**Figure S1: Methylation rate measure of each CpG site contained in the five targets for a 50% methylation standard and for Jung *et al.* and Cho *et al.* primer sets in different amplification conditions (T°C and [MgCl2]).** When no data is displayed for a particular condition, the amplification failed or no sequencing data could be obtained due to low amplification of the target.
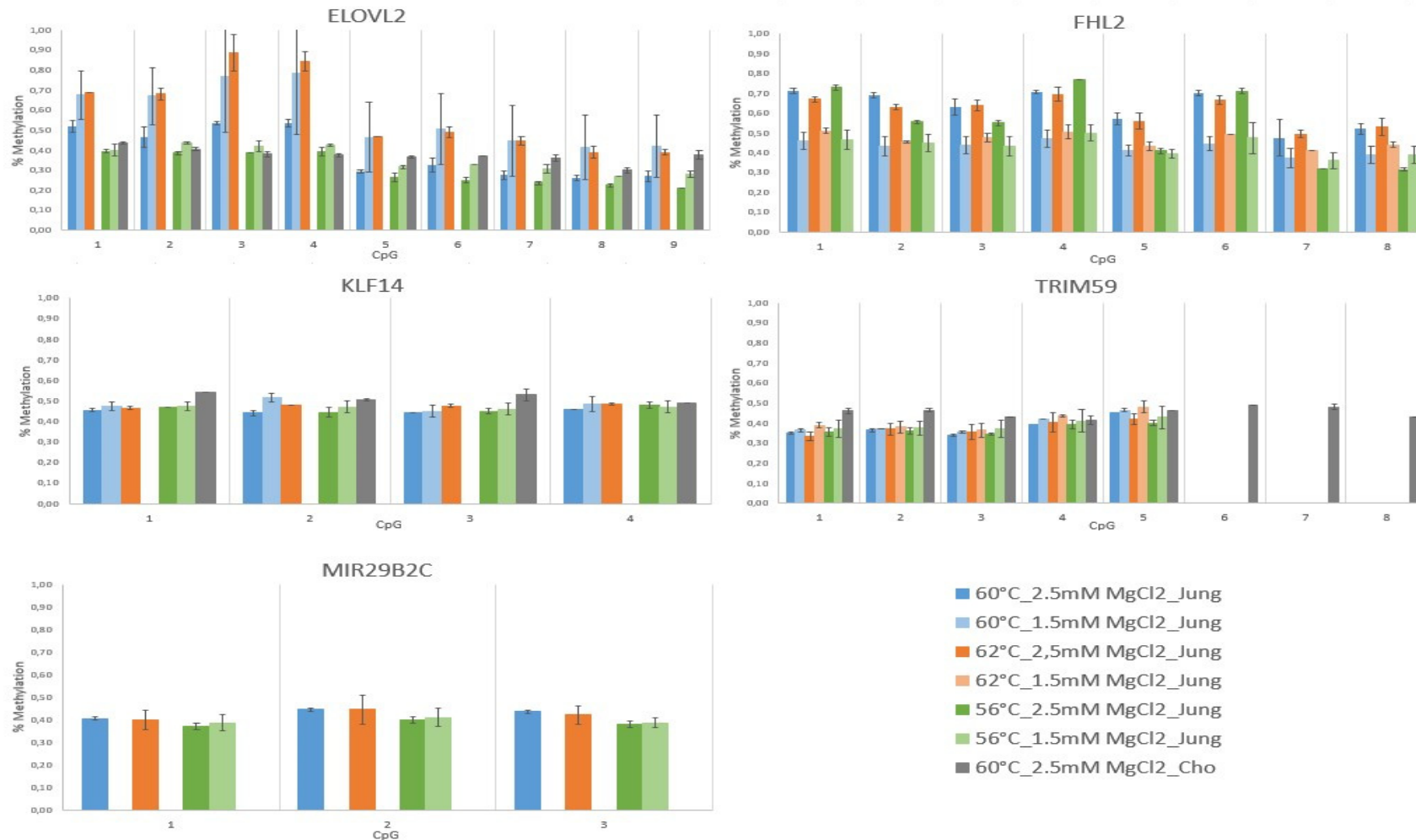
Figure S2: Correlations of the methylation rate to the chronological age for ELOVL2, FHL2, KLF14, MIR29B2C and TRIM59 CpGs in buccal swabs and saliva samples. Pearson's R and associated p-value are given for each correlation.
