Are sibship characteristics predictive of same sex marriage? An examination of fraternal birth order and female fecundity effects in population-level administrative data from the Netherlands

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Abstract: Despite historical increases in the number of individuals engaging in same-sex relations and entering same-sex unions, the causes of sexual orientation remain an open question. Two biological processes that have received some degree of empirical validation are the fraternal birth-order effect (FBOE) and the female-fecundity effect (FFE). Respectively, these processes posit that having a greater number of older brothers and being part of larger sibships independently increase the odds of male homosexuality. Nevertheless, previous studies have relied on suboptimal data and methods, including underpowered and selected samples, and models that fail to fully disentangle the two processes. In addition, they have rarely analyzed samples of women. We address these limitations using high-quality, population-level linked register data from the Netherlands (n=9,073,496). Applying a novel multivariable approach, we jointly examine the FBOE and FFE by comparing the sibship characteristics of men (n=26,542) and women (n=33,534) who entered a same-sex union against those who did not (n=4,607,785 men & 4,405,635 women). Our analyses yield robust evidence of an FBOE on both male and female homosexuality, but no support for the FFE. Additionally, we find that individuals' birth order affects the probability of entering a samesex union, regardless of the sex of older siblings.

Keywords: administrative data; fraternal birth order effect; female fecundity effect;

homosexuality; same-sex marriage.

Background

Recent decades have witnessed major shifts towards more supportive societal attitudes and legislative provisions concerning same-sex relations (Mendos, 2019; Valfort, 2017), with accompanying increases in the number of individuals adopting a non-heterosexual identity, forming same-sex couples and, more recently, entering formally recognized same-sex unions (Gates, 2015; Mishel et al., 2020). Despite this, the causal mechanisms behind the development of sexual orientation remain an open question. Understanding these mechanisms is an important endeavor, beyond a purely academic search for knowledge. This is because individuals' beliefs about the causes of sexual orientation are heavily intertwined with their degree of acceptance of sexual minorities (Bailey et al., 2016; Sheldon et al., 2007). People who believe that sexual orientation is the product of non-social factors (e.g., hormones or genetics) are more likely to express and demonstrate support for sexual minorities and their civil rights than those who believe that sexuality is the result of social processes or individual preferences. Therefore, providing robust scientific evidence on the origins of human sexual orientation can inform public debate about significant social issues affecting sexual minorities, ranging from the legalization of same-sex marriage to the criminalization of same-sex relations (see Bailey et al., 2016).

Two biological processes that have received substantial attention in the literature are the fraternal birth-order effect (FBOE) and the female-fecundity effect (FFE). The FBOE refers to the finding that men with a greater number of older brothers are more likely to identify as homosexual (Blanchard et al., 2020b). This statistical regularity was first documented by Blanchard and Bogaert (1996), following earlier research suggesting that birth order influenced the development of men's sexual orientation (Blanchard & Sheridan, 1992; Hare & Moran 1979; Slater 1962). The FFE, on the other hand, refers to the finding that the female relatives of homosexual men tend to have more children than those of heterosexual men (Blanchard et al., 2020b; Camperio-Ciani et al., 2004; Iemmola & Camperio-Ciani, 2009).¹

Aside from North America, the FBOE has been documented in Brazil (VanderLaan et al., 2017), Greece (Apostolou, 2020), Hong Kong (Li & Wong, 2018), Indonesia (Nila et al., 2019), Iran (Khorashad et al., 2020), Mexico (Gómez Jiménez et al., 2020a), the Netherlands (Schagen et al., 2012), Turkey (Bozkurt et al., 2015), Spain (Gomez-Gil et al., 2011), Samoa (VanderLaan & Vasey, 2011; Vasey & VanderLaan, 2007), and the United Kingdom (King et al., 2005; Rahman et al., 2009; Xu et al., 2019). Studies that have found empirical support for the FFE are primarily focused on European countries, such as Italy (Camperio-Ciani et al., 2004; Iemmola & Camperio-Ciani, 2009), the UK (King et al., 2005, Rahman et al., 2008), Spain, and France (Camperio-Ciani & Pellizzari, 2012). Outside of Europe, the FFE has been observed in data from Mexico (Gómez Jiménez et al., 2020b) and Samoa (Semenyna et al., 2017; VanderLaan et al., 2012; VanderLaan & Vasey, 2011; Vasey & VanderLaan, 2007).

However, despite evidence in favor of both the FBOE (Blanchard, 2018; Bogaert, 2000) and the FFE (Blanchard et al., 2020b), the existing literature suffers from three important shortcomings. First, research on both the FBOE and FFE has focused primarily on men, despite the fact that women are more likely to engage in same-sex relations and identify as non-heterosexual (Kinnish et al., 2005; Mishel et al., 2020). Early studies dismissed the existence of an FBOE for women after failing to establish a significant association between the number of older brothers and female homosexuality (Blanchard, 1997; Bogaert, 1997, 2000). With few

¹We are cognizant of competing views on the appropriateness of the term 'homosexual', including the American Psychological Association's stance against its use (American Psychological Association, 2020). In this paper, we use this term over 'gay/lesbian'—or other variations—to be consistent with the language used in previous studies of the FBOE (see e.g., Blanchard et al., 2020b; Blanchard & Bogaert, 1996; Bogaert, 2006) and FFE (see e.g., Camperio-Ciani et al., 2004; Iemmola & Camperio-Ciani, 2009). As such, our use of the term 'homosexuality' does not entail any value judgement about different sexualities, or the individuals who identify with them.

exceptions (e.g., Camperio-Ciani et al., 2018), studies of the FFE have also focused almost exclusively on men. Altogether, the FBOE and FFE remain largely unexplored and undocumented among women.

Ascertaining whether the FBOE and FFE operate for women as well as men nevertheless has significant repercussions for theory development. The focus on samples of men has skewed contemporary theoretical discussions and empirical efforts towards sexasymmetrical explanations that operate only for men. This situation applies, for example, to the Maternal Immune Hypothesis, the leading explanation for the FBOE (Blanchard and Bogaert, 1996). The Maternal Immune Hypothesis operates through a mother's exposure to H-Y antigens, which are present in a male fetus and unknown to the mother's immune system. The H-Y antigens trigger a release of maternal antibodies, which target the Y-linked NLGN4Y protein responsible for sexual differentiation in the male brain. Crucially, these antibodies are retained even after childbirth and accumulate over successive male pregnancies. This means that subsequent male fetuses are exposed to higher antibody levels, which increases the likelihood of their brain structures being altered (Bogaert et al., 2018). Ostensibly, this process results in a greater tendency towards homosexuality among men-but not women-with greater numbers of older brothers (Bogaert, 2006). However, if we were to observe evidence of the FBOE and FFE among women, this would go counter to existing sex-asymmetrical explanations for these processes, including the aforementioned Maternal Immune Hypothesis.

The second shortcoming of studies on the FBOE and FFE is that most of them have examined these two processes as independent phenomena. However, this approach may not be appropriate, since the number of older brothers is inherently correlated with the size of the sibship (Blanchard, 2012; Khovanova, 2020). Hence, it remains unclear whether or not both processes contribute to explaining male homosexuality and, if so, which of them dominates. Following a novel method to disentangle the FBOE and FFE proposed by Khovanova (2020), Blanchard and colleagues (2020b) re-analyzed 14 samples from 10 previous studies (n=5,390). Their results confirmed the presence of the FBOE, but yielded no evidence in support of the FFE. Nevertheless, this method entailed restricting their data to one-son and two-son families, triggering concerns about data losses and external validity (Blanchard et al., 2020b).² In addition, recent work building on Khovanova's (2020) method found homosexual men to be more likely to have both older brothers and older sisters (Blanchard et al., 2020a; Blanchard & Lippa, 2020). These findings suggest that male homosexuality can be related to individuals' birth order, irrespective of the sex of their older siblings. If conclusively proven, this would complicate the correlation structure further, casting doubts over the magnitude and internal validity of the FBOE estimates presented in previous studies.

Third, the external validity of existing studies is often constrained by their reliance on small and highly selected samples (Zietsch, 2018). In a recent meta-analysis by Blanchard (2018a), the number of participants in studies documenting the FBOE ranged from 121 to 4,606, and the subsamples of non-heterosexual participants ranged from 42 to 905. Furthermore, these studies largely used samples from very selective populations, including sex offenders (Blanchard & Bogaert, 1998), pedophiles (Blanchard et al., 2000; Blanchard et al., 2006; Bogaert et al., 1997), gender-dysphoric (Blanchard et al., 1996; Schagen et al., 2012) and transgender (VanderLaan & Vasey, 2011; VanderLaan et al., 2017; Vasey & VanderLaan, 2007) individuals, and individuals receiving treatments for sexually transmitted diseases (King

² Khovanova's (2020) method for separating the FBOE from the FFE entails the calculation of three parameters: (i) p_{11} , the probability that the only boy in a one-son family is homosexual; (ii) p_{12} , the probability that the first son in a two-son family is homosexual; and (iii) p_{22} , the probability that the second son in a two-son family is homosexual. The FBOE occurs when $p_{22}>p_{12}$, while the FFE occurs when $p_{12}>p_{11}$. The existence of both the FBOE and the FFE is confirmed if $p_{22}>p_{12}>p_{11}$.

et al., 2005).³ Studies of the FFE are likewise constrained by their samples, which were primarily obtained through convenience, network or snowball sampling (see e.g., Camperio-Ciani et al., 2004; Gomez-Jimenez et al., 2020b; Vasey & VanderLaan, 2007).⁴

The concerns regarding the external validity of these studies are reinforced by the findings of a handful of population-level studies (i.e., studies analyzing data representative of the broader population) investigating the same associations. Population-level studies based on large probability samples or population register data have two main advantages over these smaller scale studies based on convenience samples. The first advantage is that they are less vulnerable to sample-selection bias, yielding results that can be confidently extrapolated from the analytic sample to the overall population of interest. The second advantage is that population register data typically encompass a much larger number of cases than other datasets, which provides the statistical power required to detect statistical patterns that smaller studies are unable to capture. Our literature review yielded no population-level studies of the FFE and only a small number of population-level studies of the FBOE, most of which failed to find evidence consistent with the FBOE (Zietsch, 2018). This includes the largest study to date based on Danish register data (n=2,000,355), which did not find a significant association between the number of older brothers and the probability of entering a same-sex union (Frisch & Hviid, 2006).⁵ The contrast between significant findings of studies using convenience

³ In fact, estimates of the FBOE in Blanchard's (2018a) meta-analysis showed substantial variability, with 75% of such variability being driven by differences in the samples rather than by sampling error (Blanchard, 2018a). This indicates that sample-selection bias in these studies is more than likely, echoing concerns by Zietsch (2018) about the external validity of this pool of studies.

