

Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

A systematical association analysis of 25 common virus infection and genetic susceptibility of COVID-19 infection

Na Zhang, Yujing Chen, Chun'e Li, Xiaoyue Qin, Dan He, Wenming Wei, Yijing Zhao, Qingqing Cai, Sirong Shi, Xiaoge Chu, Yan Wen, Yumeng Jia, Feng Zhang

PII: S1286-4579(23)00073-4

DOI: https://doi.org/10.1016/j.micinf.2023.105170

Reference: MICINF 105170

To appear in: Microbes and Infection

Received Date: 26 January 2023

Revised Date: 2 June 2023

Accepted Date: 7 June 2023

Please cite this article as: N. Zhang, Y. Chen, C.'e Li, X. Qin, D. He, W. Wei, Y. Zhao, Q. Cai, S. Shi, X. Chu, Y. Wen, Y. Jia, F. Zhang, A systematical association analysis of 25 common virus infection and genetic susceptibility of COVID-19 infection, *Microbes and Infection*, https://doi.org/10.1016/j.micinf.2023.105170.

This is a PDF file of an article that has undergone enhancements after acceptance, such as the addition of a cover page and metadata, and formatting for readability, but it is not yet the definitive version of record. This version will undergo additional copyediting, typesetting and review before it is published in its final form, but we are providing this version to give early visibility of the article. Please note that, during the production process, errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

© 2023 Institut Pasteur. Published by Elsevier Masson SAS. All rights reserved.



A systematical association analysis of 25 common virus infection and genetic susceptibility

1

2	of COVID-19 infection
3	Na Zhang ^{1#} , Yujing Chen ^{1#} , Chun'e Li ¹ , Xiaoyue Qin ¹ , Dan He ¹ , Wenming Wei ¹ , Yijing Zhao ¹ ,
4	Qingqing Cai ¹ , Sirong Shi ¹ , Xiaoge Chu ¹ , Yan Wen ¹ , Yumeng Jia ¹ , Feng Zhang ^{1,2*}
5	
6	1. Key Laboratory of Trace Elements and Endemic Diseases of National Health and Family
7	Planning Commission, Key Laboratory of Environment and Genes Related to Diseases of
8	Ministry of Education of China, Key Laboratory for Disease Prevention and Control and Health
9	Promotion of Shaanxi Province, School of Public Health, Health Science Center, Xi'an Jiaotong
10	University, Xi'an, China.
11	2. Department of Psychiatry, The First Affiliated Hospital of Xi'an Jiaotong University, Xi'an,
12	China.
13	
14	#The two authors contributed equally to this work
15	
16	*Corresponding author:
17	Feng Zhang
18	Key Laboratory of Trace Elements and Endemic Diseases, National Health Commission of the
19	People's Republic of China. School of Public Health, Health Science Center, Xi'an Jiaotong
20	University
21	Email: fzhxjtu@mail.xjtu.edu.cn
22	Xi'an, P. R. China 710061

23 Abstract

Objectives: Previous studies identified a number of diseases were associated with 2019 coronavirus disease (COVID-19). However, the associations between these diseases related viral infections and COVID-19 remains unknown now.

Methods: In this study, we utilized single nucleotide polymorphisms (SNPs) related to COVID-27 19 from genome-wide association study (GWAS) and individual-level genotype data from the 28 UK biobank to calculate polygenic risk scores (PRS) of 487,409 subjects for eight COVID-19 29 clinical phenotypes. Then, multiple logistic regression models were established to assess the 30 correlation between serological measurements (positive/negative) of 25 viruses and the PRS of 31 32 eight COVID-19 clinical phenotypes. And we performed stratified analyses by age and gender. Results: In whole population, we identified 12 viruses associated with the PRS of COVID-19 33 as VZV clinical phenotypes, seropositivity for Varicella Zoster 34 such Virus (Unscreened/Exposed_Negative: $\beta = 0.1361$, P = 0.0142; Hospitalized/Unscreened: $\beta = 0.1167$, 35 Р 0.0385) and MCV seropositivity for Merkel Cell Polyomavirus 36 = (Unscreened/Exposed_Negative: $\beta = -0.0614$, P = 0.0478). After age stratification, we 37 identified seven viruses associated with the PRS of eight COVID-19 clinical phenotypes. After 38 gender stratification, we identified five viruses associated with the PRS of eight COVID-19 39 clinical phenotypes in the women group. 40

41 Conclusion: Our study findings suggest that the genetic susceptibility to different COVID-19
42 clinical phenotypes is associated with the infection status of various common viruses.

Keywords: common viral infections, coronavirus disease 2019, positive serological
measurements, genetic susceptibility, genome-wide association study

45 **1. Introduction**

The coronavirus disease 2019 (COVID-19) pandemic has resulted in over 603 million 46 infections and more than 6.4 million deaths worldwide as of July 31, 2022, casuing a significant 47 disease burden for countries around the world[1]. COVID-19 is caused by the highly contagious 48 severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which presents with a wide 49 range of clinical symptoms, from asymptomatic infection or mild illness to serious illness 50 requiring hospitalization and mechanical ventilation[2]. Previous study has found that clinical 51 variation in COVID-19 severity and symptom presentation may be due to differences in host 52 genetic factors associated with immune response[3]. Therefore, changes in immune responses 53 54 may be linked to different clinical manifestations of COVID-19. As research on COVID-19 infection has progressed, several single nucleotide polymorphisms (SNPs) and genes associated 55 with different aspects of susceptibility to infection or disease severity have been identified[4], 56 suggesting that genetic factors in the host could influence its susceptibility and severity to the 57 virus[4, 5]. 58

As COVID-19 prevention measures become normalized, identifying co-infection with one 59 or more respiratory viruses can help us understand the infection status of SARS-CoV-2. During 60 the COVID-19 pandemic, there have been increasing reports of co-infection with other 61 pathogens in COVID-19 patients [6, 7]. A retrospective study found that 242 (94.2%) patients 62 had co-infected with one or more pathogens, the most frequent of which were the Epstein virus 63 Barr virus(EBV), the rhinovirus, and the adenovirus[8]. Herpes simplex virus 1 (HSV-1) and 64 varicella zoster virus (VZV) are DNA viruses of the neurotropic alpha human herpesvirus 65 66 subfamily (HHV)[9]. The virus remains dormant in the body after recovery from the initial

infection and reactivates when the immune system is compromised, causing significant damage 67 to the host organism[10]. Although few case reports of VZV and HSV in patients with COVID-68 19 have been published, studies have suggested that VZV may be an indicator of potential 69 COVID-19 infection[11]. Previous studies have identified associations between host 70 polymorphisms in genes related to cell entry, cytokine production, and immune response with 71 multiple viruses, and antibody responses have been found to be highly heritable (32%–48%) 72 [12]. The HLA-B*46:01 allele in East Asian patients was associated with infection severity 73 during the 2003 severe acute respiratory syndrome (SARS) outbreak caused by the SARS-CoV-74 2-related β coronavirus[13]. 75

76 Researchers have discovered an association between the prevalence of COVID-19 and other viral infections^[14]. In addition to age, obesity, hypertension and other common risk 77 factors associated with increased COVID-19 severity[15], a study found that cytomegalovirus 78 (CMV) seropositivity was associated with more than twice the risk of hospitalization due to 79 SARS-CoV-2 infection[14]. Potential CMV infection influences future infection with other 80 viruses and shapes the distribution of adaptive immune cell populations[16, 17]. In SARS-CoV-81 82 2 infection, CMV seropositivity results in a severe immunological signature, which is the activation of TEMRA cells[18]. 83

The aim of our study was to investigate which viral infections are associated with the genetic susceptibility to COVID-19 by using polygenic risk scores (PRS) for COVID-19 eight clinical phenotypes. PRS is a score that aggregates genetic variants to predict disease risk. In this work, we used data from the UK Biobank cohort study and established multiple logistic regression models to assess the correlation between serological results of 25 viral infections and the PRS of COVID-19 eight clinical phenotypes.

90 2. Material and methods

91 2.1 UK Biobank Cohort

The UK Biobank cohort is a large prospective cohort study that recruited approximately 92 500,000 participants aged 40-69 between 2006 and 2010 (https://www.ukbiobank.ac.uk/learn-93 more-about-uk-biobank). Participant characteristics and other health-related indicators were 94 collected through touchscreen questionnaires, short interviews, and a series of body 95 measurements at 22 assessment centers in the United Kingdom[19]. The UK Biobank study 96 was approved by the National Health Service National Research Ethics Service(11/NW/0382), 97 and all participants provided written informed consent to participate[20]. This study was 98 conducted with the permission from the UK Biobank (application number: 46,478). 99

Multi-batch genotyping was performed using two slightly different arrays, the Applied Biosystems UK BiLEVE Axiom Array from Affymetrix and the Applied Biosystems UK Biobank Axiom Array. For quality control, sex mismatches, departures from Hardy–Weinberg equilibrium, missing genotype rate >0.05 or imputation accuracy score <0.3 were excluded. Samples identified as outliers for heterozygosity and missing rates were removed. Detailed array design, genotyping and quality control procedures can be found in previous studies[19].

106 **2.2 Common Virus Serological Measurements**

In this study, we selected serological measurements of 25 common viruses from the UK
Biobank (UK Biobank data fields: 23,050–23,071, 23,073–23,075). Detailed information was
shown in the Supplemental tables (Table S1). The serological measurements were defined as
positive or negative for each virus.

111 **2.3** Genome-wide Association Study (GWAS) Data of COVID-19 Clinical Phenotypes

The GWAS data of COVID-19 were derived from a genetic association study of the expanded 112 phenotypic definition of COVID-19, including eight clinical phenotypes associated with 113 114 COVID-19 outcomes^[5]. Detailed information of eight clinical phenotypes was presented in Supplementary tables (Table S2). Power analysis of case-control discrete traits was performed 115 using the Purcell power calculator. Array-based genotyping and SNP calling were performed 116 by Illumina with the GenotypeStudio platform or Quest/Athena Diagnostics. Genetic principal 117 components were calculated to include in the association studies to control residual population 118 structure and were computed using FlashPCA 2.0.2. Inbred-related participants were removed 119 by using AncestryDNA. Details of the array design, genotyping, and quality control procedures 120 have been described previously[5]. 121

122 2.4 Polygenic Risk Scores (PRS) Analysis

In this study, we calculated the PRS of eight COVID-19 clinical phenotypes for each subject. SNPs of $P < 1.00 \times 10^{-5}$ were selected. The PRS of eight COVID-19 clinical phenotype was calculated by PLINK2.0[21], according to the formula[22]:

126
$$PRS_m = \sum_{i=1}^n \beta_i SNP_{im}$$

PRS_m represents the PRS value of COVID-19 clinical phenotypes of the mth subject; n denotes the total number of sample size; β_i is the effect parameter of risk allele of the ith significant SNP associated with COVID-19 clinical phenotypes, which was obtained from the GWAS of COVID-19 clinical phenotypes; and SNPim denotes the dosage (0, 1, 2) of the risk allele of the ith SNP for the mth individual[22, 23]. The PRS of eight COVID-19 clinical phenotypes were used as instrumental variables to participate in the subsequent statistical analysis.

134 **2.5 Statistical Analysis**

We used logistic regression models to evaluate the correlation between common viral infections 135 and genetic predisposition to COVID-19. Serological measurements of common viruses were 136 used as outcome variables, while the calculated PRS of eight COVID-19 clinical phenotypes 137 was used as instrumental variable. Age, sex, Townsend deprivation index(TDI), frequency of 138 alcohol drinking per week, frequency of smoking per day, body mass index (BMI) and 10 139 principal components of population structure were used as covariates. We also conducted a 140 stratified analysis of age and gender. We set a threshold of P < 0.05 for suggestive significance. 141 142 All statistical analyses were performed using R software.

143 **3. Results**

144 **3.1 Descriptive characteristics of study participants**

For *C. trachomatis Definition II seropositivity for Chlamydia trachomatis*, 3887 subjects were
selected, 50.14% of them were woman, mean age was 57.30 years, standard deviation(SD) was
7.91. For *H. pylori Definition I seropositivity for Helicobacter pylori*, 2394 subjects were
selected, 53.88% of them were woman, mean age was 56.81 (SD:7.88) years. For the other
viruses, 4800 subjects were selected, 52.92% of them were women, mean age was 56.95 (SD:
7.94) years.

151 **3.2 Viruses Associated with COVID-19 Phenotypes in the Whole Population**

152 We first performed the logistic analysis in the whole population and identified 12 viruses

associated with the PRS of COVID-19 clinical phenotypes. For example, VZV seropositivity for

154 Varicella Zoster Virus was associated with Unscreened/Exposed_Negative ($\beta = 0.1361$, P =

155 0.0142), and *C. trachomatis Definition II seropositivity for Chlamydia trachomatis* was 156 associated with *Positive/Unscreened* ($\beta = 0.2174$, P = 0.0185). The detailed results were shown 157 in Table 1.

