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As you are establishing a collaborative project to build a COVID-19 coronavirus research network, I would like to offer the use of our analytics platform and team of data and biomedical scientists (freely of course) to support your efforts.

Our **precision**life platform can analyze large scale, complex multi-omic and epidemiological data to generate disease insights that are not possible with current tools. **We can turn our analyses around within hours** even for relatively large populations. We routinely work with very large anonymized patient datasets and are experienced at protecting this data.

To be effective, our tools would require data from a minimum of several hundred COVID-19 patients, ideally including genotype/whole genome sequence with additional data such as disease severity, co-morbidities, and epidemiological/phenotype information such as blood group, smoking, gender, ethnicity etc. that you may wish to correlate. Our methods work hypothesis-free and do not require training. Our studies can readily scale to over 100,000 patients if/when such data becomes available.

We have developed a uniquely capable patient stratification platform based on the association of combinations of genotypic, clinical, epidemiological and environmental features with a given disease, phenotype or outcome in large and complex (multi-factorial & heterogenous) patient populations. While we have not yet published extensively on this method, we have been developing and validating it for 9 years. Its results are superior to existing genomic analysis tools and have been **validated in over 20 complex disease studies and with multiple KOLs, development partners and in pre-clinical assays/models**.

Several of these studies have been in respiratory and immune response/auto-immune diseases. Our results are more informative than can be achieved with single-SNP/monogenic association approaches such as GWAS, and identify many more disease related associations and insights.

We believe our tools would be particularly helpful in analysing the COVID-19 patient datasets currently being generated, giving greater insights into:

- The combinatorial genomic/multi-omic signals associated with differential host response and disease severity/pathology
- Understanding the interaction of non-genomic risk factors such as smoking, air-pollution, gender, ethnicity, blood group and co-morbidities with specific genomic signatures for patient sub-groups
- Developing patient stratification biomarkers that can be used to stratify high- / low-risk people
- Systematic repurposing of existing medicines guided by the specific disease associations of a given patient sub-group, especially in those at risk of late-stage disease
- Identification of novel targets for disrupting virus/host binding and providing non-immunosuppressive targeting of relevant anti-inflammatory pathways

We can work exclusively with non-genomic information if that is more readily available, although obviously the signatures identified may be somewhat less specific.

For more information, I have attached documents with further information on the **precision**life platform and its analytical capabilities, and on one of the relevant disease studies stratifying asthma patients into immunogenic / non-immunogenic cohorts.

I know that you'll be extremely busy at the moment, nevertheless we would welcome the opportunity to help. Please contact me on **covid-19@precisionlife.com** if I can provide more information to you and your team, or if we can arrange a call to discuss our capabilities further

Kind regards and very best wishes for the success of your efforts,

Dr Steve Gardner
CEO