⁴ For example, Camperio-Ciani et al. (2004) recruited 98 homosexual men from three homosexual community groups and discotheques, while Gomez-Jimenez et al. (2020b) recruited 115 transgender and 112 cisgender androphilic males through referrals among the Mexican *muxe* community.

⁵ This study was nevertheless critiqued by Blanchard (2007) and Blanchard and VanderLaan (2015) on three grounds: its focus on homosexual marriages rather than self-identification as homosexual, measurement error in

samples and insignificant findings of studies using population-level data calls for further investigation. It is our conviction that additional population-level studies are needed to ascertain whether the FBOE and FFE can be generalized to wider populations.

In this study, we solve the three issues characterizing the literature. In doing so, we provide novel and theoretically meaningful findings that can inform the development and refinement of explanations for male and female sexual orientation. To accomplish this, we leverage unique population-level administrative data from the Netherlands. Further, we devise and apply a novel estimation method that enables us to isolate the independent influences of siblings' sex, birth order, and sibship size on male and female homosexuality, and test the FBOE and FFE in a manner that is fully consistent with their theoretical underpinnings. The Netherlands is a particularly significant case study for two reasons. First, non-heterosexual individuals in the Netherlands face comparatively low levels of stigma, given the country's long history of inclusion policies (Government of the Netherlands, 2018) and high levels of public support for same-sex relationships (Kuyper & Vanwesenbeeck, 2009). This means that fewer gay and lesbian people will remain 'in the closet' and hence unidentified in the data (Pachankis & Branstrom, 2019). Second, the Netherlands features an internationally distinct population-register system containing rich, longitudinal information on individuals' marital and family histories available for research purposes (Kabátek & Perales, 2021).

Data

Our analytical dataset was extracted from linked population registers maintained by the Dutch national statistics agency, Statistics Netherlands. The data access and release protocols are detailed in Section S1 of the Supplementary Online Appendix. Our analyses use municipal

the identification of siblings, and suboptimal modelling choices. While our study also focuses on homosexual marriages, we are able to overcome the other two issues through the use of maternal identifiers to identify siblings and the introduction of a novel estimation method.

register data, which cover the near universe of marriages and registered partnerships that took place in the Netherlands in the last 70 years (up to December 2019). Apart from the unions themselves, the register also lists select demographics of the spouses, including their sex, birth year, and immigration background. This allows us to identify same-sex unions, and also all the individuals who have ever entered same-sex unions in the Netherlands.

The population of interest consists of men and women who were born in the Netherlands between 1940 and 1990, and who were deterministically linked to their mothers and maternal siblings.⁶ To make these links, we leverage unique maternal identifiers which are sourced primarily from peoples' birth-certificate information. We exclude individuals who were born outside of the Netherlands, because very few can be linked to their mothers and maternal siblings. We observe all maternal siblings who were alive and residing in the Netherlands after October 1994. Supplementary Figure S2 shows the maternal sibling sizes across the birth cohorts included in the study.

The primary advantage of our data over those used in previous studies is the sheer number of individuals: 9,073,496 (4,634,327 men and 4,439,169 women). Of these, 60,076 (26,542 men and 33,534 women) were observed to enter a formal same-sex union, either through a marriage or a registered partnership.⁷ In comparison, the combined number of homosexual men across all 36 FBOE studies included in Blanchard's recent meta-analyses was

⁶ The birth year cut-offs were chosen based on a visual inspection of the distribution of birth years among individuals who entered a same-sex union (see Figure S1). The results are not meaningfully sensitive to the choice of cut-off years. As a robustness check, we also estimated a model using paternal siblings, yielding comparable results.

⁷ The introduction of registered partnerships for same-sex couples in the Netherlands took place in January 1998, and it was followed by the legalization of same-sex marriage in April 2001. We observe 18,155 individuals who entered same-sex partnerships and 41,921 who entered same-sex marriages. For 51,494 individuals, a same-sex union was the first formally recognized union, whereas 8,582 individuals entered the same-sex union after the dissolution of a previous different-sex union.

approximately 10,000 (Blanchard, 2018a, 2018b). The number of individuals in same-sex unions in our data is also 18 times larger than the corresponding number in Frisch and Hviid's (2006) study using Danish register data (n=3,463).

As others before us—in both this field (e.g., Frisch & Hviid, 2006) and the general literature on same-sex relations (Saxby et al., 2020)—we approximate homosexuality through an indicator of same-sex-union formation.⁸ While individuals forming these unions may be a particular subsample of non-heterosexual individuals (OECD, 2019), this would only distort the associations of interest in highly specific and—in our view—rather unlikely circumstances. For example, artificially observing an FBOE due to selection into formal same-sex partnerships would require strong correlations—net of birth cohort and maternal age at birth—between individuals' birth order and/or the sexes of their older siblings and their propensity to enter same-sex unions. We can think of no social or biological processes that would yield such correlations.

Methods

The conventional model and its shortcomings

Since our empirical method differs from the standard methods used in the FBOE and FFE literatures, we begin this section by outlining conventional approaches to measure these phenomena and discussing their shortcomings. Methodologically, the FBOE literature relies primarily on a logistic model in which the focal explanatory variables are the number of older

⁸ A cautionary note is due here. While we use same-sex marriage as a proxy for homosexuality in the manner implied in the FBOE and FFE literatures (i.e., experiencing same-sex attractions), we do not assume that all individuals in same-sex unions self-identify as 'homosexual' (or 'gay/lesbian'). Some of these individuals may instead identify as 'bisexual', for example. Nevertheless, we expect the proportion to be quite low, as an overwhelming majority of partnered bisexual people are in different-sex rather than same-sex relations (Pew Research Center, 2019). This approach is also consistent with previous literature on the FBOE and FFE, which has tended to use 'homosexuality' as an umbrella term encompassing both homosexual and bisexual people (see e.g., Blanchard et al., 2006).

brothers, number of older sisters, number of younger brothers, and number of younger sisters, and the outcome variable of interest is a dichotomous indicator of male homosexuality (see e.g., Blanchard & Bogaert, 1996; King et al., 2005). Of these variables, only the number of older brothers typically proves to have a significant influence on the odds of male homosexuality (Blanchard, 2018a). This finding, which has since been termed the FBOE, is taken as evidence that it is the *sex* of older siblings that influences male homosexuality (Bailey et al., 2016; Blanchard, 2018a).

However, a significant problem with this interpretation is that the regression coefficient corresponding to the number of older brothers captures not only the influence of siblings' sex, but also the influence of other sibship characteristics. Formally, the coefficient quantifies the change in the odds of homosexuality associated with adding one older brother to an existing sibship. In this hypothetical scenario, three sibship characteristics are being simultaneously modified: there is an increase in the number of older brothers, an increase in the size of the sibship, and also an increase in the number of older siblings, irrespective of their sex. This means that the influences of these three separate factors—all of which may be potentially affecting homosexuality—are conflated into a single regression coefficient. As a result, the conventional FBOE coefficient may prove statistically significant due to the FFE or due to a birth-order effect that is unrelated to the sex of older siblings. Indeed, it could even be the case that—out of the three interlinked sibship characteristics—the sex of older siblings is the characteristic that is least relevant for the expression of homosexuality.

To determine the actual influence of the sex of older siblings on the propensity for homosexuality, the model needs to adequately account for the confounding influences of birth order and sibship size. Rather than asking what would happen in a hypothetical scenario in which an older brother is added to an existing sibship, it is better to ask what would happen in a hypothetical scenario in which an older sister is replaced by an older brother within an existing sibship. This is a more appropriate course of action, as the latter scenario involves changing the sex of an older sibling while keeping both the sibship size and birth order fixed.

Similar arguments apply to the empirical approaches conventionally used to evaluate the FFE (see e.g., Camperio Ciani et al., 2004; Gomez et al., 2020b). Comparing the sibship sizes of homosexual and heterosexual individuals does not yield a valid test of the FFE, because imbalances between the two groups can be attributed either to the FFE or to the FBOE. Testing whether sibship size wields an independent influence on homosexuality requires accounting for the confounding influences of birth order and older siblings' sex. This corresponds to the scenario in which the sibship size increases by one, while both the birth order and older siblings' sex are kept fixed. Thus, the appropriate question to ask is what would happen if a *younger* sibling is added to an existing sibship.

