**Figure S1** The distribution of viral auxiliary CAZyme genes in each sample, including 59 CAZyme genes.



**Figure S2** The distribution **(A)** and maximum likelihood tree **(B)** of integrase genes carried by viruses under three precipitation gradients. The tree was bootstrapped with 1000 sub-replicates, and bootstrap scores > 50% are flagged with circles. The vOTU of soil across LP, MP and HP are coloured in yellow, blue and pink, respectively. ****

**Table S1** Sampling site location and description.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sample** | **Longitude** | **Latitude** | **Annual**  **precipitation** | **Altitude**  **/m** | **Land use** |
| LP\_32 | 98°00′01.581″ | 35°54′47.209″ | <200 mm | 3161 | Grassland |
| LP\_34 | 97°05′3758.789″ | 36°21′02.604″ | <200 mm | 2700 | Grassland |
| LP\_35 | 96°41′13.691″ | 36°21′12.862″ | <200 mm | 2723 | Grassland |
| LP\_36 | 95°22′28.430″ | 36°21′18.926″ | <200 mm | 2816 | Grassland |
| MP\_2 | 100°44′49.69″ | 36°21′5.22″ | 200-400 mm | 3171 | Grassland |
| MP\_7 | 98°00′33.062″ | 35°4′39.216″ | 200-400 mm | 4209 | Grassland |
| MP\_27 | 99°52′00.744″ | 36°21′57.728″ | 200-400 mm | 2930 | Grassland |
| MP\_29 | 98°06′22.870″ | 35°42′27.180″ | 200-400 mm | 3422 | Grassland |
| HP\_11 | 100°51′08.621″ | 33°17′26.637″ | >400 mm | 4326 | Grassland |
| HP\_15 | 102°07′26.130″ | 34°30′11.623″ | >400 mm | 3272 | Grassland |
| HP\_17 | 101°19′10.096″ | 34°34′58.982″ | >400 mm | 3422 | Grassland |
| HP\_22 | 101°41′29.806″ | 32°50′10.422″ | >400 mm | 3598 | Grassland |

**Table S2** Prediction of viral-host linkages in soil under three precipitation gradients.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Annual precipitation | Sample | Viral contig  number | Length /kb | Host\_id | Host\_genus | Predict\_signal | Overall\_score |
| < 200 mm | LP\_32 | 349 | 46314 | NZ\_BCQS01000026; NZ\_JNYE01000089 | *Actinomadura*; *Kitasatospora* | crispr | 1 |
|  |  | 346 | 10193 | NZ\_CP020567; CP023407; CP029254; NZ\_CP016825; NZ\_CP015726; NZ\_CP021744; NZ\_CP010519; CP029601; NZ\_CP023992; NZ\_LT963352; CP031455; LT962942; NZ\_CP031455; CP033073; CP033071; LT963352; NZ\_CP029254; NZ\_LT962942; CP034587 | *Kitasatospora*; *Streptomyces* | blast | 1 |
|  |  | 351 | 10874 | NZ\_AMXA01000002 | *Thauera* | crispr | 1 |
|  | LP\_35 | 467 | 19500 | NZ\_JDTH01000008 | *Haladaptatus* | crispr | 1 |
| 200-400 mm | MP\_2 | 320 | 11481 | NC\_013929 | *Streptomyces* | blast | 1 |
|  | MP\_7 | 553 | 12807 | NZ\_KI911420; NZ\_AZVW01000049 | *Salinispora* | crispr | 1 |
|  |  | 540 | 11060 | NZ\_FR873693 | *Streptomyces* | crispr | 1 |
|  |  | 545 | 10185 | NZ\_LFML01000079 | *Streptomyces* | crispr | 1 |
|  | MP\_27 | 93 | 64485 | NZ\_AZWY01000006 | *Salinispora* | crispr | 1 |
|  | MP\_29 | 134 | 41823 | CP030031; NZ\_CP030031 | *Acinetobacter* | crispr | 1 |
|  |  | 119 | 10656 | NZ\_CP009798 | *Burkholderia* | crispr | 1 |
|  |  | 209 | 10656 | NZ\_CP009798 | *Burkholderia* | crispr | 1 |
|  |  | 248 | 18076 | CP018911 | *Glycocaulis* | prophage | 1 |
|  |  | 245 | 27658 | NZ\_JAAN01000005 | *Luteimonas* | crispr | 1 |
|  |  | 241 | 53906 | NZ\_KB899093 | *Marinobacterium* | crispr | 1 |
|  |  | 122 | 106518 | NZ\_CP007229; LR214971 | *Mycoplasma* | crispr | 1 |
|  |  | 182 | 165467 | LR214971; NZ\_CP007229 | *Mycoplasma* | crispr | 1 |
|  |  | 259 | 11665 | LR214971 | *Mycoplasma* | crispr | 1 |
|  |  | 100 | 68474 | NZ\_CP007229 | *Mycoplasma* | crispr | 1 |
|  |  | 120 | 38490 | LR214971 | *Mycoplasma* | crispr | 1 |
