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Supplementary Information for

Regulating the terminator: SraL sRNA interaction prevents the premature transcription termination of *rho* mRNA

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Supplementary Materials and Methods
Supplementary References

Other supplementary materials for this manuscript include the following:

Dataset S1

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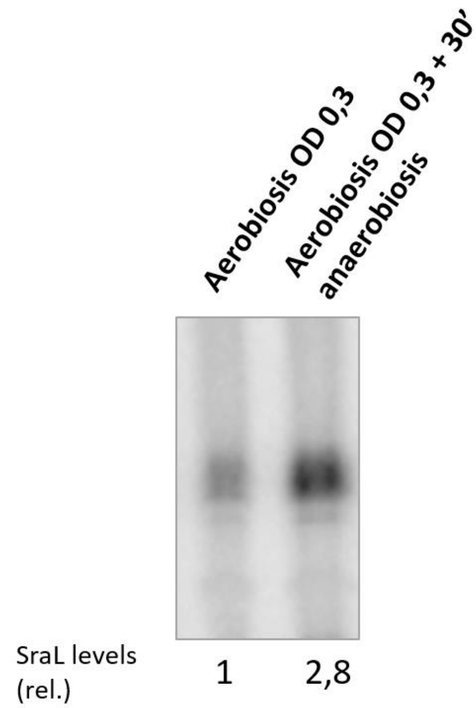

Fig. S1. SraL sRNA expression upon anaerobic shock. Total cellular RNA was extracted from *Salmonella* wild-type strain grown in LB at 37ºC and 220 rpm to an OD600 of 0.3 and then placed in a filled 50 ml Falcon tube and incubated at 37ºC without agitation during 30 min. Fifteen micrograms of total RNA were separated in a 6% PAA / 8.3 M urea to determine the expression level of SraL.

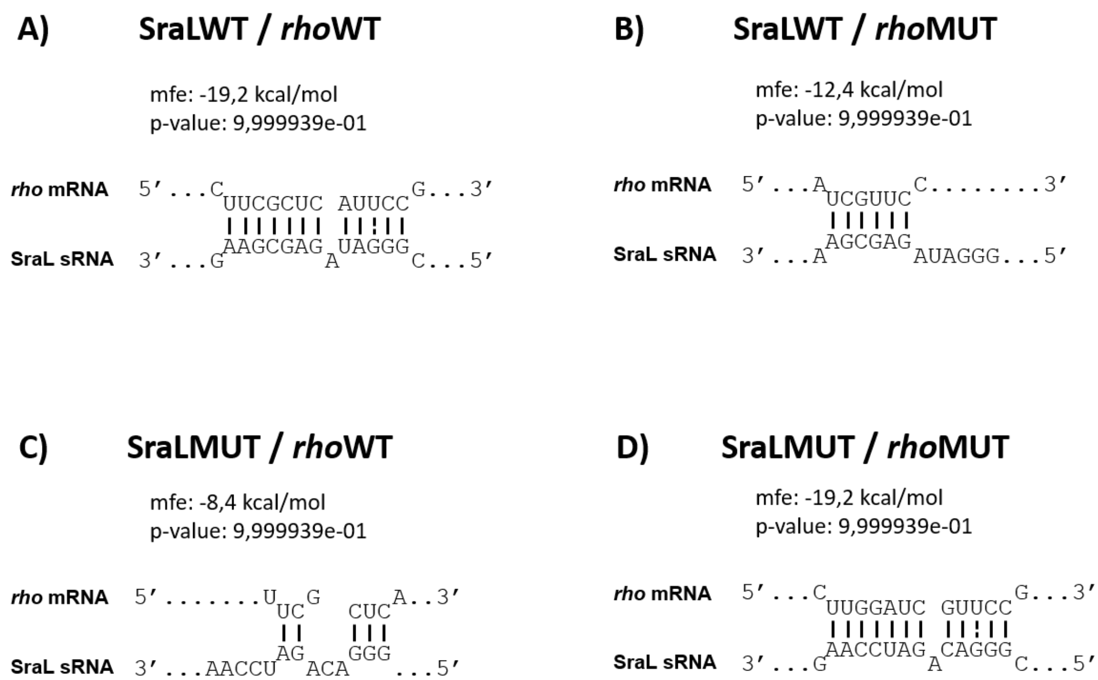

Fig. S2. Predicted interaction regions between SraL and *rho* forms. The interaction regions between SraL sRNA and *rho* mRNA were predicted by IntaRNA software (1) and RNA Hybrid (2). Minimum free energies (mfe) and p-values are indicated in the respective figure.

(A) Predicted interaction between SraLWT and *rho*WT

(B) Predicted interaction between SraLWT and *rho*MUT

(C) Predicted interaction between SraLMUT and *rho*WT

(D) Predicted interaction between SraLMUT and *rho*MUT

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STM        TTATTCTTAAATTGTCAGGATCTCTGGACGCCCGGTCTGAGTCGTGCTAAGTTAGTATTG     60
STY        TTATTCTTAAATTGTCAGGATCTCTGGACGCCCGGTCTGAGTCGTGCTAAGTTAGTATTG     60
SBO        TTATTCTTAAATTGTCAGGATCTCTGGACGCCCGGTCTGAGTCGTGCTAAGTTAGTATTG     60
SBD        -----------------------CTGGACGCCCGGCGTGAGTCATGCTAACTTAGTGTTG     37
SFL        -----------------------CTGGACGCCCGGCGTGAGTCATGCTAACTTAGTGTTG     37
SDR        -----------------------CTGGACGCCCGGCGTGAGTCATGCTAACTTAGTGTTG     37
ECO        -----------------------CTGGACGCCCGGCGTGAGTCATGCTAACTTAGTGTTG     37
CRT        -----------------GGATGACTGGACGCCCGACGTGAGTCGTGCTAAGTTAATGTTG     43
CKO        ---ATTCTAAATTATTCGGATGACTGGACGCCCGGCTTGAGTCGTGCTAACTTAGTGTTG     57
ENT        -----------------GGATCTCTGGACGCCCGGCTTTAGTCGTGCTAAGTTACTTATG     43
KPN        -----------------GGAACTCTGGACGCCCGGCAGGAGTCGTGCTAAGTTAATCCAC     43
                                  ***********     **** ****** *** *

STM        ACTTCGA--ATTAAACATACCTTATTAAGTTTGAATCTGGTTTTATCCGTCACTTCCCGT     118
STY        ACTTCGA--ATTAAACATACCTTATTAAGTTTGAATCTGGTTTTATCCGTCACTTCCCGT     118
SBO        ACTTCGA--ATTAAACATACCTTATTAAGTTTGAATCTGGTTTTATCCGTCACTTCCCGT     118
SBD        ACTTCGT--ATTAAACATACCTTATTAAGTTTGAATCTTGTAATTTCCAACGCTTCCCGT     95
SFL        ACTTCGT--ATTAAACATACCTTATTAAGTTTGAATCTTGTAATTTCCAACGCTTCCCGT     95
SDR        ACTTCGT--ATTAAACATACCTTATTAAGTTTGAATCTTGTAATTTCCAACGCTTCCCGT     95
ECO        ACTTCGT--ATTAAACATACCTTATTAAGTTTGAATCTTGTAATTTCCAACGCTTCCCGT     95
CRT        ACTACGT--AGTAAACATACCTTATTTAGTTTGAATCTTGTTATTTCCGATACTTCCCGT     101
CKO        ACTTCGT--ATTAAACATACCTTATTAAGTTTGAGTCTTGTTTTTTCCAACGCTTCCCGT     115
ENT        ACTTCGATTTAA--ACATACCTTGTC-------GTTCTTGTTTTACCCGATGCTTCCCAT     94
KPN        AGACTTCGTTTTAAACATACC---TATTGTTTGAATCTTGTTTTACCCAAAGCGTCCCGC     100
           *             *******   *          *** **  *  **    * ****

STM        TTTTT------CTCGCACGAGAAGTGGAAAGATTCCTGG-CTCTTCGCTCATTCCGTCTT     171
STY        TTTTT------CTCGCACGAGAAGTGGAAAGATTCCTGG-CTCTTCGCTCATTCCGTCTT     171
SBO        TTTTT------CTCGCACGAGAAGTGGAAAGATTCCTGG-CTCTTCGCTCATTCCGTCTT     171
SBD        TTTAT------CTTAAATGCGAAGTGAACAGATTTCTGG-CTCGTCACTCAATCCGTCTT     148
SFL        TTTAT------CTTAAATGCGAAGTGAACAGATTTCTGG-CTCGTCACTCAATCCGTCTT     148
SDR        TTTAT------CTTAAATGCGAAGTGAACAGATTTCTGG-CTCGTCACTCAATCCGTCTT     148
ECO        TTTAT------CTTAAATGCGAAGTGAACAGATTTCTGG-CTCGTCACTCAATCCGTCTT     148
CRT        TTTTT------CTCGCGCGAGAAGTGGATAGATTCTGGGCCTTATCATTCAATCCGTCTT     155
CKO        TTTTT------CTCGCGCGAGAAGTGAACAGATTCCTGG-CTTGTCACTCAATCCGTCTT     168
ENT        TGTTGACACTCACAGTGCGTGAAGTTGC-TAGATTCCGGGCTTGTCACTCAATCCGTCTT     153
KPN        A---G------ACGATGCGCGTGAGGCTAATAATTCCGGGCTTATCACTCATTCCGTCTT     151
                             * *            *   ** **  **  *** ********

