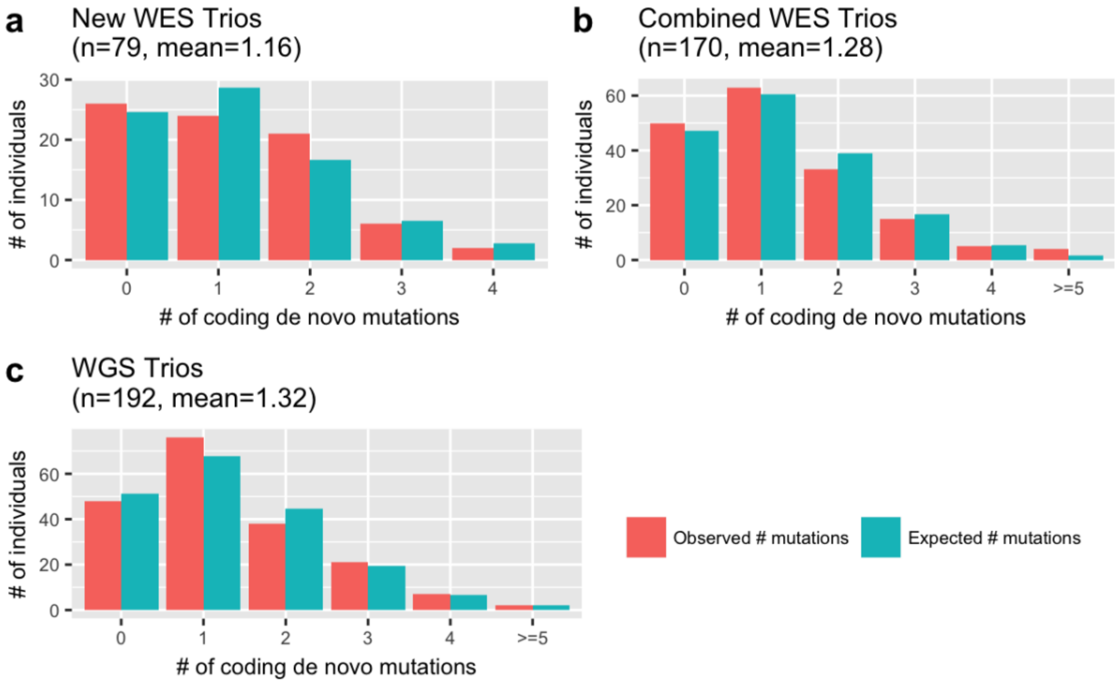
S2 Fig. Distribution of *de novo* coding variants per proband.



Distribution of number of *de novo* coding variants per proband in whole-exome (WES, top) and whole-genome sequencing (WGS, bottom) trios. The WES trios include 79 trios sequenced in this study, and 91 trios that were previously published. Twenty-seven published WES trios that were sequenced again by WGS were only included in the WGS analysis.

The observed number of variants were compared with the expectation assuming a Poisson distribution with mean equals to the average number of variants per proband.