158 **3.3 Viruses Associated with COVID-19 Phenotype After Age Stratification**

In the age \leq 65 years group, we identified seven viruses associated with PRS of the COVID-19 159 clinical phenotypes. For example, the association between HSV-2 seropositivity for Herpes 160 Simplex virus-2 and Exposed Positive/Exposed Negative ($\beta = 0.1017$, P = 0.0177) was 161 significant. Besides, HSV-2 seropositivity for Herpes Simplex virus-2 infection was also 162 associated with *Positive/Negative* ($\beta = -0.0987$, P = 0.0242). In the age > 65 years group, we 163 164 found 10 viruses associated with PRS of the COVID-19 clinical phenotypes. For example, HSV-2 seropositivity for Herpes Simplex virus-2 was associated with Continuous Severity Score (β 165 = 0.3132, P = 0.0084). In addition, *HSV-2 seropositivity for Herpes Simplex virus-2* was also 166 associated with Symptomatic/Paucisymptomatic ($\beta = 0.2436$, P = 0.0426). The detailed results 167 were shown in Table 2. 168

169 3.4 Viruses Significantly Associated with COVID-19 Phenotype After Gender 170 Stratification

In the women group, we found five viruses associated with the PRS of COVID-19 clinical phenotypes. For example, *HPV 16 Definition II seropositivity for Human Papillomavirus type-*173 *16* was associated with *Exposed_Positive /Exposed_Negative* ($\beta = -0.2766$, P = 0.0026), and 174 *HPV 18 seropositivity for Human Papillomavirus type-18* was associated with 175 *Continuous_Severity_Score* ($\beta = -0.3710$, P = 0.0054). In the men group, we found 14 viruses 176 associated with the PRS of COVID-19 clinical phenotypes, such as the association between

177 *HSV-2 seropositivity for Herpes Simplex virus-2* and *Positive/Negative* ($\beta = -0.1881$, P =178 0.0017), and the association between *JCV seropositivity for Human Polyomavirus JCV* and 179 *Exposed_Positive/Exposed_Negative* ($\beta = 0.1237$, P = 0.0023). The detailed results were 180 shown in Table 3.

181 **4. Discussion**

A previous study found that the severity of COVID-19 infection is influenced by host genetic factors[24]. We are curious if there is a potential correlation between COVID-19-related genetic information and the infection status of other viruses. In this work, we used PRS to represent an individual's genetic susceptibility to COVID-19. Logistic regression models were used to assess the association between multiple common viral infections and the PRS of COVID-19 clinical phenotypes. Our study aimed to detect which viral infections were associated with genetic susceptibility to COVID-19.

Our study builds upon previous research by adding covariates to logistic regression models 189 for correction, in order to explore whether genetic susceptibility to COVID-19 influences the 190 risk of infection by other common viruses. We found that VZV had a significant association 191 192 with Unscreened/Exposed Negative in the whole population. Herpes zoster is a viral skin disease in which herpes zoster remains dormant in the dorsal root ganglion of the cutaneous 193 nerve after chickenpox infection[25]. Among reported COVID-19 cases, infected patients 194 exhibited diverse skin manifestations, with varicella-like lesions being one of the major skin 195 manifestations during the COVID-19 outbreak [26]. Cases of herpes zoster infection have been 196 identified in recent symptomatic COVID-19 infections[27]. It is possible that this is SARS-197 CoV-2 could directly infect lymphocytes and promote apoptosis of lymphocytes, leading to 198

199 lymphopenia and impaired antiviral response, which may further favor herpes virus200 recurrence[28].

It has been found that some viruses exhibit a change in incidence with age. For example, 201 202 the zoster virus demonstrates a steady increase in incidence starting at age 50 years, with the higher incidence in people over 65 years[29]. Therefore, in our study we performed a stratified 203 analysis by controlling for age. After controlling for age variables, we found that the significant 204 associations were not the same between the age ≤ 65 years group and the age > 65 years group. 205 In the age < 65 years group, the most significant association was found between HSV-2 206 seropositivity for Herpes Simplex virus-2 and Exposed Positive/Exposed Negative. However, 207 in the age > 65 years group, the most significant association was found between HSV-2 208 seropositivity for Herpes Simplex virus-2 and Continuous Severity Score. HSV-2 causes 209 ulcerative lesions in adults and primarily affects the genital region through sexual 210 transmission[30]. Following primary infection, Herpes simplex virus enters the latent state in 211 the ganglion and may emerge later, leading to recurrent active infection[31]. Recent studies 212 been found that individuals infected with HSV could affect SARS-CoV-2 IgM/IgG serologic 213 results due to direct binding of IgM antibodies to otherwise detected surface-modified 214 polystyrene particles[32]. 215

The prevalence of common viruses is also gender-dependent. For example, the epidemiology of HSV-2 differs between women and men, with a greater probability of transmission from male-to-female than female-to-male[33]. Therefore, we conducted a gender stratified analysis. After stratifying, we found more virus in the men group may be affected by the genetic susceptibility of COVID-19. For example, 14 significant associations were found

in the men group, such as HSV-2 and Positive/Negative, which also consist with previous 221 studies[32]. In the women group, human papillomavirus (HPV)-associated virus infection is 222 associated with genetic susceptibility to COVID-19. In addition, we found human herpesvirus 223 224 (HHV) is also associated with genetic susceptibility to COVID-19. HHV reactivation was considered a positive polymerase chain reaction result taken at the time of COVID-19 225 infection[34]. The reactivation of HSV is associated with an increased risk of hospital-acquired 226 pneumonia/ventilator-associated pneumonia (HAP/VAP)[35]. Overall, co-infection with herpes 227 viruses leads to poor clinical outcomes, particularly in critically ill COVID-19 patients[11, 36]. 228 This is a new study that explores which viral infections are associated with genetic 229 susceptibility to COVID-19. Our study finally identified several viral infections that are 230 associated with genetic susceptibility to COVID-19. However, there are some limitations to 231 consider when interpreting these findings. First, our data comes from a UK biobank, which only 232 includes information from people of European descent. Therefore, our conclusions are limited 233 in their applicability to other racial and ethnic populations. Second, our work is only exploratory, 234 and the results can only demonstrate correlation rather than causation. Third, although we 235 236 controlled for confounding factors, there may still be potential confounding factors that we did not account for. Therefore, the association between viral infections and genetic susceptibility 237 should be interpreted with caution. Finally, more large-scale prospective and biological studies 238 are needed to confirm our results and elucidate the specific mechanisms involved. 239 In summary, our work identified viral infections that are associated with genetic 240

241 susceptibility to COVID-19. These findings may help clinicians to prevent and detect the

- 242 recurrence of other viruses closely related to COVID-19 in a timely manner. Moreover, this
- 243 association might assist clinicians in identifying patients with a poorer prognosis.

ournal Proproo

244 **Funding Information**

- 245 This work was supported by the National Natural Scientific Foundation of China [grant
- numbers:81922059] and the Natural Science Basic Research Program in Shaanxi Province of
- 247 China:[grant numbers:2021JCW-08].

248 Institutional Review Board Statement

249 This study has been approved by UK Biobank (Application number: 46478) and obtained

250 health-related records of participants.

251 Data Availability Statement

- 252 The data that support the findings of this study are available from the corresponding author
- 253 upon reasonable request.
- 254 **Disclosure**

255 All authors report no biomedical financial interests or potential conflicts of interest.

256 Author contributions

- 257 Na Zhang: Writing original draft, Conceptualization, Formal analysis. Yujing Chen: Writing
- 258 review & editing, Formal analysis. Chun'e Li: Formal analysis. Xiaoyue Qin: Writing –
- 259 review & editing. Dan He: Methodology. Wenming Wei: Validation. Yijing Zhao: Software.
- 260 Qingqing Cai: Software. Sirong Shi: Visualization. Xiaoge Chu: Visualization. Yan Wen:
- 261 Investigation. Yumeng Jia: Investigation. Feng Zhang: Supervision, Project administration.

262

263 References

- 264 [1] W.H. Organization, Coronavirus disease (COVID-19) Weekly Epidemiological Update and
- 265 Weekly Operational Update, (2022) 1-25.
- 266 [2] C. Huang, Y. Wang, X. Li, L. Ren, J. Zhao, Y. Hu, L. Zhang, G. Fan, J. Xu, X. Gu, Z. Cheng,
- 267 T. Yu, J. Xia, Y. Wei, W. Wu, X. Xie, W. Yin, H. Li, M. Liu, Y. Xiao, H. Gao, L. Guo, J. Xie, G.
- Wang, R. Jiang, Z. Gao, Q. Jin, J. Wang, B. Cao, Clinical features of patients infected with 2019
- 269 novel coronavirus in Wuhan, China, Lancet 395(10223) (2020) 497-506.
- 270 [3] W. Wang, Y. Xu, R. Gao, R. Lu, K. Han, G. Wu, W. Tan, Detection of SARS-CoV-2 in
- Different Types of Clinical Specimens, Jama 323(18) (2020) 1843-1844.
- [4] T.P. Velavan, S.R. Pallerla, J. Rüter, Y. Augustin, P.G. Kremsner, S. Krishna, C.G. Meyer,
- Host genetic factors determining COVID-19 susceptibility and severity, EBioMedicine 72
 (2021) 103629.
- [5] G.H.L. Roberts, R. Partha, B. Rhead, S.C. Knight, D.S. Park, M.V. Coignet, M. Zhang, N.
- 276 Berkowitz, D.A. Turrisini, M. Gaddis, S.R. McCurdy, M. Pavlovic, L. Ruiz, C. Sass, A.K. Haug
- 277 Baltzell, H. Guturu, A.R. Girshick, C.A. Ball, E.L. Hong, K.A. Rand, Expanded COVID-19
- 278 phenotype definitions reveal distinct patterns of genetic association and protective effects, Nat

279 Genet 54(4) (2022) 374-381.

- 280 [6] Q. Wu, Y. Xing, L. Shi, W. Li, Y. Gao, S. Pan, Y. Wang, W. Wang, Q. Xing, Coinfection and
- 281 Other Clinical Characteristics of COVID-19 in Children, Pediatrics 146(1) (2020).
- 282 [7] D. Lin, L. Liu, M. Zhang, Y. Hu, Q. Yang, J. Guo, Y. Guo, Y. Dai, Y. Xu, Y. Cai, X. Chen,
- Z. Zhang, K. Huang, Co-infections of SARS-CoV-2 with multiple common respiratory
 pathogens in infected patients, Sci China Life Sci 63(4) (2020) 606-609.
- [8] X. Zhu, Y. Ge, T. Wu, K. Zhao, Y. Chen, B. Wu, F. Zhu, B. Zhu, L. Cui, Co-infection with
 respiratory pathogens among COVID-2019 cases, Virus Res 285 (2020) 198005.
- [9] W.J. Ouwendijk, K.J. Laing, G.M. Verjans, D.M. Koelle, T-cell immunity to human
 alphaherpesviruses, Curr Opin Virol 3(4) (2013) 452-60.
- [10] B.M. Mitchell, D.C. Bloom, R.J. Cohrs, D.H. Gilden, P.G. Kennedy, Herpes simplex virus-
- 1 and varicella-zoster virus latency in ganglia, J Neurovirol 9(2) (2003) 194-204.
- 291 [11] P. Le Balc'h, K. Pinceaux, C. Pronier, P. Seguin, J.M. Tadié, F. Reizine, Herpes simplex

