Supplemental Figures.
Deciphering D4Z4 CpG methylation gradients in FSHD using nanopore sequencing.
Butterfield et al.

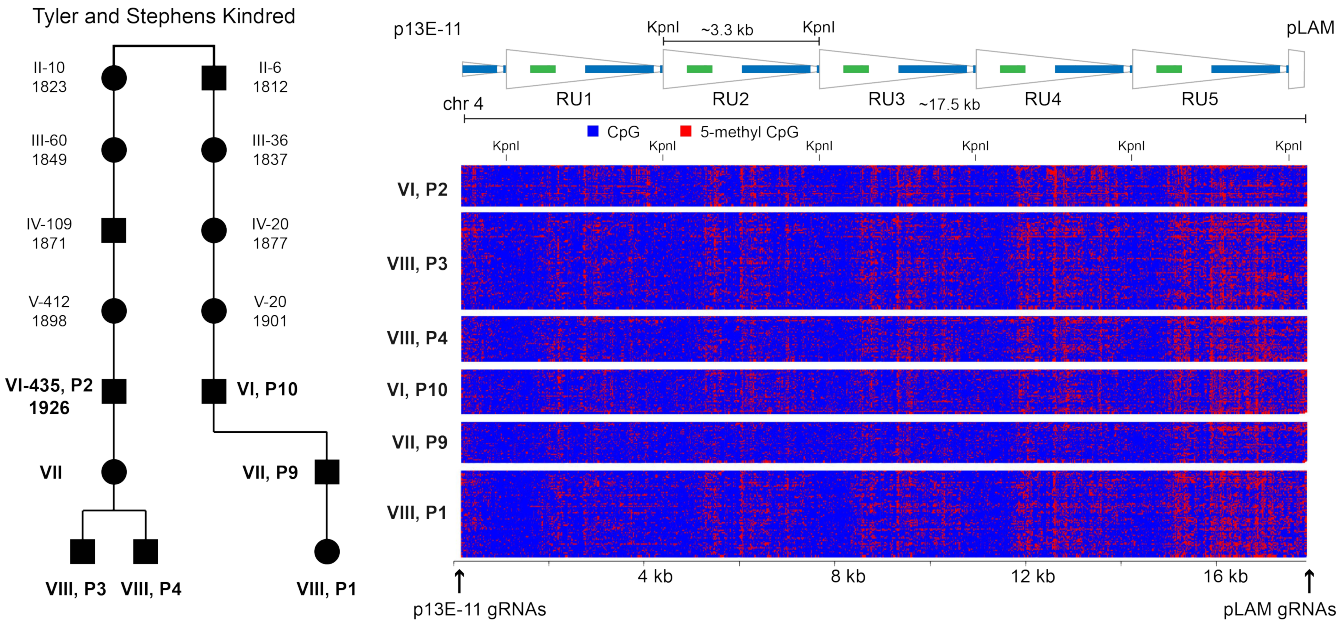

Figure S1. Intergenerational stability of the founder 5U in the historic Utah FSHD kindred. (left) Lines of descent from the founder (I-1, born 1775, England) are shown for the related participants P1, P2, P3, P4, P9. And P10. Pedigree notation indicates generation (Roman numeral) and, if followed by a hyphenated number (i.e., VI-435), the notation corresponds to the label on the original pedigree charts shown in Figure 1 and 2 from FH Tyler and FE Stephens, Ann Intern Med. 1950 Apr;32(4):640-60. doi: 10.7326/0003-4819-32-4-640. (right) Single-read *modbamtools* plots of p13E-11 to pLAM 4qA reads from the related individuals (P1, P2, P3, P4, P9, and P10) who inherited the 5U founder contraction.

