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**Supplemental information**

**Structural basis for the assembly  
of the type V CRISPR-associated transposon complex**

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**Table S1 | Cryo-EM data collection, refinement and validation statistics for Cas12k-transposon and TnsC-TniQ complexes, related to Figure 1, S1, S2, S5 and STAR Methods**

| Sample                                           | Cas12k-sgRNA-dsDNA-S15-TniQ-TnsC transposon recruitment complex (EMDB- 15975) (PDB 8BD5) | Cas12k-sgRNA-dsDNA-TnsC non-productive complex (EMDB- 15976) (PDB 8BD6) | TniQ-capped Tns-ATP-dsDNA complex (EMDB- 15974) (PDB 8BD4) |
|--------------------------------------------------|------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------------------|
| <b>Data collection and processing</b>            |                                                                                          |                                                                         |                                                            |
| Magnification                                    | 130,000                                                                                  | 130,000                                                                 | 130,000                                                    |
| Voltage (kV)                                     | 300                                                                                      | 300                                                                     | 300                                                        |
| Electron exposure (e-/Å <sup>2</sup> )           | 67.68                                                                                    | 67.68                                                                   | 66.036                                                     |
| Defocus range (µm)                               | -1.0 to -2.4 (0.2 steps)                                                                 | -1.0 to -2.4 (0.2 steps)                                                | -1.0 to -2.4 (0.2 steps)                                   |
| Pixel size (Å)                                   | 0.325                                                                                    | 0.325                                                                   | 0.325                                                      |
| Symmetry imposed                                 | C1                                                                                       | C1                                                                      | C1                                                         |
| Initial particle images (no.)                    | 3,074,932                                                                                | 3,074,932                                                               | 974,175                                                    |
| Final particle images (no.)                      | 75,146                                                                                   | 132,706                                                                 | 35,964                                                     |
| Map resolution (Å)                               | 3.28                                                                                     | 4.05                                                                    | 3.48                                                       |
| FSC threshold                                    | 0.143                                                                                    | 0.143                                                                   | 0.143                                                      |
| Map resolution range (Å)                         | 2.9-8.0                                                                                  | 3.6-10.0                                                                | 3.4-7.5                                                    |
| <b>Refinement</b>                                |                                                                                          |                                                                         |                                                            |
| Initial model used (PDB code)                    | 7PLA & 7PLH                                                                              | 7PLA & 7PLH                                                             | 7OXD & 7PLH                                                |
| Model resolution (Å)                             | 2.8                                                                                      | 4.8                                                                     | 3.5                                                        |
| FSC threshold                                    | 0.143                                                                                    | 0.143                                                                   | 0.143                                                      |
| Map sharpening <i>B</i> factor (Å <sup>2</sup> ) | -66.4                                                                                    | -109.3                                                                  | -47.3                                                      |
| Model composition                                |                                                                                          |                                                                         |                                                            |
| Non-hydrogen atoms                               | 28398                                                                                    | 29954                                                                   | 18984                                                      |
| Protein residues                                 | 2671                                                                                     | 2900                                                                    | 2285                                                       |
| Nucleotide residues                              | 328                                                                                      | 313                                                                     | 32                                                         |
| Ligands                                          | Zn:2, MG:7, ATP:7                                                                        | MG:9, ATP:9                                                             | Zn:6, MG:7, ATP:7                                          |
| <i>B</i> factors (Å <sup>2</sup> ) min/max/mean  |                                                                                          |                                                                         |                                                            |
| Protein                                          | 2.59/417.21/192.38                                                                       | 221.36/1095.42/538.71                                                   | 30.00/428.64/201.00                                        |
| Nucleotide                                       | 27.99/492.05/140.60                                                                      | 291.37/1095.42/569.01                                                   | 30.00/30.00/30.00                                          |
| Ligand                                           | 134.66/296.99/240.87                                                                     | 393.41/836.92/487.91                                                    | 30.00/299.56/234.94                                        |
| R.m.s. deviations                                |                                                                                          |                                                                         |                                                            |
| Bond lengths (Å)                                 | 0.008                                                                                    | 0.013                                                                   | 0.005                                                      |
| Bond angles (°)                                  | 0.692                                                                                    | 1.662                                                                   | 1.054                                                      |
| Validation                                       |                                                                                          |                                                                         |                                                            |
| MolProbity score                                 | 1.90                                                                                     | 2.57                                                                    | 2.05                                                       |
| Clashscore                                       | 16.11                                                                                    | 20.79                                                                   | 30.40                                                      |
| Poor rotamers (%)                                | 0.36                                                                                     | 8.44                                                                    | 0.64                                                       |
| Ramachandran plot                                |                                                                                          |                                                                         |                                                            |
| Favored (%)                                      | 96.87                                                                                    | 97.77                                                                   | 97.62                                                      |
| Allowed (%)                                      | 3.13                                                                                     | 2.23                                                                    | 2.38                                                       |
| Disallowed (%)                                   | 0.00                                                                                     | 0.00                                                                    | 0.00                                                       |
| Ramachandran Z score                             |                                                                                          |                                                                         |                                                            |
| whole                                            | 0.09                                                                                     | -2.08                                                                   | -0.08                                                      |
| helix                                            | 0.96                                                                                     | -0.84                                                                   | 0.57                                                       |
| sheet                                            | -1.61                                                                                    | -1.86                                                                   | -1.90                                                      |
| loop                                             | -1.04                                                                                    | -2.04                                                                   | -0.68                                                      |