**Additional File 3.** CRISPRs identified in 15 *S. lugdunensis* genomes using CRISPERFinder (available at: [http://crispr.i2bc.paris-saclay.fr/)](http://crispr.i2bc.paris-saclay.fr/%29)

|  |  |  |
| --- | --- | --- |
| Strain | Number of confirmed CRISPRs | Number of questionable CRISPRs |
| HKU0901 | 1 | 9 |
| N920143 | 1 | 9 |
| FDAARGOS\_141 | 0 | 4 |
| FDAARGOS\_143 | 0 | 1 |
| FDAARGOS\_222 | 0 | 4 |
| Klug93G-4 | 0 | 5 |
| FDAARGOS\_377 | 0 | 5 |
| FDAARGOS\_381 | 0 | 5 |
| VISLISI\_21 | 0 | 5 |
| VISLISI\_22 | 0 | 4 |
| VISLISI\_25 | 0 | 5 |
| VISLISI\_27 | 1 | 11 |
| VISLISI\_33 | 1 | 11 |
| VISLISI\_37 | 1 | 9 |
| C33 | 1 | 4 |

Confirmed CRISPRS characteristics

**HKU0901**

CRISPR start position: 29464

CRISPR end position: 29929

DR consensus: AATCAGAGAATACCCCGTATAAAAGGGGACGAGAAC

DR length: 36

Number of spacers: 6

|  |  |  |  |
| --- | --- | --- | --- |
| Spacer begin position |  Spacer length |  Spacer sequence | Spacer ID1 |
|  29500 |  37 |  TTCTGTATTTCTATTAACCAATTCATAAGTGTCATTA | S1 |
|  29573 |  35 |  TTCATCATATCCTTTTATATAGTTTTTGTTTTGTT | S2 |
|  29644 |  35 |  CCAGTTGCTATTTTATTTGTCAACCATTTTATTAA | S3 |
|  29715 |  32 |  TAGAATGTTTAAACAAGGTGTTTCAAAACCTG | S4 |
|  29783 |  39 | AACATTTTATTTACGTCTGTTTTTGCCTCTACTAAGTAA | S5 |
|  29858 |  36 |  TCGCTATTCAATAAGTTTTGTATTTGTTGTCTCATT | S6 |

 1 Identification number

**N920143**

CRISPR start position: 63455

CRSPR end position: 63777

DR consensus: AATCAGAGAATACCCCGTATAAAAGGGGACGAGAAC

DR length: 36

Number of spacers: 4

|  |  |  |  |
| --- | --- | --- | --- |
| Spacer begin position |  Spacer length |  Spacer sequence | Spacer ID |
|  63491 |  35 |  TAACACCTTTGATTTTATATCTTTTTCCATCAAAT | S7 |
|  63562 |  37 |  CCAAATAATACTATTAATTTATCTGTTAATGCTGTGG | S8 |
|  63635 |  35 |  TGGTAAATCTTCTACACTGTCGACTGGGTCTTCTA | S9 |
|  63706 |  36 |  TGTTCCAATTAGCTAAAGATGTTATGGACGGCAAGA | S10 |

**VISLISI\_27**

CRISPR start position: 20682

CRISPR end position: 21217

DR consensus: AATCAGAGAATACCCCGTATAAAAGGGGACGAGAACT

DR length: 37

Number of spacers: 7

|  |  |  |  |
| --- | --- | --- | --- |
| Spacer begin position | Spacer length | Spacer sequence | Spacer ID |
|  20719 |  34 | ATCAAAACATCATTTTTAATATATTTTAATTGTT | S11 |
|  20790 |  34 | GAATTTCACTTGCGAATTTTAAATAACTATCCCC | S12 |
|  20861 |  33 | TTATTAGCTATTTCATTATCTATATTATCACTA | S13 |
|  20931 |  36 | TCTGTATTTCTATTAACCAATTCATAAGTGTCATTA | S1 |
|  21004 |  34 |  TCATCATATCCTTTTATATAGTTTTTGTTTTGTT | S2 |
|  21075 |  34 |  GGTAAATCTTCTACACTGTCGACTGGGTCTTCTA | S9 |
|  21146 |  35 |  CGCTATTCAATAAGTTTTGTATTTGTTGTCTCATT | S6 |