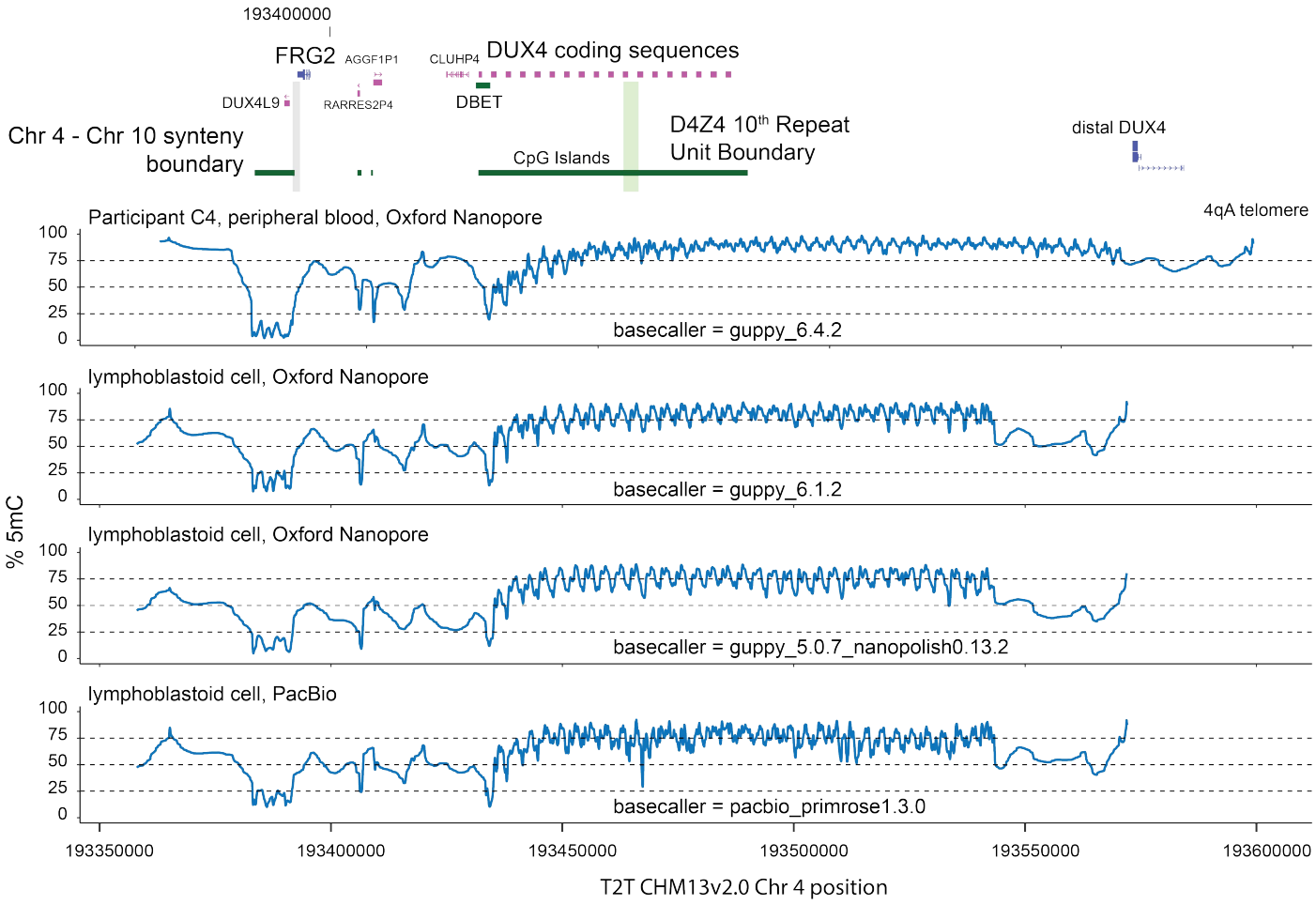

Figure S2. CpG methylation gradients in the T2T HG002/NA24385 lymphoblastoid sample. Methylation frequency plots of Oxford Nanopore (ONT) and PacBio HiFi reads. The ONT peripheral blood reads were from the control subject (R10.4.1_e8.2 nanopores) mapped to the 42U haplotype of Chr 4qA (as in Fig. 2C). The HG002/NA24385 lymphoblastoid cell line data were downloaded from the telomere-to-telomere consortium CHM13 project (https://github.com/marbl/CHM13), using the "HG002 5mC CpG and other methylation from ONT and HiFi" link to epigenetic profile data. The % 5mC plots were generated from the downloaded T2T bedMethyl files: chm13v1.1_hg002XYv2.7_hg002_CpG_ont_guppy6.1.2.bed, chm13v2.0_hg002_GpC_ont_guppy5.0.7_nanopolish0.13.2.bed, chm13v1.1_hg002XYv2.7_hg002_CpG_pacbio_primrose1.3.0_native.bed.

