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9 **SARS-CoV-2 genome sequencing at country scales**

10

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23

ABSTRACT

Background: SARS-CoV-2 has emerged in China for more than one year. Some variants are currently considered as of great concern.

Objectives: We aimed to analyze the numbers of SARS-CoV-2 genome sequences obtained in different countries worldwide until January 2021.

Study design: As on the 28th of January 2021, we downloaded from the GISAID database the deposited genome sequence origin, and from the "Our world in data" website numbers of SARS-CoV-2-diagnosed cases, numbers of SARS-CoV-2-associated deaths, population size, life expectancy, gross domestic product (GDP) per capita, and human development index per country. Files were merged and data were analyzed using the Microsoft Excel software.

Results: A total of 450,968 SARS-CoV-2 genomes originating from 135 countries on the 5 continents were available. When considering the 19 countries for which the number of genomes per 100 deaths was >100, six were in Europe, while eight were in Asia, three were in Oceania and two were in Africa. Six (30%) of these countries are beyond rank 75 regarding human development index and 4 (20%) are beyond rank 80 regarding GDP per capita. Moreover, the comparisons of the number of genomes sequenced per 100 deaths to the human development index by country show that some European Western countries have released similar or lower numbers of genomes than many African or Asian countries with a lower human development index.

Conclusions: Previous data highlight great discrepancies between the numbers of available SARS-CoV-2 genomes per 100 cases and deaths and the ranking of countries regarding wealth and development.

TEXT

27

1. Introduction

28

29   The SARS-CoV-2 pandemic, which has spread for almost a year, has generated

30 considerable global efforts in the sequencing, collection, and analysis of viral genomes.

31 Sequence databases and various tools for storing, downloading, classifying and analyzing

32 these genomes have quickly become available [1,2]. In particular, GISAID sequence database

33 hosts a collection of SARS-CoV-2 genomic sequences obtained worldwide

34 (https://www.gisaid.org/) [1]. Our team has produced, unlike other laboratories in our country,

35 a large number of genome sequences for SARS-CoV-2, in particular when the incidence of

36 cases considerably re-increased during the summer [3-6]. This enabled us very early to point

37 out the existence of variants (which are strains that differ from all others by a set of several

38 mutations and have reached a detectable population size) during summer 2020 [4]; we named

39 those identified in our institute Marseille-1 to Marseille-10. They have been responsible for

40 successive or overlapping epidemics, before it became established at our country scale. An

41 earlier study analyzed the number of SARS-CoV-2 genomes per reported COVID-19 case

42 nationwide, based on the sequences available in the GISAID database in early September

43 2020. It pointed out substantial differences between countries worldwide, including between

44 those on a same continent, as well as the good level of sequencing efforts of some low- and

45 middle-income countries [7].

46

2. Objectives

47

48   Here we wanted to analyze the numbers of genome sequences of SARS-CoV-2

49 obtained in the different countries of the world as on end of January 2021, and to relate them

50 to the numbers of SARS-CoV-2 cases and SARS-CoV-2-associated deaths and to the wealth

51   and investment into health of these countries.

52

53   **3. Materials and methods**

54   We downloaded from the GISAID database (https://www.gisaid.org/) [1] as on the

55   28th of January 2021 the nextmeta file that contains the origin of deposited genome sequences.

56   We also downloaded as on the same day from the "Our world in data" website

57   (https://ourworldindata.org/) the numbers of SARS-CoV-2-diagnosed cases and SARS-CoV-

58   2-associated deaths per country as well as various epidemiological data among which

59   population size, life expectancy, gross domestic product (GDP) per capita, or human

60   development index (https://covid.ourworldindata.org/data/owid-covid-data.xlsx). Files were

61   merged and data were analyzed using the Microsoft Excel software

62   (https://www.microsoft.com). We standardized the numbers of genomes sequenced per 100

63   SARS-CoV-2-diagnosed cases and per 100 SARS-CoV-2-associated deaths. Data were

64   plotted using the Microsoft Excel and the GraphPad Prism v.5 (https://www.graphpad.com)

65   softwares.

66

67   **4. Results**

68   A total of 450,968 SARS-CoV-2 genomes was available from the GISAID database

69   on January 28th, 2020. They originated from the 5 continents, from 135 countries and 8,919

70   laboratories. The mean (±standard deviation) number of genomes per country was

71   3,340±18,498 (range, 1-192,556). The mean number of genomes per 100 SARS-CoV-2-

72   associated deaths per country was 270±1,422 (0.06-14,397) and the mean number of genomes

73   per 100 SARS-CoV-2 diagnosed cases per country was 2,198±9,105 (0.001-70).

74   The top 100 source laboratories accounted for 72% (n= 324,837) of available

75   genomes. They were mostly, for 62% of them, located in the USA (n=24), in England (21), in

3

76 Denmark (11), and in the Netherlands (6). When considering the 19 countries for which the

77 number of genomes per 100 deaths was >100, six were in Europe (Iceland (number of

78 genomes per 100 deaths= 14,397), Denmark (1,680), Luxembourg (405), Norway (229), UK

79 (186), and Finland (174)), while eight were in Asia (Singapore (5,969), Taiwan (2,143),

80 Thailand (653), Vietnam (406), Mongolia (350), Japan (310), Brunei (167), and South Korea

81 (117)), three were in Oceania (New Zealand (4,380), Australia (1,902), and Papua New

82 Guinea (144)) and two were in Africa (Gambia (344), and Equatorial Guinea (110)) (**Figures**

83 **1, 2; Table 1**). In addition, six (30%) of these countries were beyond rank 75 regarding

84 human development index among the 135 countries studied here: Thailand (human

85 development index= 0.755), Vietnam (0.694), Mongolia (0.741), Gambia (0.460), Papua New

