

**Supplementary material:** High prevalence of SARS-CoV-2 detection and prolonged viral shedding in stools: A Systematic Review and Cohort Study

## **1. Supplementary methods**

### **RNA extraction**

Viral nucleic acid extraction from nasopharyngeal samples was carried out with the High Pure Viral Nucleic Acid kit (Roche Molecular Biochemicals, Germany). For feces samples, Trizol LS Reagent (Invitrogen, USA) was used to isolate RNA from the sample supernatants. RNA extraction was performed according to the manufacturer's instructions. Stool samples, stored in RNAlater solution, were vigorously vortexed and spanned for 5 minutes at 5000g before the nucleic acid extraction. Additionally, for RNAs extracted in feces, a PCR inhibitor clean-up was carried out with OneStep PCR Inhibitor Removal Kit (ZYMO Research, USA) following manufacturer instructions.

### **Viral genome detection**

For follow-ups SARS-CoV-2 RNA was detected using real-time one step RT-QPCR targeting Orf1b with dual-labeled hydrolysis probe as previously reported by Chu et.al.<sup>1</sup>, with some modifications. Briefly, 0.5  $\mu$ M of forward and reverse primers (HKU-ORF1b-nsp14F and HKU-ORF1b-nsp14R) and 0.25  $\mu$ M of probe (HKU-ORF1b-nsp141p) were mixed with 12.5  $\mu$ L AgPath-ID™ One-Step RT-PCR 2X master mix (Thermo Fisher Scientific), 1  $\mu$ L of 25X RT-PCR enzyme mix, and 5  $\mu$ L of extracted RNA in a final volume of 25  $\mu$ L. The reaction was conducted in a StepOnePlus™ thermal cycler (Applied Biosystems) with the following thermal profile: a reverse transcription step for 30 minutes at 50°C, an initial denaturation

for 10 minutes at 95°C followed by 45 cycles of 15 seconds at 95°C and 1 minute at 60°C. Fluorescence acquisition was conducted at annealing/extension step and the PCR cycle at which the fluorescence level meets the threshold (threshold cycle;  $C_T$ ) was recorded for each sample. The limit of detection (LOD) of the assay was established at  $C_T$  39.02, so all samples with fluorescent signal at or before this cycle were considered positive for the presence of SARS-CoV-2 RNA. Positive and negative controls were included in each run. As an amplification control we used the human RNase P (RP) housekeeping gene. RP gene primers, probe and the amplification reaction conditions were described previously (<https://www.fda.gov/media/134922/download>). The amplification reaction was prepared using 2  $\mu$ M of each primer and 0.5  $\mu$ M of dual-labeled probe, and an annealing-extension step was performed at 55°C for 1 minute. RP positive at or before 35 cycles indicated the presence of enough nucleic acid from human RNase P gene and the sample was considered of acceptable quality.

### **Search strategy and selection process**

We conducted an electronic search from December 1, 2019, to June 3, 2020 in MEDLINE (via PubMed) database. We used the following terms in the MEDLINE search: ("2019 nCoV" OR "2019nCoV" OR "2019 novel coronavirus" OR "COVID 19" OR COVID19 OR "new coronavirus" OR "novel coronavirus" OR "SARS CoV-2" OR (Wuhan AND coronavirus) OR "COVID-19" OR "SARS-CoV" OR "2019-nCoV" OR "SARS-CoV-2" OR "coronavirus disease 2019" OR "coronavirus disease-19") AND ("Stools" OR "Feces" OR "gastro" OR "gastrointestinal" OR "gastro-intestinal" OR "digestive"). References of studies searched

were also included. We hand searched (up to June 3, 2020) preprint servers (bioRxiv, medRxiv, and Social Science Research Network First Look) and coronavirus resource centers of The Lancet, JAMA, and New England Journal of Medicine. We did not limit our search by language.

## REFERENCE

1. Chu DKW, Pan Y, Cheng SMS, et al. Molecular Diagnosis of a Novel Coronavirus (2019-nCoV) Causing an Outbreak of Pneumonia. *Clinical chemistry* 2020; **66**(4): 549-55.

