Figure S1. Schematic map of the Richmond Mine, Iron Mountain, CA, USA. The locations from which biofilms were sampled for this study (samples are listed in **Table 1**) are indicated with red dots.

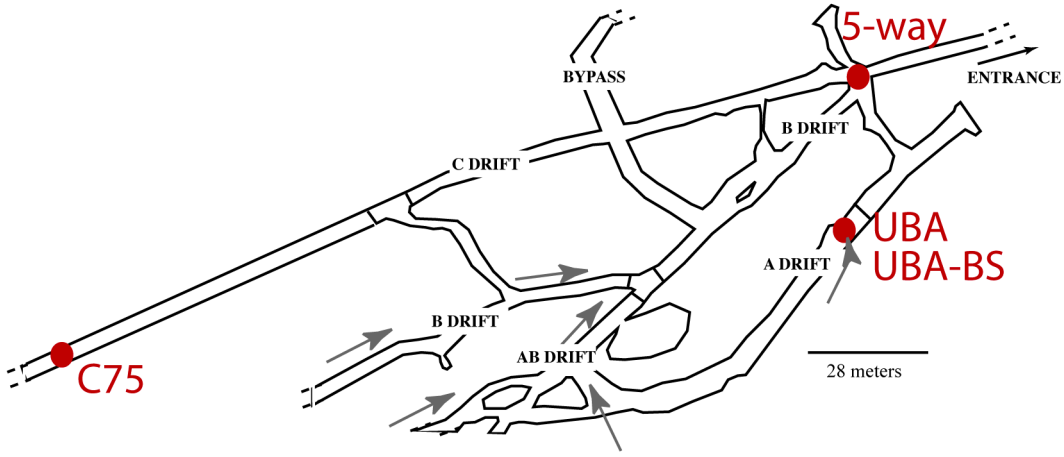

Figure S2: CRISPR-Cas system locus structure in CRISPR locus structure *Leptospirillum* group II UBA(top), *Leptospirillum* group II 5way (middle), and *Leptospirillum* group III (bottom). The code above the gene boxes present the gene ID for each dataset.

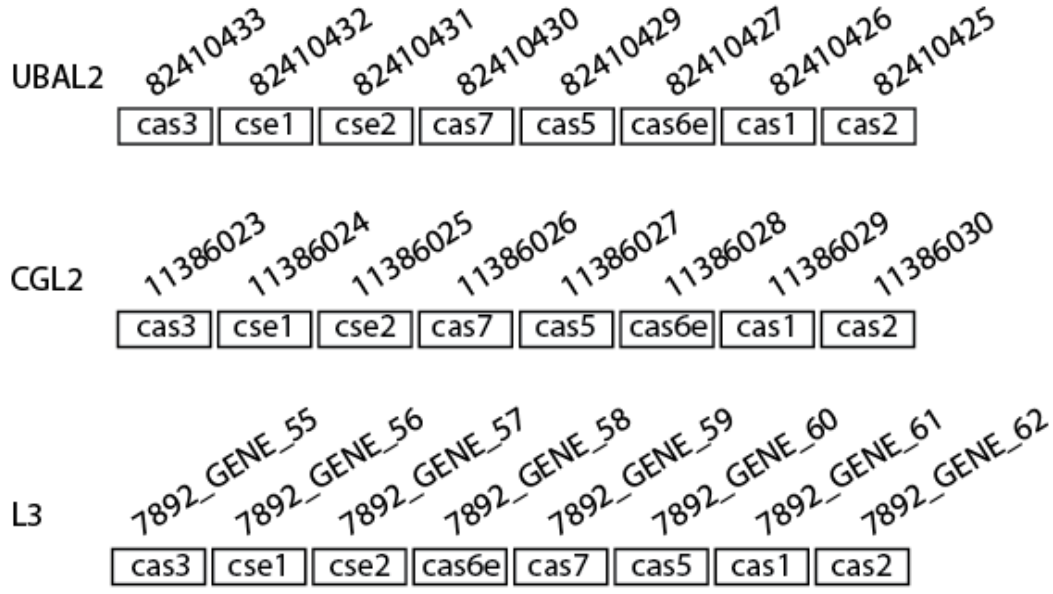

Figure S3: Phylogenetic tree of Cas1 proteins (universal marker of CRISPR systems). *Leptospirillum* group II (red) and *Leptospirillum* group III (blue) are indicated on the tree, which consists of all proteins used in the Cas1 protein tree from Makarova et al 2011(Makarova *et al.*, 2011). Proteins within the box are identified as Type I-E.