86 Guinea (0.544) and Equatorial Guinea (0.591). Moreover, 4 (20%) were beyond rank 80

87 regarding GDP per capita: Vietnam (GDP per capita= 6,172), Mongolia (11,841), Gambia

88 (1,562), and Papua New Guinea (3,823). Similarly, when considering the 24 countries for

89 which the number of genomes per 100 diagnosed cases was >1, eight were in Asia (Taiwan,

90 Vietnam, Japan, Thailand, Singapore, Brunei, South Korea, and China) and three were in

91 Africa (Gambia, Equatorial Guinea, and Democratic Republic of Congo). In addition, seven

92 (29%) of these countries were beyond rank 75 regarding human development index: Gambia

93 (human development index= 0.460), Vietnam (0.694), Thailand (0.755), Equatorial Guinea

94 (0.591), Democratic Republic of Congo (0.457), Papua New Guinea (0.544), and China

95 (0.752) , and 4 (21%) were beyond rank 100 regarding GDP per capita: Gambia (GDP per

96 capita= 1,562), Vietnam (6,172), Democratic Republic of Congo (808), and Papua New

97 Guinea (3,823). Moreover, the comparisons of the number of genomes sequenced per 100

98 deaths and the human development index by country show that some European Western

99 countries such as France (5.9 genomes per 100 deaths; human development index= 0.901),

100 Germany (8.2; 0.936), or Italy (3.4; 0.880) have released similar or lower numbers of

101   genomes than many African or Asian countries with a lower human development index,

102   among which Egypt (4.0 genomes per 100 deaths; human development index= 0.696),

103   Zimbabwe (8.7; 0.535), Nigeria (19; 0.532), Senegal (22; 0.505), Democratic Republic of

104   Congo (54; 0.457), Gambia (334; 0.460), Bangladesh (9.8; 0.608), and China (20; 0.752)

105   (**Figure 3)**. Similar observations can be done when comparing the number of genomes

106   sequenced per 100 deaths and the GPD per capita or life (**Figure 4)** expectancy by country.

107

108   **5. Discussion**

109   This analysis conducted 10 months after WHO declared COVID-19 a pandemic

110   (https://www.who.int/director-general/speeches/detail/who-director-general-s-opening-

111   remarks-at-the-media-briefing-on-covid-19---11-march-2020) shows great disparities

112   according to the country in the numbers of SARS-CoV-2 genomes available per 100 cases

113   and deaths, as well as substantial discrepancies between these numbers and the ranking of

114   countries based on their wealth and development. This shows that several developed countries

115   have either a technological or organizational delay in terms of high throughput sequencing,

116   and/or an insufficient purposefulness to monitor SARS-CoV-2 genetic and proteic diversity

117   and variability. In contrast, several developing countries exhibited wills and capacities to

118   sequence SARS-CoV-2 genomes, and scaled-up next-sequencing technologies [8]. This is

119   another example that the SARS-CoV-2 pandemic is reshuffling the cards globally.

120   Such a worldwide distribution of the availability of SARS-CoV-2 genomes is very

121   interesting. Indeed, several issues related to SARS-CoV-2 genotypic features are currently in

122   the spotlight, which are of paramount importance. Firstly, different viral variants that have

123   emerged appear to be associated with different epidemic dynamics and clinical severities.

124   What we observed for the first SARS-CoV-2 variant that we had identified in July 2020,

125   which originated from the African continent and was named Marseille-1 [5], has reproduced

126   with the Marseille-4 variant (also known as clade 20A.EU2 [9]), and is currently observed

127   with the UK (20I/501Y.V1), South African (20I/501Y.V1), and Brazilian (20I/501Y.V1)

128   variants. Thus, some of these variants have demonstrated or suspected greater

129   transmissibilities and became the predominant strains nationwide, and they were reported to

130   cause diseases with different severities [5,10-14]. In addition, all these viral variants harbor

131   amino acid changes in the viral spike, the protein that enables virus entry into human cells

132   through binding to the ACE2 receptor and is also the main target of neutralizing antibodies

133   elicited by natural infection or vaccine immunization [15-17]. Accordingly, changes in the

134   spike amino acid sequence of these variants have been reported to increase viral binding to the

135   ACE2 receptor and to allow virus escape from neutralizing antibodies induced by prior

136   infection or vaccine immunization [17-19]. Moreover, therapies such as remdesivir,

137   convalescent plasma, or cocktails of anti-spike antibodies, particularly in

138   immunocompromised patients, could increase the mutation rate of SARS-CoV-2 genomes

139   and have been associated with the rapid occurrence of several amino acid changes within the

140   spike. Among these amino acid changes, some are present in the UK, South African and

141   Brazilian variants [16,20-22]. Thus, it should have been necessary, in the cases of absence of

142   viral clearance after administration of these treatments to systematically sequence SARS-

143   CoV-2 genomes and check for the occurrence of mutations. For example, this should have

144   been performed in Hueso et al.'s study for the 5 patients who were not cleared of the virus

145   after convalescent plasmatherapy in order to determine whether mutations located in the spike

146   had not been selected by the transfused antibodies [23]. Also, cases are increasingly reported

147   of patients who experienced a second infection with SARS-CoV-2 several months after a first

148   infection was followed by viral clearance [24-26]. In our institute, two successive infections

149   with different variants have been observed to date in nearly fifty patients [27]. Systematic

150   sequencing of the genomes of the viruses involved in the two distinct infections is there too

151 essential to be able understanding which viral strains can resist, through their mutation

152 pattern, to immune responses elicited by a first infection with a distinct strain. Finally, in the

153 current setting of massive vaccine strategies that in most Western countries are exclusively

154 based on the spike protein, it is absolutely critical to analyze the viral genomes in all cases of

155 vaccine failures, in order to determine which viral mutants and variants are involved. In our

156 country, for example, the majority of SARS-CoV-2 strains that currently circulate have a

157 spike protein whose amino acid sequence differs from that used in vaccines, which

158 corresponds to strains that no longer currently exist or are very minoritary [6,10]

159 (https://nextstrain.org/groups/neherlab/ncov/france). Under these conditions, the question of

160 vaccine efficacy arises in the forefront.

