



**Supplemental Fig. S5. Concordance plots LR-AS repeat expansions called with Straglr and vamos**

Concordance plot showing a comparison of predicted sizes of the larger allele by Straglr and vamos for all RE loci. The locus specific pathogenic thresholds are shown as dashed red lines. A 1:1 correlation is shown as a dashed grey line. Individuals with no call are indicated separately to the numbered axis and are labelled nc (i.e. no genotype call).