

# Knowledge Difference in Sexually Transmitted Diseases between Hong Kong Undergraduates from Local and International Secondary Schools: A Cross-Sectional Study

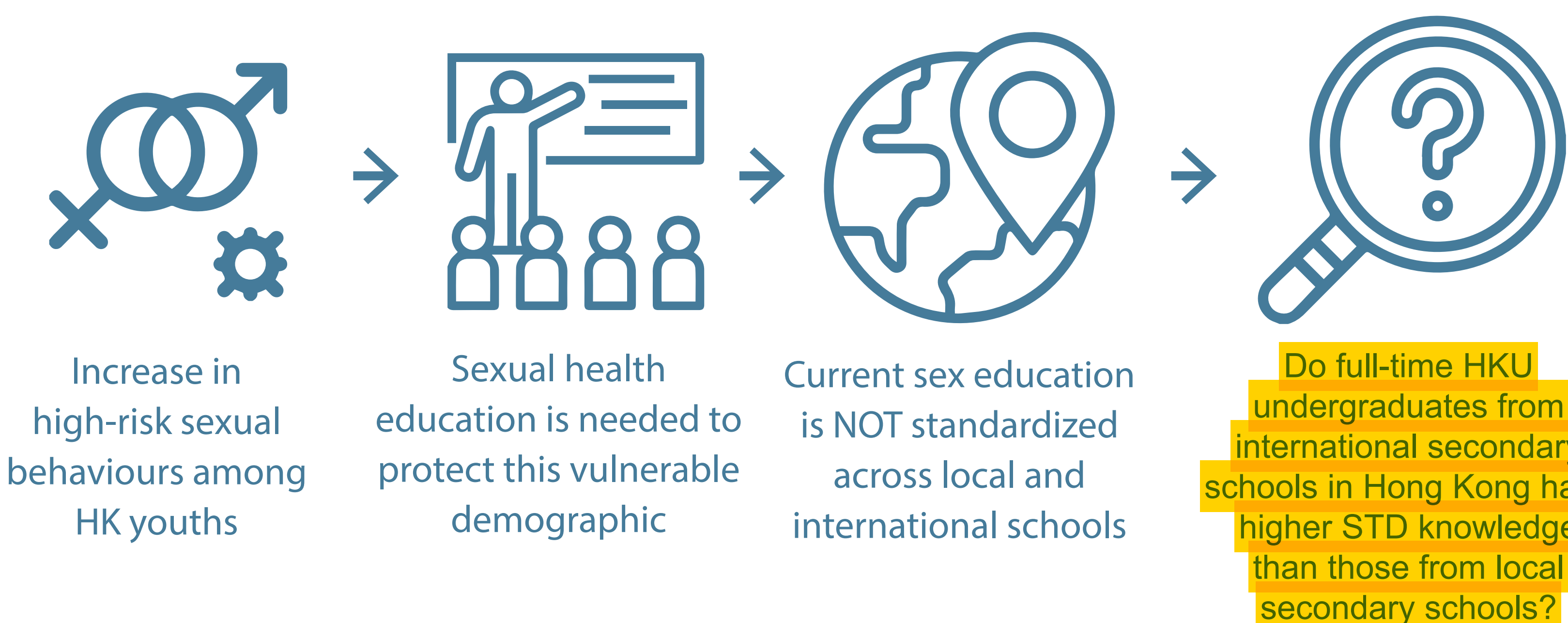
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## Highlights

- Full-time HKU undergraduates from international secondary schools demonstrated a significantly higher STD knowledge.
- The scores of 15.4 (53.1%) and 18.2 (62.8%) suggest disparities and inadequacy of STD knowledge among young adults in Hong Kong
- Warrants implementation of a standardized sex education to increase awareness, reducing the disease burden of STDs in Hong Kong.

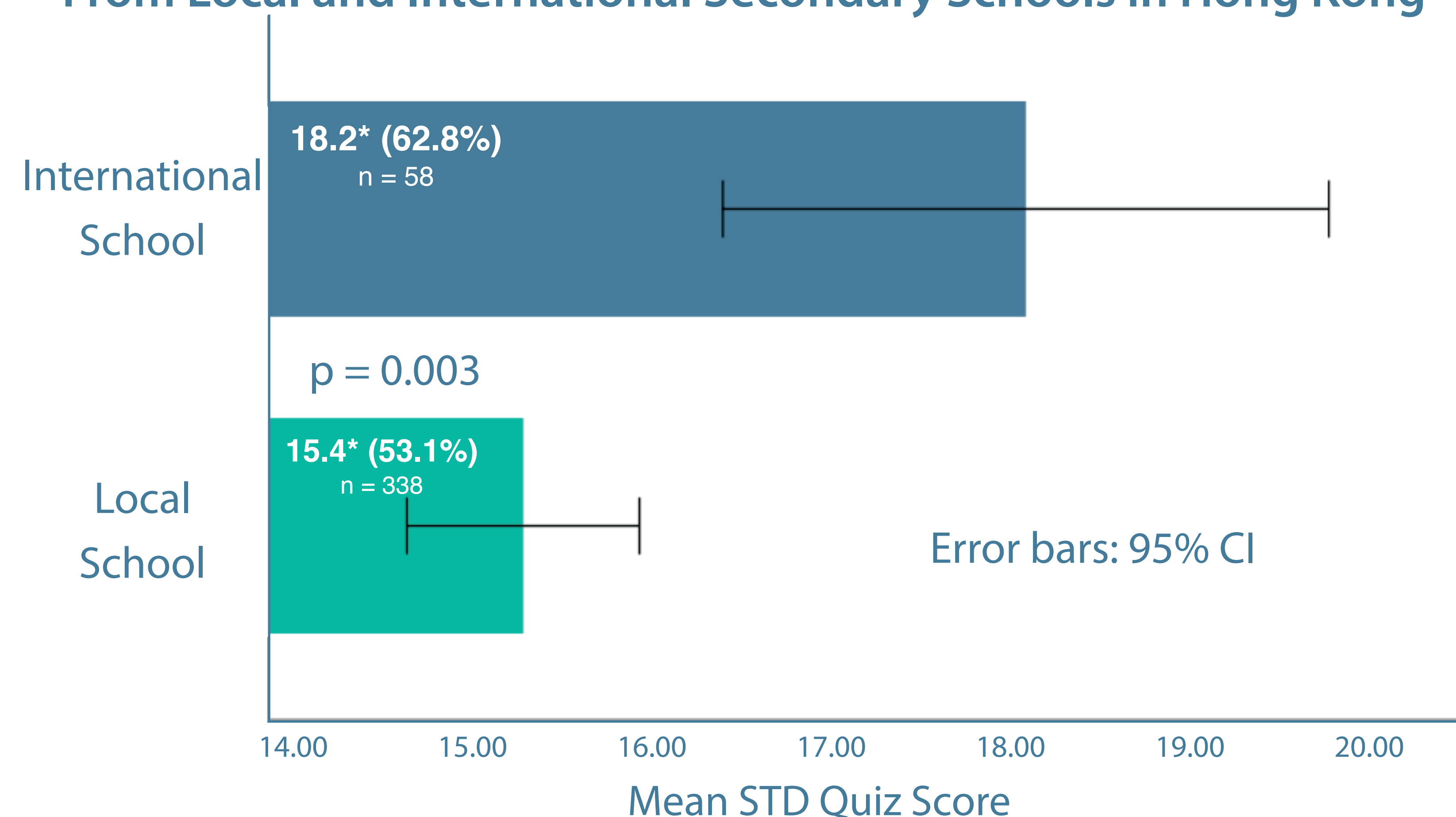
## Background



## Limitations

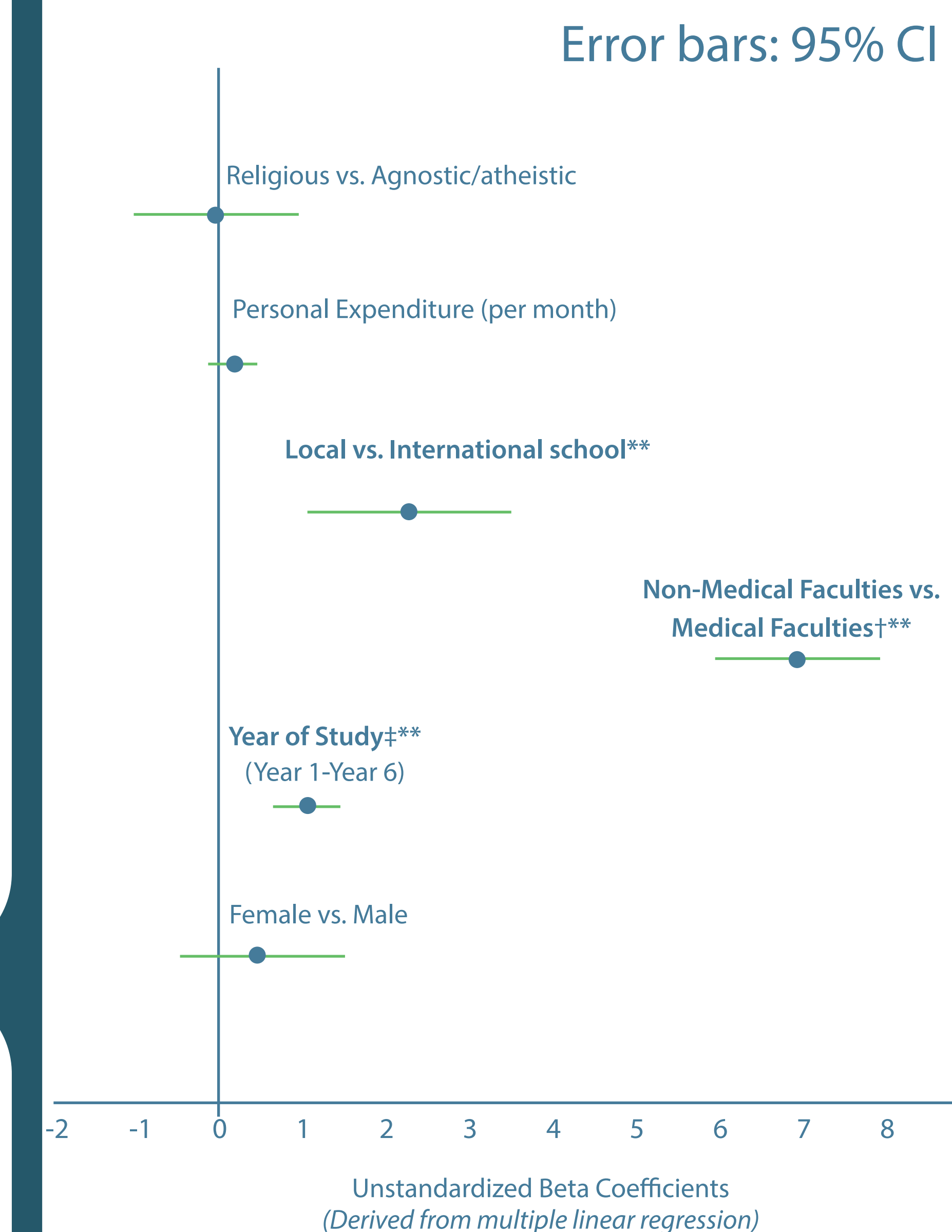
- HKU undergraduates are not representative of all Hong Kong youths
- To minimize recall bias in this study, the multiple linear regression only included objective measures.