STM        GTCGTTTCAGTTCTGCGTACT-TTCCTGTGACCAGACAGCGAACAGACATGAGTTGATAG     230
STY        GTCGTTTCAGTTCTGCGTACT-TTCCTGTGACCAGACAGCGAACAGACATGAGTTGATAG     230
SBO        GTCGTTTCAGTTCTGCGTACT-TTCCTGTGACCAGACAGCGAACAGACATGAGTTGATAG     230
SBD        GTCGTTTCAGTTCTGCGTACT-CTCCTGTGACCAGGCAGCGAAAAGACATGAGTCGATGA     207
SFL        GTCGTTTCAGTTCTGCGTACT-CTCCTGTGACCAGGCAGCGAAAAGACATGAGTCGATGA     207
SDR        GTCGTTTCAGTTCTGCGTACT-CTCCCGTGACCAGGCAGCGAAAAGATATGAGTCGATGA     207
ECO        GTCGTTTCAGTTCTGCGTACT-CTCCTGTGACCAGGCAGCGAAAAGACATGAGTCGATGA     207
CRT        GTCGTTTCAGTGCTGCGTACT-TTCCTGTGACCAGACAGCGAACAGACATGAATTGATGG     214
CKO        GTCGTTTCAGTTCTGTGTACT-TTCCTGTGACCAGACAGCGAACAGACATGAGTTGGTGG     227
ENT        GTCGTTTCAGAGCTGCGTTCTTTCCCTGTAACCAGACAGCGAACAGACATGAGTTGATGG     213
KPN        GTCGTTTCAGTTCTGCGTTCT-TTCCTGTGACCAGGCAACGTACAGACACGAGATGAAG-     209
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STM        CCGTAAACAGGCATGGATGACCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     290
STY        CCGTAAACAGGCATGGATGACCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     290
SBO        CCGTAAACAGGCATGGATGACCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     290
SBD        CCGTAAACAGGCATGGATGATCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     267
SFL        CCGTAAACAGGCATGGATGATCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     267
SDR        CCGTAAACAGGCATGGATGATCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     267
ECO        CCGTAAACAGGCATGGATGATCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     267
CRT        CCGTAAACAGGCATGGATGACCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     274
CKO        CCGTAAACAGGCATGGATGATCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     287
ENT        CCGCAAACAGGCATGGATGACCCTTCCATACCATTCACAA-ATTAAGTTCGAGATTTACC     272
KPN        CCGCTAACAGGCATGGATGTTCCTGCCATACCATTCACAACATTAAGTTCGAGATTTACC     269
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STM     CCAAGTTTAAGAACTCACACCATTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     350
STY     CCAAGTTTAAGAACTCACACCATTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     350
SBO     CCAAGTTTAAGAACTCACACCATTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     350
SBD     CCAAGTTTAAGAACTCACACCACTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     327
SFL     CCAAGTTTAAGAACTCACACCACTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     327
SDR     CCAAGTTTAAGAACTCACACCACTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     327
ECO     CCAAGTTTAAGAACTCACACCACTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     327
CRT     CCAAGTTTAAGAACTCACACCATTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     334
CKO     CCAAGTTTAAGAACTCACACCATTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     347
ENT     CCGAGTTTAAGAACCCACACCATTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     332
KPN     CCGAGTTTAAGAACCCACACCACTATGAATCTTACCGAATTAAAGAATACGCCGGTTTCT     329
        ** *********** ******* *************************************

STM     GAGCTGATCACTCTCGGCGAAAGTATGGGGCTGGAAAACCTGGCCCGTATGCGCAAGCAG     410
STY     GAGCTGATCACTCTCGGCGAAAGTATGGGGCTGGAAAACCTGGCCCGTATGCGCAAGCAG     410
SBO     GAGCTGATCACTCTCGGCGAAAGTATGGGGCTGGAAAACCTGGCCCGTATGCGTAAGCAG     410
SBD     GAGCTGATCACTCTCGGCGAAAATATGGGGCTGGAAAACCTGGCTCGTATGCGTAAGCAG     387
SFL     GAGCTGATCACTCTCGGCGAAAATATGGGGCTGGAAAACCTGGCTCGCATGCGTAAGCAG     387
SDR     GAGCTGATCACTCTCGGCGAAAATATGGGGCTGGAAAACCTGGCTCGTATGCGTAAGCAG     387
ECO     GAGCTGATCACTCTCGGCGAAAATATGGGGCTGGAAAACCTGGCTCGTATGCGTAAGCAG     387
CRT     GAGCTGATCACTCTCGGCGAAAATATGGGGCTGGAAAACCTGGCCCGTATGCGCAAGCAG     394
CKO     GAGCTGATCACTCTCGGCGAAAATATGGGGCTGGAAAACCTGGCTCGTATGCGCAAGCAG     407
ENT     GAGCTGATTACTCTCGGCGAAAACATGGGCCTTGAAAACCAGGCTCGTATGCGCAAGCAG     392
KPN     GAGCTGATTACTCTCGGCGAAAATATGGGGCTGGAAAACCTGGCTCGTATGCGTAAGCAG     389
        ******** *************  ***** ** ******* *** ** ***** ******

STM     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGCGAC     470
STY     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGCGAC     470
SBO     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGCGAC     470
SBD     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGTGAT     447
SFL     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGTGAT     447
SDR     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGTGAT     447
ECO     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGTGAT     447
CRT     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGTGAC     454
CKO     GACATTATTTTTGCCATCCTGAAGCAGCACGCAAAGAGTGGCGAAGATATCTTTGGTGAC     467
ENT     GACATCATTTTTGCCATCCTGAAGCAGCATGCTAAGAGTGGCGAAGATATCTTTGGCGAC     452
KPN     GATATTATTTTTGCCATCCTCAAGCAGCATTCGAAGAGTGGCGAAGATATCTTTGGCGAC     449
        ** ** ************** ********  * *********************** **

STM     GGTGTGCTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGTTCTGCAGACAGCTCCTAC     530
STY     GGTGTGCTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGTTCTGCAGACAGCTCCTAC     530
SBO     GGTGTGCTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGTTCCGCAGACAGCTCCTAC     530
SBD     GGCGTACTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGTTCCGCAGACAGCTCCTAC     507
SFL     GGCGTACTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGTTCCGCAGACAGCTCCTAC     507
SDR     GGCGTACTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGTTCCGCAGACAGCTCCTAC     507
ECO     GGCGTACTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGTTCCGCAGACAGCTCCTAC     507
CRT     GGTGTGCTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGCTCCGCAGACAGCTCCTAC     514
CKO     GGTGTGCTGGAGATATTGCAGGATGGATTTGGTTTCCTCCGCTCTGCAGACAGCTCCTAC     527
ENT     GGTGTACTGGAGATATTGCAAGACGGATTTGGTTTCCTCCGTTCTGGAGACAGCTCCTAC     512
KPN     GGCGTACTGGAGATACTGCAGGATGGATTTGGATTCCTCCGCTCCGCAGACAGCTCCTAC     509
        ** ** ********* **** ** ******** ******** ** * *************

STM     CTCGCCGGTCCTGATGATATCTACGTTTCCCCCAGCCAAATCCGCCGTTTCAACCTCCGC     590
STY     CTCGCCGGTCCTGATGATATCTACGTTTCCCCCAGCCAAATCCGCCGTTTCAACCTCCGC     590
SBO     CTCGCCGGCCCTGACGACATCTACGTTTCCCCCAGCCAAATCCGCCGTTTCAACCTCCGC     590
SBD     CTCGCCGGTCCTGATGACATCTACGTTTCCCCTAGCCAAATCCGCCGTTTCAACCTCCGC     567
SFL     CTCGCCGGTCCTGATGACATCTACGTTTCCCCTAGCCAAATCCGCCGTTTCAACCTCCGC     567
SDR     CTCGCCGGTCCTGATGACATCTACGTTTCCCCTAGCCAAATCCGCCGTTTCAACCTCCGC     567
ECO     CTCGCCGGTCCTGATGACATCTACGTTTCCCCTAGCCAAATCCGCCGTTTCAACCTCCGC     567
CRT     CTTGCCGGTCCTGATGACATCTACGTTTCTCCCAGCCAAATCCGCCGTTTCAACCTCCGC     574
CKO     CTCGCCGGTCCTGATGACATCTACGTTTCTCCCAGCCAAATCCGCCGTTTCAACCTCCGC     587
ENT     CTCGCCGGTCCTGATGACATCTACGTATCCCCTAGCCAAATCCGCCGTTTCAACCTCCGT     572
KPN     CTCGCCGGCCCTGACGACATCTACGTATCCCCCAGCCAAATCCGCCGTTTCAACCTTCGC     569
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STM     ACTGGTGATACCATTTCTGGTAAGATTCGCCCGCCGAAAGAAGGTGAACGCTATTTTGCG     650
STY     ACTGGTGATACCATTTCTGGTAAGATTCGCCCGCCGAAAGAAGGTGAACGCTATTTTGCG     650
SBO     ACTGGTGATACCATTTCTGGTAAGATTCGCCCGCCGAAAGAAGGTGAACGCTATTTTGCG     650
SBD     ACTGGTGATACCATCTCTGGTAAGATTCGCCCGCCGAAAGAAGGTGAACGCTATTTTGCG     627
SFL     ACTGGTGATACCATCTCTGGTAAGATTCGCCCGCCGAAAGAAGGTGAACGCTATTTTGCG     627
SDR     ACTGGTGATACCATCTCTGGTAAGATTCGCCCGCCGAAAGAAGGTGAACGCTATTTTGCG     627
ECO     ACTGGTGATACCATCTCTGGTAAGATTCGCCCGCCGAAAGAAGGTGAACGCTATTTTGCG     627
CRT     ACTGGTGATACCATCTCGGGTAAGATTCGCCCGCCGAAAGAAGGCGAACGCTACTTTGCG     634
CKO     ACTGGTGACACCATTTCTGGTAAGATTCGCCCGCCAAAAGAAGGCGAACGTTACTTTGCG     647
ENT     ACTGGTGACACCATTTCAGGTAAGATTCGTCCTCCTAAAGAGGGTGAACGCTACTTTGCG     632
KPN     ACTGGTGACACCATTTCCGGTAAGATTCGTCCTCCGAAAGAGGGTGAGCGTTACTTTGCA     629
        ******** ***** ** *********** ** ** ***** ** ** ** ** *****

