1 **Evaluation of lockdown impact on SARS-CoV-2 dynamics through viral genome**

2 **quantification in Paris wastewaters**

3

4 Wurtzer S[1], Marechal V[2+], Mouchel JM[3], Maday Y[4+], Teyssou R[5], Richard E[1], Almayrac JL[6] & Moulin

5 L[1*].

6 [1] Eau de Paris, R&D Laboratory, DRDQE 33 Avenue Jean Jaurès 94200 Ivry/Seine

7 [2] Sorbonne Université, INSERM, Centre de Recherche Saint-Antoine, F-75012, Paris, France

8 [3] Sorbonne Université, CNRS, EPHE, UMR 7619 Metis, 75005 PARIS, e-LTER Zone Atelier

9 Seine, France[4] Sorbonne Université, CNRS, Université de Paris, Laboratoire Jacques-Louis Lions

10 (LJLL), F-75005 Paris, France et Institut Universitaire de France

11 [5] Department of Virology, Institut de Recherche Biomédicale des Armées. 1Place du Général

12 Valérie André. BP73. 91223 BRETIGNY-SUR-ORGE

13 [6] SIAAP, Service process-laboratoire SIAAP site Seine Amont

14 [+] VM and YM are co-founders of the COVID-IA initiative

15

16 Corresponding author: * laurent.moulin@eaudeparis.fr

17

18 Keywords: SARS-CoV-2, COVID-19, lockdown, quantification, wastewater

19

20   **Summary**

21   SARS-CoV-2 is the etiological agent of COVID-19. Most of SARS-CoV-2 carriers are assumed to exhibit

22   no or mild non-specific symptoms. Thus, they may contribute to the rapid and mostly silent

23   circulation of the virus among humans. Since SARS-CoV-2 can be detected in stool samples it has

24   recently been proposed to monitor SARS-CoV-2 in wastewaters (WW) as a complementary tool to

25   investigate virus circulation in human populations. In the present work we assumed that the

26   quantification of SARS-CoV-2 genomes in wastewaters should correlate with the number of

27   symptomatic or non-symptomatic carriers. To test this hypothesis, we performed a time-course

28   quantitative analysis of SARS-CoV-2 by RT-qPCR in raw wastewater samples collected from several

29   major wastewater treatment plant (WWTP) of the Parisian area. The study was conducted from 5

30   March to 23 April 2020, therefore including the lockdown period in France (since 17 March 2020).

31   We confirmed that the increase of genome units in raw wastewaters accurately followed the

32   increase of human COVID-19 cases observed at the regional level. Of note, the viral genomes could

33   be detected before the beginning of the exponential growth of the epidemic. As importantly, a

34   marked decrease in the quantities of genomes units was observed concomitantly with the reduction

35   in the number of new COVID-19 cases which was an expected consequence of the lockdown. As a

36   conclusion, this work suggests that a quantitative monitoring of SARS-CoV-2 genomes in wastewaters

37   should bring important and additional information for an improved survey of SARS-CoV-2 circulation

38   at the local or regional scale.

39

Introduction

40

41   SARS-Cov-2 is a positive-sense single-stranded RNA virus of the *Coronaviridae* family and the etiologic

42   agent of COVID-19, a globalized infection affecting more than 2.5 million people worldwide and

43   causing more than 180 000 deaths in total, including more than 160 000 cases in France on April 22,

44   2020. Virus transmission is mainly associated with the projection of respiratory droplets although a

45   possible contamination through aerosols, contaminated hands and inert surfaces is likely. SARS-Cov-

46   2 causes severe complications mostly in elderly or people suffering from comorbidity factors (such as

47   diabetes, hypertension, obesity, acquired or iatrogenic immunosuppression).

48   The viral infection may initiate in the upper respiratory and/or the lower respiratory tracts. Similarly

49   to SARS-CoV-1 (1) and MERS-CoV (2), SARS-CoV-2 genome was also detected in blood and stools (3–

50   5). This argue for a possible enteric phase of the infection although isolation of infectious virus from

51   feces seems difficult (6). Of note diarrhea have been reported in some cases of COVID-19 (6).