## 2. Risk of bias assessment

**Table S1.-** Completed IHE checklist for case-series studies.

First Author	Xiong XL	Zhang J	Wang W	Zhang W1	Zhang W2	Xiao F 1	Xiao F2	Wei XS	Pan Y
<b>Study objective</b>									
1. Was the hypothesis/aim/objective of the study clearly stated?	Y	Y	Y	U	U	N	Y	Y	N
<b>Study design</b>									
2. Was the study conducted prospectively?	N	N	N	N	N	N	N	N	N
3. Were the cases collected in more than one centre?	N	N	Y	N	N	N	N	N	N
4. Were patients recruited consecutively?	N	N	N	N	N	N	N	N	N
<b>Study population</b>									
5. Were the characteristics of the patients included in the study described?	N	Y	N	N	N	N	Y	Y	N
6. Were the eligibility criteria (i.e. inclusion and exclusion criteria) for entry into the study clearly stated?	N	N	N	N	N	N	N	N	N
7. Did patients enter the study at a similar point in the disease?	U	N	N	N	N	N	N	N	N
<b>Intervention and co-intervention</b>									
8. Was the intervention of interest clearly described?	-	-	-	-	-	-	-	-	-
9. Were additional interventions (co-interventions) clearly described?	-	-	-	-	-	-	-	-	-
<b>Outcome measure</b>									
10. Were relevant outcome measures established a priori?	U	U	U	Y	Y	N	N	N	N
11. Were outcome assessors blinded to the intervention that patients received?	N	N	N	N	N	N	N	N	N
12. Were the relevant outcomes measured using appropriate objective/subjective methods?	Y	Y	Y	Y	Y	N	Y	Y	N
13. Were the relevant outcome measures made before and after the intervention?	N	N	N	N	N	N	N	N	N
<b>Statistical analysis</b>									
14. Were the statistical tests used to assess the relevant outcomes appropriate?	Y	N	N	Y	Y	N	Y	Y	N
<b>Results and conclusions</b>									
15. Was follow-up long enough for important events and outcomes to occur?	-	-	-	-	-	-	-	-	-
16. Were losses to follow-up reported?	-	-	-	-	-	-	-	-	-
17. Did the study provided estimates of random variability in the data analysis of relevant outcomes?	-	-	-	-	-	-	-	-	-
18. Were the adverse events reported?	-	-	-	-	-	-	-	-	-
19. Were the conclusions of the study supported by results?	Y	Y	Y	Y	Y	Y	Y	Y	Y
<b>Competing interests and sources of support</b>									
20. Were both competing interests and sources of support for the study reported?	Y	Y	Y	Y	Y	N	Y	Y	Y

Y: Yes; N: No; U: Unclear

**Table S2.-** Completed Newcastle-Ottawa scale checklist for cohort studies.

Author	Date	Selection	Comparability	Outcome
Chen C	March 2020	☛☛☛		☛☛
Chen Y	April 2020	☛☛☛		☛☛
Chen W	February 2020	☛☛☛		☛☛
Cheung KS	April 2020	☛☛☛		☛
Dreher M	April 2020	☛☛☛		☛
Han C	April 2020	☛☛☛		☛
Huang JT	June 2020	☛☛☛		☛
Kujawski S	March 2020	☛☛☛		☛☛
Li H	February 2020	☛☛☛		☛☛
Xu Y	April 2020	☛☛☛		☛☛
Zeng L 2	March 2020	☛☛☛		☛☛
Wu Y	March 2020	☛☛☛		☛☛
Zautner AE	April 2020	☛☛☛		☛
Zheng S	February 2020	☛☛☛		☛





