd sulA riboprobe KF0-2854 GTTTTTTTAATACGACTCACTATAGGACGACGACTATC fwd sulA riboprobe KF0-2855 GTTTTTTTTAATACGACTCACTATAGGACGACCACTGGCTATC rev sulA riboprobe KF0-1889 GTTTTTTTTAATACGACTCACTATAGGAAGAAGACAAAGACCGGAT fwd TT template DinRND KF0-1890 GTTTTTTTTAATACGACTCACTATAGGAAGAAGACGACGACGAT fwd TT template DinRND KF0-1901 GCCACCGACGCGCGACC rev T7 template DinRND KF0-1901 GCCACCGACGCCGATG rev T7 template fsZ Oligonucleotide for prime rextension rev T7 template fsZ Oligonucleotide for prime rextension rev T7 template fsZ Oligonucleotide for prime rextension gCCA Paint KF0-2725 GTGAAGACACTTCAATGCG gPCR Print KF0-2726 GTGAAGACACTTCAATGCGC gPCR Preca KF0-27275 GTGAAGAATAAAACGCAGCCTTGC gPCR Preca KF0-27276 GTGAAGAATAAAACGCAGCTATGCGTCACCC gPCR Preca KF0-27277 GTGAAGAATAAAACGCAGCTATGCGTCGCCACCC gPCR Preca KF0-27276 GTCACAGATCCAGGGTTGCGTTATAGCACGCGTCACCC 235 rRNA depletion #1							1			-	
KF0-2288 GTTTTTTTATACGACTCACTATAGGCTGGCAGCGTTAACGAG frev sul/a tiboprobe KF0-2280 CGAATGGGTTCAGTCCCC rev sul/a tiboprobe KF0-2585 CGCATTGAAGTGTCTATCGC fred sul/a tiboprobe KF0-1890 GTTTTTTTTAATACGACTCACTATAGGTACTCTGGTTTGCTCCTC fred sul/a tiboprobe KF0-1890 GTTTTTTTAATACGACTCACTATAGGTACTCTGGTTTGCTCCTC fred sul/a tiboprobe KF0-1890 GTTTTTTTAATACGACTCACTATAGGTAAGGAAGACGAAAGACCGAGAAT fred T7 template DinRNDin KF0-1891 AAAAAAAGCCGGGGCGACC rev T7 template DinRNDin KF0-1902 GTTTTTTTATATACGACTCACTATAGGTTAAGAGAACGCAGACAT fred T7 template DinRNDin KF0-1901 GCCACCGACGCCGATG rev T7 template DinRNDin KF0-1745 GGCAAAAAAGCCACATGAGGGGCCAAACCAG primer extension din/R Gligonucleotides for primer extension gCCR Prim KF0-2726 KF0-2727 GCGATAGCACTTCATGCGCGG qPCR Prim KF0-2757 GTCAAGACTCACTGCTTCGCT qPCR Prim KF0-2757 GCTCAAGACCGTCATTATACGAAAGGTACCCCGGTCACC 235 rRNA depletion #1 235_2 IBinJCCCCTTCCCCAGGGTATTCCTCGGGTTGCTCACC 235 rRNA depletion #1 235_3 IBinJCCCCTTCC	CGG	1CCC	CGGC		AAAAG	<u>;</u>					
KF0-2260 CCGAATGGGTTCAGTCCGC rev <i>sula</i> riboprobe KF0-2554 GTTITTITTATATACGACCTCACTATAGGACGCTCACCTGGCTATC fiwd <i>dini</i> riboprobe KF0-2555 CGCATTGAAGTGTCATCGC fiwd <i>dini</i> riboprobe KF0-1899 GTTITTITTAATACGACTCACTATAGGAAGAAGAACAAAGACCGGGAA fiwd T7 template DinRNo KF0-1901 GCCACCGACGCCC rev T7 template DinRNo KF0-1902 GTTITTITTAATACGACCACTAATGGAGAGAACGCAGACACTT fwd T7 template DinRNo KF0-1901 GCCACCGACCCCACTATAGGAGAGACACCAG primer extension KF0-1790 GCCACAGACACATCAATGGG primer extension <i>dinIR</i> KF0-2725 GTGAAAAAAAGCCACATGAATGGG QPCR PeinI KF0-2725 GTGAAGAATTAAAAAGCCACGCC QPCR PeinI KF0-2726 GTAAGCACTTCAATGGG QPCR PeinI KF0-2727 CTATGCGCTGACGCTTCG QPCR PeinI KF0-2727 GTAAGACCATTCAAGGTACGGTGGCTATCGGTCA QPCR PienA KF0-2726 GTGAAGATCATGCCTGGCTATGTGGTGCTATGGGTCA QPCR girR GJgonucleotides for rRNA depletion 235 IBIN_CGCGCGATAGCGCTGTGCCTATGCGGTATGGTCGCTATCGGCTA 235.1 Bin_CGGGGGAACACGCACTGGTGGCGAACTCGGGGTTGATGGCC 235 rRNA depletion #2 <th><u> </u></th> <th></th>	<u> </u>										
KF0-2554 GTITTITTATACGACTCACTATAGGACGCTCACCTGGCTATC fwd din/ itboprobe KF0-2555 CGCATTGAAGTGTCTATGCC fwd din/ itboprobe KF0-1890 GTITTITTTAATACGACTCACTATAGGTTACTCTGGTTTGCTCCCTC fwd T7 template DinRsho MG TTemplate DinRsho fwd T7 template DinRsho KF0-1691 AAAAAAAGCCGGGGCGACC rev T7 template DinRNDin KF0-1691 CCACCGACGGCGACC rev T7 template DinRNDin KF0-1791 GTITTITTTAATACGACTCACTATAGGTTAAGAGAACGCAGACAATT fwd T7 template DinRNDin KF0-1901 GCCAACGACGACGACGAC rev T7 template DinRNDin KF0-1745 GCGAAAAAAGCACAATGAAGAGAGAGACAAACCAG primer extension din/R Oligonucleotide for primer extension fwd T7 template DinRNDin fwf Template DinRNDin KF0-2726 GTGAAAGAAATAAAAACGCAGCC qPCR Pidni fwf Co2726 KF0-2726 GTAAAGCATGCATGCCTTGC qPCR Pidni fwf Co2726 KF0-2726 GTAAAGCATGCATGCCTTGCTTG qPCR Pidni fwf Co2726 GGTAAAGACATGAACGGTGCTCAGCTATCGCGGTCACC 238 rRNA depletion #1 235 23 ginnucleotides for rNA depletion fwf and the pietoin fwf	CAG	1000	CAGC	JGTTA	ACGA	AG					
KF0-2555 CCCATTGAAGTGTCTATCGC rev dini riboprobe KF0-1690 GTTTTTTTAATCGACTCACTATAGGAAGAAGACAAAGACCGGATA AG fwd T7 template DinRaho KF0-1691 AAAAAAGCCGGGGCGACC rev T7 template DinR KF0-1691 AAAAAAAGCCGGGGCGACC rev T7 template DinR KF0-1902 GTTTTTTTAATCGACTCACTATAGGTTAAGAGAACGACAGCACAATT AG fwd T7 template DinR KF0-1901 GCCACCGACGCCGATG rev T7 template fisZ oligonucleotide for prime extension rev T7 template fisZ KF0-2725 GTGAAGACACTCAATGAGGGAGCAAACCAG primer extension din/R NG02727 GTGAAGAAAAAAAACGCACGC qPCR Paini KF0-2726 GTGAAGAAATAAAACGCACGC qPCR Paini KF0-2727 GTGAAGAAATAAAACGCACGCT qPCR Paea KF0-2727 GTAAGAAATAAAACGCCGGTC qPCR Paea KF0-2727 GTAAGAAATAAACGCCGTCGCTG qPCR Paea KF0-2727 GTAAGAAATAAAACGCCGGTC QPCR SgrR KF0-2727 GTAAGAAATAAAACGCCGGTC QPCR SgrR KF0-2727 GTAAGAACCCTGCCTTGCTGCTACGGTTCGCTACCGC 235 rRNA depletion #1 235 BinJCGCGGGGAAACGCACTTCCCGGGTTGGCTACCGCGTCAC 235 rRNA depletion #3 234 BinJCGCGGGGAAAC		CTC	CACCT	TGGC							
KF0-1900 GTTTTTTTAATACGACTCACTATAGGTTACTCTGGTTTGCTCCCTC. fwd T7 template DinRsho KF0-1691 AAAAAAAGCCGGGCGACC rev T7 template DinRsho KF0-1691 AAAAAAAGCCCGGGCGACC rev T7 template DinRbin KF0-1691 GCCACCGACGCCCACTCACTATAGGTTAAGAGAACACAGACACATT fwd T7 template DinRbin KF0-1902 GTTTTTTTAATACGACTCACTATAGGTAAGAGAACGCAGACAATT fwd T7 template DinRbin KF0-1745 GCCAAAAAAGCCACATGAAGGAGCACAACCAG primer extension din/R Gligonucleotide for primer extension gCCR AAAAAAACGCAAGCC qPCR Paint KF0-2725 GTGAAGAAATAAAAACGCAGCC qPCR Paint KF0-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KF0-2727 CTATGCGCTAACTGCGTTCG qPCR PrecA KF0-2726 GTAAAGCGTCATTTACAAAGGTACGCCGTCAC 23S rRNA depletion #1 S10 BinJACCTTTGCCTCACGGCGTC qPCR sgrR Gligonucleotides for rRNA depletion T 23S 1 BinJACCTTTCCTCACGGTACTGGTTGCGTACCGCC 23S rRNA depletion #2 S2S 1 BinJGGGGGGAAACCAGCTATATTACACTGGTTCGCTGCAC 23S rRNA depletion #3 23S 4 BinJGGGGGGAAACCAGCTATATTACACTGCGTTCGCGTCAC 23S rRNA depletion #3 S2S 4 BinJGGGGGGAAACCAGCATTGAGGACCGGACTACCGACCGCC 23S rRNA deplet	JAO	5010	OROOI	1000		, 					