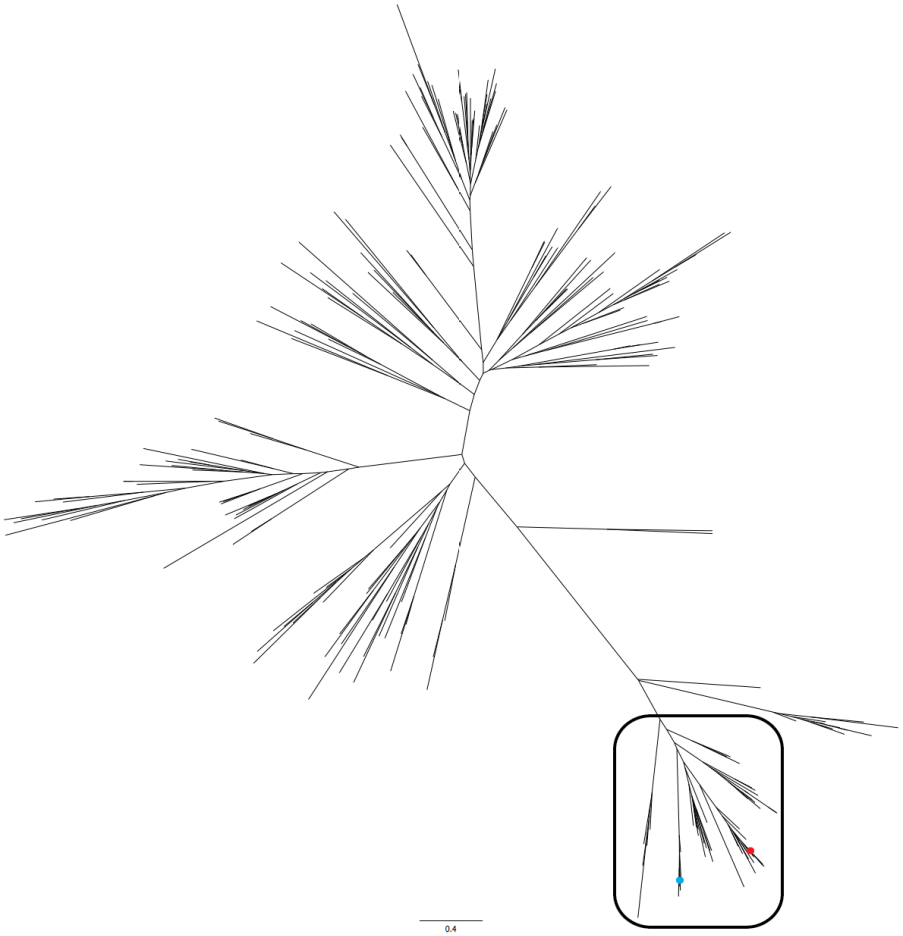

Figure S4. Spacer abundance across all datasets mapped along the reconstruction of *Leptospirillum* group II CRISPR loci from 5way, UBA, and C75 samples. Reconstructed loci are represented in the same manner as in **Figure 2**. The color gradient from black to light gray represents the most abundant spacers to the lowest abundant spacers.

