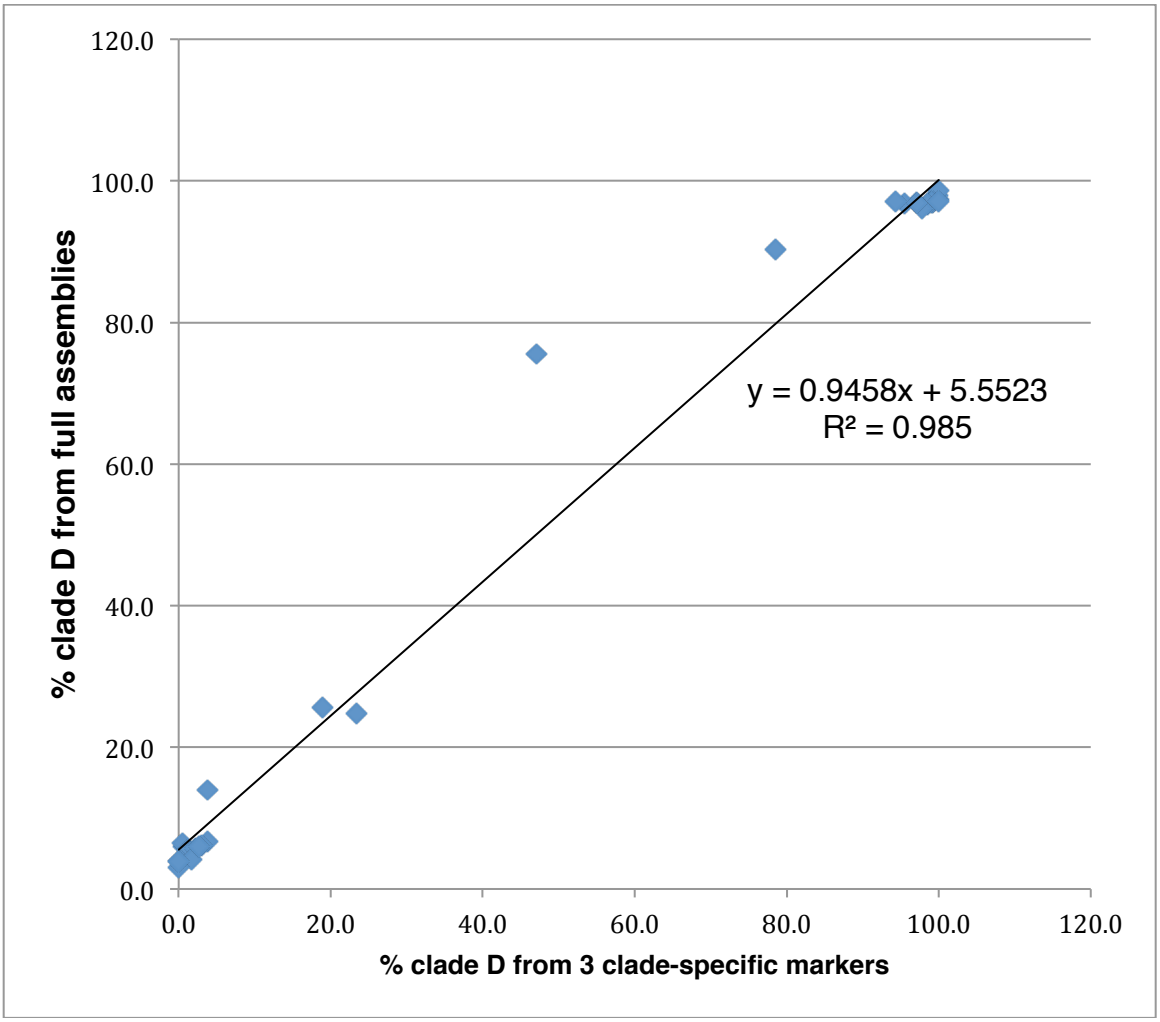

Figure S1. Correlation between two different estimates of the percentage of clade D *Symbiodinium* in each coral sample. On the x-axis is an estimate based on the number of reads aligning to three clade-specific markers (chloroplast 23S ribosomal RNA and internal transcribed spacers 1 and 2). On the y-axis is an estimate based on the total number of reads mapped to each *de novo* transcriptome assembly.