### 3. Figures

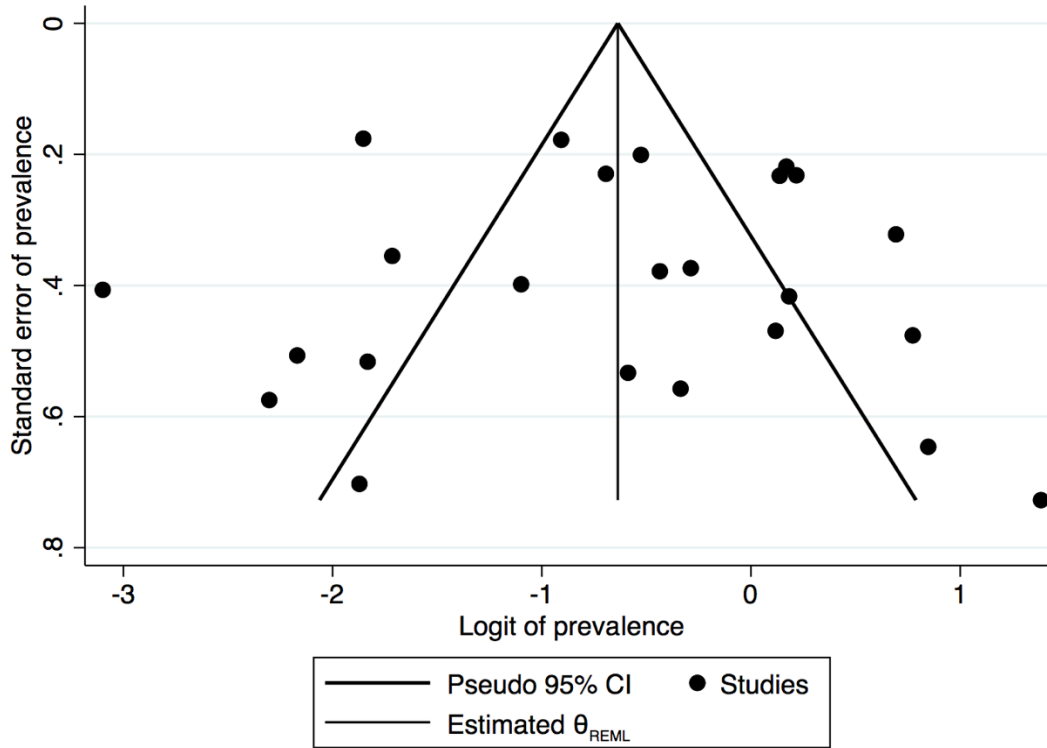
