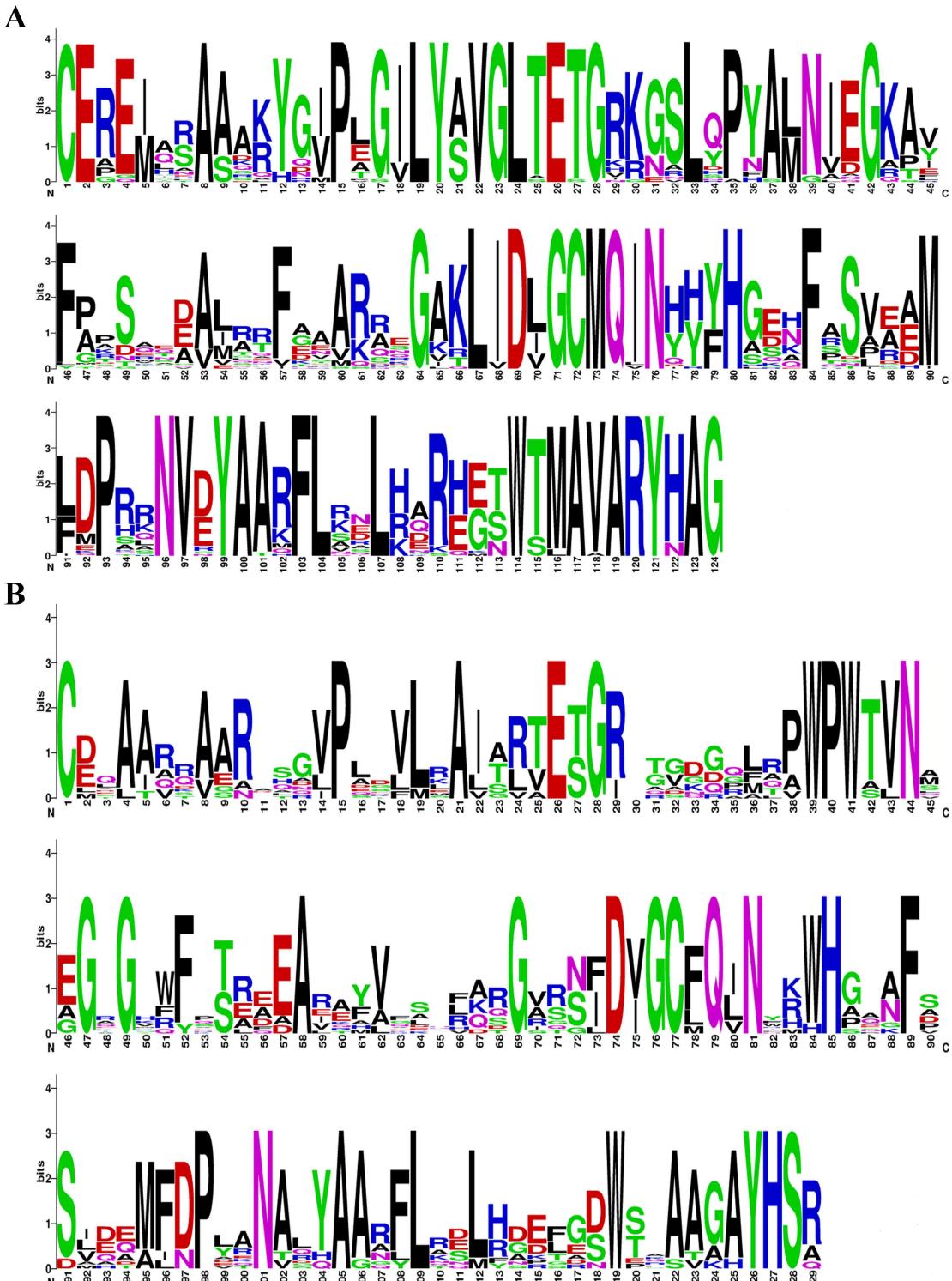


**Fig.S1 Flagellar context of lytic transglycosylases.** Graphic representation of the flagellar context of 46  $\alpha$ -proteobacteria for lytic transglycosylases and single domain scaffolding *flgJ* genes. Flagellar LT Family 1F and 1F' (SltF<sub>B5</sub> *brucella suis* (637332230), SltF<sub>Ba</sub> *Brucella abortus* (637647151), SltF<sub>Bm</sub>, *Brucella melitensis* (643747691), SltF<sub>Oa</sub>, *Ochrobactrum anthropi* (640836883) SltF<sub>Pp</sub>, *Pannomibacter phragmitetus* (2521738048), SltF<sub>Pg</sub>, *Polymorphum gilvum* (2512365150), SltF<sub>Rv</sub>, *Rhodomicrobiun vanniellii* (649746019), SltF<sub>Ms</sub>, *Methyloccella silvestris* (643463373), SltF<sub>Psp</sub>, *Pseudovibrio sp* (2511538202), SltF<sub>Mr</sub>, *Methylobacterium radiotolerans* (641627382), SltF<sub>Bsp</sub> *Bradyrhizobium sp.* (2514088350), SltF<sub>Bj</sub> *Bradyrhizobium japonicum*, (637374448), SltF<sub>Rp</sub>, *Rhodopseudomonas palustris* (637924221), SltF<sub>Bb</sub>, *Bartonella bacilliformis* (639842294), SltF<sub>Bc</sub>, *Bartonella claridgeiae* (2548760840), SltF<sub>Mo</sub>, *Mesorhizobium opportunistum* (2503200023), SltF<sub>Mt</sub>, *Mesorhizobium loti* (637075604), SltF<sub>Mc</sub>, *Mesorhizobium ciceri* (649871818), SltF<sub>Ps</sub>, *Pseudaminobacter salicylatoxidans* (2551926637), SltF<sub>Ni</sub>, *Nitratireductor indicus* (2520373292), SltF<sub>Np</sub>, *Nitratireductor