A novel approach to test the FBOE and FFE

y=1941

Our novel empirical specification addresses these issues by incorporating a more suitable parameterization of the regression model, which allows us to isolate the independent influences of siblings' sex, birth order, and sibship size. Specifically, our approach relies on a binary logistic regression model of the following form:

$$P[Y_{i} = 1 | \mathbf{x}_{i}, \boldsymbol{\beta}] = \frac{1}{1 + \exp(-\mathbf{x}_{i}'\boldsymbol{\beta})}$$
(1)
$$\mathbf{x}_{i}'\boldsymbol{\beta} = \beta_{0} + \beta_{1}N(sib.)_{i} + \beta_{2}N(older \, sib.)_{i} + \beta_{3}N(older \, br.)_{i} + \beta_{4}N(younger \, br.)_{i}$$
$$+ \sum_{i=1}^{1990} \beta_{5v}\mathbf{1}(birth \, year = y)_{i} + \sum_{i=1}^{45} \beta_{6i}\mathbf{1}(age \, at \, birth = t)_{i}$$

Here, Y is a dichotomous outcome variable denoting whether or not individual i ever entered a formal same-sex union, and the focal explanatory variables are measures of the numbers of siblings, older siblings, older brothers, and younger brothers, respectively. Following previous studies (see e.g., Blanchard & Bogaert, 1996; Bogaert, 2006; Frisch &

t=16

Hviid, 2006), we also control for birth-cohort and maternal-age-at-birth fixed effects. These variables enter the model in a robust and fully flexible manner, as a set of 50 dummy variables for specific birth years (birth cohort) and a set of 30 dummy variables for specific years of age (maternal age at birth).⁹

This model specification derives from the conventional FBOE model and uses exactly the same information. In other words, both the focal explanatory variables and the coefficients presented in Equation 1 can be reconstituted from the focal variables and coefficients corresponding to the conventional specification of the FBOE model. The two models also yield exactly the same log-likelihood. The key advantage of our specification is that we can leverage the *ceteris paribus* condition to perform more theoretically valid tests of the FBOE and the FFE.

The *ceteris paribus* condition relates to the interpretation of regression coefficients. It dictates that a coefficient in a multivariable model captures the change in the outcome variable associated with increasing the corresponding explanatory variable by one unit, *while keeping the values of the other variables fixed*. Accordingly, the coefficient β_1 in our model captures the excess probability of entering a same-sex union associated with increasing the number of siblings by one while keeping the numbers of older siblings, older brothers, and younger brothers fixed. In other words, it corresponds to a hypothetical scenario in which one younger sister is added to an existing sibship. The coefficient β_2 captures the influence of birth order

⁹ Birth-cohort fixed effects are crucial control variables in our model. This is because they capture the consequences of progressive fecundity decline (as documented in Figure S2) and any other dynamic social processes that have changed family structures over historical time. Given that the incidence of homosexuality increases over time while the average sibship size falls, failure to account for people's birth cohorts would result in a spurious negative correlation between the two variables, thus invalidating any empirical test of the FFE. Besides using birth-cohort fixed effects, we can also account for this spurious correlation by matching the homosexual and heterosexual individuals on their birth years. We do this as a sensitivity check in the Online Appendix.

within an existing sibship because the number of older siblings increases while the sibship size is kept fixed. Since the number of younger and older brothers are also fixed, it corresponds to a scenario in which an individual moves one place down the birth order, having one additional older sister, and one fewer younger sister. Following the same logic, the coefficient β_3 captures the excess probability of entering a same-sex union associated with replacing one older sister by one older brother. Finally, β_4 captures the excess probability of same-sex union entry associated with replacing one younger sister by one younger brother. An overview of the model coefficients, their definitions and interpretations is presented in Table 1.¹⁰

[TABLE 1 HERE]

Expected signs of the focal regression coefficients

The last column of Table 1 lists the expected signs of the four focal regression coefficients, based on the theoretical underpinnings of the FBOE and FFE. According to the FFE theory, the coefficient β_1 should be positive for both men and women. By adding a younger sister to the sibship, the model captures the independent influence of sibship size net of the confounding influences of birth order and older siblings' sex. The sex of younger siblings is irrelevant to the theory, which means that this coefficient can be effectively used as a test of the FFE.¹¹ The coefficient β_2 is expected to be zero, because neither the FBOE nor the FFE

¹⁰ The interpretation of the logistic-regression coefficients as measures of excess probabilities of same-sex union entry is only approximative. However, as explained in the results section, this approximation poses little risk in our application.

¹¹ A more powerful test of the FFE can be performed by averaging the excess probabilities associated with adding one younger sister and one younger brother to an existing sibship $\left(\frac{\left[\beta_1+(\beta_1+\beta_4)\right]}{2}\right)$, and testing this composite estimate against zero. Of note, averaging does not affect the statistical power of this test. An alternative approach would be to estimate a model specification that does not explicitly control for the number of younger brothers. In such a model, the coefficient β_1 would represent the influence of adding a younger *sibling* to an existing sibship, irrespective of their sex. We decided against using this model as our baseline specification because we wanted to assess whether or not the sex of younger siblings also influences the odds of same-sex union entry.

theory predicts that having one additional older sister and one fewer younger sister should affect people's propensity for homosexuality. However, we note that this coefficient represents the sororal birth order effect (SBOE), as defined by Blanchard et al. (2020a), and Blanchard & Lippa (2020). Their findings of a positive SBOE among men suggest that we might also uncover a positive coefficient estimate in our data. The coefficient β_3 is expected to be positive for men and zero for women. This is because it captures the independent influence of having an older brother (as opposed to an older sister), and the FBOE theory postulates that the sex of older siblings should affect male homosexuality only. The coefficient β_4 is expected to be zero, as neither theory predicts the sex of younger siblings to affect the propensity for homosexuality.

In addition to allowing us to evaluate the relative importance of sibship size, birth order, and siblings' sex for the expression of male and female homosexuality, another key advantage of our empirical approach is that it does not entail any data losses. Unlike other recently proposed methods to disentangle the FBOE and FFE (Blanchard et al., 2020b; Khovanova, 2020), our method accounts for all sibship configurations and allows for the inclusion of sisters in the analyses, thereby testing for the FFE and FBOE in a manner that is fully consistent with its theoretical formulation (Blanchard et al., 2020b). Together with the favorable properties of our population-level data, this approach allows us to produce internally and externally valid tests of both the FBOE and FFE and to do so with an unprecedented degree of precision.

Results

Descriptive analyses

We begin with a descriptive exercise in which we compare average sibship characteristics of individuals who did not enter a formal same-sex union (Column 1 in Table 2) and individuals who did (Column 2). On average, individuals who did not enter a same-sex union have 2.36 siblings. This number is split evenly between younger (μ =1.19) and older (μ =1.17) siblings. The average sibling sex ratio—that is, the number of brothers over the number of sisters—is 1.04 for both younger and older siblings.¹² In contrast, individuals who entered a same-sex union have fewer siblings (μ =2.14) and a greater number of older (μ =1.23) than younger (μ =0.91) siblings. Further, the sex ratio of their older siblings is skewed towards brothers (μ =1.18). All of these differences are statistically significant (Column 3).¹³

In Columns 4 and 5, we split the homosexual group further by sex to show that these patterns manifest among both men and women. Altogether, the skewness of the sex ratio among the older siblings of homosexual individuals is compatible with the FBOE, while their smaller sibship sizes are not consistent with the FFE. Nevertheless, it is worth noting that the smaller sibship sizes of homosexual individuals might be attributable to birth-cohort differences between the two groups. This means that we should not rely on unadjusted descriptive statistics to evaluate the FFE. The existence of an FFE is best inferred from the multivariable models presented below.

[TABLE 2 HERE]

Figures 1 and 2 visualize the key patterns in the data. Figure 1 shows the population shares of individuals who entered a same-sex union conditional on their sex, number of siblings, and birth order. Each of the conditioning variables visibly influences the population shares: women are more likely to enter a same-sex union than men; younger siblings are more likely to enter a same-sex union than older siblings; and individuals with more siblings are less likely to enter a same-sex union than individuals with fewer siblings. These patterns are

¹² This slight imbalance is consistent with the human sex ratio (Chahnazarian, 1988).

¹³ The need for measures of statistical uncertainty in population-level analyses—and their interpretation—has been the subject of debate. Detractors argue that these measures are intended for analyses of samples from an underlying population and uncertainty becomes irrelevant when sampling-frame coverage reaches 100% (Desbiens, 2007). Advocates argue that population-level confidence intervals and *p*-values express the chances of the observed differences manifesting in a super-population, which may consist of the same population observed under different states of the world, or the population of countries with comparable characteristics (Gelman, 2005; Graubard & Korn, 2002). Here, we follow the second approach.

apparent for both men and women, and they are measured with a high level of statistical precision. The dependence on the birth order is particularly prominent in large sibships. For example, 0.73% of men who are the youngest of five siblings entered a same sex union, compared to just 0.35% of men who are the eldest of five siblings.

[FIGURES 1 & 2 HERE]

Figure 2 shows the population shares of individuals who entered a same-sex union conditional on their sex, number of older siblings, and number of older brothers. Again, the plot shows a clear dependence: individuals whose older siblings are predominantly male are more likely to enter a same-sex union than individuals whose older siblings are predominantly female. As before, this pattern is apparent for both men and women and it is measured with a high level of precision. The dependence is again most prominent in large sibships. For example, the share of men with four older brothers entering a same-sex union is 0.96%, more than twice the share among men with four older sisters (0.46%).¹⁴

Regression modelling

Altogether, the statistics presented so far suggest that the number of siblings, birth order, and sex of older siblings wield considerable influence over the odds of entering a samesex union. To disentangle and formally quantify the magnitude of these influences, we turn to logistic regression. In Table 3, we list the estimates of coefficients and odds ratios (OR) corresponding to our principal regression models.¹⁵

¹⁴ The population shares of individuals who entered a same-sex union conditional on their sex, number of *younger* siblings, and number of *younger* brothers are shown in Figure S3. Unlike Figure 2, Figure S3 does not show any discernible pattern with regard to siblings' sex.

