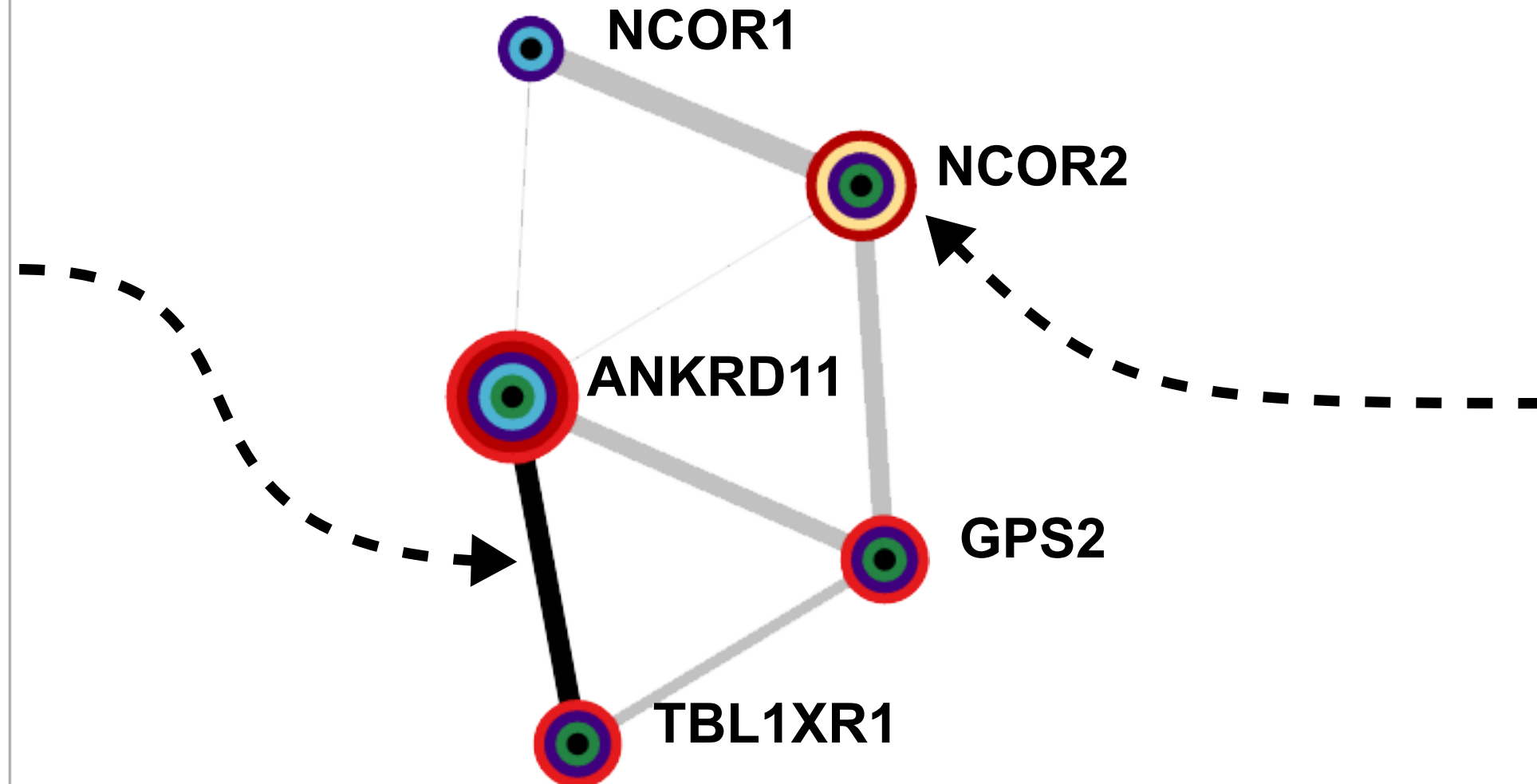
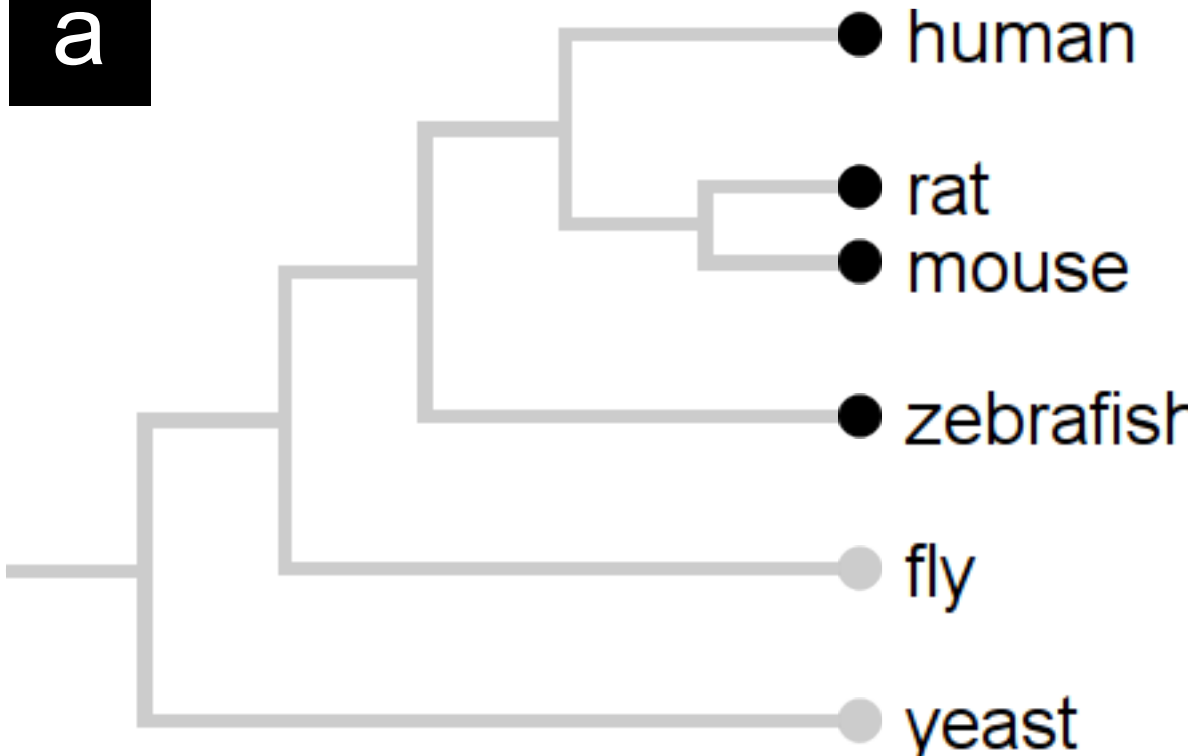


