

## **Description of Additional Supplementary Files:**

**Supplementary Data 1:** Sample metadata, also containing SRA run accessions of generated sequencing data.

**Supplementary Data 2:** Detailed information on assembled phage genomes, also including GenBank accessions, where applicable.

**Supplementary Data 3:** Results of pairwise Wilcoxon ranked sum tests on alpha diversities presented in Figure 5a and Supplementary Fig. 5a.

**Supplementary Data 4:** Detailed results of linear mixed-effects models (log relative PAPS reductase abundance vs. land use parameters).

**Supplementary Data 5:** Detailed results of logistic mixed-effects models (PAPS reductase presence vs. land use parameters).

**Supplementary Data 6:** Detailed results of linear mixed-effects models (pathogen Ct vs. land use parameters).

**Supplementary Data 7:** Detailed results of logistic mixed-effects models (pathogen presence vs. land use parameters).

**Supplementary Data 8:** Complete list of SRA run accessions for previously-generated data downloaded for this study.

**Supplementary Data 9:** Complete list of GenBank accessions for core bacterial genomes downloaded for this study.

**Supplementary Data 10:** Cropland area and estimated pesticide use around the sampling sites.