KFO-1900 GTTTTTTTAATACGACTCACTATAGGAAGAAGACAAAGACCGGATA AG fwd T7 template DinR Tev T7 template DinR/Din Wd T7 template DinR/Din Wd T7 template DinR/Din Wd T7 template frsz KFO-1902 GTTTTTTTTATACGACTCACTATAGGTTAAGAGAACGCAGACAATT AG rev T7 template frsz KFO-1901 GCCACCGACGCCGATG rev T7 template frsz oligonucleotide for prime extension rev T7 template frsz KFO-2725 GTGAAGACATTCAATGCG qPCR Painl KFO-2726 GTGAAGACATTCAATGCG qPCR Painl KFO-2726 GTGAAGCACTTCAATGCG qPCR Painl KFO-2726 GTGAAGCACATGCCCCCGCG qPCR Painl KFO-2727 CTATAGCGCTAATGTGCTTG qPCR PrecA KFO-2726 GTGAAGACATTCACTGCGTCGCT qPCR grR KFO-2727 GTCGAAGATCCATCGCTTG qPCR grR Strop GCCGTAGATCATCGCCTTG qPCR grR oligonucleotides for rNA depletion 233 gTTTTCCCTCACGGTCATTATCACGACACTCGGTCACC 235 rRNA depletion #1 235 BinJGCGCGTGCGAAATTAACCTGGTTCGCAGCGTCACC 235 rRNA depletion #2 235 rRNA depletion #2 235 BinJCCGCGGCGCGGACGGCGACTGTCTCCCGACAGC 235 rRNA depletion #3 235 BinJCCCGCGGC	TG	СТС	CTGGT	TTTGO	стосо	стс					ort
AG vert T template DinR/Din KFO-1691 AAAAAAAGCCGGGGGGACC rev T7 template DinR/Din KFO-1902 GTTTTTTTAATACGACTCACTATAGGTTAAGAGAACGCAGACAATT fwd T7 template ftsZ AG vert T1 template ftsZ vert T1 template ftsZ KFO-1901 GCCACCGACGCCGATG rev T7 template ftsZ oligonucleotide for prime extension rev T7 template ftsZ KFO-1722 GCGATAAAAAGCCAATCAATGAGGAGCAAACCAG primer extension din/R KFO-2726 GTGAAGACAATAAAAAGCCAGCC qPCR Pain! KFO-2726 GTGAAGACATAAAAAGCCAGCC qPCR Pain! KFO-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KFO-2727 CTATGCGCTGACTTCGCTCTG qPCR gr/R GGCTAAGATCCATGCTTCGCTTG qPCR gr/R gGCTAGAGTACTTCACAGCGTCATTATCCATCGGTCA 238.1 BinJACCTTTCCCTCACGGTCATGTCTGCTTCGCTCA 235 rRNA depletion #2 238.3 BinJCGGGGGAGAACCAGCTATCTCCGGGTTTGCGTGTCA 235 rRNA depletion #2 238.4 BinJGGGCTGCTGCTTTAAGCACACCGGT 235 rRNA depletion #3 238.5 BinJCGCGCGGGATAGGACCGAACTGCGACTGCCGACAGC 235 rRNA depletion #3 238.6 BinJCCCCTGCGTTGCGTTGAGCGTGCCCAAAGA<											
KFO-1902 GTTTITITTAATACGACTCACTATAGGTTAAGAGAACGCAGACATT fwd T7 template ftsZ AG rev T7 template ftsZ VFO-1901 GCCACCGACGCCGATG rev T7 template ftsZ oligonucleotide for primer extension primer extension din/R Stopartic Control of the primer extension din/R GCCAAAAAACGCACATTGAGGGAGCAAACCAG pprimer extension din/R Stopartic Control of the primer extension GCCAAAAAAAGCACACTTCAATGCGC qPCR Pdin/ KF0-2726 GTGAAAGCATAAAAAAGCCAGCC qPCR Pdin/ KF0-2727 GTGAAGCATTGCCTTCG qPCR Preca KF0-2756 GTATTGCCCTGCAGCGTC qPCR SgrR Gigonucleotides for rRNA depletion gCCASTRA depletion #1 238_1 [Bin]ACCTTTCCCTCACGGTACTGGTTGCTATCGGTCA 235 rRNA depletion #1 238_2 [Bin]GGGGCGGAACCAGCTTCACCGGTTGCATCGGCTACCGC 235 rRNA depletion #3 238_4 [Bin]GGGCAAGGAACTAACCTGACTTCCCGGCTTGCACGCC 235 rRNA depletion #3 238_5 [Bin]GGCCGGGCTGCGAACTTACCCGGCAACA 235 rRNA depletion #3 238_6 [Bin]CGGCGGGCTGCGAACTTACCCGGCACAGC 235 rRNA depletion #6 238_7 [Bin]CGCCGCGGATAGGACGACCGACCTGCCGACAGC 235 rRNA depletion #6									·		
AG rev T7 template ftsZ Oligonucleotide for primer extension primer extension din/R KF0-1901 GCCACCGACGCCGATG primer extension din/R Oligonucleotides for QPCR (ChIP analysis) KF0-2724 GCGATAGACACTTCAATGCG qPCR Pdin/ KF0-2725 GTGAAGAAATAAAAACGCAGCC qPCR PrecA KF0-2726 GTAAGACGTGTCCCTTCG qPCR PrecA KF0-2727 CTATGCGCTGAAATCTGCTCTG qPCR PrecA KF0-2757 GCTCAAGATCCATGCCTTTG qPCR SgrR KF0-2757 GCTCAAGATCCATGCCTTTGC 23S rRNA depletion #1 235_1 [Btn]ACTGCCTTGCACGGTATCTATCCGGGTTAGCCCC 23S rRNA depletion #1 235_2 [Btn]CGGGGGAACCACGCATCTATCCCGGGTTGGCCTACC 23S rRNA depletion #1 235_3 [Btn]CGGGGGAACCACGCATCTATCCCGGCTTGC 23S rRNA depletion #1 235_4 [Btn]CGGCGGGAACCGACTATCACGGACGCGT 23S rRNA depletion #1 235_3 [Btn]CGCCGGGAACGGACGAACCTACTGGTCCCGGACAGCCT 23S rRNA depletion #1 235_4 [Btn]CGCCGGGAACGGAACCTAACA 23S rRNA depletion #1 235_5 [Btn]CCCCTGTGCTGGTTGGACGTGTCCCCCGGCT 23S rRNA depletion #1 </th <th></th> <th>nRshort</th>											nRshort
KFO-1901 GCCACCGACGCCGATG rev T7 template ftsZ oligonucleotide for primer extension rev T7 template ftsZ KFO-1745 GGCAAAAAAAGCACCATGAGGGAGCAAACCAG primer extension din/R Netronal State GGCAAAAAAAGCACCATGAGGGAGCAAACCAG primer extension din/R KFO-2724 GGGATAAAAAAGCGCAGCC qPCR Pdin/ KFO-2725 GTGAAGAAATAAAAACGCAGCC qPCR Preca KFO-2726 GTAAAGCGTGTTCGCTTCG qPCR Preca KFO-2726 GTATGCCTGACGGTCTGGT qPCR Preca KFO-2726 GTATGCCTGAGCGTC qPCR Preca KFO-2756 GTATTGCCCTGCAGCGTC qPCR sgrR Gligonucleotides for rRNA depletion 235_1 Bin/ACCTGTCGCTCATTATACAAAAGGACCCCC 235 rRNA depletion #2 235_3 Bin/TGGGGGAAACCAGCATTATACCAAAAGGACCCCC 235 rRNA depletion #4 235_4 Bin/TGGGGGAACAGAACTATACCGGATTCCCTGCGGACC 235 rRNA depletion #6 235_5 Bin/GGGCGGGAACTGAGACCGAACGGT 235 rRNA depletion #7 235_6 Bin/CACCTGGTGCGAACCAACGGT 235 rRNA depletion #6 235_9 Bin/CACCGGCGTGGGAACGAACCGACGGCA 235 rRNA depletion #7<	GA	AGA	AGAAC	CGCA	GACA	ATT	fwd	T7 tem	plate <i>f</i>	ftsZ	