pacificus* (2520250528), SltF<sub>Agrh</sub>, *Agrobacterium rhizogenes* (2505292958), SltF<sub>Agr</sub>, *Agrobacterium radiobacter* (643645133), SltF<sub>Rt</sub>, *Rhizobium tropici* (2524419140), SltF<sub>Rhe</sub>, *Rhizobium etli* (640437712), SltF<sub>R</sub>, *Rhizobium phaseoli* (2549960670), SltF<sub>Rhl</sub>, *Rhizobium leguminosarum* (2510372010), SltF<sub>Agv</sub>, *Agrobacterium vitis* (643650334), SltF<sub>Agsp</sub>, *Agrobacterium Sp.* (650739020), SltF<sub>Agt</sub>, *Agrobacterium tumefaciens* (639296061), SltF<sub>Rhp</sub>, *Rhizobium sp.* (643824500), SltF<sub>Sf</sub>, *Sinorhizobium fredii* (2517638777), SltF<sub>Ef</sub>, *Ensifer fredii* (2515008689), SltF<sub>Sm</sub>, *Sinorhizobium meliloti* (637181464), SltF<sub>Sme</sub>, *Sinorhizobium medicae* (640789209), SltF<sub>Pi</sub>, *Phaeobacter inhibens* (2574253765), SltF<sub>Pga</sub>, *Phaeobacter gallaeciensis* (2558539010), SltF<sub>Sp</sub>, *Ruegeria pomeroyi* (637287661), SltF<sub>Rt</sub>, *Rubellimicrobium thermophilum* (2521341176), SltF<sub>Rs</sub>, *Rhodobacter sphaeroides* WS8N, (651575303), SltF<sub>Cn</sub>, *Catellibacterium nectariphilum* (2525538211), SltF<sub>Rl</sub>, *Roseobacter litoralis* (2510237871), SltF<sub>Rd</sub>, *Roseobacter denitrificans* (639633682), SltF<sub>Sf</sub>, *Saccharibacter floricola* (2519014188), SltF<sub>Rce</sub>, *Rhodospirillum centenum* (643411101), SltF<sub>1Rs</sub>, *Rhodobacter sphaeroides* WS8N (651573991).



