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Contextualising courtship: Exploring male body odour effects on vocal modulation

Juan David Leongómez[1#, 2], Oscar R. Sánchez[1], Milena Vásquez-Amézquita[3], S. Craig Roberts[2]

[1] Human Behaviour Lab, Faculty of Psychology, Universidad El Bosque. Bogota, Colombia.

[2] Faculty of Natural Sciences, University of Stirling. Stirling, United Kingdom.

[3] Experimental Psychology Lab, Faculty of Psychology, Universidad El Bosque. Bogota, Colombia.

*Corresponding author: Juan David Leongómez, jleongomez@unbosque.edu.co

#Current affiliation

Highlights

- Presence of male body odour does not change vocal parameters or attractiveness ratings
- Odour quality or added androstadienone do not have measurable voice effects
- Attractiveness ratings are predicted by mean F_0 and especially F_0 variability

Abstract

Voice characteristics are important to communicate socially relevant information. Recent research has shown that individuals alter their voices depending on the context of social interactions and perceived characteristics of the audience, and this affects how they are perceived. Numerous studies have also shown that the presence of bodily odours can elicit psychological changes in people. Here, we tested whether the presence of male axillary odour would influence vocal modulations in courtship contexts. We analysed differences in vocal parameters and attractiveness ratings across 950 recordings from 80 participants as they responded to opposite-sex target stimuli. Using these, we tested whether men's and women's vocal parameters and perceived attractiveness differed in the presence or absence of the odour. We expected women to speak with increased voice F_0, and men to lower their pitch, when exposed to male body odour, especially if it were of high quality. However, neither the presence of male odour, its quality, nor the addition of androstadienone produced any consistent changes in vocal parameters. Nevertheless, rated stimulus attractiveness was predicted by F_0 and especially F_0 variability, suggesting that this is a key parameter in signalling attraction during human courtship, and supporting the idea that vocal modulations are context-sensitive.

Keywords: androstadienone; fundamental frequency; male body odour; mate choice; voice modulation

1. Introduction

In recent years, numerous studies have shown that mere presence of odours can bring about psychological changes in people in a range of different contexts. For example, ambient odours can influence people's mood and creativity (Knasko, 1992) and reduce stress (Lehrner et al., 2005). Such effects are not ubiquitous but vary depending on the interaction between specific odours and situations. For example, scents that are perceived to be more associated with one or other gender alter gender-congruent shopping behaviour (Doucé et al., 2016; Spangenberg et al., 2006). Furthermore, subliminal presence of citrus scent, an odour associated with cleanliness, can influence hygienic behaviour (Holland et al., 2005; King et al., 2016), while odours associated with faeces and vomit trigger behaviour associated with disgust and avoidance, including more positive attitude towards safe sex (Tybur et al., 2011) and more conservative attitudes towards sexual behaviour (Adams et al., 2014).

Such effects are not limited to ambient fragrances and those associated with disease risk, but also involve bodily odours and their influence on social interactions. For example, the odours of people in fearful or anxious emotional states can alter brain activation, mood and cognition in others (e.g. Albrecht et al., 2011; Pause et al., 2004). Odours can also influence social judgments in other sensory modalities, as the subliminal presence of male axillary odour alters attractiveness ratings of men's faces by women (Thorne et al., 2002). This effect was supported and extended in a recent study (Mutic et al., 2016) showing that axillary odour of both sexes affected the evaluations of masculinity and femininity and the social perception of faces.

At least with attractiveness judgments, we should expect effects to vary depending on the individual odour donor, because perceived odour quality varies between individuals. Just as some individuals have faces that most people would view as relatively attractive (models would be an

extreme example), some individuals have relatively attractive body odour. Indeed, some studies report positive correlations between individual facial attractiveness and the perceived pleasantness of their axillary odour (Rikowski and Grammer, 1999; Thornhill et al., 2003; but see Roberts et al., 2011), suggesting that both are underpinned by a common biological mechanism. Although the specific components of axillary odour that are responsible for such effects remain unknown, several studies (Cornwell et al., 2004; Grosser et al., 2000; Jacob et al., 2001; Jacob and McClintock, 2000) focus on a group of naturally occurring steroids, the 16-androstenes, and mainly the compound androstadienone. Although the theoretical relevance of such studies has been questioned (e.g. Wyatt, 2020), researchers have reported numerous effects of androstadienone exposure on individuals. These include effects on positive mood (Jacob and McClintock, 2000), emotional processing (d'Ettorre et al., 2018), assessment of body movement (Hornung et al., 2017; Niu and Zheng, 2020; Parma et al., 2012; Ye et al., 2019) and facial information (Hornung et al., 2017; Niu and Zheng, 2020; Parma et al., 2012; Ye et al., 2019) Zhou et al., 2014), as well as facial attractiveness judgements, such that presence of androstadienone led to higher attractiveness ratings (Saxton et al., 2008; Verhaeghe et al., 2013).

Voice characteristics are another important means of communicating socially relevant information (e.g., Valentova et al., 2019). Recent research has shown how people alter their voices during social interactions, depending on the social context of such exchange and the perceived characteristics of the audience (for a review, see Pisanski et al., 2016). This has been demonstrated, for example, for interactions in which social status is important (Leongómez et al., 2017; Puts et al., 2006; Sorokowski et al., 2019) and in courtship scenarios (e.g. Leongómez et al., 2014; Pisanski et al., 2018). Voice modulations can increase the prospect of attracting preferred partners, for two reasons. First, the characteristics of an attractive voice can, at least to a certain extent, be imitated

47 or exaggerated (Fraccaro et al., 2011; Leongómez et al., 2014). Second, they exploit the fact that,
48 just like faces and odours, some voices are judged to be relatively more attractive than others.
49 This latter point illustrates that, in a courtship context, there may be a further correlation
50 between perception of odours and voices, as they may both give information about the underlying
51 quality of an individual as a potential partner, affecting perceived attractiveness (Feinberg et al.,
52 2005). Although the literature on this relationship is scarce, it has been found that odours,
53 according to their hedonic valence, can influence certain acoustic characteristics of voice (Millot
54 and Brand, 2001). In fact, because previous research has showed that (1) women's perception of
55 a man's attractiveness is increased both by the presence of male axillary secretion (Thorne et al.,
56 2002) and exposure to androstadienone (Saxton et al., 2008), and (2) voice modulation is
57 sensitive to attractiveness cues (Leongómez et al., 2014; Pisanski et al., 2018), it is possible that
58 body odours, as signals of the quality of a potential partner, could induce non-conscious vocal
59 modulations in courtship scenarios. However, the potential effects of body odours on voice
60 characteristics have not yet been explored in courtship contexts, for either sex.
61 In view of this, we set out here to test whether presence of male axillary odour, and
62 androstadienone in particular, would influence vocal modulation in courtship contexts. We used
63 the same experimental paradigm and measures of vocal parameters as in Leongómez et al (2014),
64 to test changes in men's and women's voices as they responded to opposite-sex targets, in the
65 presence and absence of the allocated odour. The vocal parameters we extracted were the mean
66 fundamental frequency (F_0) and its variability (both standard deviation, SD, and coefficient of
67 variation, CV; see Eguchi and Hirsh, 1969), and mean intensity. We also asked participants to
68 rate how attractive they found each target stimulus, and modelled the acoustic parameters as
69 predictors of perceived attractiveness. Despite the study being largely exploratory due to its
70 novelty, we had some specific predictions. First, we predicted that the presence of male body

odour and androstadienone would tend to increase the perceived attractiveness of male targets, causing women to speak with increased voice F_0, which tends to be attractive to gynephilic men (Feinberg et al., 2005; Jones et al., 2008). Likewise, given that low F_0 provides a cue of masculinity and dominance (Puts et al., 2007; Wolff and Puts, 2010), we expected men to lower their pitch when exposed to male body odour as a response to perceived intrasexual competition. Finally, we expected both sexes to increase pitch variability when responding to attractive target stimuli (Leongómez et al., 2014).

2. Materials and Methods

2.1 Ethics Approval

The study was performed in line with the principles of the Declaration of Helsinki. All procedures were approved by the Ethics Committee of the Department of Psychology, Faculty of Natural Sciences, University of Stirling. All participants provided written informed consent and were offered course credit for their participation.

2.2 Participants

We recruited 80 heterosexual participants who were students at the University of Stirling, half of whom were men (mean age ± SD = 20.48 ± 0.41) and half women (20.50 ± 0.49). Participants were not suffering from vocal hoarseness or nasal congestion at the time of testing. To ensure they had a normally functioning sense of smell, all participants were asked to complete a brief screening test, in which they had identify 12 odorants in a multiple choice task with 4 alternatives for each odorant (the Sniffin' Sticks Screening 12 test, www.burghart-mt.de); only data from participants who could correctly identify at least 9 odorants were included in the analysis. One participant (male, 20 years old) correctly identified only 7 and so was excluded

from the final sample, but recruitment continued until the final, balanced sample size was achieved.

2.3 Target videos

We used videos that were selected as target stimuli for a previous study (Leongómez et al., 2014). These target stimuli were selected from an initial set of 40 videos: 20 of men (mean age ± SD = 22.5 ± 2.41) and 20 of women (22.1 ± 1.65), each of 20 seconds length. Their task was presented as: "Please introduce yourself to an attractive person of the opposite sex". Each video was then scored for attractiveness by 24 opposite-sex raters. Based on the mean attractiveness scores, the videos of the 3 most and 3 least attractive men and women were selected for use in the study (12 videos in total).

2.4 Odour stimuli

Body odour samples were collected from 12 men (mean age 21.4 ± 1.9). Each wore a cotton pad in each armpit for one night. They were instructed to wash with unperfumed soap before going to bed, to avoid spicy foods, and to place the pads into the provided sealable bags on waking. These are standard and well-used procedures for axillary odour perception studies (Havlíček et al., 2005; Roberts et al., 2008, 2005). Each odour sample was then frozen immediately until use; freezing does not alter the perception of axillary odours (Lenochova et al., 2009; Roberts et al., 2008). Male odours were subsequently rated for pleasantness by a separate group of people (5 men, 5 women) using a 7-point scale ranging from -3 (very unpleasant) to +3 (very pleasant). Samples from the 4 most pleasant scoring odours were pooled to create a "high quality" (HQ) male odour, while pooling of the 4 lowest scoring odours formed a "low quality" (LQ) male odour. Pooling of such samples to create a composite odour minimises effects of individual differences in odour quality and preference while maintaining the average quality of the constituent samples (Fialová et al., 2018). To create these composites, each cotton pad was

shredded into small pieces and mixed in equal parts with the other odours in either the HQ or LQ category, before being frozen in sealable bags. Additional details on odour presentation are provided in the Supplementary Material available on-line.

2.5 Experimental procedure

Participants were recruited and participated in this study between November 2011 and May 2012. Each was asked to attend two sessions (experimental and control), spaced between 7 and 14 days apart. Participants were exposed to odour stimuli only during the experimental session; sessions were otherwise identical. Participants were randomly divided into one of 4 experimental odour conditions, according to whether they were exposed to high/low body odour quality (HQ, LQ), and whether androstadienone (ANDR) was added to that odour (the 4 conditions were thus: HQ + ANDR, HQ no ANDR, LQ + ANDR, LQ no ANDR). A group of 10 women and 10 men were allocated to each condition. Sessions were counterbalanced so that for half of the men and women in each group, the control took place in the first session, and for the other half in the second (Fig 1).

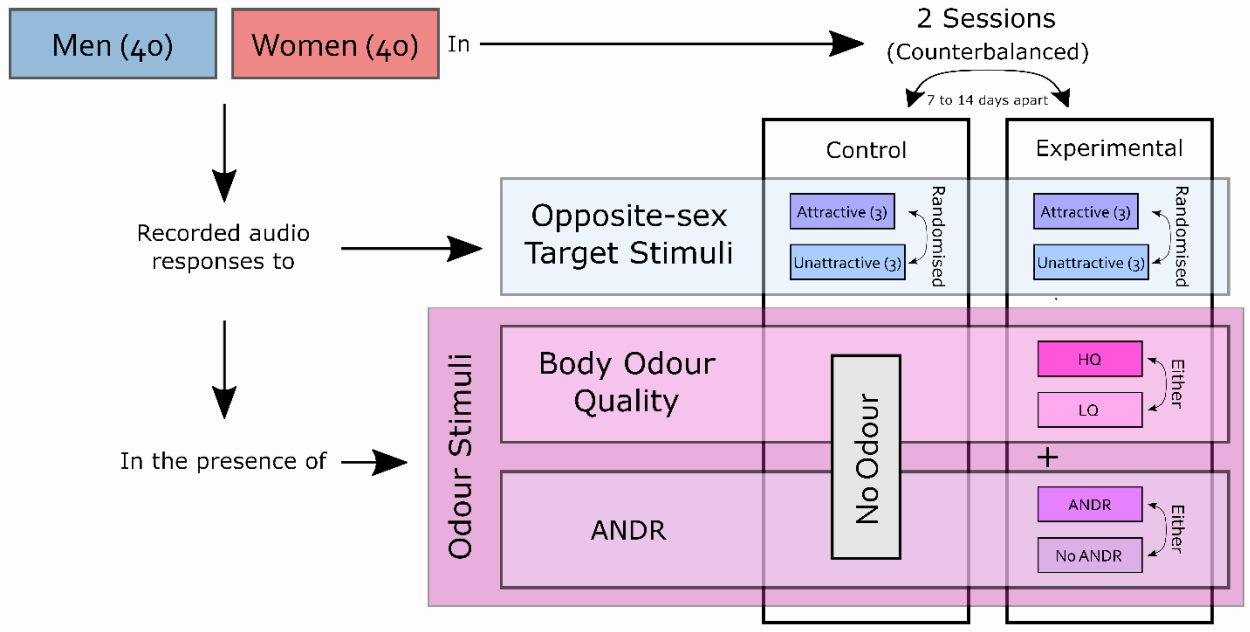


Figure 1. Experimental design. Diagram of the sessions and stimuli used in each case. The order of session was counterbalanced between participants in each odour stimuli combination (odour quality and ANDR). For body odour quality, HQ = high quality; LQ = low quality. ANDR = androstadienone.

Two hours before each experimental session, the appropriate odour sample was removed from the freezer. At this point, when testing participants from the HQ + ANDR and LQ + ANDR groups, 1ml of a 250 μM ANDR solution was added by pipette to the odour sample. We used this ANDR concentration to enable comparison with previous studies (e.g. Jacob and McClintock, 2000; Lundström and Olsson, 2005; Saxton et al., 2008) and because it is below the detection threshold for most people (Lundström et al., 2003). Fifteen minutes before the session, the odour sample was placed in the cubicle where the participant would be seated, in a small plastic container wrapped in clean aluminium foil. Odour samples were left in the cubicle for the duration of the experimental session and removed afterwards, leaving the cubicle open and empty for no less than 15 minutes before they were replaced by new odour samples to test other participants. For control sessions, clean pieces of cotton pads were placed in the same manner, so that participants could not visually differentiate between the control and experimental sessions.

Sessions were conducted in small, quiet testing cubicles with artificial light and no windows. During the session, participants were alone in the cubicle, sitting in front of a laptop, with the plastic container placed directly on the desk between the participant and the laptop, so that the odour sample was about 25 cm below the participant's nose.

The procedure from here on closely followed the methods described in Leongómez et al. (2014), but here we only analyse data from responses to opposite-sex target videos. The study was presented to participants as an experiment on selection of potential mates and relationship formation, examining the relative importance of attractiveness, self-confidence and body language on male and female preferences, as well as to understand the effect that different odours

156 have on these psychological mechanisms. The odours used in the experiment remained
157 undisclosed until participants were fully debriefed after the second session. In both sessions,
158 participants were shown the six opposite-sex target videos, and were asked to record a response
159 message to each one of them using a head mounted microphone. They were told that these
160 messages would be presented to opposite-sex participants who would judge them as a potential
161 date. Based on a study which produced demonstrable effects on mate preferences (Gangestad et
162 al., 2004), participants were instructed to explain whether and why they would like to date the
163 person in the video. Additional details are provided in the Supplementary Material available on-
164 line.