oligonucleotide for primer extension KFO-1745 GGCAAAAAAGCACATGAGGAGCAAACCAG primer extension din/R oligonucleotides for qPCR (ChIP analysis) KFO-2724 GCGATAGACACTTCAATGCG qPCR Pdin/ KFO-2725 GTGAAGAATAAAACGCAGCC qPCR Pdin/ KFO-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KFO-2726 GTATAGCCAGAGGTC qPCR sgrR KFO-2757 GCTCAAGATCAATGCTTTGG qPCR sgrR KFO-2757 GCTCAAGATCCATGCCTTTG qPCR sgrR KFO-2757 GCTCAAGGTCACAGGGTCCACGGTCGCTACCC 235 rRNA depletion #1 235_1 [BIn]AGTCGCTGCTCACAGGTACTGCTCGCGTTCGCTACCC 235 rRNA depletion #1 235_2 [BIn]GCGGCGGAGACCACACCACGTTCTCACGGATTGCCC 235 rRNA depletion #1 235_3 [BIn]GCGCTGGTTCTAAGCCAACATCTGCG 235 rRNA depletion #1 235_4 [BIn]GCGCTGGTTCGGGACCTTACCCGACAGCGT 235 rRNA depletion #1 235_5 [BIn]GAGCCGGACATGGAGGACCTTACCCGACAGCGT 235 rRNA depletion #1 235_7 [BIn]GCGCTGGCTTCAGGACCACATCCACGAC 235 rRNA depletion #1 235_8 [BIn]GCGCTGGATGGGACCGAACTTCCCACGAC 235 rRNA depletion #1 <th></th>											
KFO-1745 GGCAAAAAAGCACATGAGGGGAGCAAACCAG primer extension din/R oligonucleotides for qPCR (ChIP analysis) restension din/R KFO-2724 GCGATAGACACTTCAATGCG qPCR Pdin/ KFO-2725 GTGAAGAAATAAAAACGCAGCC qPCR Pdin/ KFO-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KFO-2727 CTATGCGCTAACTGCTTCG qPCR PrecA KFO-2726 GTATTGCCCTGCACGCTC qPCR sgrR oligonucleotides for rRNA depletion gPCR sgrR 235_1 Btn/ACCTGCTGCACGTATTACAAAAGGACCCGCCTCACC 235 rRNA depletion #1 235_3 Btn/TCGGGAGAACCAGCTATTACCAAAAGGACTACGCC 235 rRNA depletion #1 235_4 [Btn]GGGTACAGGAATATTACCTGATTCCCAGGATTACCGCC 235 rRNA depletion #14 235_6 [Btn]CGGCGGAACTGGGGTACCGACGGT 235 rRNA depletion #6 235_7 [Btn]CGGCGGAACTGGAGGTGCCAAACA 235 rRNA depletion #6 235_8 [Btn]CGGCGGGATACGAGGGGCCCAAACA 235 rRNA depletion #17 235_8 [Btn]CGGCGGGATGGGATTCACCGACAGCGGAT 235 rRNA depletion #17 235_8 [Btn]CGGCGGGATGGGATGCCCAAACA 235 rRNA depletion #17 235_8 [Btn]CGCCCGCACATGCAGAGGGCCCCAACA 235 rRNA depletion #17 235_8							rev	T7 tem	plate fi	tsZ	
oligonucleotides for qPCR (ChIP analysis) d KF0-2724 GCGATAGACACTTCAATGCG qPCR Pdin1 KF0-2725 GTGAAGAATTAAAACGCAGCC qPCR PrecA KF0-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KF0-2726 GTAAAGCGCAAATCCAGCGTC qPCR PrecA KF0-2756 GTATTGCCCTGCAGCGTC qPCR sgrR oligonucleotides for rRNA depletion z3s_1 Btn]ACTTTCCCTCACGGTACTGGTTCGCTATCGGTCAC 23s rRNA depletion #1 235_1 Btn]ACGGGGAGAACCAGCTATTATACAAAAGGTACGCCGTCACC 23s rRNA depletion #2 23s_3 Btn]CGGGCGGCTTCTAAGCCAACATCTCCGGGTTTGATTGGC 23s rRNA depletion #3 23s_4 Btn]GGGCTGCTTCAAGCCAACATCTCCGGGTTTGGATTGGC 23s rRNA depletion #3 23s_5 Btn]GGGGCGGTACGGAATTTAACCTGATTTCCATCGCACACACCC 23s rRNA depletion #4 23s_6 Btn]CGGCGGATAGGAACTTACCCGACAGGT 23s rRNA depletion #6 23s_7 Btn]CCGCCGCAACAGGGTCCAAACA 23s rRNA depletion #1 23s_7 Btn]CCGCCGCAACAGGGTCCAAACA 23s rRNA depletion #1 23s_7 Btn]CCGCCGAACAGGGACTGCCCAACAC 23s rRNA depletion #1 23s_7 Btn]CCGCCGAACAGGGACACGCCCCCCGGAC 23s rRNA depletion #1		004								-11-10	
KFÖ-2724 GCGATAGACACTTCAATGCG qPCR Pdint KFO-2725 GTGAAGAATAAAAACGCAGCC qPCR Pdint KFO-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KFO-2727 CTATGCGCTAAATCTGCTTCG qPCR PrecA KFO-2726 GTATAGACATGCTTTG qPCR PrecA KFO-2757 GCTCAAGATCCATGCCTTTG qPCR sgrR oligonucleotides for rRNA depletion apcCCTCACGGCTCATTATACAAAGGTACGCCGTCACC 235 rRNA depletion #2 235_1 BtnJACTGCGCTGGCTCATTATACAAAAGGTACGCCGTCACC 235 rRNA depletion #3 235_4 BtnJGTGGCTGGCTTCTAAGCCAACATCCTG 235 rRNA depletion #3 235_5 BtnJGGGTACAGGAATATTAACAAAGCTGATTCCATCGACTACGCC 235 rRNA depletion #3 235_6 BtnJCACCTGTGTCGGTTTGGGGTACGGT 235 rRNA depletion #3 235_6 BtnJCACCTGGCTCGACTTCCCGCACACA 235 rRNA depletion #6 235_7 BtnJCGCGGGATAGGGACCGAACTTACCCGACACA 235 rRNA depletion #6 235_9 BtnJCGCCGGACATCCAGGGCACACA 235 rRNA depletion #8 165_1 BtnJCCGCCGGGCTGCTGGCACACGGACT 165 rRNA depletion #2 165_3 BtnJACCGCCGGCTGCTGGCACACGGCTT 165 rRNA depletion #3 165_6 BtnJACCGCCGGCTGCTGGCCACGGGACT 165 rRNA depletion #3	G	UCA	1G				prin	ier exte	Insion	ainiR	
KFO-2725 GTGAAGAAATAAAAACGCAGCC qPCR PrecA KFO-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KFO-2727 CTATGCGCTAAATCTGCTCG qPCR PrecA KFO-2756 GTATTGCCCTGCAGCGTC qPCR sgrR oligonucleotides for rRNA depletion 23S_1 BtnJACTTTCCCTCACGGTACTGGTTCGCTATCGGTCA 23S rRNA depletion #1 235_1 BtnJACGCGCGGCAACCAGCTATTATACAAAAGGTACGCCGTCACC 23S rRNA depletion #2 23S_3 BtnJCGGGCGGGCAACCAGCTATTATACAAAAGGTACGCCGTCACC 23S rRNA depletion #2 23S_4 BtnJGTGGCTGCTTCAAGCCAACATCCGG 23S rRNA depletion #2 23S_5 BtnJGGGCTGCTTCAAGCCAACATCCGG 23S rRNA depletion #4 23S_6 [Btn]CAGCCGGGTGCGGAACTTACCCGACAACA 23S rRNA depletion #5 23S_7 BtnJCGGCGGGACGAACTTACCCGACAACA 23S rRNA depletion #5 23S_7 [Btn]CGGCCGGCAACTCGAGGTGCCAAACA 23S rRNA depletion #6 23S_7 [Btn]CGCCCGGCACTCGAGGACGACGTGCTCACGACA 23S rRNA depletion #8 23S_9 [Btn]CCGCTGCAACTGACGACGACTGCTCACGACA 23S rRNA depletion #1 16S_1 [Btn]CCGCGGGCTGCTGCACACGGGGTAT 16S rRNA depletion #1 16S_5 [Btn]CCACATGTCCACGCGGCTGCTGCACACGACGATC 16S rRNA depletion #1 16S_5							O	`R Ddin	1		
KFO-2726 GTAAAGCGTGTTCGCTTCG qPCR PrecA KFO-2757 CTATGCGCTAAATCTGCTCTG qPCR PrecA KFO-2756 GTATTGCCCTGCAGCGTC qPCR sgrR oligonucleotides for rRNA depletion qPCR sgrR 235_1 [Btn]AGCTTTCCCTCACGGTACTGGTTCGCTATCGGTCA 235 rRNA depletion #1 235_2 [Btn]AGTCGCTGGCTCATTATACAAAAGGTACGCCGTCACC 235 rRNA depletion #2 235_3 [Btn]GTGGCTGCTTCTAAGCAGCACATCTGCGGGTTGGTTGGC 235 rRNA depletion #3 235_4 [Btn]GGGTCGCTGCTTCTAAGCCACACTCTG 235 rRNA depletion #4 235_5 [Btn]GGGTCGGAGAACCAGGATATTACCTGATTTCCATCGACTACGCC 235 rRNA depletion #5 235_6 [Btn]CACCTGTGCGGTTGGGGTCGAACA 235 rRNA depletion #6 235_7 [Btn]CAGCCGGACTGCGAACTACGACGACC 235 rRNA depletion #7 235_8 [Btn]CGGCGGGATAGGGACCGAACTGTCTCACGACC 235 rRNA depletion #8 235_9 [Btn]CCGCCTGGACTGCACGAACTGTCTCACGAC 235 rRNA depletion #1 165_1 [Btn]CCCACTTGCAACGACTGCTGCCACGGACT 165 rRNA depletion #1 165_3 [Btn]CCACATGCTGCCACGACGGGAT 165 rRNA depletion #1 165_4 [Btn]ACCGACGGCTGGCTGCCACGAGGTT 165 rRNA depletion #1 165_7 [Btn]ACGGCGGTGTACCAGGCCGGGGCTGCGGGCCCCCG<											