¹⁵ Both the logistic-regression coefficients and the odds ratios approximate the same underlying concept: the relative increase in the probability of same-sex union entry associated with a one-unit increase in the variable of interest, all else being equal. To assess which measure is subject to a lesser approximation error, we produced direct estimates of excess probabilities of same-sex union entry (population-level average marginal effects), and

[TABLE 3 HERE]

Results from a model using the full dataset (Table 3, Column 1) indicate that, all else being equal, adding one younger sister to an existing sibship is associated with a 13.8% decrease in the probability of entering a same-sex union (OR = 0.87, p < 0.001); moving one place down the birth order while keeping the number of younger and older brothers fixed is associated with an 7.9% increase in the probability of entering a same-sex union (OR = 1.08, p < 0.001); and replacing one older sister by one older brother is associated with a 12.5% increase in the probability of entering a same-sex union (OR = 1.13, p < 0.001). Replacing one younger sister by one younger brother is associated with a 1.2% increase in the probability of entering a same-sex union (OR = 1.01), but this estimate is not statistically significant (p > 0.1).

In Columns 2 and 3 of Table 3 we present regression coefficients from models estimated separately for men and women. Both models yield estimates that are consistent with the baseline specification. Only one of the coefficients is significantly different between men and women (Column 4). This is the coefficient corresponding to the number of older siblings, indicating that men are influenced more strongly by their birth order than women.

How do these results align with the theoretical expectations formulated above and presented in Table 1? In both the baseline and the sex-specific models, the coefficient estimates of β_1 are negative and statistically significant.¹⁶ This finding is incompatible with the theoretical underpinnings of the FFE, which would predict these coefficients to be positive.

compared them with the excess probabilities corresponding to the two approximate measures. Table S1 shows that the logistic-regression coefficients approximate population-level average marginal effects better than the odds ratios, with the values of excess probabilities being virtually identical at the presented level of numerical precision. That is why we base our discussion primarily on the regression coefficient estimates, and we include odds ratios mainly to facilitate the comparisons with earlier FBOE and FFE studies.

¹⁶ The same is true for the composite coefficient estimate averaging the influences of having one younger sister and one younger brother $\left(\frac{[\beta_1+(\beta_1+\beta_4)]}{2} = -0.132, p < 0.001\right)$.

The coefficient estimates of β_2 are positive and statistically significant, thereby confirming the existence of a SBOE among both men and women. The coefficient estimates of β_3 are also positive and statistically significant, thus confirming that having an older brother (as opposed to an older sister) increases the expression of homosexuality among both men and women. While the last result is consistent with the presence of an FBOE among men, the existence of a similarly sized association among women goes counter to its current theoretical underpinnings. The coefficient estimates of β_4 are positive but not statistically significant, which is consistent with the expectation that the sex of younger siblings should not affect the odds of homosexuality.

To illustrate the combined effects of birth order and sibling sex, we use the model to predict and plot the probabilities of entering a same-sex union for individuals in all relevant permutations of two-person sibships (Figure 3). In this example, we focus on two-person sibships because they are the most common sibship type (35% of individuals) and because the corresponding number of permutations is fairly contained (n=8). Among men, the lowest predicted probability (PP) of entering a same-sex union is for those whose only sibling is a younger sister (PP = 0.55%), followed by those with a younger brother (PP = 0.56%). The ordering is the same among women: those with a younger sister (PP = 0.61%) and, finally, those with an older brother (PP = 0.68%). The ordering is the same among women: those with a younger sister (PP = 0.757%), followed by those with an older sister (PP = 0.81%), and those with an older brother (PP = 0.92%). The difference between the lowest and highest predicted probabilities is 0.12 percentage points (23.5%) for men, and 0.16 percentage points (21.2%) for women.

As before, these influences compound in larger sibships, leading to larger disparities. For example, in three-person sibships (see Figure S4 in the Supplementary Online Appendix), the difference between the lowest predicted probability—faced by eldest siblings whose younger siblings are sisters—and the highest probability—faced by youngest siblings whose older siblings are brothers—is 0.26 percentage points (or 52.6%) for men, and 0.30 percentage points (or 47%) for women. In four-person sibships, the analogous differences are 0.38 percentage points (or 88.6%) for men and 0.45 percentage points (or 78.3%) for women.

[FIGURE 3 HERE]

Alternative specifications and robustness checks

We fitted a range of additional specifications to (i) compare our results to those of earlier studies, and (ii) assess the robustness of our findings to alternative analytic decisions. First, we estimated the conventional model specification used in earlier studies of the FBOE (see Table S2, Column 1). The estimate of the key coefficient of interest (corresponding to the number of older brothers), equals 0.066 (OR = 1.07, p < 0.001). In other words, adding one older brother to an existing sibship is associated with a 6.6% increase in the probability of entering a same-sex union. Sex-specific versions of the same model (Table S2, Columns 2 and 3) yielded estimates of 0.079 (OR = 1.08, p < 0.001) for men, and 0.054 (OR = 1.06, p < 0.001) for women. Similar to our baseline specification, the conventional model yields estimates that are indicative of an FBOE among both men and women. The estimate for women is however significantly lower than the estimate for men (p < 0.001), which contrasts with the statistically indistinguishable estimates of β_3 for men and women in our baseline specification.

Second, we replicated the approach recently proposed by Khovanova (2020) to disentangle the FBOE from the FFE in our population-level dataset. This model demonstrated that second-born sons in two-son families had a higher relative risk (RR) to enter same-sex unions than first-born sons in two-son families (RR = 1.28, p < 0.001), which is compatible with the FBOE. In contrast, first-born sons in two-son families (RR = 0.90, p < 0.001), which is incompatible with the FFE. For details, see Section S2 in the Supplementary Online Appendix.

Third, we conducted a battery of additional robustness checks involving variations of our baseline model with alternative selection criteria and outcome definitions (see Section S3 in the Supplementary Online Appendix). These included specifications estimated in earlier large-scale studies (Frisch & Hviid, 2006) and specifications proposed in response to those studies (Blanchard & VanderLaan, 2015). Reassuringly, each of these supplementary analyses yielded results that were consistent with those from our baseline model.

Discussion

By exploiting population-level administrative data from the Netherlands, this study has generated distinctively robust insights into the influence of sibling characteristics on the propensity for individuals to enter a formally recognized same-sex union. Our analyses yielded strong evidence in support of the existence of an FBOE in our data: the probability of entering a same-sex marriage or registered partnership was significantly and substantially higher among individuals whose older siblings were brothers, as opposed to sisters. For example, the probability for individuals with one older brother was 12.5% higher than that for individuals with one older sister. This pattern of results was remarkably robust to a range of analytical decisions, and consistent with the findings of previous FBOE studies relying on smaller and less representative datasets (Blanchard et al., 1996, 2000; Blanchard & Bogaert, 1998; Bogaert et al., 1997; Schagen et al., 2012; VanderLaan et al., 2017; VanderLaan & Vasey, 2011; Vasey & VanderLaan, 2007). The fact that we find evidence of this association in a high-quality, population-level dataset indicates that the results reported by earlier studies are unlikely to have emerged artificially due to selection bias.

On the other hand, as others before us (Blanchard et al., 2020b), we found no empirical support of an FFE on homosexuality. Inconsistent with the FFE, our results indicated that individuals born into larger sibships face, on average, lower probabilities of same-sex union entry than individuals born into smaller sibships. Indeed, having an additional younger sibling

was associated with a 13-14% decrease in the probability of entering a same-sex union (12.6% for younger brothers and 13.8% for younger sisters).

Our analyses further demonstrated that individuals' birth order matters, regardless of siblings' sex. Our estimate of the SBOE implies that having an older sister (as opposed to a younger sister) is associated with a 9.8% increase in the probability of same-sex union entry among men, and a 6.2% increase among women. Having an older brother (as opposed to a younger brother) is associated with larger increases (19.7% for men and 18.6% for women), which is attributable to the additional influence of sibling sex.¹⁷ These results are consistent with earlier findings reported by Frisch & Hviid (2006), who showed that youngest siblings were more likely to enter formally recognized same-sex unions than older siblings in Danish register data. The results also align with recent findings of a positive SBOE among men, which has been attributed to the presence of male antibodies owing to previous miscarriages of male fetuses (Blanchard et al., 2020a; Blanchard & Lippa, 2020). We expand on these findings by demonstrating that the influence of birth order is not confined to selective samples and/or subsets of siblings, and verify that it is not attributable to confounding by birth cohort or maternal age at birth.

One important distinction between our findings and those of previous FBOE studies is that we found the sex of older siblings to be associated with homosexuality not only in men, but also women. The coefficient estimate measuring the strength of this association for women (β =0.133) was comparable in magnitude to the estimate for men (β =0.115), and both were highly statistically significant. While the pattern among men is consistent with biological

¹⁷ The corresponding estimates can be obtained by summing together the coefficient estimates of β_2 and β_3 and subtracting the coefficient estimate of β_4 . For men, this is 0.098 + 0.115 - 0.016 = 0.197.

explanations of the FBOE highlighting the role of maternal immune responses against H-Y antigens, the pattern among women is not (Bogaert et al., 2018).