165 The video targets were presented electronically to participants using E-Prime 2.0 software
166 (Psychology Software Tools, Inc., 2012; www.pstnet.com), and the order of the target videos was
167 fully randomised for each participant/session. Immediately following each video, participants
168 were asked to rate the attractiveness of each target (on a 7-point scale), and monaural audio
169 responses of the participants were digitally recorded using E-Prime (SoundIn object) on a laptop
170 PC, using a ClearChat Stereo Headset (Logitech, 2007), positioning the microphone about 2 cm
171 from the participant's mouth.

172 As each participant experienced both experimental and control sessions, they recorded a
173 total of 12 responses to opposite-sex targets (6 control, 6 experimental). A grand total of 960
174 recordings were thus obtained. Eight recordings were discarded because of technical problems or
175 background noise that affected audio quality and subsequent acoustic analysis, so 952 were
176 acoustically analysed. Of these, 2 were excluded from statistical analysis because they did not
177 produce acoustically useable data, so 950 were statistically analysed. Similar to the methods
178 described in Leongómez et al. (2014), each participant responded to 3 targets of each
179 attractiveness category (attractive, unattractive) during both the control and experimental

sessions. The values used in the analysis were, therefore, the acoustic values of each participant's 3 responses on each session/attractiveness combination: control/attractive, control/unattractive, experimental/attractive, and experimental/unattractive.

In addition, in the first session and before the experiment, participants were asked to read and sign the consent form, as well as take the short olfactory sensitivity test. In the second session, and after the experimental procedure, participants were debriefed. Their data were only retained and analysed if they still gave consent after being fully debriefed.

2.6 Acoustic analysis

Acoustical analyses of the recordings were done following the method described in Leongómez et al. (2014). We used a batch-processing script updated and optimised by Jose Joaquin Atria, based on an original script by Setsuko Shirai (https://www.ucl.ac.uk/~ucjt465/scripts/praat/get_formants_praatlist.praat), in Praat, version 6.0.41 (P. Boersma and D. Weenink, 2018; www.praat.org). Values on intensity (dB), F_0 (Hz), and the first three formants (F_1, F_2, F_3) were obtained every 10 ms. A noise-resistant autocorrelation method (75 - 300 Hz for male voices, 100 - 500 Hz for female voices) was used. Additional details are provided in the Supplementary Material available on-line.

2.7 Statistical analysis and mixed modelling

The coding for all statistical analyses, figures, and tables was created in an R Markdown file, using R version 4.0.0 (R Core Team, 2020) and RStudio version 1.3.947. This file is available from the OSF (https://doi.org/10.17605/OSF.IO/GWBHU). The output of that R Markdown file (in PDF format) constitutes the Supplementary Material to this article. All models were fitted using the *lmer* function from the *lmerTest* package (Kuznetsova et al., 2017). All statistical tests are two-tailed. Figures were created using *ggplot2* (Wickham, 2016) and *ggpubr*

(Kassambara, 2019), and tables were generated and formatted using *knirt* (Xie, 2015) and *kableExtra* (Zhu, 2019). For a full list of R packages used, see Section 4 in the Supplementary Material.

2.7.1 Models of measured variables

To test the effects of the presence or absence of body odour (i.e. control/experimental sessions), the quality of body odour (HQ, LQ), and the presence or absence of added ANDR (+ ANDR, no ANDR) on the acoustic parameters and attractiveness ratings, while taking into account the sex of the participants and the attractiveness category of the target stimuli, we used linear mixed models (LMM). Separate (but with identical factor structure) models were fitted for mean F_0, F_0 SD, F_0 CV, mean intensity, and attractiveness ratings.

Because the main focus was to test the effects of the body odour, and participants were only exposed to these in the experimental session, we only report the main effect of odour Condition, as well as all its interactions with sex, odour quality, ANDR, and Stimuli Attractiveness. We do not report here the main effects of sex, body odour quality, nor the effect of adding ANDR, as these would be confounded with characteristics other than the experimental manipulation, but full factorial models are reported in Section 2.4 of the Supplementary Material (Tables S2, S4, S6, S8 and S10). For all models, Subject (the participant ID), was also included as random factor, with correlated random slopes and intercepts for each participant between Sessions (control, experimental).

In all cases, residuals were closer to a normal or gamma (inverse link) distribution. These models, and their diagnostics (residual distribution, homoscedasticity, and linearity of each fixed factor), are detailed in Section 2.4 of the Supplementary Material.

Contrasts comparing the effect of the condition for each sex, odour quality, ANDR and target stimuli attractiveness category combination (used in model figures), were performed using the functions *emmeans* and *contrast* from the *emmeans* R package (Lenth, 2019).

2.7.2 Models to predict attractiveness ratings

Finally, to explore the association between the perceived attractiveness of each target stimulus to the participant and the acoustic characteristics of their responses, we fitted mixed linear regressions predicting the attractiveness ratings given by participants to each target stimulus, in each session.

In the initial model, fixed predictors were: participant sex, mean F_0, F_0 CV, minimum F_0, (mean) intensity, odour quality and ANDR, as well as the sex × mean F_0, sex × F_0 CV, sex × Minimum F_0, and sex × Intensity interactions. The interaction between participant ID (Subject) and Session was entered as a random intercept factor, to account for the two times that each participant rated and responded to each target stimulus (one in each condition), and to avoid pseudoreplication.

This parameterised initial model was then reduced to include only the most relevant acoustic variables (intermediate model): mean F_0, minimum F_0 and F_0 CV, as well as sex and their interactions with sex were entered as fixed predictors. Finally, this was further reduced, to include as fixed predictors only mean F_0, F_0 CV and sex, with no interactions (final model).

Initial, intermediate and final models were then compared using the Akaike information criterion (AIC) and Akaike weights and the best-supported model (i.e. the model with the lowest AIC with a ΔAIC higher than two units from the second most adequate model, and higher Akaike weight) is reported (Wagenmakers and Farrell, 2004). To do this, we used the *ICtab* function from the *bbmle* package (Bolker, 2017). Pseudo-R^2 values for these model were obtained using

the function r.*squaredGLMM* from the package *MuMIn* (Bartoń, 2020).Once a final model was fitted, model diagnostics were performed.

The residual distribution of the final model was bimodal, and hence differed from a normal distribution. Also, given that the outcome variable (attractiveness ratings) is discrete, Poisson, quasi-Poisson and negative binomial distributions could be tentatively appropriate, but none of these converged, even when separate models were fitted for women and men. Furthermore, the function *check_distribution* from the package *performance* (Lüdecke et al., 2020) showed that the most likely family distribution for this final model was the normal distribution, based on its residuals. Therefore, we used a normal distribution (i.e. a general LMM), but calculated percentile bootstrap confidence intervals for the model estimates, based on 1000 simulations, using the *confint.merMod* function, from the *lme4* package (Bates et al., 2015).

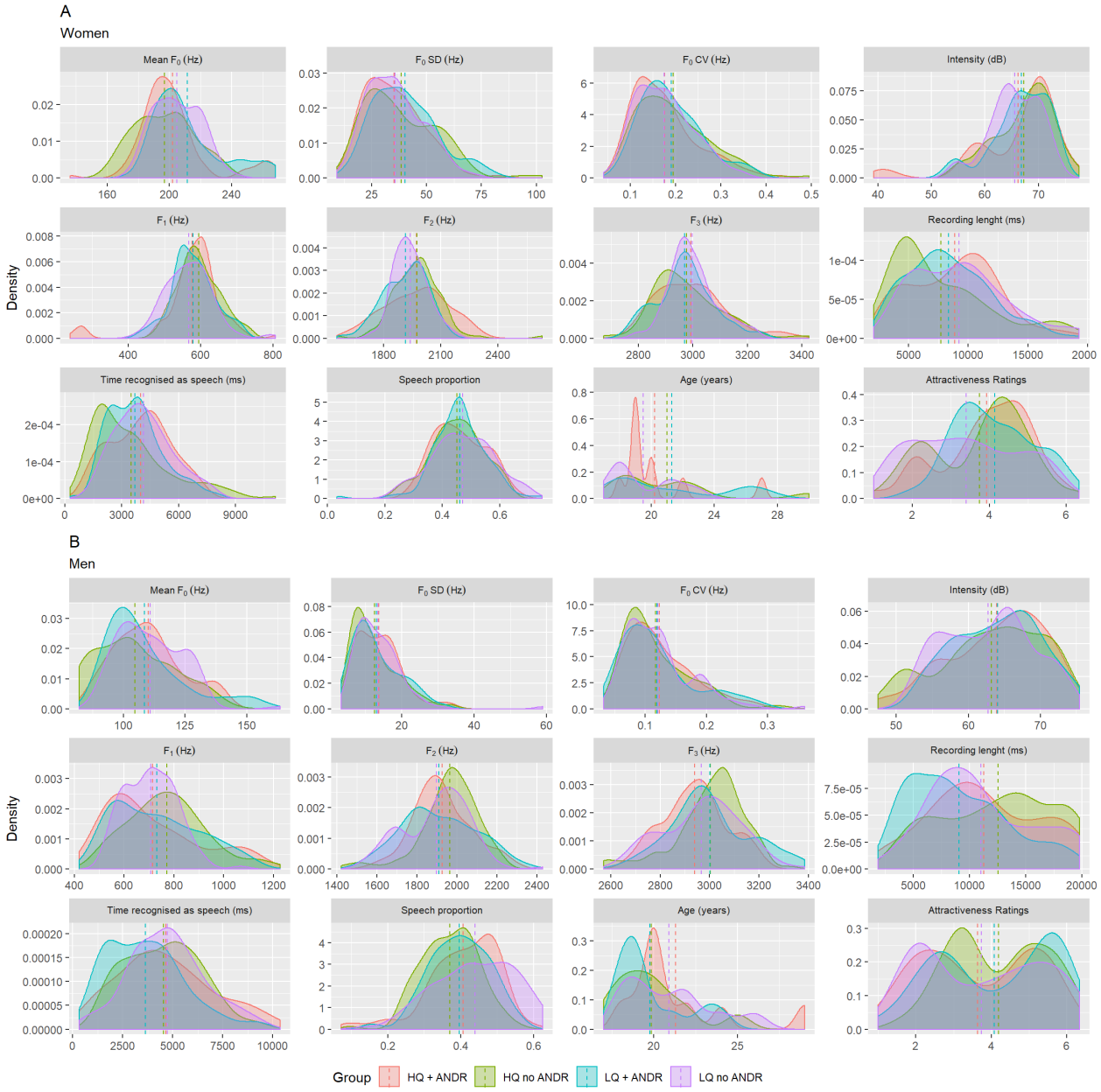
In these models we included F_0 CV and not F_0 SD, for three reasons: first, given that both are measures of F_0 variability, they are highly correlated (see Tables S3 to S5 in the Supplementary Material). Second, unlike F_0 SD, F_0 CV was not significantly correlated with mean F_0 in women, nor in men (Tables S4 and S5 in the Supplementary Material, respectively). Finally, we preferred F_0 CV given that it is a better representation of the perceptual variability, as it takes into account the mean F_0 of each recording (Eguchi and Hirsh, 1969; see also Pisanski et al., 2018). These models, and the diagnostics of the final model (residual distribution, homoscedasticity, and linearity of each fixed factor), are detailed in Section 2.5 of the Supplementary Material.

3. Results

3.1 Descriptives

Descriptive statistics for each measured variable for each group, in each session (control, experimental), and for each target attractiveness category (attractive, unattractive), are presented in Table S1 (female participants) and Table S2 (male participants) in the Supplementary Material.

Figure 2 shows the distribution of mean F_0 (Hz), F_0 SD (Hz), F_0 CV (Hz), mean intensity (dB), F_1 (Hz), F_2 (Hz), F_3 (Hz), recording length (ms), time recognised as speech (ms), speech proportion (i.e. the proportion of the length of each recording that was recognised as speech), age (years) and attractiveness ratings, for each group of women (Fig. 2A) and men (Fig. 2B).



279 **Figure 2. Distribution of all measured variables by sex and condition.** (A) Women. (B) Men. Vertical lines
280 represent the mean for each group. Detailed descriptives are found in Table S1 for women, and Table S2 for men, in
281 the Supplementary Material.

282 Bivariate (Pearson) correlations between the continuous variables included in the statistical
283 models are found in Tables S3 to S5, for all participants combined, men and women, respectively.
284 Mean F_0 was positively and significantly correlated with F_0 SD and Intensity in both men and
285 women, as well as with the length of the recording in men, and marginally positively associated (*r*

= 0.09) with the attractiveness ratings given by men. The two measures of F_0 variability, SD and CV, were highly correlated, and were positively associated with mean intensity and (particularly in women) with the attractiveness ratings given to target stimuli.

3.1.1 Time recognised as speech

Time recognized as speech was highly associated with recording length in both women and men (Fig. 3A). The actual speaking time (recognized as speech), although significantly higher for men than for women, was not affected by the presence of body odour (i.e. it did not change between sessions; Fig 3B).

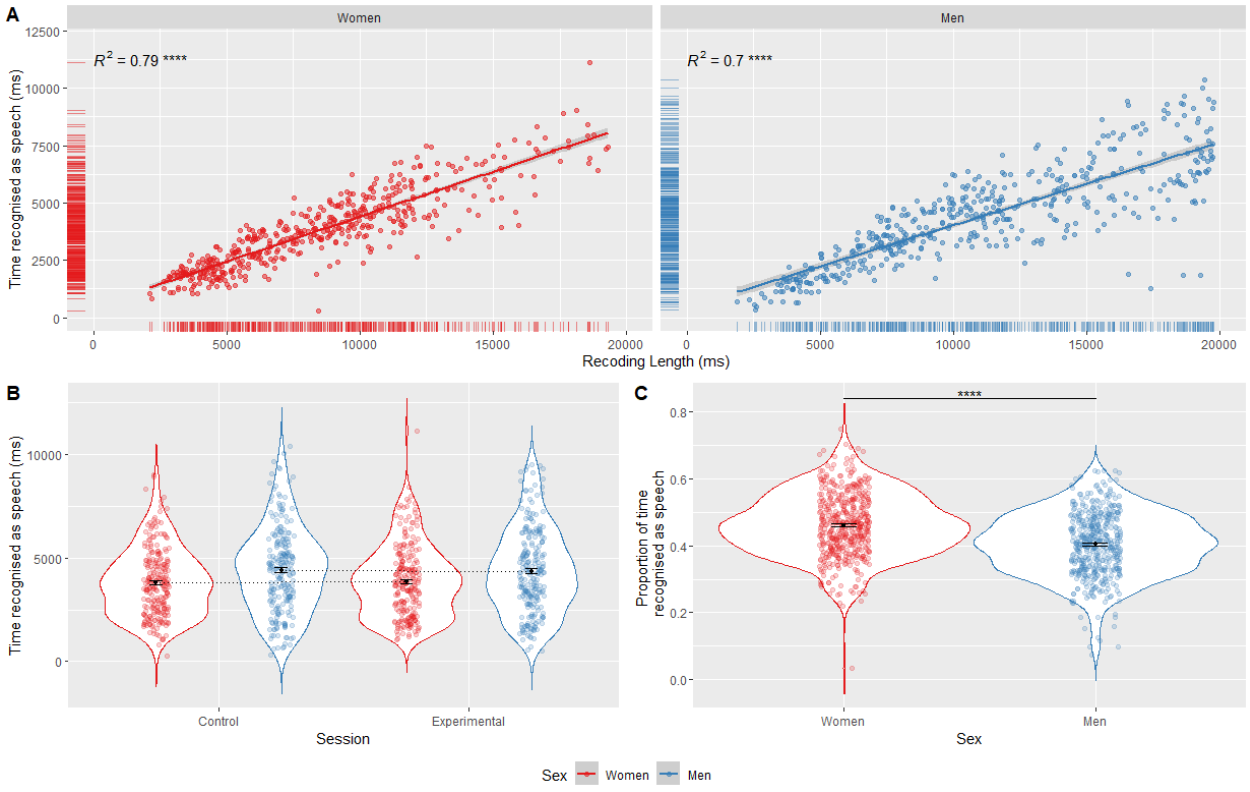


Figure 3. Differences in time recognised as speech and recoding length. (A) Correlation between time recognised as speech and recoding length. (B) Within-subject differences in time recognised as speech in responses to attractive

297 and unattractive target stimuli. (C) Proportion of time recognised as speech by sex. Comparisons between men and
298 women were performed using *t*-tests: **** $p < 0.0001$.