## Knowledge Difference in STDs Between HKU Undergraduates From Local and International Secondary Schools in Hong Kong



\* out of a 29-question STD quiz

## Demographic Characteristic Factors Affecting STD Knowledge Level

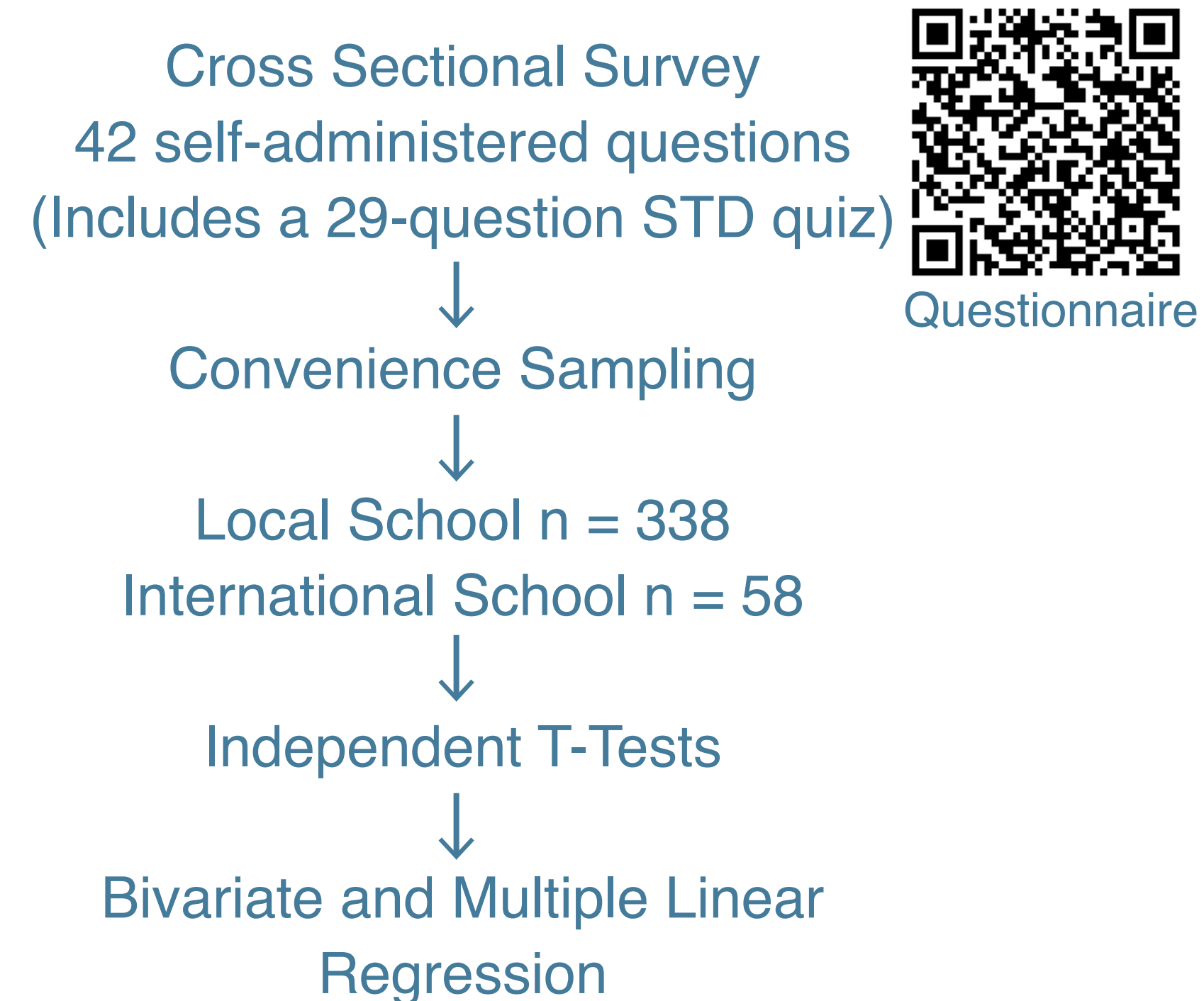


\*\* significant at p<0.05  
 Model Adjusted R<sup>2</sup>= 34.1%

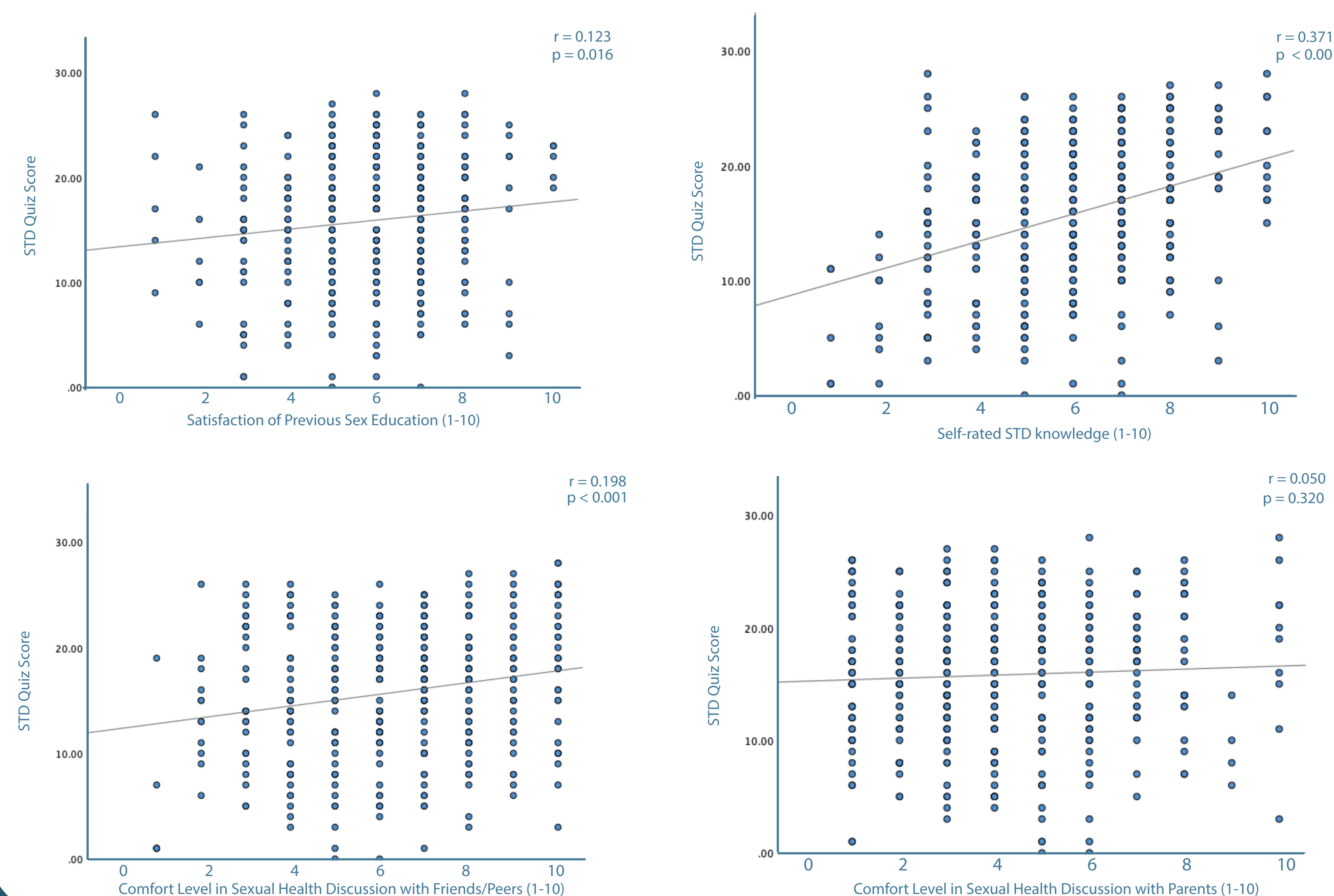
‡ Non-Medical Faculties: Departments of Science, Arts, Business and Economics, Engineering, Education, Architecture, and Law.  
 Medical Faculties: Departments of Medicine and Dentistry

‡ With the exception of a few 5-year or 6-year undergraduate degrees, most undergraduate degrees are 4-year programs.

