



**Supplementary Figure 3.** Plot of SNVs per kilobase pair versus n2n1 (majority allele frequency) for metagenome mappings to single cell amplified genomes from Piccard (yellow) and Von Damm (blue) vent fields. All y-axes reflect n2n1, or the ratio of the second most common allele to the most common allele. Bubble diameter corresponds to the average coverage of each SAG-metagenome mapping normalized by number of metagenomic reads. Bubbles are colored according to which vent field they came from; sample numbers are indicated.