**Fig.S2** N-terminus alignment flagellar lytic transglycosylases. SlrF1<sub>R</sub>*Rhodobacter sphaeroides* WSSN (651573991), SlrF2<sub>R</sub>*Rhodobacter sphaeroides* WSSN (651575303), SlrF<sub>P</sub>*Phaeobacter inhibens* (2574253765), SlrF<sub>ga</sub>*Phaeobacter gallaeciensis* (2558539010), SlrF<sub>sp</sub>*Ruegeria pomeroyi* (637287661), SlrF<sub>R</sub>*Rubellimicrobium thermophilum* (2521341176), SlrF<sub>Cn</sub>*Catellibacterium nectariphilum* (2525538211), SlrF<sub>Rd</sub>*Roseobacter litoralis* (2510257871), SlrF<sub>Rd</sub>*Roseobacter denitrificans* (639633682), SlrF<sub>sp</sub>*Saccharibacter floricola* (2519014188), SlrF<sub>R</sub>*Rhodospirillum centenum* (643411101), SlrF<sub>B</sub><sub>2</sub>*Brucella suis* (637323230), SlrF<sub>B</sub><sub>2</sub>*Brucella abortus* (637647151), SlrF<sub>B</sub><sub>2</sub>*Brucella melitensis* (643747691), SlrF<sub>B</sub><sub>2</sub>*Ochrobactrum anthropi* (640836883), SlrF<sub>P</sub>*Pannomibacter phragmitetus* (2521738048), SlrF<sub>Pg</sub>*Polymorphum gilvum* (2512365150), SlrF<sub>R</sub>*Rhodomicrobiun vannieli* (649746019), SlrF<sub>M</sub>*Methylocculus silvestris* (643463373), SlrF<sub>Pp</sub>*Pseudovibrio* sp (2511538202), SlrF<sub>M</sub>*Methylobacterium radiotolerans* (641627382), SlrF<sub>B</sub><sub>2</sub>*Bradyrhizobium* sp. (2514088350), SlrF<sub>B</sub><sub>2</sub>*Bradyrhizobium japonicum* (637374448), SlrF<sub>B</sub><sub>2</sub>*Rhodopseudomonas palustris*, (637924221), SlrF<sub>B</sub><sub>2</sub>*Bartonella bacilliformis* (639842294), SlrF<sub>B</sub><sub>2</sub>*Bartonella claridgeiae* (2548760840), SlrF<sub>M</sub>*Mesorhizobium opportunistum* (2503200023), SlrF<sub>M</sub>*Mesorhizobium loti* (637075604), SlrF<sub>M</sub>*Mesorhizobium ciceri* (649871818), SlrF<sub>P</sub>*Pseudaminobacter saliciflaxidans* (2551926637), SlrF<sub>N</sub>*Nitratreducator indicus* (2520373292), SlrF<sub>P</sub><sub>2</sub>*Nitratreducotor pacificus* (2520250528), SlrF<sub>Agp</sub>*Agrobacterium rhizogenes* (2505292958), SlrF<sub>Agp</sub>*Agrobacterium radiobacter* (643645133), SlrF<sub>R</sub>*Rhizobium tropici* (2524419140), SlrF<sub>Rh</sub>*Rhizobium etli* (640437712), SlrF<sub>Rh</sub>*Rhizobium phaseoli* (2549960670), SlrF<sub>Rh</sub>*Rhizobium leguminosarum* (2510372010), SlrF<sub>Agp</sub>*Agrobacterium vitis* (643650334), SlrF<sub>Agp</sub>*Agrobacterium* Sp. (650739020), SlrF<sub>Agp</sub>*Agrobacterium tumefaciens* (639296061), SlrF<sub>Rh</sub>*Rhizobium sp.* (643824500), SlrF<sub>S</sub>*Sinorhizobium fredii* (2517638777), SlrF<sub>E</sub>*Ensifer fredii* (2515008689), SlrF<sub>Sm</sub>*Sinorhizobium meliloti* (637181464), SlrF<sub>Sm</sub>*Sinorhizobium medicae* (640789209). Access numbers for each sequence are in accordance with IMG (Integrated Microbial Genomes : <https://img.jgi.doe.gov/>) or with GenBank. In black are shown the 17 residues of SlrF1 from *R. sphaeroides* studied in this work.