299 The proportion of time recognised as speech, however, was significantly higher in women's
300 than in men's responses. That is, although men tended to record longer voice responses, women
301 tended to spend proportionally less time in *silence* (Fig. 3C).

302 **3.2 Models of measured variables**

303 To avoid the possibility that apparent differences between groups might be an artefact of
304 between-subject differences, we tested each participant in two sessions: control (no odour stimuli),
305 and experimental (odour stimuli).

306 The within-subject effects involving Session are reported in Table 1, reflecting the
307 experimental design (full models, including Satterthwaite's approximation to degrees of freedom
308 and sum of squares, are provided in Tables S2, S4, S6, S8 and S10 in the Supplementary Material).

309 Table 1. Context-dependent variation in vocal parameters and attractiveness ratings.

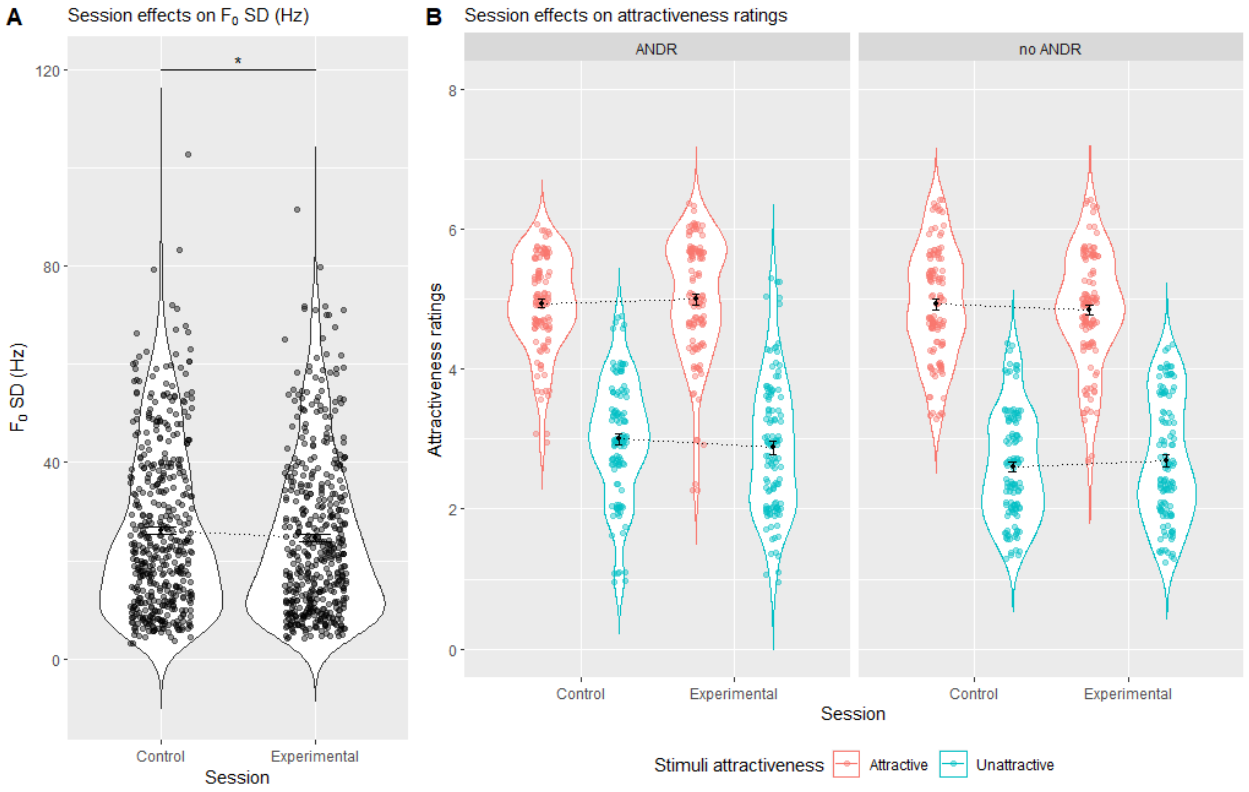
Effect	Vocal parameter								Attractiveness Ratings	
	Mean F_0		F_0 SD		F_0 CV		Intensity			
	F	***p***	***F***	***p***	***F***	***p***	***F***	***p***	***F***	***p***
S	1.44	0.234	3.97	**0.05**	2.66	0.107	0.11	0.736	0.02	0.887
S × SA	1.01	0.316	1.79	0.181	1.14	0.286	1.13	0.288	0	0.956
S × Sex	3.6	0.062	0.54	0.465	0.38	0.539	0.02	0.891	1.83	0.18
S × OQ	0.85	0.36	0.01	0.912	0.05	0.831	0.17	0.677	0.77	0.383
S × ANDR	0.46	0.499	1.19	0.279	0.95	0.334	0.41	0.524	0.06	0.812
S × SA × Sex	2.21	0.137	0.08	0.773	0.06	0.812	0.01	0.929	2.12	0.146
S × SA × OQ	0.13	0.714	0.23	0.633	0.28	0.594	0.25	0.617	0.54	0.465
S × Sex × OQ	0.77	0.382	1.32	0.254	1.32	0.253	0.03	0.856	0.98	0.325
S × SA × ANDR	0.08	0.782	0.97	0.324	1.16	0.282	0.07	0.788	8.77	**0.003**
S × Sex × ANDR	1.39	0.242	1.56	0.215	1.2	0.276	0.35	0.557	1.74	0.191
S × OQ × ANDR	0.52	0.471	1.97	0.165	2.16	0.146	1.44	0.234	0.46	0.501
S × SA × Sex × OQ	0.01	0.932	0.04	0.833	0.47	0.494	1.49	0.223	0.97	0.326
S × SA × Sex × ANDR	0.57	0.449	0.19	0.659	0.13	0.715	0.37	0.546	0.27	0.603
S × SA × OQ × ANDR	0	0.947	1.28	0.259	1.5	0.22	0.47	0.493	0.05	0.819
S × Sex × OQ × ANDR	2.23	0.14	1.36	0.247	1.33	0.252	0.04	0.851	3.08	0.083

S × SA × Sex × OQ × ANDR	1.88	0.171	0	0.947	0.01	0.933	1.72	0.19	2.09	0.149

S = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality, low quality); ANDR = androstadienone (ANDR, no ANDR); SA = target stimuli attractiveness (attractive, unattractive). For all results, including all main effects, *df* and Sums of Squares, see Tables S2, S4, S6, S8 and S10 in the Supplementary Material.

Analysis revealed that the inclusion of odour stimuli did not have a significant main effect on any of the models for measured acoustic variables (Table 1; Fig. 4A), except for variability in F_0 (measured as F_0 SD), in which the inclusion of body odour in the experimental session caused participants to decrease their pitch variability. However, this effect was only marginally significant, and it was not found when variability in F_0 was measured as F_0 CV (i.e. controlling for perceptual variability), suggesting that it was not a robust effect.

In addition, we found a significant, 3-way interaction between session, stimuli attractiveness, and ANDR for the attractiveness ratings given to target stimuli (Table 1; Fig. 4B). The inclusion of body odour (either high or low quality) with added ANDR in the experimental session caused participants to give more extreme ratings to target stimuli (i.e. higher ratings to attractive stimuli and lower ratings to unattractive stimuli). However, for participants who were exposed to male body odour without added ANDR in the experimental session, this effect was in the opposite direction (i.e. a tendency to give lower ratings to attractive, and higher ratings to unattractive, stimuli). Pairwise contrasts, however, showed that these changes (after adjustment for multiple comparisons) between the control and experimental sessions were not significant (Fig. 4B).



335 **Figure 4. Significant Session effects and interactions.** (A) Main effect of Session for F_0 SD. (B) Interaction
336 between session, target stimuli attractiveness and ANDR for Attractiveness ratings. The black dashed line represents
337 the general within-subject change across sessions (pairwise contrasts using *emmeans*; https://cran.r-
338 project.org/web/packages/emmeans/vignettes/interactions.html). Significant effects of session are represented with
339 solid lines and stars above violin plots: * $p < 0.05$.

340 ### 3.3 Models to predict attractiveness ratings

341 The initial mixed linear regressions included Sex, Mean F_0, F_0 CV, (mean) Intensity, odour
342 quality and ANDR, as well as the interactions between sex and mean F_0, sex and F_0 CV,
343 and sex and intensity were included as fixed predictors of the attractiveness rating given to each
344 target stimulus, by each participant in each session. The interaction between subject (participant
345 ID) and session was also kept as a random intercept factor.

346 In this initial model, only F_0 CV was a significant predictor of the attractiveness ratings (see
347 Table S11, in the Supplementary Material). We then reduced this highly parameterised model to
348 an intermediate model, including only the most relevant acoustic variables: mean F_0, minimum F_0

and F_0 CV, but maintaining sex and the interactions between of sex with mean F_0, minimum F_0 and F_0 CV as fixed predictors, and the interaction between subject and session as a random factor (see Table S12, in the Supplementary Material). Here, again, only F_0 CV was a significant predictor of the attractiveness ratings. This intermediate model was further reduced to only include, as fixed factors, sex, mean F_0 and F_0 CV, in an additive model with no interactions (see Table S13, in the Supplementary Material). The random term was not changed.

This final model, however, was much more likely to be the best of the three models, as revealed by AIC and w_i(AIC) (see Table S14, in the Supplementary Material). The AIC of the final model about 64 units below that of the initial model and more than 2 below the intermediate model. In addition, Akaike weights established that the final model, given its increased parsimony and similar predictive power, was most likely to be the best of the three models (in fact, more than three times more likely in comparison to the intermediate model, and several million times more likely to be the best model compared to the initial model).

The final model, however, did not meet the assumptions of residual distribution or homoscedasticity (see Fig. S11 in the Supplementary Material). In particular, the residual distribution was extremely bimodal, even when separate models were fitted for women and men, and no distribution attempted from generalised linear mixed models that converged produced an appropriate model. For this reason, and because a normal distribution was the most probable (see Table S15 in the Supplementary Material), we calculated bootstrap confidence intervals for the model estimates, as this helps in dealing with these issues (Fox, 2016) and can facilitate the assessment of associations even in the absence of *p* values.

Within this model, sex, mean F_0 and F_0 CV were found to significantly predict attractiveness ratings. Men rated the attractiveness of target stimuli by an estimate of 0.87 units higher than women. For all participants, both mean F_0 and F_0 CV positively predicted attractiveness

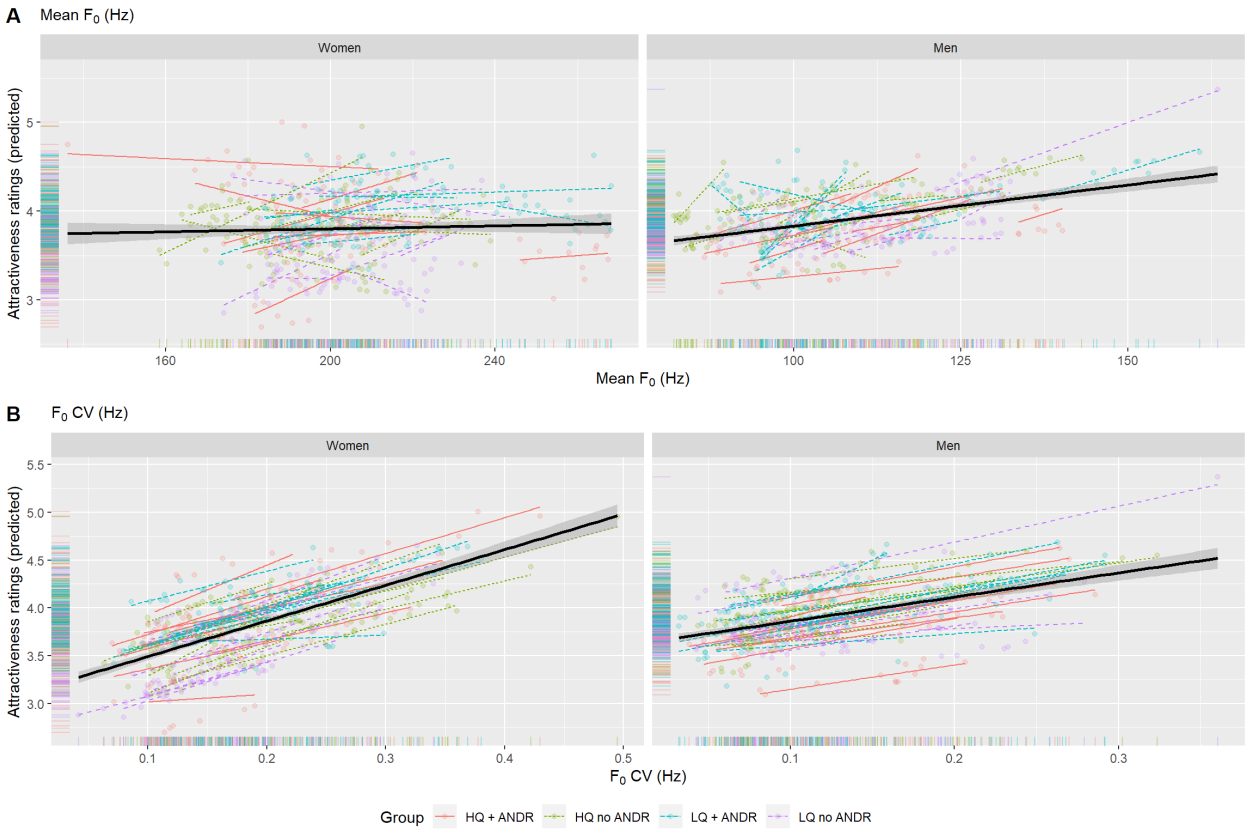
ratings (Table 2). For each increment of 1 Hz in mean F_0, ratings were estimated to increase by 0.01 units, and by each increment of 1 in F_0 CV, the model estimated an increase of 3.18 points in rated attractiveness (or, to use more realistic F_0 CV units, attractiveness ratings increased by 0.318 units for each 0.1 increment in F_0 CV).

Table 2. Final model summary (with bootstrap 95% CI).

	Estimate	***Lower 95% CI***	***Upper 95% CI***	***Std. Error***	***df***	***t***	***p***
(Intercept)	2.02	0.83	3.09	0.59	299.83	3.42	**<0.001**
Sex (men)	0.87	0.33	1.47	0.29	267	2.98	**0.003**
Mean F_0 (Hz)	0.01	0	0.01	0	274.69	2.1	**0.037**
F_0 CV (Hz)	3.18	1.86	4.61	0.72	714.5	4.39	**<0.0001**

$R^2_{marginal}$ = 0.03, $R^2_{conditional}$ = 0.13. Confidence intervals were calculated as the 2.5 and 97.5 percentiles from bootstrap (1000 simulations). Women were used as reference category for Sex. Significant effects are in bold.

Interestingly, however, while the slope of the association between mean F_0 and the attractiveness ratings predicted by this final model was close to 0 for women, and only slightly positive for men (Fig. 5A), for F_0 CV it was clearly positive not only for both men and women, but for every single participant (Fig. 5B), regardless of the odour condition to which they were exposed.



386 **Figure 5. Single term predictor slopes.** Slope of coefficients for each (single term) fixed predictor, against
387 predicted attractiveness ratings for the Final Model (linear relationship between each model term and predicted
388 response), for women (left) and men (right). (A) Mean F_0. (B) F_0 CV. Lines represent the slope for each participant,
389 according to their group. The black line with error represents the general effect.

