**Description of the Supplementary files from Shehreen et al 2018**

**1. Figure S1 Shehreen et al 2018 ARG\_CRISPRTarget.pdf**

**CRISPRTarget Output.** The output indicates whether the acquired resistance genes are targeted by the CRISPR spacers from different *Pseudomonas aeruginosa* genomes. The targets were analysed by using the default parameters of the web version of CRISPRTarget, but with a spacer match score: match reward +2, and mismatch penalty -1

**2. Document S1 Shehreen et al 2018 CRISPR\_cas\_acr.docx**

Table 1 and Table 2: Distribution of CRISPR, *cas* and anti-CRISPR in representative and all bacterial genomes

The table describes the distribution of CRISPR arrays, *cas* genes and anti-CRISPR (*acr)* genes in the tested bacterial genomes. The tables are generated from the raw data and **Figure 2** in the main paper is based on these tables.

**3. Table S2 Shehreen et al 2018 ARG\_CRISPR\_Cas.csv**

**Association of CRISPR-Cas with Acquired resistance in tested bacterial species:** The table is composed of all the raw statistical data we used to generate heat map of **Figure 3.** The header denotes as following:

ARG\_Name: Antibiotic Class

SPECIES: Scientific name of the corresponding bacterial species

GENOMES: Number of genomes of that particular species were analysed

ARG: Number of genomes resistant to specific drug class

NO CRISPR-Cas: Number of genomes having no CRISPR-Cas

BOTH CRISPR-Cas and ARG: Number of genomes with CRISPR-Cas and antibiotic resistance

EXCLUSION OBS (ARG not CRISPR-Cas): Observed number of genomes with resistance but not CRISPR-Cas

EXCLUSION EXP (ARG not CRISPR-Cas): Expected number of genomes with resistance but not CRISPR-Cas

EXCLUSION OBS (ARG not CRISPR-Cas) +PSC: Observed number of genomes with resistance but not CRISPR-Cas+ pseudo count

EXCLUSION EXP (ARG not CRISPR-Cas) + PSC: Expected number of genomes with resistance but not CRISPR-Cas + Pseudo count

OE: observed no. of genomes/expected no. of genomes

LOG\_OE: log of observed no. of genomes/expected no. of genomes

LOG\_OE\_CAT: category of log of observed no. of genomes/expected no. of genomes

QTL\_0005 and QTL\_9995: Quartile

SIG: Significance

CRISPR-Cas (%): Proportion of genomes with CRISPR-Cas for that particular species

**4. Table S3 Shehreen et al 2018 PA\_AB\_Mutation.csv**

**Association of CRISPR-Cas and Anti-CRISPR with Point Mutations in *Pseudomonas aeruginosa***: The table was generated by merging the output of the command line version of Resistance Gene Identifier (RGI v 3.2.1), anti-CRISPR, and CRISPR-Cas data of *Pseudomonas aeruginosa* genomes (2021). Then, the statistical calculation was performed.

ARG\_NAME: Antibiotic Class

SPECIES: Scientific name of the corresponding bacterial species

COEXIT\_WITH: The tested association (CRISPR-Cas & resistance or Anti-CRISPR and resistance)

GENOMES: Number of genomes of that particular species were analysed

ARG: Number of genomes resistant to specific drug class

NO CRISPR-Cas: Number of genomes having no CRISPR-Cas

BOTH ARG and Acr/CRISPR-Cas: Number of genomes with Anti-CRISPR/ CRISPR-Cas and antibiotic resistance

OBS (ARG and ACR/CRISPR-Cas): Observations with ARG and Anti-CRISPR/CRISPR-Cas

EXP (BOTH ARG and ACR/CRISPR-Cas): Expected number of genomes with resistance and anti-CRISPR/ CRISPR-Cas

OBS (Both ARG and Acr/CRISPR-Cas) + PSC: Observations with ARG and Anti-CRISPR/CRISPR-Cas + pseudo count

EXP (Both ARG and CRISPR-Cas/ACR) +PSC: Expected number of genomes with resistance and anti-CRISPR/ CRISPR-Cas + pseudo count

OE: observed no. of genomes/expected no. of genomes

LOG\_OE: log of observed no. of genomes/expected no. of genomes

LOG\_OE\_CAT: category of log of observed no. of genomes/expected no. of genomes

QTL\_0005 and QTL\_9995: Quartile

**5. Table S4 Shehreen et al 2018 PA\_spacer\_target\_ARG.csv**

Blastn result to detect potential targets within ARGs of the CRISPR spacers (Details are in Methods section)

**6. Table S5 Shehreen et al 2018 ARG\_database.xlsx**

The resistance genes database were downloaded from ResFinder (v 2.1) and Resistance Gene Identifier (RGI v 3.2.1). These were used to detect resistance genes of the tested genomes.

**7. Table S6 Shehreen et al 2018 CRISPR\_target\_results.txt**

This text file contains the outputs generated by CRISPRTarget. The targets (acquired resistance genes) of different *Pseudomonas aeruginosa* spacers were analysed by using the default parameters of web version of CRISPRTarget, but with a spacer match score: match reward +2, and mismatch penalty -1.

**8. Table S7 Shehreen et al 2018 ARG\_ACR.csv**

**Association of Anti-CRISPR with ARG.** The table is composed of all the raw statistical data we used to generate heat map of **Figure 4.** The header denotes as following:

ARG\_Name: Antibiotic Class

SPECIES: Scientific name of the corresponding bacterial species

GENOMES: Number of genomes of that particular species were analysed

ARG: Number of genomes resistant to specific drug class

ACR: Number of genomes having Anti-CRISPR

BOTH ACR and ARG: Number of genomes with Anti-CRISPR and antibiotic resistance

EXP (ARG and ACR): Expected number of genomes with resistance and Anti-CRISPR

OBS (ARG and ACR): Observed number of genomes with resistance and Anti-CRISPR

OBS (ARG and ACR) +PSC: Observed number of genomes with anti-CRISPR and resistance + pseudo count

EXP (ARG and ACR) + PSC: Expected number of genomes with anti-CRISPR and resistance + Pseudo count

OE: observed no. of genomes/expected no. of genomes

LOG\_OE: log of observed no. of genomes/expected no. of genomes

LOG\_OE\_CAT: category of log of observed no. of genomes/expected no. of genomes

QTL\_0005 and QTL\_9995: Quartile

SIG: Significance

GENOME with ACR (%): Proportion of genomes with Anti-CRISPR for that particular species

**9. Table S8 Shehreen et al 2018 ARG\_CRISPR-Cas\_Acr\_pseudomonas.docx**

Table S8 refers the distribution of different types resistance (both acquired and point mutation mediated) among CRISPR-Cas and anti-CRISPR containing *Pseudomonas aeruginosa*. The table is generated from S3 and S7.

**10. Table S9 Shehreen et al 2018 anti-CRISPR list.csv**

Table S9 provides a summary table of anti-CRISPR sequences which we used as query of anti-CRISPR search (details in the Methods section)

**11. Table S10 Shehreen et al 2018 Shehreen et al 2018 S10 Summary\_blast\_anti-CRISPR.xlxs**

Table S10 provides a summary table showing which anti-CRISPR protein sequence was used as a query, how many hits there were, and which species the anti-CRISPR homologues were found for both 104947 genomes and 5677 representative genomes. The table is generated from the raw data table provided at github (https://github.com/davidchyou).