**Fig.S3 Amino acid frequency analysis.** Frequency analysis of residues within the catalytic site of SltF from subfamily 1F (Panel A) y 1F' (Panel B). This was achieved using WebLogo v2.8 (Crooks GE, Hon G, Chandonia JM, Brenner SE. 2004, WebLogo: A sequence logo generator, *Genome Research*, 14:1188-1190)

Mesorhizobium loti MAFF303099  
 Mesorhizobium opportunistum WSM2075 (final version from ORNL)

Mesorhizobium ciceri CC1192

Agrobacterium vitis bv. III S4

Agrobacterium tumefaciens C58-UWash  
 Agrobacterium sp. H13-3

Rhizobium sp. 10195

Agrobacterium radiobacter K84

Rhizobium tropici CIAT899

Agrobacterium rhizogenes ATCC 15834

Rhizobium leguminosarum bv. trifolii CB782

Rhizobium phaseoli DSM 30137

Rhizobium etli CFN 42, DSM 11541

Sinorhizobium fredii USDA 257

Sinorhizobium medicae WSM419

Sinorhizobium melliloti SM11

Bartonella bacilliformis ATCC 35685D-5

Bartonella clarridgeiae 73

Ochrobactrum anthropi ATCC 49188

Brucella melitensis ATCC 23457

Brucella abortus A13334

Brucella suis ATCC 23445

Rhodomicrobium vannielii ATCC 17100

Pseudovibrio sp. FO-BEG1

Polymorphum gilvum SL003B-26A1

Pannonibacter phragmitetus DSM 14782

Methylobacterium radiotolerans JCM 2831

Methylocella silvestris BL2, DSM 15510

Rhodopseudomonas palustris BisA53

Bradyrhizobium sp. BF49

Bradyrhizobium japonicum USDA 110

Saccharibacter floricola DSM 15669

Rhodospirillum centenum SW

Rubellimicrobium thermophilum DSM 16684

Gemmobacter nectariphilus DSM 15620

Rhodobacter sphaeroides WS8N

Roseobacter litoralis Och 149

Roseobacter denitrificans DSM 7001

Ruegeria pomeroyi DSS-3

Phaeobacter gallaeciensis DSM 17395

Phaeobacter inhibens T5, DSM 16374

Pseudaminobacter salicylatoxidans DSM 6986

Nitratireductor pacificus pht-3B

Nitratireductor indicus C115

### Short conserved C-terminus

### Long nonconserved C-terminus

### Short conserved C-terminus

**Fig.S4 Phylogenetic tree based on 16S ribosomal RNA sequences.** The phylogenetic tree was built with sequences from 46  $\alpha$ -proteobacteria that possess single domain SltFs.

**Table S1** Sec signal sequence prediction for Transglycosylases found in this work. Access numbers correspond to the data base from IMG. Signal sequence was predicted with SignalP V 4.1 Nielsen H. 2017. Predicting Secretory Proteins with SignalP. Methods Mol Biol Clifton NJ 1611:59–73.

| SlfF proteins | Signal sequence* |
|---------------|------------------|
| 639296061     | ✓                |
| 650739020     | ✓                |
| 643650334     | ✓                |
| 2548760840    | ✗                |
| 639842294     | ✓                |
| 637374448     | ✓                |
| 2514088350    | ✓                |
| 643747691     | ✓                |
| 637332230     | ✓                |
| 637647151     | ✓                |
| 637181464     | ✓                |
| 640789209     | ✓                |
| 643824500     | ✓                |
| 2515008689    | ✓                |
| 2517638777    | ✓                |
| 637075604     | ✗                |
| 649871818     | ✓                |
| 2503200023    | ✓                |
| 641627382     | ✓                |
| 640836883     | ✓                |

|            |   |
|------------|---|
| 643463373  | X |
| 2512365150 | X |
| 2511538202 | X |
| 2510372010 | ✓ |
| 640437712  | ✓ |
| 643645133  | ✓ |
| 2524419140 | ✓ |
| 649746019  | ✓ |
| 637924221  | ✓ |
| 2521738048 | X |
| 2549960670 | ✓ |
| 2520250528 | ✓ |
| 2551926637 | ✓ |
| 2520373292 | ✓ |
| 2505292958 | ✓ |
| 2558539010 | X |
| 2574253765 | X |
| 643411101  | X |
| SltF       | ✓ |
| SltF2      | ✓ |
| 637287661  | ✓ |
| 639633682  | ✓ |
| 2510237871 | ✓ |
| 2521341176 | ✓ |

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2525538211

✓

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2519014188

✓

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\* The software used was SignalP V 4.1