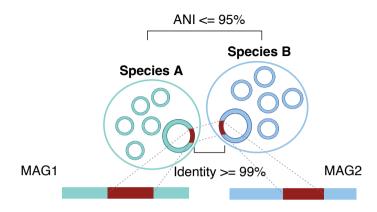
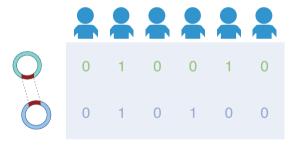
HDMI workflow

1. HGT events candidate detection



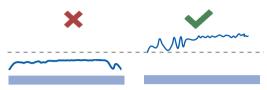
2.4. Cohort-based Validation



Across the cohort the HGT should be found in the two genomes of an HGT event

2. HGT events quality check

2.1 Species presence/ absence



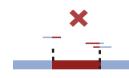
A minimum of average 0.8X median depth

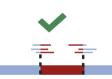
2.2 HGT region covergae



The HGT region has a minimum of 90% horizontal Coverage

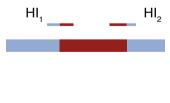
2.3 Split reads support:





The HGT region has a minimum of 3 split reads spanning the start and end sites.

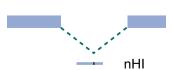
3. HGTs Profiling



sequence of with HGT



HI₁: reads spanning the start of the split site with HGT Insersion HI₂: reads spanning the end of the split site with HGT Insersion nHI: reads spanning the site with no HGT Insersion



simulate sequence without HGT

 $HI = min(HI_1, HI_2)$ if $min(HI_1, HI_2) >= 3$ else 0 nHI = nHI if nHI >= 3 else 0

HGT presence = HI/(HI + nHI) > 0HGT absence = HI/(HI + nHI) = 0