- virus and cytomegalovirus reactivations among severe COVID-19 patients, Crit Care 24(1)
 (2020) 530.
- [12] A.D. Kenney, J.A. Dowdle, L. Bozzacco, T.M. McMichael, C. St Gelais, A.R. Panfil, Y.
- 295 Sun, L.S. Schlesinger, M.Z. Anderson, P.L. Green, C.B. López, B.R. Rosenberg, L. Wu, J.S.
- 296 Yount, Human Genetic Determinants of Viral Diseases, Annu Rev Genet 51 (2017) 241-263.
- [13] M. Lin, H.K. Tseng, J.A. Trejaut, H.L. Lee, J.H. Loo, C.C. Chu, P.J. Chen, Y.W. Su, K.H.
- Lim, Z.U. Tsai, R.Y. Lin, R.S. Lin, C.H. Huang, Association of HLA class I with severe acute
 respiratory syndrome coronavirus infection, BMC Med Genet 4 (2003) 9.
- 300 [14] C. Alanio, A. Verma, D. Mathew, S. Gouma, G. Liang, T. Dunn, D.A. Oldridge, J. Weaver,
- 301 L. Kuri-Cervantes, M.B. Pampena, M.R. Betts, R.G. Collman, F.D. Bushman, N.J. Meyer, S.E.
- 302 Hensley, D. Rader, E.J. Wherry, Cytomegalovirus Latent Infection is Associated with an
- 303 Increased Risk of COVID-19-Related Hospitalization, J Infect Dis 226(3) (2022) 463-473.
- 304 [15] J.T. Wu, K. Leung, M. Bushman, N. Kishore, R. Niehus, P.M. de Salazar, B.J. Cowling,
- M. Lipsitch, G.M. Leung, Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China, Nat Med 26(4) (2020) 506-510.
- 307 [16] M.J. Cannon, D.S. Schmid, T.B. Hyde, Review of cytomegalovirus seroprevalence and
- demographic characteristics associated with infection, Rev Med Virol 20(4) (2010) 202-13.
- 309 [17] D. Furman, V. Jojic, S. Sharma, S.S. Shen-Orr, C.J. Angel, S. Onengut-Gumuscu, B.A.
- 310 Kidd, H.T. Maecker, P. Concannon, C.L. Dekker, P.G. Thomas, M.M. Davis, Cytomegalovirus
- infection enhances the immune response to influenza, Sci Transl Med 7(281) (2015) 281ra43.
- 312 [18] E. Patin, M. Hasan, J. Bergstedt, V. Rouilly, V. Libri, A. Urrutia, C. Alanio, P. Scepanovic,
- 313 C. Hammer, F. Jönsson, B. Beitz, H. Quach, Y.W. Lim, J. Hunkapiller, M. Zepeda, C. Green, B.
- 314 Piasecka, C. Leloup, L. Rogge, F. Huetz, I. Peguillet, O. Lantz, M. Fontes, J.P. Di Santo, S.
- 315 Thomas, J. Fellay, D. Duffy, L. Quintana-Murci, M.L. Albert, Natural variation in the
- 316 parameters of innate immune cells is preferentially driven by genetic factors, Nat Immunol 19(3)
- 317 (2018) 302-314.
- 318 [19] C. Bycroft, C. Freeman, D. Petkova, G. Band, L.T. Elliott, K. Sharp, A. Motyer, D.
- 319 Vukcevic, O. Delaneau, J. O'Connell, A. Cortes, S. Welsh, A. Young, M. Effingham, G. McVean,
- 320 S. Leslie, N. Allen, P. Donnelly, J. Marchini, The UK Biobank resource with deep phenotyping
- and genomic data, Nature 562(7726) (2018) 203-209.

- 322 [20] C. Sudlow, J. Gallacher, N. Allen, V. Beral, P. Burton, J. Danesh, P. Downey, P. Elliott, J.
- 323 Green, M. Landray, B. Liu, P. Matthews, G. Ong, J. Pell, A. Silman, A. Young, T. Sprosen, T.
- Peakman, R. Collins, UK biobank: an open access resource for identifying the causes of a wide range of complex diseases of middle and old age, PLoS Med 12(3) (2015) e1001779.
- 326 [21] S. Purcell, B. Neale, K. Todd-Brown, L. Thomas, M.A. Ferreira, D. Bender, J. Maller, P.
- 327 Sklar, P.I. de Bakker, M.J. Daly, P.C. Sham, PLINK: a tool set for whole-genome association
 328 and population-based linkage analyses, Am J Hum Genet 81(3) (2007) 559-75.
- 329 [22] S. Cheng, X. Qi, M. Ma, L. Zhang, B. Cheng, C. Liang, L. Liu, P. Li, O.P. Kafle, Y. Wen,
- 330 F. Zhang, Assessing the Relationship Between Gut Microbiota and Bone Mineral Density, Front
- 331 Genet 11 (2020) 6.
- [23] F. Dudbridge, Polygenic Epidemiology, Genet Epidemiol 40(4) (2016) 268-72.
- 333 [24] D. Zhu, R. Zhao, H. Yuan, Y. Xie, Y. Jiang, K. Xu, T. Zhang, X. Chen, C. Suo, Host Genetic
- Factors, Comorbidities and the Risk of Severe COVID-19, J Epidemiol Glob Health (2023)
 1-13.
- [25] R.R. Dayan, R. Peleg, Herpes zoster typical and atypical presentations, Postgrad Med
 129(6) (2017) 567-571.
- [26] U. Wollina, A.S. Karadağ, C. Rowland-Payne, A. Chiriac, T. Lotti, Cutaneous signs in
 COVID-19 patients: A review, Dermatol Ther 33(5) (2020) e13549.
- 340 [27] A. Ferreira, T.T. Romão, Y.S. Macedo, C. Pupe, O.J.M. Nascimento, COVID-19 and herpes
- zoster co-infection presenting with trigeminal neuropathy, Eur J Neurol 27(9) (2020) 17481750.
- 343 [28] H.Y. Zheng, M. Zhang, C.X. Yang, N. Zhang, X.C. Wang, X.P. Yang, X.Q. Dong, Y.T.
- 344 Zheng, Elevated exhaustion levels and reduced functional diversity of T cells in peripheral
- blood may predict severe progression in COVID-19 patients, Cell Mol Immunol 17(5) (2020)
 541-543.
- [29] K. Kawai, B.G. Gebremeskel, C.J. Acosta, Systematic review of incidence and
 complications of herpes zoster: towards a global perspective, BMJ Open 4(6) (2014) e004833.
- 349 [30] A.J. Nahmias, B. Roizman, Infection with herpes-simplex viruses 1 and 2. II, N Engl J
- 350 Med 289(14) (1973) 719-25.
- 351 [31] D.T. Fleming, G.M. McQuillan, R.E. Johnson, A.J. Nahmias, S.O. Aral, F.K. Lee, M.E. St

- Louis, Herpes simplex virus type 2 in the United States, 1976 to 1994, N Engl J Med 337(16)
 (1997) 1105-11.
- 354 [32] L. Vandervore, E. Van Mieghem, V. Nowé, S. Schouwers, C. Steger, P. Abrams, J. Van
- 355 Schaeren, A. Meskal, T. Vandamme, False positive Herpes Simplex IgM serology in COVID-
- 356 19 patients correlates with SARS-CoV-2 IgM/IgG seropositivity, Diagn Microbiol Infect Dis
- 357 103(1) (2022) 115653.
- 358 [33] A. Wald, A.G. Langenberg, K. Link, A.E. Izu, R. Ashley, T. Warren, S. Tyring, J.M.
- 359 Douglas, Jr., L. Corey, Effect of condoms on reducing the transmission of herpes simplex virus
- 360 type 2 from men to women, Jama 285(24) (2001) 3100-6.
- 361 [34] A. Shafiee, M.M. Teymouri Athar, M.J. Amini, H. Hajishah, S. Siahvoshi, M. Jalali, B.
- 362 Jahanbakhshi, S.H. Mozhgani, Reactivation of herpesviruses during COVID-19: A systematic
- review and meta-analysis, Rev Med Virol 33(3) (2023) e2437.
- 364 [35] A. Meyer, N. Buetti, N. Houhou-Fidouh, J. Patrier, M. Abdel-Nabey, P. Jaquet, S. Presente,
- 365 T. Girard, F. Sayagh, S. Ruckly, P.H. Wicky, E. de Montmollin, L. Bouadma, R. Sonneville, D.
- 366 Descamps, J.F. Timsit, HSV-1 reactivation is associated with an increased risk of mortality and
- 367 pneumonia in critically ill COVID-19 patients, Crit Care 25(1) (2021) 417.
- [36] J. Katz, S. Yue, W. Xue, Herpes simplex and herpes zoster viruses in COVID-19 patients,
- 369 Ir J Med Sci 191(3) (2022) 1093-1097.
- 370

371 Legends for Figures and Tables

- 372 **Figure 1:** Forest plots of the results of logistic regression analysis in the whole population.
- 373 (a) Continuous Severity Score;
- 374 (b) *Exposed_Positive/Exposed_Negative*;
- 375 (c) Hospitalized/Not Hospitalized;
- 376 (d) *Hospitalized/Unscreened*
- 377 Note: Odds ratio (OR) forest plot of the PRS of COVID-19 clinical phenotypes . Use forest plot
- to visualize logistic regression analysis. The outcome variables were serological measurements
- of 25 viruses. The instrumental variables were the PRS of COVID-19 clinical phenotypes.
- **Figure 2:** Forest plots of the results of logistic regression analysis in the whole population.
- 381 (a) *Positive/Negative*;
- 382 (b) *Positive/Unscreened*;
- 383 (c) *Symptomatic/Paucisymptomatic*;
- 384 (d) Unscreened/Exposed_Negative
- 385 Note: Odds ratio (OR) forest plot of the PRS of COVID-19 clinical phenotypes . Use forest plot
- to visualize logistic regression analysis. The outcome variables were serological measurements
- of 25 viruses. The instrumental variables were the PRS of COVID-19 clinical phenotypes.
- 388 Table 1: Viral infections associated with COVID-19 clinical phenotypes in the whole
 389 population
- **Table 2:** Viral infections associated with COVID-19 clinical phenotypes in the age < 65 years
- 391 group and the age > 65 years group
- 392 **Table 3:** Viral infections associated with COVID-19 clinical phenotypes in the women group

and the men group

Journal Pre-proof

Outcome Variable	Instrumental Variable	β	P
Unscreened/Exposed_Negative	VZV seropositivity for Varicella Zoster Virus	0.1361	0.0142
Positive/Unscreened	C. trachomatis Definition II seropositivity for Chlamydia trachomatis	0.2174	0.0185
Exposed_Positive/Exposed_Negative	HSV-2 seropositivity for Herpes Simplex virus-2	0.0935	0.0192
Positive/Negative	HSV-1 seropositivity for Herpes Simplex virus-1	0.0718	0.0213
Exposed_Positive/Exposed_Negative	HBV seropositivity for Hepatitis B Virus	0.2722	0.0219
Hospitalized/Unscreened	VZV seropositivity for Varicella Zoster Virus	0.1167	0.0385
Positive/Unscreened	HCV seropositivity for Hepatitis C Virus	<mark>0.7220</mark>	0.0398
Exposed_Positive/Exposed_Negative	KSHV seropositivity for Kaposi's Sarcoma-Associated Herpesvirus	-0.1044	0.0444
Positive/Negative	HSV-2 seropositivity for Herpes Simplex virus-2	-0.0814	0.0446
Unscreened/Exposed_Negative	MCV seropositivity for Merkel Cell Polyomavirus	-0.0614	0.0478
Unscreened/Exposed_Negative	T. gondii seropositivity for Toxoplasma gondii	0.0677	0.0481
Unscreened/Exposed_Negative	HSV-2 seropositivity for Herpes Simplex virus-2	0.0817	0.0493

Table 1: Viral infections associated with COVID-19 clinical phenotypes in whole population

Note: The threshold of significance is P < 0.05.

is P <

	05 years group			
Group	Outcome Variable	Instrumental Variable	β	Р
Age ≤ 65 years	Exposed_Positive/Exposed_Negative	HSV-2 seropositivity for Herpes Simplex virus-2	0.1017	0.0177
	Positive/Negative	HHV-6B seropositivity for Human Herpesvirus-6	-0.0869	0.0226
	Positive/Negative	HSV-2 seropositivity for Herpes Simplex virus-2	-0.0987	0.0242
	Positive/Negative	HSV-1 seropositivity for Herpes Simplex virus-1	0.0748	<mark>0.0270</mark>
	Exposed_Positive/Exposed_Negative	KSHV seropositivity for Kaposi's Sarcoma-Associated Herpesvirus	-0.1208	0.0353
	Unscreened/Exposed_Negative	VZV seropositivity for Varicella Zoster Virus	0.1206	0.0432
	Hospitalized/Not_Hospitalized	HBV seropositivity for Hepatitis B Virus	-0.2565	0.0464
Age > 65 years	Continuous_Severity_Score	HSV-2 seropositivity for Herpes Simplex virus-2	0.3132	0.0084
	Positive/Negative	HHV-6B seropositivity for Human Herpesvirus-6	<mark>0.2150</mark>	0.0149
	Hospitalized/Unscreened	KSHV seropositivity for Kaposi's Sarcoma-Associated Herpesvirus	-0.3371	0.0171
	Unscreened/Exposed_Negative	BKV seropositivity for Human Polyomavirus BKV	0.3491	0.0208
	Continuous_Severity_Score	HHV-6 overall seropositivity for Human Herpesvirus-6	-0.2731	0.0323
	Exposed_Positive/Exposed_Negative	HPV 18 seropositivity for Human Papillomavirus type-18	-0.5712	0.0343
	Hospitalized/Not_Hospitalized	C. trachomatis Definition I seropositivity for Chlamydia trachomatis	-0.2309	0.0367
	Symptomatic/Paucisymptomatic	HPV 16 Definition I seropositivity for Human Papillomavirus type-16	-0.5834	0.0368
	Symptomatic/Paucisymptomatic	HSV-2 seropositivity for Herpes Simplex virus-2	0.2436	0.0426
	Positive/Unscreened	HHV-6B seropositivity for Human Herpesvirus-6	0.1801	0.0465

Table 2: Viral infections associated with COVID-19 clinical phenotypes in the age \leq 65 years group and the age >

65 years group

Note: The threshold of significance is P < 0.05.