390 # 4. Discussion

391 ## 4.1 Odour effects on voice modulation and attractiveness ratings

392 Previous research showed that men's perceived attractiveness to women is increased by the
393 presence of male axillary secretions (Thorne et al., 2002), as well as by exposure to
394 androstadienone (Saxton et al., 2008). Because of this, we expected that men portrayed in the target
395 videos would be regularly perceived as more attractive during the experimental session than the
396 control session, leading women to speak with increased voice F_0, which tends to be attractive to
397 gynephilic men (Feinberg et al., 2005; Jones et al., 2008). Similarly, and because low F_0 signals

masculinity and is a robust cue of dominance (Puts et al., 2007; Wolff and Puts, 2010), we expected men to lower their pitch when exposed to male body odour, especially if it was of high quality, as the perception of competition was likely to increase. Contrary to these expectations, the addition of male odour did not produce any consistent changes in vocal parameters. There was only a main effect of pitch variability when measured as F_0 SD, but not when measured as F_0 CV, and the latter could thus be an artefact of the measurement of variability without controlling for perceptual differences arising from tone (and sex) of the voice.

However, we did find that the presence of body odour with added ANDR caused participants to tend to give target videos more extreme ratings corresponding to the attractiveness category of the targets, while the presence of body odour without added ANDR caused the opposite tendency in participants of both sexes. While the reasons for these effects are unclear, we speculate that this could be because the presence of male body odour may decrease selectiveness in both women and men, or make targets appear as more similarly attractive (because the odour stimulus, a signal of quality, was always the same for each participant, regardless of the target evaluated). However, the addition of ANDR seem to have had the opposite effect: increasing selectiveness. For example, in women, this could be because the presence of ANDR may increase the preference for attractive targets. In men, instead of increasing the perception of competition for men, ANDR may have boosted their own confidence and/or self-perceived attractiveness, affecting their selectiveness. An explanation for these results would require future studies to specifically control for changes in variables such as self-confidence and self-perceived attractiveness in the presence of ANDR. However, it is important to note that pairwise contrasts revealed that the difference in attractiveness ratings between the control and experimental sessions (for participants exposed to odours either with or without added ANDR, separately), did not reach significance after adjustment for multiple comparisons (see Fig. 4B).

It was unexpected that neither high-quality odour nor added androstadienone had additional effects. It may be that the difference in odour quality between the high and low quality composites was insufficient to elicit quality-related changes in modulation. Using a larger sample of odour donors, and therefore accentuating differences between high- and low-quality odours, could potentially make the effect of odour quality measurable. In addition, measuring participants' subjective evaluations of intensity and pleasantness of the odour stimuli would enable a manipulation check and further exploration of differences in odour condition (e.g., Oren and Shamay-Tsoory, 2019). Alternatively, lack of effects could be due to methodological choices, including the time that odour samples were left in the cubicle before each session (15 minutes), and the time that cubicles were left open before testing another participant (>15 minutes), that may have been insufficient to avoid the residual presence of previously used stimuli, potentially creating some level of smell mixture and confounding any effects of different odour stimuli.

With respect to added androstadienone, there are several possibilities: for example, other constituents of the axillary odour could have a more prominent role in odour evaluation (see d'Ettorre et al., 2018), or these other constituents may be more perceivable in the odour mixture. A more general, evolutionary hypothesis for the lack of effects of ANDR on voice modulation, could be related to an inactivation of the vomeronasal system that would have occurred in catarrhines with the appearance of trichromacy in primates (Gilad et al., 2004; Zhang and Webb, 2003). This tendency can also be observed in primates when comparing nocturnal and diurnal lineages: the former maintain a much greater olfactory brain structure, while the latter have larger cerebral visual structures (Barton et al., 1995). This inactivation could be associated with pseudogenization, in this case leading to decreased functions or changes in the genes related to the vomeronasal organ. In addition, the main olfactory system suffered a progressive inactivation, such that only 70% of the olfactory receptor genes are functional in Old World primates, and only 40%

446 in humans (Gilad et al., 2003), potentially leading to a reduced (or non-existent) role of at least
447 *some* molecules that function as social chemosignals in related species.
448 Nevertheless, the lack of consistent ANDR effects in our study is consistent with Hare et
449 al. (2017), who found no effects of ANDR on sex perception or evaluation of masculinity-related
450 sex-specific characteristics. Ultimately, the null effect is also in line with recent doubts cast on the
451 existence of specific pheromones in humans and thus should not be expected to have any special
452 effects on any and all cognitive functions and human behaviours (Wyatt, 2015).
453
454 **4.2 Voice characteristics as predictors of perceived attractiveness**
455 Our experimental paradigm was closely based on Study 1 of Leongómez et al. (2014), but
456 there were some important differences. First, of course, the current study incorporated the addition
457 of male body odour and androstadienone in the experimental sessions. Second, it enabled further
458 investigation of vocal modulation in courtship contexts by asking participants to rate each target
459 video, in the two experimental sessions, providing us with the opportunity to test how voice
460 characteristics are related to perceived attractiveness.
461 Voice modulation, and specifically vocal modulation during courtship, is a complex
462 phenomenon that has gained increasing interest in recent years (e.g. Farley et al., 2013; Fraccaro
463 et al., 2013, 2011; Hughes et al., 2010; Leongómez et al., 2014; Pisanski et al., 2018).
464 Understanding what voice parameters are modulated, in which direction, and what social and
465 perceptual effects these modulations have, are still matters of debate that call for more research.
466 For example, in a tightly controlled experiment, Leongómez et al. (2014) found that both men and
467 women increase pitch variability when responding to attractive target stimuli. The same finding in
468 both sexes suggests pitch variability is a key parameter, but women did so when competing with
469 an attractive woman. In a less controlled but more ecologically valid experiment, Pisanski et al.

(2018) recorded participants during real, face-to-face interactions in a speed-dating game, finding that women increased both their average fundamental frequency and its variability (measured as either F_0 SD or F_0 CV) with people they selected as dates. However, although men lowered their F_0 towards individuals selected as dates, their pitch variability (either F_0 SD or F_0 CV) was not correlated with selection of dates.

Such disparities in results could be due to differences in experimental design, such as between responses to muted videos (Leongómez et al., 2014) (to avoid possible effects of pitch convergence; see Gregory et al., 2001), and real-life interactions (Pisanski et al., 2018). Furthermore, participants in the former study were instructed to explain whether and why they would like to go on a date with the person in the video, and this was done in isolation in a cubicle, while in the latter recordings were of free conversations between two participants in a noisy and busy speed-dating game setting. This suggests two things: first, that voice modulations do occur during courtship, and so can play an important part in shaping how we are perceived by others. And second, that vocal modulations are very context sensitive.

Our results, mostly congruent with Leongómez et al. (2014), suggest that pitch variability is modulated according to the attractiveness of the listener in this courtship scenario. Here, our model of perceived attractiveness (measured as attractiveness ratings given to target stimuli), shows that pitch variability (measured as F_0 CV) was a better predictor than mean F_0. Moreover, F_0 CV was predicted to be robust across participants and conditions, and in all fitted models regardless of their complexity. Importantly, F_0 CV is a measure of pitch variability, that controls for perceptual differences that depend on the average pitch of a voice sample.

4.3 Conclusions

Our study is the first to test the effects of male odour quality and ANDR in voice modulation and attractiveness ratings. We did not find support for either odour quality or ANDR effects.

Furthermore, we did not detect any consistent effects of the presence of body odour. Although the null effects of ANDR are in line with recent evidence (Hare et al., 2017), the lack of effects of odour quality, and especially of the presence of body odour (vs responses in a no-odour, control session), are somewhat surprising.

However, consistent with evidence of vocal modulations in courtship scenarios, we found that voice characteristics predict attractiveness ratings given to target videos, regardless of the presence or absence of any body odour. Recent evidence, however, is inconsistent regarding the expected direction of such modulations and the relative importance of each acoustic parameter found in different studies (Leongómez et al., 2014; Pisanski et al., 2018). This, we think, suggests that human voice modulation is extremely context-sensitive; for example, it could be that an attractive opposite-sex person could elicit an increase in pitch variability (Leongómez et al., 2014), while the presence of people nearby (as in Pisanski et al., 2018) could create an opposite tendency to decrease these modulations, therefore confounding these effects. If this is true, experimental tests of vocal modulation in courtship (and likely other) scenarios would need to consider these differences and their potential confounding effects.

5. Declarations

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5.2 Compliance with Ethical Standards

All procedures performed in studies involving human participants were in accordance with the ethical standards of the institutional research committee and with the 1964 Helsinki Declaration

and its later amendments or comparable ethical standards. Written informed consent was obtained from all individual adult participants included in the study.

5.3 Conflicts of Interest

The authors declare that they have no conflict of interest.

5.4 Data and Code availability

All data used for this article are openly available at the OSF (https://doi.org/10.17605/OSF.IO/53BZK). Code to perform data wrangling, tables, figures, and all analyses, is available in PDF ('Supplementary-Material.pdf') and *R Markdown* ('Supplementary-Material.Rmd') formats, so that it can be fully reproduced and explored in depth (https://doi.org/10.17605/OSF.IO/GWBHU).

5.5 Author contributions

Juan David Leongómez: Conceptualisation, Methodology, Formal analysis, Software, Data curation, Writing- Original draft preparation, Visualization, Investigation, Funding acquisition. **Oscar R. Sánchez**: Writing- Original draft preparation, Funding acquisition. **Milena Vásquez-Amézquita**: Writing- Original draft preparation, Writing - Review & Editing. **S. Craig Roberts**: Conceptualisation, Methodology, Writing- Original draft preparation, Writing - Review & Editing, Supervision.

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Supplementary Material

Supplementary Materials and Methods and Results (code and analyses) for **Contextualising courtship: Exploring male body odour effects on vocal modulation**

Juan David Leongómez*

26 June, 2020

Description

This `R Markdown` document contains the supplementary materials and methods, as well as results, including all code, and step by step detailed explanations for all analyses, figures and tables included in Leongómez, J.D., Sánchez, O.R., Vásquez-Amézquita, M., & Roberts, S.C. (2019). *Contextualising courtship: Exploring male body odour effects on vocal modulation.* Data available from the Open Science Framework (OSF): https://osf.io/px7m6/.

Contents

*Human Behaviour Lab, Faculty of Psychology, Universidad El Bosque. Bogota, Colombia. jdleongomez@unbosque.edu.co, jdleongomez.info

1 Supplementary Materials and Methods

1.1 Odour stimuli

Between-individual differences in attractiveness of body odour, when averaged across a number of different raters, likely reflect a measure of absolute quality such as psychosocial dominance (Havlíček et al., 2005) or low fluctuating asymmetry (Gangestad, 2003; Rikowski and Grammer, 1999), rather than a relative measure of mate compatibility based on MHC, because the latter effect will differ between different odour donor/rater pairs. Differences in mean ratings of pleasantness given by each rater to the composite odours in the HQ category ($M = 0.35$, $SD = 0.57$) were significantly higher than those given in the LQ category ($M =$ -1.35, $SD = 0.27$) (paired-samples t-test: $t_9 = 10.52$, $p < 0.001$). Note also that use of composite samples (i.e. pooling odours of 4 men in each category) further avoids the potential confounding influence of differences in genetic similarity between sniffer and odour donor (Roberts et al., 2008; Wedekind et al., 1995), and that composite body odours preserve comparable hedonic perceived qualities as the individual odours (Fialová et al., 2018).

1.2 Experimental procedure

To avoid possible effects of pitch convergence (Gregory et al., 2001), all videos were played without sound.

Participants were told that "at this stage" (to maintain the illusion that they might meet the judges) they had to base their responses only on visual characteristics of the person in the video (e.g. attractiveness, body language and clothing style). Additionally, the laptop video camera was on (but not recording) during the experiment, to create the illusion that their videos were going to be shown to opposite-sex participants; to assure this, the experimenters highlighted the video by adjusting the videorecorder in the presence of participants, while they viewed a real-time image of themselves on the monitor.

1.3 Acoustic analysis

Acoustic relevant variables were analysed and compiled using R version 4.0.0 (R Core Team, 2020), for each output produced by Praat (one for each recording), using a custom script (https://osf.io/6vcu4/). This script first creates subsets of data from each Praat output, eliminating data from times in which there are no registered values of F_0 or intensity, to avoid times when the participant was silent could affect acoustic mean, minimum, or SD values. Then, it computes the relevant values for each recording: mean F_0, F_0 SD, F_0 CV (F_0 SD/mean F_0), minimum and maximum F_0 (all in Hz), mean intensity (dB), mean F_1, F_2, and F_3 (Hz), as well as the length of the recording, the time recognised as speech (in ms), and the proportion of the length of each recording recognised as speech.

All Praat outputs, as well as the custom script to create the final database with the relevant variables, are available at the Open Science Framework, in the Acoustic data folder of this project's data component (https://osf.io/53bzk/), so that this procedure can be reproduced and explored in depth.

2 Supplementary Results

2.1 Preliminaries

2.1.1 Load Packages

Used packages include `osfr` to download and open data files directly from the Open Science Framework (OSF), using the `osf_retrieve_file` and `osf_download` functions. All packages used in this file (full list in the code below) can be directly installed from the Comprehensive R Archive Network (CRAN).

```
library(tidyverse)
library(plyr)
library(ggpubr)
library(gridExtra)
library(xtable)
library(kableExtra)
library(data.table)
library(lemon)
library(car)
```

```
library(dplyr)
library(psych)
library(lme4)
library(lmerTest)
library(emmeans)
library(gridExtra)
library(osfr)
library(rstatix)
library(sciplot)
library(bbmle)
library(performance)
library(broom)
library(MuMIn)
```

2.1.2 Custom functions

2.1.2.1 `lmeSig` Function to bold significant effects from anova-type tables, specifying correctly formatted predictor names for the models here reported. This function highlights significant p values, and formats the output table in HTML using `kable`.

```
#List of predictor names ordered and formatted.
prednames <- c("S",
               "SA",
               "Sex",
               "OQ",
               "ANDR",
               "S $\\times$ SA",
               "S $\\times$ Sex",
               "SA $\\times$ Sex",
               "S $\\times$ OQ",
               "SA $\\times$ OQ",
               "Sex $\\times$ OQ",
               "S $\\times$ ANDR",
               "SA $\\times$ ANDR",
               "Sex $\\times$ ANDR",
               "OQ $\\times$ ANDR",
               "S $\\times$ SA $\\times$ Sex",
               "S $\\times$ SA $\\times$ OQ",
               "S $\\times$ Sex $\\times$ OQ",
               "SA $\\times$ Sex $\\times$ OQ",
               "S $\\times$ SA $\\times$ ANDR",
               "S $\\times$ Sex $\\times$ ANDR",
               "SA $\\times$ Sex $\\times$ ANDR",
               "S $\\times$ OQ $\\times$ ANDR",
               "SA $\\times$ OQ $\\times$ ANDR",
               "Sex $\\times$ OQ $\\times$ ANDR",
               "S $\\times$ SA $\\times$ Sex $\\times$ OQ",
               "S $\\times$ SA $\\times$ Sex $\\times$ ANDR",
               "S $\\times$ SA $\\times$ OQ $\\times$ ANDR",
               "S $\\times$ Sex $\\times$ OQ $\\times$ ANDR",
               "SA $\\times$ Sex $\\times$ OQ $\\times$ ANDR",
               "S $\\times$ SA $\\times$ Sex $\\times$ OQ $\\times$ ANDR")

#Function
lmeSig <- function(modTab, capti){
  anoTab <- anova(modTab)
  anoTab[,6] <- ifelse(anoTab[,6] < 0.0001, "\\textbf{<0.0001}",
```

```
                      ifelse(anoTab[,6] < 0.001, "\\textbf{<0.001}",
                             ifelse(anoTab[,6] < 0.05,
                                    paste0("\\textbf{", round(anoTab[,6], 3), "}"),
                                    round(anoTab[,6], 3))))
  rownames(anoTab) <- prednames
  anoTab$DF <- paste0(anoTab$NumDF, " - ",
                      round(anoTab$DenDF, 2))
  anoTab <- anoTab[,c(1, 7, 5:6)]
finTab <- kable(anoTab,
                digits = 2,
                caption = capti,
                align = "c",
                col.names = c("Sum of Squares",
                              "$df$" ,
                              "$F$",
                              "$p$"),
                booktabs = TRUE,
                escape = FALSE) %>%
  kable_styling(latex_options = "HOLD_position") %>%
  footnote(general = "S = Session (control, experimental);
           Sex = participants sex (women, men);
           OQ = odour quality (high quality, low quality);
           ANDR = androstadienone (added, not added);
           SA = stimuli attractiveness (attractive, unattractive).",
           threeparttable = TRUE,
           escape = FALSE)
  return(finTab)
}

#Function
lmeSigFin <- function(modTab, capti){
  anoTab <- anova(modTab)
  anoTab[,6] <- ifelse(anoTab[,6] < 0.0001, "\\textbf{<0.0001}",
                      ifelse(anoTab[,6] < 0.001, "\\textbf{<0.001}",
                             ifelse(anoTab[,6] < 0.05,
                                    paste0("\\textbf{", round(anoTab[,6], 3), "}"),
                                    round(anoTab[,6], 3))))
  rownames(anoTab) <- prednames
  anoTab$DF <- paste0(anoTab$NumDF, " - ",
                      round(anoTab$DenDF, 2))
  anoTab <- anoTab[,c(1, 7, 5:6)]
  colnames(anoTab) <- c("Sum of Squares",
                        "$df$" ,
                        "$F$",
                        "$p$")
  return(anoTab)
}
```