KFO-2727 CTATGCGCTAAATCTGCTCTG qPCR sgrR KFO-2756 GTATTGCCCTGCAGCGTC qPCR sgrR oligonucleotides for rRNA depletion 235_1 [Btn]ACCTTTCCCTCACGGTACTGGTTCGCTACTGGTCA 235 rRNA depletion #2 235_2 [Btn]AGTCGCTGGCTCATTATACAAAAGGTACGCCGTCACC 235 rRNA depletion #3 235_4 [Btn]GTGGCTGCTTCTAAGCCAACATCCTG 235 rRNA depletion #3 235_5 [Btn]GGGTACAGGAATATTAACCAAAGGTACGCGT 235 rRNA depletion #4 235_6 [Btn]GGGCACATGGATTGGGTTCGATTCCCAGGACTACCC 235 rRNA depletion #5 235_7 [Btn]CACCTGTGCGGTCGGAACTTACCCGACAGG 235 rRNA depletion #6 235_8 [Btn]CGGCGGATAGGGACCGAACTGTCCAACA 235 rRNA depletion #7 235_8 [Btn]CGGCGGATAGGGACCGAACTGTCACAGAC 235 rRNA depletion #7 235_9 [Btn]CGGCGGATGAGGACCGACGTCCCAACA 235 rRNA depletion #7 235_8 [Btn]CCGCTCGACTTGCAGGGACTTCCCAACA 235 rRNA depletion #1 165_1 [Btn]CCGCTGCACATGGAAGGTCCCAACAC 235 rRNA depletion #1 165_1 [Btn]CCGCGTGGACACTGCCACGGACT 165 rRNA depletion #1 165_2 [Btn]ACGGCGTGGACACACGTCCCCCGT 165 rRNA depletion #2 165_6 [Btn]ACGCACTGTGTACAAGGACCGCGGGAGACT 165 rRNA depleti											
KFO-2756 GTATTGCCCTGCAGCGTC qPCR sgrR KFO-2757 GCTCAAGATCCATGCCTTTG qPCR sgrR Oligonucleides for rRNA depletion 235_1 [Btn]ACTCGCTGCCTCATTATACAAAAGGTACGCCGTCACC 235 rRNA depletion #2 235_3 [Btn]GTGGCGGCTCATTATACAAAAGGTACGCCGTCACC 235 rRNA depletion #2 235_4 [Btn]GTGGCGGCTCATTATACACAAAGGTACGCCGGTTGGCC 235 rRNA depletion #3 235_5 [Btn]GTGGCTGCTTCTAAGCCAACATCCTG 235 rRNA depletion #4 235_6 [Btn]CCGCGGGTCGGAACTAGCGGGT 235 rRNA depletion #6 235_7 [Btn]CGGCGGATCGGGGTCGGAACTTACCCGACGGT 235 rRNA depletion #6 235_8 [Btn]GCGCCGACATCGAGGTGCCAAACA 235 rRNA depletion #6 235_9 [Btn]CGGCGGATAGGGACCGAACTGTCTCACGAC 235 rRNA depletion #7 165_1 [Btn]CCGCTGCACTGGCACAGCGACCGACTGCGCCCCGT 165 rRNA depletion #1 165_2 [Btn]CCCCATTGTCAACGACGACTGCTCACGCGCCCCG 165 rRNA depletion #1 165_3 [Btn]ACCGCGGCACACCACGGGAT 165 rRNA depletion #1 165_5 [Btn]ACCGCGGGATTCCACCGGGGAT 165 rRNA depletion #1 165_5 [Btn]ACCGCGGGATGCCACCGGGGGGGGGGGGGGGGA 165 rRNA depletion #1 165_5 [Btn]ACCGCGGGGTGTGCCACGGGGGGGGGGGGGGGGGGGGGG											
KFO-2757 GCTCAAGATCCATGCCTTTG qPCR sgrR oligonucleotides for rRNA depletion											
235_1[Btn]ACCTTTCCCTCACGGTACTGGTTCGCTATCGGTCA23S rRNA depletion #1235_2[Btn]AGTCGCTGGCTCATTATACAAAAGGTACGCCGTCACC23S rRNA depletion #2235_3[Btn]CGGGGAGAACCAGCTATCTCCGGGTTTGATTGGC23S rRNA depletion #4235_4[Btn]GTGGCTGCTTCTAAGCCAACATCCTG23S rRNA depletion #4235_5[Btn]GGGTACAGGAATATTAACCTGATTTCCATCGACTACGCC23S rRNA depletion #5235_6[Btn]CACCTGTGCGGTTGGGGACCGACCGACGGT23S rRNA depletion #6235_7[Btn]CGGCGGGCTGGGACCTACCGCACAG23S rRNA depletion #7235_8[Btn]CGGCCGACATCGAGGTGCCAAACA23S rRNA depletion #8235_9[Btn]CCGCTCGACTGCATGGTAGCAGCGACCGACAGCCGACAGCGTTCG16S rRNA depletion #2165_1[Btn]CCCCTTGGCAAGGTCCCACTGCTGCCTCCCGT16S rRNA depletion #3165_2[Btn]CCCATTGCAAGATTCCCTACTGCTGCCTCCCGT16S rRNA depletion #3165_3[Btn]ACCGCGGGTGGACCGACGGAGT16S rRNA depletion #3165_4[Btn]ACCGCGGGTGGACCACCGGGTAT16S rRNA depletion #4165_5[Btn]ACCAACATCTCACACGCTTGGCGGGCCCCCG16S rRNA depletion #5165_6[Btn]ACCAACATCTCACACGCGTGACGACGACA16S rRNA depletion #7165_8[Btn]ACCGCACTGTGTACAAGGCCCGGGA16S rRNA depletion #7165_8[Btn]CACCACCCCGGCCTATCAACGCGGGGCCCAAGGCATCC16S rRNA depletion #7165_9ram-1[Btn]CACGCTCTTCATCGCCTTTCACGCGGGGTCCAACGCGCTA15S rRNA depletion #7165_gram-1[Btn]CCACACCCCGGCCTATCAACGTGGGGTCCCAACGCGCTA16S rRNA depletion #7165_911[Btn]CACGCCCCACCCCGGCAAGGGGTCCCAACGCGCCTA15S rRNA depletion #7165_gram-2[Btn]AG											
235_2[Btn]AGTCGCTGGCTCATTATACAAAAGGTACGCCGTCACC23S rRNA depletion #2235_3[Btn]TCGGGGAGAACCAGCTATCTCCGGGTTTGGTTGGC23S rRNA depletion #3235_4[Btn]GTGGCTGCTTCTAAGCCAACATCCTG23S rRNA depletion #4235_5[Btn]GGGTACAGGAATATTAACCTGATTTCCATCGACTACGCC23S rRNA depletion #5235_6[Btn]CACCTGTGTCGGTTGGGGTCGGACTTACCCGACAAG23S rRNA depletion #6235_7[Btn]CACCTGGGGTCGGGACTTACCCGACAAG23S rRNA depletion #7235_8[Btn]CGCCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #7235_9[Btn]CGCCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #1165_1[Btn]CGCCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #1165_2[Btn]CCCATTGTGCAGGATCGCTGCTGCGCGCCCCGT16S rRNA depletion #1165_3[Btn]ACCGCGGCGCGCGCGGCGCCCCG16S rRNA depletion #1165_5[Btn]ACCGCGGCGTGGCACAGGGGTAT16S rRNA depletion #4165_5[Btn]ACCGCGGCGTGGCACCGGGGA16S rRNA depletion #5165_6[Btn]ACCCAACATCCACAGGCCGGGA16S rRNA depletion #6165_7[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion #6165_7[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion #6165_7[Btn]CACGCCCCCCACGCCTATCAACGTGGTGCTTCGACG16S rRNA depletion #6165_7[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion #6165_7[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion #6165_7[Btn]CACGCCCACCCCCCCCCCCCCCGCAG16S rRNA depletion #6165_8[Btn]CACGCCCCACCCCCCCCCCCCCCCCCCCCCCCCCCCCC											