Group	Outcome Variable	Instrumental Variable	β	Р
Women	Exposed_Positive/Exposed_Negative	HPV 16 Definition II seropositivity for Human Papillomavirus type-16	-0.2766	0.0026
	Continuous_Severity_Score	HPV 18 seropositivity for Human Papillomavirus type-18	<mark>-0.3710</mark>	0.0054
	Hospitalized/Not_Hospitalized	HHV-7 seropositivity for Human Herpesvirus-7	-0.2380	<mark>0.0230</mark>
	Symptomatic/Paucisymptomatic	HPV 16 Definition II seropositivity for Human Papillomavirus type-16	-0.2105	0.0252
	Hospitalized/Unscreened	BKV seropositivity for Human Polyomavirus BKV	-0.1802	0.0356
Men	Positive/Negative	HSV-2 seropositivity for Herpes Simplex virus-2	-0.1881	0.0017
	Exposed_Positive/Exposed_Negative	JCV seropositivity for Human Polyomavirus JCV	0.1237	0.0023
	Positive/Negative	HHV-6 overall seropositivity for Human Herpesvirus-6	-0.1986	0.0048
	Positive/Unscreened	C. trachomatis Definition II seropositivity for Chlamydia trachomatis	0.3021	0.0078
	Unscreened/Exposed_Negative	T. gondii seropositivity for Toxoplasma gondii	0.1269	0.0122
	Positive/Negative	KSHV seropositivity for Kaposi's Sarcoma-Associated Herpesvirus	-0.1936	0.0126
	Unscreened/Exposed_Negative	H. pylori Definition I seropositivity for Helicobacter pylori	0.1633	0.0162
	Positive/Unscreened	HPV 16 Definition II seropositivity for Human Papillomavirus type-16	0.2164	0.0256
	Positive/Negative	HSV-1 seropositivity for Herpes Simplex virus-1	0.0989	0.0285
	Positive/Negative	HHV-6A seropositivity for Human Herpesvirus-6	<mark>-0.1090</mark>	0.0308
	Exposed_Positive/Exposed_Negative	H. pylori Definition I seropositivity for Helicobacter pylori	0.1312	0.0333
	Unscreened/Exposed_Negative	VZV seropositivity for Varicella Zoster Virus	0.1913	0.0364
	Hospitalized/Not_Hospitalized	JCV seropositivity for Human Polyomavirus JCV	-0.0876	0.0417
	Exposed_Positive/Exposed_Negative	HSV-2 seropositivity for Herpes Simplex virus-2	0.1158	0.0445

Table 3: Viral infections associated with COVID-19 clinical phenotypes in the women group and the men group

Note: The threshold of significance is P < 0.05.