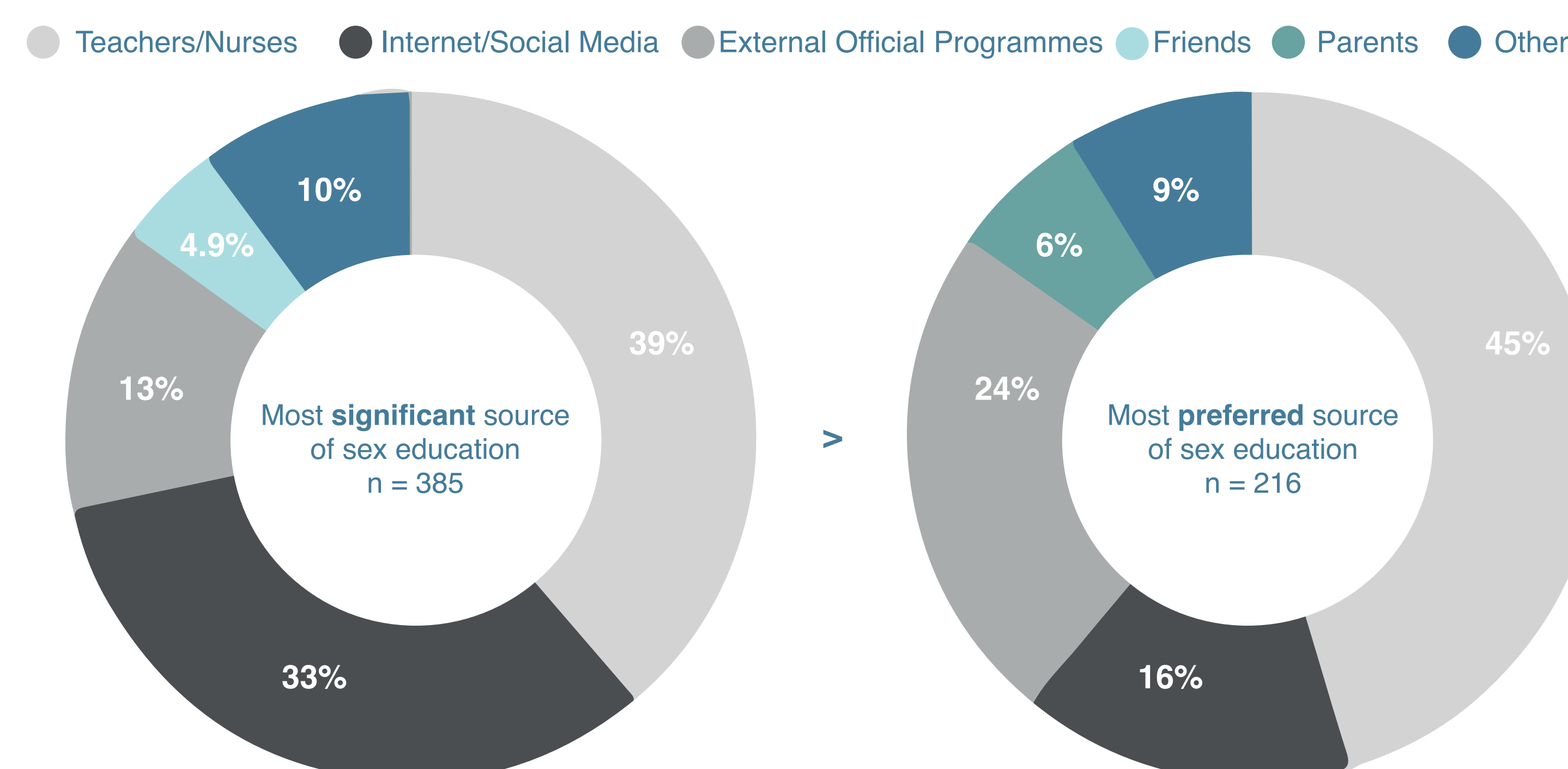
## Methods



## Correlation Between STD Quiz Scores and Parameters of Previous Sex Education and Attitudes Towards Sexual Health



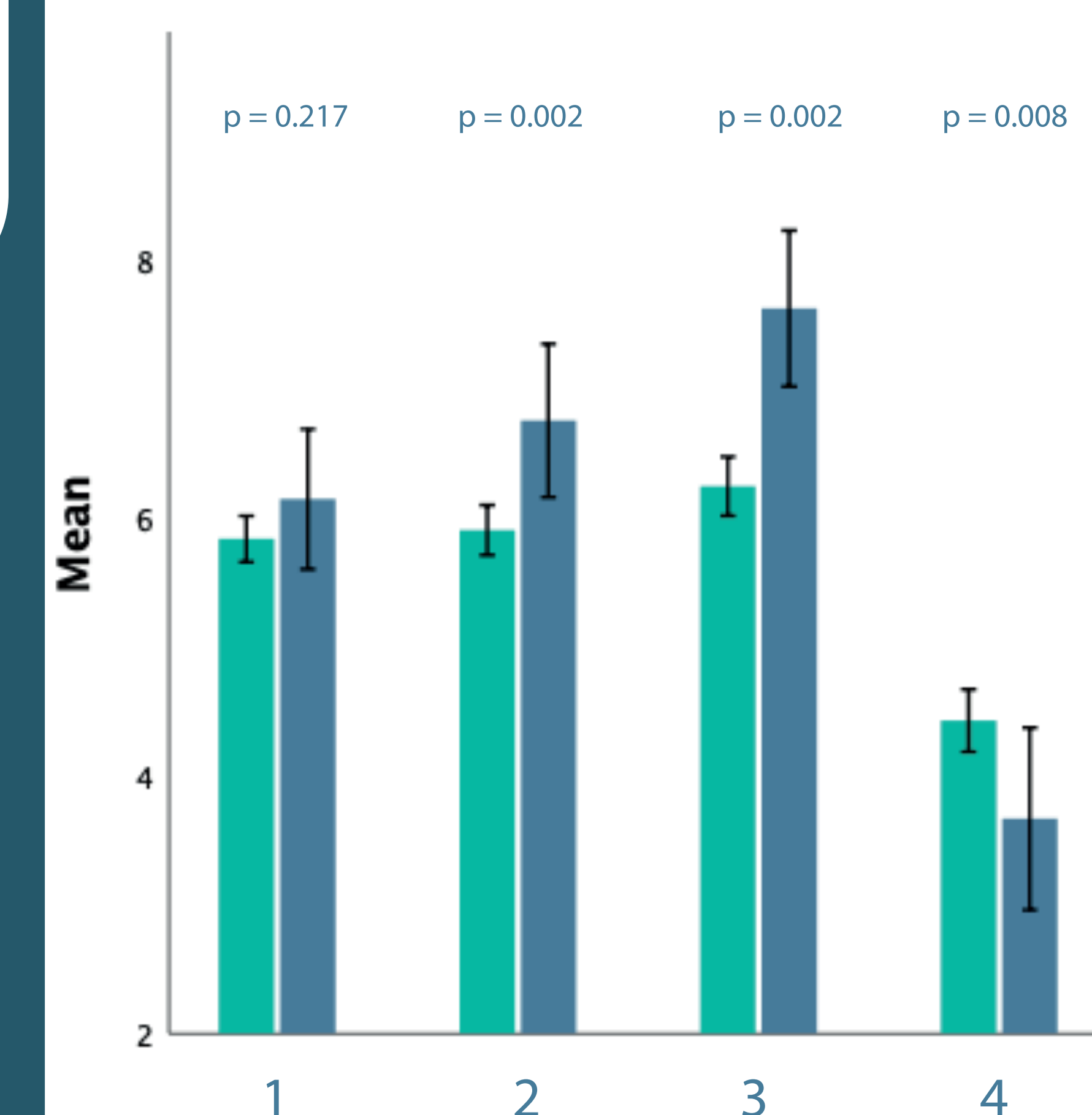
## Most Significant and Preferred Sources of Sex Education



"Other" includes the sources "Television", "Books/magazines/newspapers" and "Siblings"

## Parameters of Previous Sex Education and Attitudes Towards Sexual Health

● International School  
 ● Local School  
 Error bars: 95% CI



1: Satisfaction of Previous Sex Education  
 2: Self-rated STD knowledge  
 3: Comfort level in sexual health discussion with peers/friends  
 4: Comfort level in sexual health discussion with parents



# Remdesivir for the treatment of SARS-CoV-2 (COVID-19): a systematic review and meta-analysis



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## INTRODUCTION

- COVID-19 is caused by SARS-CoV-2 infection, with 19% patients progressing to its severe form<sup>1</sup>.
- Remdesivir is a RNA-dependent RNA polymerase inhibitor used in Ebola and Marburg virus infections, with effective outcomes.

## AIM

- To define the efficacy of remdesivir for the treatment of severe COVID-19 patients

## MATERIALS & METHODS

- Systematic review on databases (Pubmed, Embase, Medline, Cochrane) on 29 May 2020. Keywords: remdesivir, COVID-19, SARS-CoV-2, RCT, cohort study.
- Inclusion criteria:
  1. Peer reviewed high-quality evidence with clinical data (i.e. cohort studies and RCT)
  2. Laboratory confirmed severe COVID-19 adults, fulfilling:
    - a) PaO<sub>2</sub> saturation ≤ 94% with ambient air, OR
    - b) PaO<sub>2</sub>/FiO<sub>2</sub> ≤ 300mmHg

- Definition of clinical improvement:
  - 1) Clinical improvement from a higher score to score 1,2,3; OR
  - 2) Reduction of ≥ 2 points from baseline score

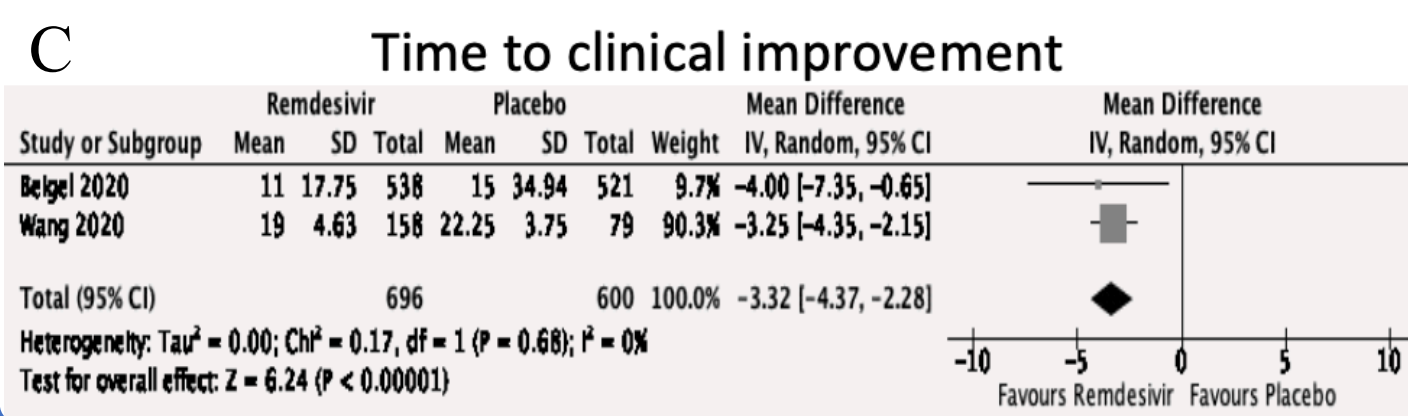
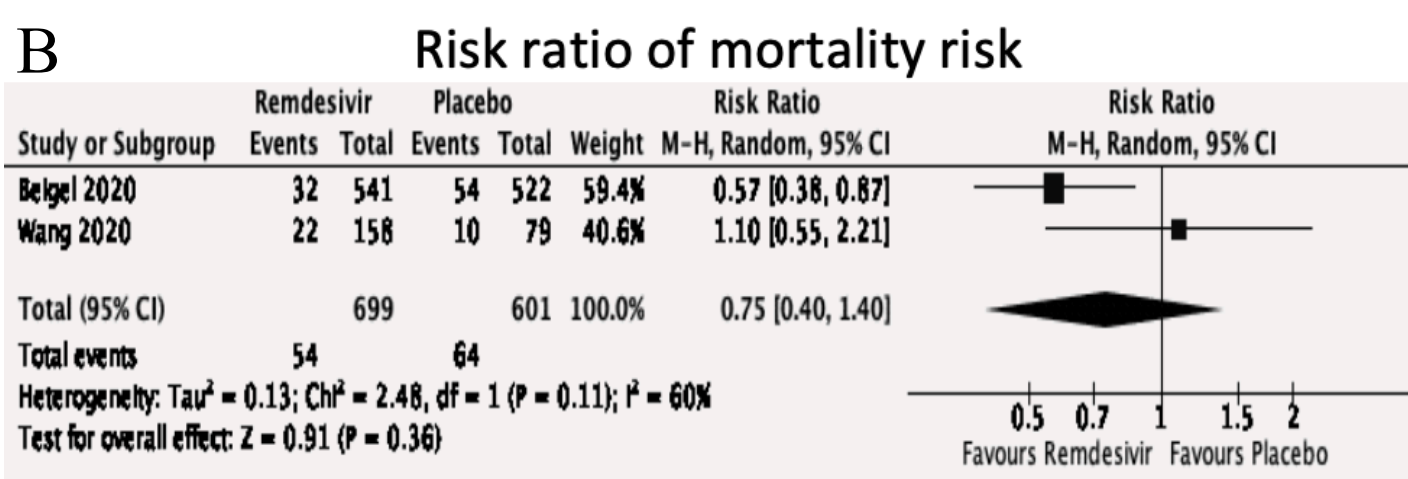
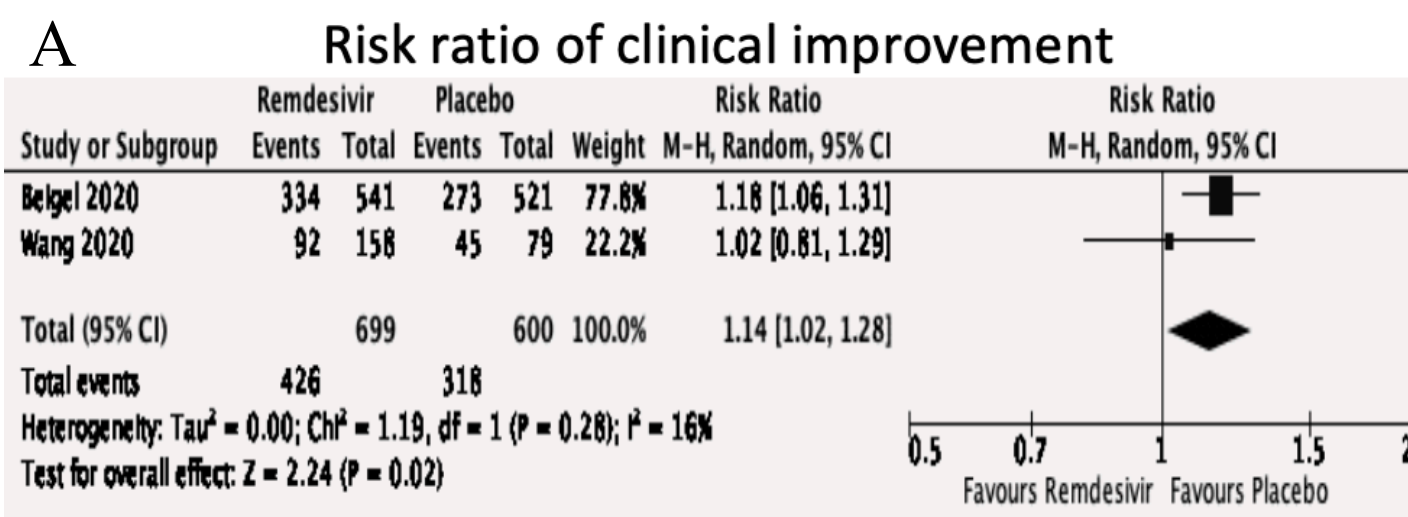
Table 1. Eight-point ordinal score

Score	Descriptions
1	Not hospitalized, no limitations of activities
2	Not hospitalized, limitation of activities, home oxygen requirement or both
3	Hospitalized, not requiring supplemental without ongoing medical care
4	Hospitalized, not requiring supplemental oxygen and no longer requiring ongoing medical care
5	Hospitalized, requiring any supplemental oxygen
6	Hospitalized, requiring non-invasive or use of high-flow oxygen devices
7	Hospitalized, receiving invasive mechanical ventilation of extracorporeal membrane oxygenation (ECMO)
8	Death

## Clinical efficacy (Figure 2)

- Higher chance of clinical improvement compared with placebo (risk ratio 1.14, 95% CI 1.02-1.28, p=0.02)
- Not associated with reduction of mortality. (risk ratio 0.75, 95% CI 0.40-1.40, p=0.36)
- Reduced mean time of clinical improvement by 3.32 days (95% CI -4.37 to -2.28, p<0.001)

Figure 2. Clinical efficacy of remdesivir



## Results

### Subgroup analysis within remdesivir group (Figure 3)

- More favorable clinical improvement in patients with baseline score less than 7:
    - Risk ratio 1.90, 95% CI 1.58-2.29, p<0.001;
    - Hazard ratio 2.22, 95% CI, 1.64-3.02, p<0.001).
    - Younger patients\* had a better chance of improvement compared with the older. (hazard ratio 2.14, 95% CI 1.39 – 3.28, p<0.001).
- \*Beigel et al<sup>2</sup> & Goldman et al<sup>3</sup> used 65 years old as cutting age; while Grein et al<sup>4</sup> used 70 years old.

