#### Supplemental text for

# Genome-wide mapping of TnrA-binding sites provides new insights into the TnrA regulon in *Bacillus subtilis*

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#### Supplemental Figures Legend.

## Figure S1. Direct involvement of TnrA as repressor in the control of *yuiA*, *yvgT*, *hom*, *pycA*, *pucI* and *yumC* expression.

Strains were cultivated in minimal medium with glutamate (left panels A, C, E, G, I and K) or with glutamate + glutamine (right panels B, D, F, H, J and L) as nitrogen source. Growth ( $OD_{600nm}$ ) was monitored every 5 min: blue circles, wild-type; red circles,  $\Delta tnrA$ . Promoter activity (RLU/OD) of each transcriptional fusion with the *luc* reporter gene is indicated: blue lines, in the wild-type; red lines, in  $\Delta tnrA$  cells. Growth and promoter activity were followed for the 6 genes *yuiA*, *yvgT*, *hom*, *pycA*, *pucI* and *yumC*. For each strain, one representative curve, out of three independent replicates realized, is shown. Note that the X-axes are different for paired panels to get a better view of the data.

## Figure S2. Direct involvement of TnrA as activator in the control of *appD*, *dtpT*, *yrbD*, *pucR*, *ysnD*, *yfiR* and *pucA* expression.

Strains were cultivated in minimal medium with glutamate (left panels A, C, E, G, I, K and M) or with glutamate + glutamine (right panels B, D, F, H, J, L and N) as nitrogen source. Growth ( $OD_{600nm}$ ) was monitored every 5 min: blue circles, wild-type; green circles,  $\Delta tnrA$ . Promoter activity (RLU/OD) of each transcriptional fusion with the *luc* reporter gene is indicated: blue lines, in the wild type; green lines, in  $\Delta tnrA$ cells. Growth and promoter activity were followed for the 7 genes *appD*, *dtpT*, *yrbD*, *pucR*, *ysnD*, *yfiR* and *pucA*. For each strain, one representative curve, out of three independent replicates realized, is shown. Note that the Y-axes are different for some paired panels to get a better view of the data. Figure S3. Alignment of TnrA box sequences from the TnrA primary and secondary regulon.









#### Mirouze et al., Figure S3

glnQ	(+)	-28	GGTCAAA TTT TCT GAT A	
nasA	(-)	-82	TGTAAGT TTT TGT GACA	
nasD	(+)	-85	TGTTACA TTT TAT AAC A	
nrgA	(-)	-102	TGTAAGATTTCCTGACA	
oppA	(-)	-231	CGTTAGTTTTTCTTCCA	
pucJ	(+)	-140	TGTTACA TTT TCT TACA	
tnrA	(+)	-124	TGTTAAT TTT TCT TCCG	
<i>ykzB</i>	(-)	-87	TGTTAAT TTT TCT TCCG	
ureA	(-)	-938	TGTTATA TTTATTCACA	
vcsF	(+)	-145	TGGTAGGTTTTCTGACA	
- vcsF	(-)	-52	TGTCATT TAT TGT CCC G	
_ gabP	(+)	-103	TGGTATA TTT TCT TACA	
yrbD	(-)	-96	TGTCACATTATATGACC	
_ appD	(-)	-119	AGTTGTATATTATTACA	
dtpT	(+)	-212	TCTAAAATTTTTATTAAA	
- dtpT	(-)	-175	CGTGAGA TTT TCT TACA	
pucR	(+)	-140	TGTCAGT TTA TGTAACA	
ysnD	(+)	-141	TGGAAGATTTTATAACA	
- ysnD	(+)	-97	TGACAGATCATCTTGCA	Tan Annaissan an an Ion
- ywrD	(+)	-83	CGTC <mark>A</mark> CTTTTTCTGCCG	InrA primary regulon
glnR	(+)	-82	TGTTAAGAATCCTTACA	
glnR	(-)	-59	TGTTATATTATGTGTCA	
gltA	(+)	-51	TGTT <mark>AGA</mark> TTTTATG <mark>A</mark> CC	
ilvB	(-)	-736	TGACAGATCATCTTGCA	
<i>ilv</i> B	(-)	-692	TGGAAGATTTTATAACA	
pel	(+)	-27	TGTGAGA TTTTATTCCA	
yoyD	(+)	-61	TGTGATC TTT TCT TACA	
ywdI	(-)	-92	TGTTATTTTTTTCTGACA	
уусС	(+)	-66	TGTGACA TCT TCT TACA	
yttA	(-)	-69	TGTT <mark>AGA</mark> TTTTTTCACG	
ywlF	(-)	-154	TTGCAGATTTTCTGACA	
alsT	(-)	-61	TGTTAGATTTTTTAACA	
degU	(-)	-159	TGTCATCGTTCCTTCCA	
yuiA	(-)	-78	AGTCAGATCATGTGACA	
уvgT	(-)	-39	TGTTAAA TTTTCTGACG	
yfiR	(-)	-31	TCTGCAA TTT TCT TACC	
hom	(-)	-203	AGTCAGATTTTCTCCTC	
русА	(+)	-87	TGTTTATCTGTAAAAAA	
braB	(-)	-55	TGTT <mark>AGA</mark> TTTTCTTCCT	
ydaB	(-)	-55	TGTTAGATTTTCTTCCT	
yflL	(+)	-345	CG'ICAGATTTTCTCCAA	
уккС	(-)	-243 +20		TnrA secondary regulon
ypqP vuak	(-)	+20 -45		
y agn kamA	() (+)	+168	CGTCAGAATTTCTACCA	
ykoH	(-)	+330	CGTCAGGTTTCCTCACA	
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