Table S5. Cross-BLASTn analysis of the mosquito metagenomes. A sequence was considered to be shared by two metagenomes if each sequence was the best BLASTn similarity for the other when the two metagenomes were compared with BLASTn.

Sample	SD-BVL	SD-RB	SD-WAP
SD-BVL	100.00%	12.00%	11.40%
SD-RB	12.00%	100.00%	5.21%
SD-WAP	11.40%	5.21%	100.00%