| Annual precipitation | Sample | Viral contig  number | Length /kb | Host\_id | Host\_genus | Predict\_signal | Overall\_score |
| 200-400 mm | MP\_29 | 97 | 92794 | NZ\_LZQK01000223 | *Pseudomonas* | crispr | 1 |
|  |  | 247 | 18112 | NZ\_KQ089365; NZ\_KQ089406; NZ\_KQ089701; NZ\_GL882852; NZ\_CP011624; NZ\_MPYK01000084; NZ\_MPYL01000018; NZ\_ARRZ01000040; NZ\_JWRK01000001; NZ\_JQDX01000015; NZ\_JQDY01000013; NZ\_LLWB01000118; NZ\_JQCX01000013; NZ\_LXNC01000004; NZ\_AOPN02000190; NZ\_JQCW01000004; NZ\_JRRF01000004; NZ\_FLJW01000005; NZ\_LNHK01000027; NZ\_LNHF01000038; NZ\_LNHE01000037; NZ\_FLIS01000011; NZ\_FLDR01000006; NZ\_LAFX01000003; NZ\_LAFW01000003; NZ\_JXBF01000003; NZ\_CCGZ01000033; NZ\_FLEP01000006; NZ\_LAFV01000003;  NZ\_FLIO01000002; NZ\_FLIM01000003; NZ\_LAFU01000002; NZ\_CCHJ01000296; NZ\_FLEK01000006; NZ\_MPCF01000002; NZ\_FLEL01000005; NZ\_MNAI01000003; NZ\_FLIH01000005; NZ\_CCGX01000012; NZ\_FLEM01000002; NZ\_LJCD01000008; NZ\_FLIE01000005; NZ\_FBRA01000004; NZ\_FLHA01000002; NZ\_CCIL01000001; NZ\_CCHH01000003; NZ\_CCJA01000016; NZ\_CCID01000021; NZ\_CCGB01000034; CP025963; CP036442; CP029582; CP031795; CP023249; CP023839; CP032222; CP024429; CP019160; CP027042; CP024916; NZ\_CP018695; NZ\_CP019160; NZ\_CP024834; NZ\_CP014755; NZ\_CP024429; NZ\_CP012426; NZ\_CP017934; NZ\_CP017985; NZ\_CP021757; NZ\_CP023249; NZ\_CP013322; NZ\_CP025963; NZ\_CP018719; NZ\_CP024458; NZ\_CP029582; NZ\_CP021939; NZ\_CP024916; NZ\_CP024838; NZ\_CP018707; NZ\_CP018701; NZ\_CP015025; NZ\_CP021740; NZ\_CP018713; NZ\_CP023913; NZ\_CP015500; NZ\_CP021944; NZ\_LN824133; NZ\_CP018140; NZ\_CP018686 | *Klebsiella* | crispr | 1 |
|  |  | 118 | 28560 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 115 | 37983 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 117 | 15722 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 94 | 95973 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
| Annual precipitation | Sample | Viral contig  number | Length /kb | Host\_id | Host\_genus | Predict\_signal | Overall\_score |
| 200-400 mm | MP\_29 | 107 | 17806 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 129 | 62268 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 110 | 103350 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 181 | 20342 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 179 | 102212 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 203 | 14926 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 185 | 103327 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 152 | 62485 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 192 | 20935 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
| 1 |  | 149 | 13566 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 156 | 15716 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 169 | 38560 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 190 | 37980 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 274 | 34910 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 304 | 10534 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
|  |  | 281 | 14826 | NZ\_KE557322 | *Rubellimicrobium* | crispr | 1 |
| > 400 mm | MP\_11 | 4 | 45002 | NZ\_CM001475; LR134533 | *Methylomicrobium*; *Neisseria* | crispr | 1 |
|  | MP\_15 | 15 | 35224 | NZ\_LIRL01000794 | *Streptomyces* | crispr | 1 |
|  | MP\_17 | 30 | 34548 | NZ\_CP015606 | Not know | crispr | 1 |
|  | MP\_22 | 74 | 21854 | NZ\_LBHA01000124; NZ\_CP020568 | Kitasatospora | crispr | 1 |
|  |  | 80 | 15134 | NZ\_KK853998 | Kitasatospora | crispr | 1 |
|  |  | 77 | 32919 | NZ\_AZWL01000023 | Streptomyces | crispr | 1 |

