Figure X. Evolutionary conservation in different contexts. (a) Examining sequence conservation of homologous sequences across multiple species looks at a longer evolutionary timescale. (b) Examining the enrichment of rare variants (or depletion of common variants) in the same genomic element across multiple individuals within a single species or population looks at a shorter evolutionary timescale. (c) Examining sequence conservation of similar domain sequences within a single genome, (d) reveals species- and domain-specific conservation that might be important to the structure or function of the domain family. Genomic variant profile across the domain can be further analysed, e.g. by comparing the number of non-synonymous (ns) relative to synonymous (s) variants and comparing the number of rare (r) relative to common (c) variants. Here, we use ankyrin domains found in the human genome as an example. The sequence profile of an ankyrin repeat motif is painted green to yellow, corresponding to the structure of each of six ankyrin repeats found in the human Notch 1 ankyrin domain (PDB ID: 1YYH).