

Figure S1. Integration-dependent immunity systems. Sequences are shown for phage (phiGDxx) and prophage (prophiGDxx) sequences at the 3' ends of the repressor genes; if the phage sequence is reconstructed from the prophage sequence it is designated in apostrophes. The amino acid sequence of the repressor is highlighted in green, and tRNA genes in grey shading. Common core sequences are underlined. Integrative recombination occurs within the repressor coding region, giving rise to a C-terminally truncated repressor expressed from the prophage. For MabH with example of prophiGD36-2 we show the sequences of *attL* and *attR* and deduced *attB* and *attP* sequences, highlighting changes in DNA and amino acid sequences.

Figure S2. Genome organization of prophiGD17-2, Cluster MabA1. Genome organization of prophiGD17-2 (MabA1). The prophage prophiGD17-2 genome is represented with predicted genes shown as boxes either above or below the genome indicating rightward- and leftward-transcription, respectively, with gene numbers in each gene box. Family designations are shown above or below each gene with the numbers of family members in parentheses; genes are colored according to the family designations. White boxes represent 'orphans', genes with no close relatives in this dataset. Family assignments were determined using Phamerator and database Actino_prophage (version 5). Predicted gene functions are indicated. The prophage is represented from *attL* to *attR*.

Figure S3. Genome comparisons of Cluster MabA1. See Fig. S2 for details. Spectrum-colored shading between genomes indicated nucleotide sequence similarity determined by BlastN with violet being the most similar, and red the least similar but above a threshold E value of 10^{-4} .

Figure S4. Genome organization of prophiGD02-2, Cluster MabA2. See Fig. S2 for details.

Figure S5. Genome comparisons of Cluster MabA2. See Figs. S2 and S3 for details.

Figure S6. Genome organization of prophiGD91-2, Cluster MabA3. See Fig. S2 for details.

Figure S7. Genome organization of prophigD08-2, Cluster MabB. See Fig. S2 for details.

Figure S8. Genome comparisons of Cluster MabB. See Figs. S2 and S3 for details.

Figure S9. Genome organization of prophigD57-1, Cluster MabC. See Fig. S2 for details.

Figure S10. Genome comparisons of Cluster MabC. See Figs. S2 and S3 for details.

Figure S11. Genome organization of prophigD12-2, Cluster MabD. See Fig. S2 for details.

Figure S12. Genome comparisons of Cluster MabD. See Figs. S2 and S3 for details.

Figure S13. Genome organization of prophigD25-1, Cluster MabE1. See Fig. S2 for details.

Figure S14. Genome comparisons of Cluster MabE1. See Figs. S2 and S3 for details.

Figure S15. Genome organization of prophigD91-4, Cluster MabE2. See Fig. S2 for details.

Figure S16. Genome organization of prophigD11-3, Cluster MabF. See Fig. S2 for details.

Figure S17. Genome comparisons of Cluster MabF. See Figs. S2 and S3 for details.

Figure S18. Genome organization of prophigD21-3, Cluster MabG. See Fig. S2 for details.

Figure S19. Genome comparisons of Cluster MabG. See Figs. S2 and S3 for details.

Figure S20. Genome organization of prophigD36-2, Cluster MabH. See Fig. S2 for details.

Figure S21. Genome comparisons of Cluster MabH. See Figs. S2 and S3 for details.

Figure S22. Genome organization of prophigD54-2, Cluster Mabl. See Fig. S2 for details.

Figure S23. Genome organization of prophigD24-3, Cluster MabJ. See Fig. S2 for details.

Figure S24. Genome organization of prophigD43A-5, Cluster MabK. See Fig. S2 for details.

Figure S25. Genome organization of prophigD43A-6, Cluster MabL. See Fig. S2 for details.

Figure S26. Genome comparisons of Cluster MabL. See Figs. S2 and S3 for details.

Figure S27. Genome organization of prophigD05-3, Cluster MabM. See Fig. S2 for details.

Figure S28. Genome organization of prophigD62-3, Cluster MabN. See Fig. S2 for details.

Figure S29. Genome comparisons of Cluster MabN. See Figs. S2 and S3 for details.

Figure S30. Genome organization of prophigD91-3, Cluster MabO. See Figs. S2 for details.

Figure S31. Genome organization of prophigD51-2, Cluster MabP. See Figs. S2 for details.

Figure S32. Genome organization of prophigD79-1, Cluster MabQ. See Figs. S2 for details.

Figure S33. Genome organization and comparisons of Cluster pA plasmids. Linear representations of Cluster pA plasmid genomes are represented with predicted genes shown as boxes either above or below the genome indicating rightward- and leftward-transcription, respectively, with gene numbers in each gene box. Phamily designations are shown above or below each gene with the numbers of phamily members in parentheses; genes are colored according to the phamily designations. White boxes represent 'orphams', genes with no close relatives in this dataset. Phamily assignments were determined using Phamerator and database 'Abscessus_plasmids' (version 6). Predicted gene functions are indicated. Spectrum-colored shading between genomes indicated nucleotide sequence similarity determined by BlastN with violet being the most similar, and red the least similar but above a threshold E value of 10^{-4} .

Figure S34. Genome organization of plasmid pGD18, Cluster pB. See Fig. S2 for details.

Figure S35. Genome organization and comparisons of Cluster pB plasmids. See Fig. S33 for details.

Figure S36. Genome organization and comparisons of Cluster pC plasmids. See Fig. S33 for details.

Figure S37. Genome organization and comparisons of Cluster pD plasmids. See Fig. S33 for details.

Figure S38. Genome organization and comparisons of Cluster pE plasmids. See Fig. S33 for details.

Figure S39. Genome organization and comparisons of Cluster pF plasmids. See Fig. S33 for details.

Figure S40. Genome organization of plasmid pGD25-2, Cluster pG. See Fig. S33 for details.

Figure S41. Genome organization and comparisons of Cluster pG plasmids. See Fig. S33 for details.

Figure S42. Genome organization of plasmid pGD58, Cluster pH. See Fig. S33 for details.

Figure S43. Genome organization of plasmid pATCC19977, singleton. See Fig. S33 for details.

Figure S44. Genome organization of plasmid pGD13, singleton. See Fig. S33 for details.

Figure S45. Genome organization of plasmid pGD21-1, singleton. See Fig. S33 for details.

Figure S46. Genome organization of plasmid pGD21-2, singleton. See Fig. S33 for details.

Figure S47. Genome organization of plasmid pGD22-1, singleton. See Fig. S33 for details.

Figure S48. Genome organization of plasmid pGD25-3, singleton. See Fig. S33 for details.

Figure S49. Genome organization of plasmid pGD51, singleton. See Fig. S33 for details.

Figure S50. Genome organization of plasmid pGD52, singleton. See Fig. S2 for details.

Figure S51. Genome organization of plasmid pGD104, singleton. See Fig. S2 for details.