STM     CTGTTGAAAGTTAACGAAGTTAACTACGACAAACCGGAAAACGCCCGTAACAAAATCCTC     710
STY     CTGTTGAAAGTTAACGAAGTTAACTACGACAAACCGGAAAACGCCCGTAACAAAATCCTC     710
SBO     CTGTTGAAAGTTAACGAAGTTAACTACGACAAACCAGAAAACGCCCGTAACAAAATCCTG     710
SBD     CTGCTGAAAGTTAACGAAGTTAACTTCGACAAACCTGAAAACGCCCGCAACAAAATCCTC     687
SFL     CTGCTGAAAGTTAACGAAGTTAACTTCGACAAACCTGAAAACGCCCGCAACAAAATCCTC     687
SDR     CTGCTGAAAGTTAACGAAGTTAACTTCGACAAACCTGAAAACGCCCGCAACAAAATCCTC     687
ECO     CTGCTGAAAGTTAACGAAGTTAACTTCGACAAACCTGAAAACGCCCGCAACAAAATCCTC     687
CRT     CTGCTGAAAGTTAACGAAGTTAACTACGACAAACCGGAAAACGCCCGTAACAAAATTCTC     694
CKO     CTGTTGAAAGTTAACGAAGTTAACTACGACAAACCTGAAAACGCCCGTAATAAAATCCTC     707
ENT     CTGTTGAAAGTTAACGAAGTTAACTACGATAAACCTGAAAACTCGCGCAATAAGATCCTG     692
KPN     CTGTTGAAAGTTAACGAAGTTAACTACGACAAGCCGGAAAACGCGCGTAACAAGATCCTG     689
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STM     TTTGAGAACTTAACCCCGCTGCACGCAAACTCTCGTCTGCGTATGGAGCGTGGTAACGGT     770
STY     TTTGAGAACTTAACCCCGCTGCACGCAAACTCTCGTCTGCGTATGGAGCGTGGTAACGGT     770
SBO     TTTGAGAACTTAACCCCGCTGCACGCGAACTCTCGTCTGCGTATGGAGCGTGGTAACGGT     770
SBD     TTTGAGAACTTAACCCCGCTGCACGCAAACTCTCGTCTGCGTATGGAACGTGGTAACGGT     747
SFL     TTTGAGAACTTAACCCCGCTGCACGCAAACTCTCGTCTGCGTATGGAACGTGGTAACGGT     747
SDR     TTTGAGAACTTAACCCCGCTGCACGCAAACTCTCGTCTGCGTATGGAACGTGGTAACGGT     747
ECO     TTTGAGAACTTAACCCCGCTGCACGCAAACTCTCGTCTGCGTATGGAACGTGGTAACGGT     747
CRT     TTCGAAAACTTAACTCCGCTGCATGCCAACTCACGTCTGCGCATGGAACGTGGTAACGGT     754
CKO     TTTGAGAACTTAACGCCGCTGCACGCGAACTCACGTCTGCGTATGGAACGTGGTAACGGT     767
ENT     TTTGAAAACTTAACGCCGCTGCACGCGAACTCTCGCCTGCGCATGGAGCGTGGTAACGGT     752
KPN     TTCGAGAACTTAACGCCGCTGCACGCGAATTCTCGCCTGCGTATGGAACGTGGTAACGGT     749
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STM     TCTACCGAAGACTTAACGGCGCGCGTTCTGGATCTGGCTTCGCCGATCGGTCGCGGCCAG     830
STY     TCTACCGAAGACTTAACGGCGCGCGTTCTGGATCTGGCTTCGCCGATCGGTCGCGGCCAG     830
SBO     TCTACAGAAGACTTAACGGCGCGGGTACTGGATCTGGCTTCACCGATTGGTCGCGGTCAG     830
SBD     TCTACGGAAGATTTAACCGCTCGCGTACTGGATCTGGCATCACCTATCGGTCGTGGTCAG     807
SFL     TCTACTGAAGATTTAACTGCTCGCGTACTGGATCTGGCATCACCTATCGGTCGTGGTCAG     807
SDR     TCTACGGAAGATTTAACTGCTCGCGTACTGGATCTGGCATCACCTATCGGTCGTGGTCAG     807
ECO     TCTACTGAAGATTTAACTGCTCGCGTACTGGATCTGGCATCACCTATCGGTCGTGGTCAG     807
CRT     TCTACCGAAGACTTAACGGCGCGCGTGCTGGATCTGGCTTCGCCAATCGGTCGCGGTCAG     814
CKO     TCTACTGAAGATTTAACGGCTCGCGTACTGGATTTGGCTTCCCCGATTGGCCGTGGTCAG     827
ENT     TCTACCGAAGACCTGACGGCTCGCGTTCTGGATCTGGCGTCTCCAATTGGTCGTGGTCAG     812
KPN     TCTACCGAAGACTTAACCGCTCGCGTACTGGATCTGGCCTCCCCGATTGGCCGCGGCCAG     809
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STM     CGCGGTCTGATTGTCGCGCCGCCGAAAGCGGGTAAAACCATGCTGCTGCAGAACATCGCG     890
STY     CGCGGTCTGATTGTCGCGCCGCCGAAGGCGGGTAAAACCATGCTGCTGCAGAACATCGCG     890
SBO     CGTGGTCTGATTGTTGCGCCGCCGAAAGCGGGTAAAACCATGCTGCTGCAGAATATCGCG     890
SBD     CGTGGTCTGATTGTGGCACCGCCGAAAGCCGGTAAAACTATGCTGCTGCAGAACATTGCT     867
SFL     CGTGGTCTGATTGTGGCACCGCCGAAAGCCGGTAAAACTATGCTGCTGCAGAACATTGCT     867
SDR     CGTGGTCTGATTGTGGCACCGCCGAAAGCCGGTAAAACCATGCTGCTGCAGAACATTGCC     867
ECO     CGTGGTCTGATTGTGGCACCGCCGAAAGCCGGTAAAACCATGCTGCTGCAGAACATTGCT     867
CRT     CGTGGTCTGATTGTCGCGCCGCCGAAAGCGGGTAAAACCATGCTGCTGCAGAATATCGCG     874
CKO     CGTGGTCTGATCGTCGCACCGCCGAAAGCGGGTAAAACTATGCTGTTGCAGAACATCGCG     887
ENT     CGTGGCCTGATCGTGGCACCACCGAAAGCAGGTAAGACCATGCTGCTGCAGAACATCGCG     872
KPN     CGTGGTTTGATTGTCGCGCCGCCGAAAGCCGGTAAAACGATGCTGCTGCAGAACATCGCG     869
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STM     CAGAGCATCGCGTATAACCACCCGGACTGCGTGCTGATGGTGCTGCTGATTGACGAACGT    950
STY     CAGAGCATCGCGTATAACCACCCAGACTGCGTGCTGATGGTGCTGCTGATTGACGAACGT    950
SBO     CAGAGCATTGCGTACAACCATCCAGACTGCGTGCTGATGGTCTTGCTGATTGACGAACGT    950
SBD     CAGAGCATTGCTTACAACCACCCGGATTGTGTGCTGATGGTTCTGCTGATCGACGAACGT    927
SFL     CAGAGCATTGCTTACAACCACCCGGATTGTGTGCTGATGGTTCTGCTGATCGACGAACGT    927
SDR     CAGAGCATTGCTTACAACCACCCGGATTGTGTGCTGATGGTTCTGCTGATCGACGAACGT    927
ECO     CAGAGCATTGCTTACAACCACCCGGATTGTGTGCTGATGGTTCTGCTGATCGACGAACGT    927
CRT     CAGAGCATCGCCTACAACCATCCGGACTGCGTGCTGATGGTGCTGCTGATTGACGAACGT    934
CKO     CAGAGCATTGCTTACAACCACCCTGACTGCGTACTGATGGTGCTGCTGATCGACGAACGT    947
ENT     CAGAGCATTGCTTACAACCATCCTGATTGCGTACTGATGGTTCTGCTGATCGATGAGCGT    932
KPN     CAGAGCATCGCTTACAACCACCCGGACTGCGTGCTGATGGTGCTGCTGATCGACGAACGT    929
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STM     CCGGAAGAAGTGACCGAGATGCAGCGTCTGGTGAAAGGCGAAGTGGTTGCTTCTACCTTT    1010
STY     CCGGAAGAAGTAACCGAGATGCAGCGTCTGGTGAAAGGCGAAGTGGTTGCCTCTACCTTT    1010
SBO     CCGGAAGAAGTGACCGAGATGCAGCGTCTGGTGAAAGGCGAAGTGGTTGCGTCTACCTTT    1010
SBD     CCGGAAGAAGTAACCGAGATGCAGCGTCTGGTAAAAGGTGAAGTTGTTGCTTCTACCTTT    987
SFL     CCGGAAGAAGTAACCGAGATGCAGCGTCTGGTAAAAGGTGAAGTTGTTGCTTCTACCTTT    987
SDR     CCGGAAGAAGTAACCGAGATGCAGCGTCTGGTAAAAGGTGAAGTTGTTGCTTCTACCTTT    987
ECO     CCGGAAGAAGTAACCGAGATGCAGCGTCTGGTAAAAGGTGAAGTTGTTGCTTCTACCTTT    987
CRT     CCGGAAGAAGTGACCGAGATGCAGCGTCTGGTGAAAGGCGAAGTGGTCGCTTCCACCTTC    994
CKO     CCAGAAGAAGTAACCGAAATGCAGCGTCTGGTAAAAGGTGAAGTGGTTGCTTCCACCTTC    1007
ENT     CCAGAAGAAGTAACAGAGATGCAGCGTCTGGTGAAAGGTGAAGTGATTGCATCTACCTTT    992
KPN     CCGGAAGAAGTGACCGAGATGCAGCGTCTGGTGAAAGGTGAAGTGGTTGCTTCCACCTTT    989
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STM     GACGAACCGGCATCCCGCCACGTTCAGGTTGCCGAAATGGTTATCGAGAAGGCGAAGCGT    1070
STY     GACGAACCGGCATCCCGCCACGTTCAGGTTGCCGAAATGGTTATCGAGAAGGCGAAACGT    1070
SBO     GACGAACCGGCATCCCGCCACGTTCAGGTTGCGGAAATGGTTATTGAGAAGGCGAAACGC    1070
SBD     GACGAACCCGCATCTCGCCACGTTCAGGTTGCGGAAATGGTGATCGAGAAGGCCAAACGC    1047
SFL     GACGAACCCGCATCTCGCCACGTTCAGGTTGCGGAAATGGTGATCGAGAAGGCCAAACGC    1047
SDR     GACGAACCCGCATCTCGCCACGTTCAGGTTGCGGAAATGGTGATCGAGAAGGCGAAACGC    1047
ECO     GACGAACCCGCATCTCGCCACGTTCAGGTTGCGGAAATGGTGATCGAGAAGGCCAAACGC    1047
CRT     GACGAACCGGCATCCCGTCACGTTCAGGTAGCTGAAATGGTTATCGAGAAGGCGAAACGT    1054
CKO     GACGAACCGGCATCCCGTCACGTTCAGGTTGCTGAAATGGTAATCGAGAAGGCGAAGCGT    1067
ENT     GATGAGCCAGCCTCTCGCCACGTTCAGGTTGCTGAAATGGTTATCGAGAAAGCTAAGCGT    1052
KPN     GACGAGCCGGCATCCCGCCACGTGCAGGTTGCCGAGATGGTTATCGAGAAAGCAAAACGT    1049
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STM     CTGGTTGAACACAAGAAAGACGTTATCATCCTGCTCGACTCCATCACCCGTCTGGCGCGC    1130
STY     CTGGTTGAACACAAGAAAGACGTCATCATCCTGCTCGACTCCATCACCCGTCTGGCGCGT    1130
SBO     CTGGTTGAGCACAAAAAAGACGTTATCATCCTGCTCGACTCTATTACACGTCTGGCGCGT    1130
SBD     CTGGTTGAGCACAAGAAAGACGTTATCATTCTGCTCGACTCCATCACTCGTCTGGCGCGC    1107
SFL     CTGGTTGAGCACAAGAAAGACGTTATCATTCTGCTCGACTCCATCACTCGTCTGGCGCGC    1107
SDR     CTGGTTGAGCACAAGAAAGACGTTATCATTCTGCTCGACTCCATCACTCGTCTGGCGCGC    1107
ECO     CTGGTTGAGCACAAGAAAGACGTTATCATTCTGCTCGACTCCATCACTCGTCTGGCGCGC    1107
CRT     CTGGTTGAACATAAGAAAGACGTTATCATTCTGCTCGACTCCATCACCCGTCTGGCGCGT    1114
CKO     CTGGTTGAACACAAAAAAGACGTCATCATTCTGCTCGACTCCATCACTCGTCTGGCTCGC    1127
ENT     CTGGTCGAGCACAAGAAAGACGTTATTATTCTGCTCGACTCCATCACTCGTCTGGCGCGT    1112
KPN     CTGGTTGAACACAAGAAAGACGTTATCATCCTGCTCGACTCCATTACTCGTCTGGCGCGA    1109
        ***** ** ** ** ******** ** ** *********** ** ** ******** **

