



**Figure S2. Comparison of tiling and sequence data for *smg-1(r861)* mutant.** (a) correlation of gene intensities (left) and exon intensities (right) at two different developmental shows very high positive correlation. (b) Nearly 90% of genes expressed by tiling arrays are found to be expressed by sequencing as well. (c) As seen for the wild-type N2 sequence reads, nearly 95% of the sequencing reads from the mutants map to known transcripts.