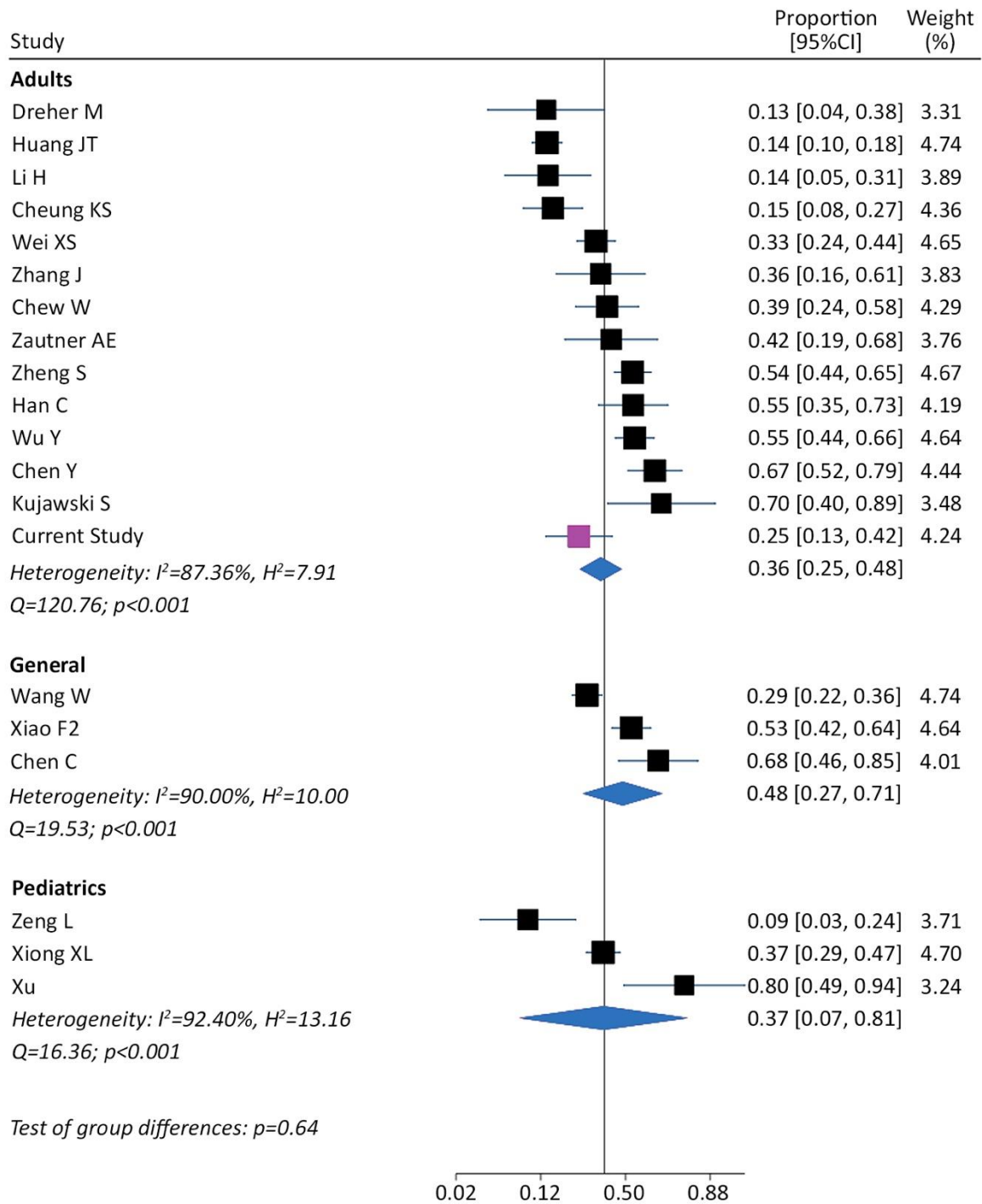
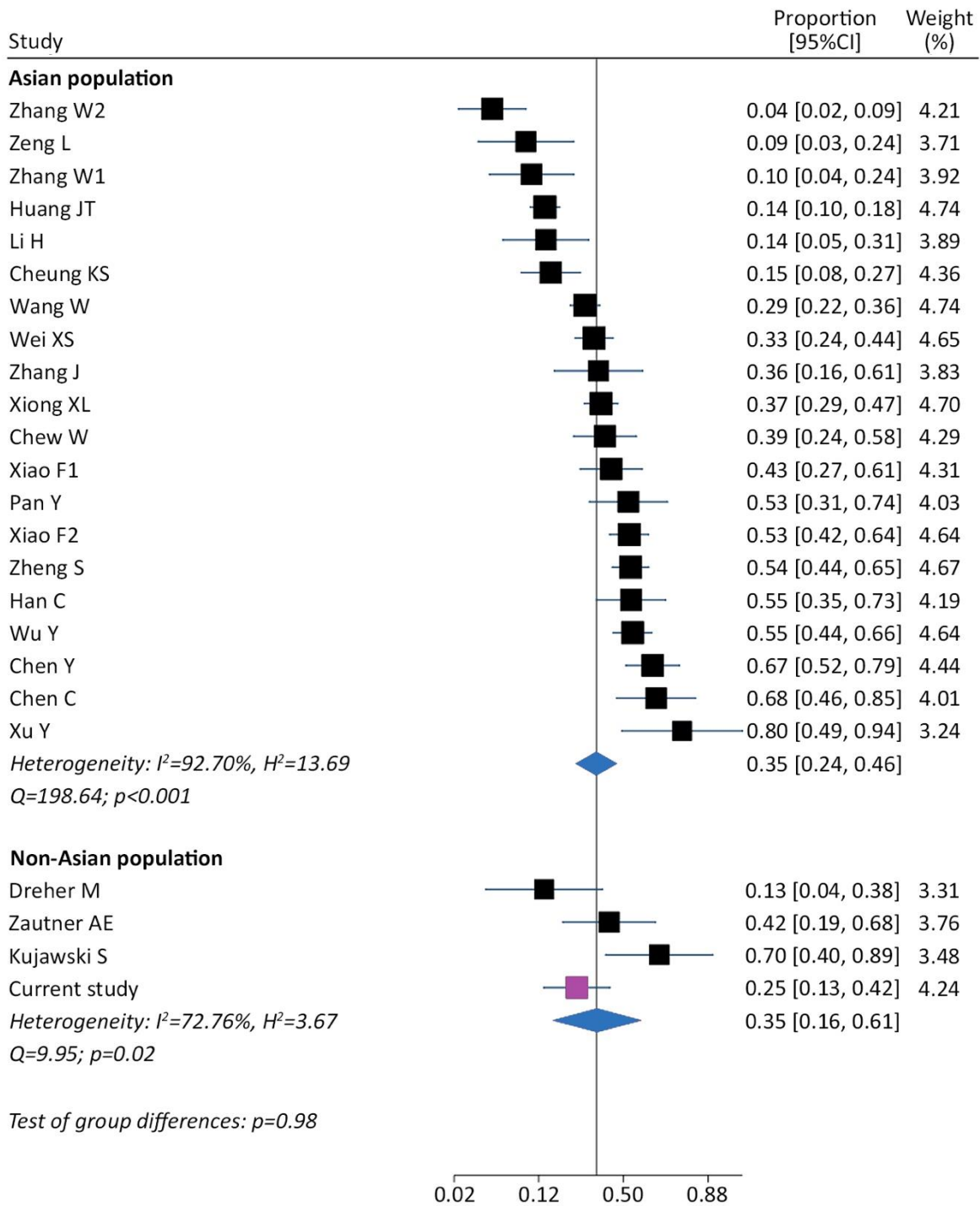