161 Overall, in a new disease caused by viruses with a high mutation rate, as we have

162 learned for a long time with human immunodeficiency virus and hepatitis C virus, it is

163 absolutely necessary to survey and monitor viral genome sequences to detect mutants and

164 variants, in order to identify possible differences in terms of transmissibility, clinical severity,

165 resistance to treatments, and escape from vaccine immunity as well as natural immunity.

166 Considering previous data, we believe that broad scale SARS-CoV-2 genomic surveillance

167 should have been mandatory for all developed countries that had the means to perform it.

168

169

170 **Availability of data and materials**

171 Data analyzed have been downloaded from and are available in the GISAID database

172 (https://www.gisaid.org/) and the "Our world in data" website (https://ourworldindata.org/).

173

174 **Authors' contributions**

175 Conceived and designed the experiments: DR and PC. Contributed for the materials/analysis

176 tools: PC. Analyzed the data: DR and PC. Wrote the paper: DR and PC.

177

178 **Acknowledgments**

185

186 **Competing interests**

187 The authors have no conflicts of interest to declare. There are no financial or personal

188 relationship with other people or organisations that could inappropriately influence their

189 work.

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FIGURE LEGEND

286

287 **Figure 1.** Number of SARS-CoV-2 genomes per 100 SARS-CoV-2-diagnosed cases (left,

288 orange) and per 100 deaths (right, blue) according to continent/region.

289

290 **Figure 2.** Number of SARS-CoV-2 genomes per 100 SARS-CoV-2-associated deaths

291 according to continent/region**.**

292

293 **Figure 3.** Number of SARS-CoV-2 genomes per 100 SARS-CoV-2-associated deaths vs.

294 human development index.

295 For a better legibility of the graph only countries with more than 100 SARS-CoV-2 genomes

296 are shown.

297

298 **Figure 4.** Number of SARS-CoV-2 genomes per 100 SARS-CoV-2-associated deaths vs.

299 gross domestic product per capita.

300 For a better legibility of the graph only countries with more than 100 SARS-CoV-2 genomes

301 are shown.

302

303

304 **TABLE**

305 **Table 1.** Number of genomes, of SARS-CoV-2-diagnosed cases, and of SARS-CoV-2-associated deaths per country, and various

306 epidemiological data among which population size, life expectancy, gross domestic product (GDP) per capita, or human development index

307

Country	Continent/region	Number of genomes	Number of genomes per 100 cases	Number of genomes per 100 deaths	Number of cases	Number of deaths	Population	GDP per capita	Number of hospital beds per thousand	Life expectancy (years)	Human development index
Iceland	Europe	4 175	69,6	14397	6 001	29	341 250	46 483	2,9	83,0	0,935
Singapore	Asia	1 731	2,9	5969	59 425	29	5 850 343	85 535	2,4	83,6	0,932
New Zealand	Oceania	1 095	47,5	4380	2 305	25	4 822 233	36 086	2,6	82,3	0,917
Taiwan	Asia	150	16,8	2143	895	7	23 816 775	-	-	80,5	-
Australia	Oceania	17 290	60,0	1902	28 799	909	25 499 881	44 649	3,8	83,4	0,939
Denmark	Europe	34 819	17,6	1680	197 892	2 072	5 792 203	46 683	2,5	80,9	0,929
Thailand	Asia	496	3,1	653	16 221	76	69 799 978	16 278	2,1	77,2	0,755
Vietnam	Asia	142	8,6	406	1 651	35	97 338 583	6 172	2,6	75,4	0,694
Luxembourg	Europe	2 325	4,6	405	50 228	574	625 976	94 278	4,5	82,3	0,904
Mongolia	Asia	7	0,4	350	1 710	2	3 278 292	11 841	7,0	69,9	0,741
Gambia	Africa	427	10,6	334	4 019	128	2 416 664	1 562	1,1	62,1	0,460
Japan	Asia	17 052	4,5	310	380 644	5 503	126 476 458	39 002	13,1	84,6	0,909
IHU Méditerranée Infection	*Europe*	*1 585*	*5,2*	*250*	*30 237*	*633*	-	-	-	-	-
Norway	Europe	1 278	2,1	229	62 276	557	5 421 242	64 800	3,6	82,4	0,953
United Arab Emirates	Asia	1 845	0,6	225	293 052	819	9 890 400	67 293	1,2	78,0	0,863
United Kingdom	Europe	192 556	5,1	186	3 754 448	103 324	67 886 004	39 753	2,5	81,3	0,922
Finland	Europe	1 154	2,6	174	44 039	664	5 540 718	40 586	3,3	81,9	0,920
Brunei	Asia	5	2,8	167	180	3	437 483	71 809	2,7	75,9	0,853
Papua New Guinea	Oceania	13	1,5	144	851	9	8 947 027	3 823	-	64,5	0,544