Our results thus bear substantial implications for contemporary theories aimed at explaining biological influences on the expression of human homosexuality (Bailey et al., 2016). This includes the Maternal Immune Hypothesis, which in its current formulation, applies only to men (Bogaert et al., 2018). Our finding of an FBOE for women suggests that this hypothesis may need to be reconsidered or refined to incorporate women. Some authors have pointed to biological mechanisms that may extend the logic of the Maternal Immune Hypothesis to accommodate female homosexuality (LeVay, 2016; Nielsen et al., 2007). For example, LeVay (2016) noted that older brothers reduce the birthweight of their later-born male and female siblings, and that this lower birthweight can be linked to the same maternal immune response implicated in the Maternal Immune Hypothesis (Nielsen et al., 2007). In particular, the maternal immune response that initially targets only male-specific proteins may lose specificity over time and spread to closely related female proteins, or to non-sex-specific proteins, through a process known as 'determinant spreading' (Nielsen et al., 2007; Nielsen, 2011). Admittedly, the administrative data at our disposal are not fit-for-purpose to test this or any other biological mechanisms, yet our results call for future research that addresses these processes with suitable data. More broadly, our findings serve as a cautionary note about theoretical explanations of the FBOE that overlook female homosexuality.

Another important distinction between our findings and those of other studies is that the coefficient estimate that we used to test the FBOE hypothesis is not directly comparable to the estimates reported in earlier research. Due to our novel model parameterization, our preferred coefficient estimate corresponds to a hypothetical scenario in which one older sister is *replaced* by one older brother. This estimate captures the independent influence of older siblings' sex on the propensity for homosexuality, which makes it particularly suitable for testing the FBOE and its theoretical underpinnings. Most of the earlier FBOE estimates correspond to a hypothetical scenario in which one older brother is *added* to an existing sibship (Blanchard & Bogaert, 1996; Bogaert, 2006; Kishida & Rahman, 2015; VanderLaan et al., 2017). The latter is in our view a suboptimal approach, because it conflates (i) the positive influence of having an older brother (instead of an older sister), (ii) the positive influence of moving one place down the birth order, and (iii) the negative influence of increasing the sibship size by one. Our supplementary analyses showed that the conventional approach yielded a coefficient estimate that is also consistent with the FBOE hypothesis. However, in terms of magnitude, the conventional estimate was half the size of our preferred estimate, which means that the independent influence of older siblings' sex on the expression homosexuality is much greater than what would the conventional FBOE estimate suggests.¹⁸ The fact that our preferred coefficient estimate is substantially and significantly larger than the conventional estimate may therefore prove valuable in explaining previous null results. Applying our novel regression parameterization to the samples used in studies that yielded insignificant estimates of the FBOE (e.g., Frisch & Hviid, 2006; Francis, 2008; Kishida & Rahman, 2015) may overturn these null findings.

Similarly, the failure of earlier studies to find evidence of an FBOE among women may also stem from the use of suboptimal modelling specifications. When we fitted sex-specific versions of the *conventional* model, we found that the FBOE coefficient estimate for men was approximately 50% greater than the estimate for women. Taken in isolation, this finding could be interpreted as evidence of lesser importance of older siblings' sex for the expression of

¹⁸ We note that the conventional FBOE estimate (0.066) can be fully reconstituted from our baseline coefficients (see Column 1 in Table 3). It combines the 12.5% increase in the probability of entering a same-sex union associated with having an older brother (instead of an older sister) with the 7.9% increase associated with moving one place down the birth order, and the 13.8% decrease associated with adding one sibling to the existing sibship: 0.125 + 0.079 - 0.138 = 0.066.

female homosexuality. However, our preferred model showed that this is an incorrect interpretation. The independent influence of older siblings' sex was actually comparable across men and women (if anything, it was marginally stronger for women), and the only sibship characteristic that wielded significantly greater influence on men's homosexuality was individuals' own birth order (captured by the coefficient β_2). Since the FBOE coefficient in the conventional model conflates the influence of birth order, siblings' sex, and sibship size, the stronger influence of birth order among men increases the magnitude of their FBOE estimate. Critically, this means that the conventional FBOE estimates for men are bound to be larger and more likely to prove statistically significant than the estimates for women, even though the sex of women's older siblings is just as important a predictor of homosexuality as the sex of men's older siblings. Again, applying our novel regression parameterization to the datasets used in earlier studies of the FBOE among women may yield statistically significant estimates.

Despite the strengths of the present study, an important limitation is that we could only identify homosexuality through entry into a same-sex registered partnership or a same-sex marriage. Because a small portion of these individuals may be bisexual rather than homosexual, the results represent conservative estimates of the effect of sibship characteristics on homosexuality—strictly defined. This expectation is based on work by Apostolou (2020), who found evidence of an FBOE among homosexual people, but not among bisexual or heterosexual people with same-sex attractions. More broadly, our results might not apply to homosexual individuals who are either single, or in a *de facto* relationship. We are also unable to assess whether the reported pattern of results emerges for other measures of homosexuality based on sexual identity, attraction, and behavior (Bearman & Bruckner, 2002; Currin et al., 2015). Future studies using high-quality data and different markers of homosexuality for both single and partnered individuals could thus expand on our findings. In terms of the FFE, it is important to note that our study considered only maternal siblings, in a similar manner as other

recent tests of the FFE hypothesis (see e.g., Blanchard, 2012; Blanchard et al., 2020b). However, other approaches to operationalizing the FFE underscore the potential importance of other female relatives, such as sisters, maternal aunts, and maternal grandmothers (Camperio-Ciani & Pellizari, 2012; Iemmola & Camperio-Ciani, 2009). We therefore cannot disregard the existence of an FFE that operates through those other channels, and this should be the focus of future studies.

Despite these shortcomings, our results tell a clear, consistent and reliable story: sibship characteristics are an important piece of the unresolved puzzle of human sexuality. The evidence gathered through this study aligns squarely with perspectives emphasizing that sexual orientation is an innate trait and a reflection of individuals' true selves, rather than the product of lifestyle choices (Bailey et al., 2016). The implications of our findings for public debate on policies aimed at improving the health, wellbeing and social standing of sexual minorities are far-reaching.

Disclosure statement. The authors declare no competing interests for this study.

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Tables and Figures

Table 1. An overview of the focal coefficients in our specification of the logistic regression model of sexual preference, with the outcome variable being a binary indicator of entering a same-sex union.

Model coefficient	Formal definition	Interpretation	Expected sign, men/women	
β_1 (no. of siblings)	Approximate predicted percent change in the probability of entering a same-sex union associated with increasing the number of siblings by one, holding the number of older siblings, older brothers, and younger brothers constant.	This coefficient corresponds to a situation in which one younger sister is added to an existing sibship.	+/+ (FFE)	
β_2 (no. of older siblings)	Approximate predicted percent change in the probability of entering a same-sex union associated with increasing the number of older siblings by one, holding the number of siblings, older brothers, and younger brothers constant.	This coefficient corresponds to a situation in which an individual moves one place down the birth order, having one additional older sister and one fewer younger sister (SBOE). ^a	0 ^b / 0	
β_3 (no. of older brothers)	Approximate predicted percent change in the probability of entering a same-sex union associated with increasing the number of older brothers by one, holding the number of siblings, older siblings, and younger brothers constant.	This coefficient corresponds to a situation in which one older sister is replaced by an older brother in an existing sibship.	+ / 0 (FBOE)	
β_4 (no. of younger brothers)	Approximate predicted percent change in the probability of entering a same-sex union associated with increasing the number of younger brothers by one, holding the number of siblings, older siblings, and older brothers constant.	This coefficient corresponds to a situation in which one younger sister is replaced by a younger brother in an existing sibship.	0 / 0	

^a The male counterpart to this association (having one additional older brother and one fewer younger brother) can be expressed as a composite coefficient ($\beta_2 + \beta_3 - \overline{\beta_4}$). This coefficient is intrinsically related to the FBOE-FF risk ratio proposed by Khovanova (2020) and used by Blanchard et al. (2020a), and Blanchard & Lippa (2020). ^b While the theories underlying the FFE and FBOE do not predict any association with sororal birth order, the findings presented in recent studies of Blanchard et al. (2020a), and Blanchard et al.

	(1)	(2)	(3)	(4)	(5)	(6)
Variables	Individuals who did not enter a same-sex union	Individuals who entered a same-sex union	Difference between (1) and (2)	Men who entered a same-sex union	Women who entered a same-sex union	Difference between (4) and (5)
Number of siblings	2.36	2.14	0.22***	2.25	2.05	0.20^{***}
	(1.96)	(1.76)	[0.11]	(1.87)	(1.66)	[0.11]
Number of older siblings	1.19	1.23	-0.04^{***}	1.32	1.16	0.16***
	(1.50)	(1.48)	[-0.03]	(1.57)	(1.40)	[0.10]
Number of younger siblings	1.17	0.91	0.26^{***}	0.94	0.88	0.06^{***}
	(1.41)	(1.15)	[0.19]	(1.19)	(1.11)	[0.04]
Sex ratio, older siblings	1.04	1.18	-0.14^{***}	1.17	1.19	-0.02^{\dagger}
	(1.94)	(2.18)	[-0.08]	(2.09)	(2.27)	[-0.01]
Sex ratio, younger siblings	1.04	1.05	-0.01	1.06	1.05	0.01
	(1.93)	(2.22)	[-0.01]	(2.21)	(2.24)	[0.01]
Number of individuals	9,013,420	60,076		26,542	33,534	

Table 2. Summary statistics for key variables used in the analyses

Notes: Statistics are extracted from linked population register data from the Netherlands. The sibling sex ratios measure the shares of male to female siblings. Columns 3 and 6 list differences between the means presented in Columns 1 and 2, and Columns 4 and 5. The statistical significance of the differences was tested using two-sided *t*-tests of the equality of means with unequal variances. Statistical significance: ***p < 0.001, **p < 0.05, *p < 0.10. Standard deviations in parentheses. Values of Cohen's d corresponding to the differences between the means are presented in square brackets.