2.1.2.2 `summaSig` Function to bold significant p values from model tables, including `summary$coefficients`, and `lmerTest::ranova`. It highlights significant p values, and formats the output table in LaTeX, ready to be used with `kable`.

```
summasig <- function(modTab, pcol) {
    modTab[, pcol] <- ifelse(modTab[, pcol] < 1e-04, "\\textbf{0.0001}",
        ifelse(modTab[, pcol] < 0.001, "\\textbf{0.001}",
               ifelse(modTab[, pcol] < 0.05,
```

```
                    paste0("\\textbf{", round(modTab[, pcol],3), "}"),
                    round(modTab[, pcol], 3))))
    return(modTab)
}
```

2.1.2.3 modDiag and lmerDiag Functions to create a plot of model diagnostics, including residual distribution, homoscedasticity (constant variance of residuals) and linearity in each (single term) predictor.

```
modDiag <- function(model){
  pa <- qplot(residuals(model,
                        type = "pearson"),
              geom = "blank") +
    geom_histogram(aes(y = ..density..),
                   bins = 30,
                   alpha = 0.4) +
    stat_density(fill = "red",
                 alpha = 0.4) +
    labs(y = "Density",
         x = "Residuals")
  pb <- ggplot(augment(model), aes(.fitted, .resid)) +
    geom_point() +
    stat_smooth(method="loess") +
    geom_hline(yintercept=0,
               col="red",
               linetype="dashed") +
    labs(x = "Fitted values",
         y = "Residuals")
  pc1 <- ggplot(data.frame(x1 = db$Session,
                           pearson = residuals(model,
                                               ype = "pearson")),
                aes(x = x1,
                    y = pearson)) +
    geom_jitter(alpha = 0.1,
                width = 0.1) +
    geom_boxplot(width=0.2,
                 notch = TRUE,
                 alpha = 0.5) +
    geom_smooth(method = "lm",
                aes(group=1)) +
    labs(x = "Session",
         y = "Pearson residuals")
  pc2 <- ggplot(data.frame(x1 = db$Sex,
                           pearson = residuals(model,
                                               ype = "pearson")),
                aes(x = x1,
                    y = pearson)) +
    geom_jitter(alpha = 0.1,
                width = 0.1) +
    geom_boxplot(width=0.2,
                 notch = TRUE,
                 alpha = 0.5) +
    geom_smooth(method = "lm",
                aes(group=1)) +
    labs(x = "Sex",
         y = "")
  pc3 <- ggplot(data.frame(x1 = db$ANDR,
```

```
                              pearson = residuals(model,
                                                  ype = "pearson")),
                    aes(x = x1,
                        y = pearson)) +
    geom_jitter(alpha = 0.1,
                width = 0.1) +
    geom_boxplot(width=0.2,
                 notch = TRUE,
                 alpha = 0.5) +
    geom_smooth(method = "lm",
                aes(group=1)) +
    labs(x = "ANDR",
         y = "")
  pc4 <- ggplot(data.frame(x1 = db$Odour_Quality,
                              pearson = residuals(model,
                                                  ype = "pearson")),
                    aes(x = x1,
                        y = pearson)) +
    geom_jitter(alpha = 0.1,
                width = 0.1) +
    geom_boxplot(width=0.2,
                 notch = TRUE,
                 alpha = 0.5) +
    geom_smooth(method = "lm",
                aes(group=1)) +
    labs(x = "Odour Quality",
         y = "")
  pc5 <- ggplot(data.frame(x1 = db$Stimuli_Attractiveness,
                              pearson = residuals(model,
                                                  ype = "pearson")),
                    aes(x = x1,
                        y = pearson)) +
    geom_jitter(alpha = 0.1,
                width = 0.1) +
    geom_boxplot(width=0.2,
                 notch = TRUE,
                 alpha = 0.5) +
    geom_smooth(method = "lm",
                aes(group=1)) +
    labs(x = "Stimuli Attractiveness",
         y = "")
  Fig <- ggarrange(ggarrange(pa, pb,
                             ncol = 2,
                             labels = "AUTO"),
                   ggarrange(pc1, pc2, pc3, pc4, pc5,
                             nrow = 1,
                             labels = "C"),
                   nrow = 2,
                   heights = c(1, 2))
  return(Fig)
}

lmerDiag <- function(model, data){
  pa <- qplot(residuals(model,
                        type = "pearson"),
              geom = "blank") +
```

```
    geom_histogram(aes(y = ..density..),
                   alpha = 0.4,
                   bins = 30) +
    stat_density(fill = "red",
                 alpha = 0.4) +
    labs(y = "Density",
         x = "Residuals")
  pb <- ggplot(augment(model), aes(.fitted, .resid)) +
    geom_point() +
    stat_smooth(method="loess") +
    geom_hline(yintercept=0,
               col="red",
               linetype="dashed") +
    labs(x = "Fitted values",
         y = "Residuals")
  pc1 <- ggplot(data.frame(x1 = data$Mean_F0,
                           pearson = residuals(model,
                                               type = "pearson")),
                aes(x = x1,
                    y = pearson)) +
    geom_point() +
    geom_smooth(method = "lm") +
    labs(x = expression(paste("Mean F"[0], " (Hz)")),
         y = "Pearson residuals")
  pc2 <- ggplot(data.frame(x1 = data$F0_CV,
                           pearson = residuals(model,
                                               type = "pearson")),
                aes(x = x1,
                    y = pearson)) +
    geom_point() +
    geom_smooth(method = "lm") +
    labs(x = expression(paste("F"[0], " CV (Hz)")),
         y = "")
  Fig <- ggarrange(ggarrange(pa, pb,
                             ncol = 2,
                             labels = "AUTO"),
                   ggarrange(pc1, pc2,
                             nrow = 1,
                             labels = "C"),
                   nrow = 2)
  return(Fig)
}
```

2.1.2.4 `corstarsl` Function to create a correlation matrix, and display significance (from http://myowelt.blogspot.com/2008/04/beautiful-correlation-tables-in-r.html)

```
corstarsl <- function(x){
  require(Hmisc)
  x <- as.matrix(x)
  R <- rcorr(x)$r
  p <- rcorr(x)$P

  ## define notions for significance levels; spacing is important.
  mystars <- ifelse(p < .001, "***", ifelse(p < .01, "** ", ifelse(p < .05, "* ", " ")))

  ## trunctuate the matrix that holds the correlations to two decimal
```

```
  R <- format(round(cbind(rep(-1.11, ncol(x)), R), 2))[,-1]

  ## build a new matrix that includes the correlations with their apropriate stars
  Rnew <- matrix(paste(R, mystars, sep = ""), ncol = ncol(x))
  diag(Rnew) <- paste(diag(R), " ", sep = "")
  rownames(Rnew) <- colnames(x)
  colnames(Rnew) <- paste(colnames(x), "", sep = "")

  ## remove upper triangle
  Rnew <- as.matrix(Rnew)
  Rnew[upper.tri(Rnew, diag = TRUE)] <- ""
  Rnew <- as.data.frame(Rnew)

  ## remove last column and return the matrix (which is now a data frame)
  Rnew <- cbind(Rnew[1:length(Rnew)-1])
  return(Rnew)
}
```

2.1.2.5 `contr.stars` Function to create a dataframe of model contrasts, representing significance levels from an `emmeans::emmeans` output. These dataframes are formatted to be called by the `ggpubr::stat_pvalue_manual` function used in model figures.

```
contr.stars <- function(emms){
  require(emmeans)
  x <- as.data.frame(contrast(emms, interaction = "pairwise"))
  x <- separate(x,
                col = 1,
                into = c("group1", "group2"),
                sep = " - ",
                remove = TRUE)
  x$p.signif <- ifelse(x[,7] < 0.0001, "****",
                       ifelse(x[,7] < 0.001, "***",
                              ifelse(x[,7] < 0.01, "**",
                                     ifelse(x[,7] < 0.05, "*",
                                            ifelse(x[,7] < 0.10, "†", NA)))))
  return(x)
}
```

2.1.2.6 `data.summary` Function to calculate standard errors. Used in model figures.

```
data.summary <- function(x) {
  m <- mean(x)
  ymin <- m - se(x)
  ymax <- m + se(x)
  return(c(y=m,ymin=ymin,ymax=ymax))
}
```

2.1.2.7 `pvalr` This function takes p-values and formats them (from rawr).

```
pvalr <- function(pvals, sig.limit = .001, digits = 3, html = FALSE) {

  roundr <- function(x, digits = 1) {
    res <- sprintf(paste0('%.', digits, 'f'), x)
    zzz <- paste0('0.', paste(rep('0', digits), collapse = ''))
    res[res == paste0('-', zzz)] <- zzz
    res
  }
```

```
  sapply(pvals, function(x, sig.limit) {
    if (x < sig.limit)
      if (html)
        return(sprintf('&lt; %s', format(sig.limit))) else
          return(sprintf('< %s', format(sig.limit)))
    if (x > .1)
      return(roundr(x, digits = 2)) else
        return(roundr(x, digits = digits))
  }, sig.limit = sig.limit)
}
```

2.1.3 Load and organise data

All individual Praat outputs were compiled into the `Database.csv` file using an R script (https://osf.io/6vcu4/). Attractiveness ratings given to each target stimulus by each participant in each session are available in the `Attractiveness Ratings.csv` file. Both files are available from the **Data** component in the Open Science Framework (OSF) project site (https://osf.io/53bzk/).

```
#Download and load acoustic data
aco <- osf_retrieve_file("bdf3g") %>%
  osf_download(conflicts = "overwrite")

db.1 <- read.csv(aco$local_path,
                 sep = ";",
                 dec = ".")

#Download and load attractiveness ratings
rat <- osf_retrieve_file("srpg6") %>%
  osf_download(conflicts = "overwrite")

AttRatings <- read.csv(rat$local_path,
                       sep = ",",
                       dec = ".")
```

Merge both acoustic data and attractiveness ratings.

```
#Merge acoustic data and attractiveness ratings
db <- inner_join(db.1,
                 AttRatings,
                 by = c("Subject",
                        "Sex",
                        "Group",
                        "Odour_Quality",
                        "ANDR",
                        "Session",
                        "Stimuli_Attractiveness",
                        "Stimuli_Sex"))

#Change sex to factor
db$Sex <- factor(db$Sex,
                 levels = c("Women", "Men"))
db <- db[,c(1:21,23:24,22)]
```

Final dataframe structure

```
str(db)
```

```
## 'data.frame':    950 obs. of  24 variables:
```

```
##  $ Recording             : chr  "F_A_01_Con_OS_Att_01.txt" "F_A_01_Con_OS_Att_02.txt" "F_A_01_Con_OS_At
##  $ Subject               : chr  "F_A_01" "F_A_01" "F_A_01" "F_A_01" ...
##  $ Sex                   : Factor w/ 2 levels "Women","Men": 1 1 1 1 1 1 1 1 1 1 ...
##  $ Group                 : chr  "HQ no ANDR" "HQ no ANDR" "HQ no ANDR" "HQ no ANDR" ...
##  $ Odour_Quality         : chr  "HQ" "HQ" "HQ" "HQ" ...
##  $ ANDR                  : chr  "no ANDR" "no ANDR" "no ANDR" "no ANDR" ...
##  $ Session               : chr  "Control" "Control" "Control" "Control" ...
##  $ Stimuli_Sex           : chr  "Opposite Sex" "Opposite Sex" "Opposite Sex" "Opposite Sex" ...
##  $ Stimuli_Attractiveness: chr  "Attractive" "Attractive" "Attractive" "Unattractive" ...
##  $ Mean_F0               : num  172 178 169 169 174 ...
##  $ F0_SD                 : num  17.2 27.2 22.5 23.7 35.5 ...
##  $ F0_CV                 : num  0.0996 0.153 0.1337 0.1402 0.2044 ...
##  $ Min_F0                : num  113.3 100.1 99.9 102.9 101.5 ...
##  $ Max_F0                : num  229 383 250 262 499 ...
##  $ Intensity             : num  76.4 77.3 74.9 75.1 77 ...
##  $ F1                    : num  523 537 556 542 550 ...
##  $ F2                    : num  1970 1942 1730 1859 1847 ...
##  $ F3                    : num  2933 2876 2887 2880 2821 ...
##  $ Recording_length      : int  6140 5430 10430 9490 12560 18140 8320 11240 12260 8510 ...
##  $ Voice_length          : int  3460 2940 5670 5470 6130 9020 3910 5660 6640 4830 ...
##  $ Prop                  : num  0.564 0.541 0.544 0.576 0.488 ...
##  $ Age                   : int  23 23 23 23 23 23 23 23 23 23 ...
##  $ AttractivenessRatings : num  5.33 5.33 5.33 4.33 4.33 ...
##  $ Stimulus_ID           : int  1 2 3 4 5 6 1 2 3 4 ...
```

2.1.4 Figure 1. Experimental design

2.1.4.1 Colour version Online version.

```
Fig1 <- osf_retrieve_file("w6c4s") %>%
  osf_download(conflicts = "overwrite")

knitr::include_graphics("Fig1_col.pdf")
```

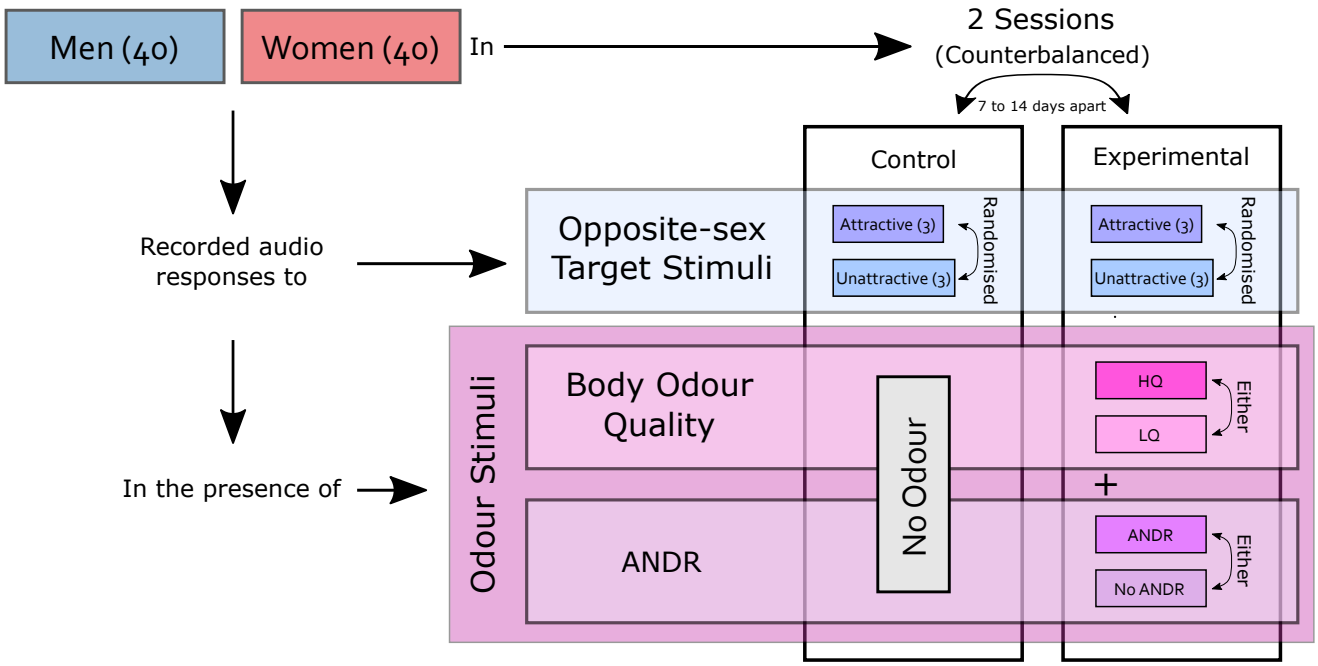

Figure 1. Experimental design. Diagram of the sessions and stimuli used in each case. The order of session was counterbalanced between participants in each odour stimuli combination (odour quality and ANDR). For body odour quality, HQ = high quality; LQ = low quality. ANDR = androstadienone.