233_3[Btn]CCGGGGAGAACCAGCTATCTCCGGGTTTGATTGGC23S rRNA depletion #3235_4[Btn]GGGTACAGGAATATTAACCTGACTCCTG23S rRNA depletion #4235_5[Btn]GGGTACAGGAATATTAACCTGATTTCCATCGACTACGCC23S rRNA depletion #5235_6[Btn]CACCTGTGTCGGGTTGGGGTACGGT23S rRNA depletion #6235_7[Btn]CGGCGGGATAGGGACCTACCCGACAAG23S rRNA depletion #7235_8[Btn]CGGCGGATAGGACCGAACTGTCCCGACAAG23S rRNA depletion #7235_9[Btn]CCGCTCGACTTGCAGGTGCTAAGCACGCGCCGCG16S rRNA depletion #9165_1[Btn]CCGCTGGACTACGAGATTCCTCACGAC23S rRNA depletion #1165_2[Btn]CCGCTGGCGCGCTGCTGGCACGGAGT16S rRNA depletion #1165_3[Btn]ACCGCGGCTGCTGCACGGAGT16S rRNA depletion #3165_4[Btn]ACCGCGGCTGCTGCACCGGGGTT16S rRNA depletion #4165_5[Btn]ACCGCACTGCTCCACCGCTTGTGCGGGCCCCCG16S rRNA depletion #4165_6[Btn]ACCACATCTCACACGCTTGTGCGGGCCCCCG16S rRNA depletion #4165_6[Btn]ACCACATCTCACACGCGTGACGACAA16S rRNA depletion #4165_7[Btn]CGCAGTGTGTACAAGGCCCGGGA16S rRNA depletion #6165_7[Btn]GCGCAGTGTGTACAAGGCCCGGGA16S rRNA depletion #6165_7[Btn]CACGCCCCTTCAACGCGCCGCAG16S rRNA depletion #7165_8[Btn]CCACGTCCTTCACCGCCTTTCACGCCGCAG16S rRNA depletion #816S-gram1[Btn]CCACACCCGGCCTATCAACGTGGGGTCCAACGCGCTA5S rRNA depletion #1155_2[Btn]GCACACCCCACATCACACGCGCTA5S rRNA depletion #1155_2[Btn]AGACCCCACATACCAGCGGCGGGATACCACGCGCTA5S rRNA depletion #1155_2[Btn											
235_4[Btn]GTGGCTGCTTCTAAGCCAACATCCTG23S rRNA depletion #4235_5[Btn]GGGTACAGGAATATTAACCTGATTTCCATCGACTACGCC23S rRNA depletion #5235_6[Btn]CACCTGTGCGGTTTGGGGTACGGT23S rRNA depletion #6235_7[Btn]CACCGGGTCGGAACTTACCCGACAAG23S rRNA depletion #7235_8[Btn]CGGCGGATAGGGACCGAACTGCCGACAACA23S rRNA depletion #7235_9[Btn]CCGCTCGACTTGCATGTGTTAAGCATGCCGACAGCGTTCG16S rRNA depletion #9165_1[Btn]CCGACTTGCAAGATTCCCTACTGCTGCACGAC23S rRNA depletion #1165_2[Btn]CCCACTGTGCAAGATTCCCTACTGCTGCCTCCGT16S rRNA depletion #2165_3[Btn]ACCGCGGCTGCTGCACAGGGTAT16S rRNA depletion #4165_5[Btn]ACCGCGGTGGACTACCAGGGTAT16S rRNA depletion #4165_6[Btn]ACCCACATGCTCACCGCGTGGCGCCCCGG16S rRNA depletion #4165_7[Btn]ACCGCAGTGTGTACAAGGCCGGGAC16S rRNA depletion #5165_6[Btn]ACCCACATCCTCACCAGCGCGAA16S rRNA depletion #6165_7[Btn]GCACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion #6165_8[Btn]AAGGAGGTGATCCAGCCGCGAG16S rRNA depletion #7165_8[Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion #7165_8[Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion #816S-gram2[Btn]CCACACCCGGCCTATCAACGTGGGTCCAACGCGCTA5S rRNA depletion #1155_2[Btn]AGACCCCACATACCAGTCGGGTCCAACGCGCTA5S rRNA depletion #1155_2[Btn]AGACCCCACATCCACACTACCATCGCGATACCGCG5S rRNA depletion #125_2[Btn]AGACCCCACATCCACACTCCGAT5S rRNA depletion #1<					C						
233_5Btn]GGGTACAGGAATATTAACCTGATTTCCATCGACTACGCC23S rRNA depletion #5235_6[Btn]CACCTGTGTCGGTTTGGGGTACGGT23S rRNA depletion #6235_7[Btn]CACCTGGGTCGGAACTTACCCGACAGG23S rRNA depletion #7235_8[Btn]GAGCCGACATCGAGGTGCCAAACA23S rRNA depletion #7235_9[Btn]CGGCGGATAGGGACCGACGACTGTCTCACGAC23S rRNA depletion #9165_1[Btn]CCGCTCGACTTGCATGTGTTAAGCATGCCGACAGCGTTCG16S rRNA depletion #1165_2[Btn]ACCGCGGCTGCTGCAAGATTCCCTACTGCTGCCTCCCGT16S rRNA depletion #2165_3[Btn]ACCGCGGCTGCTGCGACCAGGAGT16S rRNA depletion #3165_4[Btn]ACCGCGGGCTGCCCAGGGGTAT16S rRNA depletion #3165_5[Btn]ACCCAACATCTCACAGGGTAT16S rRNA depletion #4165_6[Btn]ACCCAACATCTCACAGGCCCGGGA16S rRNA depletion #6165_7[Btn]ACCCAACATCTCACAACACGAGCCGGAAC16S rRNA depletion #7165_8[Btn]AAGGAGGTGATCCAGCCCCGGGA16S rRNA depletion #7165_9ram1[Btn]CCACACCCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion #116S-gram2[Btn]GTCCGGAAGGGGTCAGCGGGGTCCAACGCGCTA5S rRNA depletion #116S-gram2[Btn]GTCCGGAAGGGGTCAGGTGGGTCCAACGCGCTA5S rRNA depletion #115S_2[Btn]AGACCCCACACTACCATCGGCGATACGTCG16S rRNA depletion #15S_1[Btn]AGACCCCACACTACCATCGGCGATACGTCG5S rRNA depletion #15S_2[Btn]AGACCCCACACTACCATCGGCGATACGTCG5S rRNA depletion #15S_2[Btn]AGACCCCACACTACCATCGCGATCGCGAT5S rRNA depletion #20ilgonucleotides for RIL-seq3TP-AGATCGGAAGAGCACACGTCGTGCATA-dCli	GAT		GATT	GGC							
23S_6[Btn]CACCTGTGTCGGTTTGGGGTACGGT23S rRNA depletion #623S_7[Btn]TCGTGCGGGTCGGAACTTACCCGACAAG23S rRNA depletion #723S_8[Btn]CGGCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #823S_9[Btn]CGGCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #916S_1[Btn]CCGCTCGACTTGCATGTGTTAAGCATGCCGACAGCGTTCG16S rRNA depletion #116S_2[Btn]CCCATTGTGCAAGATTCCCTACTGCTGCCTCCGT16S rRNA depletion #216S_3[Btn]ACCGCGGCTGCTGGCACGGAGT16S rRNA depletion #316S_4[Btn]ACCGCGGTGGACTACCAGGGTAT16S rRNA depletion #416S_5[Btn]TCCACATGTCCACCGCTTGTGCGGGCCCCCG16S rRNA depletion #416S_6[Btn]ACCGACGTGTACAACGCGCGGA16S rRNA depletion #616S_7[Btn]GGCAGTGTACAAGGCCCGGGA16S rRNA depletion #616S_7[Btn]GGCAGTGTACAAGGCCCGGCA16S rRNA depletion #716S_8[Btn]ACGGCGTGTACAAGGCCCGGCA16S rRNA depletion #716S_9ram1[Btn]CCCACACCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion #816S-gram2[Btn]GTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA5S rRNA depletion #15S_2[Btn]AGACCCCACCACTACCATCGGCGATACGTCG5S rRNA depletion #2oligonucleotides for RIL-seq161616373P-AGATCGGAAGGGCACACGTCTG-ddCligation to the cDNA 3' end8C5_adaptorP-AACACTTGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' end8C6_adaptorP-ACCAAGTCGAAGAGCGACGGAGGGTCGTGTGTA-ddCligation to the RNA 3' end				OT 1 O	~~~						