Figure 3. Sub-group analysis of clinical efficacy

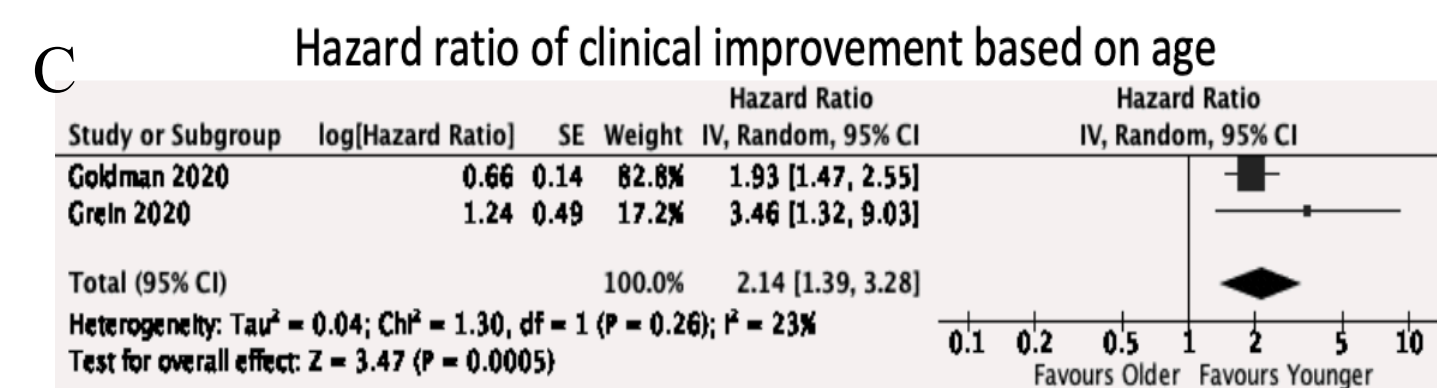
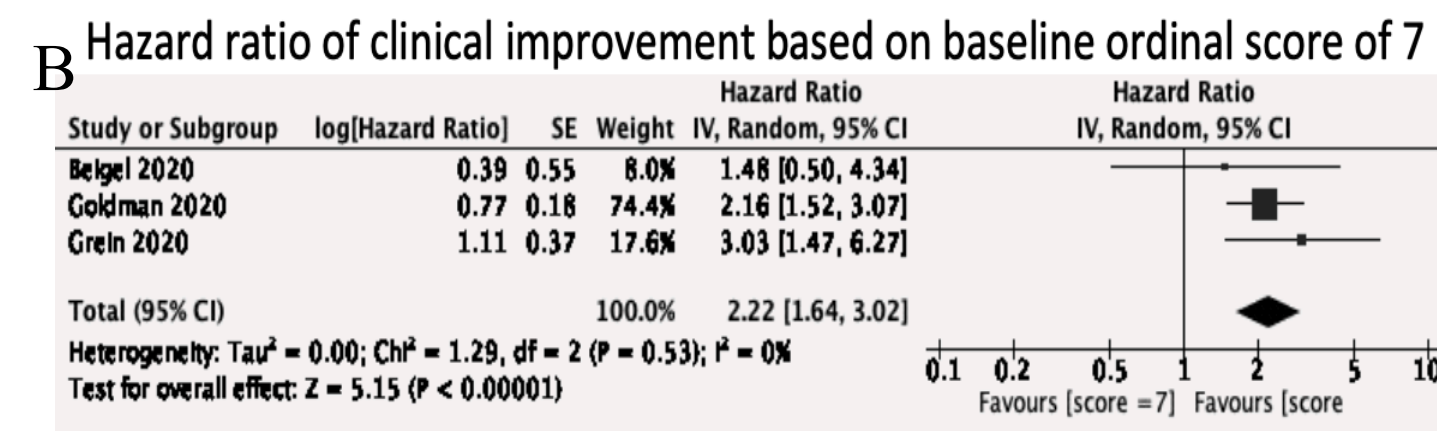
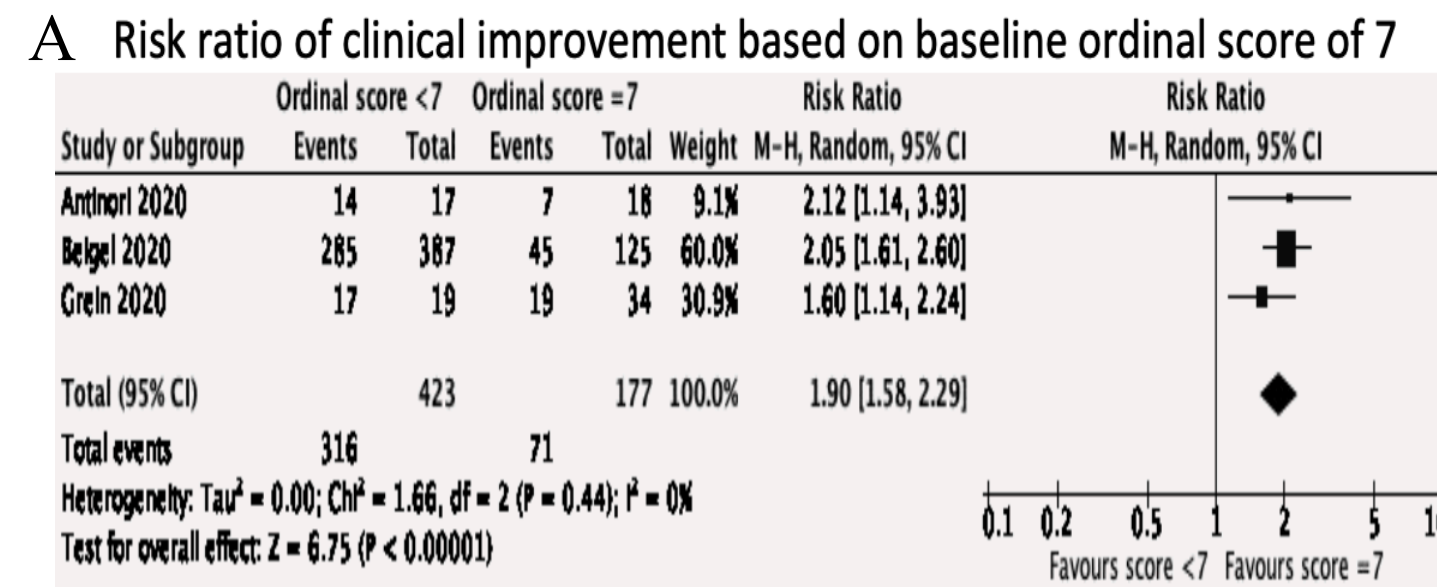
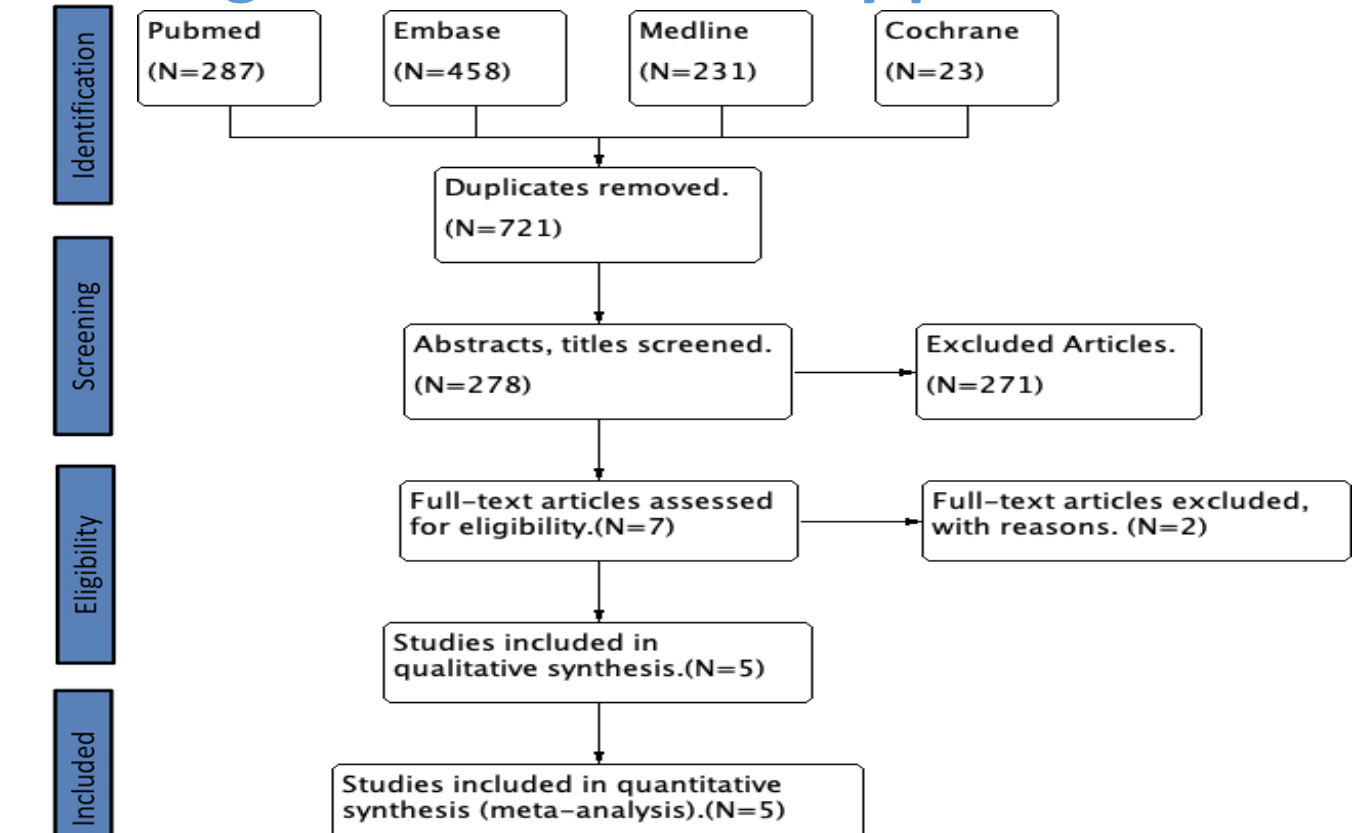


Figure 1. PRISMA study profile



## DISCUSSION

- Remdesivir is more effective for patients without invasive ventilations, possibly due to the absence of irreversible alveolar damage.
- It significantly reduced viral load in the first 10 days in the treatment group, but comparable viral load in the end with placebo-group<sup>5</sup>. Combination therapy to maximize viral-load reductions should be considered.

## CONCLUSION

Remdesivir is effective for the treatment of severe COVID-19 patients, especially those without invasive ventilation.

## REFERENCES

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2. Beigel JH, Tomashek KM, Dodd LE, et al. Remdesivir for the Treatment of Covid-19 - Preliminary Report. *N Engl J Med* 2020. DOI:10.1056/NEJMoa2007764.
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## Disclosure

Prof. Ching-Lung Lai gave sponsored lectures on viral hepatitis for Gilead Sciences Inc. Other authors declared as no conflict of interests.

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# Understanding and Perception of Direct-to-Consumer Genetic Testing (DTCGT) in Hong Kong

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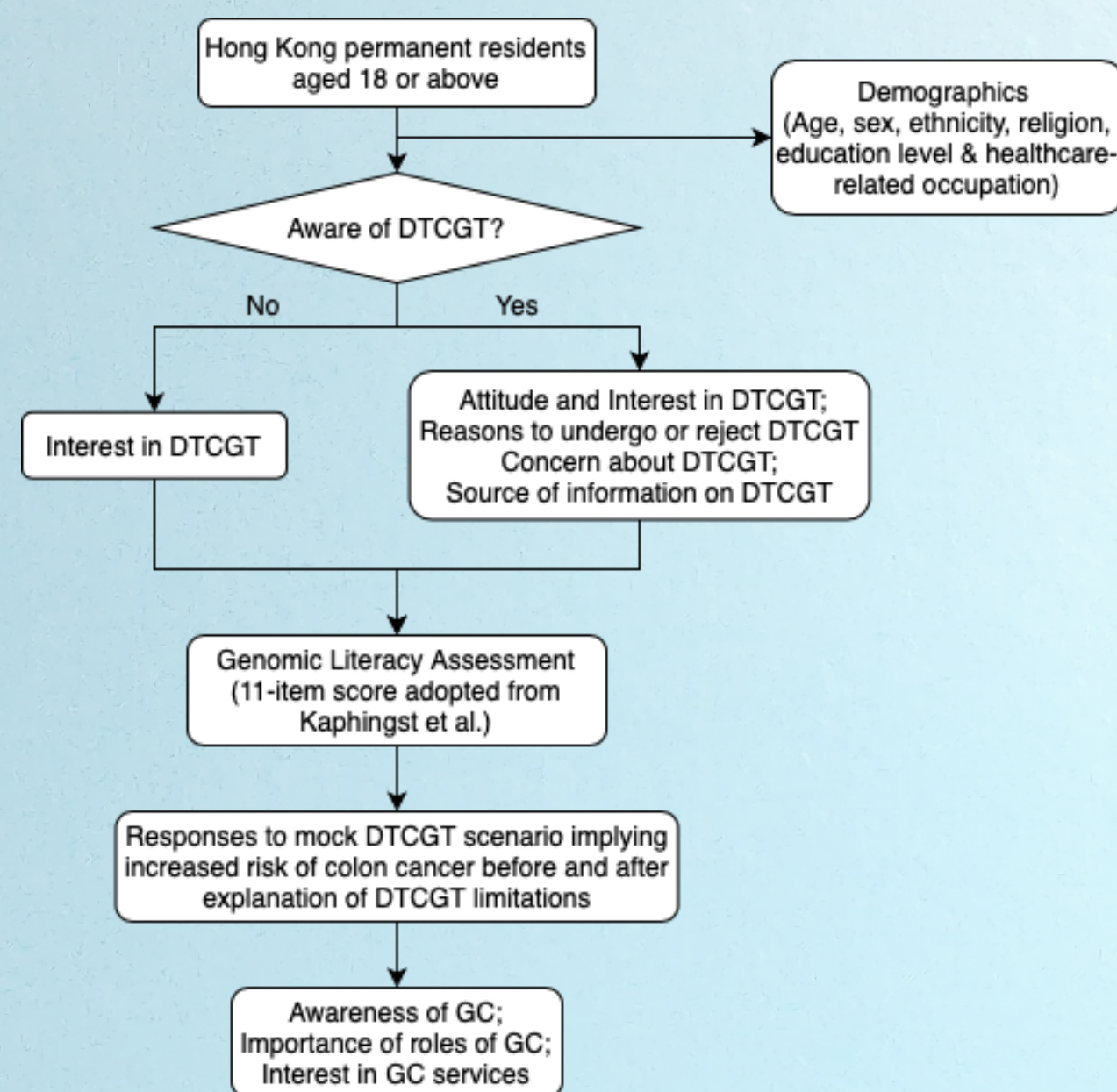