		(1)	(2)	(3)	(4)
Variables	Coefficient interpretation	Full sample	Men	Women	Sex difference
Coefficients					
Number of siblings	This coefficient corresponds to a situation in which one younger sister is added to an existing sibship.	-0.138^{***} (0.006)	-0.134^{***} (0.009)	-0.140^{***} (0.008)	0.006 (0.012)
Number of older siblings	This coefficient corresponds to a situation in which an individual moves one place down the birth order, having one additional older sister, and one fewer younger sister.	0.079^{***} (0.008)	0.098 ^{***} (0.012)	0.062 ^{***} (0.012)	0.036 [*] (0.016)
Number of older brothers	This coefficient corresponds to a situation in which one older sister is replaced by an older brother in an existing sibship.	0.125 ^{***} (0.007)	0.115 ^{***} (0.011)	0.133 ^{***} (0.010)	-0.018 (0.015)
Number of younger brothers	This coefficient corresponds to a situation in which one younger sister is replaced by a younger brother in an existing sibship.	0.012 (0.009)	0.016 (0.013)	0.009 (0.012)	0.008 (0.017)
Odds ratios					
Number of siblings	This odds ratio corresponds to a situation in which one younger sister is added to an existing sibship.	0.871^{***} (0.005)	0.874^{***} (0.008)	0.869 ^{***} (0.007)	0.005 (0.010)
Number of older siblings	This odds ratio corresponds to a situation in which an individual moves one place down the birth order, having one additional older sister, and one fewer younger sister.	1.083 ^{***} (0.009)	1.103 ^{***} (0.013)	1.063 ^{***} (0.011)	0.040^{*} (0.017)
Number of older brothers	This odds ratio corresponds to a situation in which one older sister is replaced by an older brother in an existing sibship.	1.133 ^{***} (0.008)	1.122 ^{***} (0.012)	1.142 ^{***} (0.011)	-0.020 (0.017)
Number of younger brothers	This odds ratio corresponds to a situation in which one younger sister is replaced by a younger brother in an existing sibship.	1.012 (0.009)	1.016 (0.013)	1.008 (0.012)	0.008 (0.017)
Birth-cohort fixed effects		Yes	Yes	Yes	
Maternal-age-at-birth fixed effects		Yes	Yes	Yes	
Number of individuals		9,073,496	4,634,327	4,439,169	

Table 3. Coefficients from binary logistic regression models of same-sex union entry, baseline model estimates

Notes: The models use linked population register data from the Netherlands. Robust standard errors in parentheses. Columns 1 to 3 list coefficients from binary logistic regression models of entry into same-sex unions. Column 4 lists differences between the coefficients corresponding to the male and female populations; that is, Column 2 minus Column 3. To determine whether sex differences are statistically significant, we estimated a fully-interacted binary logistic regression model using two sets of controls: the principal set of controls, and the same set of controls interacted with the male indicator variable. The coefficients listed in Column 4 correspond to the set of interacted controls. Statistical significance: ***p < 0.001, **p < 0.01, *p < 0.05, †p < 0.10.

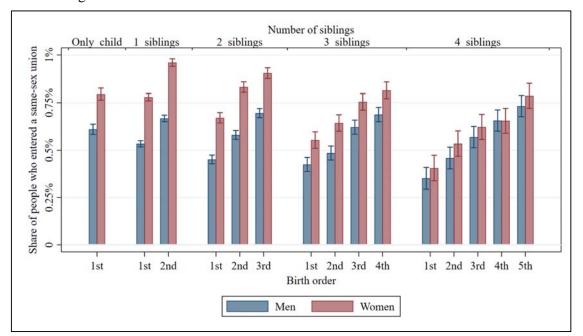


Figure 1. Population shares of individuals who entered a same-sex union, by sex, number of older siblings and birth order

Notes: Population shares are extracted from linked population register data from the Netherlands. Whiskers denote 95% confidence intervals.

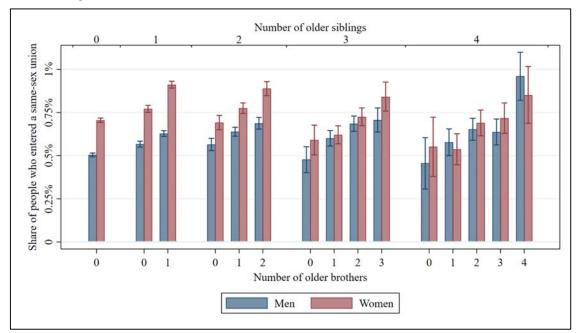


Figure 2. Population shares of individuals who entered a same-sex union, by sex, number of older siblings and number of older brothers

Notes: Population shares are extracted from linked population register data from the Netherlands. Whiskers denote 95% confidence intervals.



Figure 3. Predicted probabilities of entering a same-sex union for individuals in two-person sibships

Notes: Predicted probabilities from sex-specific logistic regression models of entry into samesex unions adjusted for birth-cohort and maternal-age-at-birth fixed effects (Table 3, Columns 2 and 3). The models use linked population register data from the Netherlands. Whiskers denote 95% robust confidence intervals.

Supplementary Online Appendix

Appendix S1. Accessing Dutch linked administrative data

The linked, administrative data used in this study are maintained by the Dutch national statistical office (Statistics Netherlands) and they can be accessed by authorized researchers through a remote-access environment. To ensure individual privacy, all retrieved statistics and model estimates must be vetted by Statistics Netherlands. The release protocols stipulate that a statistic (such as a mean or variance) can be published only if it is based on more than 10 individual records.

To gain access to these data, researchers submit proposals which outline the aims of their research projects. Each project must involve a researcher who is affiliated with a university of research institution within the Netherlands. Statistics Netherlands evaluates the project proposals on the basis of their feasibility. An ethics board is not involved in the evaluation process. Approved projects are issued a contract which stipulates access conditions and costs. The costs vary depending on the duration of the project, number of data modules used, and other services provided by Statistics Netherlands. Further inquiries regarding the data access should be addressed to microdata@cbs.nl.

Researchers who obtain access to these data will be able to replicate our findings. Authors can be contacted to obtain a list of all the data modules used in the empirical analyses, as well as copies of the statistical software syntax used to generate the results.

Appendix S2. Supplementary analysis using Khovanova's method

We conducted a supplementary analysis using the FBOE-FF-model proposed by Khovanova (2020). The model uses a subset of the full dataset consisting of men in one-son and two-son families. Following the original manuscript, the number of female siblings was left unrestricted, which resulted in an average sibship size of 2.36 siblings.

Using this selective sample, we estimated a logistic regression model of same-sex union entry, with the control variables being three dummy variables corresponding to the individual being (i) the first son in a one-son family, (ii) the first son in a two-son family, and (iii) the second son in a two-son family. The models also controlled for birth-cohort and maternal-age-at-birth fixed effects. Using the model estimates, we predicted the average probabilities of same-sex union entry for men in the three aforementioned categories. Table S3 presents these probabilities together with the corresponding risk ratios.

The predicted probability for first sons in one-son families (p_{11}) is 0.57%, the predicted probability for first sons in two-son families (p_{12}) is 0.51%, and the predicted probability for second sons in two-son families (p_{22}) is 0.66%. We note that the predicted probabilities p_{12} and p_{22} are significantly lower than the ones corresponding to two-child families presented in Figure 3. This is because the average sibship size in the FBOE-FF sample is larger than two, and the influence of the larger sibship size pulls the predicted probabilities downwards.

The risk ratio p_{12}/p_{11} is 0.901, and it is significantly different from one. This result is inconsistent with the FFE, which would predict the risk ratio to be larger than one. The risk ratio p_{22}/p_{12} is 1.281, and it is also significantly different from one. This result is consistent with the FBOE, showing that the second-born sons in two-son sibships are more likely to enter same-sex unions than first-born sons in two-son sibships.

In terms of magnitude, the risk ratio p_{12}/p_{11} implies a 9.9% decrease in the probability of entering a same-sex union associated with having an additional male sibling. This is consistent with our baseline model for men, which predicts a 11.8% decrease.¹⁹ Accordingly, we confirm that the FBOE-FF model yields consistent predictions of the FBOE. The risk ratio p_{22}/p_{12} implies that second-born sons face 28.1% higher probabilities of entering a same-sex union than first-born sons in two-son sibships. This estimate is significantly higher (p < 0.001)

¹⁹ This prediction corresponds to the combination of coefficients for the number of siblings (-0.134) and the number of younger brothers (0.016), reported in Column 2 in Table 3.

than the baseline estimate we use to evaluate the FBOE hypothesis (11.5%, see Column 2 in Table 3). This is because the FBOE-FF risk ratio combines the positive influence of an older brother with the positive influence of higher birth order irrespective of siblings' sex.

Qualitatively, the model reaches the same conclusions as our baseline specification, yielding results that are inconsistent with the FFE and consistent with the FBOE. However, the fact that the ratio combines two distinct influences poses a clear methodological issue: due to the positive influence of birth order regardless of siblings' sex, the model would predict the existence of an FBOE even if the sex of elder siblings did not matter. This means that the FBOE-FF model may not yield consistent predictions of the FBOE.

