Supplementary Fig. 10. *SpRag1L* exon 3 sequence. The third 2,578 bp exon of *SpRag1L* contains a 2,070 bp region with 57 repeated variants of a 24 bp motif (consensus: ACAGCCCCTTTAACCCCAACTGCC; alternating black and white background) and 4 variants of a 126 bp region (blue background). We determined the sequence of this region by direct sequencing from two BAC clones (149P17 and 78F1). Nucleotides that vary from the consensus (shown in red) were used to maintain continuity across the sequence. The sequence of a 308 bp region that was impossible to resolve by direct BAC sequencing in the context of these repeats was unambiguously bridged using a WGS trace sequence (214582154; http://www.ncbi.nlm.nih.gov/Traces/trace.cgi). Our sequence differs from the genome assembly, but is consistent with restriction mapping (using *Eae1* and *Sml1*), and PCR measurements made on both BAC clone DNAs and on genomic DNA from the animal used for the genome sequence (data not shown). The exon encodes an open reading frame of 859 amino acids. Four separate cDNA sequences from this region taken from different animals track the genomic sequence at each end of the repeats, but are missing internal regions. Each of these cDNAs maintains the correct reading frame throughout this region and into flanking exons. These length differences may result from polymorphism or a more complex form of non-canonical splicing. Yellow highlighting indicates non-repetitive coding sequence. Splice junction dinucleotides are highlighted in green.