308

Table 1 - *Continued*

Country	Continent/region	Number of genomes	Number of genomes per 100 cases	Number of genomes per 100 deaths	Number of cases	Number of deaths	Population	GDP per capita	Number of hospital beds per thousand	Life expectancy (years)	Human development index
South Korea	Asia	1 631	2,1	117	77 395	1 399	51 269 183	35 938	12,3	83,0	0,903
Equatorial Guinea	Africa	95	1,7	110	5 492	86	1 402 985	22 605	2,1	58,7	0,591
Switzerland	Europe	8 071	1,6	87	519 404	9 308	8 654 618	57 410	4,5	83,8	0,944
Burkina Faso	Africa	85	0,8	71	10 377	120	20 903 278	1 703	0,4	61,6	0,423
Ireland	Europe	1 973	1,0	62	193 645	3 167	4 937 796	67 335	3,0	82,3	0,938
Democratic Republic of Congo	Africa	360	1,6	54	22 322	665	89 561 404	808	-	60,7	0,457
Netherlands	Europe	7 422	0,8	53	979 702	13 925	17 134 873	48 473	3,3	82,3	0,931
Saint Vincent and the Grenadines	North America	1	0,1	50	827	2	110 947	10 727	2,6	72,5	0,723
Surinam	South America	71	0,9	46	8 293	154	586 634	13 767	3,1	71,7	0,720
Malaysia	Asia	321	0,2	45	198 208	717	32 365 998	26 808	1,9	76,2	0,802
Canada	North America	8 613	1,1	44	770 433	19 659	37 742 157	44 018	2,5	82,4	0,926
Côte d'Ivoire	Africa	65	0,2	43	27 694	151	26 378 275	3 601	-	57,8	0,492
Uganda	Africa	133	0,3	42	39 424	318	45 741 000	1 698	0,5	63,4	0,516
Bahrain	Asia	150	0,1	40	101 503	372	1 701 583	43 291	2,0	77,3	0,846
Uruguay	South America	129	0,3	31	39 887	415	3 473 727	20 551	2,8	77,9	0,804
Kenya	Africa	514	0,5	29	100 422	1 753	53 771 300	2 993	1,4	66,7	0,590
Ghana	Africa	114	0,2	29	63 883	390	31 072 945	4 228	0,9	64,1	0,592
Mozambique	Africa	94	0,3	27	35 833	347	31 255 435	1 136	0,7	60,9	0,437
Benin	Africa	12	0,3	25	3 786	48	12 123 198	2 064	0,5	61,8	0,515
Israel	Asia	1 128	0,2	24	628 895	4 669	8 655 541	33 132	3,0	83,0	0,903
Senegal	Africa	136	0,5	22	25 711	614	16 743 930	2 471	-	67,9	0,505
Portugal	Europe	2 422	0,4	21	685 383	11 608	10 196 707	27 937	3,4	82,1	0,847
USA	North America	89 814	0,3	21	25 766 681	433 196	331 002 647	54 225	2,8	78,9	0,924
Latvia	Europe	233	0,4	20	63 992	1 148	1 886 202	25 064	5,6	75,3	0,847
Sri Lanka	Asia	60	0,1	20	61 586	297	21 413 250	11 669	3,6	77,0	0,770
China	Asia	949	1,0	20	99 746	4 813	1 439 323 774	15 309	4,3	76,9	0,752
Nigeria	Africa	290	0,2	19	127 024	1 547	206 139 587	5 338	-	54,7	0,532
Rwanda	Africa	34	0,2	18	14 529	186	12 952 209	1 854	-	69,0	0,524
Belgium	Europe	3 743	0,5	18	702 437	20 982	11 589 616	42 659	5,6	81,6	0,916

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Table 1 - *Continued*

Country	Continent/region	Number of genomes	Number of genomes per 100 cases	Number of genomes per 100 deaths	Number of cases	Number of deaths	Population	GDP per capita	Number of hospital beds per thousand	Life expectancy (years)	Human development index
Austria	Europe	1 344	0,3	18	410 230	7 607	9 006 400	45 437	7,4	81,5	0,908
Antigua and Barbuda	North America	1	0,5	17	215	6	97 928	21 491	3,8	77,0	0,780
Saudi Arabia	Asia	953	0,3	15	367 276	6 366	34 813 867	49 045	2,7	75,1	0,853
Sierra Leone	Africa	11	0,3	14	3 282	77	7 976 985	1 390	-	54,7	0,419
Jordan	Asia	581	0,2	14	324 169	4 269	10 203 140	8 337	1,4	74,5	0,735
Oman	Asia	205	0,2	13	133 728	1 527	5 106 622	37 961	1,6	77,9	0,821
Spain	Europe	7 431	0,3	13	2 705 001	57 806	46 754 783	34 272	3,0	83,6	0,891
Trinidad and Tobago	North America	17	0,2	13	7 520	134	1 399 491	28 763	3,0	73,5	0,784
Sweden	Europe	1 388	0,2	12	564 557	11 520	10 099 270	46 949	2,2	82,8	0,933
Bangladesh	Asia	792	0,1	9,8	533 953	8 087	164 689 383	3 524	0,8	72,6	0,608
Botswana	Africa	13	0,1	9,7	21 293	134	2 351 625	15 807	1,8	69,6	0,717
Lithuania	Europe	258	0,1	9,4	180 160	2 749	2 722 291	29 524	6,6	75,9	0,858
Zimbabwe	Africa	101	0,3	8,7	32 646	1 160	14 862 927	1 900	1,7	61,5	0,535
Germany	Europe	4 582	0,2	8,2	2 194 562	55 883	83 783 945	45 229	8,0	81,3	0,936
Mali	Africa	24	0,3	7,3	8 056	328	20 250 834	2 014	0,1	59,3	0,427
Guinea	Africa	6	0,0	7,3	14 435	82	13 132 792	1 999	0,3	61,6	0,459
South Africa	Africa	3 062	0,2	7,1	1 437 798	43 105	59 308 690	12 295	2,3	64,1	0,699
Costa Rica	North America	181	0,1	7,0	192 637	2 599	5 094 114	15 525	1,1	80,3	0,794
Qatar	Asia	16	0,0	6,5	150 280	248	2 881 060	116 936	1,2	80,2	0,856
Panama	North America	314	0,1	6,0	316 808	5 196	4 314 768	22 267	2,3	78,5	0,789
Gabon	Africa	4	0,0	5,9	10 536	68	2 225 728	16 562	6,3	66,5	0,702
France	Europe	4 379	0,1	5,9	3 166 145	74 601	65 273 512	38 606	6,0	82,7	0,901
Liechtenstein	Europe	3	0,1	5,8	2 475	52	38 137	-	2,4	82,5	0,916
Chile	South America	966	0,1	5,3	714 143	18 174	19 116 209	22 767	2,1	80,2	0,843
Malta	Europe	13	0,1	5,0	17 400	261	441 539	36 513	4,5	82,5	0,878
Estonia	Europe	20	0,0	4,9	42 656	406	1 326 539	29 481	4,7	78,7	0,871
Palestine	Asia	88	0,1	4,9	157 593	1 812	5 101 416	4 450	-	74,1	0,686
Cameroon	Africa	22	0,1	4,8	29 617	462	26 545 864	3 365	1,3	59,3	0,556
Slovenia	Europe	162	0,1	4,7	163 235	3 448	2 078 932	31 401	4,5	81,3	0,896
Cyprus	Europe	8	0,0	4,1	30 538	197	875 899	32 415	3,4	81,0	0,869
Egypt	Africa	366	0,2	4,0	164 282	9 169	102 334 403	10 550	1,6	72,0	0,696

