

**Table S4. Validation of the CRISPR-Cas systems detection on systems with *in vivo* effects listed in the review by Bondy-Denomy et. al 2014 (Table 1) [1]**

Bacterial species	Type	References	Detection
<i>Campylobacter jejuni</i>	II-C	[2]	YES*
<i>Clostridium difficile</i>	I-B	[3]	YES
<i>Enterococcus</i> sp.	II-A	[4]	YES
<i>Escherichia coli</i>	I-E, I-F	[5-7]	YES
<i>Francisella tularensis</i> subsp. <i>novicida</i>	II-B	[8,9]	YES
<i>Haloferax volcanii</i>	I-B	[10]	YES
<i>Mycoplasma gallisepticum</i>	II	[11]	YES - One II-U detected
<i>Neisseria meningitidis</i>	II-C	[12]	YES*
<i>Pectobacterium atrosepticum</i>	I-F	[13]	YES
<i>Porphyromonas gingivalis</i>	I-C, III-B	[14]	YES
<i>Pseudomonas aeruginosa</i>	I-F	[15,16]	YES
<i>Salmonella enterica</i> serovar Typhimurium	I-E	[17]	YES
<i>Staphylococcus epidermidis</i>	III-A	[18]	YES
<i>Streptococcus agalactiae</i>	II-A	[19]	YES
<i>Streptococcus pyogenes</i>	II-A, I-C	[20,21]	YES
<i>Streptococcus thermophilus</i>	II-A	[22]	YES
<i>Sulfolobus</i> spp.	I-A	[23-25]	YES
<i>Thermococcus kodakarensis</i>	I-A, I-B	[26]	YES
<i>Xanthomonas oryzae</i>	I-C	[27]	YES
<i>Yersinia pestis</i>	I-F	[28]	YES
<i>Erwinia amylovora</i>	I-E	[29]	YES <sup>§</sup>
<i>Lactococcus lactis</i>	III-A	[30]	NA - Plasmids not in our dataset
<i>Leptospirillum</i> group II	III	[31,32]	NA - Environmental sample
<i>Vibrio cholerae</i>	I-F	[33]	NA - <i>V. cholerae</i> variant not in our dataset

NA - Not applicable because the data were not in our genomic dataset; green "Detection" cells mean the systems were detected. \*Type II-C: detected clusters containing only Cas1, Cas2 and Cas9 recently proposed as Type II-C [34]. Because they are difficult to distinguish with degraded Type II-A or Type II-B systems, we preferred classify them as Type II-U (U for unclassified). <sup>§</sup>In the paper by Bondy-Denomy et. al 2014 [1] (Table 1), a type I-F is attributed to *Erwinia amylovora* based on a publication by Rezzonico et. al. 2011 [29]. However in this paper, the Type I-F was described in *E. pyrifoliae* and *tasmaniensis*, not in *E. amylovora* (Figure 1).

## References

1. Bondy-Denomy J, Davidson AR (2014) To acquire or resist: the complex biological effects of CRISPR-Cas systems. *Trends Microbiol* 22: 218-225.
2. Dugar G, Herbig A, Forstner KU, Heidrich N, Reinhardt R, et al. (2013) High-resolution transcriptome maps reveal strain-specific regulatory features of multiple *Campylobacter jejuni* isolates. *PLoS Genet* 9: e1003495.
3. Soutourina OA, Monot M, Boudry P, Saujet L, Pichon C, et al. (2013) Genome-wide identification of regulatory RNAs in the human pathogen *Clostridium difficile*. *PLoS Genet* 9: e1003493.
4. Palmer KL, Gilmore MS (2010) Multidrug-resistant enterococci lack CRISPR-cas. *MBio* 1.
5. Almendros C, Guzman NM, Diez-Villasenor C, Garcia-Martinez J, Mojica FJ (2012) Target motifs affecting natural immunity by a constitutive CRISPR-Cas system in *Escherichia coli*. *PLoS ONE* 7: e50797.