Appendix S3. Robustness checks

To verify the reliability of our baseline estimates and examine heterogeneity in the association between sibship characteristics and same-sex union entry, we estimated a battery of supplementary models. In this section, we discuss the specifications and key results from these additional models. The models use the full set of control variables that corresponds to our baseline model specification listed in Table 3. We discuss the specifications in the order in which they appear in Table S4.

- 1. Model 1 replicates the empirical design of Frisch and Hviid (2006), in that the outcome is a binary indicator equal to one if the *first* formally recognized union was a same-sex union, and zero otherwise. The corresponding model estimates are not meaningfully different from the baseline specification.
- 2. Model 2 restricts the analytic sample to individuals who entered at least one formally recognized union (same-sex or different-sex). This is to avoid making implicit assumptions regarding the sexual orientation of individuals who are single or living out of wedlock. The coefficients are largely similar to the baseline specification (the coefficient for the number of siblings is slightly larger in magnitude).
- 3. Model 3 expands on Model 2 by restricting the sample to individuals who entered a formally recognized union (same-sex or different-sex) after the date of legalization of same-sex registered partnerships in the Netherlands (March 1998). This is a response to a commentary by Blanchard and VanderLaan (2015), who argued that the results of Frisch and Hviid (2006) could be distorted by the fact that the same-sex unions were compared to different-sex unions that were initiated prior to the legalization of same-sex unions. The coefficients are similar to those in our baseline specification (the coefficients for the number of siblings and the number of older siblings are slightly smaller in magnitude).
- 4. Model 4 restricts the sample to individuals who entered a formally recognized union (same-sex or different-sex) after the date of legalization of same-sex marriage in the Netherlands (April 2001). The estimates are similar to those in our baseline specification, although the coefficients for the number of siblings and the number of older siblings are slightly smaller in magnitude.
- 5. Model 5 restricts the analytic sample to individuals who had four or fewer maternal siblings. This is to ensure that our estimates are not distorted by idiosyncrasies of very

large sibships. The corresponding model estimates are not meaningfully different from the baseline specification.

- 6. Model 6 restricts the analytic sample by randomly selecting one individual per maternal sibship. This is to evaluate whether our estimates might be affected by idiosyncratic features of families with multiple homosexual individuals. The corresponding model estimates are not meaningfully different from the baseline specification.
- 7. Model 7 restricts the analytic sample to all individuals who entered a formally recognized same-sex union, and a matched sample of individuals who entered a formally recognized different-sex union. The two samples are matched on birth years and the year of wedding/registration. The coefficients are similar to those in our baseline specification, although the coefficients for the number of siblings and the number of older siblings are slightly smaller in magnitude.
- 8. Model 8 uses the full analytic sample and controls for the characteristics of paternal siblings (instead of maternal siblings). The corresponding model estimates are not meaningfully different from those in our baseline specification.
- Model 9 evaluates whether sibship characteristics also influence entry into different-sex 9. unions. The outcome is a binary indicator equal to one if an individual entered a formally recognized different-sex union, and zero otherwise. The estimates reveal that different-sex union entry is also influenced by sibship characteristics. The probability of entering a different-sex union increases with the number of siblings in the sibship ($\hat{\beta}=0.071$), increases with birth order ($\hat{\beta}=0.034$), decreases with the number of older brothers $(\hat{\beta}=-0.013)$, and increases with the number of younger brothers $(\hat{\beta}=0.007)$. All of these associations are statistically significant. The association with the number of siblings has the opposite sign than the association corresponding to the model of same-sex union entry $(\hat{\beta}=-0.138)$. The negative association with sibship size therefore appears to be unique to same-sex unions. The association with the number of older siblings has a positive sign $(\hat{\beta}=0.034)$, however it is considerably weaker than the one corresponding to the model of same-sex-union entry ($\hat{\beta}$ =0.080). This implies that individuals with higher birth order are more likely to enter both same-sex and different-sex unions, however this dependence is twice as strong for same-sex union entry. The association with the number of older brothers has a negative sign and its magnitude is almost ten times smaller than the

magnitude of the same-sex association ($\hat{\beta}=0.125$). This result is, again, consistent with the FBOE: if the presence of older brothers increases the likelihood of homosexuality, we should observe fewer different-sex marriages among individuals with a greater number of older brothers than older sisters. Finally, the association with the number of younger brothers has a positive sign, and it is smaller in magnitude than the insignificant association in the model for same-sex-union entry ($\hat{\beta}=0.012$). This result cannot be explained by the biological theories outlined in our manuscript, but might be attributable to different socialization mechanisms among individuals with younger brothers and younger sisters.

- 10. Model 10 restricts the outcome variable to entry into a same-sex registered partnership. The corresponding model estimates are not meaningfully different from the baseline specification.
- 11. Model 11 restricts the outcome variable to entry into a same-sex marriage. The corresponding model estimates are not meaningfully different from the baseline specification.
- 12. Model 12 expands the analytic sample by also including first-generation immigrants who could be linked to their maternal siblings. The coefficients are largely similar to the baseline specification (the coefficient for the number of siblings is slightly larger in magnitude). The qualitative results of our analyses remain unaffected.
- 13. Model 13 is an extension of Model 3 that uses an alternative analytic sample of individuals born in the Netherlands between 1980 and 1999. This model estimates the probability of entering a same-sex union among those individuals who were legally able to enter same-sex unions from age 18 onwards. The coefficient estimate for the number of siblings is larger in magnitude, and the coefficient estimate for the number of older brothers is smaller in magnitude compared to the coefficients corresponding to the baseline specification. Yet the qualitative results drawn from the analyses remain unaffected.

Supplementary Figures and Tables

	(1)	(2)	(3)
Variables	Population-level average marginal effects	Regression coefficients	Transformed odds ratios
Number of siblings	-0.137***	-0.138***	-0.129***
	(0.006)	(0.006)	(0.005)
Number of older siblings	0.079^{***}	0.079^{***}	0.083***
	(0.008)	(0.008)	(0.009)
Number of older brothers	0.124***	0.125***	0.133***
	(0.007)	(0.007)	(0.008)
Number of younger brothers	0.012	0.012	0.012
	(0.009)	(0.009)	(0.009)
Birth-cohort fixed effects		Yes	
Maternal-age-at-birth fixed effects		Yes	
Number of individuals		9,073,496	

Table S1. Population-level average marginal effects, regression coefficients, and transformed odds ratios from the baseline binary logistic regression model of same-sex union entry

Notes: The model uses linked population register data from the Netherlands. Robust standard errors in parentheses. Column 1 lists the average marginal effects from binary logistic regression models of entry into same-sex unions, Column 2 lists the regression coefficients, and Column 3 lists the transformed odds ratios which are commonly interpreted as excess probabilities, defined as (*OR*-1). Statistical significance: ${}^{***}p < 0.001$, ${}^{**}p < 0.01$, ${}^{**}p < 0.05$, ${}^{\dagger}p < 0.10$.

1 6	1			
	(1)	(2)	(3)	(4)
Variables	Full sample	Men	Women	Sex difference
Coefficients				
Number of older brothers	0.066***	0.079***	0.054***	0.025***
	(0.005)	(0.007)	(0.007)	(0.009)
Number of older sisters	-0.058^{***}	-0.036***	-0.078^{***}	0.042***
	(0.005)	(0.007)	(0.007)	(0.010)
Number of younger brothers	-0.125***	-0.118^{***}	-0.132***	0.014
	(0.006)	(0.008)	(0.008)	(0.012)
Number of younger sisters	-0.138***	-0.134***	-0.140^{***}	0.006
	(0.006)	(0.009)	(0.008)	(0.012)
Odds Ratios				
Number of older brothers	1.069***	1.082^{***}	1.055***	0.027***
	(0.005)	(0.007)	(0.007)	(0.010)
Number of older sisters	0.943***	0.964***	0.924***	0.040^{***}
	(0.005)	(0.007)	(0.007)	(0.010)
Number of younger brothers	0.882^{***}	0.888^{***}	0.876^{***}	0.012
	(0.005)	(0.008)	(0.007)	(0.009)
Number of younger sisters	0.871***	0.874^{***}	0.869***	0.005
	(0.005)	(0.008)	(0.007)	(0.010)
Birth-cohort fixed effects	Yes	Yes	Yes	
Maternal-age-at-birth fixed effects	Yes	Yes	Yes	
Number of individuals	9,073,496	4,634,327	4,439,169	

Table S2. Coefficients from binary logistic regression models of same-sex union entry, estimates corresponding to the conventional parameterization of the model

Notes: The models use linked population register data from the Netherlands. Robust standard errors in parentheses. Columns 1 to 3 list coefficients from binary logistic regression models of entry into same-sex unions. Column 4 lists differences between the coefficients corresponding to the male and female populations; that is, Column 2 minus Column 3. To determine whether sex differences are statistically significant, we estimated a fully-interacted binary logistic regression model which used two sets of controls: the principal set of controls, and the same set of controls interacted with the male indicator variable. The coefficients listed in Column 4 correspond to the set of interacted controls from an auxiliary regression model. Statistical significance: ***p < 0.001, **p < 0.01, *p < 0.05, †p < 0.10. Standard errors in parentheses.

