**SUPPLEMENTAL MATERIAL**

**LEGENDS**

**TABLE S1** List of proteins significantly upregulated and downregulated of growing cell ($OD_{600}$ of 1) of *S. lugdunensis* N920143 compared to Δ*agrA* mutant.

**TABLE S2** List of all genes differentially expressed in *S. lugdunensis* N920143 cells compared to Δ*agrA* mutant cells ($OD_{600}$ of 1).

**TABLE S3** Summary of RNAseq results of the samples of *S. lugdunensis* N920143 and Δ*agrA* mutant.

**TABLE S4** List of oligonucleotides used in this study.

**FIG S1** Complementation experiments. **A** growth curves in BHI with 10% NaCl of *S. lugdunensis* Δ*agrA* mutant containing the empty plasmid pRB473 (continuous line), and Δ*agrA* mutant with the plasmid pRB473-*agr* (complemented strain) (dotted line). **B** growth curves in BHI with 0.4 mM $H_2O_2$ of *S. lugdunensis* Δ*agrA* containing the empty plasmid pRB473 (continuous line), and Δ*agrA* mutant with the plasmid pRB473-*agr* (complemented strain) (dotted line). **C** Transcriptional changes ($Log_2FC$) of RNAIII, *crtM*, *crtN*, *slushABC*, and *SLUG_07290* in the Δ*agrA* mutant compared to the wild type strain (black bars) and in complemented strain (Δ*agrA* mutant with the plasmid pRB473-*agr*) compared to the Δ*agrA* strain (white bars). Asterisks indicate $p$ values < 0.05.

**FIG S2** Volcano plots of proteins differentially expressed of growing cell ($OD_{600}$ of 1) of *S. lugdunensis* N920143 compared to Δ*agrA* mutant.

**FIG S3** Volcano plots of genes differentially expressed of growing cell ($OD_{600}$ of 1) of *S. lugdunensis* N920143 compared to Δ*agrA* mutant.

## **TABLE S3** Summary of RNAseq results of the samples of *S. lugdunensis* N920143 and Δ*agrA* mutant.

| | ***S. lugdunensis* N920143 wild type** | | | | ***S. lugdunensis* N920143 *agr* deleted** | | | |
|---|---|---|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 1 | 2 | 3 | 4 |
| **Overall results** | | | | | | | | |
| Number of input reads | 29827506 | 33177543 | 34470980 | 31888778 | 32495196 | 31285384 | 29215079 | 31391569 |
| Average input read length | 50 | 50 | 50 | 50 | 50 | 50 | 50 | 50 |
| Mean Quality | 39.8 | 39.81 | 39.83 | 39.8 | 39.42 | 39.43 | 39.40 | 39.44 |
| (%) > Q30 | 98.46 | 98.5 | 98.52 | 98.48 | 99.57 | 99.61 | 99.56 | 99.60 |
| **Unique reads** | | | | | | | | |
| Uniquely mapped reads number (%) | 28976728<br>(97.15 %) | 32320911<br>(97.42 %) | 33762650<br>(97.95 %) | 31205204<br>(97.86 %) | 31426765<br>(96.71 %) | 30426886<br>(97.26 %) | 28239556<br>(96.66 %) | 30783448<br>(98.06 %) |
| Average mapped length | 49.94 | 49.94 | 49.94 | 49.94 | 49.94 | 49.95 | 49.94 | 49.95 |
| **Multi-mapping reads** | | | | | | | | |
| Number of reads mapped to multiple loci (%) | 594203<br>(1.99 %) | 492013<br>(1.48 %) | 410947<br>(1.19 %) | 518997<br>(1.63 %) | 968870<br>(2.98 %) | 550622<br>(1.76 %) | 648812<br>(2.22 %) | 485314<br>(1,55 %) |
| Number of reads mapped to too many loci | 31 | 22 | 12 | 14 | 24 | 11 | 17 | 9 |
| **Unmapped reads** | | | | | | | | |
| Number of reads unmapped: too many mismatches | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| Number of reads unmapped: too short (%) | 256245<br>(0.86 %) | 364066<br>(1.10 %) | 297024<br>(0.86 %) | 164342<br>(0.52 %) | 99284<br>(0.31 %) | 307564<br>(0.98 %) | 326342<br>(1.12 %) | 122274<br>(0.39 %) |
| Number of reads unmapped: other | 299 | 531 | 347 | 221 | 253 | 301 | 353 | 524 |