23S_7[Btn]TCGTGCGGGTCGGAACTTACCCGACAAG23S rRNA depletion #723S_8[Btn]GAGCCGACATCGAGGTGCCAAACA23S rRNA depletion #823S_9[Btn]CGGCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #823S_9[Btn]CCGCTCGACTTGCATGGTAAGCATGCCGACAGCGTTCG16S rRNA depletion #916S_1[Btn]CCGCTCGACTGCAAGATTCCTACTGCTGCCGCACAGCGTTCG16S rRNA depletion #116S_2[Btn]CCCATTGTGCAAGATTCCCTACTGCTGCCTCCGT16S rRNA depletion #216S_3[Btn]ACCGCGGCTGGACTACCAGGGTAT16S rRNA depletion #316S_4[Btn]ACCGCGGCTGGACTACCAGGGTAT16S rRNA depletion #416S_5[Btn]ACCAATGCTCACCGCGTGTGCGGGGCCCCCG16S rRNA depletion #616S_6[Btn]ACCAACATCTCACAACACGAGCTGACGACA16S rRNA depletion #616S_7[Btn]GGGAGTGTACAAGGCCCGGGA16S rRNA depletion #616S_8[Btn]ACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion #716S_8[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion - Gra negative bacteria #116S-gram1[Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion - Gra negative bacteria #116S-gram2[Btn]GTCCGGAAGGGGTCAGGTGGGTCCAACGCGCTA5S rRNA depletion - Gra negative bacteria #25S_1[Btn]GACCCCACACACACACCAGTCGGGTCCAACGCGCTA5S rRNA depletion #2oligonucleotides for RIL-seqI3Tr3P-AGATCGGAAGAGCACACGTCTG-ddCligation to the cDNA 3' endRR2TACACGGACGACGGAGAGAGCGTCGTGTA-ddCligation to the RNA 3' endBC5_adaptorP-ACCAAGTCGGAAGAGCGACGGTCGTGTA-ddCligation to the RNA 3' endBC6_adapto	CGA	CAT	CGAU	JIACO							
23S_8[Btn]GAGCCGACATCGAGGTGCCAAACA23S rRNA depletion #823S_9[Btn]CCGCCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #916S_1[Btn]CCGCTCGACTTGCATGTGTTAAGCATGCCGACAGCGTTCG16S rRNA depletion #116S_2[Btn]CCCATTGTGCAAGATTCCCTACTGCTGCCTCCCGT16S rRNA depletion #216S_3[Btn]ACCGCGGCTGCTGGCACGGAGT16S rRNA depletion #316S_4[Btn]ACCGCGTGCTGGCACGGCTCTGCGCGCGCCCCG16S rRNA depletion #416S_5[Btn]ACCACATGCTCACCAGGGTAT16S rRNA depletion #516S_6[Btn]ACCAACATCTCACAACGCGTGGACGACCAACA16S rRNA depletion #616S_7[Btn]GGGCAGTGTGTACAAGGCCCGGGA16S rRNA depletion #716S_8[Btn]AGGAGGTGATCCAGCCGCAG16S rRNA depletion - Gra negative bacteria #116S-gram1[Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion - Gra negative bacteria #116S_7_2[Btn]CCACACCCGGCCTATCAACGTGGTGGTCCAACGCGCTA5S rRNA depletion - Gra negative bacteria #116S-gram2[Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion #20igonucleotides for RIL-seq3Tr3P-AGATCGGAAGGGGTCAGGTGGGTCCAACGCGCTA5S rRNA depletion #20igonucleotides for RIL-seq3Tr3P-AGATCGGAAGAGCACACGTCTG-ddCligation to the RNA 3' endBC5_adaptorP-ACAAGTCGGAAGAGCGGAGGAGGGTCGTGTA-ddCligation to the RNA 3' endBC6_adaptorP-ACCAAGTCGGAAGAGCGGCGCGTGTGTA-ddCligation to the RNA 3' end		AAG	2								
23S_9[Btn]CGGCGGATAGGGACCGAACTGTCTCACGAC23S rRNA depletion #916S_1[Btn]CCGCTCGACTTGCATGTGTTAAGCATGCCGACAGCGTTCG16S rRNA depletion #116S_2[Btn]CCCATTGTGCAAGATTCCCTACTGCTGCCTCCCGT16S rRNA depletion #216S_3[Btn]ACCGCGGGCTGCTGGCACGGGACT16S rRNA depletion #316S_4[Btn]ACGGCGTGGACTACCAGGGTAT16S rRNA depletion #416S_5[Btn]ACCCAACATGCTCCACCGCTTGTGCGGGCCCCCG16S rRNA depletion #416S_6[Btn]ACCCAACATCTCACACCGCTGTGCGGGCCCCCG16S rRNA depletion #516S_6[Btn]ACCCAACATCTCACAACACGAGCTGACGACA16S rRNA depletion #616S_7[Btn]GGGCAGTGTGTACAAGGCCCGGGA16S rRNA depletion #716S_8[Btn]AAGGAGGTGATCCAGCCGCGCAG16S rRNA depletion #616S-gram-1[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion - Gra negative bacteria #116S-gram-2[Btn]CCACACCCGGCCTATCAACGGCGTCCAACGCGCTA5S rRNA depletion - Gra negative bacteria #25S_1[Btn]GTCGGGAAGGGGTCAGGTGGGGTCCAACGCGCTA5S rRNA depletion #20ligonucleotides for RIL-seg3Tr3P-AGATCGGAAGAGCACACGTCTG-ddCligation to the cDNA 3' enAR2TACACGACGCTCTTCCGATreverse transcription primBC5_adaptorP-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' endBC6_adaptorP-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' end			,								
16S_1[Btn]CCGCTCGACTTGCATGTGTTAAGCATGCCGACAGCGTTCG16S rRNA depletion #116S_2[Btn]CCCATTGTGCAAGATTCCCTACTGCTGCCTCCCGT16S rRNA depletion #216S_3[Btn]ACCGCGGCTGCTGGCACGGAGT16S rRNA depletion #316S_4[Btn]ACGGCGTGGACTACCAGGGTAT16S rRNA depletion #416S_5[Btn]TCCACATGCTCCACCGCTTGTGCGGGCCCCCG16S rRNA depletion #416S_6[Btn]ACCCAACATCTCACAACACGAGGTGACGACA16S rRNA depletion #616S_6[Btn]ACCCAACATCTCACAACACGAGCTGACGACA16S rRNA depletion #616S_7[Btn]GGGCAGTGTGTACAAGGCCGGGGA16S rRNA depletion #716S_8[Btn]AAGGAGGTGATCCAGCCGCAG16S rRNA depletion - Gra negative bacteria #116S-gram-1[Btn]CCACACCCCGGCCTATCAACGTGGTGGTCCAACGCGCTA16S rRNA depletion - Gra negative bacteria #116S_gram-2[Btn]CCACACCCCGGCCTATCAACGTGGTGGTCCAACGCGCTA5S rRNA depletion - Gra negative bacteria #25S_1[Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA5S rRNA depletion #15S_2[Btn]AGACCCCACACTACCATCGGCGATACGTCG5S rRNA depletion #10ligonucleotides for RIL-seq33Tr3P-AGATCGGAAGAGCACACGTCTG-ddCligation to the cDNA 3' enRR2TACACGACGCTCTTCCGATreverse transcription primBC5_adaptorP-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' endBC6_adaptorP-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' end	SAC	ACG	GAC								
16S_2[Btn]CCCATTGTGCAAGATTCCCTACTGCTGCCTCCCGT16S rRNA depletion #216S_3[Btn]ACCGCGGGCTGCTGGCACGGAGGT16S rRNA depletion #316S_4[Btn]ACCGCGTGGACTACCAGGGTAT16S rRNA depletion #416S_5[Btn]TCCACATGCTCCACCGCTTGTGCGGGCCCCCG16S rRNA depletion #516S_6[Btn]ACCCAACATCTCACAACGCGGGCCGGGA16S rRNA depletion #616S_7[Btn]GGGCAGTGTGTACAAGGCCCGGGA16S rRNA depletion #716S_8[Btn]AAGGAGGTGATCCAGCCGCAG16S rRNA depletion #816S-gram1[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion - Gra negative bacteria #116S-gram2[Btn]CCACACCCGGCCTATCAACGTGGTGGTCCTACGACGCGTA16S rRNA depletion - Gra negative bacteria #25S_1[Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA5S rRNA depletion #15S_2[Btn]AGACCCCACACTACCATCGGCGATACGTCG5S rRNA depletion #2oligonucleotides for RIL-seq3173P-AGATCGGAAGAGCACACGTCG-ddC118C5_adaptorP-ACCAAGTCGGAAGAGCGTCGGAAGAGCGTCGTGTA-ddC11118C5_adaptorP-ACCAAGTCGGAAGAGCGACGGAAGAGCGTCGTGTA-ddC11118C6_adaptorP-ACCAAGTCGGAAGAGCGACGGAAGAGCGTCGTGTA-ddC11118C6_adaptorP-ACCAAGTCGAGAAGAGCGACGGAAGAGCGTCGTGTA-ddC11118C6_adaptorP-ACCAAGTCGGAAGAGCGACGGAAGAGCGTCGTGTA-ddC11118C6_adaptorP-ACCAAGTCGGAAGAGCGTCGTGTA-ddC11118C6_adaptorP-ACCAAGTCGAGAAGAGCGTCGTGTA-ddC1111118C6_adaptorP-ACCAAGTCGAGAAGAGCGTCGTGTA-ddC111111 </th <th></th> <th></th> <th></th> <th>AGCC</th> <th>STTCG</th> <th>3</th> <th></th> <th></th> <th></th> <th></th> <th></th>				AGCC	STTCG	3					