Table 1 - *Continued*

Country	Continent/region	Number of genomes	Number of genomes per 100 cases	Number of genomes per 100 deaths	Number of cases	Number of deaths	Population	GDP per capita	Number of hospital beds per thousand	Life expectancy (years)	Human development index
Czech Republic	**Europe**	614	0,1	3,9	964 660	15 944	10 708 982	32 606	6,6	79,4	0,888
Jamaica	**North America**	13	0,1	3,8	15 435	344	2 961 161	8 194	1,7	74,5	0,732
France minus IHU Méditerranée Infection	*Europe*	*2 794*	*0,1*	*3,8*	*3 135 908*	*73 968*	-	-	-	-	-
Serbia	**Europe**	146	0,0	3,7	390 637	3 965	6 804 596	14 049	5,6	76,0	0,787
Italy	**Europe**	2 974	0,1	3,4	2 515 507	87 381	60 461 828	35 220	3,2	83,5	0,880
India	**Asia**	4 778	0,0	3,1	10 720 048	154 010	1 380 004 385	6 427	0,5	69,7	0,640
North Macedonia	**Europe**	82	0,1	2,9	91 891	2 831	2 083 380	13 111	4,3	75,8	0,757
Slovakia	**Europe**	122	0,1	2,8	243 427	4 411	5 459 643	30 155	5,8	77,5	0,855
Russia	**Europe**	1 820	0,0	2,6	3 752 548	70 533	145 934 460	24 766	8,1	72,6	0,816
Greece	**Europe**	141	0,1	2,5	154 796	5 742	10 423 056	24 574	4,2	82,2	0,870
Kuwait	**Asia**	23	0,0	2,4	163 450	958	4 270 563	65 531	2,0	75,5	0,803
Hungary	**Europe**	278	0,1	2,3	363 450	12 291	9 660 350	26 778	7,0	76,9	0,838
Madagascar	**Africa**	6	0,0	2,2	18 743	279	27 691 019	1 416	0,2	67,0	0,519
Belarus	**Europe**	35	0,0	2,1	242 851	1 688	9 449 321	17 168	11,0	74,8	0,808
Turkey	**Asia**	493	0,0	1,9	2 457 118	25 605	84 339 067	25 129	2,8	77,7	0,791
Kazakhstan	**Asia**	53	0,0	1,7	231 716	3 040	18 776 707	24 056	6,7	73,6	0,800
Montenegro	**Europe**	12	0,0	1,5	60 288	790	628 062	16 409	3,9	76,9	0,814
Morocco	**Africa**	122	0,0	1,5	469 139	8 224	36 910 558	7 485	1,1	76,7	0,667
Ecuador	**South America**	208	0,1	1,4	246 000	14 766	17 643 060	10 582	1,5	77,0	0,752
Argentina	**South America**	662	0,0	1,4	1 905 524	47 601	45 195 777	18 934	5,0	76,7	0,825
Belize	**North America**	4	0,0	1,3	11 845	298	397 621	7 824	1,3	74,6	0,708
Myanmar	**Asia**	41	0,0	1,3	139 152	3 103	54 409 794	5 592	0,9	67,1	0,578
Poland	**Europe**	473	0,0	1,3	1 496 665	36 443	37 846 605	27 216	6,6	78,7	0,865
Tunisia	**Africa**	78	0,0	1,2	204 351	6 508	11 818 618	10 849	2,3	76,7	0,735
Peru	**South America**	441	0,0	1,1	1 113 970	40 272	32 971 846	12 237	1,6	76,7	0,750
Brazil	**South America**	2 414	0,0	1,1	9 058 687	221 547	212 559 409	14 103	2,2	75,9	0,759
Indonesia	**Asia**	313	0,0	1,1	1 037 993	29 331	273 523 621	11 189	1,0	71,7	0,694
Romania	**Europe**	191	0,0	1,1	721 513	18 105	19 237 682	23 313	6,9	76,1	0,811
Croatia	**Europe**	50	0,0	1,0	230 978	4 943	4 105 268	22 670	5,5	78,5	0,831
Andorra	**Europe**	1	0,0	1,0	9 779	100	77 265	-	-	83,7	0,858