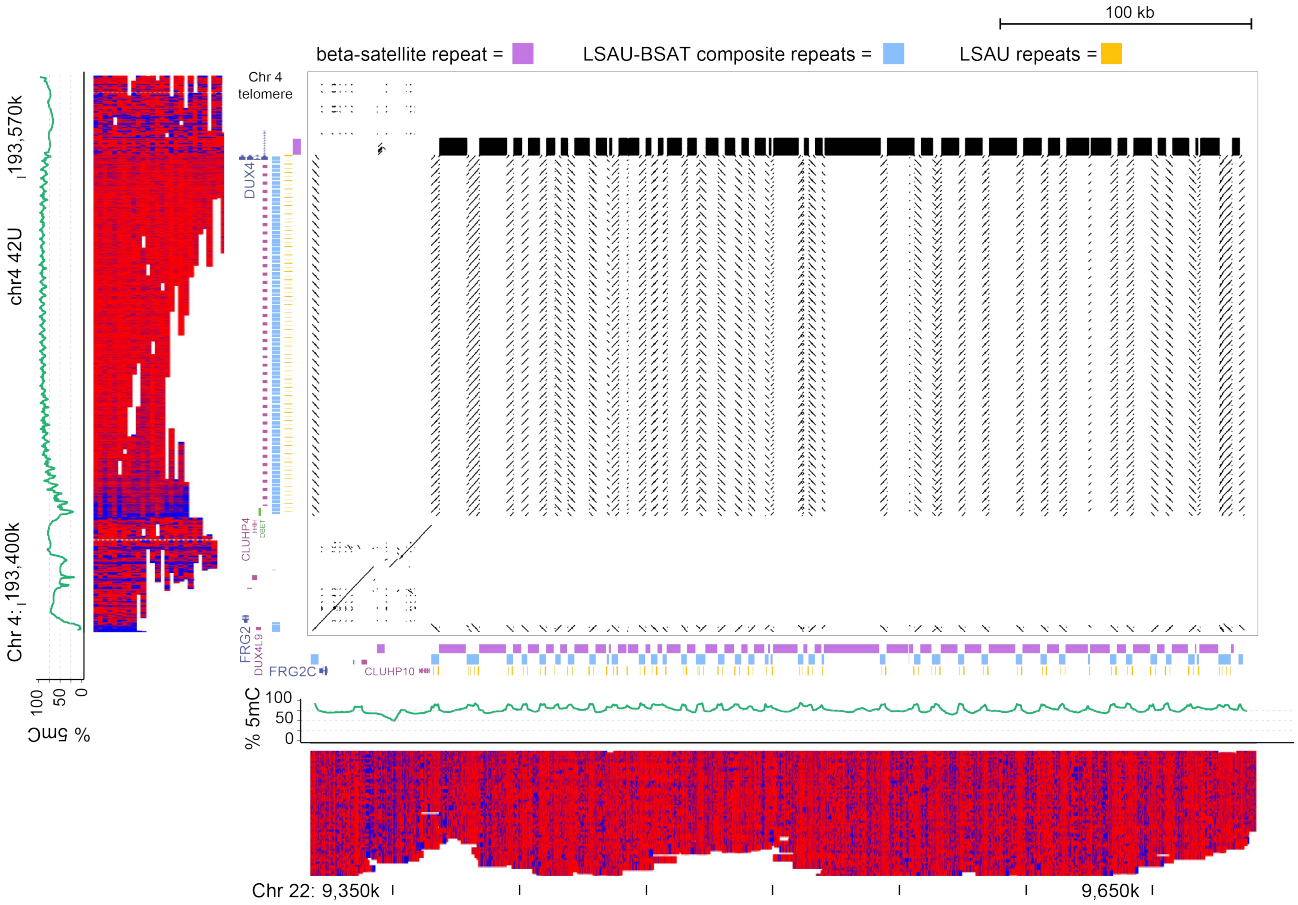

Figure S3. Paralogous Chr22 D4Z4 cluster retains the FRG2 region. LASTZ alignment dot plot between the 4qA array from CHM13 v2.0 Chr 4:193,389,177-193,574,945 and the divergent D4Z4 cluster on Chr 22:9,317,908-9,717,807. The Chr 4qA sequence has been composited to a length of 42 full-length D4Z4 repeats with a distal 4qAL-pLAM sequence. The data for methylation plots were from participant C4, using Promethion R10.4.1_e8.2 nanopores for sequencing. Modified basecalling was performed with guppy (v.6.4.2) and the dna_r10.4.1_e8.2_400bps_modbases_5mc_cg_sup.cfg config file.