## BACKGROUND

- As **direct-to-consumer genetic testing (DTCGT)** is gaining popularity, concerns have been raised by healthcare professionals regarding its validity, utility, as well as the public's ability to understand and interpret the test results
- Genetic counselling (GC)** is consistently recommended to facilitate understanding in DTCGT results
- DTCGT is highly consumer-centric; thus understanding the perception of potential users i.e. the general public, is important
- This study aims to investigate the Hong Kong public's genomic literacy, perception towards DTCGT, and importance of GC in DTCGT

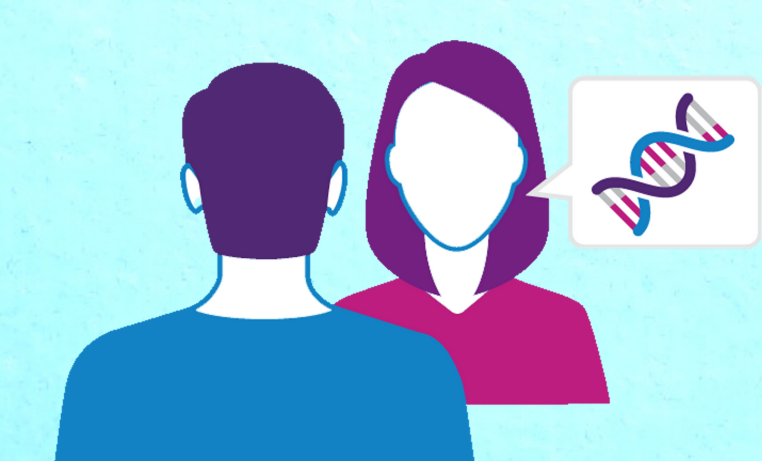
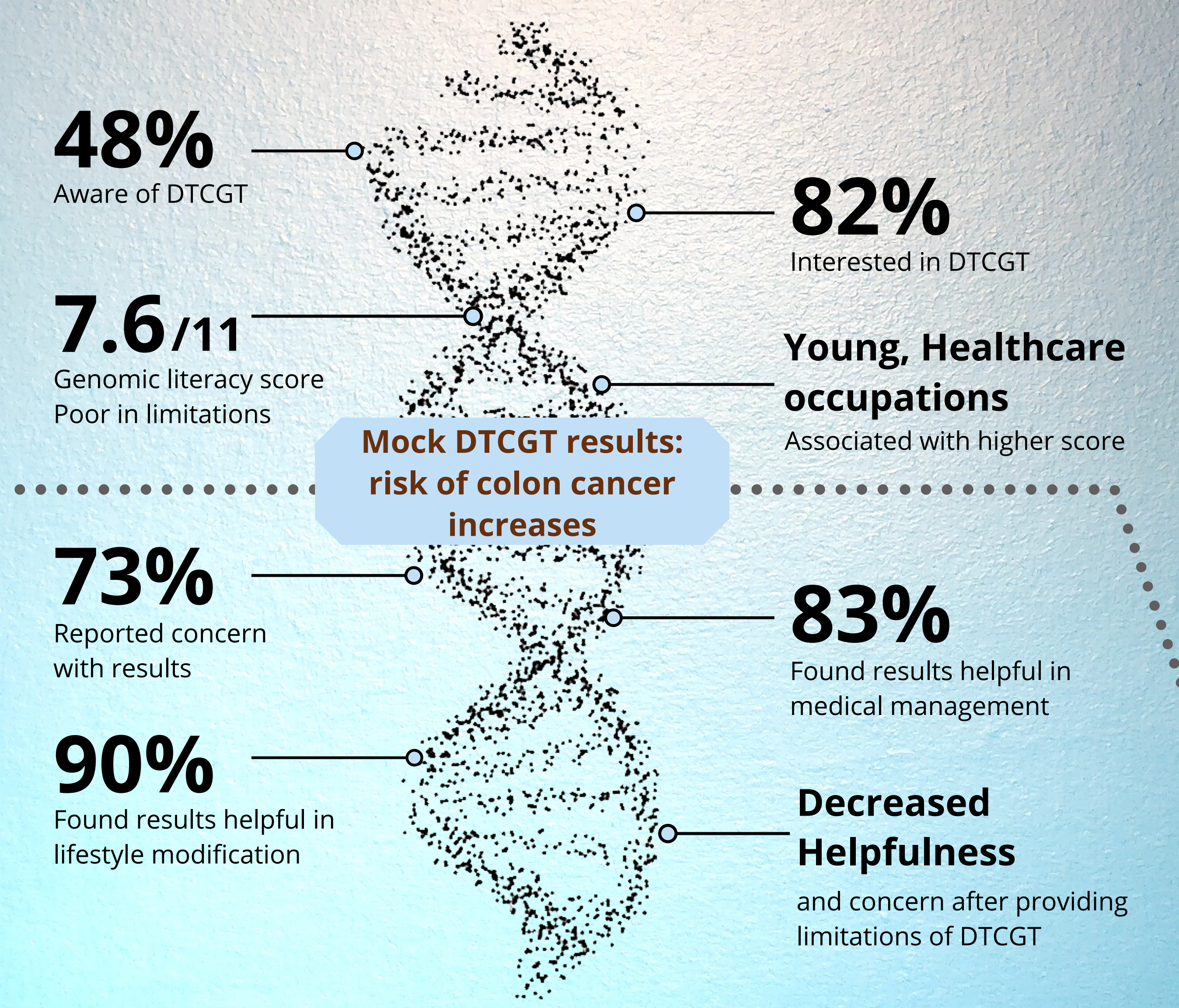
## METHODS

- 304 Hong Kong citizens aged  $\geq 18$  years old completed an anonymous web-based survey distributed mainly via researchers' personal connections and HKU mailing list from January to February 2020.
- Data analysis**  
SPSS package was used. Analyses include descriptive statistics, logistic regression, chi-square tests, t-tests, ANOVA, Pearson correlation.



## REFERENCES

- Horrow C, Pacyna JE, Sutton EJ, Sperry BP, Breitkopf CR, Sharp RR. Assessing optimism and pessimism about genomic medicine: Development of a genomic orientation scale. *Clin Genet.* 2019;95(6):704-12
- Kaphingst KA, Facio FM, Cheng MR, Brooks S, Eidem H, Linn A, et al. Effects of informed consent for individual genome sequencing on relevant knowledge. *Clin Genet.* 2012;82(5):408-15



**30%** Aware of genetic counselling (GC)  
**73%** among those who needed / considered GC services did not know how to access

## CONCLUSIONS

- This Hong Kong population has a high level of awareness and interest in DTCGT
- As potential DTCGT users, they might experience excess concern and overestimate the usefulness of positive DTCGT results, particularly in terms of medical management
- The importance of GC to educate and guide interpretation of DTCGT results is supported; yet there is inadequate awareness and access of GC services

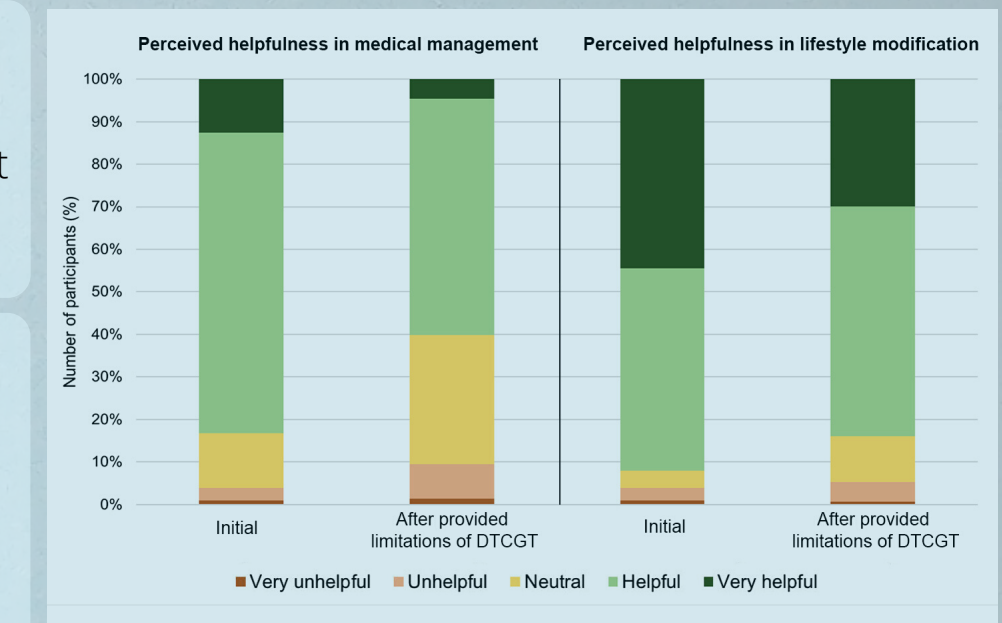
## RESULTS & DISCUSSION

- Participant characteristics**
- Young age (18-30; 72%)
  - Tertiary-educated (90%)
  - Never experienced DTCGT (98%)
  - Healthcare-related occupation (38%)
- Genomic literacy**
- Mean score: 7.6 / 11 (95% CI: 7.3 - 7.9)
  - Higher score associated with young age ( $p = 0.002$ ) and healthcare-related occupation ( $p < 0.001$ )
  - Weaker in limitations of genomic testing compared to benefits ( $p < 0.001$ )
  - Lower than a similar US population (8.1/11,  $p = 0.001$ ) (Horrow et al.)

- Perception on DTCGT**
- High awareness (48%)
  - High interest (82%)
  - Internet (72%) and mass media advertisements (48%) are the major sources of information, which are potentially biased

- Top motivations to undergo DTCGT:**
- Curiosity (63%)
  - Health-related motivation: early detection of diseases (62%)
- Top reasons to decline DTCGT:**
- Cost (66%)
  - Concerns with ethical issues (41%)
  - Unreliable results (30%)

- INITIAL receipt of positive report**
- 73% reported concern
  - 83% found results helpful in medical management
  - 90% found results helpful in lifestyle modification



- AFTER being provided limitations of DTCGT**
- 40% had decreased level of concern
  - Significant reduction in perceived helpfulness of medical management (35%) and lifestyle modification (27%)

- Perception on Genetic Counselling (GC)**
- Low awareness (30%)
  - Moderate interest in using GC for DTCGT (50%)
  - Higher awareness and interest associated with tertiary education ( $p = 0.004$ ,  $p < 0.001$ ) and health-related occupation ( $p < 0.001$ ,  $p = 0.004$ )
  - Inadequate access to GC services (79% of those who were aware of GC did not know how to access GC services)

# A Bayesian age-period-cohort analysis and projection of diabetes incidence in Hong Kong from 2007 to 2027

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## OBJECTIVES

Our study primarily aimed to examine the effects of age (biological changes), time period (current population-wide factors), and birth cohort (generational factors) on incidence rate of diabetes and generate projections of the trends in Hong Kong Chinese population.