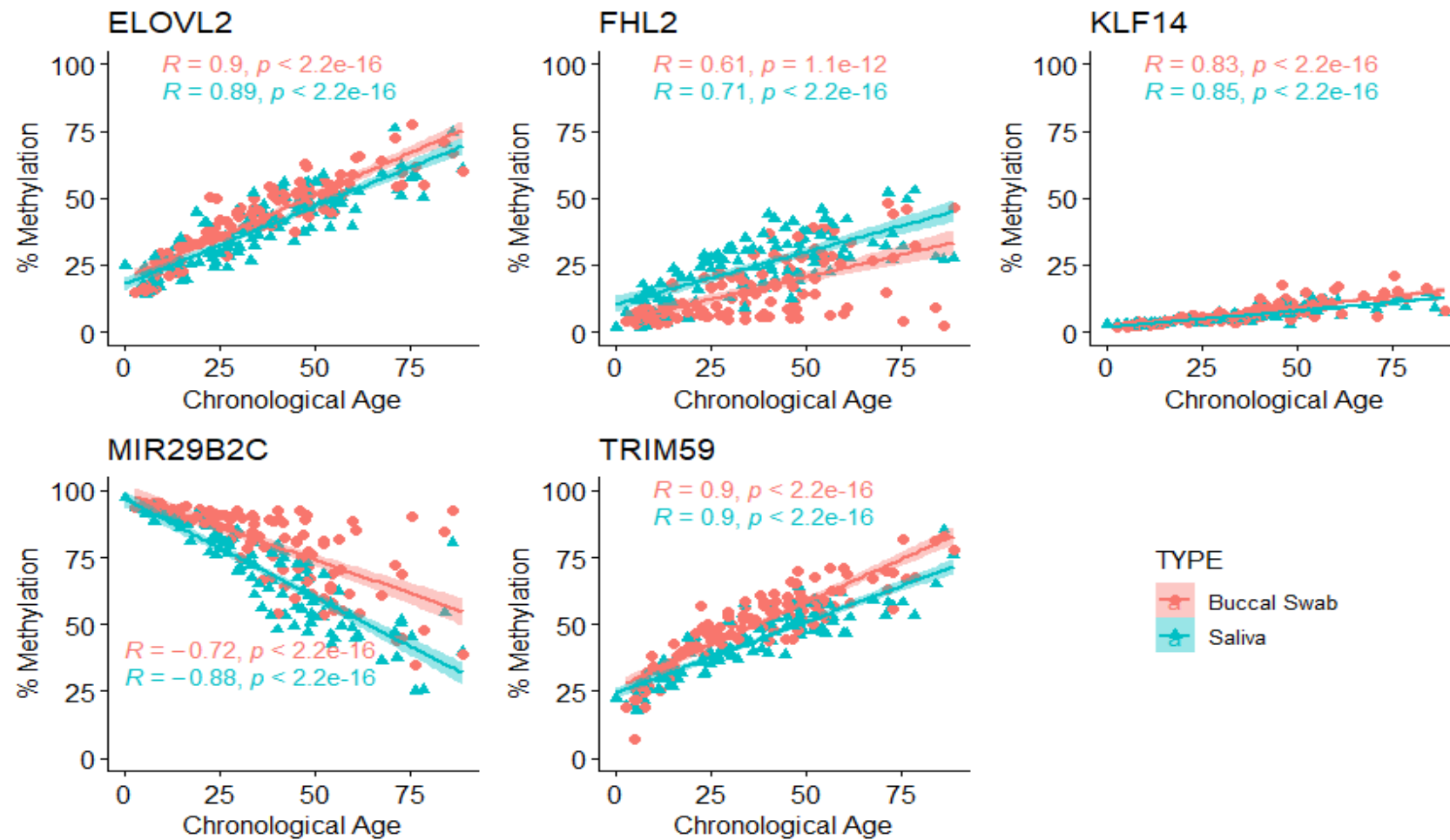
Figure S3A: Residue analysis for the saliva model from 0 to 88 y.o. individuals (up) and 18 to 75 y.o. individuals (down).