**VISLISI\_33**

CRISPR start position: 20195

CRISPR end position: 20952

DR consensus: AATCAGAGAATACCCCGTATAAAAGGGGACGAGAAC

DR length: 36

Number of spacers: 10

|  |  |  |  |
| --- | --- | --- | --- |
| Spacer begin position |  Spacer length |  Spacer sequence | Spacer ID |
|  20231 |  40 | CCACCTTTACTTTTCGTCATATCATTTTTCTTTTGAGCGA | S14 |
|  20307 |  36 |  TCCCAGTTTGGTAAGTTCATTTTTAATCATCCTTTT | S15 |
|  20379 |  36 |  ATAATCAATTGTTAAATACATTTCATTTGGATTAAT | S16 |
|  20451 |  37 |  TTCTGTATTTCTATTAACCAATTCATAAGTGTCATTA | S1 |
|  20524 |  35 |  TTCATCATATCCTTTTATATAGTTTTTGTTTTGTT | S2 |
|  20595 |  35 |  TGGTAAATCTTCTACACTGTCGACTGGGTCTTCTA | S9 |
|  20666 |  35 |  TGTGCACTTTTACACTATTAGTTTAAATATCTCCA | S17 |
|  20737 |  37 |  CTTTATATACAGTAGTTAATGACTTATGAAAGGTTTC | S18 |
|  20810 |  35 |  CCAGTTGCTATTTTATTTGTCAACCATTTTATTAA | S3 |
|  20881 |  36 |  TCGCTATTCAATAAGTTTTGTATTTGTTGTCTCATT | S6 |

**VISLISI\_37**

CRISPR start position: 182355

CRISPR end position: 182608

DR consensus: CTAATCAGAGAATACCCCGTATAAAAGGGGACGAGAAC

DR length: 38

Number of spacers: 3

|  |  |  |  |
| --- | --- | --- | --- |
| Spacer begin position |  Spacer length |  Spacer sequence | Spacer ID |
|  182393 |  35 |  ATATTTTACTATATGCTCATATCCGCCGTTTGTTT | S18 |
|  182466 |  33 |  TGGTAAATCTTCTACACTGTCGACTGGGTCTTC | S9 |
|  182537 |  34 | TGTTCCAATTAGCTAAAGATGTTATGGACGGCAA | S10 |

**C33**

CRISPR start position: 98485

CRISPR end position: 99241

DR consensus: GTTTTAGTACTCTGTAATTTTAGGTATAAGTGATAC

DR length: 36

Number of spacers: 11

|  |  |  |
| --- | --- | --- |
| Spacer begin position |  Spacer length |  Spacer sequence |
|  98521 |  29 |  TGTTCGTCCATTTGTCTTTAAAATTATAT |
|  98586 |  30 | TTGGTGGCGGAGCTATCATTGCAGTAGCAG |
|  98652 |  29 |  GTATAAAAAAACACCGTATCAACTAAGAT |
|  98717 |  30 |  ATTATGACATCAATAGTATCACTTTCCCAG |
|  98783 |  29 |  TGAAGGTAAAGACAGAGGACATAGTCCTA |
|  98848 |  29 |  CGGTTTAGGTGCTGTTGCAATGGCTGGAA |
|  98913 |  30 |  GTTTTTCGAATGAGTTGATAGTGACGTCTG |
|  98979 |  30 | TCACATCATTCGAACGTAAGAATGAGGCTG |
|  99045 |  29 |  TCTGTGTTCAATCCATGCAGTCTGTCCAA |
|  99110 |  30 | GTATTGAAGATGTAAGAAAAGACACGGTTC |
|  99176 |  30 | ACTAAAAACTGACTGCTACGGCAGAGATCA |

Questionable CRISPRS

Recurrent motif

DR: TGATTGAGAAGTCAGTCGAAAAAC

DR length: 24

Spacer sequence

TATTGCAAAAGAAAAACGATTATGTATAATAAAGTTATAAAT

Spacer length: 42