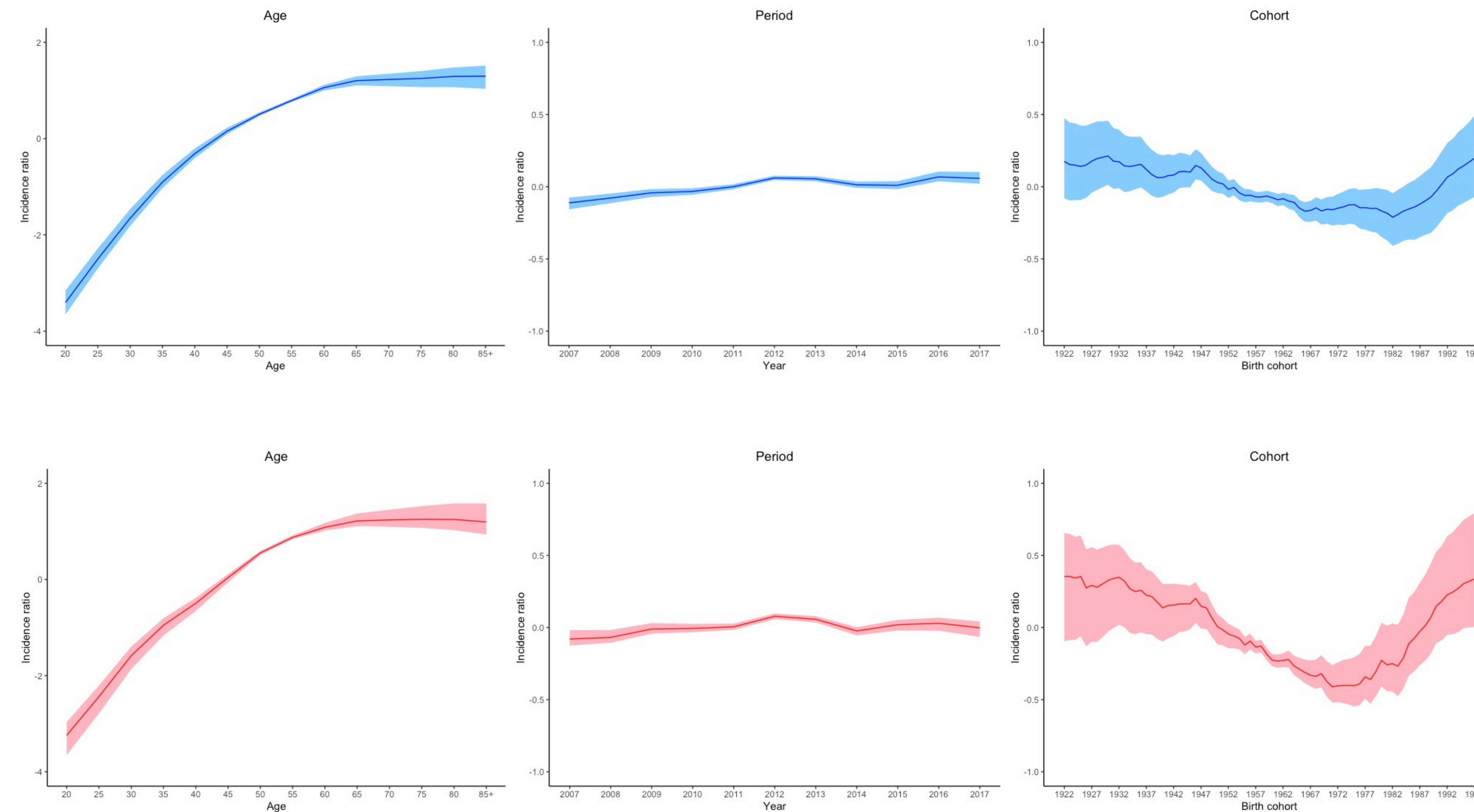
## METHODS

We identified all individuals who had a recorded diagnosis for diabetes from 1 January 2007 to 31 December 2017. We analysed diabetes incidence data from the electronic medical record database of Hospital Authority (Clinical Management System) in Hong Kong from 2007 to 2017. We included those aged from 20 years old (14 age groups at 5-year intervals) with birth cohorts from 1922 to 1997. Population estimated from 2007 to 2017 were obtained from the Census and Statistics Department, HKSAR. We applied a Bayesian age-period-cohort model which decomposed the age, period, and cohort effects on diabetes incidence trends separately for males and females. Based on past data from 2007 to 2017, we projected future trends for the next decade to 2027.

## RESULTS

We identified 469,325 incident cases of diabetes from 2007 to 2017. As expected, we observed clear age effects on incidence in both sexes. Overall incidence rates increased among successive birth cohorts from 1980s to 1990s while period effects remained negligible. In the projection model, incidence rate increased with older age groups in a progressive manner in male. We noticed an increasing trend projection for the 30-39 age group and a decreasing trend projection for the 70-79 age group. The other age groups in male remained a stable trend with no rise or decline for incidence rate. For female, incidence rate also progressively increased with older age groups in a pattern similar as male. 20-29 age group had a stable projected trend. The next 30-39 and 40-49 age groups showed a small rising trend. While for the remaining age groups with patients above 50 years old, they all revealed declining trends in the projected years.

FIGURE 1: APC EFFECTS ON INCIDENCE OF DIABETES (Male/Female)



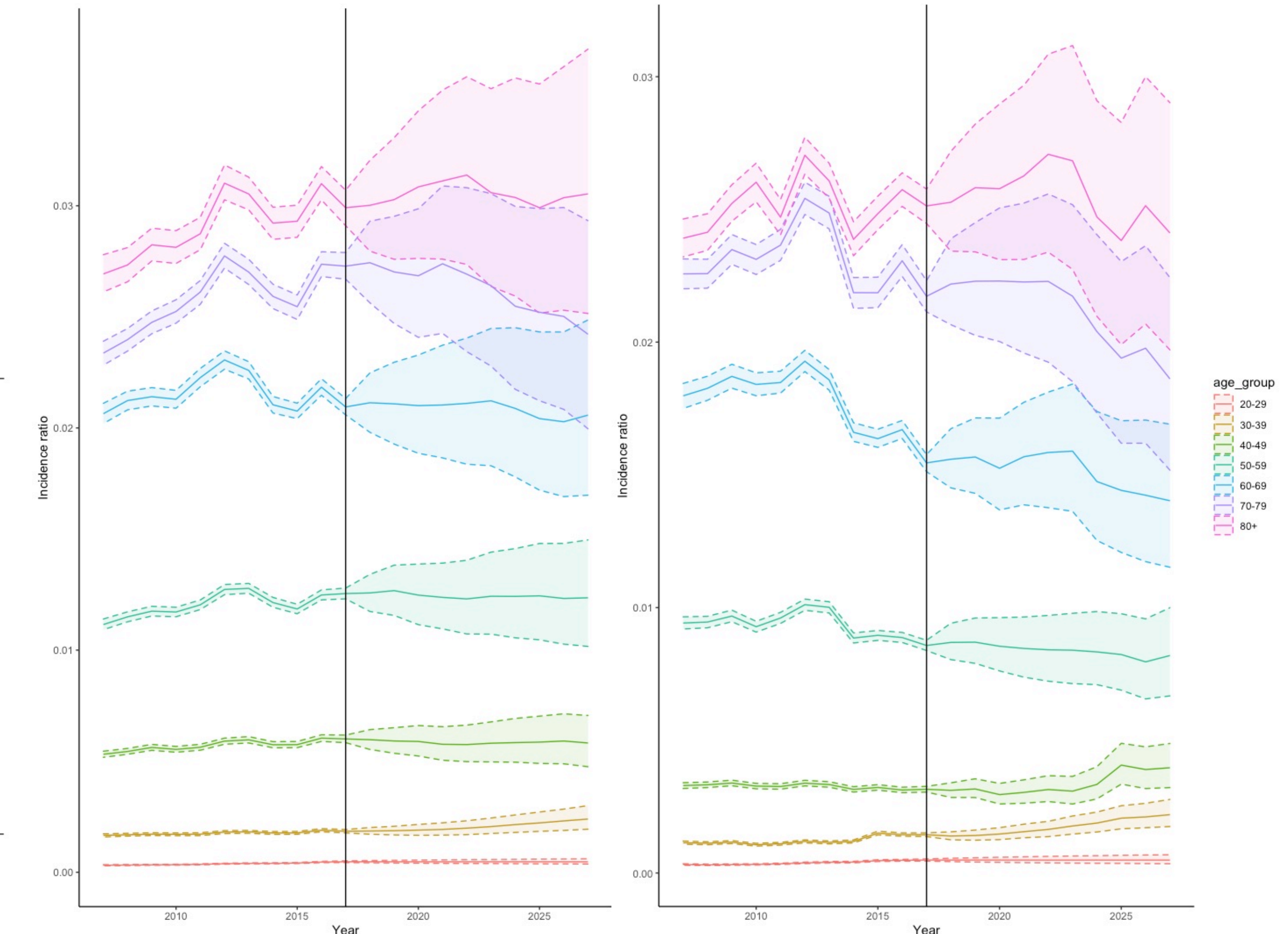
## DISCUSSION

Age had the greatest impact on incidence rates among people with diabetes, while period had negligible impact. The increase in cohort effects from 1980s in both sexes could be due to the increasing prevalence of obesity for the millennials in Hong Kong. We could observe that the age of onset of diabetes had a decreasing projected trend. This could represent an actual earlier onset of diabetes at younger age or due to earlier detection of diabetes. Further studies should be done in Hong Kong to evaluate the relationship between diabetes trends and its related risk factors such BMI, waist-to-hip ratio, systolic and diastolic blood pressure.

## LIMITATION

Age-period-cohort analyses described trends so we could only speculate the aetiologies that lead to the incidence trends observed. We could not study the causal factor related to the concomitant changes in trends. With limited data covering from 2007 to 2017, our projection of future trends had large confidence intervals in incidence projection.

FIGURE 2: DIABETES PROJECTION (Male/Female)

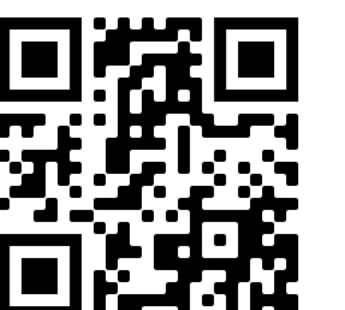


## ACKNOWLEDGEMENTS

We thank the Hospital Authority and the Census and Statistics Department of the Government of the Hong Kong Special Administrative Region for their support and assistance in providing the data, although they have no role in study design, data analysis or interpretation of the work. We would also like to thank our other team members for assistance in statistical analysis.

## CONTACT INFORMATION

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# Positions 241/3037/14408/23403 of SARS-CoV-2 genomes can be well fitted by first order dynamic models which suggests natural selection.

## Analysis of SARS-CoV-2 Genomes Regarding Time and Geographical Regions

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School of Biomedical Sciences, HKU

### Background

- SARS-CoV-2 had developed into a pandemic and infected over 15 million people around the globe.
- As a single-stranded RNA virus, SARS-CoV-2 genome can easily undergo nucleotide mutation.
- We aim to track mutation of the virus regarding time and geographical regions.

### Methods

- We first download nearly 26,000 complete genomes from GISAID Initiative.
- For the sake of quality control, we only analyse samples with high coverage (i.e. <1% missing value coded in Ns).
- We apply multiple sequence alignment on these samples to include samples with slightly different lengths (-495 positions).
- We then perform correlation analysis between SARS-CoV-2 mutations and a set of covariates including time, geographical regions, sequencing technology, etc.