2.1.4.2 Greyscale version

Print version.

```
Fig1 <- osf_retrieve_file("5ftgh") %>%
  osf_download(conflicts = "overwrite")

knitr::include_graphics("Fig1_BW.pdf")
```

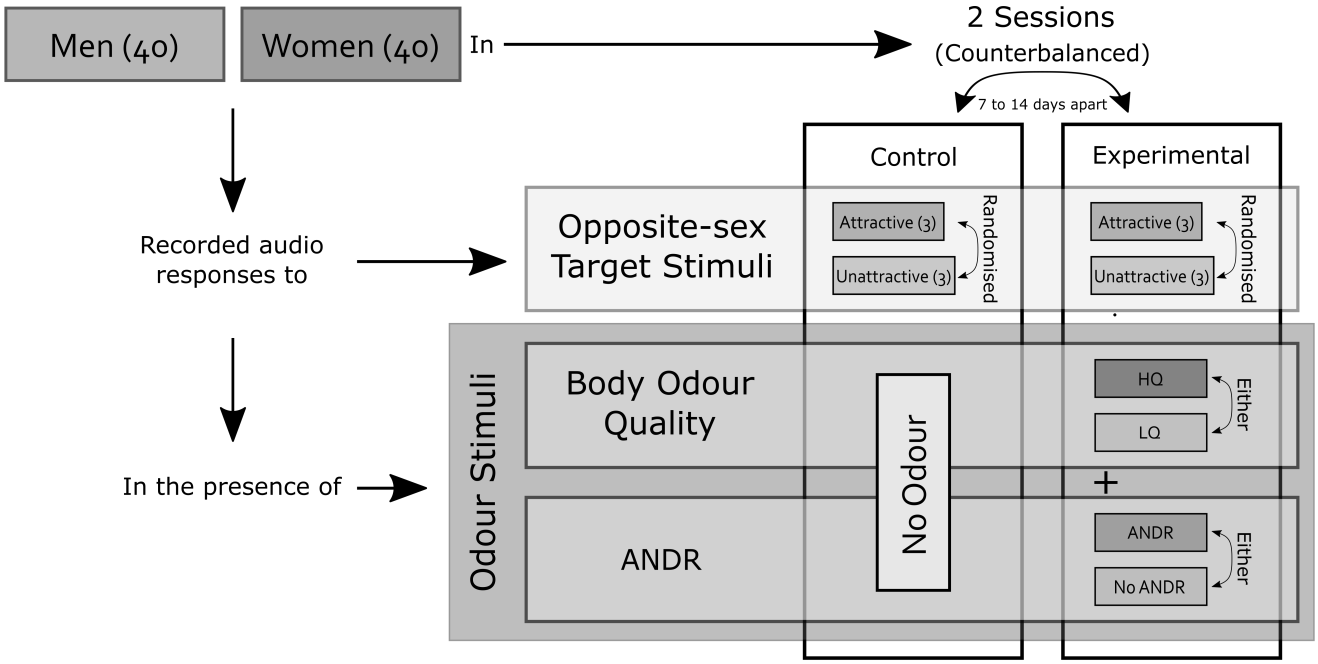

Figure 1. Experimental design. Diagram of the sessions and stimuli used in each case. The order of session was counterbalanced between participants in each odour stimuli combination (odour quality and ANDR). For body odour quality, HQ = high quality; LQ = low quality. ANDR = androstadienone.

2.2 Descriptives

```
#Subsets of men and women
WomD <- subset(db, db$Sex ==  "Women")
MenD <- subset(db, db$Sex ==  "Men")

#List of corrected variable names with Markdown syntax
varnames <- c("Mean $F_{0}$ (Hz)",
              "$F_{0}$ SD (Hz)",
              "$F_{0}$ CV (Hz)",
              "Minimum $F_{0}$ (Hz)",
              "Maximum $F_{0}$ (Hz)",
              "Intensity (dB)",
              "$F_{1}$ (Hz)",
              "$F_{2}$ (Hz)",
              "$F_{3}$ (Hz)",
              "Recording lenght (ms)",
              "Time recognised as speech (ms)",
              "Attractiveness Ratings")

#List of descriptive variables to include with Markdown syntax
varinames = c("Measured\ncharacteristic",
              "Group",
              "Session",
              "Stimuli\nattractiveness",
              "$n$",
              "Mean",
              "$SD$",
              "Median",
              "Min",
```

```
              "Max")

#Descriptives of women
descF <- describeBy(WomD[c(10:20,23)],
                    list(WomD$Stimuli_Attractiveness,
                         WomD$Session, WomD$Group),
                    mat = TRUE, digits = 2)
#Select only relevant descriptives
descF <- descF[,c(4,3,2,6:9,12:13)] %>%
  rownames_to_column("Measured characteristic")
#Add correct variable names
descF$`Measured characteristic` <- rep(varnames, each = 16)

#Descriptives of men
descM <- describeBy(MenD[c(10:20,23)],
                    list(MenD$Stimuli_Attractiveness,
                         MenD$Session, MenD$Group),
                    mat = TRUE, digits = 2)
#Select only relevant descriptives
descM <- descM[,c(4,3,2,6:9,12:13)] %>%
  rownames_to_column("Measured characteristic")
#Add correct variable names
descM$`Measured characteristic` <- rep(varnames, each = 16)
```

2.2.1 Table S1. Women

```
kable(
  descF,
  booktabs = TRUE,
  align = c("l", "l", "l", "l", "c", "c", "c", "c", "c", "c"),
  caption = "\\textbf{Table S1.} Descriptive statistics of
  measured variables for women",
  col.names = linebreak(varinames,
              align = "c"),
  longtable = TRUE,
  escape = FALSE) %>%
  kable_styling(latex_options = c("HOLD_position"),
                font_size = 6) %>%
  collapse_rows(1:3)
```

Table S1. Descriptive statistics of measured variables for women

Measured characteristic	Group	Session	Stimuli attractiveness	*n*	Mean	*SD*	Median	Min	Max
	HQ + ANDR	Control	Attractive	30	203.98	21.06	200.01	179.13	267.45
			Unattractive	30	201.05	22.36	192.79	177.89	264.45
		Experimental	Attractive	30	201.89	25.95	198.52	136.27	267.12
			Unattractive	29	201.87	22.32	199.97	170.35	264.65
	HQ no ANDR	Control	Attractive	30	196.02	21.04	198.37	160.30	237.20
			Unattractive	30	195.66	18.75	195.10	158.54	229.50
		Experimental	Attractive	30	196.13	17.87	195.05	164.02	231.53
			Unattractive	30	199.08	19.56	196.43	165.52	238.85
	LQ + ANDR	Control	Attractive	30	214.11	23.38	206.18	184.52	264.03
			Unattractive	30	206.43	19.38	201.94	173.44	251.90
		Experimental	Attractive	30	214.27	22.99	207.17	187.75	268.07
			Unattractive	30	211.11	24.26	203.79	183.87	268.27

Mean F_0 (Hz)									
	LQ no ANDR	Control	Attractive	30	209.04	15.64	208.77	179.62	243.62
			Unattractive	30	202.25	15.25	201.89	174.21	226.17
		Experimental	Attractive	30	207.72	13.37	204.84	188.26	236.74
			Unattractive	30	200.61	14.48	199.16	176.40	224.64
F_0 SD (Hz)	HQ + ANDR	Control	Attractive	30	37.94	15.11	37.31	18.01	83.24
			Unattractive	30	31.73	12.85	27.20	14.55	62.16
		Experimental	Attractive	30	37.74	13.16	35.64	14.83	71.10
			Unattractive	29	33.29	11.16	32.70	12.17	52.89
	HQ no ANDR	Control	Attractive	30	42.10	13.85	41.88	17.17	66.58
			Unattractive	30	41.02	19.45	34.78	15.24	102.77
		Experimental	Attractive	30	34.88	12.78	33.37	11.95	59.04
			Unattractive	30	36.21	18.78	28.01	16.68	91.46
	LQ + ANDR	Control	Attractive	30	41.62	12.92	39.99	20.62	72.13
			Unattractive	30	39.92	14.03	38.81	12.39	79.36
		Experimental	Attractive	30	41.08	17.10	37.81	14.98	79.62
			Unattractive	30	38.17	14.28	35.03	16.27	71.30
	LQ no ANDR	Control	Attractive	30	40.21	11.94	38.57	21.60	66.92
			Unattractive	30	31.84	10.51	29.37	13.85	53.67
		Experimental	Attractive	30	37.31	13.92	35.25	9.24	71.79
			Unattractive	30	33.06	12.56	30.33	16.34	61.74
F_0 CV (Hz)	HQ + ANDR	Control	Attractive	30	0.19	0.08	0.19	0.10	0.43
			Unattractive	30	0.16	0.07	0.14	0.07	0.32
		Experimental	Attractive	30	0.19	0.08	0.17	0.08	0.38
			Unattractive	29	0.17	0.06	0.15	0.07	0.30
	HQ no ANDR	Control	Attractive	30	0.21	0.07	0.21	0.10	0.35
			Unattractive	30	0.21	0.09	0.19	0.08	0.49
		Experimental	Attractive	30	0.18	0.07	0.17	0.06	0.36
			Unattractive	30	0.18	0.08	0.15	0.09	0.42
	LQ + ANDR	Control	Attractive	30	0.19	0.06	0.19	0.10	0.31
			Unattractive	30	0.19	0.07	0.19	0.07	0.37
		Experimental	Attractive	30	0.19	0.08	0.17	0.08	0.38
			Unattractive	30	0.18	0.07	0.17	0.09	0.34
	LQ no ANDR	Control	Attractive	30	0.19	0.06	0.19	0.10	0.34
			Unattractive	30	0.16	0.05	0.15	0.08	0.29
		Experimental	Attractive	30	0.18	0.06	0.17	0.04	0.33
			Unattractive	30	0.17	0.07	0.15	0.08	0.34
Minimum F_0 (Hz)	HQ + ANDR	Control	Attractive	30	114.28	28.66	100.40	99.77	216.22
			Unattractive	30	110.50	19.75	101.03	99.77	176.33
		Experimental	Attractive	30	116.07	25.61	102.48	99.81	179.28
			Unattractive	29	111.50	26.93	100.64	99.80	229.75
	HQ no ANDR	Control	Attractive	30	107.02	15.11	100.69	99.79	164.30
			Unattractive	30	112.07	22.88	101.50	99.82	178.94
		Experimental	Attractive	30	110.75	20.05	102.37	99.82	176.80
			Unattractive	30	110.01	18.01	101.89	99.78	167.82
	LQ + ANDR	Control	Attractive	30	114.57	30.24	102.59	99.84	211.55
			Unattractive	30	109.64	20.12	101.40	99.79	202.46
		Experimental	Attractive	30	124.46	36.09	104.54	99.78	212.19
			Unattractive	30	113.00	25.44	102.21	99.80	211.07
	LQ no ANDR	Control	Attractive	30	113.33	24.39	102.59	99.82	178.27
			Unattractive	30	108.16	20.55	100.94	99.81	176.62
		Experimental	Attractive	30	113.26	27.05	100.78	99.81	187.42
			Unattractive	30	106.48	16.31	100.86	99.76	178.45

Maximum F_0 (Hz)	HQ + ANDR	Control	Attractive	30	404.23	102.76	460.36	232.44	499.79
			Unattractive	30	394.18	104.13	454.03	228.12	499.83
		Experimental	Attractive	30	367.82	90.90	323.78	252.34	497.72
			Unattractive	29	346.20	92.12	305.33	219.73	499.90
	HQ no ANDR	Control	Attractive	30	372.07	105.89	378.57	204.68	499.57
			Unattractive	30	385.00	106.92	423.14	216.09	499.22
		Experimental	Attractive	30	349.11	104.72	283.74	222.20	499.61
			Unattractive	30	356.46	100.75	310.89	235.05	499.85
	LQ + ANDR	Control	Attractive	30	379.67	84.95	393.99	249.23	499.61
			Unattractive	30	392.20	98.23	431.27	213.53	499.16
		Experimental	Attractive	30	397.87	96.04	442.01	239.05	499.41
			Unattractive	30	381.25	97.57	429.02	242.76	496.86
	LQ no ANDR	Control	Attractive	30	407.57	91.14	437.60	262.95	499.41
			Unattractive	30	350.84	97.76	305.12	219.22	493.99
		Experimental	Attractive	30	360.75	94.44	321.11	220.01	497.75
			Unattractive	30	317.85	69.85	297.79	236.27	481.83
Intensity (dB)	HQ + ANDR	Control	Attractive	30	67.17	4.91	69.95	56.09	73.81
			Unattractive	30	67.59	5.30	70.28	56.01	73.00
		Experimental	Attractive	30	65.09	9.83	69.14	40.59	77.65
			Unattractive	29	65.11	10.38	69.40	39.22	76.18
	HQ no ANDR	Control	Attractive	30	67.03	6.02	68.24	54.10	77.30
			Unattractive	30	66.78	6.62	69.00	55.16	77.04
		Experimental	Attractive	30	67.61	4.75	67.87	58.45	74.83
			Unattractive	30	67.75	3.91	68.03	60.61	74.16
	LQ + ANDR	Control	Attractive	30	67.18	5.46	67.05	54.15	74.21
			Unattractive	30	66.49	5.41	65.99	53.40	73.40
		Experimental	Attractive	30	66.72	5.05	67.91	54.55	72.98
			Unattractive	30	66.82	5.34	67.90	52.64	74.52
	LQ no ANDR	Control	Attractive	30	65.59	3.32	65.63	59.90	70.62
			Unattractive	30	65.44	3.72	66.02	56.07	70.70
		Experimental	Attractive	30	65.86	5.70	65.15	54.06	74.00
			Unattractive	30	65.63	5.61	65.35	54.30	73.35
F_1 (Hz)	HQ + ANDR	Control	Attractive	30	598.46	52.07	588.94	496.07	698.50
			Unattractive	30	594.99	50.48	590.61	484.78	721.89
		Experimental	Attractive	30	557.07	115.22	573.03	259.86	807.04
			Unattractive	29	553.29	111.21	591.72	240.25	717.77
	HQ no ANDR	Control	Attractive	30	572.86	57.46	567.70	472.42	695.74
			Unattractive	30	597.37	60.82	592.65	477.99	729.40
		Experimental	Attractive	30	607.41	63.98	594.46	504.95	738.77
			Unattractive	30	603.59	41.46	595.48	513.32	714.39
	LQ + ANDR	Control	Attractive	30	569.82	55.60	576.43	428.62	715.33
			Unattractive	30	587.26	54.77	568.71	488.12	713.16
		Experimental	Attractive	30	575.99	68.18	574.35	445.05	697.93
			Unattractive	30	583.26	60.15	577.20	482.32	711.72
	LQ no ANDR	Control	Attractive	30	558.36	57.88	566.54	445.58	671.49
			Unattractive	30	565.90	68.76	578.56	440.17	664.84
		Experimental	Attractive	30	567.03	61.80	557.96	458.66	783.20
			Unattractive	30	577.41	69.34	566.78	417.09	800.50
	HQ + ANDR	Control	Attractive	30	1995.37	158.19	2015.55	1702.32	2315.69
			Unattractive	30	1944.17	156.24	1951.02	1723.10	2244.60
		Experimental	Attractive	30	1986.91	177.20	1982.20	1609.49	2278.17
			Unattractive	29	1961.78	171.27	1979.67	1612.21	2202.21
			Attractive	30	1981.53	118.99	1968.19	1729.62	2297.70

