Figure 4 Reproducible workflows with continuous analysis.
(**a**,**b**) Phylogenetic tree building with four mRNA samples (MouseTw1,
HumanTw1, MouseTw2 and FlyTw) (**a**) and an additional gene
(HumanTw2) (**b**). (**c**,**d**) RNA-seq differential expression experiment
principal component (PC) analysis before (**c**) and after (**d**) addition of
a sample (mT8).