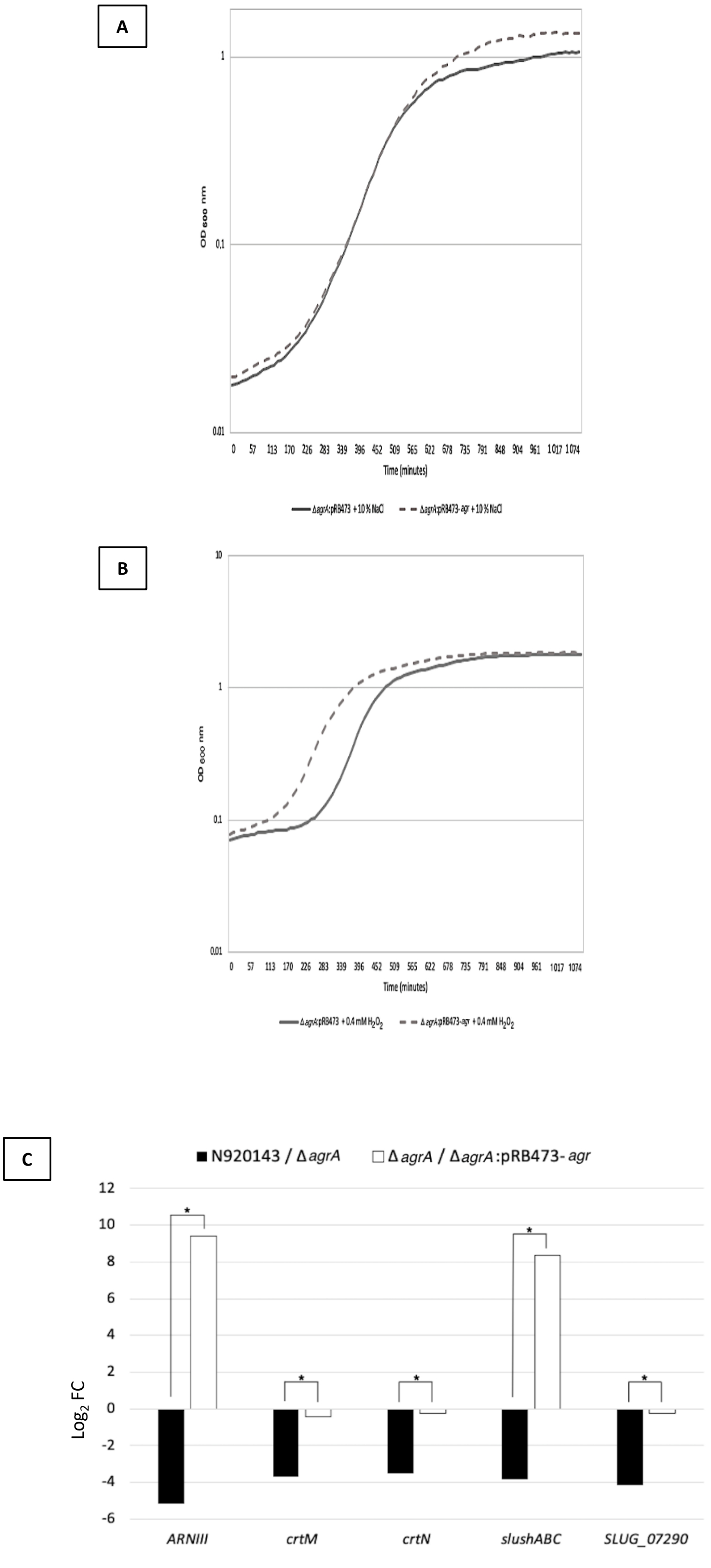