F_2 (Hz)	HQ no ANDR	Control	Unattractive	30	1993.66	169.72	1978.53	1730.25	2631.69
		Experimental	Attractive	30	1971.38	100.66	2003.17	1803.55	2132.80
			Unattractive	30	1959.54	113.98	1985.17	1557.19	2160.75
	LQ + ANDR	Control	Attractive	30	1956.81	126.28	1994.09	1618.41	2151.79
			Unattractive	30	1931.18	96.40	1962.02	1708.99	2108.90
		Experimental	Attractive	30	1915.28	100.07	1926.59	1711.96	2121.35
			Unattractive	30	1856.58	113.64	1858.42	1565.90	2040.78
	LQ no ANDR	Control	Attractive	30	1933.58	83.88	1935.68	1722.09	2095.48
			Unattractive	30	1908.73	70.42	1914.56	1758.21	2037.50
		Experimental	Attractive	30	1977.62	91.71	1977.24	1804.17	2187.74
			Unattractive	30	1945.21	88.19	1918.32	1817.08	2156.79
F_3 (Hz)	HQ + ANDR	Control	Attractive	30	3003.44	106.71	3006.00	2815.01	3199.91
			Unattractive	30	2972.03	106.54	2969.69	2766.93	3161.56
		Experimental	Attractive	30	3008.31	143.48	2999.56	2851.38	3392.23
			Unattractive	29	2985.90	151.14	2946.64	2790.06	3307.27
	HQ no ANDR	Control	Attractive	30	2975.58	132.96	2938.51	2672.73	3369.74
			Unattractive	30	2975.80	149.76	2949.96	2709.09	3426.78
		Experimental	Attractive	30	2973.43	105.60	2947.89	2862.75	3230.57
			Unattractive	30	2980.93	111.46	2981.55	2790.82	3205.30
	LQ + ANDR	Control	Attractive	30	2994.92	114.77	2982.85	2777.96	3249.45
			Unattractive	30	2974.64	115.06	2971.71	2781.94	3249.23
		Experimental	Attractive	30	2966.25	86.53	2963.69	2805.52	3128.70
			Unattractive	30	2945.75	101.24	2972.90	2744.19	3124.36
	LQ no ANDR	Control	Attractive	30	2997.53	88.63	2974.30	2828.34	3220.25
			Unattractive	30	2978.48	85.70	2989.99	2788.96	3159.88
		Experimental	Attractive	30	3012.95	83.94	2993.68	2864.48	3235.28
			Unattractive	30	3003.48	92.88	2986.39	2884.83	3211.54
Recording lenght (ms)	HQ + ANDR	Control	Attractive	30	8352.67	3153.36	8155.00	3180.00	14680.00
			Unattractive	30	10020.00	3862.51	11005.00	2860.00	18600.00
		Experimental	Attractive	30	8211.67	3569.81	8660.00	2630.00	16620.00
			Unattractive	29	8933.79	3936.55	9680.00	3000.00	18620.00
	HQ no ANDR	Control	Attractive	30	7059.67	3415.50	5900.00	3260.00	16650.00
			Unattractive	30	8681.00	4986.63	7815.00	2190.00	18140.00
		Experimental	Attractive	30	7409.00	4057.22	6220.00	2650.00	18530.00
			Unattractive	30	7650.33	4111.44	6010.00	2100.00	18610.00
	LQ + ANDR	Control	Attractive	30	7590.33	2997.11	7210.00	2830.00	14690.00
			Unattractive	30	9069.33	3727.17	8275.00	3120.00	16550.00
		Experimental	Attractive	30	8002.67	2825.56	8065.00	2740.00	14950.00
			Unattractive	30	8682.33	3920.16	8405.00	3290.00	18760.00
	LQ no ANDR	Control	Attractive	30	8813.00	2607.19	9140.00	3280.00	14090.00
			Unattractive	30	10265.00	4321.47	9930.00	3340.00	19230.00
		Experimental	Attractive	30	8744.00	4370.40	7795.00	3890.00	19300.00
			Unattractive	30	9174.33	3883.70	8510.00	2980.00	17810.00
	HQ + ANDR	Control	Attractive	30	3652.00	1367.86	3865.00	1240.00	6690.00
			Unattractive	30	4431.67	1576.84	4695.00	1080.00	6720.00
		Experimental	Attractive	30	3742.00	1441.12	3895.00	1220.00	7340.00
			Unattractive	29	4178.97	1880.03	4390.00	1310.00	7210.00
	HQ no ANDR	Control	Attractive	30	3116.00	1710.57	2730.00	1070.00	8330.00
			Unattractive	30	3743.67	2353.83	3170.00	810.00	9020.00
		Experimental	Attractive	30	3507.33	2011.92	3230.00	1290.00	8420.00
			Unattractive	30	3582.67	2210.25	3340.00	1030.00	11120.00
		Control	Attractive	30	3352.67	1497.90	3115.00	280.00	6820.00
			Unattractive	30	3819.00	1477.65	3580.00	1870.00	7750.00

Time recognised as speech (ms)	LQ + ANDR	Experimental	Attractive	30	3628.00	1072.63	3805.00	1610.00	5700.00
			Unattractive	30	3996.33	1646.48	3765.00	1890.00	7960.00
	LQ no ANDR	Control	Attractive	30	3883.67	976.26	3805.00	1800.00	5860.00
			Unattractive	30	4477.33	1521.89	4570.00	2190.00	7930.00
		Experimental	Attractive	30	4122.00	1785.03	3790.00	1700.00	7520.00
			Unattractive	30	4132.00	1615.00	4180.00	1090.00	7720.00
Attractiveness Ratings	HQ + ANDR	Control	Attractive	30	4.37	0.63	4.50	3.00	5.00
			Unattractive	30	3.30	0.95	3.33	2.00	4.67
		Experimental	Attractive	30	4.60	1.00	4.67	2.33	6.00
			Unattractive	29	3.46	1.36	3.67	1.00	5.33
	HQ no ANDR	Control	Attractive	30	4.77	0.70	4.67	4.00	6.33
			Unattractive	30	2.80	0.92	2.50	1.67	4.33
		Experimental	Attractive	30	4.60	0.45	4.67	3.67	5.33
			Unattractive	30	2.83	0.93	2.67	1.33	4.00
	LQ + ANDR	Control	Attractive	30	4.90	0.66	4.67	3.67	6.00
			Unattractive	30	3.30	0.60	3.33	2.00	4.00
		Experimental	Attractive	30	5.07	0.72	5.00	4.00	6.33
			Unattractive	30	3.30	0.39	3.33	2.67	4.00
	LQ no ANDR	Control	Attractive	30	4.50	0.78	4.67	3.33	5.33
			Unattractive	30	2.20	0.68	2.17	1.33	3.33
		Experimental	Attractive	30	4.40	1.05	4.33	2.67	5.67
			Unattractive	30	2.47	0.91	2.17	1.33	4.00

2.2.2 Table S2. Men

```
kable(
  descM,
  booktabs = TRUE,
  align = c("l", "l", "l", "l", "c", "c", "c", "c", "c", "c"),
  caption = "\\textbf{Table S2.} Descriptive statistics of
  measured variables for men",
  col.names = linebreak(varinames),
  longtable = TRUE,
  escape = FALSE) %>%
  kable_styling(latex_options = c("HOLD_position"),
                font_size = 6) %>%
  collapse_rows(1:3)
```

Table S2. Descriptive statistics of measured variables for men

Measured characteristic	Group	Session	Stimuli attractiveness	n	Mean	SD	Median	Min	Max
	HQ + ANDR	Control	Attractive	26	112.67	14.23	108.00	88.43	139.36
			Unattractive	27	109.16	14.01	109.37	87.61	137.73
		Experimental	Attractive	30	110.70	13.21	110.64	88.63	140.26
			Unattractive	30	107.74	14.43	106.58	85.56	137.55
	HQ no ANDR	Control	Attractive	29	104.16	15.10	103.21	83.70	136.30
			Unattractive	30	105.27	16.58	105.30	83.04	138.37
		Experimental	Attractive	30	105.19	15.57	100.32	82.55	133.72
			Unattractive	30	104.52	15.98	103.36	82.12	143.07
	LQ + ANDR	Control	Attractive	29	111.55	17.43	104.86	89.91	153.90
			Unattractive	30	111.35	17.52	106.99	87.86	160.76
		Experimental	Attractive	30	107.21	15.33	100.99	90.60	153.11
			Unattractive	30	104.56	14.52	97.70	89.01	145.36

Mean F_0 (Hz)									
	LQ no ANDR	Control	Attractive	30	113.11	15.19	110.34	91.90	163.45
			Unattractive	30	110.27	12.07	106.90	90.43	132.45
		Experimental	Attractive	30	110.88	12.47	111.76	88.94	131.03
			Unattractive	30	109.23	11.63	109.28	90.72	128.42
	HQ + ANDR	Control	Attractive	26	15.47	7.64	14.82	4.92	33.08
			Unattractive	27	11.80	4.77	10.89	4.37	22.04
		Experimental	Attractive	30	14.21	5.64	14.46	6.59	28.24
			Unattractive	30	13.10	6.33	13.66	5.06	33.90
	HQ no ANDR	Control	Attractive	29	13.41	7.46	11.65	5.67	33.07
			Unattractive	30	11.80	6.40	10.41	4.53	33.79
		Experimental	Attractive	30	12.67	6.45	10.81	4.59	29.01
			Unattractive	30	12.18	5.38	10.78	5.56	26.16
F_0 SD (Hz)	LQ + ANDR	Control	Attractive	29	13.56	7.04	13.67	3.26	26.29
			Unattractive	30	14.22	7.19	11.58	5.76	31.48
		Experimental	Attractive	30	12.45	6.66	10.54	4.52	27.69
			Unattractive	30	11.66	5.39	10.39	4.19	21.75
	LQ no ANDR	Control	Attractive	30	15.24	9.90	14.11	6.18	58.96
			Unattractive	30	12.82	5.10	13.00	4.47	20.07
		Experimental	Attractive	30	12.84	5.32	12.00	4.68	25.46
			Unattractive	30	12.66	5.48	10.88	4.12	26.92
	HQ + ANDR	Control	Attractive	26	0.14	0.06	0.12	0.05	0.26
			Unattractive	27	0.11	0.04	0.10	0.04	0.22
		Experimental	Attractive	30	0.13	0.05	0.12	0.06	0.29
			Unattractive	30	0.12	0.05	0.10	0.05	0.27
	HQ no ANDR	Control	Attractive	29	0.12	0.06	0.10	0.06	0.30
			Unattractive	30	0.11	0.05	0.10	0.05	0.24
		Experimental	Attractive	30	0.12	0.06	0.10	0.04	0.32
			Unattractive	30	0.12	0.05	0.11	0.05	0.21
F_0 CV (Hz)	LQ + ANDR	Control	Attractive	29	0.12	0.06	0.11	0.03	0.27
			Unattractive	30	0.13	0.07	0.11	0.06	0.29
		Experimental	Attractive	30	0.12	0.06	0.10	0.05	0.27
			Unattractive	30	0.11	0.05	0.10	0.04	0.23
	LQ no ANDR	Control	Attractive	30	0.13	0.06	0.13	0.06	0.36
			Unattractive	30	0.12	0.05	0.12	0.04	0.20
		Experimental	Attractive	30	0.12	0.05	0.11	0.05	0.24
			Unattractive	30	0.12	0.05	0.10	0.04	0.26
	HQ + ANDR	Control	Attractive	26	84.80	9.99	81.10	74.80	109.83
			Unattractive	27	82.18	10.35	76.96	74.83	105.19
		Experimental	Attractive	30	81.07	9.68	77.17	74.74	113.87
			Unattractive	30	83.46	11.43	78.41	74.75	112.44
	HQ no ANDR	Control	Attractive	29	80.45	8.44	75.19	74.77	102.72
			Unattractive	30	84.80	12.02	77.57	74.75	107.03
		Experimental	Attractive	30	81.79	10.00	76.21	74.75	109.39
			Unattractive	30	81.61	9.63	75.85	74.76	105.11
Minimum F_0 (Hz)	LQ + ANDR	Control	Attractive	29	83.79	9.07	79.54	74.77	101.74
			Unattractive	30	82.65	9.50	78.35	74.76	115.39
		Experimental	Attractive	30	81.13	7.75	77.30	74.77	99.61
			Unattractive	30	79.75	5.75	77.14	74.76	95.57
	LQ no ANDR	Control	Attractive	30	81.22	9.88	77.06	74.78	115.82
			Unattractive	30	84.68	12.29	78.74	74.80	117.88
		Experimental	Attractive	30	84.03	11.00	79.66	74.77	113.96
			Unattractive	30	82.08	12.03	76.81	74.76	114.74
			Attractive	26	199.72	63.37	182.39	110.16	299.01