**Table S3** Physical and chemical properties.

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample | LP\_32 | LP\_34 | LP\_35 | LP\_36 | MP\_2 | MP\_7 | MP\_27 | MP\_29 | HP\_11 | HP\_15 | HP\_17 | HP\_22 |
| Average annual precipitation | < 200 mm | < 200 mm | < 200 mm | < 200 mm | 200-400 mm | 200-400 mm | 200-400 mm | 200-400 mm | > 400 mm | > 400 mm | > 400 mm | > 400 mm |
| SWC (%) | 6.9±0.5 | 12.8±1.1 | 1.4±0.3 | 1.0±0.1 | 11.8±0.2 | 9.8±0.1 | 2.7±0.5 | 29.5±1.2 | 49.8±0.6 | 41.7±1.9 | 39.1±1.4 | 55.8±4.4 |
| pH | 8.7±0.1 | 8.5±0.1 | 8.5±0.1 | 8.4±0.1 | 8.1±0.0 | 8.2±0.0 | 8.6±0.1 | 8.5±0.1 | 5.8±0.0 | 6.8±0.2 | 7.4±0.1 | 5.6±0.0 |
| EC (μS/cm) | 117±9 | 19093±  2100 | 39420±  16011 | 5485±  2624 | 169±8 | 122±5 | 73±6 | 2936±376 | 95±3 | 100±16 | 131±6 | 90±14 |
| TC (g/kg) | 22.0±1.5 | 20.0±1.0 | 15.9±1.6 | 13.1±0.6 | 31.4±0.2 | 21.1±0.1 | 11.1±0.3 | 21.9±1.4 | 51.0±1.4 | 33.9±2.3 | 34.1±1.2 | 61.2±3.5 |
| TN (g/kg) | 0.5±0.1 | 0.4±0.0 | 0.5±0.0 | 0.1±0.0 | 2.0±0.1 | 0.9±0.0 | 0.4±0.0 | 0.6±0.1 | 4.7±0.1 | 3.3±0.2 | 3.1±0.1 | 5.5±0.2 |
| C/N | 48.3±9.4 | 58.2±3.3 | 35.2±6.1 | 155.3±27.7 | 16.1±0.8 | 24.4±0.5 | 29.9±1.5 | 41.3±6.0 | 11.0±0.1 | 10.4±0.2 | 11.1±0.2 | 11.2±0.2 |
| SOM (g/kg) | 10.9±2.9 | 12.9±0.6 | 19.3±4.8 | 3.3±0.8 | 33.2±0.6 | 19.1±0.7 | 9.0±0.4 | 14.2±1.9 | 87.3±1.8 | 59.1±3.9 | 58.6±2.1 | 104.0±5.5 |
| TP (g/kg) | 6.1±0.1 | 0.4±0.0 | 5.5±0.2 | 4.8±0.2 | 5.8±0.1 | 3.4±0.0 | 2.7±0.1 | 6.0±0.1 | 10.2±0.1 | 7.8±0.1 | 6.9±0.1 | 10.3±0.1 |
| NH4+-N (mg/kg) | 14.7±0.6 | 14.1±0.9 | 50.0±12.7 | 18.9±3.0 | 16.1±2.0 | 11.4±1.0 | 11.6±2.8 | 10.4±3.3 | 13.7±0.8 | 17.4±1.3 | 8.4±1.4 | 19.3±2.1 |
| NO3--N (mg/kg) | 17.8±3.9 | 78.4±33.1 | 721.6±313.3 | 325.6±214.8 | 79.9±42.7 | 84.4±20.6 | 21.1±6.1 | 22.5±15.4 | 179.1±13.6 | 93.0±2.8 | 93.9±10.5 | 170.0±22.3 |

**TABLE S4** Integrase gene annotation of metagenome.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| vOTU | Kegg\_id | Kegg\_hit | Viral\_id | Viral\_hit | Pfam\_hits | Vogdb\_description |
| 15\_S1\_k57\_5168085\_flag\_0\_multi\_55.5672\_len\_44718 | K14059 | integrase | NP\_852561.1 | NP\_852561.1 DNA integration/  recombination/invertion protein  [Bacillus phage phBC6A52] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 15\_S1\_k57\_8941988\_flag\_0\_multi\_15.3233\_len\_24344 | K06400 | site-specific  DNA recombinase | YP\_009950750.1 | YP\_009950750.1 serine integrase  [Mycobacterium phage Leston] | Resolvase, N terminal domain  [PF00239.23]; Recombinase  [PF07508.15] | sp|P03014|PINE\_ECOLI Serine recombinase PinE; Xr |