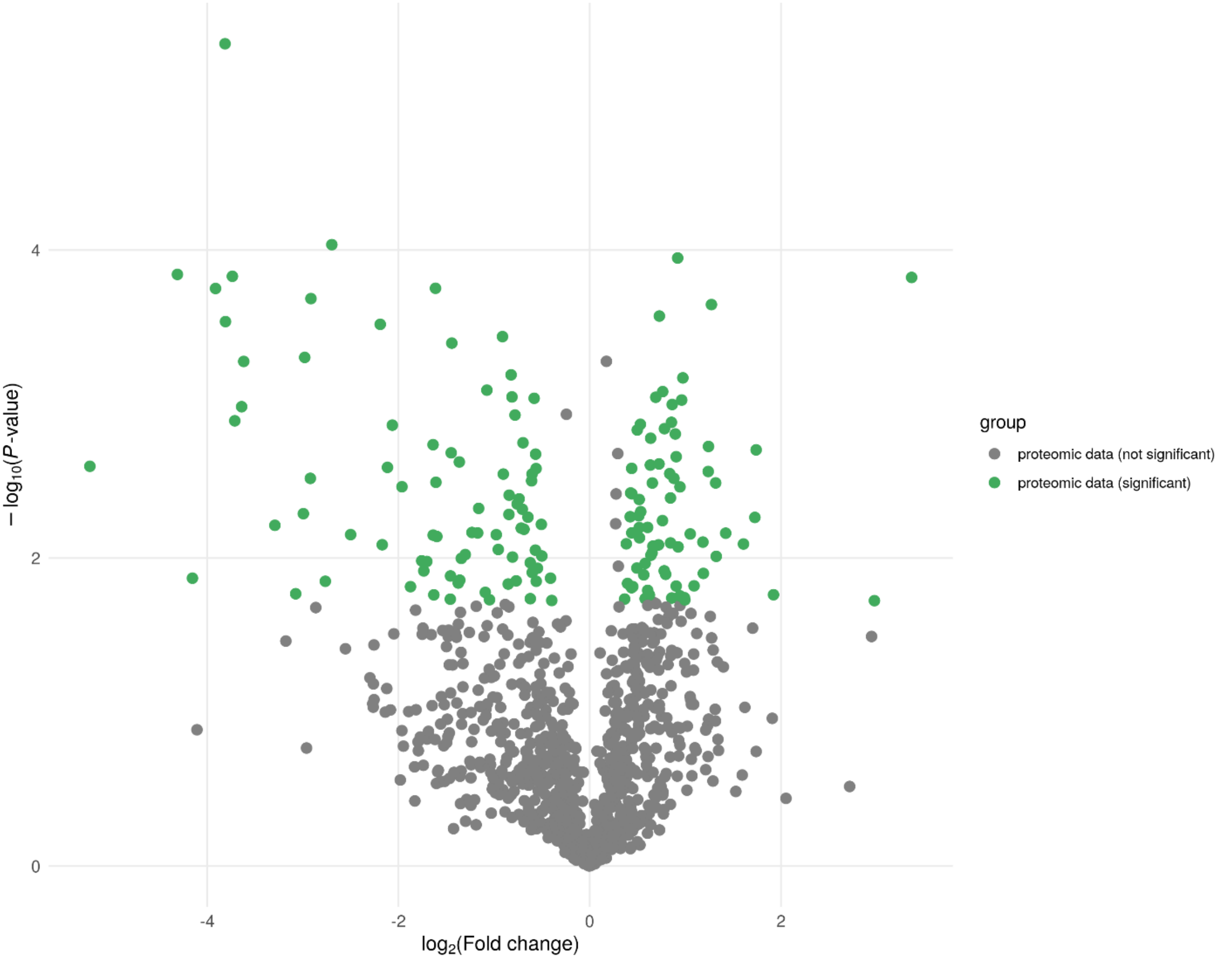