Supporting Organisms

ANKRD11 - TBL1XR1

a



Variations

b

NCOR2

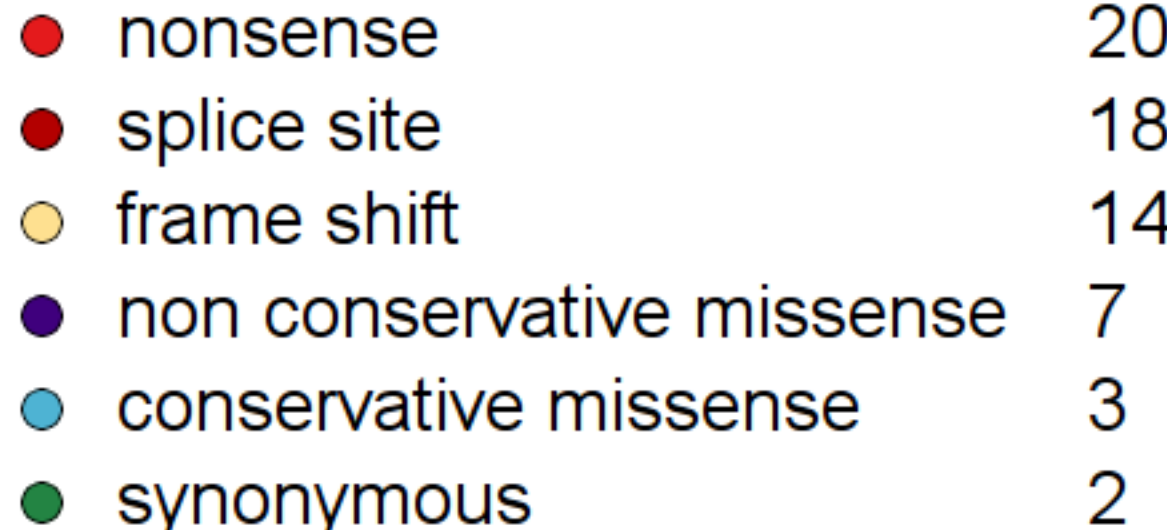


Fig.3

Fig.3 The value of integrating data across multiple MOD-InterMine databases when investigating sequence variation and interaction networks (or pathways). The thickness/color density of graph edges reflects the level of phylogenetic support for them, as shown in (a). Nodes (proteins) are surrounded by colored circles representing the types of variations (b) observed. For the set of individuals/strains being examined, (c) shows how variations are distributed across individuals, perhaps showing, as has been observed in cancer studies, that mutations in members of a complex tend to be mutually exclusive (Ciriello et al 2013).

Variations × Individuals

C