STM     GCCTACAACACCGTGGTGCCGGCTTCCGGTAAAGTATTGACCGGTGGTGTGGACGCTAAC    1190
STY     GCCTACAACACCGTGGTGCCGGCTTCCGGTAAAGTACTGACCGGTGGTGTGGATGCTAAC    1190
SBO     GCCTACAACACCGTGGTGCCAGCTTCTGGTAAGGTGCTGACTGGTGGTGTGGATGCCAAC    1190
SBD     GCTTACAACACTGTTGTTCCGGCGTCAGGTAAAGTGTTGACCGGTGGTGTGGACGCCAAT    1167
SFL     GCTTACAACACTGTTGTTCCGGCGTCAGGTAAAGTGTTGACCGGTGGTGTGGACGCCAAT    1167
SDR     GCTTACAACACCGTTGTTCCGGCGTCAGGTAAAGTGTTGACTGGTGGTGTGGACGCCAAT    1167
ECO     GCTTACAACACCGTTGTTCCGGCGTCAGGTAAAGTGTTGACCGGTGGTGTGGATGCCAAC    1167
CRT     GCGTATAACACCGTTGTTCCGGCCTCCGGTAAAGTGTTGACCGGTGGTGTGGATGCCAAC    1174
CKO     GCCTACAACACCGTGGTGCCGGCTTCTGGTAAAGTCCTGACCGGTGGTGTGGACGCCAAC    1187
ENT     GCTTACAACACCGTAGTTCCTGCTTCCGGTAAAGTACTGACCGGTGGTGTGGATGCGAAC    1172
KPN     GCCTACAACACCGTGGTACCGGCTTCTGGTAAAGTCCTGACCGGTGGTGTGGACGCCAAC    1169
        ** ** ***** ** ** ** ** ** ***** **  **** *********** ** **
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STM     GCCCTGCATCGTCCGAAGCGTTTCTTCGGCGCGGCGCGTAACGTGGAAGAGGGCGGTAGC     1250
STY     GCCCTGCATCGTCCGAAGCGCTTCTTCGGCGCGGCGCGTAACGTGGAAGAGGGCGGTAGC     1250
SBO     GCCCTGCATCGTCCGAAGCGTTTCTTCGGTGCCGCGCGTAACGTGGAAGAGGGCGGCAGC     1250
SBD     GCCCTTCATCGTCCGAAACGCTTCTTCGGTGCGGCGCGTAACGTGGAAGAGGGCGGCAGC     1227
SFL     GCCCTTCATCGTCCGAAACGCTTCTTTGGTGCGGCGCGTAACGTGGAAGAGGGCGGCAGC     1227
SDR     GCCCTTCATCGTCCGAAACGCTTCTTTGGTGCGGCGCGTAACGTGGAAGAGGGCGGCAGC     1227
ECO     GCCCTGCATCGTCCGAAACGCTTCTTTGGTGCGGCGCGTAACGTGGAAGAGGGCGGCAGC     1227
CRT     GCCCTGCACCGTCCGAAGCGTTTCTTCGGCGCGGCGCGTAACGTTGAAGAGGGCGGTAGC     1234
CKO     GCCCTGCACCGTCCGAAGCGTTTCTTCGGCGCGGCGCGTAACGTGGAAGAGGGCGGCAGC     1247
ENT     GCATTACACCGTCCGAAGCGTTTCTTTGGTGCCGCGCGTAACGTTGAAGAGGGAGGAAGC     1232
KPN     GCCCTGCACCGTCCGAAGCGTTTCTTCGGTGCGGCACGTAACGTCGAAGAGGGCGGCAGC     1229
        **  * ** ******** ** ***** ** ** ** ******** ******** ** ***