Figure S1.- Funnel plot of the studies included for SARS-CoV-2 detection in stools.

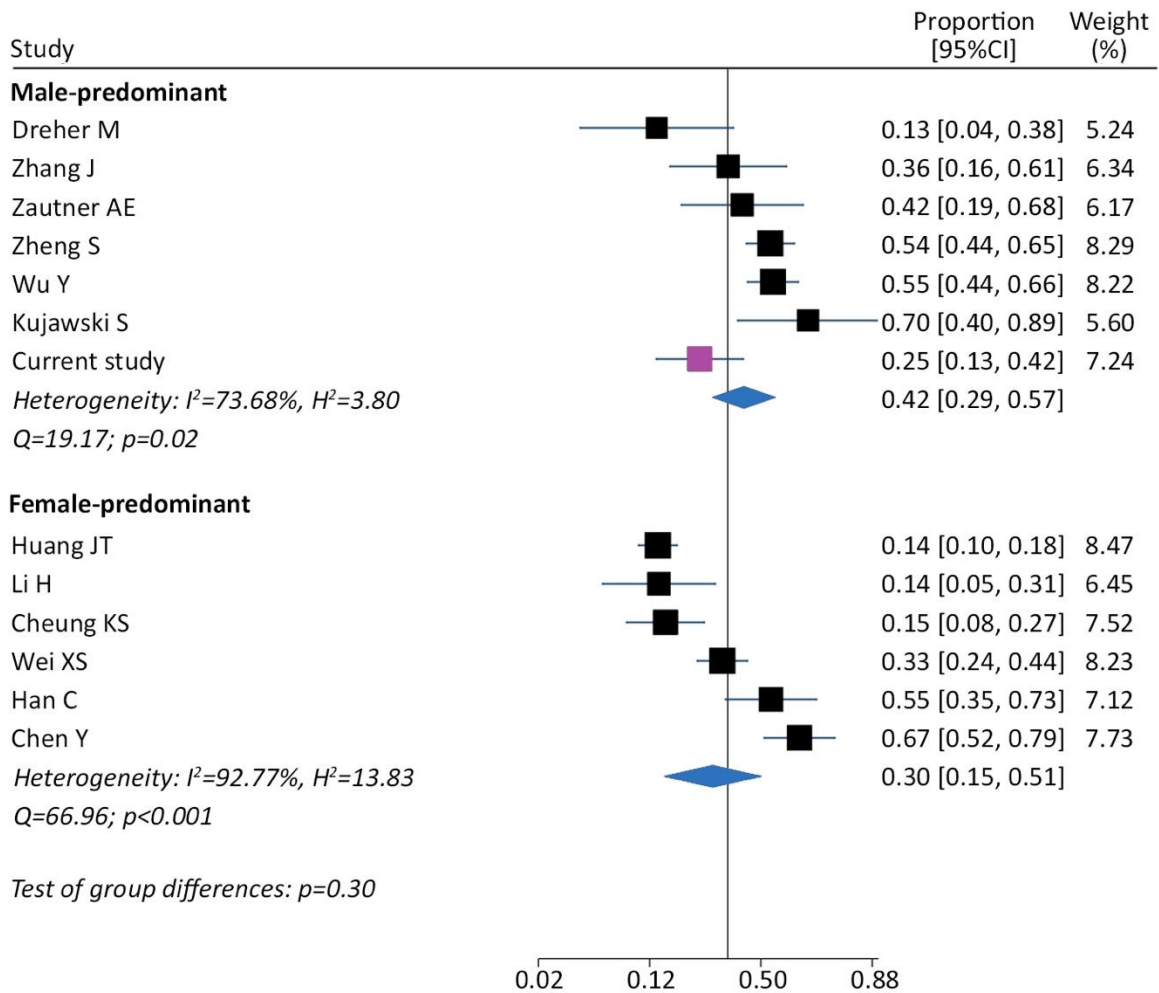




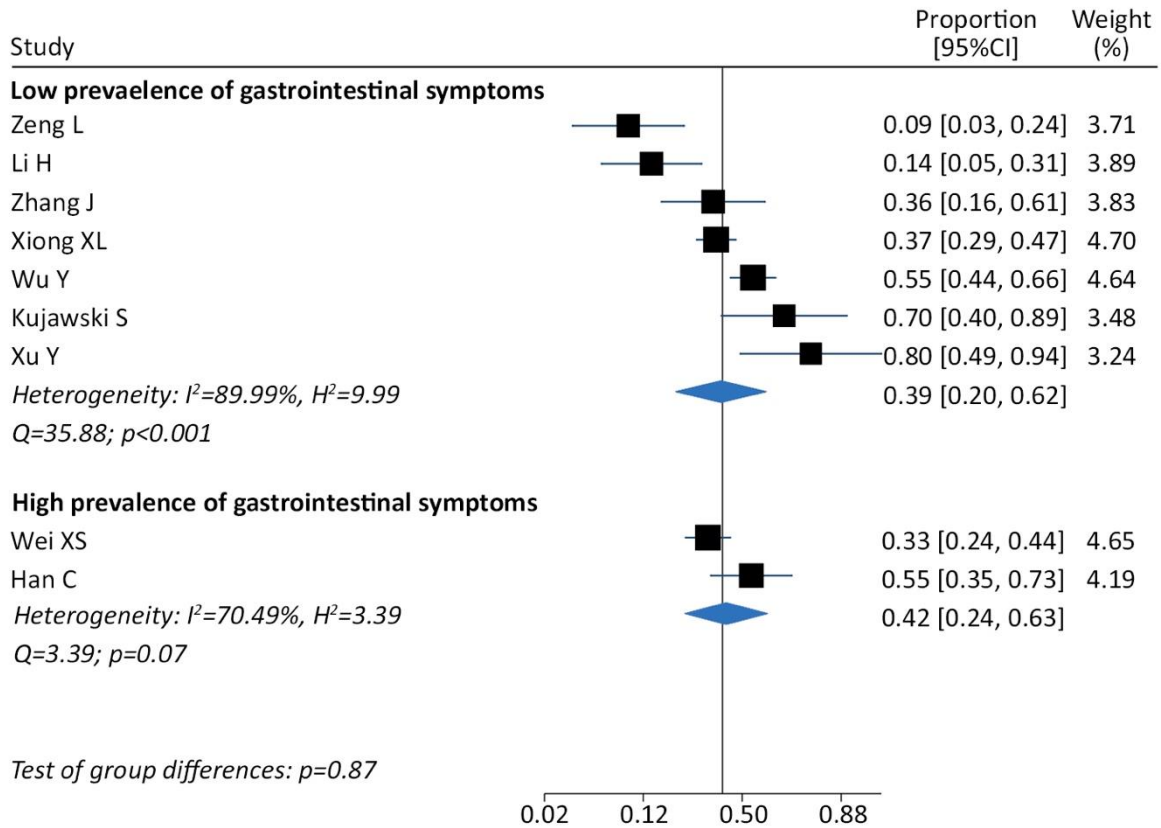
**Figure S2.-** Forest plots of prevalence of viral detection in stools from SARS-CoV-2 infected patients according to age (subgroup analysis).