52   Importantly, SARS-CoV-2 genomes could be detected in feces several weeks after it could not be

53   detected anymore in oral swabs, suggesting that viral excretion in tools may be longer than oral

54   secretion (7). The presence of viral genomes in stools may open new perspective in the survey of

55   SARS-CoV-2 carriers. It would notably suggest that the virus could possibly be transmitted by a feco-

56   oral route, an hypothesis that should likely deserve a careful examination (8) .

57   Management of an epidemic, such as lockdown decision, requires a careful monitoring of the

58   infected population by detecting the virus in carriers through massive or targeted testing.

59   Investigating the proportion of people that have been infected through sero-epidemiological surveys

60   is equally important but antibodies against SARS-CoV-2 will appear only weeks after initial infection

61   (9,10). In the case of COVID-19, due to the lack of systematic and repeated screening of the

62   population, the precise number of infected people is difficult to assess, especially because of the high

63   proportion of infected people that exhibit only few or no symptoms but could secrete and silently

64   transmit the virus (11–14). Depending on screening kit availability and public health policy, testing

65   strategy varies between countries which may explain some discrepancy between worldwide data.

66   Estimating the effective proportion of infected individuals is essential for monitoring the epidemic

67   spread and to propose adapted and efficient control procedures, such as partial or total lockdown.

68   France went into lockdown on the March 17 2020, a decision that was expected to have a major

69   impact on virus circulation especially when asymptomatic carriers are considered to have a strong

70   impact on virus transmission. This decision was motivated by the urgent need to limit exposure of so-

71   called fragile people who are at highest risk to develop the most severe forms of the disease

72   (11,13,15).

73   Analysis of raw wastewaters collected at the inlet of wastewater treatment plants (WWTP) may

74   provide essential information on the health of the human population that is connected to the WWTP.

75   It may notably allow measurement and identification of pathogens or drugs that may be difficult to

76   assess otherwise. Using this method, the European Monitoring Center for Drugs and Drug Addiction

77   follows drugs and their metabolites in the wastewater of several European cities (16). In addition

78   previous works on human enteric viruses in urban river and in raw and treated wastewaters

79   demonstrated that the presence of these viruses was directly linked to epidemic state in the

80   population (17,18). This strongly argue for a close monitoring of fecal viruses in wastewater as a new

81   and complementary tool for investigating human epidemics.

82   Enveloped viruses like coronaviruses are expected to be less resistant than naked viruses that are

83   usually tracked in waste and environmental waters. There is still little information on the persistence

84   of coronaviruses in waters and most of our current knowledge has been inferred from experiments

85   made on surrogate viruses. Recent data suggested that infectious SARS-CoV-2 is particularly resistant

86   in environmental conditions: 3.5 half-life days in the air, 7 days on some surfaces, any reduction at

87   pH between 3 and 10 (6,19). Previous studies on SARS-CoV-1 indicated a significant persistence at 4

88   °C even in wastewater (more than 20 days), or a persistence of at least 1 or 2 days at summer

89   temperatures (1,20,21).

90   Altogether these results led us and others to suggest that the detection of SARS-CoV-2 genomes in

91   wastewater could provide an early and global tool to monitor virus circulation in addition to human

92   epidemiological data (22–24).

93   A first publication underlined the putative benefit of a qualitative approach for monitoring SARS-CoV-

94   2 in wastewaters (24). Other studies used quantitative measurements of viral genomes but the

95   survey only started at the apex of the epidemic (25). Here, we used a specific reverse-transcription

96   quantitative PCR (RT-qPCR) method to precisely quantify SARS-CoV-2 genome equivalents in raw

97   wastewaters of the Parisian area. A 2-months survey covering the lockdown period allowed to

98   observe an increase and a decrease in the total quantities of viral genomes that paralleled the

99   number of new COVID-19 cases in the same region. To our knowledge, this is the first real-time

100   indirect survey of SARS-CoV-2 circulation during a lockdown period.