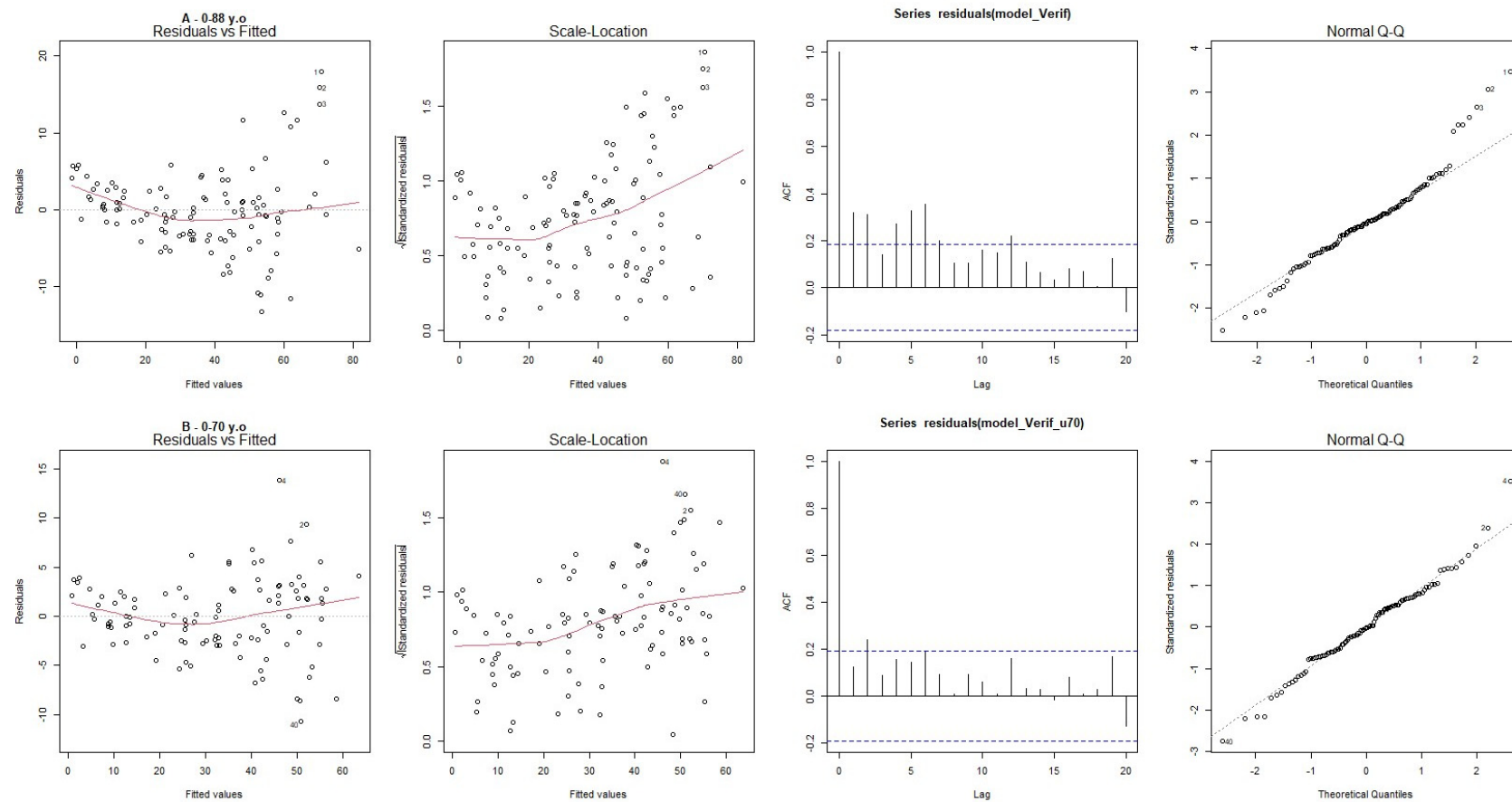
Figure S3B: Residue analysis for the buccal swab model from 0 to 88 y.o. individuals (up) and 18 to 75 y.o. individuals (down).