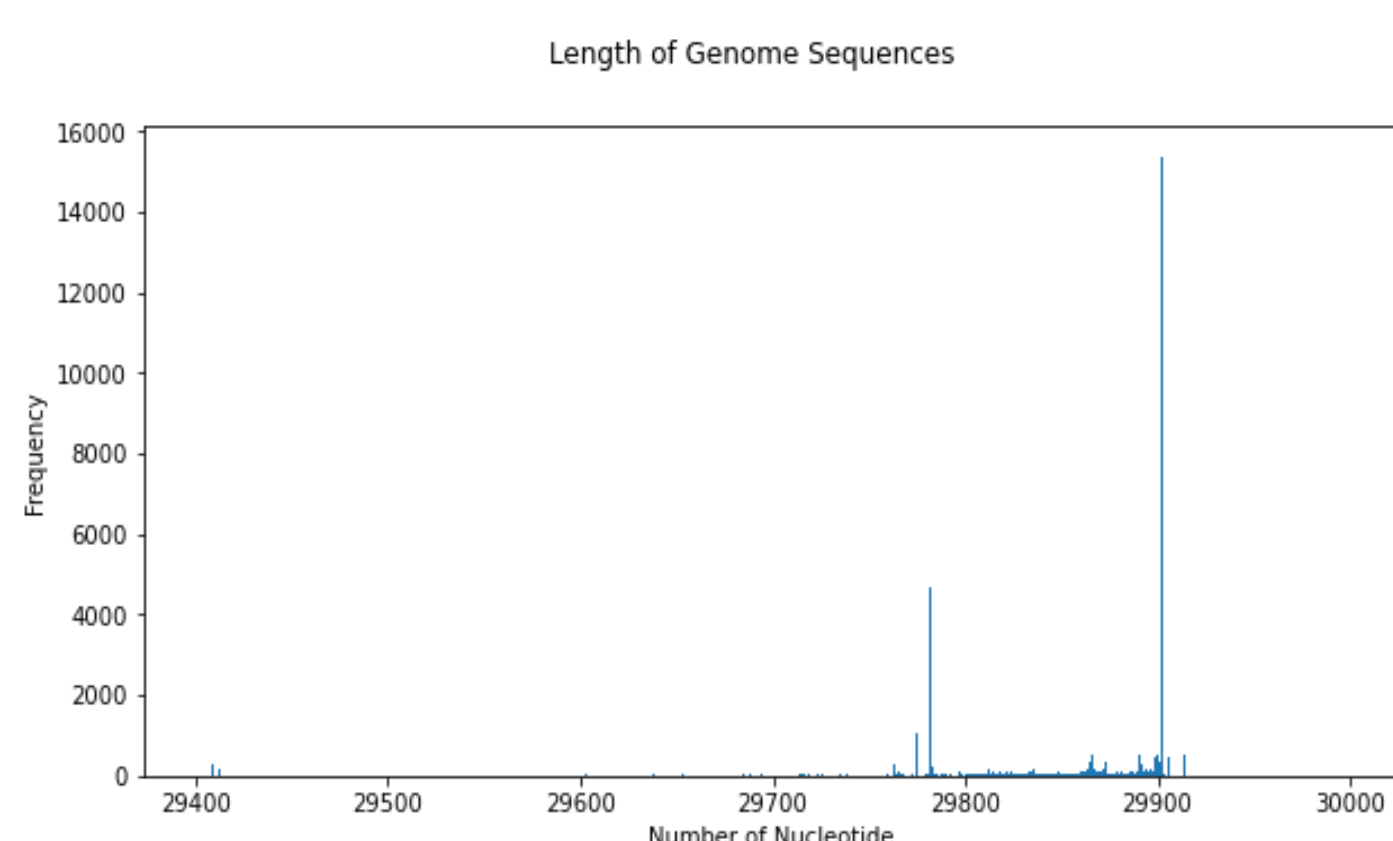


Fig.1. The histogram shows the distribution of length of genome sequences downloaded from GISAID Initiative. The mode is 29903, which is the same as the reference genome in Wuhan. We performed multiple sequence alignment on lengths with high frequency.

### Results

- There is no distinct correlation between mutation and sequencing technology or assembly technology. This strengthens the reliability of viral genotyping.
- Positions 241/3037/14408/23403 (from 5' to 3' end) co-mutated in 76.5% of samples and co-conserved in 21.6% of samples.
- This clade was first introduced in China on 1st February, and can be very well fitted by first-order dynamical models which suggests natural selection of SARS-CoV-2 with time.
- The mutation at position 23403 (i.e. D614G) mutation has been suggested to be more infectious in a recent study. (Kerbor et al, Cell, 2020, July 2nd).

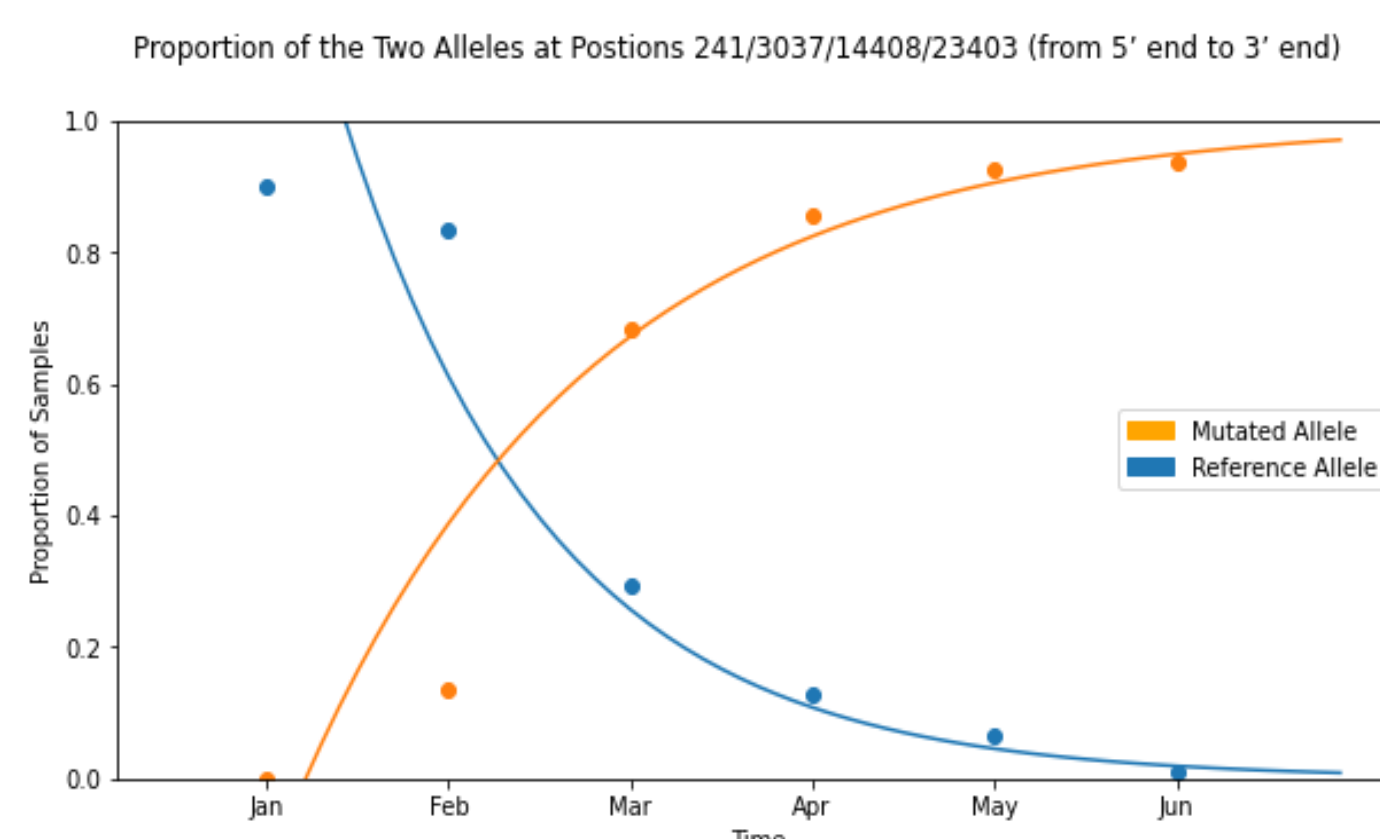


Fig.2. The graph shows the trending of alleles at positions 241/3037/14408/23403. The fitted curve for the reference allele is  $\exp(1.2391 - 0.8658*t)$ ,  $p$ -value = 0.001, Mean Absolute Error = 0.144,  $R = 0.971$ . The fitted curve for the mutated allele is  $1 - \exp(0.7592 - 0.6253*t)$ ,  $p$ -value = 0.001, Mean Absolute Error = 0.0783,  $R = 0.980$ . The half-life of the reference allele is 0.80 month inferred from the reference allele or 1.11 month inferred from the mutated allele.

### Discussion

- The global sampling of genomes in GISAID Initiative is biased towards USA and European countries.
- Using a spatial-temporal model will have better power to reveal further insights on the evolution of SARS-CoV-2.

## Extra Graphs

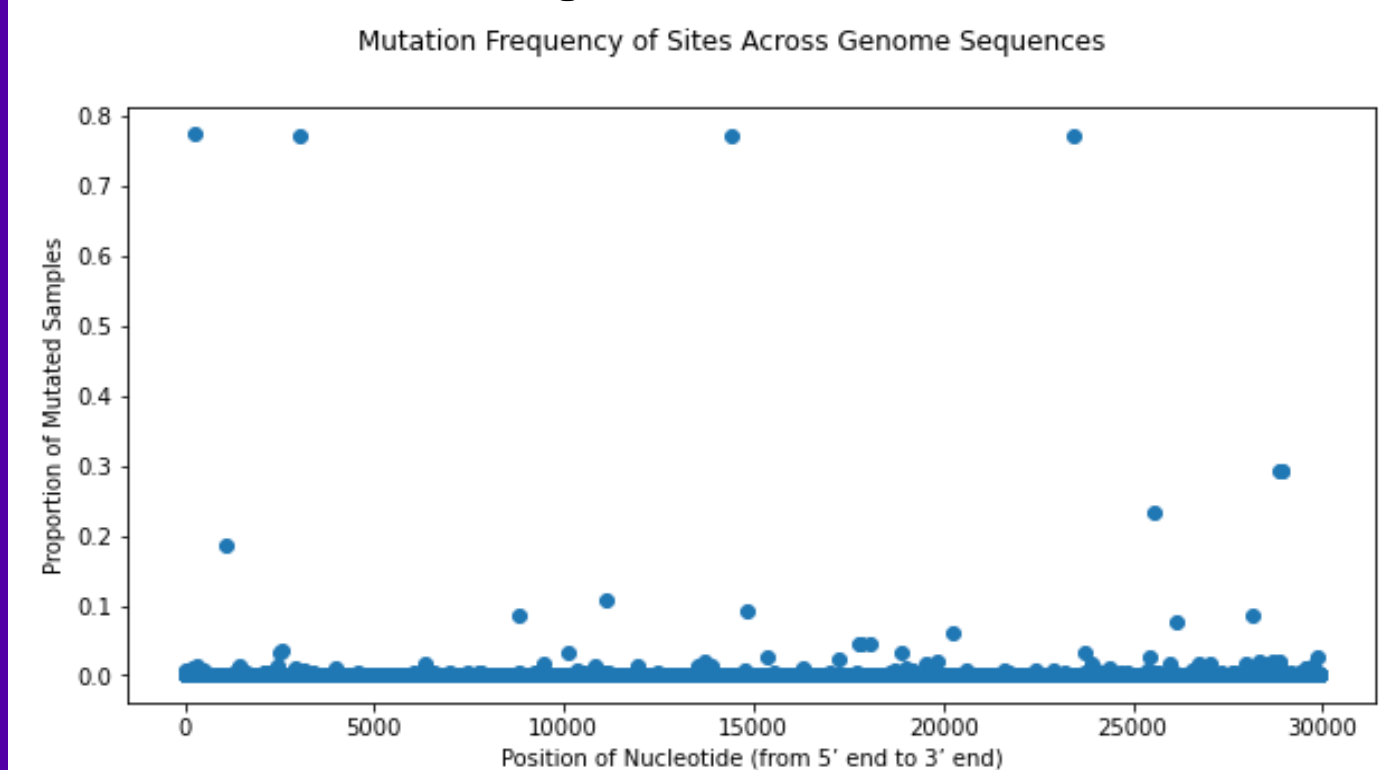


Fig.3. The scatter plot shows mutation frequency of every nucleotide position. The 4 dots around 0.8 are positions 241, 3037, 14408 and 23403 respectively.