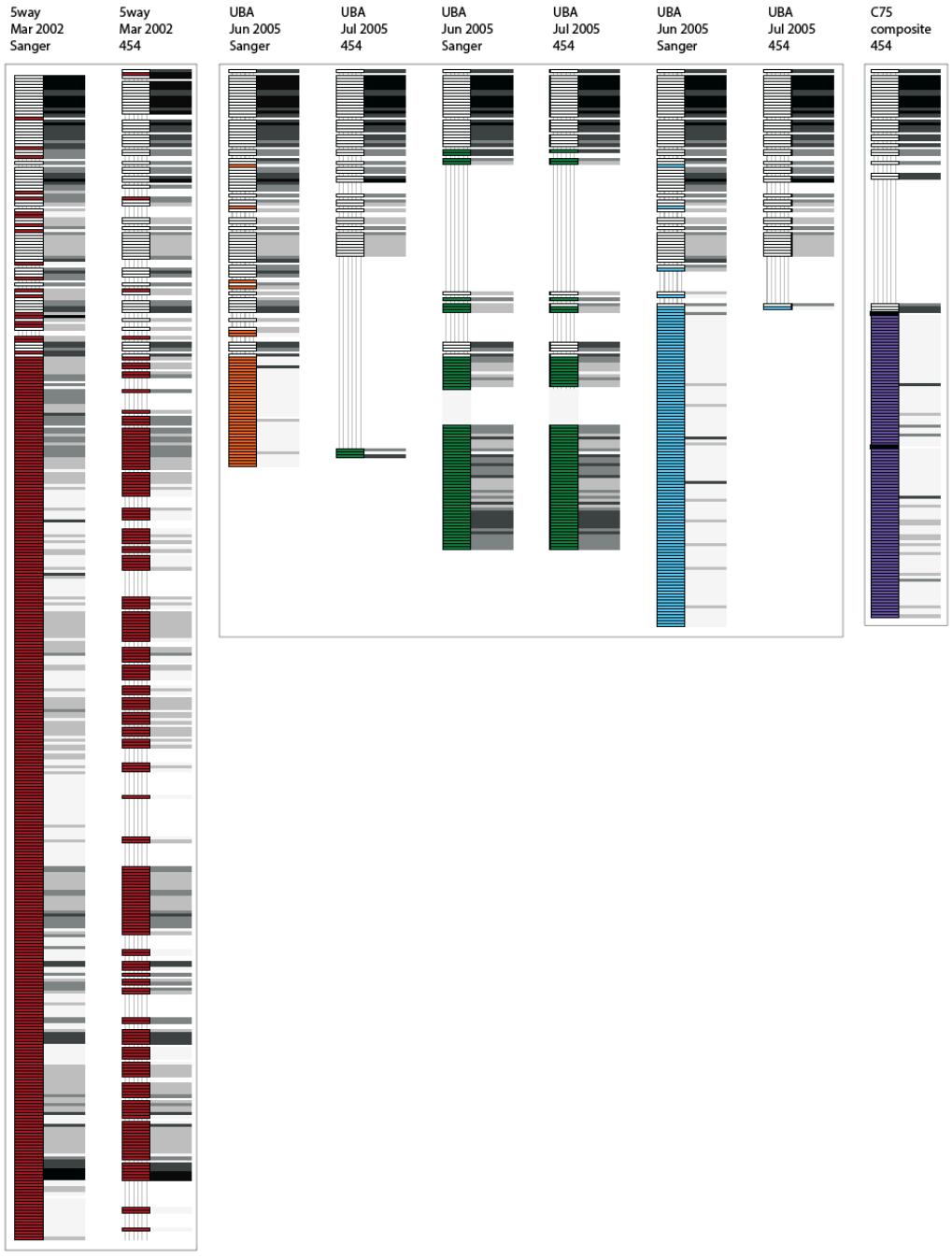

Figure S5. Reconstruction of the *Leptospirillum* group III from 5way and UBA datasets. Loci are shown vertically from trailer to leader end, with spacers represented as wide rectangles. Colors and symbols employed are consistent with Figure 2.

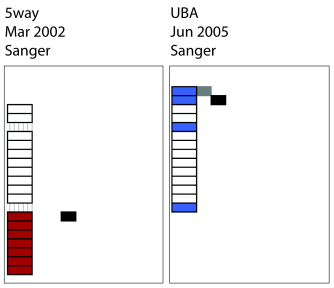

Figure S6. Histogram showing the spacer targeting on a 17 kb genomic region of AMDV1 (Contig209). Histogram bins report the number of spacer matches per 500 bp.