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Table 1 - *Continued*

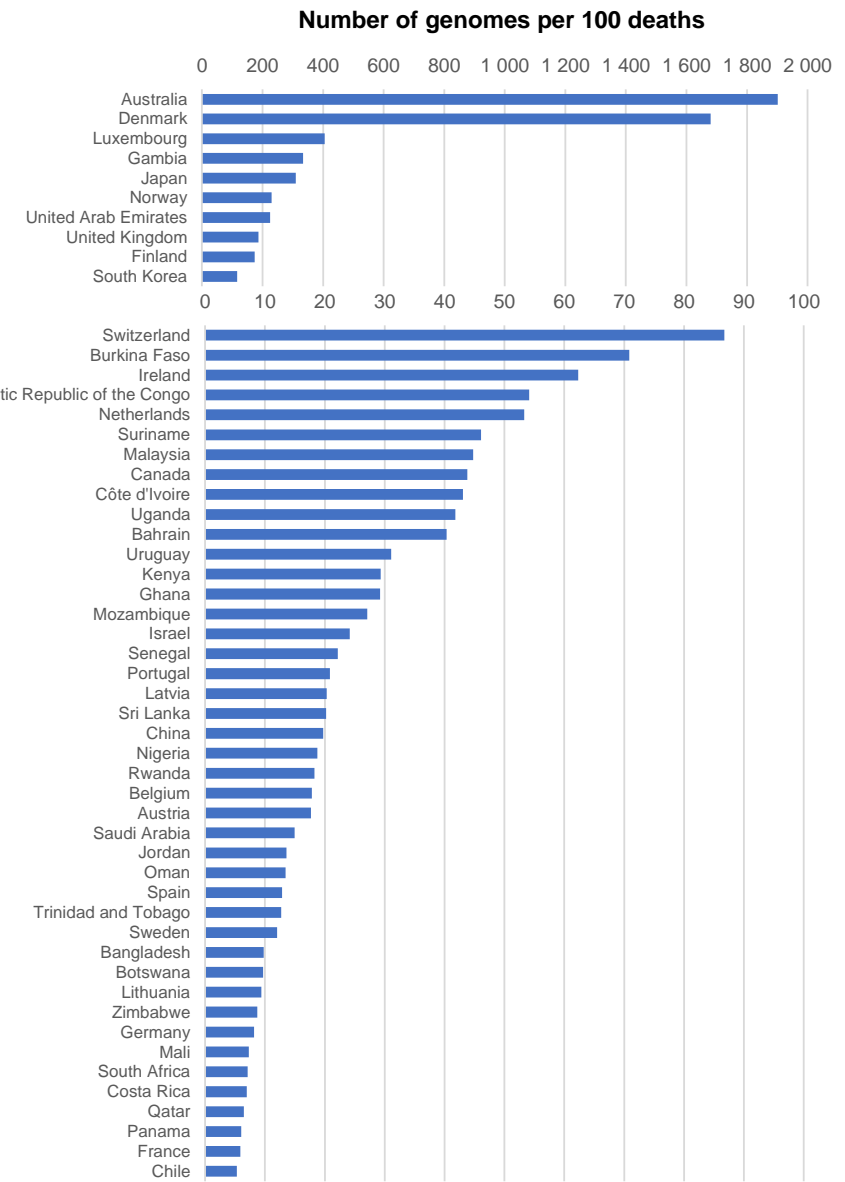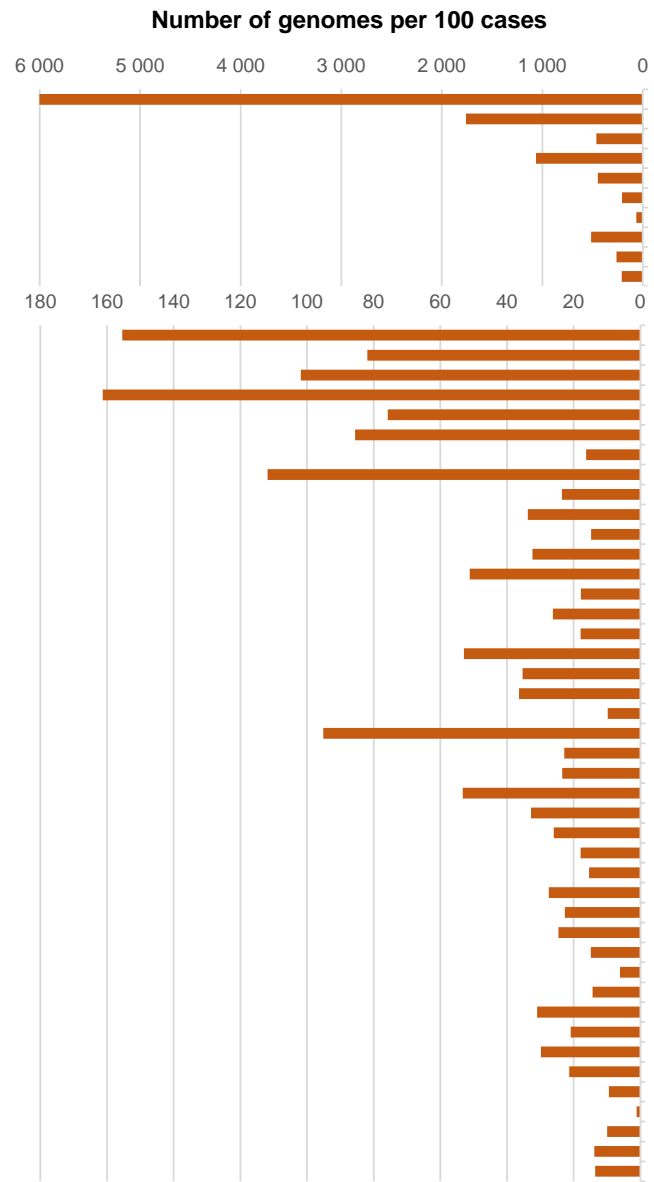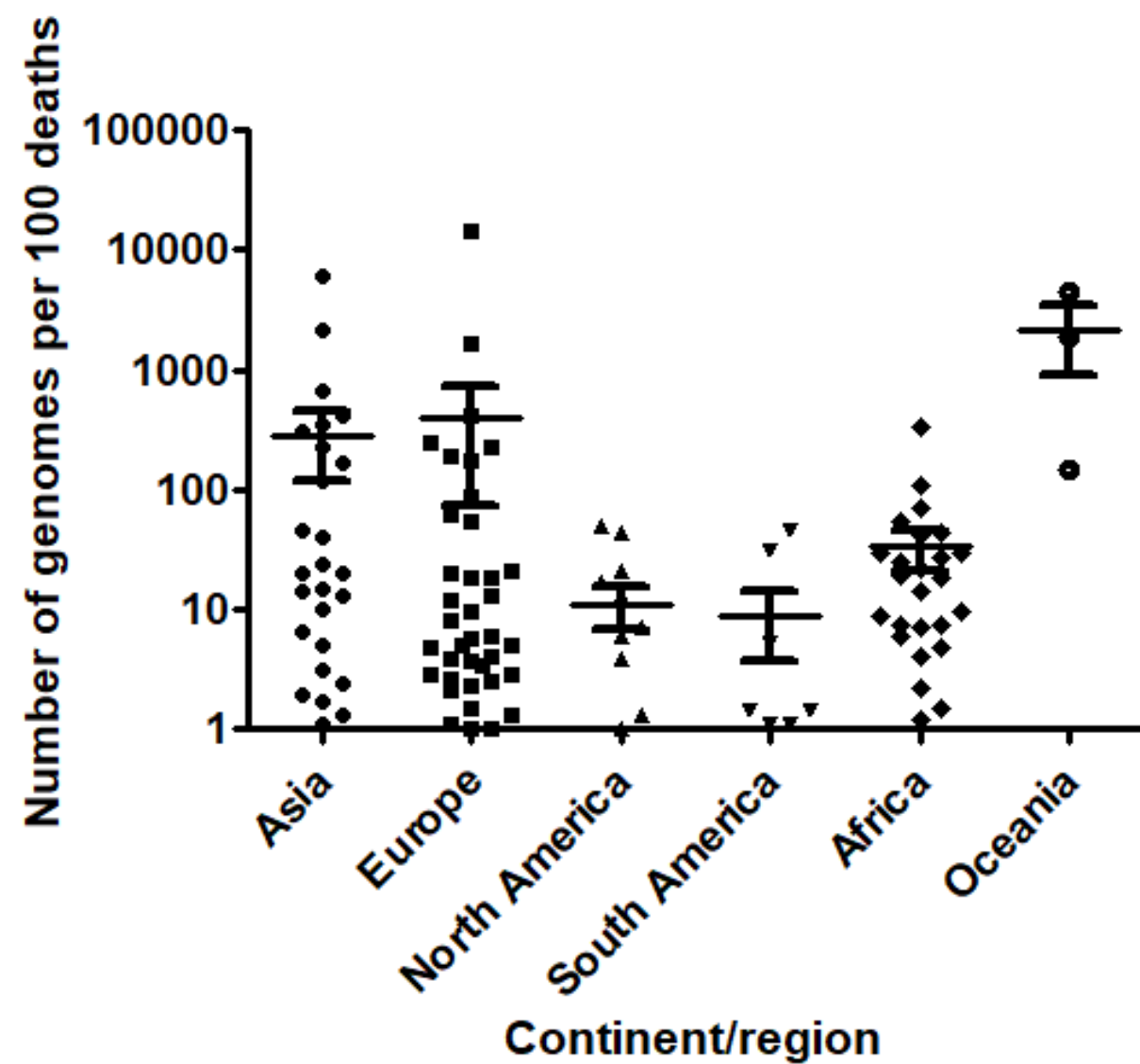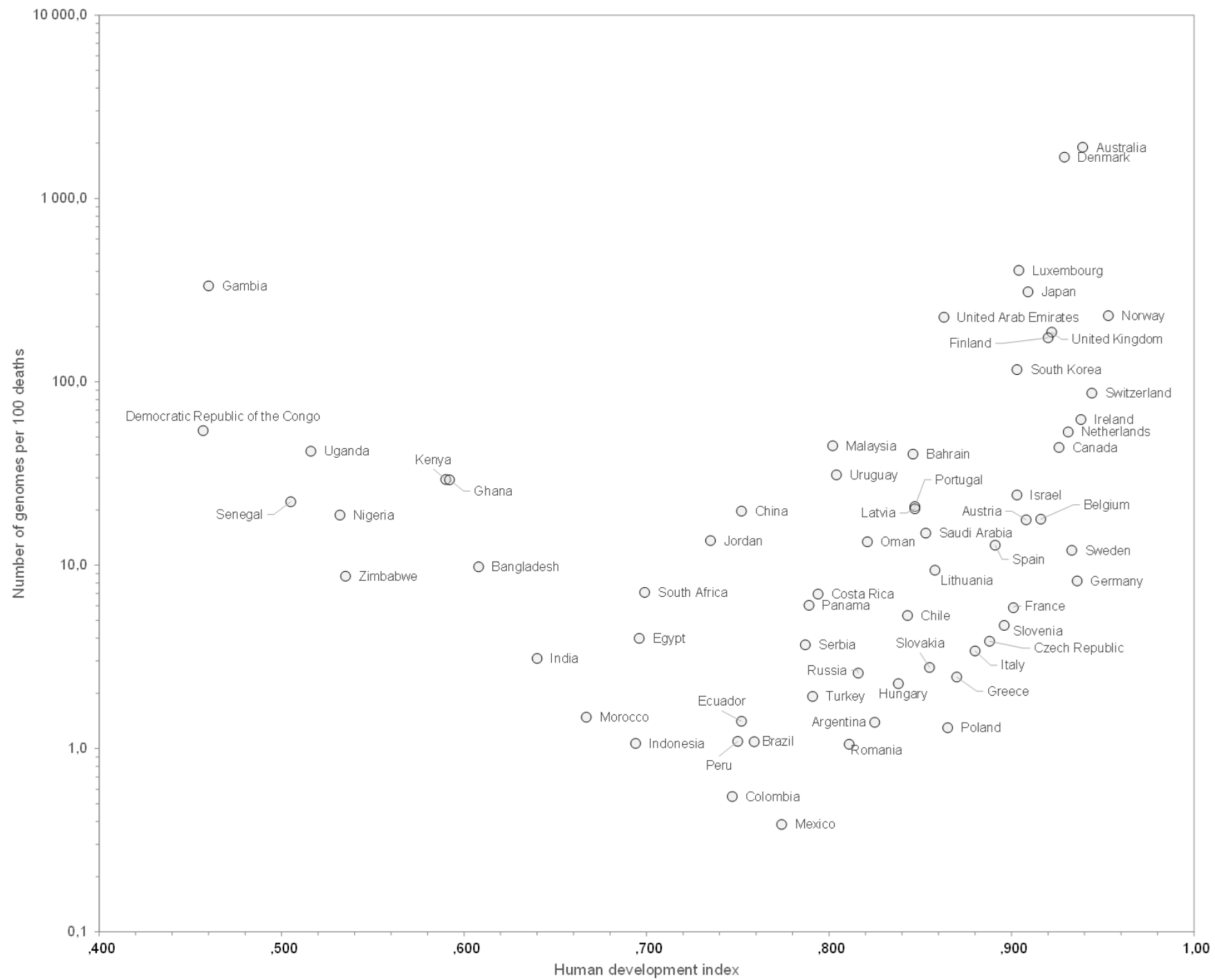| Country	Continent/region	Number of genomes	Number of genomes per 100 cases	Number of genomes per 100 deaths	Number of cases	Number of deaths	Population	GDP per capita	Number of hospital beds per thousand	Life expectancy (years)	Human development index
Cuba	North America	2	0,0	1,0	24 105	208	11 326 616	-	5,2	78,8	0,777
Lebanon	Asia	23	0,0	0,9	293 157	2 621	6 825 442	13 368	2,9	78,9	0,757
Georgia	Asia	26	0,0	0,8	256 287	3 127	3 989 175	9 745	2,6	73,8	0,780
Kosovo	Europe	12	0,0	0,8	58 988	1 479	1 932 774	9 796	-	-	-
Nepal	Asia	15	0,0	0,7	270 588	2 020	29 136 808	2 443	0,3	70,8	0,574
Bosnia and Herzegovina	Europe	33	0,0	0,7	121 194	4 659	3 280 815	11 714	3,5	77,4	0,768