| 15\_S2\_k57\_8135724\_flag\_3\_multi\_12.9942\_len\_47262 | K04763 | integrase/recombinase XerD | YP\_009196981.1 | YP\_009196981.1 integrase/Rec-ombinase [Bacillus phage Stills] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 22\_S1\_k57\_6559383\_flag\_1\_multi\_11.5133\_len\_30737 | K06400 | site-specific DNA recombinase | YP\_009950844.1 | YP\_009950844.1 serine integrase  [Mycobacterium phage Paola] | Resolvase, N terminal domain  [PF00239.23]; Recombinase  [PF07508.15] | sp|P03014|PINE\_ECOLI Serine recombinase PinE; Xr |
| 27\_S1\_k57\_4090296\_flag\_0\_multi\_12\_8346\_len\_10309-cat\_2 | K14059 | integrase | NP\_852561.1 | NP\_852561.1 DNA integration/re-combination/invertion protein  [Bacillus phage phBC6A52] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S1\_k57\_3840950\_flag\_0\_multi\_12\_8658\_len\_41823-cat\_2 |  |  |  |  | Phage integrase family [PF00589.24]; Arm DNA-binding domain  [PF13356.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S1\_k57\_6063795\_flag\_1\_multi\_11\_0000\_len\_61403-cat\_2 |  |  | YP\_007237580.1 | YP\_007237580.1 site-specific  Integrase [Cronobacter phage  ENT47670] | Phage integrase family [PF00589.24]; Phage integrase, N-terminal SAM-like domain [PF02899.19]; Phage  integrase, N-terminal SAM-like  domain [PF13495.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| vOTU | Kegg\_id | Kegg\_hit | Viral\_id | Viral\_hit | Pfam\_hits | Vogdb\_description |
| 29\_S1\_k57\_6919927\_flag\_1\_multi\_7.0876\_len\_24440 |  |  |  |  | Phage integrase family [PF00589.24]; Phage integrase, N-terminal SAM-like domain [PF02899.19] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S2\_k57\_1022647\_flag\_0\_multi\_13.6825\_len\_38148 |  |  | YP\_007237580.1 | YP\_007237580.1 site-specific  integrase [Cronobacter phage  ENT47670] | Phage integrase family [PF00589.24]; Phage integrase, N-terminal SAM-  like domain [PF02899.19]; Phage  integrase, N-terminal SAM-like  domain [PF13495.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S2\_k57\_103201\_flag\_0\_multi\_15.4283\_len\_102212 |  |  |  |  | Phage integrase family [PF00589.24] |  |
| 29\_S2\_k57\_1882072\_flag\_1\_multi\_10\_9899\_len\_47535-cat\_2 |  |  | YP\_024945.1 | YP\_024945.1 putative integrase  protein [Burkholderia virus  BcepC6B] | Phage integrase family [PF00589.24]; Arm DNA-binding domain  [PF13356.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S2\_k57\_3207518\_flag\_1\_multi\_9\_0000\_len\_30771-cat\_2 | K14059 | integrase | YP\_001552358.1 | YP\_001552358.1 integrase  [Mycobacterium phage Giles] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S2\_k57\_3590775\_flag\_1\_multi\_21\_6770\_len\_13378-circular-cat\_2 |  |  |  |  | Phage integrase family [PF00589.24]; Arm DNA-binding domain  [PF13356.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S2\_k57\_4504829\_flag\_0\_multi\_65\_8771\_len\_43392-cat\_2 |  |  |  |  |  | sp|P22877|INTR\_SACER Integrase; XhXr |
| 29\_S2\_k57\_8184121\_flag\_0\_multi\_10.6982\_len\_13141 |  |  |  |  | Phage integrase family [PF00589.24] |  |