101

102　**Methods**

103　**Sample collection**

104　Three WWTP (more than 100 000 inhabitants linked to the station from the Parisian area were

105　sampled since the start of the epidemic (March 5th, 2020). Samples were kept at 4°C and processed

106　less than 24 hours after sampling.

107　**Concentration methods**

108　Samples were homogenized, then 11 ml were centrifugated at 200 000 x g for 1 hour at +4°C. Viral

109　pellets were resuspended in 400 µL of PBS 1X buffer.

110　200µL of viral concentrate were lysed and extracted using PowerFecal Pro kit (QIAGEN) on a

111　QIAsymphony automated extractor (QIAGEN) according to a modified manufacturer's protocol.

112　Extracted nucleic acids were filtered through OneStep PCR inhibitor removal kit (Zymoresearch)

113　according the manufacturer's instructions.

114　**Molecular detection method**

115　The RT-qPCR primers and PCR conditions used herein have been previously described (26). The

116　amplification was done using Fast virus 1-step Master mix 4x (Lifetechnologies) with oligonucleotide

117　concentrations recommended previously. Detection and quantification were carried on the E gene by

118　RT-qPCR. Positive results were confirmed by amplification of a region located within the gene

119　encoding for the viral RNA-dependent RNA polymerase (RdRp). An internal positive control (IPC) was

120　added to evaluate the presence of residual inhibitors. The detection limit was estimated to be

121　around 10^3 genome units per liter of raw wastewater.

122　The quantification was performed using a standard curve based on synthetic oligonucleotide

123　corresponding to the full-length amplicon on the E gene (SARS-Cov2 Wuhan-Hu isolate sequence

124　NC_045512.2). Amplification reaction and fluorescence detection were performed on Viaa7 Real

125　Time PCR system (Lifetechnologies).

126　**Modelization of Viral RNA excretion**

127　Even if the real number of infected people is unknown, we attempted to compute the expected

128　amount of viral RNA shed in stools, using available information. Since the very beginning of the

129　epidemic, the daily number of patients consulting at the emergency department of greater Paris

130　hospitals　and　diagnosed　with　COVID　symptoms　was　published

131　(https://www.santepubliquefrance.fr/). Wölfel et al. measured the daily amount of vRNA in swab

132　samples for few patients (27). This data was used as an estimation of viral expression for all infected

133   people and we also assume that people with symptoms would consult 2 days after the onset of the

134   illness, and that at any moment the number of patients with strong symptoms was proportional to

135   the total number of infected people. Accepting the above hypothesis, the convolution of two dataset

136   (i.e. number of consulting patient and model of excretion) is an emission-proxy, proportional to the

137   total amount of viral RNA shed in stools in a given population.

138   **Results**

139   Three major wastewater treatment plants (WWTP) managing over 75 000 cubic meters per day, were

140   sampled at the inlet of the plant from March 5th to April 23th 2020. All processed samples scored

141   positive for the presence of SARS-CoV-2 genomes as assessed by RT-qPCR on the viral E gene. All

142   positive samples were confirmed by RT-qPCR on the viral RdRp gene (Figure 1). The COVID-19

143   epidemic in the same region was illustrated by various indicators such as the total number of COVID-

144   19 cases treated in the regional hospitals, the accumulation of hospitalized patients or the daily

145   death toll linked to COVID 19. Based on these epidemiologic statistics and on published data on virus

146   shedding quantity and delay, an estimated indicator of the viral excretion in the region was

147   calculated and compared to the viral load in wastewaters.

148   Briefly, the concentration of vRNA in raw wastewater was around 5.10^4 genome units /L on the 5th of

149   March 2020. At the same date, less than 10 COVID-19 confirmed patients were reported and only

150   404 individuals were tested positive in France. For the Parisian area more specifically, 91 confirmed

151   cases were reported at that time (on a total number of more than 12 million inhabitants) and no

152   death was recorded. Altogether this information indicated that the COVID-19 epidemic was at an

153   early stage in the Parisian area.

