New LOINC term and observation component for Region of interest

Term name:

Short name; Genetic sequencing coverage

Description: a number between 0 and 100 describing the average number (Depth) of mapped reads at each base position is obtained by counting the total number of mapped reads and dividing by the number of bases in the region sequenced. It only applies when the method is a sequencing method and is especially important to next generation sequencing. The depth will not necessarily be uniform over the region. They are reported as integer followed by “x”. e.g. 50x or a percent.. The required read coverage varies with the kind of study, region studied and intent of the analysis.Some laboratories report a histogram of the read depth across the length of the studied sequence and some report and the interquartile range. Ilumina suggests 30-50x for whole genome sequencing, 100x for whole exome sequencing and 100x for chip sequencing.

Referene: <https://www.illumina.com/science/technology/next-generation-sequencing/plan-experiments/coverage.html>

In LOINC property terms it is really a rati and would be a decimal number So think we should call it a percent and give it units of %