| 29\_S3\_k57\_2770978\_flag\_0\_multi\_19.0874\_len\_62944 |  |  | YP\_009194162.1 | YP\_009194162.1 putative integrase |  | REFSEQ hypothetical protein; Xu |
| vOTU | Kegg\_id | Kegg\_hit | Viral\_id | Viral\_hit | Pfam\_hits | Vogdb\_description |
| 29\_S3\_k57\_4566374\_flag\_0\_multi\_12.9983\_len\_69651 |  |  |  |  | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 32\_S1\_k57\_8005552\_flag\_0\_multi\_23.1115\_len\_36384 |  |  | YP\_002321479.1 | YP\_002321479.1 integrase arm-  type DNA-binding domain-  containing protein  [Stenotrophomonas phage S1] | Arm DNA-binding domain  [PF13356.8]; Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 32\_S2\_k57\_11087896\_flag\_0\_multi\_13.9981\_len\_68123 |  |  | YP\_009188643.1 | YP\_009188643.1 putative integra-se [Gordonia phage GMA3] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 32\_S2\_k57\_11443506\_flag\_3\_multi\_31.0006\_len\_50684 |  |  |  |  | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 32\_S2\_k57\_771536\_flag\_0\_multi\_12.4558\_len\_24435 | K04763 | integrase/recombinase XerD | YP\_009199114.1 | YP\_009199114.1 putative recom-binase XerD [Brevibacillus phage Jenst] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 32\_S3\_k57\_3088676\_flag\_1\_multi\_11.0000\_len\_46314 |  |  | YP\_009012282.1 | YP\_009012282.1 integrase  [Mycobacterium phage BigNuz] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 32\_S3\_k57\_5168632\_flag\_1\_multi\_7.8168\_len\_37784 |  |  | YP\_007112444.1 | YP\_007112444.1 integrase [Enterobacterial phage mEp390] | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 35\_S1\_k57\_2071602\_flag\_0\_multi\_25\_3611\_len\_11665-cat\_2 | K04763 | integrase/recombinase XerD | YP\_009199114.1 | YP\_009199114.1 putative recom-binase XerD [Brevibacillus phage Jenst] | Phage integrase family [PF00589.24];  Phage integrase, N-terminal SAM-  like domain [PF02899.19]; Phage  integrase, N-terminal SAM-like  domain [PF13495.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| vOTU | Kegg\_id | Kegg\_hit | Viral\_id | Viral\_hit | Pfam\_hits | Vogdb\_description |
| 35\_S1\_k57\_3346215\_flag\_0\_multi\_9.6000\_len\_15680 |  |  |  |  | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 35\_S1\_k57\_5120045\_flag\_0\_multi\_76.0154\_len\_15370 |  |  | YP\_008059154.1 | YP\_008059154.1 integrase [Halo-virus HCTV-5] | Phage integrase family [PF00589.24] | sp|P96629|INT\_BACSU ICEBs1 integrase; Xr |
| 35\_S1\_k57\_5412590\_flag\_0\_multi\_74.4810\_len\_15082 |  |  |  |  | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 35\_S1\_k57\_6397365\_flag\_0\_multi\_72.7471\_len\_16129 |  |  |  |  | Phage integrase family [PF00589.24];  Phage integrase, N-terminal SAM-  like domain [PF02899.19]; Phage  integrase SAM-like domain  [PF13102.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 35\_S1\_k57\_6397365\_flag\_0\_multi\_72.7471\_len\_16129 |  |  |  |  | Phage integrase family [PF00589.24] |  |
