



Figure S2. Scatter plots of *Osedax japonicus* transcriptome. Root specific genes are indicated as magenta plots. Gray plots in the root specific area (X-axis < 0, Y-axis \geq 0) are genes whose fragments per kilobase per million reads (FPKM) values of the other sample were above the threshold (\geq 0). For example, gray plots in the root specific area of the left graph are genes whose trunk FPKM values were above the threshold.