16S_3[Btn]ACCGCGGCTGCTGGCACGGAGT16S rRNA depletion #316S_4[Btn]ACGGCGTGGACTACCAGGGTAT16S rRNA depletion #416S_5[Btn]TCCACATGCTCCACCGCTTGTGCGGGCCCCCG16S rRNA depletion #516S_6[Btn]ACCCAACATCTCACAACACGAGCTGACGACA16S rRNA depletion #616S_7[Btn]GGGCAGTGTGTACAAGGCCCGGGA16S rRNA depletion #716S_8[Btn]AAGGAGGTGATCCAGCCGCAG16S rRNA depletion #816S-gram1[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion - Granegative bacteria #116S-gram2[Btn]CCACACCCGGCCTATCAACGTGGTGTCCAACGCGCTA5S rRNA depletion #25S_1[Btn]GTTCGGGAAGGGGTCAACGTCGGCAACGCGCTA5S rRNA depletion #2oligonucleotides for RIL-seq3P-AGATCGGAAGAGCACACGTCTG-ddCligation to the cDNA 3' endRR2TACACGACGCTCTTCAGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' endBC5_adaptorP-ACAAGTCGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' end							16S	rRNA	depleti	ion #2	
16S_5[Btn]TCCACATGCTCCACCGCTTGTGCGGGCCCCCG16S rRNA depletion #516S_6[Btn]ACCCAACATCTCACAACACGAGCTGACGACA16S rRNA depletion #616S_7[Btn]GGGCAGTGTGTACAAGGCCCGGGA16S rRNA depletion #716S_8[Btn]AAGGAGGTGATCCAGCCGCAG16S rRNA depletion #816S-gram1[Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC16S rRNA depletion - Granegative bacteria #116S-gram2[Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG16S rRNA depletion - Granegative bacteria #25S_1[Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA5S rRNA depletion #2oligonucleotides for RIL-seq31r3P-AGATCGGAAGAGCACACGTCTG-ddCligation to the cDNA 3' end8C5_adaptorP-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' endBC6_adaptorP-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddCligation to the RNA 3' end											
16S_6 [Btn]ACCCAACATCTCACAACACGAGCTGACGACA 16S rRNA depletion #6 16S_7 [Btn]GGGCAGTGTGTACAAGGCCCGGGA 16S rRNA depletion #7 16S_8 [Btn]AAGGAGGTGATCCAGCCGCAG 16S rRNA depletion #8 16S-gram1 [Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC 16S rRNA depletion - Granegative bacteria #1 16S-gram2 [Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG 16S rRNA depletion - Granegative bacteria #2 5S_1 [Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA 5S rRNA depletion #1 5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' end RR2 TACACGACGCTCTTCCGAT P-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end											
16S_7 [Btn]GGGCAGTGTGTACAAGGCCCGGGA 16S rRNA depletion #7 16S_8 [Btn]AAGGAGGTGATCCAGCCGCAG 16S rRNA depletion #8 16S-gram1 [Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC 16S rRNA depletion - Granegative bacteria #1 16S-gram2 [Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG 16S rRNA depletion - Granegative bacteria #2 5S_1 [Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA 5S rRNA depletion #1 5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' end RR2 TACACGACGCTCTTCCGAT P-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end				<u> </u>			-				
16S_8 [Btn]AAGGAGGTGATCCAGCCGCAG 16S rRNA depletion #8 16S-gram1 [Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC 16S rRNA depletion - Granegative bacteria #1 16S-gram2 [Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG 16S rRNA depletion - Granegative bacteria #2 5S_1 [Btn]AGACCCCACACTACCATCGGCGGTCCAACGCGCTA 5S rRNA depletion #1 5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' end RR2 TACACGACGCTCTTCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end	ACA	<u>\CG</u>	ACA								
16S-gram1 [Btn]CACGTCCTTCATCGCCTTTTACTGCCAAGGCATCC 16S rRNA depletion - Granegative bacteria #1 16S-gram2 [Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG 16S rRNA depletion - Granegative bacteria #2 5S_1 [Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA 5S rRNA depletion #1 5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' en AR2 TACACGACGCTCTTCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end											
negative bacteria #1 16S-gram2 [Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG 16S rRNA depletion - Granegative bacteria #2 5S_1 [Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA 5S rRNA depletion #1 5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' en AR2 TACACGACGCTCTTCCGAT reverse transcription prim BC5_adaptor P-AGCAAGTCGGAAGAGCACACGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end	000			TCC							<u>a</u> m
16S-gram2 [Btn]CCACACCCGGCCTATCAACGTGGTGGTCTTCGACG 16S rRNA depletion - Granegative bacteria #2 5S_1 [Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA 5S rRNA depletion #1 5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' end AR2 TACACGACGCTCTTCCGAT reverse transcription prime BC5_adaptor P-ACCAAGTCGGAAGACCCGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end	100/	AAG	JGCAI	100							alli
