



Correlation of expression values between reference transcripts and Trinity transcript components according to percent length agreement in *S. pombe*. Blue: shown is the average correlation across four *S. pombe* samples (left Y axis; Pearson r^2) between the expression levels computed for matching reference and Trinity assembled transcripts at different levels of agreement between the matching transcripts (X axis; % length agreement computed as the length of the shorter transcript divided by length of the longer transcript, comparing the Trinity contig to the corresponding reciprocal best hit reference transcript, and reported as a percentage). More complete transcripts (those with greatest percent length agreement) are more highly correlated with reference transcript expression profiles across the four growth conditions. Orange: Proportion of Trinity contigs (right Y axis) in each bin of % transcript length agreement (X axis). Most Trinity transcripts are nearly complete (>80%), with increasing fractions in the higher percentage length bins (orange).