



**Figure S1.** Comparison of results at 16p12.2 using single molecules or *de novo* assembled contigs as input to OMGenSV. Results are shown for all three groups of configurations, as in Figure 4. Stacked bar graphs are shown, with numbers representing how many times each configuration was detected with each input source. Counts for molecule and contig analyses may not add up to the same total, since the number of samples with usable data differed in the two approaches.