(a)				(b)		
Virus	P	OR(95%CI)		P	OR(95%CI)	
HSV-1 seropositivity for Herpes Simplex virus-1	0.639	1.015(0.953- 1.082)	Ť	0.204	1.039(0.979- 1.103)	in the second seco
HSV-2 seropositivity for Herpes Simplex virus-2	0.397	0.965(0.888- 1.048)	+	0.019	1.098(1.015- 1.187)	-
EBV sempositivity for Enstein-Barr Virus	0.518	1.038(0.926-1.164)	Ť.	0.912	0.994(0.893-1.106)	
CMV seropositivity for Human Cytomegalovirus	0.144	1.046(0.985-1.110)		0.762	0.958(0.915-1.023)	T
HHV-6 overall seropositivity for Human Herpesvirus-6	0.175	0.934(0.846- 1.031)	-	0.748	0.985(0.898- 1.081)	
HHV-6A seropositivity for Human Herpesvirus-6	0.884	0.995(0.928-1.057)	+	0.634	0.984(0.922-1.051)	-
HHV-68 seropositivity for Human Herpesvirus-6	0.227	0.957(0.892- 1.028)	-	0.259	1.039(0.972-1.110)	-
HHV-7 seropositivity for Human Herpesvirus-7	0.914	0.993(0.873- 1.130)	-	0.586	1.033(0.918- 1.163)	-
KSHV seropositivity for Kaposi's Sarcoma-Associated Herpesvirus	0.615	0.972(0.868- 1.087)	+	0.044	0.901(0.814- 0.997)	-
HBV seropositivity for Hepatitis B Virus	0.349	1.117(0.895-1.408)		0.022	1.313(1.040- 1.657)	
HCV seropositivity for Hepatitis C Virus	0.996	1.002(0.468- 2.144)		0.173	1.700(0.792-3.649)	
T. gondii seropositivity for Toxoplasma gondii	0.090	1.061(0.991-1.135)		0.280	1.036(0.972-1.104)	
HTLV-1 seropositivity for Human T-Lymphotropic Virus 1	0.191	0.850(0.665-1.085)		0.760	1.035(0.830- 1.291)	
HIV-1 seropositivity for Human Immunodeliciency Virus	0.239	1.484(0.769-2.861)		0.691	1.139(0.600-2.161)	
101 sensesibility for Human Polysmaulaus 101	0.104	0.993(0.935-1.053)	T	0.123	1.040(0.984-1.029)	
MCV seropositivity for Merkel Cell Polyomavirus	0.366	0.972(0.913- 1.034)	1	0.834	1.002(0.946- 1.052)	
HPV 16 Definition I seropositivity for Human Papillomavirus type-16	0.673	0.969(0.836-1.123)		0.306	1.076(0.935-1.238)	
HPV 18 seropositivity for Human Papillomavirus type-18	0.149	0.861(0.703- 1.055)		0.539	1.061(0.878- 1.283)	
C. trachomatis Definition I seropositivity for Chlamydia trachomatis	0.412	0.969(0.897-1.046)		0.452	1.028(0.957- 1.105)	-
C. trachomatis Definition II seropositivity for Chlamydia trachomatis	0.441	1.076(0.893- 1.295)		0.251	1.109(0.930- 1.323)	
H. pylori Definition I seropositivity for Helicobacter pylori	0.235	0.947(0.865-1.036)	+	0.333	1.042(0.958- 1.134)	-
H. pylori Definition II seropositivity for Helicobacter pylori	0.856	1.006(0.941- 1.076)	+	0.507	1.021(0.960- 1.087)	+
HPV 16 Definition II seropositivity for Human Papillomavirus type-16	0.398	1.061(0.925-1.217)		0.117	0.905(0.798- 1.025)	-
(c)			65 60 65 20	24 (1)		<u></u>
(C)		ODIOFN CIL	UN	(a)	OD/OFF CI	1.01
VITUS HSV-1 seropositivity for Herpes Simplex virus-1	0.166	0.957(0.899- 1.018)	-+;	0.176	0.959(0.902-1.019)	
HSV-2 seropositivity for Herpes Simplex virus-2	0.368	0.964(0.889- 1.045)	-	0.681	0.984(0.908- 1.065)	-
VZV seropositivity for Varicella Zoster Virus	0.456	1.043(0.933- 1.166)		0.038	1.124(1.008-1.255)	
EBV seropositivity for Epstein-Barr Virus	0.701	1.025(0.904- 1.163)	-	0.392	1.056(0.932-1.196)	
CMV seropositivity for Human Cytomegalovirus	0.949	1.002(0.945- 1.062)	-	0.695	0.989(0.933- 1.047)	4
HHV-6 overall seropositivity for Human Herpesvirus-6	0.430	0.962(0.874- 1.059)	+	0.495	1.034(0.940- 1.138)	+
HHV-6A seropositivity for Human Herpesvirus-6	0.393	0.971(0.907- 1.039)	-	0.978	1.001(0.936- 1.070)	+
HHV-6B seropositivity for Human Herpesvirus-6	0.779	0.990(0.924- 1.061)	+	0.269	1.040(0.971- 1.113)	
HHV-7 seropositivity for Human Herpesvirus-7	0.548	0.962(0.849-1.091)		0.737	1.022(0.902-1.157)	+
KSHV seropositivity for Kaposi's Sarcoma-Associated Herpesvirus	0.220	0.933(0.835-1.042)		0.369	0.952(0.854-1.060)	+
HBV seropositivity for Hepatitis B Virus	0.119	0.830(0.856-1.050)		0.073	0.805(0.634-1.020)	77
T conditionersithith for Toxonisma condition	0.738	0.995(0.922; 1.054)	-	0.605	1.021(0.407-1.088)	
HTI V-1 servicesitistis for Human T-J venhotmoir Virus 1	0.992	1.001(0.794- 1.262)		0.954	1.007(0.801+1.266)	
HIV-1 seropositivity for Human Immunodeficiency Virus	0.400	1.317(0.694-2.499)		0.234	1.468(0.780-2.761)	
BKV seropositivity for Human Polyomavirus BKV	0.309	1.073(0.937- 1.230)		0.121	0.902(0.792-1.028)	
JCV seropositivity for Human Polyomavirus JCV	0.699	0.989(0.933- 1.048)	+	0.672	0.988(0.933-1.046)	
MCV seropositivity for Merkel Cell Polyomavirus	0.823	1.007(0.948- 1.070)	-	0.972	0.999(0.941-1.060)	
HPV 16 Definition I seropositivity for Human Papillomavirus type-16	0.811	1.018(0.881+ 1.176)	+	0.235	1.087(0.947-1.248)	-
HPV 16 Definition I seropositivity for Human Papillomavirus type-16 HPV 18 seropositivity for Human Papillomavirus type-18	0.811	1.018(0.881- 1.176) 1.017(0.837- 1.236)		0.235 0.309	1.087(0.947- 1.248) 1.102(0.914- 1.328)	
HPV 16 Definition I seropositivity for Human Papillomavirus type-16 HPV 18 seropositivity for Human Papillomavirus type-18 C. trachomatis Definition I seropositivity for Chiamydia trachomatis	0.811 0.866 0.341	1.018(0.881-1.176) 1.017(0.837-1.236) 0.864(0.894-1.039)		0.235 0.309 0.102	1.087(0.947- 1.248) 1.102(0.914- 1.328) 0.940(0.874- 1.012)	
HPV 16 Definition I seropositivity for Human Papilomavirus type-16 HPV 18 seropositivity for Human Papilomavirus type-18 C. trachomatis Definition I seropositivity for Chiamydia trachomatis C. trachomatis Definition II seropositivity for Chiamydia trachomatis	0.811 0.956 0.341 0.810	1.018(0.881- 1.176) 1.017(0.837- 1.236) 0.964(0.894- 1.039) 1.022(0.853- 1.226)		0.235 0.309 0.102 0.488	1.087(0.947-1.248) 1.102(0.914-1.328) 0.940(0.874-1.012) 0.938(0.780-1.128)	
HPV 16 Definition I seropositivity for Human Papiliomavirus type-16 HPV 16 Beropositivity for Human Papiliomavirus type-16 C. trachematis Definition I seropositivity for Chiamydia trachematis C. trachematis Definition II seropositivity for Chiamydia trachematis H, pylori Definition I seropositivity for Nelicobarder pylori	0.811 0.856 0.341 0.810 0.410	1.018(0.881-1.176) 1.017(0.837-1.236) 0.964(0.894-1.039) 1.022(0.853-1.226) 1.038(0.949-1.136) 4.0170.260-1.736)		0.235 0.309 0.102 0.498 0.303	1.087(0.947-1.248) 1.102(0.914-1.328) 0.940(0.874-1.012) 0.938(0.780-1.128) 1.047(0.958-1.143)	
HP114 Definition i semopatitivity for Human Papilomaniva type-16 HP11 i semopatitivity for Human Papilomaniva type-18 C stathomatis Definition i semopatitivity for Chiamyda trathomatis C stathomatis Definition i semopatitivity for Chiamyda trathomatis L hydro Definition i semopatitivity for trathomater physic H j hydro Definition II semopatitivity for Halcobacter pytori HD116 Definition II semopatitivity for Halcobacter pytori HD116 Definition II semopatitivity for Halcobacter Dytori	0.811 0.856 0.341 0.810 0.410 0.709	1.018(0.881-1.176) 1.017(0.837-1.236) 0.684(0.884-1.039) 1.022(0.855-1.226) 1.038(0.949-1.136) 1.038(0.949-1.136) 1.012(0.849-1.080) 1.012(0.849-1.180)		0 235 0 309 0.102 0.488 0 303 0.604	1.087(0.947-1.248) 1.102(0.914-1.328) 0.940(0.874-1.012) 0.938(0.780-1.128) 1.047(0.958-1.143) 1.017(0.954-1.084) 1.012(2.1.188)	
HP1 16 Distriction Lemposatility for Human Papilotenetrics type-16 HP7 18 sereposatility for Human Papilotenetrics type-18 C: stachenetas Bufferition Lemposatility for Chlemyde tarbonnets C: stachenetas Bufferition Lemposatility for Chlemyde tarbonnets H sylort Definition Lemposatility for Chlemyde tarbonnets H sylort Definition Lemposatility for Holicobacter pylori HP7 18 Definition Lemposatility for Human Papilotenetrics type-16	0.811 0.856 0.341 0.810 0.410 0.709 0.954	1.018(0.881+1.176) 1.017(0.457+1236) 0.964(0.894+1.039) 1.022(0.465+1.266) 1.038(0.946+1.136) 1.012(0.466+1.080) 1.023(0.87+1.148)		0 235 0 309 0.102 0.488 0 303 0.604 0.549	1.087(0.547-1.248) 1.102(0.914-1.328) 0.940(0.874-1.012) 0.938(0.780-1.128) 1.047(0.9864-1.143) 1.017(0.954-1.084) 1.041(0.912-1.188)	
HPV 16 Dictriton I sergosativity for Intram Paptitementus type-16 HPV 18 exceptible for Human Paptitements type-18 C. tradnematik Definition I sergosativity for Otlamyda tradnomatik C. tradnematik Definition I sergosativity for Policenyda tradnomati I pylori Definition I sergosativity for Holeszber gylori HPV 16 Definition II sergosativity for Heleszber gylori HPV 16 Definition II sergosativity for Helmen Paptitementus type-16	0.811 0.856 0.341 0.810 0.410 0.709 0.954	1.016(0.081-1.178) 1.017(0.037-1.29) 0.964(0.084-1.039) 1.022(0.085-1.228) 1.026(0.449-1.158) 1.012(0.449-1.080) 1.000(0.877-1.148)		0.235 0.309 0.402 0.488 0.303 0.604 0.549	1.067(0.947-1.248) 1.102(0.914-1.328) 0.940(0.874-1.012) 0.938(0.780-1.128) 1.047(0.958-1.143) 1.017(0.954-1.084) 1.041(0.912-1.188)	
IPV 16 Direfront in service/sitely for Human Papilonenicus type-16 IPV 18 service/sitely for Human Papilonenicus type-18 IPV 18 service/sitely in Service/sitely for Human Papilonenicus type-18 C: tractorestis Definition I service/sitely for Citerry-la technomis H cyclor Definition I service/sitely for Citerry-la technomis H cyclor Definition I service/sitely for Hercobacter pylori H (PVI 16 Definition II service/sitely for Hercobacter pylori HPV 16 Definition II service/sitely for Human Papilonenicus type-16	0.811 0.896 0.341 0.810 0.410 0.709 0.954	1.016(0.881-1.176) 1.017(0.837-1.239) 0.646(0.081-1.039) 1.022(0.853-1.228) 1.012(0.849-1.080) 1.012(0.849-1.080) 1.000(0.877-1.188)		0.235 0.309 0.102 0.498 0.303 0.694 0.549	1.067(0.947-1.248) 1.102(0.914-1.328) 0.940(0.874-1.012) 0.938(0.780-1.128) 1.047(0.958-1.143) 1.017(0.954-1.084) 1.041(0.912-1.188)	
HPV 16 Didnition Langozatility for Human Papitomenius type-16 HPV 18 serepositivity for Human Papitomenius type-18 LPV 18 serepositivity for Human Papitomenius type-18 C: trachomatis Dufficient Langozativity for Chlemyda trachomatis H pytor Definition I serepositivity for Helicobacter pytori H pytor Definition I serepositivity for Human Papitomenius type-18 HPV 18 Didnition II serepositivity for Human Papitomenius type-18	0.811 0.886 0.341 0.810 0.410 0.709 0.954	1.018(0.881-1.178) 1.017(0.837-1.296) 0.864(0.884-1.039) 1.022(0.653-1.228) 1.023(0.646-1.080) 1.023(0.869-1.080) 1.003(0.877-1.148)		0.235 0.309 0.402 0.468 0.303 0.649 0.569	1.687(0.547-1.248) 1.102(0.514-1.328) 0.540(0.874-1.012) 0.930(0.780-1.128) 1.647(0.568-1.143) 1.647(0.568-1.143) 1.641(0.912-1.188)	
HPV 16 Didnition I serepositivity for Human Psylotenetric type-16 HPV 16 serepositivity for Human Psylotenetric type-16 C. trachomitis Definition I serepositivity for Olimpida Instromatis C. trachomitis Definition I serepositivity for Olimpida Instromatis H polori Definition I serepositivity for Holizenter pylori H polori Definition I serepositivity for Holizenter pylori HPV 18 Definition II serepositivity for Human Psylotenetrics type-18	0.811 0.856 0.341 0.810 0.410 0.709 0.964	1.018(0.081-1.776) 1.017(0.037-1.236) 0.0940(0.081-1.039) 1.022(0.053-1.236) 1.023(0.045-1.136) 1.023(0.047-1.146) 1.023(0.047-1.146)		0.235 0.309 0.402 0.488 0.303 0.664 0.549	1.067(0.547-1.248) 1.102(0.514-1.328) 0.940(0.874-1.012) 0.940(0.874-1.012) 0.947(0.960-1.143) 1.047(0.960-1.143) 1.041(0.912-1.188)	
IPV 16 Diarkoto Lanopasitiky for Human Papitometrus type-16 IPV 18 seropositiky for Human Papitometrus type-18 IPV 18 seropositiky for Human Papitometrus type-18 C. trachentias Buffelion Lanopasitiky for Charrysia trachematis D. for buffelion Lanopasitiky for Charrysia trachematis La polyco Duffelion seropositiky for Halicobacter pylori H pylors Definition II seropositiky for Halicobacter pylori IPV 16 Definition II seropositiky for Halicobacter pylori IPV 16 Definition II seropositiky for Haman Papitometrika type-18	0.811 0.896 0.341 0.810 0.410 0.410 0.709 0.964	1.019(0.081-1.176) 1.017(0.081-1.039) 0.04(0.081-1.039) 1.022(0.085-1.239) 1.022(0.085-1.239) 1.022(0.085-1.039) 1.022(0.081-1.039) 1.022(0.087-1.146)		0.235 0.309 0.482 0.483 0.303 0.664 0.549	1.087(0.947-1.248) 1.102(0.944-1.328) 0.940(0.874-1.012) 0.938(0.746-1.142) 1.047(0.968-1.143) 1.047(0.968-1.143) 1.041(0.912-1.188)	