154   The time-course monitoring of viral load in WW displayed an exponential increase (from 5.10^4 GU/L

155   on March 5th to 3.10^6 GU/L, a 2-log increase in average). A peak was observed on the 9th of April,

156   followed by a marked decrease (1-log reduction in average). The shape of the concentration curve

157   was reminiscent of the disease dynamics at the regional level, with an 8-day temporal shift.

158   Altogether these results underline that essential information could be obtain from wastewater

159   epidemical monitoring, such as early starting of the epidemics, evolution of the infections, and

160   impact of the lockdown procedures.

161

162   **Discussion**

163   It is demonstrated here for the first time that a quantitative detection of SARS-CoV-2 in wastewaters
164   could reflect the circulation of the virus in human populations in the Parisian area, a region called Ile-
165   de-France. Since similar results were obtained from three independent and distant WWTP around
166   Paris with striking similarities, the time-course survey that has been done is likely to be a direct
167   reflect of SARS-CoV-2 dynamic in Parisian inhabitants that are connected to these WWTP. It is to note
168   that at home lockdown is effective since March 17th 2020, therefore limiting daily transport.
169   Importantly no significant rain fall was recorded in the Parisian area that could have had an impact
170   on virus concentration in wastewaters. More surprisingly this decrease stopped after 7 days, and the
171   virus concentration has been stable since. This plateau is intriguing, although the emission-proxy
172   suggests that it can partly be explained by the duration of the virus shedding period, and several
173   hypotheses can be made. First, one may suggest that many infected people are still secreting viruses
174   in their feces whereas the virus is not present anymore in the ORL region. This hypothesis has
175   recently been confirmed in Chinese patients with longer periods of excretion than reported by Wölfel
176   (7). Second, lockdown has been partial since some specific workers have been allowed to pursue
177   essential activities that were not compatible with homeworking. These people are usually not
178   considered at risk of severe infections (i.e. more pauci-symptomatic case), but they may promote
179   virus circulation at a low level notably in their family if they do not strictly respect hands cleaning and
180   mask wearing. Third, one may suggest that lockdown is not respected by few people that maintain
181   virus circulation at a low but significant level. Virus survey in the same WWTP will likely provide some
182   answers in the following weeks.

183   The observed delay between epidemiological curves in humans compared to virus quantification in
184   wastewaters is probably due to several parameters. This may include the effective number of
185   infected people, the timing and temporal kinetics of viral shredding in feces and other causes that
186   are still to be investigated. Nevertheless, our data are in very good agreement with epidemiological
187   parameters such as the number of confirmed COVID-19 patients or our excretion model. To that
188   respect, let us note that our study provides a strong indirect evidence for a significant reduction of
189   virus transmission in response to lockdown. According to our results, the number of people
190   producing SARS-CoV-2 is likely underestimated when based on individual testing, especially during a
191   pandemic where a limited quantity of virological tests did not allow for extensive testing so far. As a
192   comparison the quantity of human enteric virus concentration in raw wastewater is around 10^6 per
193   liter (17).

194   Epidemiological investigations that have been conducted on the Diamond Princess cruise ship
195   suggested that less than 20% of infected people were asymptomatic (12). Most of the infected
196   people were reported to exhibit moderate nonspecific symptoms including fever, headache, body
197   aches, intense tiredness and/or dry cough. However infected people can produce SARS-CoV-2 for a
198   few days before the onset of symptoms and up to several days after recovery (2,7,28). Another
199   extensive study based on Iceland population shows that 43% of SARS-CoV-2 positive patients did not
200   report any symptoms (29). In this context, a clear majority of infected carriers may silently
201   contaminate sensitive people. This led us to suggest that the contamination of raw wastewaters may
202   occur before the significative appearance of clinical cases. The evolution of SARS-CoV-2 viral load in
203   wastewater was in good agreement with the dynamics of pandemic during the first wave of infection
204   in urbanized area, which is also in agreement with the excretion model that is proposed here. To our
205   knowledge this is the first report demonstrating that the quantitative monitoring of SARS-CoV-2 in
206   raw wastewater is a time-related relevant indicator of the evolution of the health status of a
207   population linked to a sewage network. This quantitative approach was especially useful to
208   unrevealed the dynamics of the pandemic and follow impact of government measures such as
209   containment.