STM     CTGACTATCATCGCGACGGCGCTAATCGATACCGGTTCCAAGATGGACGAAGTTATCTAC     1310
STY     CTGACTATCATCGCGACGGCGCTAATCGATACCGGTTCCAAGATGGACGAAGTTATCTAC     1310
SBO     CTGACCATTATCGCGACGGCGTTGATCGACACCGGCTCCAAGATGGATGAAGTTATCTAC     1310
SBD     CTGACCATTATCGCGACGGCGCTTATCGATACCGGTTCTAAAATGGACGAAGTTATTTAC     1287
SFL     CTGACCATTATCGCGACGGCGCTTATCGATACCGGTTCTAAAATGGACGAAGTTATTTAC     1287
SDR     CTGACCATTATCGCGACGGCGCTTATCGATACCGGTTCTAAAATGGACGAAGTTATTTAC     1287
ECO     CTGACCATTATCGCGACGGCGCTTATCGATACCGGTTCTAAAATGGACGAAGTTATCTAC     1287
CRT     CTGACCATCATCGCGACCGCGCTTATCGATACCGGCTCCAAGATGGACGAGGTTATCTAC     1294
CKO     CTGACCATTATCGCAACGGCGCTGATCGACACCGGTTCTAAGATGGATGAAGTGATCTAC     1307
ENT     CTGACGATTATCGCAACCGCTCTGGTTGATACCGGCTCTAAAATGGATGAAGTTATCTAC     1292
KPN     CTGACCATCATTGCCACGGCGCTGATTGACACCGGCTCCAAAATGGACGAAGTGATCTAC     1289
        ***** ** ** ** ** **  *  * ** ***** ** ** ***** ** ** ** ***

STM     GAAGAGTTTAAAGGCACCGGTAACATGGAGCTGCATCTCTCGCGTAAGATCGCTGAAAAA     1370
STY     GAAGAGTTTAAAGGCACCGGTAACATGGAGCTGCATCTCTCGCGTAAGATCGCTGAAAAA     1370
SBO     GAAGAGTTTAAAGGTACAGGCAACATGGAACTGCACCTCTCTCGTAAGATCGCTGAAAAA     1370
SBD     GAAGAGTTTAAAGGTACAGGCAACATGGAACTGCACCTCTCTCGTAAGATCGCTGAAAAA     1347
SFL     GAAGAGTTTAAAGGTACAGGCAACATGGAACTGCACCTCTCTCGTAAGATCGCTGAAAAA     1347
SDR     GAAGAGTTTAAAGGTACAGGCAACATGGAACTGCACCTCTCTCGTAAGATCGCTGAAAAA     1347
ECO     GAAGAGTTTAAAGGTACAGGCAACATGGAACTGCACCTCTCTCGTAAGATCGCTGAAAAA     1347
CRT     GAAGAGTTCAAGGGCACCGGTAACATGGAACTGCACCTTTCCCGTAAGATCGCGGAAAAA     1354
CKO     GAAGAGTTTAAAGGCACCGGTAACATGGAGCTGCACCTCTCCCGTAAGATCGCTGAAAAA     1367
ENT     GAAGAGTTTAAAGGCACCGGTAACATGGAGCTGCACCTGGCACGTAAAATCGCCGAGAAG     1352
KPN     GAAGAGTTTAAAGGCACCGGTAACATGGAGCTGCACCTCTCTCGTAAGATTGCCGAAAAA     1349
        ******** ** ** ** ** ******** ***** **  * ***** ** ** ** **

STM     CGTGTCTTCCCGGCTATCGACTACAACCGTTCCGGTACCCGTAAAGAAGAGCTGCTCACC     1430
STY     CGTGTCTTCCCGGCTATCGACTACAACCGTTCCGGTACCCGTAAAGAAGAGCTGCTCACC     1430
SBO     CGCGTCTTCCCGGCTATCGACTATAACCGTTCCGGTACGCGTAAAGAAGAGCTGCTTACC     1430
SBD     CGCGTCTTCCCGGCTATCGACTACAACCGTTCCGGTACCCGTAAAGAAGAGCTGCTCACG     1407
SFL     CGCGTCTTCCCGGCTATCGACTACAACCGTTCCGGTACCCGTAAAGAAGAGCTGCTCACG     1407
SDR     CGCGTCTTCCCGGCTATCGACTACAACCGTTCTGGTACCCGTAAAGAAGAGCTGCTCACG     1407
ECO     CGCGTCTTCCCGGCTATCGACTACAACCGTTCTGGTACCCGTAAAGAAGAGCTGCTCACG     1407
CRT     CGCGTCTTCCCGGCCATTGACTACAACCGTTCCGGTACGCGTAAAGAAGAGCTGCTTACC     1414
CKO     CGCGTCTTCCCGGCTATCGACTACAACCGTTCCGGTACGCGTAAAGAAGAGCTGCTCACC     1427
ENT     CGCGTCTTCCCAGCGATTGATTACAACCGTTCAGGGACGCGTAAAGAAGAGCTGCTCACC     1412
KPN     CGCGTCTTCCCGGCTATCGATTACAACCGTTCCGGCACCCGTAAAGAAGAACTGCTCACC     1409
        ** ******** ** ** ** ** ******** ** ** *********** ***** **

STM     ACTCAGGAAGAGCTGCAGAAAATGTGGATCCTGCGTAAAATCATCCATCCGATGGGTGAA     1490
STY     ACTCAGGAAGAGCTGCAGAAAATGTGGATCCTGCGTAAAATCATCCATCCGATGGGTGAG     1490
SBO     ACTCAGGAAGAGCTGCAGAAAATGTGGATCCTACGTAAAATCATTCATCCAATGGGTGAA     1490
SBD     ACTCAGGAAGAACTGCAGAAAATGTGGATCCTGCGCAAAATCATTCACCCGATGGGCGAA     1467
SFL     ACTCAGGAAGAACTGCAGAAAATGTGGATCCTGCGCAAAATCATTCACCCGATGGGCGAA     1467
SDR     ACTCAGGAAGAACTGCAGAAAATGTGGATCCTGCGCAAAATCATTCACCCGATGGGCGAA     1467
ECO     ACTCAGGAAGAACTGCAGAAAATGTGGATCCTGCGCAAAATCATTCACCCGATGGGCGAA     1467
CRT     ACTCAGGAAGAACTGCAGAAAATGTGGATCCTGCGTAAGATCATTCACCCAATGGGCGAA     1474
CKO     ACTCAGGAAGAGCTACAGAAAATGTGGATCCTGCGCAAAATCATCCATCCGATGGGTGAA     1487
ENT     ACTCAGGAAGAGCTGCAGAAAATGTGGATCCTGCGTAAGATCATTCACCCGATGGGCGAA     1472
KPN     ACTCAGGAAGAGCTGCAGAAAATGTGGATCCTGCGCAAAATTATTCATCCGATGGGTGAG     1469
        *********** ** ***************** ** ** ** ** ** ** ***** **
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STM     ATTGACGCGATGGAATTCCTCATTAACAAACTGGCGATGACCAAAACTAATGACGACTTT      1550
STY     ATTGACGCGATGGAATTCCTCATTAACAAACTGGCGATGACCAAAACTAATGACGACTTT      1550
SBO     ATCGACGCAATGGAATTCCTCATCAATAAATTGGCGATGACCAAAACCAATGATGACTTC      1550
SBD     ATCGATGCAATGGAATTCCTCATTAATAAACTGGCCATGACCAAGACCAATGACGATTTC      1527
SFL     ATCGATGCAATGGAATTCCTCATTAATAAACTGGCCATGACCAAGACCAATGACGATTTC      1527
SDR     ATCGATGCAATGGAATTCCTCATTAATAAACTGGCAATGACCAAGACCAATGACGATTTC      1527
ECO     ATCGATGCAATGGAATTCCTCATTAATAAACTGGCAATGACCAAGACCAATGACGATTTC      1527
CRT     ATCGACGCGATGGAATTTCTCATTAACAAGCTGGCAATGACCAAGACCAACGACGACTTC      1534
CKO     ATCGACGCGATGGAATTCCTCATTAACAAGCTGGCAATGACCAAGACCAACGACGACTTC      1547
ENT     ATCGACGCAATGGAGTTCCTCATCAATAAGCTGGCAATGACAAAGACCAACGATGATTTC      1532
KPN     ATCGATGCAATGGAATTCCTCATTAACAAGCTGGCGATGACCAAGACGAATGATGACTTC      1529
        ** ** ** ***** ** ***** ** **   **** ***** ** ** ** ** ** **

