



Figure S3: Fractional read depth in the Polypolish algorithm.

A: hypothetical read alignments for three 100 bp reads to a 1200 bp assembly. Read A aligned to a single location, read B to two locations and read C to four locations.

B: Polypolish read depths resulting from the alignments. Each alignment contributes $1/n$ depth, where n is the total number of alignments for that read. This results in a mean depth of 0.25 for the entire assembly, the same value which would be obtained if each read only had a single alignment.