

## Supplementary Material: Overview of putative CRISPR sequences

Direct repeats are shown in yellow and spacers are marked in grey. Blast hits to similar sequences in the Direct Repeats and Spacer databases [1,2] are shown below each sequence (e-value cut-off 0.01).

### >5-SewaE-CRISPR\_1

TCCGTAGCCTTCTAAGTGAAGCCGCAAGTAATCTCGGAGAGAAATCAAACCTCTCAGAAATC  
ATTGCAAAGTATCTTAACCTTAAGGTACAAGAACAACCACAAGCAGGTGGGCAAGAAGGCG  
GTGGAGAAGGTGGAATGCCAGACTTGCCTTCTCTATTGGGTGGACAAGCAGGTGGGCAGGAA  
GGCGATCAAGAAACCGGTGGACAGGAAGCACAAACAAGTGATGAATCTCAGAAATTCC  
TCGAACAGGCTTTGGCTCCGGGACTAGGTGAAACCGTCCCGGA

No hit to direct repeat database and spacer database.

### >5-SewaE-CRISPR\_2

GATTGTTCTTTGAAAAGTTATTGATAAATGTTTCATCTCATCATGGGTTGCGGAAACGTGAAA  
ATAAACCCGTGATTATCAAGGCCTTAAGTGGCCTACC GTTGCGCCCCGCAGGGGCGCATGAA  
TTGAAACCTGTTTGGGCGATGCTTGGGGCATTCAACCGGA GTTGCGCCCCGCAGGGGCGCAT  
GAATTGAAACACAAACGCGCCGTATGTGCATCTGCTTCCAC GTTGCGCCCCGCAGGGGCGC  
ATGAATTGAAACACAGGCAATACAGACAAGCCGGTGAAGCACAAAGAA GTTGCGCCCCGCAG  
GGGCGCATGAATTGAAACGAAAAACGCCGGATATACATCTCTAAAAAGACA GTTGCGCCCCG  
CAGGGGCGCATGAATTGAAACAGGTTCTCCGGGGTTGGGAACGTCAGATGTGCGAGTTGCGC  
CCCGCAGGAGCGCATGAATTGAAAC TGTGTTACAAATCCCAAATCCCTTTAAGATCCTGTTG  
CGCCCCGCAGGGGCGCATGAATTGAAACAGGCAAGCGCAATTCAATTGGCAGAAGCCTACT  
TGAAGGCAAAATGGAATGGAAGGATTAAGATGAACAATGTTCAAATTTGTGAACACCACC  
TGTTCT

Direct repeats 1 - 6:

CAS-Type I-C with 93% identity to CRISPR locus CP015249\_6

Direct repeat 7:

CAS-Type I-C with 93% identity to CRISPR locus CP015249\_4

No hit for spacers.

### >6-SewaF-CRISPR\_1

GAACATCTTATCACAGTGGACACATTACCGCCACCAACCCGGTGGCCCCCTCGCAAAGCCAG  
GACGACACTTCTGATTTACAATCAGTTACAGAGATACTCTAGCAGTACCCAAGTAAATTTCAA  
GGTAATGCGAGCAAACGGATGCTGGCCTATTCCAGCGTCGAGCACATGCTAGCAGTACCCAA  
GTAAATTTCAAGGTAATGCGAGTCCCTGGATTATTGCGAGCCGTCGATGCCCCAGAACTAGC  
AGTACCCAAGTAAATTTCAAGGTAATGCGAGGTATAAATGGGAGACGGATAAAATTATCGAA  
AAGGTGCTAGCAGTGCCCAAGTAAATTTCAAGGTAATGCGAGAAGATGTCTCTCGCAGGTTTT  
ATAAGAAACGGGACACTAGCAGTACCCAAGTAAATTTCAAGGTAATGCGGGCAGCACCTGG  
CTGAGCACCGTGCGACTGGGAAGAATAATTTATTACTATGAATAAATTTCAAAATGCAATAGA  
TATAATTAAACAATTAACCATTAACA

No hit to direct repeat database and spacer database.

>6-SewaF-CRISPR\_2

CCGGTGGCGGCATCTTTTAAAGTTACGTAGGAAGGTTCCGGTGGTGTACCTAGCCGGTTAACT  
TTCCATAATAATGTGCTAATTTTTTCATCTTTCTCATACACTTCACTTTTTAGTTCGTTTGGGCG  
TTGCAAGATGCAGTTTTTAACACCACACGAGTACGTCCTGTTGGACTCACATCACCTTTTAGTT  
CGTTTGGGCGTTGCGAGCAGCGTATGTTAGTCATGGCGGCACGCCATATAGCGGCTCACATCA  
CCTTTTAGTTCGTTTGGGCGTTGCGAGGGGTTGTAACGTACACCACCATTGGCAATGCTGTC  
ACTCACATCACCTTTTAGTTTCGTTTGGGCGTTGCGAGAGCTTCTCTGTAACGTCCTGTATTGCA  
ATGCCGTCGTCCTGTCTTTGCGAGGGGCCACCGGATTGGTGGCGGTGAATGTGTCCACTGTGA  
TAAGATGTTT

No hit to direct repeat database and spacer database.

>6-SewaF-CRISPR\_3

CATGATAAAGAAGAATTTGAAGATTATCCGGTAGATGCAATGTAAGAGTTGAAATATTAAAA  
TGGGAGTTGACATTTGTGAAAAGTCTGATATAATGAGAGGCGAAAATTGAAATGCCAAAGAA  
AAATTGAAAAAAAAAATCGAAAAAGAGTTGACATTGATTAAGTCTGGTATAATGGTTGG  
CGAAAATTGAAATACCAAAGAAAAATTGGTAAAAAACAAAAATTGAACACTATTTATCTGGTA  
GTATGAGAAATCGATTACAAAAACGGAATAGAGCCGAGGGCGATTGGACGCTCAATAGTAA  
G

No hit to direct repeat database and spacer database.

## References

1. Grissa, I.; Vergnaud, G.; Pourcel, C. CRISPRFinder: A Web Tool to Identify Clustered Regularly Interspaced Short Palindromic Repeats. *Nucleic Acids Res* **2007**, *35*, W52-57, doi:10.1093/nar/gkm360.
2. Couvin, D.; Bernheim, A.; Toffano-Nioche, C.; Touchon, M.; Michalik, J.; Néron, B.; Rocha, E.P.C.; Vergnaud, G.; Gautheret, D.; Pourcel, C. CRISPRCasFinder, an Update of CRISPRFinder, Includes a Portable Version, Enhanced Performance and Integrates Search for Cas Proteins. *Nucleic Acids Res* **2018**, *46*, W246–W251, doi:10.1093/nar/gky425.