Algeria	Africa	18	0,0	0,6	106 610	2 881	43 851 043	13 914	1,9	76,9	0,754
Guatemala	North America	32	0,0	0,6	157 595	5 543	17 915 567	7 424	0,6	74,3	0,650
Colombia	South America	290	0,0	0,5	2 067 575	52 913	50 882 884	13 255	1,7	77,3	0,747
Pakistan	Asia	58	0,0	0,5	541 031	11 560	220 892 331	5 035	0,6	67,3	0,562
Mexico	North America	598	0,0	0,4	1 825 519	155 145	128 932 753	17 336	1,4	75,1	0,774
El Salvador	North America	6	0,0	0,4	53 989	1 599	6 486 201	7 292	1,3	73,3	0,674
Philippines	Asia	38	0,0	0,4	519 575	10 552	109 581 085	7 599	1,0	71,2	0,699
Dominican Republic	North America	8	0,0	0,3	208 610	2 603	10 847 904	14 601	1,6	74,1	0,736
Ukraine	Europe	67	0,0	0,3	1 247 674	23 469	43 733 759	7 894	8,8	72,1	0,751
Zambia	Africa	2	0,0	0,3	50 319	705	18 383 956	3 689	2,0	63,9	0,588
Bolivia	South America	27	0,0	0,3	210 726	10 226	11 673 029	6 886	1,1	71,5	0,693