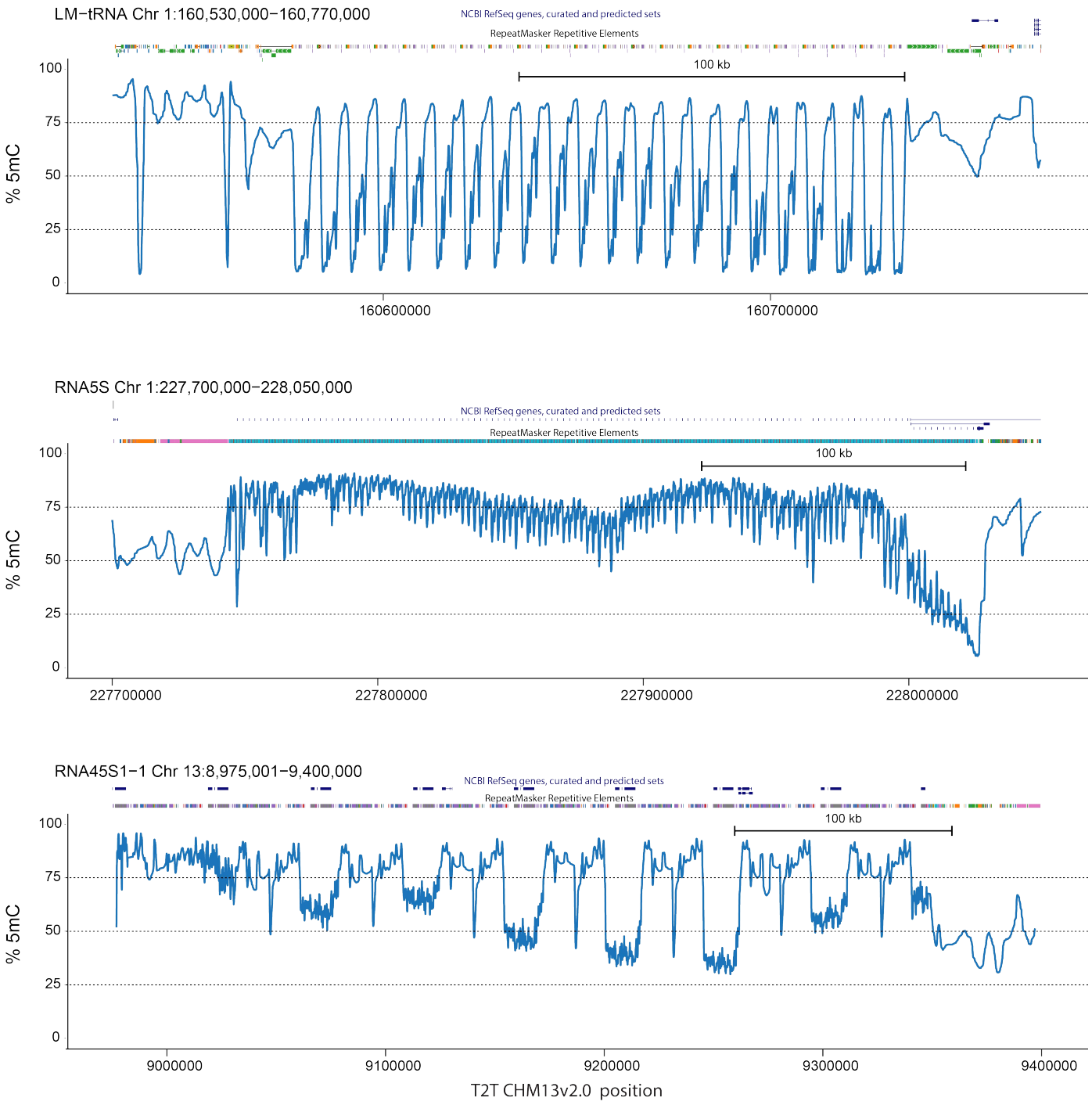

Figure S4. Methylation gradients in CpG-dense repeat regions in the T2T HG002/NA24385 lymphoblastoid cells. Methylation frequency plots of Oxford Nanopore (ONT) reads from the tRNA cluster on Chromosome 1, the 5S rRNA cluster on Chromosome 1, and one end of the RNA45S1 rRNA cluster on Chromosome 13. The % 5mC plots were generated from the T2T bedMethyl files: chm13v1.1_hg002XYv2.7_hg002_CpG_ont_guppy6.1.2.bed downloaded from the telomere-to-telomere consortium CHM13 project (https://github.com/marbl/CHM13), using the “HG002 5mC CpG and other methylation from ONT and HiFi” link to epigenetic profile data.