

**Background:**

Genetic factors are likely to affect susceptibility to infectious disease, and the severity of the outcome (Hill 2006). Several results suggest that genetic predisposition plays a role in susceptibility and clinical severity of Covid-19 (Shelton *et al.* 2020; Roberts *et al.* 2020; The Severe Covid-19 GWAS Group 2020).

**Aim:**

We are interested in determining if polymorphisms in lncRNAs are among the genetic factors affecting such susceptibility, with the further, future, aim of identifying lncRNAs that influence susceptibility to Covid-19.

**Methodology:**

Results of meta-analysis of GWAs performed by the COVID-19 Host Genetics Initiative (<https://www.covid19hg.org/>) were processed to scan for SNPs significantly associated to COVID-19 severity according to different clinical parameters, described in the Results section of the COVID-19 web-site (<https://www.covid19hg.org/results/>). As a first step we processed the results coded by COVID-19 Host Genetics Initiative as A2\_ALL, representing a meta-analysis of GWAs of “Very severe respiratory confirmed covid vs. population” and B1\_ALL, representing a meta-analysis of “hospitalized covid vs non-hospitalized covid”.

For each SNP identified in the meta-analysis we searched in the current annotation of the Human Genome the gene(s) whose 3' and 5' end were closest to the SNP. If one of these was a lncRNA, we noted the name in a result table.

The operation was performed using an R function that we developed for this project, and that is made publicly available under GPL 3.0 in github ([https://github.com/fabiomarroni/covid\\_severity\\_lncRNA](https://github.com/fabiomarroni/covid_severity_lncRNA)).

**Results:**

In the A2\_ALL results we identified several SNPs moderately associated to severe COVID vs population for which the closest gene was a lncRNA. In this study, a locus on chromosome 3 (including more than 100 SNPs) showed a strikingly significant association. Several of the SNPs had a lncRNA as their closest gene.

We identified several SNPs moderately associated to COVID severity for which the closest gene was a lncRNA. Strikingly, two lncRNAs (LOC107986082 and LOC107986083) the closest genes to several genome-wide significant SNPs in chromosome 3.

While this does not ensure that lncRNA have a causal role in COVID-19 severity or infection, it warrants the need for further investigation.

**Bibliography:**

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