	(1)	(2)	(3)
	Predicted probability of same-sex-union entry	Risk ratio p_{xy}/p_{11}	Risk ratio p_{xy}/p_{12}
First son in a one-son family (p_{11})	0.569% (0.006)	1.000	1.110***
First son in a two-son family (p_{12})	0.512% (0.008)	0.901***	1.000
Second son in a two-son family (p_{22})	0.656% (0.009)	1.153***	1.281***
Birth-cohort fixed effects	Ye	es	
Maternal-age-at-birth fixed effects	Ye	es	
Number of individuals	3,239),384	

Table S3. Predicted average probabilities of same-sex union entry and risk ratios for men in one-son and two-son sibships, based on Khovanova's FBOE-FF-model

Notes: Predicted average probabilities and risk ratios from a logistic model of same-sex union entry for men in one-son and two-son families. Figures in bold represent the two ratios proposed by Khovanova to disentangle the FFE (p_{12}/p_{11}) from the FBOE (p_{22}/p_{12}) . The model uses linked population register data from the Netherlands, and controls for birth-cohort and maternal-age-at-birth fixed effects. Robust standard errors in parentheses. Statistical significance: ***p < 0.001, **p < 0.01, *p < 0.05, †p < 0.10.

	(1)	(2)	(3)	(4)	(5)	(6)	(7)
Variables	First unions	Ever in a union	Unions past 1998	Unions past 2001	Less than 5 siblings	1 sibling per sibship	Matched diff sex
Coefficients							
Number of	-0.144^{***}	-0.153***	-0.120^{***}	-0.121***	-0.147^{***}	-0.148***	-0.100^{***}
siblings ^a	(0.007)	(0.006)	(0.006)	(0.007)	(0.008)	(0.011)	(0.008)
Number of older	0.081***	0.067^{***}	0.057^{***}	0.051***	0.095***	0.078^{***}	0.053***
siblings ^b	(0.009)	(0.008)	(0.008)	(0.009)	(0.010)	(0.015)	(0.010)
Number of older	0.117^{***}	0.125***	0.132***	0.135***	0.126***	0.137***	0.135***
brothers ^c	(0.008)	(0.007)	(0.007)	(0.008)	(0.009)	(0.014)	(0.010)
Number of younger	0.010	0.010	0.016^{\dagger}	0.014	0.019^{\dagger}	0.019	0.015
brothers ^d	(0.010)	(0.009)	(0.009)	(0.009)	(0.010)	(0.016)	(0.012)
Odds Ratios							
Number of	0.866***	0.858***	0.887***	0.886***	0.864***	0.862***	0.905***
siblings ^a	(0.006)	(0.005)	(0.005)	(0.006)	0.007	(0.010)	0.007
Number of older	1.084***	1.070***	1.059***	1.052***	1.099***	1.082***	1.055***
siblings ^b	(0.009)	(0.008)	(0.009)	(0.009)	0.010	(0.016)	0.011
Number of older	1.125***	1.133***	1.142***	1.145***	1.134***	1.147***	1.144***
brothers ^c	(0.009)	(0.008)	(0.008)	(0.009)	0.010	(0.016)	0.012
Number of younger	1.010	1.010	1.016†	1.014	1.019†	1.019	1.015
brothers ^d	(0.010)	(0.009)	(0.009)	(0.010)	0.010	(0.016)	0.012
Birth-cohort fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Maternal-age-at-birth fixed effects	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Number of individuals	9,073,496	6,491,498	2,659,397	2,263,142	7,996,529	3,816,904	120,152

Table S4. Robustness checks

	(8) Determel	(9) Diff	(10) Descistante d	(11) Marria and	(12) Jachudia a	(13) Domin
Variables	Paternal siblings	Diff. sex unions	Registered partners	Marriages only	Including immigrants	Born in 1980-99
Coefficients	sionings	unions	purmers	omy	mingrants	1900 99
Number of	-0.142^{***}	0.071^{***}	-0.129***	-0.144^{***}	-0.158^{***}	-0.219***
siblings ^a	(0.008)	(0.001)	(0.009)	(0.007)	(0.006)	(0.015)
Number of older	0.087^{***}	0.034***	0.071^{***}	0.087^{***}	0.092^{***}	0.086^{***}
siblings ^b	(0.010)	(0.002)	(0.012)	(0.010)	(0.008)	(0.020)
Number of older	0.120***	-0.013***	0.124***	0.129***	0.119***	0.076^{***}
brothers ^c	(0.009)	(0.002)	(0.011)	(0.009)	(0.007)	(0.019)
Number of younger	0.022^{*}	0.007^{***}	0.025^{\dagger}	0.001	0.010	0.026
brothers ^d	(0.009)	(0.002)	(0.013)	(0.010)	(0.008)	(0.021)
Odds Ratios						
Number of	0.867***	1.074***	0.879***	0.866***	0.854***	0.804***
siblings ^a	(0.005)	(0.001)	(0.008)	(0.006)	(0.005)	(0.012)
Number of older	1.091***	1.035***	1.074***	1.091***	1.096***	1.090***
siblings ^b	(0.009)	(0.002)	(0.013)	(0.010)	(0.008)	(0.022)
Number of older	1.127***	0.987***	1.132***	1.137***	1.127***	1.079***
brothers ^c	(0.009)	(0.002)	(0.013)	(0.010)	(0.008)	(0.021)
Number of younger	1.023*	1.007***	1.027*	1.001	1.010	1.026
brothers ^d	(0.009)	(0.002)	(0.014)	(0.010)	(0.009)	(0.021)
Birth-cohort fixed effects	Yes	Yes	Yes	Yes	Yes	Yes
Maternal-age-at-birth fixed effects	Yes	Yes	Yes	Yes	Yes	Yes
Number of individuals	8,034,806	9,073,496	9,073,496	9,073,496	9,610,934	3,742,087

Notes: The models use linked population register data from the Netherlands. Robust standard errors in parentheses. ^a This estimate corresponds to a situation in which one younger sister is added to an existing sibship. ^b This estimate corresponds to a situation in which an individual moves one

place down the birth order, having one additional older sister, and one fewer younger sister. ^c This estimate corresponds to a situation in which one older sister is replaced by an older brother in an existing sibship. ^d This estimate corresponds to a situation in which one younger sister is replaced by a younger brother in an existing sibship. Statistical significance: ***p < 0.001, *p < 0.01, *p < 0.05, †p < 0.10.

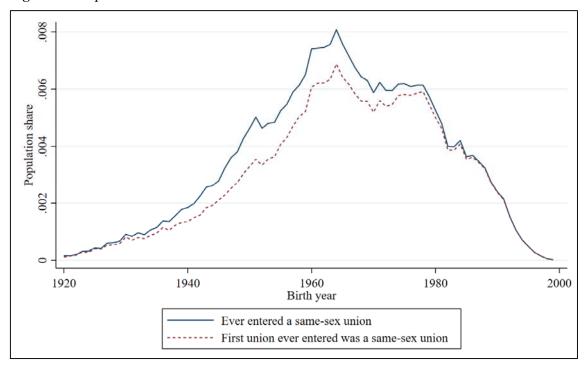
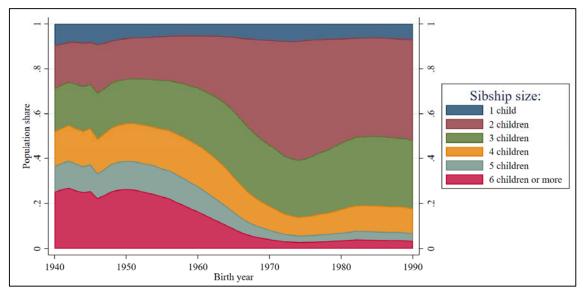


Figure S1. Population shares of individuals who entered a same-sex union

Notes: Population shares are extracted from linked population register data from the Netherlands.

Figure S2. Eventual sibship size, by birth year



Notes: This figure shows the population shares of sibship sizes observed among individuals born in the given year. Rather than measuring the sibship size at birth, we measure the eventual sibship size, counting all maternal siblings born prior to the individual in question as well as those born afterwards. This includes siblings born prior to 1940, as well as those born past 1990 (up to 2019). The shares were extracted from linked population register data from the Netherlands.

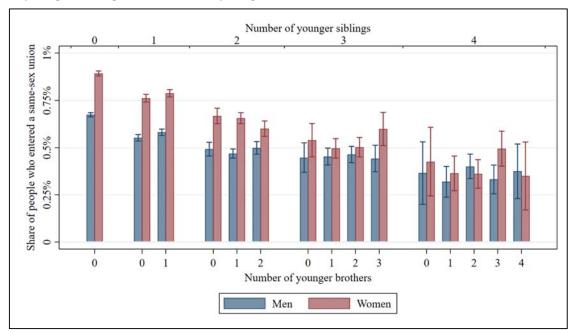


Figure S3. Population shares of individuals who ever entered a same-sex union, by sex, number of younger siblings and number of younger brothers

Notes: Population shares are extracted from linked population register data from the Netherlands. Whiskers denote 95% confidence intervals.

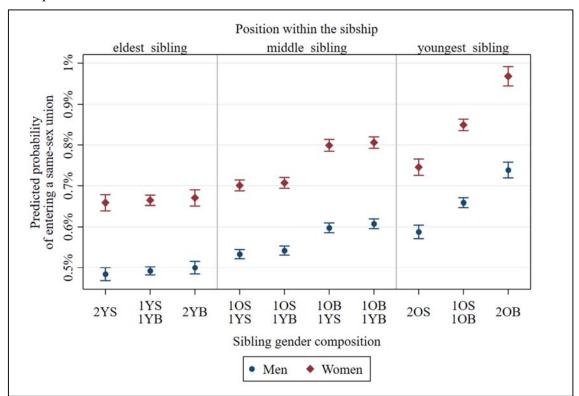


Figure S4. Predicted probabilities of entering a same-sex union for individuals in three-person sibships

Notes: Predicted probabilities from sex-specific logistic regression models of entry into samesex unions adjusted for birth-cohort and maternal-age-at-birth fixed effects (Table 3, Columns 2 and 3). The models use linked population register data from the Netherlands. Whiskers denote 95% robust confidence intervals.