MIDAS2 SNV Track Plot

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Contents

1 Questions **1**

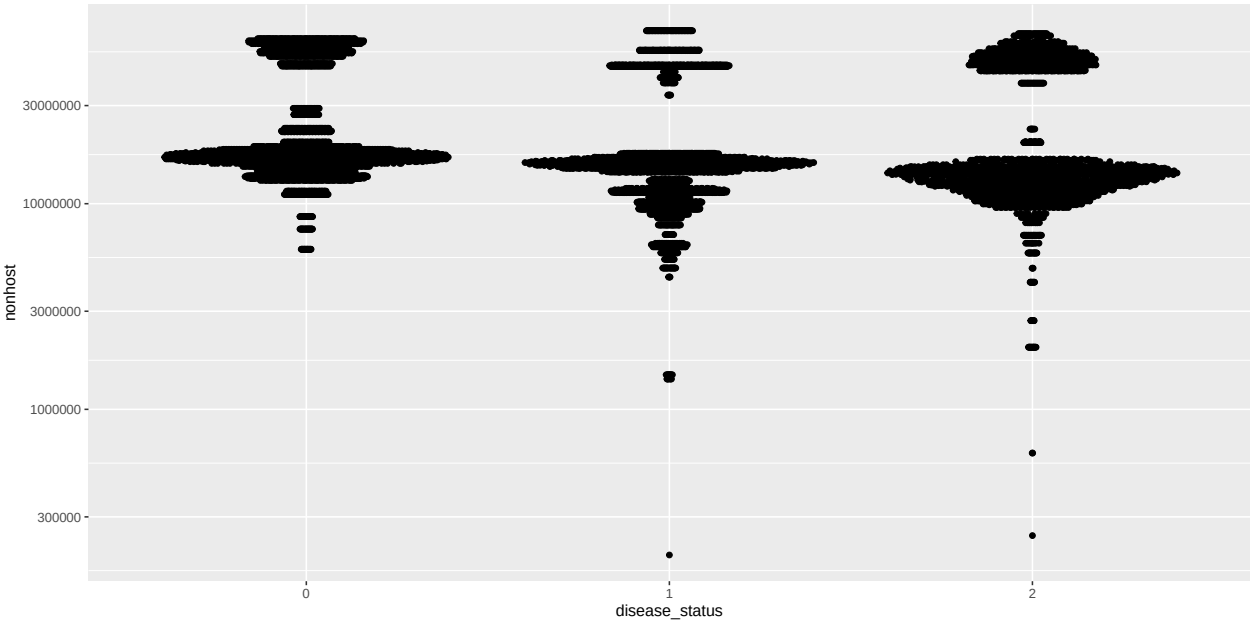
2 Correlation **1**

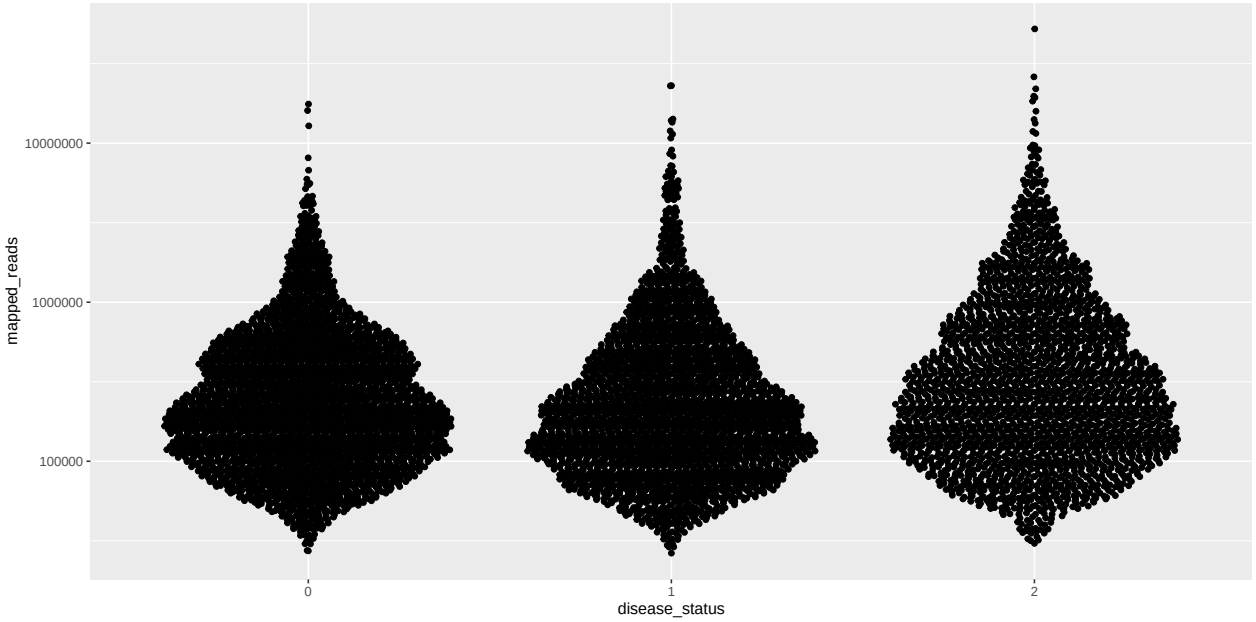
1 Questions

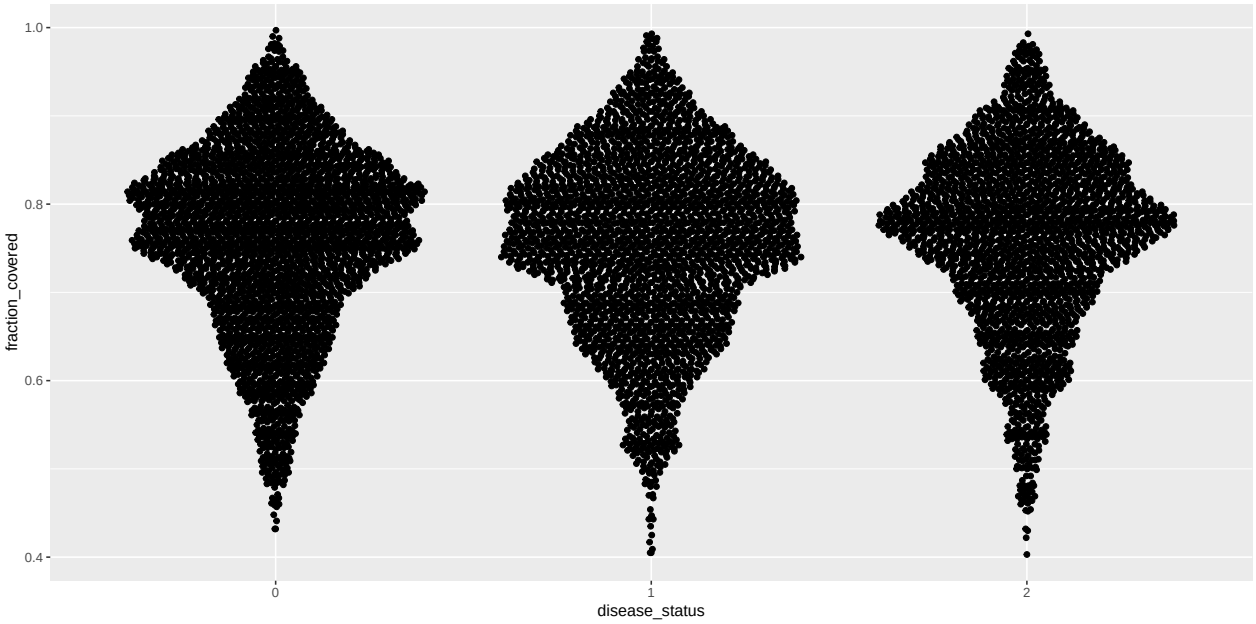
1. Does the marker_coverage is consistent with the species_median_coverage from the Species flow?
2. Apply <gene, sample> filter
3. Define core genes
4. Expected output

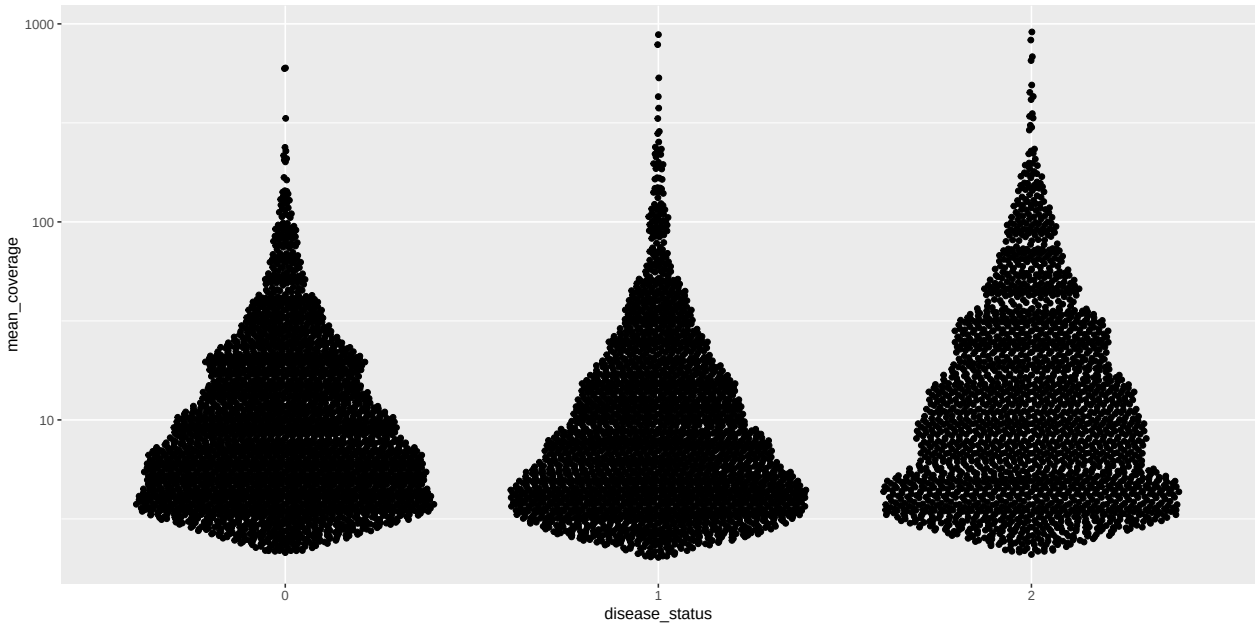
2 Correlation

TODO: remove samples with low total read counts: e.g. minimal 1M (?)




mapped_reads
10000000
1000000
100000
0
1
2
disease_status


fraction_covered
1.0
0.8
0.6
0.4
0
1
2
disease_status

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##
## [[2]]
## NULL
##
## [[3]]
## NULL
##
## [[4]]
## NULL
##
## [[5]]
## NULL
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## [[6]]
## NULL
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