210   To finish, this data, if carefully utilized, could help to describe the proportion of SARS-CoV-2 excretors
211   during all the monitored pandemic event and allow to calculate the immunity of the population,
212   especially at the local level.

213   **Conclusions**

214   Our results strongly argue for the use of a quantitative monitoring of SARS-CoV-2 genomes in urban
215   wastewaters. This would also argue for a long-time conservation of wastewater samples in dedicated
216   local i.e. wastewater-bank, which would allow a retrospective investigation of pathogens circulation.
217   Additionally, wastewaters survey may provide an alternative and possibly early tool to detect
218   pathogens in populations when investigations in humans are difficult to conduct for logistic, ethical
219   or economic reasons, notably in poor countries that are strongly exposed to COVID-19 epidemic.

220

221

222   **Reference**

223   1.   Wang X-W, Li J-S, Guo T-K, Zhen B, Kong Q-X, Yi B, et al. Concentration and detection of SARS
224   coronavirus in sewage from Xiao Tang Shan Hospital and the 309th Hospital. Journal of Virological
225   Methods. sept 2005;128(1‑2):156‑61.

226   2.   Zhou J, Li C, Zhao G, Chu H, Wang D, Yan HH-N, et al. Human intestinal tract serves as an alternative
227   infection route for Middle East respiratory syndrome coronavirus. Sci Adv. nov
228   2017;3(11):eaao4966.

229   3.   Zhang W, Du R-H, Li B, Zheng X-S, Yang X-L, Hu B, et al. Molecular and serological investigation of
230   2019-nCoV infected patients: implication of multiple shedding routes. Emerging Microbes &
231   Infections. 1 janv 2020;9(1):386‑9.

232   4.   Zhang H, Kang Z, Gong H, Xu D, Wang J, Li Z, et al. The digestive system is a potential route of 2019-
233   nCov infection: a bioinformatics analysis based on single-cell transcriptomes [Internet].
234   Microbiology; 2020 janv [cité 28 avr 2020]. Disponible sur:
235   http://biorxiv.org/lookup/doi/10.1101/2020.01.30.927806

236   5.   Wu Y, Guo C, Tang L, Hong Z, Zhou J, Dong X, et al. Prolonged presence of SARS-CoV-2 viral RNA in
237   faecal samples. Lancet Gastroenterol Hepatol. 19 mars 2020;

238   6.   Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y, et al. Epidemiological and clinical characteristics of 99
239   cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. The Lancet. févr
240   2020;395(10223):507‑13.

241   7.   Chen C, Gao G, Xu Y, Pu L, Wang Q, Wang L, et al. SARS-CoV-2–Positive Sputum and Feces After
242   Conversion of Pharyngeal Samples in Patients With COVID-19. Ann Intern Med [Internet]. 30 mars
243   2020 [cité 28 avr 2020]; Disponible sur: https://annals.org/aim/fullarticle/2764036/sars-cov-2-
244   positive-sputum-feces-after-conversion-pharyngeal-samples

245   8.   Yeo C, Kaushal S, Yeo D. Enteric involvement of coronaviruses: is faecal–oral transmission of SARS-
246   CoV-2 possible? The Lancet Gastroenterology & Hepatology. avr 2020;5(4):335‑7.

247   9.   Grzelak L, Temmam S, Planchais C, Demeret C, Huon C, Guivel F, et al. SARS-CoV-2 serological
248   analysis of COVID-19 hospitalized patients, pauci-symptomatic individuals and blood donors.
249   [Internet]. Infectious Diseases (except HIV/AIDS); 2020 avr [cité 28 avr 2020]. Disponible sur:
250   http://medrxiv.org/lookup/doi/10.1101/2020.04.21.20068858

251   10.   Assis RR de, Jain A, Nakajima R, Jasinskas A, Felgner J, Obiero JM, et al. Analysis of SARS-CoV-2
252   Antibodies in COVID-19 Convalescent Plasma using a Coronavirus Antigen Microarray [Internet].
253   Immunology; 2020 avr [cité 28 avr 2020]. Disponible sur:
254   http://biorxiv.org/lookup/doi/10.1101/2020.04.15.043364

255   11.   Li R, Pei S, Chen B, Song Y, Zhang T, Yang W, et al. Substantial undocumented infection facilitates the
256   rapid dissemination of novel coronavirus (SARS-CoV2). Science. 16 mars 2020;eabb3221.