STM     TTCGAGATGATGAAGCGCTCATAA      1574
STY     TTCGAGATGATGAAGCGCTCATAA      1574
SBO     TTTGAGATGATGAAGCGCTCATAA      1574
SBD     TTCGAAATGATGAAACGCTCATAA      1551
SFL     TTCGAAATGATGAAACGCTCATAA      1551
SDR     TTCGAAATGATGAAACGCTCATAA      1551
ECO     TTCGAAATGATGAAACGCTCATAA      1551
CRT     TTCGACATGATGAAGCGTTCGTAA      1558
CKO     TTCGACATGATGAAGCGTTCGTAA      1571
ENT     TTCGACATGATGAAACGCTCGTAA      1556
KPN     TTCGATATGATGAAGCGCTCGTAA      1553
        ** ** ******** ** ** ***
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Fig. S3. Alignment of *rho* genes including the upstream promoter region in several enterobacteria. All nucleotides are colored regarding their degree of conservation (red: high conservation; blue: partial conservation; black: little or no conservation). The asterisks (*) below the sequences are indicating the nucleotides conserved between all the species analyzed. *rho* coding sequence is given in bold letters. The *rho* interaction region with SraL is also indicated in yellow. STM: *Salmonella enterica* serovar Typhimurium; STY: *Salmonella enterica* serovar Typhi; SBO: *Salmonella bongori*; SBD: *Shigella boydii*; SFL: *Shigella flexneri*; SDR: *Shigella dysenteriae*; ECO: *Escherichia coli*; CRT: *Citrobacter rodentium*; CKO: *Citrobacter koseri*; ENT: *Enterobacter*; KPN: *Klebsiella pneumoniae*

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                                                                       1                 20                       40
STM AAAAATTTCGGCTAAAAAAT-CAGCATTTCG-CTGGCGAACAGGGCGTCGTCGCTTACACTTACAGTATCAACACAAACCGGAACCTCCACCACG----TGCTCGATA-TGA
STY AAAAATTTCGGCTAAAAAAT-CAGCATTTCG-CTGGCGAACAGGGCGTCGTCGCTTACACTTACAGTATCAACACAAACCGGAACCTCCACCACG----TGCTCAATA-TGA
SBO AAAAATTTCGGCTAAAAAAT-CAGCATTTCA-CTGGCAAACAGAACGCCGTGACATACACTTACAGTATCAACACAAACCGGAACCTCCACCACG----TGCTCGATA-TGA
SBD AAATATTGCGGTTAAAAAGTATACTTTTACA-CTGGCGAAGAAACGTCGGTGACATACAATTAAAGCATCAACACCAACCGGAACCTCCACCACG----TGCTCGA-A-TGA
SFL AAATATTGCGGCTAAAAAGTATACTTTTACA-CTGGCGAAGAAACGTCGGTGACATACAATTAAAGCATCAACACCAACCGGAACCTCCACCACG----TGCTCGA-A-TGA
SDR AAATATTGCGGCTAAAAAGTATACTTTTACA-CTGGCGAAGAAACGCCGGTGACATACAATTAAAGCATCAACACCAACCGGAACCTCCACCACG----TGCTCGA-A-TGA
ECO AAATATTGCGGCTAAAAAGTGTACTTTTACA-CTGGCGAAGAAACGCCGGTCACATACAATTAAAGCATCAACACCAACCGGAACCTCCACCACG----TGCTCGA-A-TGA
CRT AAAAATTT-GGCTAAAAAAT-CATCATTACGGCTGGAAAACCGAAGGCCGCGGCATACAATTACAGTATCAACACAAACCGGAACCTCCACCACG----TGCCCGA-A-TGA
CKO AAAAATTTCGGCTAAAAAAC-AGACAATACA-CTGGCAAACGGGCGGGCATGGCATACAATTACAGTATCAACACAAACCGGAACCTCCACCACG----TGCTCGAC--TGA
ENT AAAAATTTTGGCTAAAATCTGAACATCCGCG-CTGGCGAAGATGACGATTTGCATACAATTAAAGTGTCAGCACAAACCGGAACCTCC-CCAAC----TGCTCGACA-TGA
KPN GAAAATTTCGGCAAAATAGTAAG-----------GAAAAAATGGCAGCAGCTGC-CATAGTTAAAGTGTCGACGCAAACCGGAACCTCCATCAACAGATTGCGCAATACTGA
     ** ***  **  ***                  *   **             *  * * *** **  **  * * *************  **      *** * *   ***

                      60                    80                 100                   120                  140
STM GGGGTGTTGACGTCGGGGGAAACCCTCCTGTAA--TCAGCGGGATAGAGCGAAAGACAAAGACCGG--AAACAAACTAAAGCGCCCTTA-GCGGCGCTTTAGTTT
STY GAGGTGTTGACGTCGGGGGAAACCCTCCTGTAA--TCAGCGGGATAGAGCGAAAGACAAAGACCGG--AAACAAACTAAAGCGCCCTTA-GCGGCGCTTTAGTTT
SBO GGGGTGTTGACGTCGGGGGAAACCCTCCTGTAAA-TCAGCGGGATAGAGCGAAAGACAAAGACCGG--AAACAAACTAAAGCGCCCTTA-GCGGCGCTTTAGTTT
SBD GGTGTGTTGACGTCGGGGGAAACCCTCCTGTGTA-CCAGCGGGATAGAGAGAAAGACAAAGACCGGA-AAACAAACTAAAGCGCCCTT--GTGGCGCTTTAGTTT
SFL GGTGTGTTGACGTCGGGGGAAACCCTCCTGTGTT-CCAGCGGGATAGAGAGAAAGACAAAGACCGGA-AAACAAACTAAAGCGCCCTT--GTGGCGCTTTAGTTT
SDR GGTGTGTTGACGTCGGGGGAAGCCCTCCTGTGTA-CCAGCGGGATAGAGAGAAAGACAAAGACCGGA-AAACAAACTAAAGCGCCCTT--GTGGCGCTTTAGTTT
ECO GGTGTGTTGACGTCGGGGGAAACCCTCCTGTGTA-CCAGCGGGATAGAGAGAAAGACAAAGACCGGA-AAACAAACTAAAGCGCCCTT--GTGGCGCTTTAGTTT
CRT GGGGTGTTGATGTCGGGGGAAACCCTCCCGTGATATAAGCGGGATAGAGCGAAAGACAAAGACCGGGGAAAAAAACTAAAGCGCCCTT--GCGGCGCTTTAGTTT
CKO GGGGTGTTGATGTCGGGGGAAACCCTCCCGTGAA-CCAACGGGATAGAGCGAAAGACAAAGACCGG--AAACAAACTAAAGCGCCCTT--GCGGCGCTTTAGTTT
ENT GGGGTGTTGATGTCGGGGGAAACCCTCCCGTGAA-CCAGCGGGATAGAGAGAAAGACAAAGACCGGG--AATAAACTAAAGCGCCTTAGTCTGGCGCTTTAGTTT
KPN GGGACGTCGATGTCGGGGGAAACCCTCTCGTGAA-CCAGCGAGATAATGCGAAAGACAAAGACCGG--AAAACAACTAAAGCGCCCAGTTGTGGCGCTTTAGTTT
    *    ** ** ********** *****  **      * ** ****  * ****************   **  ************       *************
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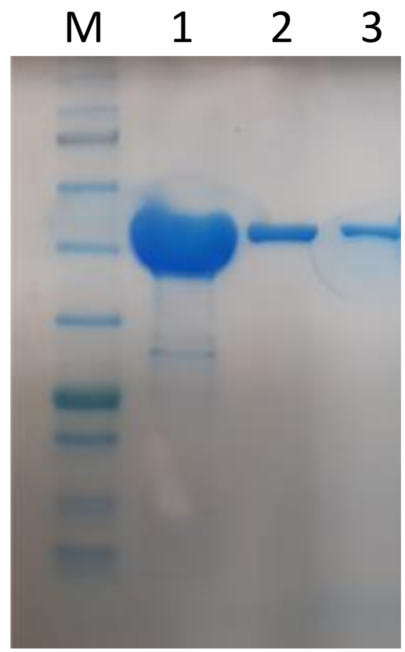
Fig. S4. Alignment of *sraL* genes including the upstream promoter region in several enterobacteria. All nucleotides are colored regarding their degree of conservation (red: high conservation; blue: partial conservation; black: little or no conservation). The asterisks (*) below the sequences are indicating the nucleotides conserved between all the species analyzed. The SraL interaction regions with *tig* mRNA and *rho* mRNA are also indicated in yellow and green, respectively. STM: *Salmonella enterica* serovar Typhimurium; STY: *Salmonella enterica* serovar Typhi; SBO: *Salmonella bongori*; SBD: *Shigella boydii*; SFL: *Shigella flexneri*; SDR: *Shigella dysenteriae*; ECO: *Escherichia coli*; CRT: *Citrobacter rodentium*; CKO: *Citrobacter koseri*; ENT: *Enterobacter*; KPN: *Klebsiella pneumoniae*



1 – Rho protein after purification (17,2 µM)
2 – Rho protein in Buffer 2 without glycerol (2,8 µM)
3 – Rho protein in Buffer 2 (1,4 µM)

Fig. S5. SDS-PAGE analysis of purified Rho protein.

Protein samples were visualized by BlueSafe (Nzytech). Molecular weight marker (NZYBlue Protein Marker - Nzytech) is shown on the left side of the image. Purified recombinant *Salmonella* Rho (~42,7 kDa) after purification and after buffer exchange (without and with 50% glycerol) were separated on a 10 % polyacrylamide gel.

