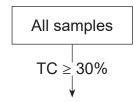
Sample categories per patient

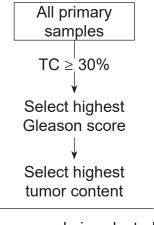


Select samples with mutations that are present in minority of samples

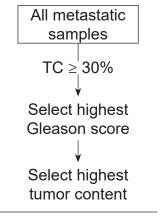
For each mutation:

Select highest Gleason score

Select highest tumor content



If no sample is selected, repeat with $TC \ge 20\%$.



If no sample is selected, repeat with $TC \ge 20\%$.