HPV 16 Dictritors I sergesativity for Human Papelitementus type-16 HPV 16 sergespoints by termine Papelitements type-18 C. tradematik Definition I sergesativity for Otlamyda tradematik C. tradematik Definition I sergesativity for Holmeyda tradematik I polori Definition I sergesativity for Holmeyda tradematik HPV 10 Definition II sergesativity for Helicobater givel HPV 10 Definition II sergesativity for Helicobater givel HPV 10 Definition II sergesativity for Hennen Papeltomevices type-18	0.811 0.886 0.341 0.810 0.410 0.709 0.964	1.019(0.081-1.176) 1.017(0.037-126) 0.094(0.048-1.09) 1.022(0.063-12.00) 1.022(0.064-1.09) 1.021(0.064-1.09) 1.021(0.064-1.09) 1.021(0.067-1.148)		0235 0309 0409 0488 0303 0804 0569	1.087(0.547-1.248) 1.102(0.914-1.328) 0.540(0.874-1.012) 0.0380(0.780-1.128) 1.047(0.964-1.128) 1.047(0.964-1.084) 1.041(0.912-1.188)	
IPV 16 Diartoto Langozatility for Liman Papitomenicus type-18 IPV 18 sengozisity for Human Papitomenicus type-18 C statutomits Diartotion Langozatility for Clamyda Instruments C statutomits Diartotion Langozatility for Clamyda Instruments Lypolfor Diattinis representitivity for Educator priori H polfor Diattinis and Langozatility for Halcobater priori HPV 18 Diartotion II seespositivity for Halcobater priori IHV 18 Diafettion II seespositivity for Haman Papitomenicus type-16	0.811 0.866 0.341 0.810 0.410 0.709 0.864	1.0140.081-1.070 1.0710021 2390 0.9640.084-1.039 1.02020.055-1.239 1.02020.065-1.239 1.02020.065-1.039 1.02020.064-1.039 1.02020.067.1146		0.235 0.162 0.488 0.333 0.664 0.669	1 067(0.947-1.246) 1 102(0.944-1.328) 0.940(0.974-1.012) 0.938(0.786-1.143) 1 047(0.968-1.143) 1 047(0.968-1.044) 1 041(0.912-1.188)	
IPV 16 Didition Langosativity for Human Papelenewise type-16 IPV 18 second/ord for Human Papelenewise type-18 C trademats Definition Lengositivity for Chamyda tradematis C trademats Definition II empositivity for Chamyda tradematis C trademats Definition II empositivity for Chamyda tradematis H pplori Definition II empositivity for Halesbacker pylot H pplori Definition II empositivity for Halesbacker pylot HPV 10 Definition II empositivity for Human Papelonenivia type-10	0.811 0.966 0.341 0.810 0.410 0.410 0.709	1.018(0.081-1.179) 1.07(0.037-1.203) 1.02(0.057-1.203) 1.02(0.053-1.203) 1.02(0.054-1.105) 1.02(0.044-1.105) 1.02(0.047-1.146)		0.235 0.102 0.402 0.488 0.303 0.654 0.569	1 687(0.947-1.248) 1.102(0.944-1.328) 0.6940(0.874-1.802) 0.6940(0.874-1.128) 1.647(0.864-1.132) 1.647(0.864-1.133) 1.647(0.912-1.188)	
IPV 16 Distribution Langozatifuty for Limana Papelitementus type-16 IPV 16 secondult for Human Papelitementus type-16 C. trachomatik Dahriton Langozatifuty for Chlamyda Istadonatik C. trachomatik Dahriton Langozatifuty for Chlamyda Istadonatik I polori Dahriton Langozatifuty for Human Papelitementus I polori Dahriton I anergozatifuty for Human Papelitementus type-16 HPV 10 Dahriton II anergozatifuty for Human Papelitementus type-16	0.811 0.866 0.341 0.810 0.410 0.410 0.709	1.010(0.011.170) 1.01(0.011.120) 0.04(0.004.1030) 1.02(0.015.42.10) 1.02(0.045.42.10) 1.02(0.045.41.00) 1.02(0.045.41.00) 1.02(0.0457.1140) 	++ + + +	0.236 0.509 0.689 0.030 0.689 0.689	1.027(0.947-1.249) 1.102(0.944-1.329) 0.9340(0.874-1.329) 0.9340(0.874-1.128) 1.047(0.968-1.133) 1.047(0.968-1.139) 1.041(0.912-1.188)	
IPV 16 Diartoto Langozatility for Irlinan Papitomenicus type-18 IPV 18 seropozatility for Human Papitomenicus type-18 IPV 18 seropozatility for Human Papitomenicus type-18 C: tractorentia Bufferiton Langozatility for Citamyola tractorentia Di polor Dufferito II seropozatility for Infectorentia IP oplor Dufferito II seropozatility for Infectorentia priori IPV 18 Diartoton II seropozatility for Helicobater priori IPV 18 Diartoton II seropozatility for Helicobater priori IPV 18 Diartoton II seropozatility for Human Papitomenicus type-16	0.011 0.056 0.341 0.410 0.410 0.709 0.964	1.0140.081-1.070 1.0170.027 1230 0.05440.084-1.039 1.0202.015-1.230 1.0202.045-1.030 1.0202.046-1.030 1.0202.046-1.030 1.0202.047-1.146		0.236 0.507 0.402 0.409 0.303 0.004 0.569	1087(0.947-1.248) 1182(0.944-1.328) 0.640(0.874-1.012) 0.640(0.874-1.128) 10.647(0.868-1.143) 10.77(0.964-1.032) 10.41(0.912-1.188)	
IPV 16 Didn'toto I serviçatility for I-Imma Paştitementus type-16 IPV 16 serviçatility for Human Paştitementus type-18 C. tradnematik Definition I serviçatility for Otlamyda tradnematik C. tradnematik Definition I serviçatility for Otlamyda tradnematik I polori Definition I serviçatility for I-Imma Paştitementus I polori Definition I serviçatility for I-Imma Paştitementus type-18 IPV 10 Definition II serviçatility for I-Imma Paştitementus type-18	0.011 0.066 0.341 0.010 0.410 0.709 0.964	1.018(0.081-1.179) 1.07(0.037-1.20) 0.084(0.084-1.039) 1.020(0.054-1.039) 1.020(0.064-1.139) 1.020(0.064-1.139) 1.020(0.067-1.148)		0.236 0.300 0.402 0.488 0.333 0.664 0.569	1.027(0.547-1.249) 1.102(0.544-1.329) 0.540(0.874-1.012) 0.530(0.728-1.133) 1.047(0.964-1.043) 1.047(0.964-1.045) 1.041(0.972-1.189)	
IPV 16 Diartoto I serepatitivy for Imma Papitometrus type-16 IPV 16 serepatitivy for Imma Papitometrus type-18 IPV 16 serepatitivy for Immo Papitometrus type-18 C: transmits Definition I serepatitivy for Chamyda Instruments D: type/of Definition I serepatitivy for Instrument type I IPV 16 Diartotom II serepatitivy for Instrument type I IPV 16 Diartotom II serepatitivy for Haman Papitometrus type-18	0.011 0.054 0.341 0.410 0.410 0.750 0.954	1.01(2)(0.01		0.236 0.507 0.612 0.648 0.533 0.644 0.549	10270.047.1245	
IPV 16 Didition Langoatility for Human Papelementus type-16 IPV 18 secondult of Human Papelementus type-18 CI: bathornals Didition Langoatility for Chamyda trachomatis CI: bathornals Didition Langoatility for Chamyda trachomatis H: pylori Didition Langoatility for Halebatter pylot H: pylori Didition Langoatility for Halebatter pylot H: pylori Didition II angoatility for Halebatter pylot H:PV 10 Didition II angoatility for Halebatter pylot H:PV 10 Didition II angoatility for Human Papelonenivia type-10	0.011 0.054 0.341 0.010 0.410 0.756 0.954	1.018(0.087-1.076) 1.017(0.087-1.026) 0.944(0.084-1.026) 1.022(0.053-1026) 1.023(0.044-1.026) 1.023(0.047-1.016) 1.023(0.047-1.016) 3.003(0.077-1.016)		0.256 0.507 0.508 0.508 0.509 0.664 0.669	1.007.007.1240 1.1002.007.1240 0.008.007874-1020 0.008.007874-1020 0.007070.005-1120 1.0070.006-1100 1.0070.006-1100 1.0070.0071-1180	
IPV 16 Didnition I surgozativly for I-Imma Papitomerkus type-16 IPV 16 sergovisito for Human Papitomerkus type-17 C. trachomatik Didnition I surgozativly for Otlanyda Itadonnalis C. trachomatik Didnition I surgozativly for Otlanyda Itadonnalis I pylori Didnition I surgozativly for Human Papitomerkus type-18 H pylori Didnition II surgozativly for Human Papitomerkus type-18 HPV 10 Didnition II surgozativly for Human Papitomerkus type-18	0.811 0.854 0.841 0.810 0.410 0.759 0.854	1.01(0.0147.128) 1.01(0.0147.128) 0.04(0.0147.128) 0.02(0.015.128) 1.02(0.0147.128) 1.02(0.0147.128) 1.02(0.0147.118) 1.02(0.047.118) 1.02(0.047.118) 3.00(0.077.118)		0.236 0.500 0.402 0.489 0.533 0.694 0.649	1007.0047.200 11000.014.12007 0000.0047.12007 0000.0047.12007 00070.0064.12007 10770.0064.12007 10770.0064.1200 10410.072.1100	
IPV 16 Diartoton Lanopatihity for Irlama Papitomenicus type-16 IPV 16 seropatihity for Human Papitomenicus type-18 C statuantis Buffiniton Lanopatihity for Chamyda Itautoantis C statuantis Buffiniton Lanopatihity for Chamyda Itautoantis I Lypofor Dathitos II aeropatihity for Irlatostater pixel I Lypofor Dathitos II aeropatihity for Irlatostater pixel I PV 16 Dafriton II aeropatihity for Haltostater pixel I PV 16 Dafriton II aeropatihity for Haltostater pixel	0.011 0.0541 0.0410 0.410 0.700 0.064	1.01(7)(0.057) (236) 0.064(0.084 - 10.05) 1.02(0.065 - 12.08) 1.02(0.065 - 12.08) 1.02(0.065 - 10.08) 1.02(0.065 - 10.08) 1.02(0.067 - 11.08) 1.02(0.067 - 11.08) 1.02(0.		0.236 0.512 0.412 0.489 0.333 0.644 0.549	10071097-240 11020391-1200 008000284-1020 00800284-1020 00800284-1020 10070086-1100 1070086-1080 10410392-1100	
IPV 16 Didnition I sergositivity for I-Imma Papitomevicus type-16 IPV 19 sergositivity for Humin Papitomives type-18 C tradvenate Didnition I sergositivity for Ottanyola tradvenate C tradvenate Didnition I sergositivity for Ottanyola tradvenate I pytori Didnitis regressitivity for Induced and pytori H pytori Didnitis and sergositivity for Induced and pytori H pytori Didnitis ni sergositivity for Induced and pytori H PV 10 Didnitis ni sergositivity for Human Papitomevica type-18 HPV 10 Didnitis ni sergositivity for Human Papitomevica type-18	0.811 0.854 0.341 0.410 0.410 0.964	1 (117) 1 (0.236 0.307 0.402 0.488 0.337 0.644 0.569	10071047 - 201 11020 974 - 201 11020 974 - 201 00080784 - 1020 00080784 - 1020 10770 954 - 108 10770 954 - 108 10770 954 - 108	
IPV 16 Districtor Langozatifuty for Linnan Papitometruk typ-16 IPV 16 secondult for Kinann Papitometruk typ-16 C. taxhonalik Dahrinon Langozatifuty for Olimyda Isahonalis C. taxhonalik Dahrinon Langozatifuty for Dianyda Isahonalis I. polori Dahrinon Langozatifuty for Halicobater pylori H pylori Dahrinon Langozatifuty for Halicobater pylori H PV 10 Dahrinon II aeropatifuty for Halicobater pylori HPV 10 Dahrinon II aeropatifuty for Halicobater pylori IPV 10 Dahrinon II aeropatifuty for Human Papitometruk typ-16	0.011 0.956 0.341 0.810 0.410 0.750 0.750 0.954	1 0.17(0.137.128) 1.07(0.137.128) 0.064(0.084.1039) 1.02(0.063.128) 1.02(0.063.128) 1.02(0.064.1039) 1.02(0.064.10		0.236 0.507 0.689 0.333 0.694 0.569	1007.0047 - 240 11020.014 - 1207 005800784 - 1020 005800784 - 1020 005800784 - 1020 10270.0064 - 1040 10270.0064 - 1040 102410.027 - 1180	
IPV 16 Dictritor I sergestifully for Human Psychian-turk typ-16 IPV 16 sergestifully for Human Psychian-turk typ-18 C tachematis Definition I sergestifully for Chamyda tachematis C tachematis Definition II sergestifully for Chamyda tachematis II spirol Definition II sergestifully for Human Psychian track (H psychian) (H Human Psychian Human Psychian Human) H psychiantian II sergestifully for Human Psychianesius typ-10 IPV 10 Definition II sergestifully for Human Psychianesius typ-10	0.811 0.866 0.341 0.810 0.410 0.410 0.709 0.964	1 0170 0147 - 1283 1 0170 0147 - 1283 1 0170 0147 - 1283 1 0170 0147 - 1283 1 0170 0148 - 1180 1 0170 0148 - 1180 1 0170 0148 - 1180 1 0170 0148 - 1180 1 0170 0147 - 1180		0.236 0.507 0.508 0.518 0.518 0.519 0.549	1007007-200 11020-97-200 0000028-1020 0000028-1020 0000028-1020 1070008-108 1070008-108 1041092-1180	
IPV 16 Districtor Langozatifuty for I-Imma Papitamentus type-16 IPV 16 seconductor type-18 C. trachematik Definition I seropozitifuty for Otlanryda Istachomatik C. trachematik Definition I seropozitifuty for Otlanryda Istachomatik I papirol Definition I seropozitifuty for Induced program I PDV 10 Definition II seropozitifuty for Induced program IPV 10 Definition II seropozitifuty for Induced program Induced program I PV II Definition II seropozitifuty for Induced program IPV 10 Definition II seropozitifuty for Induced p	0.011 0.066 0.066 0.070 0.070 0.070 0.070 0.070 0.070	1 01070 0137 1293 1 01070 0137 1293 1 02070 0137 1293 1 02070 0137 1293 1 02070 0147 1293 1 02070 0147 1 02070 01		0.236 0.500 0.602 0.689 0.699 0.649	10071047-20) 11020-014-1207 000800748-10207 000800748-1020 000800748-1020 100700568-1100 100700568-1000 10410092-1100	