A
1
0,1
0,01
OD 600 nm
0 57 113 170 226 283 339 396 452 509 565 622 678 735 791 848 904 961 1017 1074
Time (minutes)
ΔagrA:pRB473 + 10 % NaCl
ΔagrA:pRB473-agr + 10 % NaCl
B
10
1
0,1
0,01
OD 600 nm
0 57 113 170 226 283 339 396 452 509 565 622 678 735 791 848 904 961 1017 1074
Time (minutes)
ΔagrA:pRB473 + 0.4 mM H2O2
ΔagrA:pRB473-agr + 0.4 mM H2O2
C
■ N920143 / ΔagrA
☐ ΔagrA / ΔagrA:pRB473-agr
12
10
8
6
4
2
0
-2
-4
-6
Log2 FC
*
*
*
*
*
ARNIII
crtM
crtN
slushABC
SLUG_07290

**FIG S1**



4
2
0
− log10(P-value)
-4
-2
0
2
log2(Fold change)
group
● proteomic data (not significant)
● proteomic data (significant)

**FIG S2**

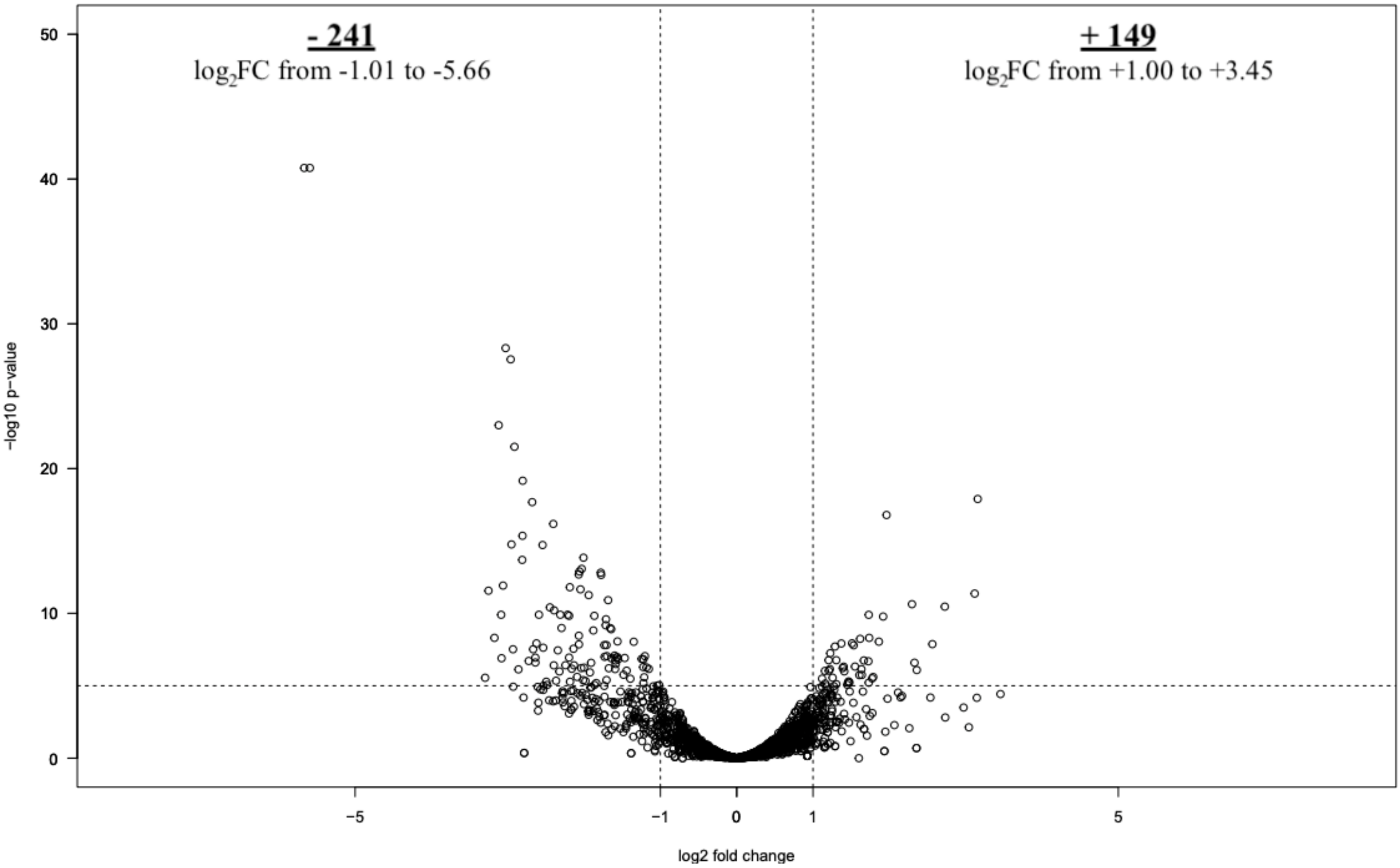

- 241
log2FC from -1.01 to -5.66
+ 149
log2FC from +1.00 to +3.45
50
40
30
20
10
0
−log10 p−value
−5
−1
0
1
5
log2 fold change

**FIG S3**