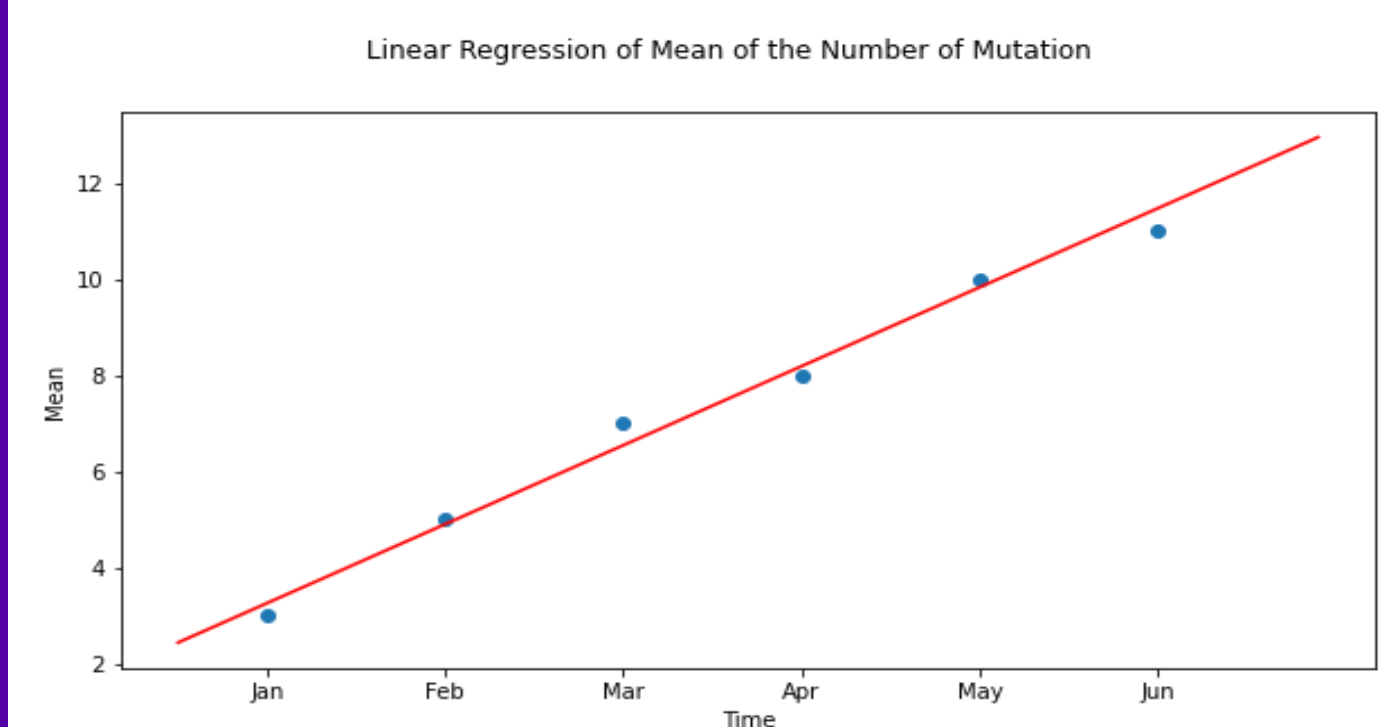


Fig.4. The linear regression line for mean of the number of mutation is  $1.64*t + 1.63$ , Standard Error = 0.071,  $p$ -value = 0.00,  $R = 0.996$ .

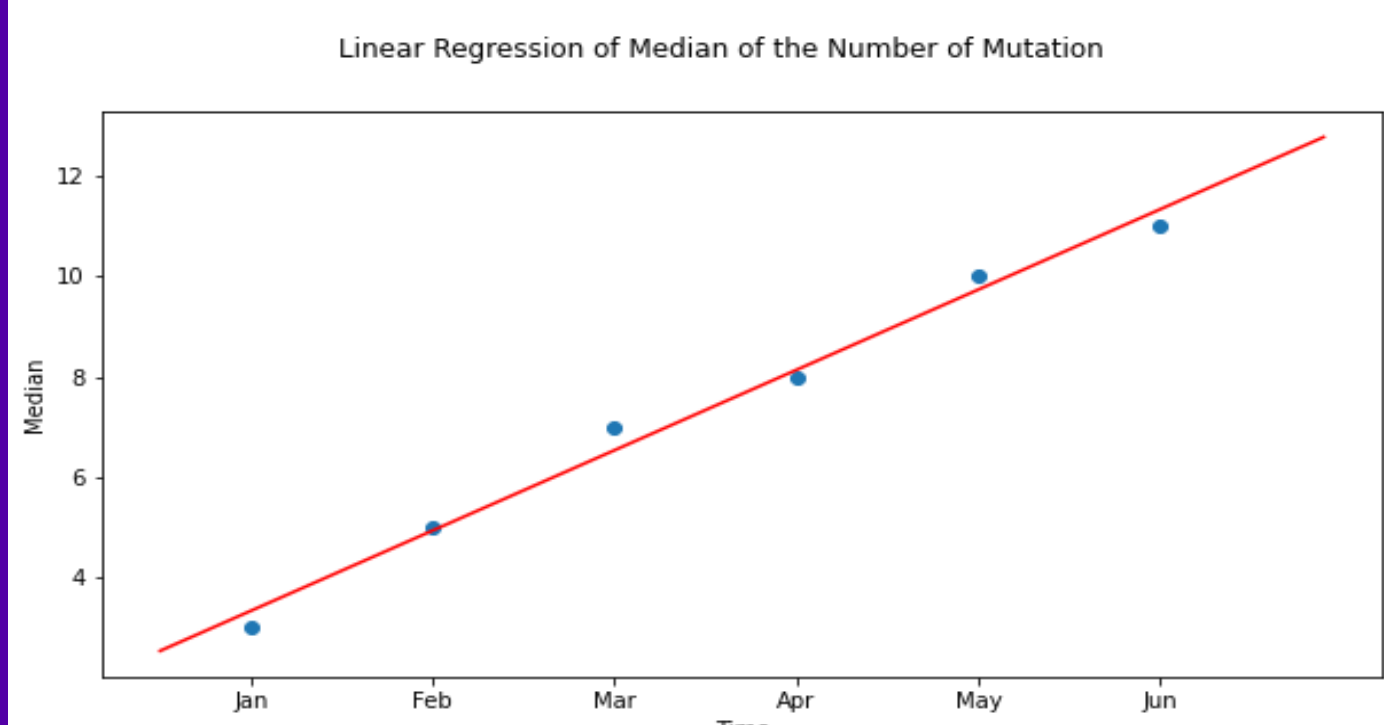


Fig.5. The linear regression line for median of the number of mutation is  $1.60*t + 1.73$ , Standard Error = 0.087,  $p$ -value = 0.00,  $R = 0.994$ .

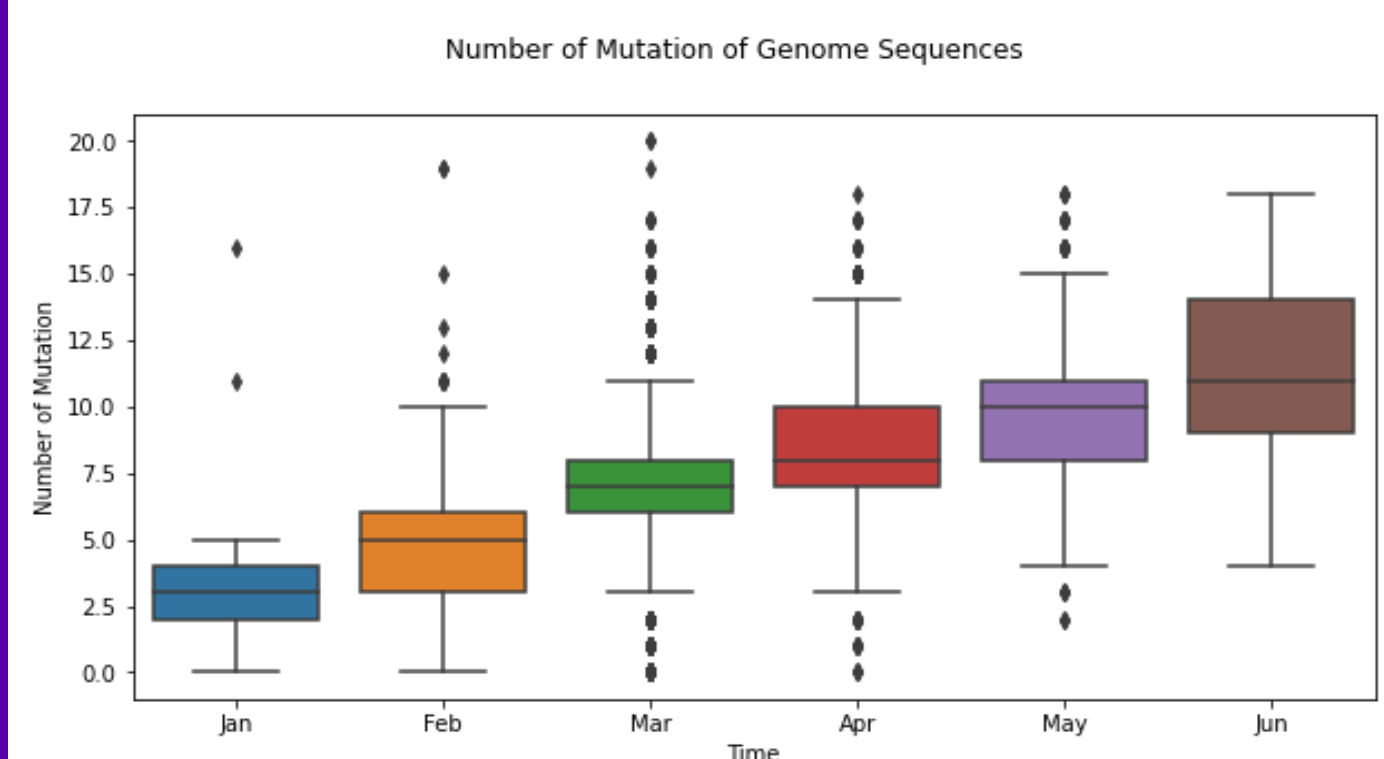


Fig.6. The box plot shows a consistent increasing trend of number of mutation from January (mean = 3.06, S.D. = 2.66) to June (mean = 11.3, S.D. = 3.31).

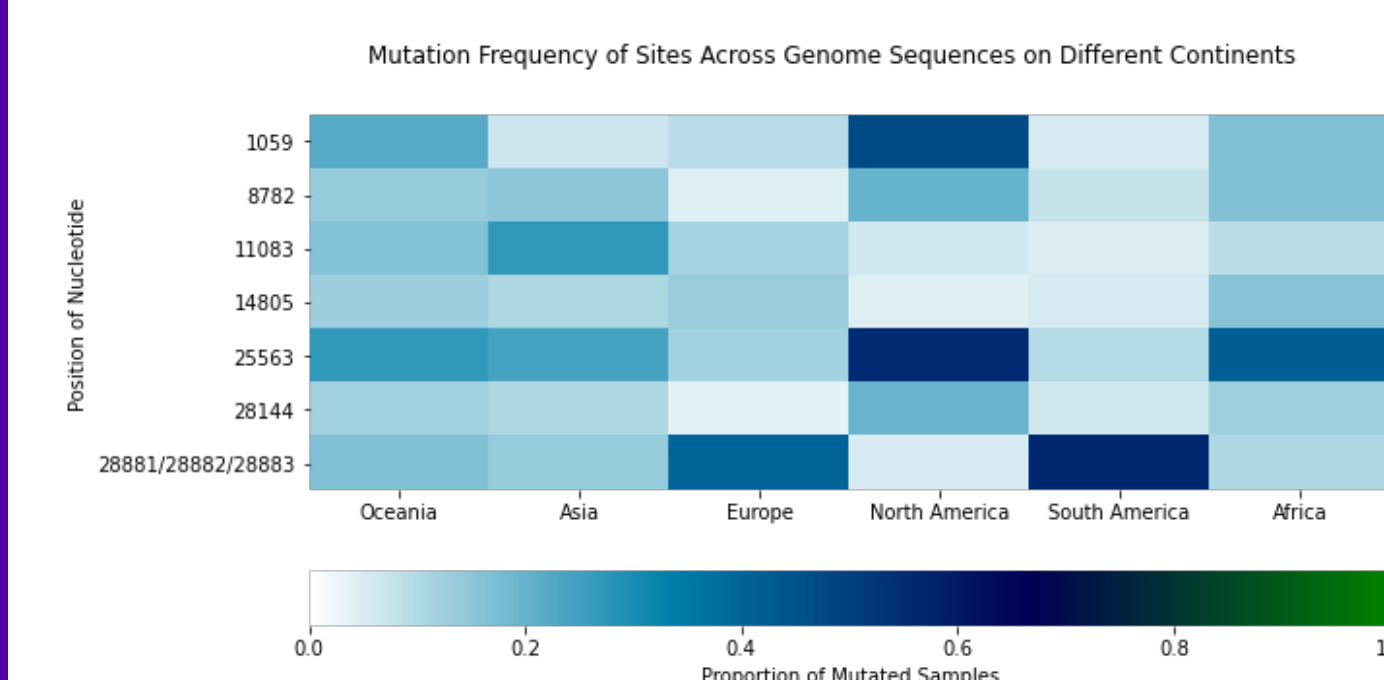


Fig.7. The heatmap shows mutation frequency of particular nucleotide positions in different continents. There is a co-mutation at positions 28881/28882/28883.