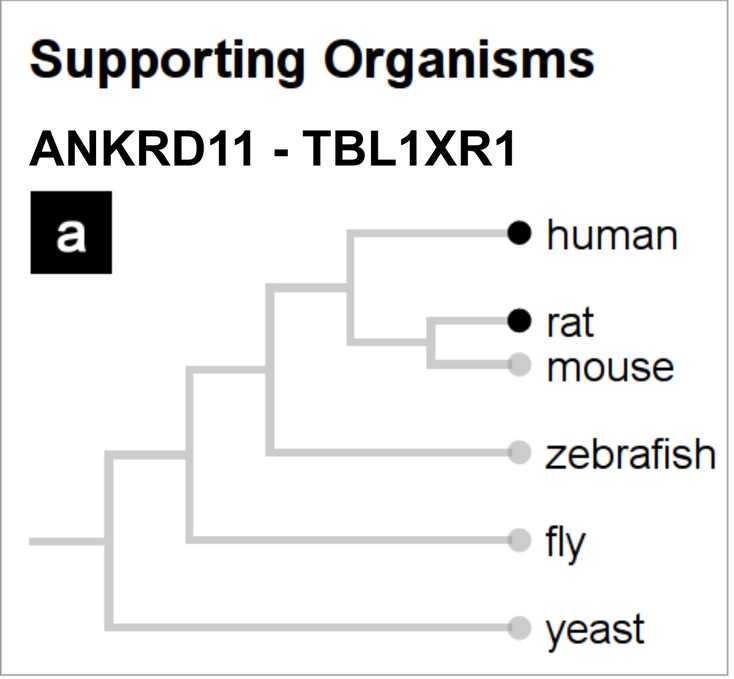

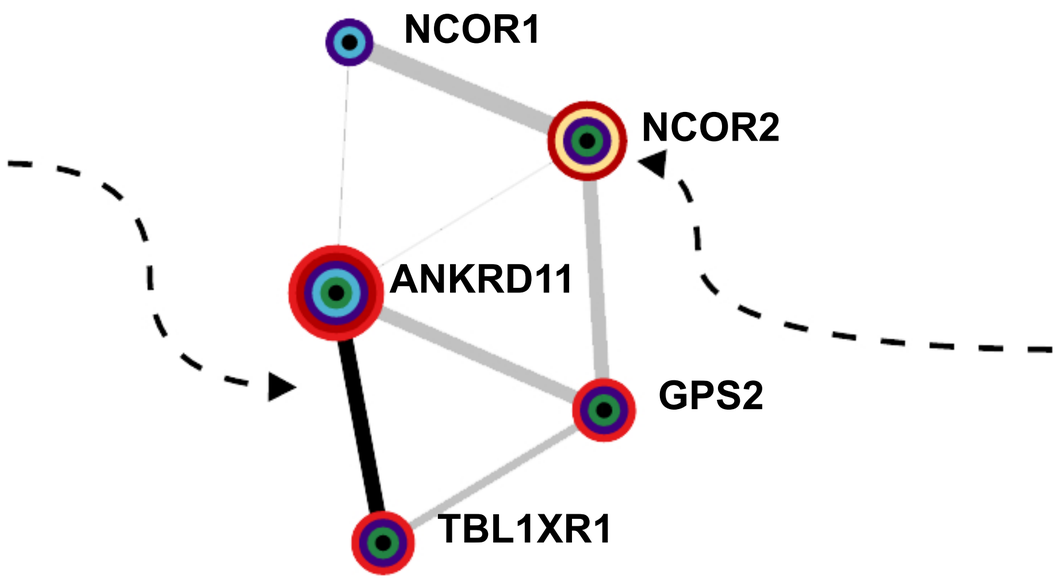

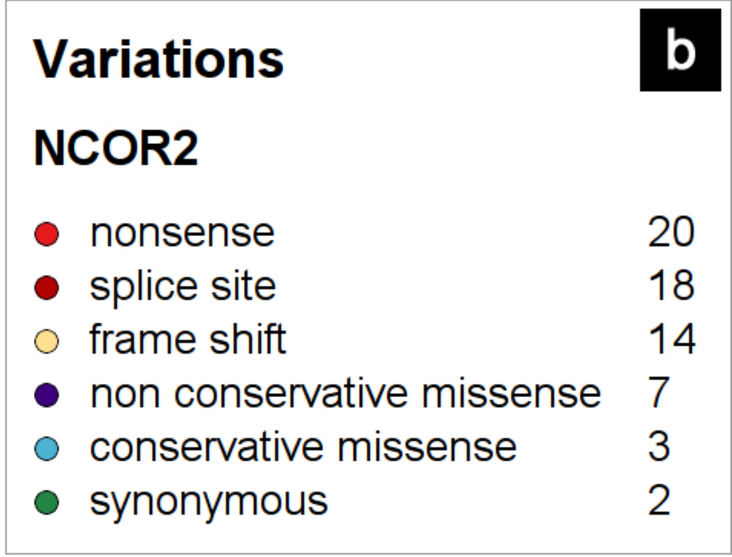

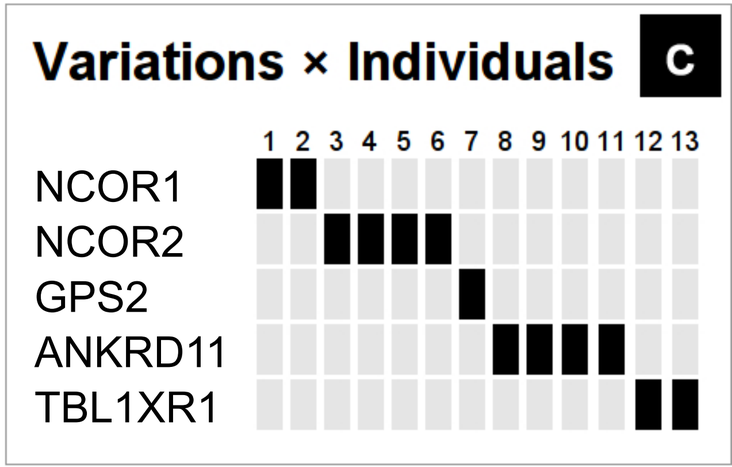

Fig.2 The value of integrating data across multiple MOD InterMine databases when investigating sequence variation and interaction networks (or pathways). Here the thickness/colour density of graph edges reflects the level of phylogenetics support for them, as show in (a). Nodes are surrounded by coloured circules representing the types of variations (b) observed for that gene. For the set of patients/strains being examined, (c) shows how variations are distributed across individuals, or instance showing that, in particular cancer types, mutations in members of a complex tend to be mutually exclusive (Sander et al. 2013).