(a)				(b)		
Virus	P	OR(95%CI)		P	OR(95%CI)	
HSV-1 seropositivity for Herpes Simplex virus-1	0.021	1.075(1.011-1.142)	7**	0.861	0.995(0.935-1.058)	†
HSV-2 seropositivity for Herpes Simplex virus-2	0.045	0.922(0.852-0.998)	-	0.316	0.960(0.886- 1.040)	+
VZV seropositivity for Varicella Zoster Virus	0.563	0.959(0.859-1.079)	+	0.353	1.053(0.944-1.176)	-
EBV seropositivity for Epstein-Barr Virus	0.158	0.916(0.810-1.035)		0.163	0.916(0.809-1.036)	-
CMV seropositivity for Human Cytomegalovirus	0.301	0.970(0.916- 1.028)	+	0.777	1.008(0.952-1.059)	+
HHV-6 overall seropositivity for Human Herpesvirus-6	0.088	0.921(0.838-1.012)	-	0.379	0.958(0.871-1.054)	-
HHV-6A seropositivity for Human Herpesvirus-6	0.207	0.958(0.896- 1.024)	+	0.488	1.024(0.957-1.096)	+
HHV-6B seropositivity for Human Herpesvirus-6	0.272	0.953(0.899-1.030)	+	0.519	0.978(0.913-1.047)	+
HHV-7 seropositivity for Human Herpesvirus-7	0.618	1.032(0.912-1.168)	-	0.644	1.030(0.908- 1.169)	+
KSHV seropositivity for Kaposi's Sarcoma-Associated Herpesvirus	0.394	0.954(0.857-1.063)	-	0.838	1.012(0.907-1.127)	+
HBV seropositivity for Hepatitis B Virus	0.695	0.956(0.761-1.199)	+	0.773	0.967(0.768-1.217)	
HCV seropositivity for Hepatitis C Virus	0.118	1.742(0.868-3.497)		0.040	2.059(1.034-4.098)	
T. gondii seropositivity for Toxoplasma gondii	0.721	1.012(0.948-1.080)	-	0.502	1.023(0.958-1.093)	
HTLV-1 seropositivity for Human T-Lymphotropic Virus 1	0.489	0.923(0.735-1.158)		0.598	0.939(0.743-1.187)	-
HIV-1 seropositivity for Human Immunodeficiency Virus	0.089	1.719(0.920-3.210)		0.081	1.754(0.933-3.296)	
BKV seropositivity for Human Polyomavirus BKV	0.371	0.941(0.824-1.075)	+	0.165	0.914(0.800-1.044)	-
JCV seropositivity for Human Polyomavirus JCV	0.498	0.981(0.926-1.038)		0.636	0.905(0.931-1.044)	-
MCV seropositivity for Merkel Cell Polyomavirus	0.342	0.972(0.916-1.031)	1	0.617	0.985(0.928-1.046)	+
HPV 16 Definition I seropositivity for Human Papillomavirus type-16	0.537	0.957(0.832-1.101)	+	0.533	0.956(0.830-1.101)	+
HPV 18 seropositivity for Human Papillomawirus type-18	0.985	1.002(0.828- 1.213)		0.423	1.081(0.894-1.305)	
C. trachomatis Definition I seropositivity for Chlamydia trachomatis	0.616	1.019(0.947- 1.096)	Ť	0.519	0.976(0.907-1.051)	+
C. trachomatis Definition II seropositivity for Chlamydia trachomatis	0.182	1.131(0.944-1.355)		0.018	1.243(1.037-1.489)	
H. pylori Definition I seropositivity for Helicobacter pylori	0.865	1.008(0.921- 1.102)		0.350	1.043(0.964- 1.140)	
H. pylori Definition II seropositivity for Helicobacter pylori	0.697	1.013(0.950- 1.080)	Ť	0.309	1.034(0.969-1.103)	-
HPV 16 Definition II seropositivity for Human Papillomavirus type-16	0.242	0.924(0.809-1.055)		0.291	1.074(0.941-1.227)	
(c)			a a a a a a a a	(d)		a a a a a
(c)			i i i i i i i i a	(d)		j j j i OK
(C) Virus HSV-1 semendikity for Hernes Simpley virus-1	P	OR(95%CI)	ni ni ni ni ni ni mi	(d) P	OR(95%CI)	i i j i i
(C) Virus HSV-1 seropositivity for Herpes Simplex virus-1 HSV-2 seropositivity for Herpes Simplex virus-2	P 0.246	OR(95%CI) 0.984(0.907-1.028) 0.99900.895-1.0491	u u u u u u u u	(d) P 0.446	OR(95%CI)	
(C) Virus HSV-1 seropositivity for Herpes Simplex virus-1 HSV-2 seropositivity for Herpes Simplex virus-2 V/2 werenotity the Variantial Zoeter Virus	P 0.246 0.434	OR(95%CI) 0.964(0.907-1.028) 0.969(0.895-1.049) 1.0200.915-1.1371	10 0 0 0 0 0 0 0 0	(d) P 0.446 0.049	OR(95%Cl) 1.024(0.963-1.090) 1.085(1.000-1.177)	È 🖌
(C) Virus HSV-1 sengoalikity for Harpes Simplex virus-1 HSV-2 sengoalikity for Harpes Simplex virus-2 V2V sengoality for Variantial Zostar Virus EV sengoality for Scateful Barry Virus	P 0.246 0.434 0.723	OR(95%CI) 0.984(0.107-1.028) 0.989(0.885-1.049) 1.020(0.915-1.137) 0.9590 845-1.087)	й й й й й й й й 	(d) P 0.446 0.049 0.014	OR(95%Cl) 1.024(0.963-1.090) 1.085(1.000-1.177) 1.146(1.028-1.278) 1.0190/988-1.155)	Ē K
(C) Virus HSV-1 sensositivity for Herpos Bimplax Vius-1 HSV-2 sensositivity for Herpos Bimplax Vius-2 V2V sensositivity for Hanola Zoster Vius EBV sensopolitivity for Epidenic Barr Vinas CMV sensositivity for Hanna Channasativitas	P 0.246 0.434 0.723 0.509	OR(95%,Cl) 0.584(0.107-1.028) 0.589(0.895-1.049) 1.620(0.915-1.137) 0.559(0.845-1.087) 0.599(0.845-1.087)		(d) P 0.446 0.049 0.014 0.779 0.570	OR(95%Cl) 1.024(0.963-1.090) 1.085(1.000-1.177) 1.140(1.028-1.278) 1.018(0.888-1.155) 0.08211.0421	
(C) Virus HSV-1 empositivly for Heyses Simplex virus-1 HSV-2 empositivly for Heyses Simplex virus-2 V2V eneropositivly for Heysen Sam Virus EVM eneropositivly for Epidem Sam Virus CMM eneropositivly for Heiman Chomegalovirus	P 0.246 0.434 0.723 0.559 0.970	OR(95%Cl) 0.9640(0.807-1.028) 0.9640(0.805-1.040) 1.020(0.915-1.137) 0.9690(0.845-1.087) 0.9990(0.943-1.058) 1.020(0.964-1.132)		(d) P 0.446 0.049 0.014 0.779 0.670 0.933	OR(95%Cl) 1.024(0.363-1.050) 1.005(1.000-1.177) 1.046(1.028-1.278) 1.018(0.888-1.156) 0.367(0.301-1.047) 1.044(0.311-1.168)	
(C) Virus 1953 sangadahij far Herpas Binglas visus 1 1952 angadahij far Herpas Binglas visus 2 2024 angadahij far Vanasa Zandri Yula 1954 angadahij far Jaman Cjanagabara 1964 da vengadahij far Jaman Cjanagabara 1964 da vengadahij far Jaman Cjanagabara	P 0.246 0.434 0.723 0.509 0.970 0.556 0.521	OR(95%Cl) 0.884(0.897-1.028) 0.889(0.885-1.049) 1.620(0.815-1.137) 0.696(0.845-1.087) 0.696(0.945-1.057) 1.620(0.506-1.132) 1.620(0.506-1.132)	**************************************	(d) P 0.446 0.049 0.014 0.779 0.670 0.833 0.853	OR(95%Cl) 1.024(0.983-1.090) 1.005(1.005-1.177) 1.146(1.028-1.278) 1.018(0.888-1.156) 0.997(0.301-1.047) 1.040(0.911-1.106) 0.994(0.302-1.054)	
(C) Virus 1993 sangestihly for Herps Binglex virus-1 1992 angestihly for Herps Binglex virus 2004 angestihly for Herps Binglex virus EBF parquetisky for Epitain Barr Virus CMF angestihly for Human Herpsenson HerV-d angestihly for Human Herpsenson 4	P 0.246 0.434 0.723 0.970 0.576 0.521 0.855	OR(95%CI) 0.884(0.897-1.028) 0.888(0.895-1.049) 1.020(0.915-1.137) 0.999(0.845-1.087) 0.999(0.845-1.087) 1.020(0.395-1.152) 1.022(0.395-1.033) 0.9840(0.395-1.054)	* * * * * * * * * * * *	(d) P 0.446 0.049 0.014 0.014 0.014 0.014 0.013 0.064 0.023	OR(95%Cl) 1.024(0.383-1.090) 1.085(1.000-1.177) 1.146(1.028-1.278) 1.018(0.888-1.155) 0.897(0.831-1.047) 1.048(0.322-1.054) 0.594(0.322-1.120)	
(C) Virus 18%1 sampatihily for Herpes Bimplex rhss 1 18%2 ampathility for Herpes Bimplex rhss 2 18%2 execution for Vessel Zeark from EdV execution for Vessel Zeark from CAV execution for Herman Chempenhania 18%6 execution for Herman Telepresitiva 18%6 execution for Herman Telepresitiva 18%6 execution for Herman Telepresitiva	P 0.246 0.434 0.723 0.509 0.556 0.555 0.855	OR(95%C) 0.584(0.587-1.028) 0.588(0.885-1.049) 1.020(0.945-1.157) 0.598(0.845-1.057) 0.598(0.545-1.058) 1.020(0.508-1.152) 1.020(0.508-1.054) 0.594(0.528-1.054)	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	(d) P 0.446 0.049 0.014 0.014 0.014 0.014 0.013 0.084 0.213 0.749	OR(95%Cf) 1.024(0.363-1.080) 1.005(1.000-1.177) 1.146(1.088-1.278) 1.018(0.888-1.555) 0.597(0.361-1.047) 1.004(0.391-1.106) 0.594(0.302-1.054) 1.042(0.302-1.159)	
(C) Virus 1954: sampatiship for Herpes Simplex virus-1 1952: angeoathip for Herpes Simplex virus-2 1954: angeoathip for Herpes Simplex virus-2 1954: angeoathip for Herpes Herpes virus-3 1964: angeoathip for Herpes Herpes virus-3 HerV-1 angeoathip for Herpes Virus-1 HerV-1 angeoathip for Herpes Virus-1 Herpes virus-3 HerV-1 angeoathip for Herpes Virus-1 HerPes Virus-1 HerV-1 Herpes Virus-1 HerV-1 Herpes Virus-1 HerV-1	P 0.246 0.434 0.723 0.500 0.570 0.556 0.521 0.855 0.857 0.550	OR(05%C0) 0.64(0:107-1.020) 0.69(0:805-1.040) 1.02(0:945-1.137) 0.69(0:945-0.857) 1.02(0:806-1.132) 1.02(0:806-1.132) 1.02(0:806-1.143)	* * * * * * * * * * * * * * * * * * *	(d) P 0.446 0.049 0.014 0.379 0.670 0.833 0.884 0.213 0.749 0.489	OR(85%C0) 1.024(0.985-1.030) 1.0182(1.002-1.177) 1.018(0.088-1.155) 0.987(0.983-1.047) 0.984(0.932-1.044) 1.044(0.917-1.130) 1.024(0.962-1.150) 1.029(0.962-1.160)	
(C) Virus 10%1 sempositivity for Merges Einspise visus 1 10%2 sempositivity for Merges Einspise visus 2 10%2 visuspositivity for Visus 20x0 vitis 10%2 visuspositivity for Visus Mergesonia 10%2 visuspositivity for Minum Mergesonia 10%2 visuspositivity for Manum Mergesonia 10%	P 0.246 0.434 0.723 0.370 0.556 0.551 0.555 0.521 0.355 0.857 0.500 0.405	DR(09%C0) 0.984(0.307-1.028) 0.989(0.885-1.049) 1.020(0.914-1.137) 0.999(0.943-1.058) 1.020(0.964-1.132) 1.020(0.964-1.132) 1.020(0.964-1.132) 0.994(0.328-1.044) 1.030(0.964-1.144) 1.030(0.311-1.157)	* * * * * * * * * * * * * * * * * * *	(d) P 0.446 0.049 0.014 0.014 0.014 0.013 0.033 0.033 0.033 0.035 0.033 0.035 0.033 0.049 0.033 0.049 0.033 0.049 0.049 0.014 0.049 0.014 0.033 0.033 0.055 0.045 0.045 0.033 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.045 0.055 0.055 0.055 0.055 0.055 0.055 0.055 0.045 0.055 0.055 0.055 0.055 0.045 0.055 0.055 0.055 0.045 0.055 0	OR(05%C0) 1.024(0.082-1.080) 1.032(1.000-1.177) 1.146(1.002-1.278) 0.987(0.931-1.047) 1.04(0.931-1.047) 1.04(0.932-1.047) 1.04(0.932-1.158) 1.04(0.932-1.159) 1.04(0.932-1.158)	
(C) Virus Hors Inspectively for herpes Empire virus -1 Hors Inspectively for herpes Empire virus -2 Low Annowable Virus Allower Mail Edit Annovable Virus Allower Mail Hord Annovable Virus Allower Mail Hord Annovable Virus Herpenina -3 Hord Management -3 Hord Man	P 0.246 0.454 0.723 0.570 0.570 0.556 0.521 0.555 0.521 0.855 0.857 0.565 0.405 0.348	DR(95%Cf) 0.944(-0.07-1.038) 0.950(2.045-1.049) 0.950(2.045-1.047) 0.990(0.045-1.017) 0.990(0.045-1.018) 1.020(0.066-1.013) 0.944(0.045-1.013) 0.944(0.045-1.144) 1.030(0.051-1.157) 1.144(0.475-1.322)	* * * * * * * * * * * * * * * * * * *	(d) P 0.448 0.049 0.014 0.779 0.833 0.884 0.213 0.749 0.459 0.459 0.394	DR(95%C0) 1.045(1.002-1.177) 1.045(1.002-1.177) 1.045(1.002-1.177) 1.045(0.088-1.165) 0.967(0.081-1.047) 0.94(0.928-1.044) 1.944(0.978-1.178) 1.944(0.978-1.178) 1.945(0.978-1.178) 1.947(0.978-1.186) 1.947(0.988-1.847)	
