**Table S1.** Phylum level distributions in toombak metagenome from IMG/M-ER system (Phylogenetic Distributions). Based on 30%+ protein identity.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Domain** | **Phylum** | **Genome Count** | **Gene Copies** | **Percent**  **Abundance (%)** |
| Bacteria | Actinobacteria | 13423 | 12922659 | 74.7 |
| Bacteria | Unclassified | 3288 | 815504 | 4.72 |
| Bacteria | Firmicutes | 21459 | 3333085 | 19.3 |
| Bacteria | Proteobacteria | 41292 | 85260 | 0.49 |
| Viruses | Mostly DNA Virus, no RNA Stage | 5087 | 65454 | 0.38 |
| Eukaryota | Mostly Streptophyta | 650 | 34374 | 0.20 |
| Bacteria | Others | 10631 | 25445 | 0.15 |
| Archaea | Mostly Euryarchaeota | 1313 | 4042 | 0.023 |

**Table S2.** Results from ICEBERG and CARD database mapping.ICEBERG matches are in yellow, while the CARD matches are in green.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **GenBank Accession#** | **#ID** | **Avg. Fold** | **Length** | **Ref GC%** | **Covered %** | **Covered bases** | **Plus Reads** | **Minus Reads** | **Read GC%** |
| FJ231270 | Integrating conjugative element ICE6013  [*Staphylococcus aureus* strain HDG2] | 18.7 | 19905 | 0.30 | 76.6 | 15248 | 656 | 669 | 0.32 |
| FN433596 | Putative integrating conjugative element ICESauTW20-1 [*Staphylococcus aureus* subsp. *aureus* TW20] | 4.15 | 19906 | 0.30 | 12.7 | 2526 | 152 | 152 | 0.32 |
| AE009948 | Integrating conjugative element ICESa2603  [*Streptococcus agalactiae* 2603V/R] | 3.66 | 54349 | 0.38 | 11. 6 | 6282 | 361 | 382 | 0.37 |
| GU951538 | TN6079 Antimicrobial-resistance associated  [Uncultured bacterium MID12] | 2.69 | 28411 | 0.38 | 12.5 | 3559 | 137 | 151 | 0.36 |
| CP002643 | Putative integrating conjugative element ICESauT0131-1 [*Staphylococcus aureus* subsp. *aureus* T0131] | 1.86 | 19899 | 0.30 | 7.08 | 1408 | 72 | 65 | 0.34 |
| AM180066 | Macrolide phosphotransferase *mphC*  [*Staphylococcus equorum*] | 62.1 | 900 | 0.37 | 100 | 900 | 117 | 106 | 0.36 |
| AF015628 | Virginiamycin B lyase *VgbB*  [*Staphylococcus cohnii*] | 57.0 | 889 | 0.39 | 100 | 889 | 100 | 94 | 0.42 |
| NC\_013450 | HTH-type transcriptional regulator *mgrA*  [*Staphylococcus aureus* subsp. *aureus* ED98] | 53.5 | 445 | 0.33 | 100 | 445 | 43 | 50 | 0.34 |
| AF015628 | Streptogramin A acetyl transferase *vatC*  [*Staphylococcus cohnii*] | 47.3 | 640 | 0.36 | 99.1 | 634 | 62 | 57 | 0.40 |
| NC\_002951 | Multidrug resistance ABC transporterhomolog *sav1866* [*Staphylococcus aureus subsp. aureus COL*] | 33.4 | 1738 | 0.33 | 95.1 | 1653 | 100 | 113 | 0.32 |
| AY566250 | Efflux-mediated resistance transporter norA  [*Staphylococcus epidermidis*] | 29.4 | 1165 | 0.32 | 93.8 | 1093 | 70 | 65 | 0.35 |
| X98831.1 | EF-Tu mutants conferring resistance to elfamycin [*Streptomyces cinnamoneus*] | 26.0 | 1194 | 0.63 | 96.4 | 1151 | 66 | 68 | 0.60 |
| NC\_010419.1 | Fosfomycin-resistance gene FosB  [*Staphylococcus aureus*] | 17.0 | 420 | 0.30 | 100 | 420 | 15 | 16 | 0.32 |
| NC\_009632 | Erythromycin ribosome methylase ErmA  [*Staphylococcus aureus* subsp. *aureus* JH1] | 16.5 | 733 | 0.32 | 100 | 733 | 22 | 27 | 0.36 |
| NC\_013452 | Tetracycline-resistance gene *tetK*  [*Staphylococcus aureus* subsp. *aureus* ED98] | 12.4 | 1381 | 0.28 | 100 | 1381 | 38 | 37 | 0.30 |