Moldova	Europe	9	0,0	0,3	158 309	3 413	4 033 963	5 190	5,8	71,9	0,700
Azerbaijan	Asia	8	0,0	0,3	229 793	3 113	10 139 175	15 847	4,7	73,0	0,757
Venezuela	South America	3	0,0	0,3	125 364	1 171	28 435 943	16 745	0,8	72,1	0,761
Iraq	Asia	31	0,0	0,2	617 202	13 024	40 222 503	15 664	1,4	70,6	0,685
Bulgaria	Europe	15	0,0	0,2	217 574	8 973	6 948 445	18 563	7,5	75,1	0,813
Armenia	Asia	3	0,0	0,1	166 669	3 067	2 963 234	8 788	4,2	75,1	0,755
Albania	Europe	1	0,0	0,1	75 454	1 350	2 877 800	11 803	2,9	78,6	0,785
Iran	Asia	36	0,0	0,1	1 398 841	57 736	83 992 953	19 083	1,5	76,7	0,798
Saint Kitts and Nevis	North America	3	8,1	0,0	37	-	53 192	24 654	2,3	76,2	0,778
Cambodia	Asia	4	0,9	0,0	463	-	16 718 971	3 645	0,8	69,8	0,582
Hong Kong	Asia	344	0,0	0,0	-	-	7 496 988	56 055	-	84,9	0,933

Fig. 1

Number of genomes per 100 cases | Number of genomes per 100 deaths

Fig. 2

Fig. 3

Fig. 4