(C) Virus 1951: sensedavity for Marsas Einspise virus 1 1952: sensedavity for Marsas Einspise virus 2 1954: encounted for Marsas Einspise virus 1954: encounted for Marsas Einspise 1954: encounted for Marsas Teleparas 1954: encounted for Marsas Teleparas	P 0.246 0.334 0.723 0.350 0.350 0.556 0.555 0.555 0.855 0.855 0.855 0.855 0.855 0.855 0.855 0.855 0.855 0.948	DR(95%C0) 0.0%(0.07-1.028) 0.0%(0.007-1.028) 0.0%(0.007-1.028) 0.0%(0.045-1.047) 0.0%(0.045-1.018) 1.0%(0.045-1.018) 1.0%(0.069-1.044) 1.0%(0.069-1.044) 1.0%(0.069-1.147) 1.0%(0.057-1.312) 1.0%(0.045-1.212) 1.0%(0.045-2.122) 1.0%(0.045-2.123)		(d) P 0.446 0.049 0.014 0.079 0.833 0.854 0.213 0.554 0.459 0.459 0.336 0.544 0.459 0.396	DR(95%C0) 1.04(0.0813-1.080) 1.04(0.082-1.172) 1.04(0.084-1.172) 1.04(0.091-1.047) 1.04(0.091-1.1160) 0.04(0.097-1.120) 1.04(0.097-1.120) 1.04(0.097-1.110)	
(C) Virus HSV Iampachily for Herpas Binglas visus 1 HSV associativity for Herpas Binglas visus 2 HSV associativity for Visus 2 HSV associativity for Visus 2 HSV associativity for Human Herpensiva HSV Associativity HSV Human Herpensiva HSV Herpens	P 0.446 0.453 0.523 0.500 0.575 0.524 0.525 0.521 0.525 0.526 0.521 0.525 0.526 0.521 0.525 0.526 0.521 0.525 0.526 0.521 0.525 0.526 0.521 0.520 0.521 0.525 0.527 0.526 0.527 0.528 0.529	DR(95%C0) 0.96(2),977-1029) 0.96(2),987-1029) 0.96(2),984-1027) 0.96(2),984-1027) 0.96(2),984-1027) 1.02(2),984-1023) 0.96(2),984-1023) 0.96(2),984-1023) 0.96(2),984-1023) 1.04(2),845-2122) 1.04(2),845-2122) 1.04(2),845-2123)		(d) P 0.440 0.049 0.014 0.073 0.073 0.083 0.084 0.213 0.740 0.449 0.394 0.046	OR(85%C0) 1.52(4)085-1.020) 1.54(4)084-1.020) 1.54(4)084-1.150) 0.54(0)084-1.150) 0.54(0)085-1.160) 1.62(0)085-1.160) 1.62(0)085-1.150) 1.62(0)085-1.150) 1.62(0)085-1.120) 1.62(0)085-1.120) 1.62(0)085-1.120)	
(C) Virus 1951: empediating termines timples virus 1 1952: empediating termines timples virus 2 1954: empediating termines timples virus 2 1954: empediating termines timples 1954: empediating termines tim	 P 0.246 0.723 0.559 0.559 0.551 0.551 0.855 0.855 0.856 0.948 0.948 0.927 0.853 	CP(4954/CC) O (496/007 - 102/00 O (496/007 - 102/00 O (496/004 - 104/00 O (496/004 - 104/004 O (496/004))		(d) P 0.440 0.014 0.014 0.014 0.014 0.014 0.014 0.021 0.213 0.213 0.213 0.213 0.213 0.213 0.214 0.439 0.394 0.040 0.040 0.040 0.054	DR(95%C0) 1.024(0.08-1.030) 1.034(1.00-1.177) 1.44(0.08-1.120) 1.04(0.08-1.103) 1.04(0.097-1.103) 1.04(0.097-1.103) 1.04(0.097-1.103) 1.04(0.097-1.103) 1.02(0.08-1.103) 1.07(0.08-1.104) 1.07(0.08-1.104) 1.07(0.08-1.104) 1.02(0.08-1.1	
(C) Virus HSI anspatiship for Herpes Binglas russ 1 HSI anspatiship for Herpes Binglas russ 2 Virus equatiship for Herpes Binglas russ 2 HSI de Sampathip for Herpes Herpeshol HSI de Sampathip for Herpeshol HSI de Sa	P 0.246 0.434 0.723 0.570 0.576 0.576 0.576 0.576 0.576 0.576 0.576 0.576 0.576 0.576 0.576 0.576 0.577 0.576 0.577 0.576 0.577 0.573 0.587 0.587	CR(85%CC) O(840/037-1020) O(840/034-0140) O(840/034-1040) O(840/034-1040) O(840/034-1040) O(840/034-1040)		(d) P 0.440 0.014 0	DR(85%C0) 1.04(4.004-1.020) 1.04(4.004-1.020) 1.04(4.004-1.020) 0.04(0.001-1.010) 0.04(0.021-1.010) 0.04(0.021-1.010) 1.04(0.005-1.100) 1.04(0.005-1.100) 1.04(0.005-1.100) 1.04(0.005-1.010) 1.04(0.005-1.010) 0.070(1.041-1.010) 0.070(1.041-1.010) 0.08(0.045-1.010) 0.08(0.045-1.010) 0.04(0.045-1.010) 0.04(0.045-1.010)	
(C) Virus 10% semanticity for Messes Employe who 4 10% semanticity for Messes Employe who 2 10% semanticity for Messes Employe who 2 10% semanticity for Messes Messes 10% semanticity for Messes 10%	 P 0.246 0.434 0.723 0.506 0.856 0.865 0.865 0.950 0.405 0.950 0.95	OR(2054)C() 0.084(0.007-1.028) 0.084(0.007-1.028) 0.094(0.045-1.024) 0.094(0.045-1.024) 0.094(0.045-1.024) 0.094(0.045-1.024) 0.094(0.045-1.024) 1.094(0.045-1.024) 0.094(0.045-1.024) 0.094(0.045-1.024) 0.094(0.045-1.024) 0.094(0.045-1.024) 0.094(0.045-1.024) 0.097(0.047-1.045) 0.097(0.047-1.045) 0.097(0.047-1.045) 0.097(0.047-1.045)		(d) P 0.446 0.044 0.014 0.014 0.014 0.014 0.014 0.014 0.014 0.014 0.014 0.405 0.833 0.834 0.046 0.046 0.046 0.054 0.046 0.054 0.055 0.054 0.055 0	DR(95%CC) 1.024(008-1.000) 1.034(1002-1077) 1.040(1008-1.077) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017) 1.040(008-1.017)	
(C) Virus 1951: Instructional for largenese linespines runs a 1 1952: Assessments for largenese linespines runs a 2 2054: respectively for largenese linespines runs a 2 2054: Respectively for largenese linespines runs a 2 1954: Respectively for largenese linespines runs a 2 1954: Respectively for largenese linespines runs a 2 1955: Respectively for largenese linespines runs a 1 1955: Respectively for largenese linespines runs a 1 1954: Respectively for largenese linespinespines runs a 1 1955: Respectively for largenese linespinespinespinespinespinespinespinesp	P 0.244 0.723 0.509 0.556 0.556 0.556 0.857 0.550 0.454 0.956 0.857 0.560 0.454 0.857 0.853 0.853 0.853 0.853 0.854	OR(1951)C(1) 0 64(4):02(7)-11(2) 0 64(4):02(7)-11(2) 0 64(4):04(7)-11(2) 0 64(4):04(7)-11(2) 0 64(4):04(7)-11(2) 1 02(4):04(7)-11(2) 1 02(4):04(7)-11(2) 1 02(4):04(7)-11(2) 1 02(4):04(7)-11(2) 1 02(4):04(7)-11(2) 1 02(4):04(7)-11(2) 1 02(4):04(7)-11(2) 0 64(4):04(7)-11(2) 0 64(7)-11(2) 0 64(7)-11((d) P 0.440 0.040 0.014 0.014 0.014 0.014 0.014 0.014 0.014 0.014 0.014 0.021 0.053 0.054 0.054 0.054 0.054 0.054	02(895),C() 1.624(0.963-1.070) 1.146(0.63-1.270) 1.146(0.961-1.071) 1.146(0.961-1.071) 1.040(0.931-1.041) 1.040(0.931-1.041) 1.040(0.951-1.160) 1.040(0.951-1.160) 1.047(0.951-1.160) 1.047(0.951-1.160) 1.047(0.951-1.160) 1.040(0.951-0.160) 1.040(0.951-0.	
(C) Virus 10 ⁻¹ series and the Means Employ series 1 10 ⁻¹ series and the Means Employ series 2 10 ⁻¹ series and the Means Employ series 2 10 ⁻¹ series and the Means Telepassis 2 10 ⁻¹ series and the Means 1 10 ⁻¹ series and the Means Telepassis 2 10 ⁻¹ series and th	 P 0.246 0.434 0.723 0.556 0.877 0.868 0.887 0.888 0.887 0.405 0.405 0.945 0.947 0.863 0.947 0.863 0.867 0.867 0.867 0.773 0.864 0.877 0.73 0.845 	OR(4954C0) O(4940) 0074 - 1028) O (2020) 0484 - 1028) O (2020) 0484 - 1027) O (2020) 0484 - 1027) O (2020) 0484 - 1028) O (2020) 0484 - 1028) O (2020) 0484 - 1028) O (2020) 048 - 1028) O (2020) 048 - 1028) O (2020) 047 - 1086) O (2020) 047 - 1087) O (2020) 047) O (2020) 04		(d) P 0.446 0.009 0.014 0.770 0.853 0.864 0.469 0.465 0.455 0.455 0.455 0.465 0.455 0	08(854,C) 1.02(4):055-107 1.04(2):05-107 1.04(2):05-107 0.04(2):05-107 0.04(2):05-107 0.04(2):05-107 1.04(2):05-107 1.07(2):05-107 1.	
(C) Viru Br: Iangenative for Heppes Binglew data 1 Hor: Jangenative for Heppes Binglew data 2 Vir vespectave for Vespecial Spectra Viru Comparative Virus Zauge Virus Comparative Virus Comparative Virus Hori Van Vespecial Virus Virus Virus Hori Van Vespecial Virus Virus Virus Virus Vespecial Virus Virus Virus Virus Vespecial Virus Virus Virus Virus Virus Virus Vespecial Virus Virus Virus Virus Virus Virus Virus Vespecial Virus Virus Virus Vespecial Virus	 P 0.246 0.454 0.723 0.506 0.877 0.506 0.885 0.886 0.886 0.946 0.946 0.946 0.947 0.8603 0.6673 0.773 0.840 0.285 	08(8954) 0 5802087 - 100 0 5802087 - 100 0 5802087 - 101 0 6890288 - 108 1 02002 - 101 1 02002 - 101 0 64402 - 101 0 6		(d) P 0.440 0.049 0.0514 0.573 0.670 0.833 0.845 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.214	08(89545) 1.562(335-100) 1.562(335-107) 1.5	
(c) Virus 10 ⁻¹ series and the Means Singles with st. 10 ⁻¹ series and the Means Singles with st. 10 ⁻¹ series and the Weath Single with st. 10 ⁻¹ series and the Weath Single with st. 10 ⁻¹ series and the Means Chematophysical 10 ⁻¹ series and the Means Chematophysical 10 ⁻¹ series and the Means Chematophysical 10 ⁻¹ series and the Means Theoretical 10 ⁻¹ series and the Means Theoreti	 P 0.246 0.454 0.723 0.590 0.561 0.825 0.845 0.846 0.946 0.947 0.833 0.847 0.733 0.849 0.243 0.849 0.243 0.849 0.243 0.325 	04(4954) 048(2003-114) 048(2003-14) 048(2		(d) P 0.440 0.040 0.041 0.773 0.870 0.870 0.873 0.984 0.439 0.374 0.439 0.374 0.439 0.374 0.454 0.524 0.854 0	04(95454) 1080(1054) 1080(1054) 1080(1054) 1040(10	
(C) Vira Morian electronic de la construit d	 P 0.246 0.434 0.759 0.509 0.509 0.509 0.501 0.852 0.852 0.867 0.946 0.927 0.868 0.946 0.927 0.864 0.927 0.864 0.927 0.864 0.927 0.864 0.927 0.864 0.927 0.864 0.926 0.773 0.864 0.225 0.734 0.352 	04(6954) 04800007-1007 04800007-1007 04800007-1007 049000041-007 049000041-007 049000041-007 049000007-1007 0490000000-1007 04900000000-1007 0490000000-1007 0490000000-1007 0490000000-1007 049000000-1007 0490000000-1007 0490000000-1007 0490000000-1007 0490000000-1007 0490000000-1007 0490000000-1007 04900000000000000000000000000000000000		(d) P 0.440 0.009 0.077 0.670 0.670 0.670 0.670 0.670 0.690 0.779 0.670 0.690 0.740 0.465 0.524 0.520 0.540 0	0(8)(8)(4)(8)(4) 1.9(4)(4)(4)(4)(4)(4)(4)(4)(4)(4)(4)(4)(4)(
(c) Virus Viru	 P 3.46 3.43 3.52 3.59 3.59 3.59 3.54 3.54 3.54 3.54 3.54 3.55 3.25 3.25 3.25 3.25 3.25 3.25 3.25 	04(654(5)) 04(6)(24)) 04(6)((d) P 0.440 0.040 0.040 0.040 0.040 0.040 0.053 0.054 0.054 0.040 0.040 0.054 0.054 0.054 0.054 0.054 0.054 0.054 0.054 0.054 0.054 0.056 0.055 0	04(954)-(34)-(34)-(34)-(34)-(34)-(34)-(34)-(3	
(c) Vira Morian electronic and a second a seco	 P 2.46 0.424 0.425 0.509 0.509 0.509 0.504 0.521 0.546 0.547 0.546 0.547 0.546 0.547 0.546 0.547 0.548 0.541 0.542 0.541 0.542 	04(954C) 04800207-1109 04800208-1109 04800208-1109 04800208-1109 04800208-1109 04800208-1009 04800208-1009 04800208-1009 04800208-1100000000-1000000000000000000000		(d) P 0.446 0.074 0.077 0.670 0.870 0.820 0.824 0.420 0.445 0.624 0.624 0.624 0.624 0.624	0(848) 48-1(84) 1.08(2) 48-1(8) 1.08(2) 48-1(8) 1.08(2	
(c) Viru Monitory of the part in the part in the part of the par	 P 0.246 0.434 0.723 0.500 0.570 0.574 0.586 0.887 0.846 0.946 0.946 0.947 0.803 0.846 0.846 0.846 0.235 0.235 0.734 0.846 0.235 0.734 0.846 0.846 0.846 0.235 0.734 0.846 0	04(8545,01) 04800,021,102 04800,024,102 04800,02		(d) P 0.466 0.077 0.0779 0.0773 0.0733 0.083 0.083 0.084 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.213 0.2244 0.2244 0.2244 0.2244 0.2244 0.2244 0.2244 0.2244 0.2244 0.2244 0.22444 0.2244 0.2244 0.2244 0.2244 0.22444 0.22444 0.2244	04(954) 40(2010	