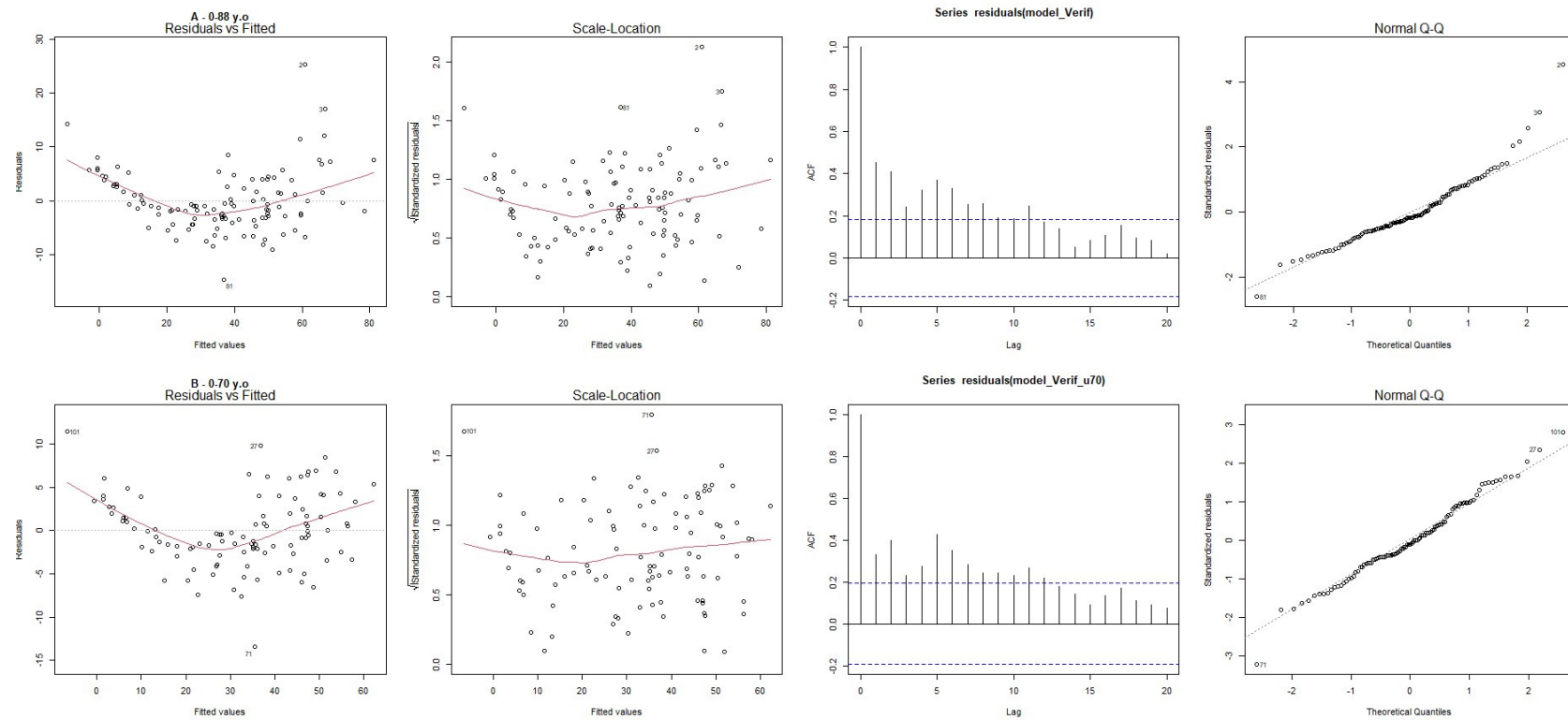
Figure S3C: Residue analysis for the multi-tissue model from 0 to 88 y.o. individuals (up) and 18 to 75 y.o. individuals (down).