257   12.   Mizumoto K, Kagaya K, Zarebski A, Chowell G. Estimating the asymptomatic proportion of
258   coronavirus disease 2019 (COVID-19) cases on board the Diamond Princess cruise ship, Yokohama,
259   Japan, 2020. Eurosurveillance [Internet]. 12 mars 2020 [cité 28 avr 2020];25(10). Disponible sur:
260   https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.10.2000180

261   13.   Al-Tawfiq JA. Asymptomatic coronavirus infection: MERS-CoV and SARS-CoV-2 (COVID-19). Travel
262   Med Infect Dis. 27 févr 2020;101608.

263   14.   Rothe C, Schunk M, Sothmann P, Bretzel G, Froeschl G, Wallrauch C, et al. Transmission of 2019-
264   nCoV Infection from an Asymptomatic Contact in Germany. N Engl J Med. 5 mars
265   2020;382(10):970⬚1.

266   15.   Ng SC, Tilg H. COVID-19 and the gastrointestinal tract: more than meets the eye. Gut. 9 avr 2020;

267   16.   González-Mariño I, Zuccato E, Santos MM, Castiglioni S. Monitoring MDMA metabolites in urban
268   wastewater as novel biomarkers of consumption. Water Research. mai 2017;115:1⬚8.

269   17.   Bisseux M, Colombet J, Mirand A, Roque-Afonso A-M, Abravanel F, Izopet J, et al. Monitoring human
270   enteric viruses in wastewater and relevance to infections encountered in the clinical setting: a one-
271   year experiment in central France, 2014 to 2015. Vol. 23, Eurosurveillance. 2018. p. 17⬚00237.

272   18.   Prevost B, Lucas FS, Ambert-Balay K, Pothier P, Moulin L, Wurtzer S. Deciphering the Diversities of
273   Astroviruses and Noroviruses in Wastewater Treatment Plant Effluents by a High-Throughput
274   Sequencing Method. Appl Environ Microbiol. oct 2015;81(20):7215⬚22.

275   19.   van Doremalen N, Bushmaker T, Morris DH, Holbrook MG, Gamble A, Williamson BN, et al. Aerosol
276   and Surface Stability of SARS-CoV-2 as Compared with SARS-CoV-1. N Engl J Med. 17 mars 2020;

277   20.   Gundy PM, Gerba CP, Pepper IL. Survival of Coronaviruses in Water and Wastewater. Food Environ
278   Virol. mars 2009;1(1):10.

279   21.   Ye Y, Ellenberg RM, Graham KE, Wigginton KR. Survivability, Partitioning, and Recovery of Enveloped
280   Viruses in Untreated Municipal Wastewater. Environ Sci Technol. 17 mai 2016;50(10):5077⬚85.

281   22.   Lodder W, de Roda Husman AM. SARS-CoV-2 in wastewater: potential health risk, but also data
282   source. Lancet Gastroenterol Hepatol. 1 avr 2020;

283   23.   Mallapaty S. How sewage could reveal true scale of coronavirus outbreak. Nature. avr
284   2020;580(7802):176⬚7.

285   24.   Medema G, Heijnen L, Elsinga G, Italiaander R, Brouwer A. Presence of SARS-Coronavirus-2 in
286   sewage. medRxiv. 1 janv 2020;2020.03.29.20045880.

287   25.   Wu F, Xiao A, Zhang J, Gu X, Lee WL, Kauffman K, et al. SARS-CoV-2 titers in wastewater are higher
288   than expected from clinically confirmed cases. medRxiv. 1 janv 2020;2020.04.05.20051540.

