Table 1. Suboptimal solutions of INTARNA, RNAHYBRID and RNAPLEX for interactions without correct optimal solution.

sRNA - target	Tool	Subopt. energy	Mfe	Sensitivity	PPV
DsrA-*rpoS*	RNAHYBRID	-46.500	-47.700	0.808	0.488
GcvB-*argT*	RNAPLEX	-26.300	-30.400	0.950	0.950
GcvB-*gltI*	INTARNA	-18.284	-18.356	0.375	0.500
GcvB-*STM4351*	RNAHYBRID	-15.700	-87.800	0.000	0.000
GcvB-*STM4351*	RNAPLEX	-9.700	-33.600	0.000	0.000
MicC-*ompC*	RNAPLEX	-16.400	-28.000	0.000	0.000
SgrS-*ptsG*	RNAHYBRID	-13.100	-92.100	0.000	0.000

For every sRNA-target pair, all suboptimal solutions within an energy range of 0.5*mfe kcal/cal of the mfe energy were analyzed until a solution with sensitivity and PPV other than zero was found. If no solution within that range exists, only the suboptimal solution with the highest energy was used.

Table 2. Prediction accuracy of INTARNA without seed features on our test set (see Results section)

sRNA - target	Sensitivity INTARNA (without seed)	PPV INTARNA (without seed)
DsrA-*rpoS*	0.462	0.667
GcvB-*argT*	0.950	0.950
GcvB-*dppA*	1.000	0.586
GcvB-*gltI*	0.000	0.000
GcvB-*livJ*	0.000	0.000
GcvB-*livK*	0.542	0.565
GcvB-*oppA*	1.000	0.957
GcvB-*STM4351*	0.760	0.905
IstR-*tisAB*	0.806	0.690
MicA-*ompA*	1.000	0.821
MicA-*lamB*	1.000	1.000
MicC-*ompC*	1.000	0.537
MicF-*ompF*	0.960	0.960
OxyS-*fhlA*	0.375	1.000
RyhB-*sdhD*	0.588	1.000
RyhB-*sodB*	1.000	0.818
SgrS-*ptsG*	0.739	1.000
Spot42-*galK*	0.409	0.643
Average	0.699	0.728

For every sRNA-target pair, sensitivity and positive predictive value (PPV) were calculated for the highest-scoring interaction predicted.

Table 3. Changes in SD sequence accessibility as result of interaction between sRNA and target gene

sRNA - target	Regulation	Target site	SD location	ΔPU_{SD}
DsrA-*rpoS*	Activation	(-126,-97)	(-12,-7)	**0.07**
GcvB-*argT*	Repression	(-57,-37)	(-10,-5)	0.01
GcvB-*dppA*	Repression	(-43,-11)	(-12,-7)	**[SD]**
GcvB-*gltI*	Repression	(-62,-45)	(-10,-5)	0.00
GcvB-*livJ*	Repression	(-51,-28)	(-18,-13)	0.06
GcvB-*livK*	Repression	(-44,-17)	(-13,-8)	**-0.46**
GcvB-*oppA*	Repression	(-8,16)	(-15,-10)	**[SD]**
GcvB-*STM4351*	Repression	(-45,-19)	n/a	n/a
IstR-*tisAB*	Repression	(-145,-102)	(-11,-6)	0.00
MicA-*ompA*	Repression	(-21,-6)	(-14,-9)	**[SD]**
MicA-*lamB*	Repression	(-17,18)	(-10,-5)	**[SD]**
MicC-*ompC*	Repression	(-62,-15)	(-15,-10)	**[SD]**
MicF-*ompF*	Repression	(-16,10)	(20,25)	0.00
OxyS-*fhlA*	Repression	(34,41)	(15,20)	0.00
RyhB-*sdhD*	Repression	(-33,-13)	(-12,-7)	**[SD]**
RyhB-*sodB*	Repression	(-6,5)	(-12,-7)	**[SD]**
SgrS-*ptsG*	Repression	(-28,-9)	(-16,-11)	**[SD]**
Spot42-*galK*	Repression	(-18,14)	(-13,-8)	**[SD]**

The INTARNA predicted mRNA target sites and the predicted SD sequence locations are given relative to the start codon. GcvB-*gltI* shows the first suboptimal target prediction. "n/a" indicates that no significant SD sequence location could be found. ΔPU_{SD} represents the change, due to sRNA binding, in the probability that the SD sequence is unpaired. "[SD]" indicates that either ΔPU_{SD} can not be calculated because the sRNA binds at the predicted SD sequence or the target site is in the immediate vicinity of the predicted SD sequence location (distance at most 2 nt). The regulatory effects were successfully predicted for all sRNA-mRNA interactions marked in bold in the last column.