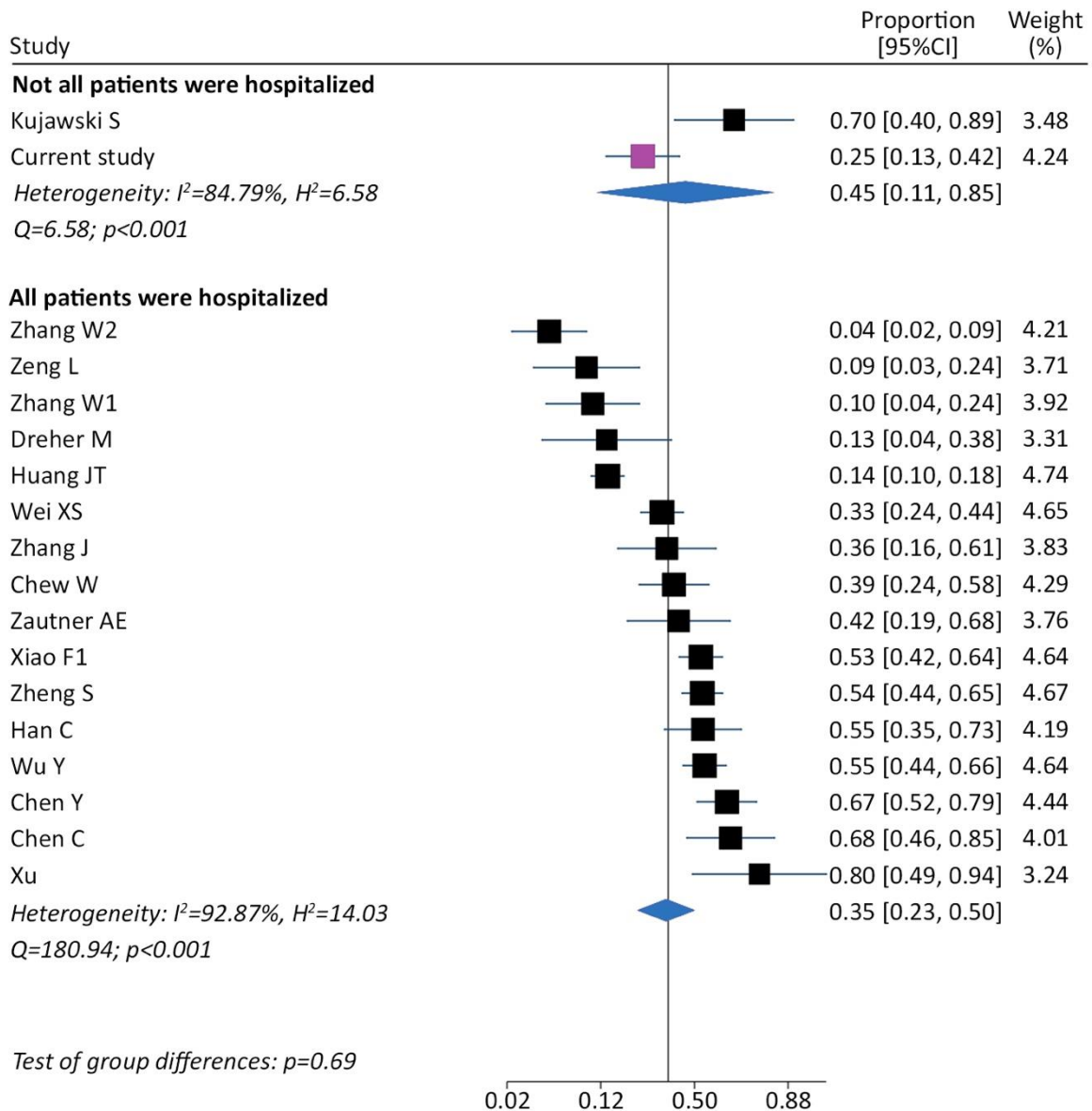
**Figure S3.-** Forest plots of prevalence of viral detection in stools from SARS-CoV-2 infected patients according to ethnicity (subgroup analysis).



**Figure S4.-** Forest plots of prevalence of viral detection in stools from SARS-CoV-2 infected patients according to gender (subgroup analysis).



**Figure S5.-** Forest plots of prevalence of viral detection in stools from SARS-CoV-2 infected patients according to gastrointestinal symptoms (subgroup analysis).



**Figure S6.-** Forest plots of prevalence of viral detection in stools from SARS-CoV-2 infected patients according to hospitalization (subgroup analysis).