289   26.   Corman VM, Landt O, Kaiser M, Molenkamp R, Meijer A, Chu DKW, et al. Detection of 2019 novel
290   coronavirus (2019-nCoV) by real-time RT-PCR. Euro Surveill. janv 2020;25(3).

291   27.   Wölfel R, Corman VM, Guggemos W, Seilmaier M, Zange S, Müller MA, et al. Virological assessment
292   of hospitalized patients with COVID-2019. Nature [Internet]. 1 avr 2020 [cité 28 avr 2020];
293   Disponible sur: http://www.nature.com/articles/s41586-020-2196-x

294   28.   Atkinson B, Petersen E. SARS-CoV-2 shedding and infectivity. The Lancet. avr
295   2020;395(10233):1339⬚40.

296   29.   Gudbjartsson DF, Helgason A, Jonsson H, Magnusson OT, Melsted P, Norddahl GL, et al. Spread of
297   SARS-CoV-2 in the Icelandic Population. N Engl J Med. 14 avr 2020;NEJMoa2006100.

298

299

Contribution

306 SW, ER performed the virus measurements; SW, LM started the project; JLA, SW provided samples;
307 LM, VM, JMM, SW for the redaction of the manuscript; YM, RT, JLA technical and theorical discussion
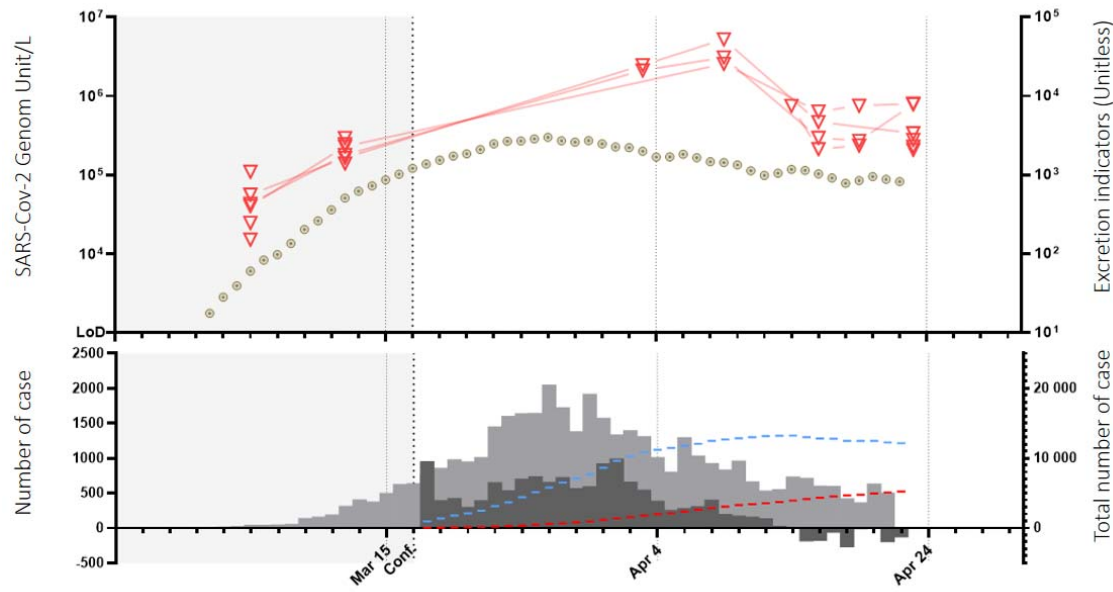308 .

311

Figure 1: Upper panel: Quantification of SARS-Cov-2 in wastewater samples in Parisian Area in different WWTP (open inverted red triangles for important WWTP, purple open inverted triangles for smaller WWTP) in circle estimators of the viral excretion.

Lower panel : In Light grey area, daily number of consultation for COVID 19 Symptoms in hospital of the Parisian area. Dark grey daily growth of hospitalized patient. Blue bar total hospitalized patient in the Parisian area, red bar cumulative deaths each day, in Parisian area.

Both panel : grey background, pre-lockdown period.

322 **Supplementary data**

323 None

324