5S_1 [Btn]GTTCGGGAAGGGGTCAGGTGGGTCCAACGCGCTA 5S rRNA depletion #1 5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' en AR2 TACACGACGCTCTTCCGAT reverse transcription prim BC5_adaptor P-ACAAGTCGGAAGACCGACGACGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGGAAGACCGACGACGCGTCGTGTA-ddC ligation to the RNA 3' end	ттс	GTC	TTCG	SACG			16S	rRNA	depleti	ion - Gr	am
5S_2 [Btn]AGACCCCACACTACCATCGGCGATACGTCG 5S rRNA depletion #2 oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' en AR2 TACACGACGCTCTTCCGAT reverse transcription prim BC5_adaptor P-ACCAAGTCGGAAGAGCACCGACGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGGAAGAGCGTCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end	CGC	CAAC	CGCG	ACTA							
oligonucleotides for RIL-seq 3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' en AR2 TACACGACGCTCTTCCGAT reverse transcription prim BC5_adaptor P-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end				U 171							
3Tr3 P-AGATCGGAAGAGCACACGTCTG-ddC ligation to the cDNA 3' en AR2 TACACGACGCTCTTCCGAT reverse transcription prim BC5_adaptor P-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end											
AR2 TACACGACGCTCTTCCGAT reverse transcription prim BC5_adaptor P-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end							ligat	ion to t	he cDI	NA 3' er	nd
BC5_adaptor P-AATCACTTGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end							-				
BC6_adaptor P-ACCAAGTCGAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end	-dd(GTA	\-ddC						· ·	· ·	
							-				
Indition to the KNA 3' end							-				
BC8_adaptor P-ACCCGTCTTAGATCGGAAGAGCGTCGTGTA-ddC ligation to the RNA 3' end										A 3' en	a
P5_Enr AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACG PCR enrichment CTCTTCCGATCT PCR enrichment PCR enrichment	TTT	стст	TTTCC	CCTA	CACG	ACG	PCF	R enrich	nment		
P7_BC1_Enr CAAGCAGAAGACGGCATACGAGATTCGTGTGCGTGACTGGAGTTC PCR enrichment AGACGTGTGCTCTTCCGATCT PCR enrichment PCR enrichment	CG1	GTG	CGTG	SACTO	GGAG	TTC	PCF	R enrich	nment		

Supplementary References

- 1. Kim D, *et al.* (2012) Comparative analysis of regulatory elements between Escherichia coli and Klebsiella pneumoniae by genome-wide transcription start site profiling. *PLoS Genet* 8(8):e1002867.
- 2. Corpet F (1988) Multiple sequence alignment with hierarchical clustering. *Nucleic Acids Res* 16(22):10881-10890.
- 3. Fernandez De Henestrosa AR, *et al.* (2000) Identification of additional genes belonging to the LexA regulon in Escherichia coli. *Mol Microbiol* 35(6):1560-1572.
- 4. Wade JT, Reppas NB, Church GM, & Struhl K (2005) Genomic analysis of LexA binding reveals the permissive nature of the Escherichia coli genome and identifies unconventional target sites. *Genes Dev* 19(21):2619-2630.
- 5. Katoh K, Rozewicki J, & Yamada KD (2019) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Brief Bioinform* 20(4):1160-1166.
- 6. Huang TW, *et al.* (2014) Capsule deletion via a lambda-Red knockout system perturbs biofilm formation and fimbriae expression in Klebsiella pneumoniae MGH 78578. *BMC Res Notes* 7:13.
- 7. Sharma CM, Darfeuille F, Plantinga TH, & Vogel J (2007) A small RNA regulates multiple ABC transporter mRNAs by targeting C/A-rich elements inside and upstream of ribosome-binding sites. *Genes Dev* 21(21):2804-2817.
- 8. Fröhlich KS, Papenfort K, Fekete A, & Vogel J (2013) A small RNA activates CFA synthase by isoform-specific mRNA stabilization. *EMBO J* 32(22):2963-2979.
- 9. Papenfort K, *et al.* (2006) s^E-dependent small RNAs of *Salmonella* respond to membrane stress by accelerating global *omp* mRNA decay. *Mol Microbiol* 62(6):1674-1688.
- 10. Huber M, *et al.* (2022) An RNA sponge controls quorum sensing dynamics and biofilm formation in Vibrio cholerae. *Nat Commun* 13(1):7585.
- 11. Culviner PH, Guegler CK, & Laub MT (2020) À Simple, Cost-Effective, and Robust Method for rRNA Depletion in RNA-Sequencing Studies. *mBio* 11(2).
- 12. Siemers M, Lippegaus A, & Papenfort K (2023) ChimericFragments: Computation, analysis, and visualization of global RNA networks. *bioRxiv* DOI: 10.1101/2023.12.21.572723.
- 13. Bar A, Argaman L, Altuvia Y, & Margalit H (2021) Prediction of Novel Bacterial Small RNAs From RIL-Seq RNA-RNA Interaction Data. *Front Microbiol* 12:635070.
- 14. Bruchmann S, *et al.* (2015) Deep transcriptome profiling of clinical Klebsiella pneumoniae isolates reveals strain and sequence type-specific adaptation. *Environ Microbiol* 17(11):4690-4710.
- 15. Hör J, Matera G, Vogel J, Gottesman S, & Storz G (2020) Trans-Acting Small RNAs and Their Effects on Gene Expression in Escherichia coli and Salmonella enterica. *EcoSal Plus* 9(1).
- 16. losub IA, *et al.* (2021) The mRNA derived MaIH sRNA contributes to alternative carbon source utilization by tuning maltoporin expression in E. coli. *RNA Biol* 18(6):914-931.
- 17. Bailey TL & Elkan C (1994) Fitting a mixture model by expectation maximization to discover motifs in biopolymers. *Proc Int Conf Intell Syst Mol Biol* 2:28-36.
- 18. Thelin KH & Taylor RK (1996) Toxin-coregulated pilus, but not mannose-sensitive hemagglutinin, is required for colonization by Vibrio cholerae O1 El Tor biotype and O139 strains. *Infect Immun* 64(7):2853-2856.
- 19. Figueroa-Bossi N, Valentini M, Malleret L, & Bossi L (2009) Caught at its own game: regulatory small RNA inactivated by an inducible transcript mimicking its target. *Gene Dev* 23(17):2004-2015.
- 20. Hoyos M, Huber M, Forstner KU, & Papenfort K (2020) Gene autoregulation by 3' UTR-derived bacterial small RNAs. *Elife* 9.