**Statistical analysis**

In this study, we are focusing on a missense functional snp (rs2257167) located in IFNAR1 and its association with a “lung disease severity”. The reference allele was a G and the SNP variant was C. One important phenotype of interest was a clinically defined “severe” and “mild” status, which served as a dichotomous dependent variable of interest. To test the genetic effected, we formulated three hypotheses (1) the additive model, which contained all three genotypes: GG, GC, and CC (2) a dominant model of variant effect, GG vs. GC/CC (3) and a recessive model of variant effect: GG/GC vs. CC. For each of these three hypotheses, we performed the logistic regression and for the dominant/recessive model, we derived the odds ratio of the genotype effect and its corresponding 95% confident interval for each estimate. During the patient recruiting, we also collected other related information including gender, breastfeeding, region, and social economic status. In our analyses, we included each factor in the statistic model as a covariate. All the tests and estimates were made and adjusted for the covariate accordingly. All tests were conducted with R and R packages which are freely available.

**Results**

The SNP st2257167 was located in human genome chromosome 21:33343393, the minor allele frequency (MAF) in 1000 genome population was 0.2288. In our study cohort, the overall MAF was 0.2687; in the sub-population with RSV tested positive, the MAF was 0.2681. (Supplemental table S1).

**Table Legend**

S1. Minor allele frequency assessment.