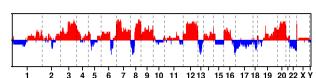
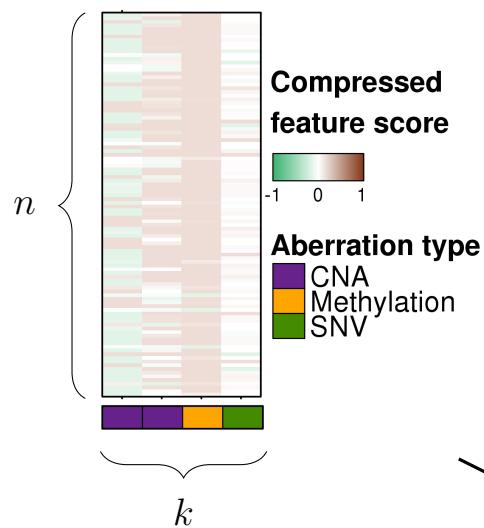


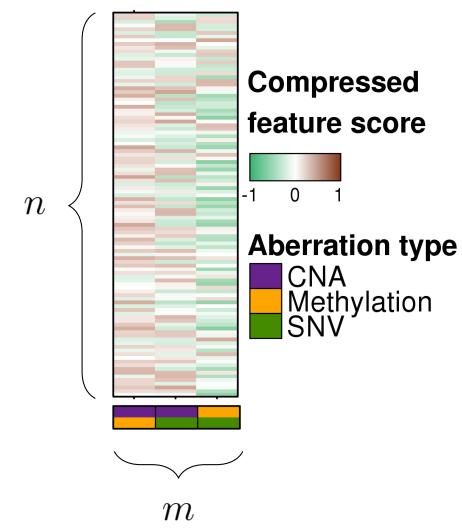
Patient molecular aberration profiles



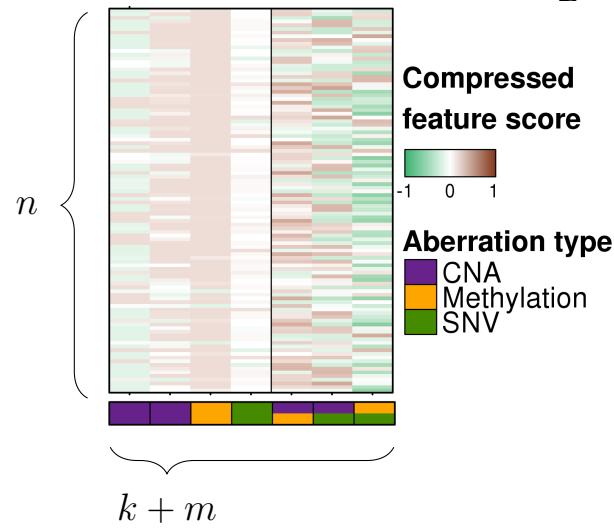
Feature reduction



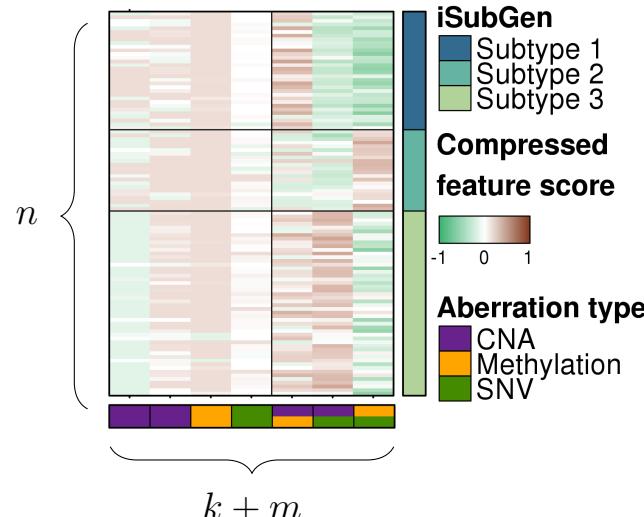
Pairwise similarity measures



Reweight & merge



Pattern discovery



n = # of patients being subtyped
 $k = \sum_{i=1}^d f_i$
 f_i = # of compressed features for aberration type i
 $m = \frac{d(d-1)}{2}$
 d = # of aberration types