Table S1. List of Oligonucleotides used in this work

Oligo	Sequence 5' to 3'
pIS-021	ATCAACACAAACCGGAAC
pIS-022	**GTTTTTTTTTTAATACGACTCACTATAG**GGAGGTAAGGGCGCTTTAGTTTG
pIS-023	CTACGGCGTTTCACTTCTGAGTTC
pIS-024	ACGGCTACCTTGTTACGACTT
pIS-027	TGGTAAGGCAACGCCAGCTC
pIS-030	GATGAGCTGGACGGTTGTATC
pIS-041	AGGCGCTGTATGGTCAGGCGTCTGTCATTCGACGAATGATTAAGGTATCAGTGTAGGCTGGAGCTGCTTC
pIS-042	TCCTGACAATTTAAGAATAACGTAAGGACAACAGACGCCACGAAACTGCCGGTCCATATGAATATCCTCCTTAG
pIS-043	AAACGGCGAAGTGGCGGCAAC
pIS-044	GTGGAAAGATTCCTGGCTCTTGGATCGTTCCGTCTTGTCGTTTCA
pIS-045	TGAAACGACAAGACGGAACGATCCAAGAGCCAGGAATCTTTCCAC
pIS-046	TCGCCGAGAGTGATCAGCTCAG
pIS-047	CCCTCCTGTAATCAGCGGGACAGATCCAAAGACAAAGACCGGAAA
pIS-048	TTTCCGGTCTTTGTCTTTGGATCTGTCCCGCTGATTACAGGAGGG
pIS-049	**GTTTTTTTTTTAATACGACTCACTATAG**TTCACCAGACGCTGCATCTC
pIS-050	CGTTCTGGATCTGGCTTCGC
pIS-051	CGATGCTCTGCGCGATGTTC
pIS-052	ATCACTCTCGGCGAAAGTATGG
pIS-053	TCCATCCTGCAATATCTCCAGC
pIS-054	CTCGCACGAGAAGTGGAAAG
pIS-055	CGCTGTCTGGTCACAGGAAAG
pIS-056	TAAGCGTCGCTGCCG
pIS-057	AAAGAAAGCGTAATAGCTCACTGGTC
pIS-058	GTTTTTT**CATATG**AATCTTACCGAATTAAAG

pIS-059	GTTTTTT**AAGCTT**GCGCATATCCCGATGACCAGTTT
pIS-060	**GTCTAACCTATAGGATACTTACAGCC**GACTTCGAATTAAACATACCTTATTAAG
pIS-061	TTACCACGCTCCATACGCAGACGAGAGTTTGCG
pIS-062	**TTATCAAAAAGAGTATTGACTTAAA**GTCTAACCTATAGGATACTTACAGCC
pIS-063	**GTTTTTTTTAATACGACTCACTATAGG**ATCAACACAAACCGGAACCTC
pIS-064	AAAACTAAAGCGCCGCTAAG
pIS-065	GGAATGAGCGAA
pIS-066	**GTTTTTTTTAATACGACTCACTATAGG**ACATCAGATTTCCTGGTGTAACG
pIS-067	AAAAAATCCCGGCCCTACGGGTC
pIS-068	CAACGGATAACGTAGCAATTACTGATGGCGTCATTATAATGTGTAGGCTGGAGCTGCTTC
pIS-069	CGGTTTATCAGCGCGAGGTTTACGTTCAGCGCCTTCTTTACGGTCCATATGAATATCCTCCTTAG
pIS-070	GTCGCACAGCTTGAAACC
pIS-071	CTGCGCGTACAATCAAAGAC
pIS-072	GTTTTT**TCTAGA**TGACGCCTGTTCATGCCTGCTG
pIS-073	GTTTTTT**AAGCTT**ATGCAAGCAGGCCAGCTAAC
EM1724	GACTGA**GAATTC**CAGACCCTGATGGTGTCTG
EM2883	CCG**CTCGAG**CGTACACCATCAGGGTACGTTTT
EM2884	CAGTT**GAATTC**ATCAACACAAACCGGAACCTC
EM2885	CCC**AAGCTT**CACTCGGCCATCGGGCTG
EM2886	CCG**CTCGAG**ATCAACACAAACCGGAACCTC
EM2888	CCTCGAGCCCGGGGAGCTCG
EM2889	AATTCGAGCTCCCCGGGCTCGAGGACGT

Table S2. List of strains used in this work

Strain	Relevant Markers / Genotype	Source/Reference
S. Typhimurium, SL1344	Str^R*hisG rpsL xyl*	(3)
E. coli DH5	*rec*A1 *end*A1 *gyr*A96 thi-*hsd*R17 *sup*E44 *rel*A1 Δ*lac*ZYA-*arg* FU169 f80dLacZDM15	New England Biolabs
BL21(DE3)	*fhuA2 [lon] ompT gal (λ DE3) [dcm] ΔhsdS* *λ DE3 = λ sBamHIo ΔEcoRI-B int::(lacI::PlacUV5::T7 gene1) i21 Δnin5*	New England Biolabs
CMA-651	SL1344 *sraL* (Δ*sraL*::Cm^R)	(4)
CMA-654	SL1344 [*sraL-STM4267*]IG::Cm^R	(4)
CMA-659	SL1344 [*trxA-rho*]IG::Cm^R	This study
CMA-660	SL1344 [*trxA-rho*]IG::Cm^R $rho_{C98G/C100A/A103G}$	This study
CMA-661	SL1344 [*sraL-STM4267*]IG::Cm^R $sraL_{U83C/G87U/G89C}$	This study
CMA-662	SL1344 $sraL_{U83C/G87U/G89C}$	This study
CMA-663	SL1344 [*trxA-rho*]IG::Cm^R $rho_{C98G/C100A/A103G}$ $sraL_{U83C/G87U/G89C}$	This study
CMA-664	SL1344 *proQ* (Δ*proQ*::Cm^R)	This study
CMA-665	SL1344 *sraL* (Δ*sraL*)	This study
CMA-666	SL1344 *sraL proQ (*Δ*sraL* Δ*proQ*::Cm^R)	This study
JVS-0255	SL1344 Δ*hfq*::Cm^R	(5)
MA11598	LT2 *pgaA*1(ΔL)-*lacZY aph* Δ*csrA*::cat *sup2*	(6)

Table S3 - List of plasmids used in this work

Plasmid	Comments	Origin/Marker	Source / Reference
pKD3	Template for mutants construction; carries chloramphenicol-resistance cassete	oriRγ/Amp^R	(7)
pKD46	Temperature-sensitive lambda-red recombinase expression plasmid	oriR101/Amp^R	(7)
pCP20	Temperature-sensitive FLP recombinase expression plasmid	Amp^R/Cm^R	(7)
pET-28a	Inducible expression vector, N-terminal His Tag	Kan^R	Novagen
pWSK29	Constitutive expression plasmid	pSC101/Amp^R	(8)
pZE12Luc	P_{LlacO} promoter; constitutive expression plasmid	ColE1/Amp^R	(9)
pISVA-001	pZE12luc derivative; P_{LlacO} promoter; constitutive plasmid expressing SraL	ColE1/Amp^R	(4)
pISVA-004	pET-28a encoding His-Rho protein	Kan^R	This study
pISVA-005	pWSK29 derivative; constitutive plasmid expressing ProQ	pSC101/Amp^R	This study
pBAD-MS2	pBAD24 + MS2 aptamer; arabinose inducible plasmid	pBR322/Amp^R	(10)
pBR-p*lac*	P_{LlacO} promoter expression vector	pBR322/Amp^R	(11)
pBR-p*lac*2	P_{LlacO} promoter expression vector	pBR322/Amp^R	This study
pBR-p*lac*2-*sraL*	P_{LlacO} promoter expression vector; plasmid expressing SraL; IPTG inducible promoter	pBR322/Amp^R	This study
pBR-p*lac*2 *MS2*	P_{LlacO} promoter expression vector	pBR322/Amp^R	This study
pBR-p*lac*2 *MS2*-sraL	P_{LlacO} promoter expression vector; plasmid expressing MS2-SraL; IPTG inducible promoter	pBR322/Amp^R	This study
pSVA-6	pWSK29 derivative; constitutive plasmid expressing Hfq	pSC101/Amp^R	(12)

Supplementary Materials and Methods

Bacterial strains and plasmids

The chromosomal point mutants in *rho* (CMA-660) and *sraL* (CMA-661) were obtained by a multiple-step PCR process. The strain CMA-659 was constructed by inserting a Cm^R cassette 89 nucleotides upstream of *rho* transcription start site, in the intergenic region between *rho* and its upstream gene *trxA*. The Cm^R was amplified from plasmid pKD3 using the primers pair pIS-041/pIS-042. The resulting PCR product was integrated into SL1344 wild-type chromosome using the λ-red recombinase method (7). Subsequently, DNA fragments containing the Cm^R cassette and the nucleotides substitutions in *rho* were prepared using two primers pairs pIS-043/pIS-045 and pIS-044/pIS-046 and using CMA-659 genomic DNA as template. In the case of *sraL*, the DNA fragments were prepared using the primers pairs pIS-027/pIS-048 and pIS-047/pIS-030 and the previously constructed CMA-654 (4) genomic DNA as template. The two resulting DNA fragments of each gene were mixed and used as PCR templates to obtain a DNA fragment containing Cm^R cassette and the nucleotides substitutions using the primers pair pIS-043/pIS-046 for *rho* and pIS-027/pIS-030 for *sraL*. The resulting DNA fragments were purified and integrated into SL1344 by the λ-red recombinase method (7). The mutants were subsequently transferred to a fresh genetic background (SL1344 strain) by P22 HT105/1 int-201 transduction (13). The presence of the expected substitutions was confirmed by DNA sequencing (STAB Vida, Portugal). The strains CMA-662 and CMA-665 were obtained by eliminating chloramphenicol resistance gene from strains CMA-661 and CMA-651, respectively, using plasmid pCP20 (7). The double mutants (CMA-663 and CMA-666) were constructed using P22 HT105/1 int-201 transduction method (13).

proQ null mutant (CMA-664) was also constructed using the λ-red recombinase method (7) using the primer pair pIS-068/pIS-069. Chloramphenicol-resistance cassette of plasmid pKD3 replaces nucleotides -56 to +439 of *proQ* gene. Gene deletion was confirmed by colony PCR with primer pair pIS-070/pIS-071.