6. Touchon M, Charpentier S, Clermont O, Rocha EP, Denamur E, et al. (2011) CRISPR distribution within the *Escherichia coli* species is not suggestive of immunity-associated diversifying selection. *J Bacteriol* 193: 2460-2467.
7. Westra ER, Pul U, Heidrich N, Jore MM, Lundgren M, et al. (2010) H-NS-mediated repression of CRISPR-based immunity in *Escherichia coli* K12 can be relieved by the transcription activator LeuO. *Mol Microbiol* 77: 1380-1393.
8. Schunder E, Rydzewski K, Grunow R, Heuner K (2013) First indication for a functional CRISPR/Cas system in *Francisella tularensis*. *International journal of medical microbiology : IJMM* 303: 51-60.
9. Sampson TR, Saroj SD, Llewellyn AC, Tzeng YL, Weiss DS (2013) A CRISPR/Cas system mediates bacterial innate immune evasion and virulence. *Nature* 497: 254-257.
10. Fischer S, Maier LK, Stoll B, Brendel J, Fischer E, et al. (2012) An archaeal immune system can detect multiple protospacer adjacent motifs (PAMs) to target invader DNA. *The Journal of biological chemistry* 287: 33351-33363.
11. Delaney NF, Balenger S, Bonneaud C, Marx CJ, Hill GE, et al. (2012) Ultrafast evolution and loss of CRISPRs following a host shift in a novel wildlife pathogen, *Mycoplasma gallisepticum*. *PLoS Genet* 8: e1002511.
12. Zhang Y, Heidrich N, Ampattu BJ, Gunderson CW, Seifert HS, et al. (2013) Processing-independent CRISPR RNAs limit natural transformation in *Neisseria meningitidis*. *Mol Cell* 50: 488-503.
13. Vercoe RB, Chang JT, Dy RL, Taylor C, Gristwood T, et al. (2013) Cytotoxic chromosomal targeting by CRISPR/Cas systems can reshape bacterial genomes and expel or remodel pathogenicity islands. *PLoS Genet* 9: e1003454.
14. Watanabe T, Nozawa T, Aikawa C, Amano A, Maruyama F, et al. (2013) CRISPR regulation of intraspecies diversification by limiting IS transposition and intercellular recombination. *Genome Biol Evol* 5: 1099-1114.
15. Cady KC, Bondy-Denomy J, Heussler GE, Davidson AR, O'Toole GA (2012) The CRISPR/Cas adaptive immune system of *Pseudomonas aeruginosa* mediates resistance to naturally occurring and engineered phages. *J Bacteriol* 194: 5728-5738.
16. Bondy-Denomy J, Pawluk A, Maxwell KL, Davidson AR (2013) Bacteriophage genes that inactivate the CRISPR/Cas bacterial immune system. *Nature* 493: 429-432.
17. Medina-Aparicio L, Rebollar-Flores JE, Gallego-Hernandez AL, Vazquez A, Olvera L, et al. (2011) The CRISPR/Cas immune system is an operon regulated by LeuO, H-NS, and leucine-responsive regulatory protein in *Salmonella enterica* serovar Typhi. *J Bacteriol* 193: 2396-2407.
18. Marraffini LA, Sontheimer EJ (2008) CRISPR interference limits horizontal gene transfer in staphylococci by targeting DNA. *Science* 322: 1843-1845.
19. Lopez-Sanchez MJ, Sauvage E, Da Cunha V, Clermont D, Ratsima Hariniaina E, et al. (2012) The highly dynamic CRISPR1 system of *Streptococcus agalactiae* controls the diversity of its mobilome. *Mol Microbiol* 85: 1057-1071.
20. Deltcheva E, Chylinski K, Sharma CM, Gonzales K, Chao Y, et al. (2011) CRISPR RNA maturation by trans-encoded small RNA and host factor RNase III. *Nature* 471: 602-607.
21. Nozawa T, Furukawa N, Aikawa C, Watanabe T, Haobam B, et al. (2011) CRISPR inhibition of prophage acquisition in *Streptococcus pyogenes*. *PLoS ONE* 6: e19543.
22. Barrangou R, Fremaux C, Deveau H, Richards M, Boyaval P, et al. (2007) CRISPR provides acquired resistance against viruses in prokaryotes. *Science* 315: 1709-1712.
23. Manica A, Zebec Z, Teichmann D, Schleper C (2011) In vivo activity of CRISPR-mediated virus defence in a hyperthermophilic archaeon. *Mol Microbiol* 80: 481-491.
24. Gudbergsdottir S, Deng L, Chen Z, Jensen JV, Jensen LR, et al. (2011) Dynamic properties of the *Sulfolobus* CRISPR/Cas and CRISPR/Cmr systems when challenged with vector-borne viral and plasmid genes and protospacers. *Mol Microbiol* 79: 35-49.
25. Erdmann S, Garrett RA (2012) Selective and hyperactive uptake of foreign DNA by adaptive immune systems of an archaeon via two distinct mechanisms. *Mol Microbiol* 85: 1044-1056.
26. Elmore JR, Yokooji Y, Sato T, Olson S, Glover CV, 3rd, et al. (2013) Programmable plasmid interference by the CRISPR-Cas system in *Thermococcus kodakarensis*. *RNA Biol* 10: 828-840.
27. Semenova E, Nagorniykh M, Pyatnitskiy M, Artamonova, II, Severinov K (2009) Analysis of CRISPR system function in plant pathogen *Xanthomonas oryzae*. *FEMS Microbiol Lett* 296: 110-116.
28. Cui Y, Li Y, Gorge O, Platonov ME, Yan Y, et al. (2008) Insight into microevolution of *Yersinia pestis* by clustered regularly interspaced short palindromic repeats. *PLoS ONE* 3: e2652.
29. Rezzonico F, Smits TH, Duffy B (2011) Diversity, evolution, and functionality of clustered regularly interspaced short palindromic repeat (CRISPR) regions in the fire blight pathogen *Erwinia amylovora*. *Appl Environ Microbiol* 77: 3819-3829.

30. Millen AM, Horvath P, Boyaval P, Romero DA (2012) Mobile CRISPR/Cas-mediated bacteriophage resistance in *Lactococcus lactis*. *PLoS ONE* 7: e51663.
31. Tyson GW, Banfield JF (2008) Rapidly evolving CRISPRs implicated in acquired resistance of microorganisms to viruses. *Environ Microbiol* 10: 200-207.
32. Andersson AF, Banfield JF (2008) Virus population dynamics and acquired virus resistance in natural microbial communities. *Science* 320: 1047-1050.
33. Seed KD, Lazinski DW, Calderwood SB, Camilli A (2013) A bacteriophage encodes its own CRISPR/Cas adaptive response to evade host innate immunity. *Nature* 494: 489-491.
34. Chylinski K, Le Rhun A, Charpentier E (2013) The tracrRNA and Cas9 families of type II CRISPR-Cas immunity systems. *RNA Biol* 10: 726-737.