**Table S3. Genetic Content from IMG/M-ER: Clusters of Orthogonal Genes (COGs)**

|  |  |  |  |
| --- | --- | --- | --- |
| **COG** | **Description** | **Gene Hits** | **Gene Copy Estimate (Abundance)** |
| COG0600 | ABC-type nitrate/sulfonate/bicarbonate transport system, permease component (NrtA) | 65 | 10560 |
| COG0715 | ABC-type nitrate/sulfonate/bicarbonate transport system, periplasmic component (NrtB) | 79 | 18251 |
| COG1116 | ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component (NrtC) | 63 | 11148 |
| COG1140 | Nitrate reductase beta subunit (NarH) | 25 | 3348 |
| COG2180 | Nitrate reductase assembly protein NarJ, required for insertion of molybdenum cofactor | 19 | 4727 |
| COG2181 | Nitrate reductase gamma subunit (NarI) | 18 | 4637 |
| COG2223 | Nitrate/nitrite transporter NarK/NarT | 26 | 5332 |
| COG3005 | Tetraheme cytochrome c subunit of nitrate or TMAO reductase | 1 | 13 |
| COG3043 | Nitrate reductase cytochrome c-type subunit | 1 | 19 |
| COG3062 | Cytoplasmic chaperone NapD for the signal peptide of periplasmic nitrate reductase NapAB | 0 | 0 |
| COG3850 | Signal transduction histidine kinase, nitrate/nitrite-specific | 0 | 0 |
| COG4459 | Periplasmic nitrate reductase system, NapE component | 0 | 0 |
| COG5000 | Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation | 5 | 555 |
| COG5013 | Nitrate reductase alpha subunit (NarG) | 61 | 14085 |
| **Antimicrobial Resistance** | |  |  |
| COG0456 | Ribosomal protein S18 acetylase RimI and related acetyltransferases | 265 | 35903 |
| COG0480 | Translation elongation factor EF-G, a GTPase | 36 | 7331 |
| COG0744 | Membrane carboxypeptidase (penicillin-binding protein) | 115 | 10016 |
| COG0745 | DNA-binding response regulator, OmpR family, contains REC and winged-helix (wHTH) domain | 255 | 32696 |
| COG0768 | Cell division protein FtsI/penicillin-binding protein 2 | 122 | 18250 |
| COG1131 | ABC-type multidrug transport system, ATPase component | 445 | 48634 |
| COG1132 | ABC-type multidrug transport system, ATPase and permease component | 399 | 39530 |
| COG1566 | Multidrug resistance efflux pump | 7 | 714 |
| COG1670 | Protein N-acetyltransferase, RimJ/RimL family | 191 | 12382 |
| COG2274 | ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain | 26 | 2060 |
| COG2720 | Vancomycin resistance protein YoaR (function unknown), contains peptidoglycan-binding and VanW domains | 22 | 5882 |
| COG3559 | Putative exporter of polyketide antibiotics | 45 | 5554 |
| COG4767 | Glycopeptide antibiotics resistance protein | 24 | 3099 |
| COG5009 | Membrane carboxypeptidase/penicillin-binding protein | 3 | 2102 |
| **Horizontal Gene Transfer** | |  |  |
| COG3316 | Transposase (or an inactivated derivative) | 50 | 24749 |
| **PhyloMarker COGs** | |  |  |
| COG0556 | Excinuclease UvrABC helicase subunit UvrB | 51 | 8304 |
| COG0497 | DNA repair ATPase RecN | 41 | 5748 |
| COG1200 | RecG-like helicase | 43 | 9103 |