| 35\_S2\_k57\_3598456\_flag\_0\_multi\_7.4215\_len\_10204 |  |  |  |  | Phage integrase family [PF00589.24]; Phage integrase, N-terminal SAM-  like domain [PF13495.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 35\_S2\_k57\_3713203\_flag\_0\_multi\_12.5028\_len\_25743 |  |  |  |  | Phage integrase family [PF00589.24]; Phage integrase, N-terminal SAM-  like domain [PF13495.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 35\_S2\_k57\_6861616\_flag\_0\_multi\_13.4062\_len\_12254 |  |  |  |  | Phage integrase family [PF00589.24] |  |
| 7\_S2\_k57\_11632576\_flag\_3\_multi\_13.9753\_len\_42552 |  |  | YP\_009785037.1 | YP\_009785037.1 site-specific  integrase | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| vOTU | Kegg\_id | Kegg\_hit | Viral\_id | Viral\_hit | Pfam\_hits | Vogdb\_description |
| 7\_S1\_k57\_7699859\_flag\_1\_multi\_7.0000\_len\_39892 | K04763 | integrase/recombinase XerD | YP\_009194042.2 | YP\_009194042.2 tyrosine-type  recombinase/integrase [Bacillus  phage vB\_BtS\_BMBtp3] | Phage integrase family [PF00589.24]; Phage integrase, N-terminal SAM-  like domain [PF02899.19]; Phage  integrase, N-terminal SAM-like  domain [PF13495.8] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 7\_S2\_k57\_1756606\_flag\_1\_multi\_6.5682\_len\_32454 | K06400 | site-specific DNA recombinase | YP\_009953031.1 | YP\_009953031.1 serine integrase Mycobacterium phage Curiosium | Resolvase, N terminal domain  [PF00239.23]; Recombinase  [PF07508.15] | sp|P03014|PINE\_ECOLI Serine recombinase  PinE; Xr |
| 7\_S2\_k57\_350917\_flag\_3\_multi\_18.0000\_len\_39184 | K06400 | site-specific DNA recombinase | YP\_009616548.1 | YP\_009616548.1 serine integrase [Streptomyces phage Hydra] | Resolvase, N terminal domain  [PF00239.23]; Recombinase  [PF07508.15] | sp|P03014|PINE\_ECOLI Serine recombinase  PinE; Xr |
| 7\_S3\_k57\_10080475\_flag\_1\_multi\_6.4180\_len\_13590 |  |  | YP\_008129787.1 | YP\_008129787.1 integrase  [Mycobacterium phage Leo] | Phage integrase family [PF00589.24] |  |
| 7\_S3\_k57\_12141746\_flag\_3\_multi\_26.0004\_len\_61025 |  |  |  |  | Phage integrase family [PF00589.24] | sp|P22877|INTR\_SACER Integrase; XhXr |
| 7\_S3\_k57\_12141775\_flag\_3\_multi\_23.0004\_len\_59157 |  |  | YP\_009784265.1 | YP\_009784265.1 putative  integrase/recombinase protein  [Burkholderia phage Bp-AMP1] |  | sp|P22877|INTR\_SACER Integrase; XhXr |
| 7\_S3\_k57\_7386454\_flag\_0\_multi\_59.8804\_len\_56826 | K14059 | integrase | YP\_009952554.1 | YP\_009952554.1 tyrosine  integrase [Mycobacterium phage  Amelie] | Phage integrase family [PF00589.24]; Integrase [PF12835.9] | sp|P22877|INTR\_SACER Integrase; XhXr |