The pBR-p*lac*2-*sraL* plasmid was constructed as follow. The multi-cloning site of the pBR-p*lac* (11) was modified to introduce new endoribonuclease cleavage sites (XhoI, SmaI, SacI) by annealing oligonucleotides EM2888 and EM2889 and cloned into pBR-p*lac* AatII/EcoRI-digested. The resulting plasmid was called pBR-p*lac*2. The *sraL* gene was PCR-amplified from *Salmonella* Typhimurium SL1344 with primers EM2886 and EM2885. PCR product was then digested with XhoI and HindIII and inserted in pBR-p*lac*2 cut with the same enzymes to generate the pBR-p*lac*2-*sraL* plasmid. Note: *sraL* was not cloned directly at the +1 of the pBR-p*lac*2 plasmid due to the presence of an AatII cleavage site in its sequence.

The plasmid pBR-p*lac*2 *MS2*-*sraL* was constructed as follow. Plasmid pBR-p*lac*2 *MS2* was generated using a PCR reaction from the plasmid pBAD-*MS2* (14) with the following oligonucleotides, EM2883 and EM1724. The PCR product was digested with appropriate restriction enzymes and ligated into an equivalently digested pBR-p*lac*2. Plasmid pBR-p*lac*2 *MS2*-*sraL* was generated using a PCR reaction with EM2884 and EM2885 with *Salmonella* Typhimurium SL1344 genomic DNA as matrix. The PCR product and plasmid pBR-p*lac*2 *MS2* were then digested with EcoRI and HindIII and ligated. In this construct, *MS2* aptamer was fused to the 5'-end of SraL.

To overexpress *Salmonella* Rho protein, SL1344 *rho* coding region was amplified with primer pair pIS-058/pIS-059. The purified PCR product was digested with NdeI and

HindIII and ligated to the pET-28a plasmid previously digested with the same enzymes, giving rise to pISVA-004. The plasmid was first transformed into *E. coli* DH5α and was subsequently cloned into BL21(DE3) strain.

To obtain pISVA-005 plasmid expressing ProQ, the entire *proQ* sequence was amplified from SL1344 chromosome using the primer pair pIS-072/pIS-073. The resultant PCR fragment was digested with XbaI and HindIII and ligated into pWSK29 plasmid previously digested with the same enzymes.

All these constructs were verified by sequencing.

MS2-affinity purification coupled with RNA sequencing

Salmonella Typhimurium SL1344 strains were grown in LB medium at 37°C (100 mL). Cells were harvested in (A) exponential phase after anaerobic shock and in (B) late stationary phase. MAPS was performed as previously described in (14, 15). Briefly, the expression of MS2-*sraL* (or *sraL* control) was induced by addition of 1 mM IPTG for 10 minutes. Then, harvested cells were chilled for 20 minutes on ice. Cells were then centrifuged, resuspended in 1 mL of buffer A (20 mM Tris-HCl at pH 8.0, 150 mM KCl, 1 mM $MgCl_2$, 1 mM DTT). Cells were then transferred to screw cap tubes containing 200 μL of glass beads (0.1 mm bead diameter; BioSpec). Cells were disrupted using Precellys®24 Homogenizer (three cycles: 6500 rpm for 20 seconds, followed by 1 minute on ice; Bertin). The lysate was centrifuged at 17,000g for 30 minutes at 4°C and the supernatant was applied to the column for affinity purification. MS2-affinity purification was performed as previously described (15). Both lysates were applied on the same column (200 pmol of the MS2-MBP protein immobilized on an amylose resin). Afterward, RNA samples (output) were treated with TURBO™DNase (Ambion). cDNA libraries were prepared with ScriptSeq™ v3 RNA-Seq Library Preparation Kit (Illumina) and sequenced (MiSeq sequencing system; Illumina). We used Galaxy Project (16) to analyze data. The whole list of genes enriched is available in Supplementary Dataset S1. The GEO accession number is GSE108234.

In vitro transcription termination assays

DNA templates for the *in vitro* transcription assays were prepared by PCR using genomic DNA from SL1344 wild-type strains for the wild-type transcripts, and the chromosomal DNA from the CMA-660 for the *rho*MUT transcript, and the following primer pairs: pIS-060/pIS-061 and pIS-062/pIS-061 for *rho*WT; pIS-063/pIS-064 for *sraL*; and pIS-066/pIS-067 for *dsrA*. *In vitro* transcription using T7 RNA polymerase and "riboprobe *in vitro* transcription system" (Promega) was performed to obtain *sraL* and *dsrA* transcripts. The transcripts were then purified by electrophoresis on an 8.3 M urea / 8% polyacrylamide gel, identified by ethidium bromide staining, and cut out from the gel. The RNA was eluted (3 M ammonium acetate at pH 5.2, 1 mM EDTA, 2.5% [v/v] phenol at pH 4.3) overnight at room temperature. The RNA was ethanol precipitated and resuspended in RNase free water. Transcription termination experiments were performed as described previously (17). Briefly, DNA template (5 nM; *rho*WT or *rho*MUT), *E. coli* RNA polymerase (0.0135 U/µl; New English Biolabs), Rho (0 nM or 70 nM, hexamer concentration) and RNasin (0,4 U/µl; Promega) were mixed in transcription buffer (40 mM Tris-HCl pH 8, 5 mM $MgCl_2$, 1.5 mM DTT, 0.05 mg/ml BSA and 100 mM KCl). After 10 min at 37ºC, the indicated sRNAs (SraL, DsrA or Anti) were added at a final concentration of 0.433 µM. After addition of transcription initiation mixture (0.2 mM rATP, 0.2 mM rCTP, 0.2 mM rGTP, 0.02 mM rUTP, 0.2 µCi/µl of ^{32}P-αUTP, 25 µg/ml rifampicin in transcription buffer) the samples were incubated for 20 min at 37ºC. Each reaction was stopped with 4 µl of EDTA (0.5 M pH 7.5), 2 µl of Yeast tRNA (0.25 mg/ml; Invitrogen) and 10 ul of sodium acetate (3 M pH 5.2), and subjected to phenol-chlorophorm extraction and ethanol precipitation as described (17). Reaction pellets were dissolved in resuspension buffer (10 mM MOPS, 1 mM EDTA, pH 7.5), mixed with RNA loading buffer (95% [v/v] formamide, 0.1% [w/v] xylene cyanol, 0.1% [w/v] bromophenol blue, 10 mM EDTA) and analysed by denaturing 8.3 M urea / 6% polyacrylamide gel electrophoresis.

β-Galactosidase activity assays

β-Galactosidase activity was assayed as previously described by Miller (18), with some modifications. Bacterial cells in middle exponential phase (OD_{600} of 1), stationary phase (OD_{600} of 2 plus 6 h) and upon anaerobic shock were harvested and resuspended in Buffer 1 (60 mM $NA_2HPO_4.7H_2O$, 40 mM $NaH_2PO_4 \cdot H_2O$, 10 mM KCl, 1 mM $MgSO_4$, and 50 mM β-mercaptoethanol, pH 7). The optical density at 600 nm was determined and a specific volume of cells was used to access LacZ expression using *o*-nitrophenyl- β-D-galactopyranoside (ONPG; Sigma) as substrate. The reaction was stopped with 1 M of Na_2CO_3 when the suspension reached a light-yellow color. OD_{420} and OD_{500} were measured and β-Galactosidase activity expressed in Miller Units. Paired t-test statistical analysis was carried out using GraphPad Prism 6 software.

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Additional data table S1 (separate file)

Dataset S1 - Summary table of all enriched RNAs using MAPS in *sraL*$^{-}$ background. Genes are named according to *Salmonella enterica* serovar Typhimurium SL1344 nomenclature (NCBI Genome Database NC_016810.1). Reads were normalized by coverage. gene1_gene2 represents the intergenic region between gene1 and gene2 (including 5' and 3'-UTR). The first entry corresponds to SraL; the previous described SraL target (trigger factor) and Rho are highlighted.