	HQ + ANDR	Control	Unattractive	27	178.71	58.28	163.13	113.57	295.87
		Experimental	Attractive	30	187.04	59.35	170.74	109.75	298.96
			Unattractive	30	185.18	59.52	175.02	114.03	299.91
	HQ no ANDR	Control	Attractive	29	175.15	63.83	155.44	106.69	295.86
			Unattractive	30	165.69	57.26	149.61	102.96	299.40
		Experimental	Attractive	30	175.70	62.79	150.95	111.79	299.06
			Unattractive	30	180.68	55.77	163.96	107.80	292.27
	LQ + ANDR	Control	Attractive	29	200.34	71.83	165.08	107.52	297.31
			Unattractive	30	205.32	70.59	188.41	114.93	298.45
Maximum F_0 (Hz)		Experimental	Attractive	30	170.76	58.29	143.63	113.25	297.54
			Unattractive	30	174.72	69.16	139.42	106.35	297.07
	LQ no ANDR	Control	Attractive	30	178.86	43.21	171.26	121.61	290.10
			Unattractive	30	193.42	60.82	168.75	116.13	299.97
		Experimental	Attractive	30	191.02	56.89	173.32	123.05	291.62
			Unattractive	30	180.21	50.13	169.19	112.39	298.67
	HQ + ANDR	Control	Attractive	26	65.40	8.12	67.12	47.51	73.69
			Unattractive	27	63.83	7.76	66.89	47.52	73.32
		Experimental	Attractive	30	63.56	5.24	64.39	53.73	70.76
			Unattractive	30	63.03	4.77	64.43	54.55	71.68
	HQ no ANDR	Control	Attractive	29	63.07	6.84	61.58	51.12	73.12
			Unattractive	30	62.77	7.26	62.70	47.48	73.00
		Experimental	Attractive	30	63.29	7.48	65.22	50.11	73.34
			Unattractive	30	63.71	6.81	65.36	50.35	72.96
	LQ + ANDR	Control	Attractive	29	63.73	6.28	64.05	53.20	73.44
			Unattractive	30	63.49	6.17	62.92	53.29	72.98
Intensity (dB)		Experimental	Attractive	30	64.72	5.72	66.60	55.38	75.37
			Unattractive	30	64.19	5.39	65.40	56.74	75.43
	LQ no ANDR	Control	Attractive	30	63.24	6.82	62.75	53.64	73.25
			Unattractive	30	63.10	6.81	62.12	53.91	73.30
		Experimental	Attractive	30	62.31	4.95	64.76	52.57	70.68
			Unattractive	30	62.31	5.27	64.56	52.88	72.84
	HQ + ANDR	Control	Attractive	26	686.82	173.56	633.59	418.75	1095.34
			Unattractive	27	720.63	196.38	669.27	477.24	1167.50
		Experimental	Attractive	30	718.17	192.16	693.07	462.56	1105.45
			Unattractive	30	725.08	205.87	639.54	494.63	1103.38
	HQ no ANDR	Control	Attractive	29	728.06	140.85	718.07	498.82	1011.90
			Unattractive	30	762.85	141.52	746.95	525.02	1011.78
		Experimental	Attractive	30	796.28	174.58	798.86	471.99	1190.78
			Unattractive	30	801.13	165.24	787.20	514.68	1227.95
	LQ + ANDR	Control	Attractive	29	734.37	183.70	739.33	507.75	1105.10
			Unattractive	30	742.42	196.66	729.11	462.22	1091.47
F_1 (Hz)		Experimental	Attractive	30	733.30	167.67	729.79	536.35	1075.42
			Unattractive	30	718.59	141.33	704.05	498.81	1107.56
	LQ no ANDR	Control	Attractive	30	738.97	115.91	742.22	536.59	1066.51
			Unattractive	30	713.09	98.68	729.09	550.01	902.43
		Experimental	Attractive	30	682.29	94.86	670.85	539.12	901.99
			Unattractive	30	690.92	98.16	690.85	514.93	897.06
	HQ + ANDR	Control	Attractive	26	1898.70	120.10	1905.63	1657.65	2194.62
			Unattractive	27	1937.75	158.01	1932.60	1615.65	2289.40
		Experimental	Attractive	30	1935.42	148.75	1932.32	1562.56	2218.35
			Unattractive	30	1932.45	152.20	1895.05	1646.29	2218.82
		Control	Attractive	29	1939.80	173.97	1963.69	1421.50	2147.59
			Unattractive	30	1937.22	173.36	1979.37	1485.39	2212.95

F_2 (Hz)	HQ no ANDR	Experimental	Attractive	30	1980.33	110.38	1968.27	1784.07	2210.72
			Unattractive	30	1998.15	111.41	2002.40	1701.48	2236.46
	LQ + ANDR	Control	Attractive	29	1949.81	185.41	1954.55	1577.34	2200.72
			Unattractive	30	1954.96	176.05	1954.90	1622.21	2255.36
		Experimental	Attractive	30	1879.92	182.16	1821.84	1567.29	2341.10
			Unattractive	30	1860.75	194.06	1811.94	1497.63	2333.35
	LQ no ANDR	Control	Attractive	30	1904.66	203.47	1953.71	1542.51	2429.13
			Unattractive	30	1898.28	187.49	1935.75	1558.25	2179.69
		Experimental	Attractive	30	1906.77	132.34	1918.25	1682.55	2205.14
			Unattractive	30	1879.01	124.39	1914.89	1628.28	2053.03
F_3 (Hz)	HQ + ANDR	Control	Attractive	26	2902.65	121.47	2886.84	2681.71	3175.36
			Unattractive	27	2930.39	108.21	2942.94	2757.86	3222.86
		Experimental	Attractive	30	2961.21	134.36	2963.44	2737.88	3182.37
			Unattractive	30	2961.33	145.12	2969.62	2659.34	3188.47
	HQ no ANDR	Control	Attractive	29	2986.42	203.84	3071.29	2571.09	3217.87
			Unattractive	30	2998.97	157.32	3050.77	2659.23	3218.58
		Experimental	Attractive	30	3005.10	80.25	3001.82	2873.01	3177.04
			Unattractive	30	3024.18	101.87	3036.73	2769.35	3324.97
	LQ + ANDR	Control	Attractive	29	3017.30	163.74	3022.14	2796.63	3379.84
			Unattractive	30	3023.80	159.30	3012.26	2738.82	3360.95
		Experimental	Attractive	30	2985.38	162.76	2972.39	2686.06	3313.89
			Unattractive	30	2980.03	166.79	2966.53	2620.79	3324.20
	LQ no ANDR	Control	Attractive	30	2968.34	190.74	2997.81	2675.26	3385.35
			Unattractive	30	2964.27	193.30	3014.02	2618.93	3273.17
		Experimental	Attractive	30	2972.08	118.24	2951.79	2791.19	3205.89
			Unattractive	30	2965.73	114.10	2989.13	2747.52	3145.89
Recording lenght (ms)	HQ + ANDR	Control	Attractive	26	9707.31	3961.49	9445.00	1880.00	18660.00
			Unattractive	27	11392.22	4877.01	10350.00	2340.00	19660.00
		Experimental	Attractive	30	12004.33	5134.80	11925.00	2620.00	19720.00
			Unattractive	30	11836.67	4990.77	11780.00	2530.00	19210.00
	HQ no ANDR	Control	Attractive	29	12270.00	4757.07	12570.00	3580.00	19550.00
			Unattractive	30	12588.67	4775.83	13220.00	4630.00	19380.00
		Experimental	Attractive	30	12466.33	4973.77	12505.00	4840.00	19220.00
			Unattractive	30	12749.67	5275.41	14220.00	3410.00	19770.00
	LQ + ANDR	Control	Attractive	29	9775.17	4823.64	8790.00	3330.00	18050.00
			Unattractive	30	10233.33	4588.38	11230.00	3730.00	18630.00
		Experimental	Attractive	30	7610.33	3296.80	7410.00	3640.00	19180.00
			Unattractive	30	8602.00	4163.50	7545.00	3850.00	19400.00
	LQ no ANDR	Control	Attractive	30	10804.67	4401.40	10365.00	2550.00	19730.00
			Unattractive	30	11583.00	4690.28	11070.00	2910.00	19720.00
		Experimental	Attractive	30	10763.33	4817.68	9365.00	4660.00	19690.00
			Unattractive	30	10859.33	4445.80	9710.00	3760.00	19660.00
	HQ + ANDR	Control	Attractive	26	4108.46	2207.40	3960.00	680.00	9650.00
			Unattractive	27	4384.44	2468.10	3680.00	790.00	10380.00
		Experimental	Attractive	30	5050.33	2467.22	4955.00	490.00	9510.00
			Unattractive	30	4964.00	2314.64	4750.00	580.00	9290.00
	HQ no ANDR	Control	Attractive	29	4512.76	1715.03	4350.00	1520.00	8700.00
			Unattractive	30	4643.33	1741.09	4930.00	1790.00	7630.00
		Experimental	Attractive	30	4454.67	1744.70	4400.00	1720.00	7820.00
			Unattractive	30	4539.33	2310.22	4440.00	1150.00	9410.00
		Control	Attractive	29	3808.28	2217.17	3600.00	630.00	8890.00
			Unattractive	30	4129.67	2245.53	4285.00	1120.00	9370.00
			Attractive	30	3094.67	1302.33	3120.00	1220.00	7350.00

Time recognised as speech (ms)	LQ + ANDR	Experimental	Unattractive	30	3518.67	1703.92	3650.00	1490.00	6960.00
	LQ no ANDR	Control	Attractive	30	4502.33	1934.00	4555.00	320.00	9060.00
			Unattractive	30	5110.67	1988.15	5110.00	850.00	8320.00
		Experimental	Attractive	30	4392.67	1631.35	4405.00	1090.00	8210.00
			Unattractive	30	4902.33	1980.59	4660.00	1330.00	9420.00
Attractiveness Ratings	HQ + ANDR	Control	Attractive	26	5.00	0.54	5.00	4.00	6.00
			Unattractive	27	2.52	0.83	2.67	1.00	4.00
		Experimental	Attractive	30	4.90	0.90	5.17	3.00	5.67
			Unattractive	30	2.20	0.57	2.00	1.33	3.33
	HQ no ANDR	Control	Attractive	29	5.22	0.57	5.67	4.00	5.67
			Unattractive	30	2.90	0.57	3.17	1.67	3.33
		Experimental	Attractive	30	5.37	0.63	5.00	4.67	6.33
			Unattractive	30	3.30	0.56	3.33	2.67	4.33
	LQ + ANDR	Control	Attractive	29	5.52	0.26	5.67	5.00	5.67
			Unattractive	30	2.83	0.82	3.00	1.00	4.00
		Experimental	Attractive	30	5.43	0.61	5.67	4.33	6.00
			Unattractive	30	2.57	0.71	2.50	1.67	4.33
	LQ no ANDR	Control	Attractive	30	5.23	0.87	5.17	4.00	6.33
			Unattractive	30	2.50	0.72	2.17	1.67	4.00
		Experimental	Attractive	30	5.03	0.73	5.17	3.33	5.67
			Unattractive	30	2.17	0.61	2.17	1.33	3.67

2.2.3 Figure 2. Distribution by Sex and Group

Kernel density plot for all measured variables by `Group` and `Sex`.

2.2.3.1 Colour version

Online version.

```
#Arrange data for density plots
datp <- melt(db,
             id.vars = 3:4,
             measure.vars = c(10:12, 15:23),
             variable.name = "Measure",
             value.name = "Value")

#Variable names with ggplot syntax
levels(datp$Measure) <- c("Mean~F[0]~(Hz)",
                          "F[0]~SD~(Hz)",
                          "F[0]~CV~(Hz)",
                          "'Intensity (dB)'",
                          "F[1]~(Hz)",
                          "F[2]~(Hz)",
                          "F[3]~(Hz)",
                          "'Recording lenght (ms)'",
                          "'Time recognised as speech (ms)'",
                          "'Speech proportion'",
                          "'Age (years)'",
                          "'Attractiveness Ratings'")

#Subsets by sex
datpF <- subset(datp, datp$Sex == "Women")
datpM <- subset(datp, datp$Sex == "Men")

#Fig 2A, women
Fig2A <- ggplot(datpF,
```

```
                aes(Value,
                    fill = Group,
                    colour = Group)) +
  geom_density(alpha = 0.3) +
  facet_wrap(~ Measure,
             scales = "free",
             ncol = 4,
             labeller = label_parsed) +
  labs(y = "Density",
       x = NULL, title = "A",
       subtitle = "Women") +
  theme(strip.text.x = element_text(size = 8))

#Fig 2B, men
Fig2B <- ggplot(datpM,
                aes(Value,
                    fill = Group,
                    colour = Group)) +
  geom_density(alpha = 0.3) +
  facet_wrap(~ Measure,
             scales = "free",
             ncol = 4,
             labeller = label_parsed) +
  labs(y = "Density",
       x = NULL, title = "B",
       subtitle = "Men") +
  theme(strip.text.x = element_text(size = 8))

#Fig 2 COMPLETE
Fig2 <- ggarrange(Fig2A,
          Fig2B,
          common.legend = TRUE,
          legend = "bottom",
          labels = "AUTO",
          nrow = 2,
          ncol = 1)
Fig2
```

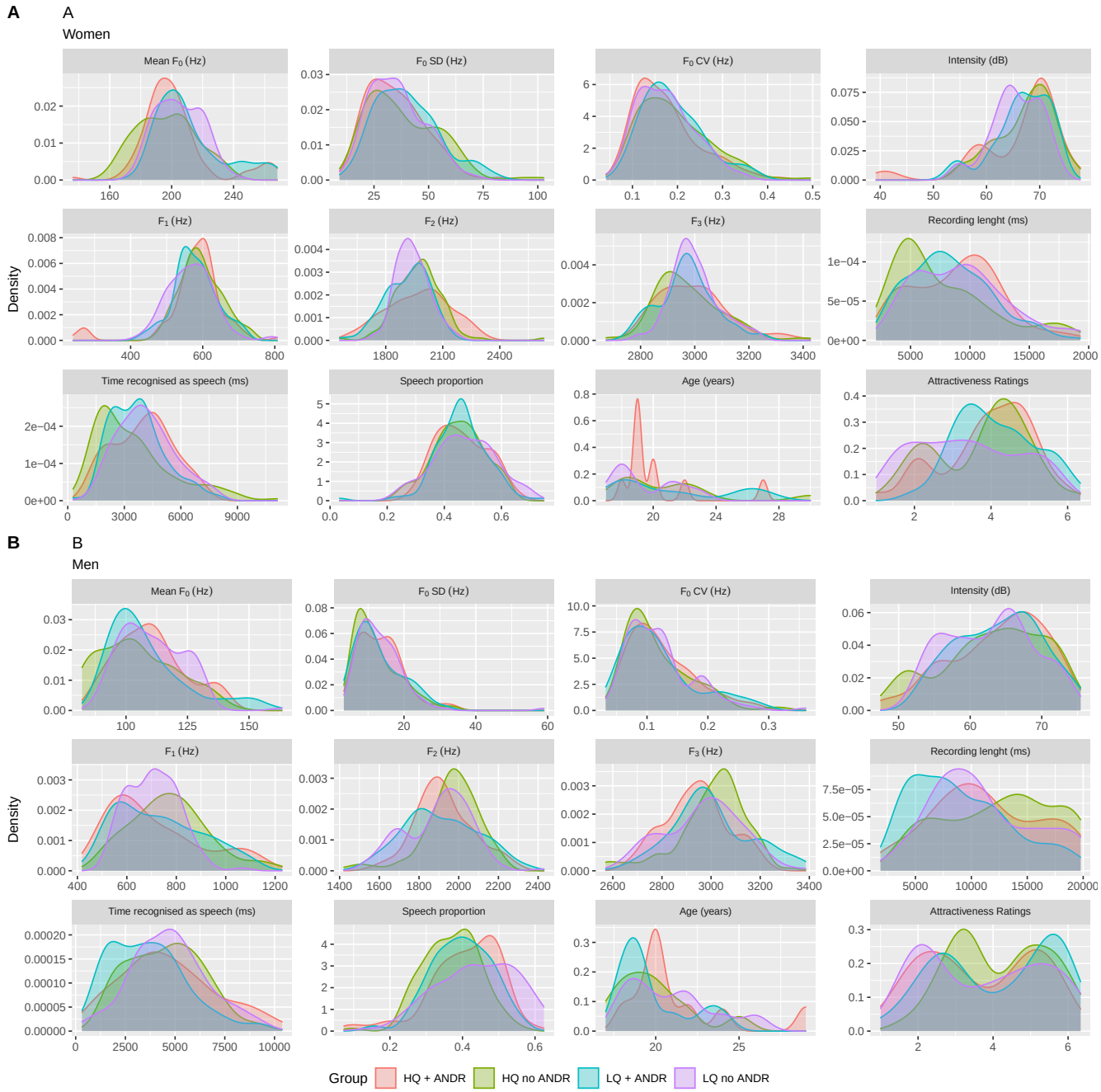

Figure 2. Distribution of all measured variables by sex and group. (A) Women. (B) Men. Vertical lines represent the mean for each group. Detailed descriptives are found in Table S1 for women, and Table S2 for men.

2.2.3.2 Greyscale version

Print version.

```
#Fig 2A, women
Fig2Abw <- Fig2A +
  scale_color_grey() +
  scale_fill_grey() +
  theme_light() +
  theme(strip.text.x = element_text(size = 8,
                                    color = "black"))

#Fig 2B, men
```

```
Fig2Bbw <- Fig2B +
  scale_color_grey() +
  scale_fill_grey() +
  theme_light() +
  theme(strip.text.x = element_text(size = 8,
                                    color = "black"))

#Fig 2 COMPLETE
Fig2bw <- ggarrange(Fig2Abw,
          Fig2Bbw,
          common.legend = TRUE,
          legend = "bottom",
          labels = "AUTO",
          nrow = 2,
          ncol = 1)
Fig2bw
```

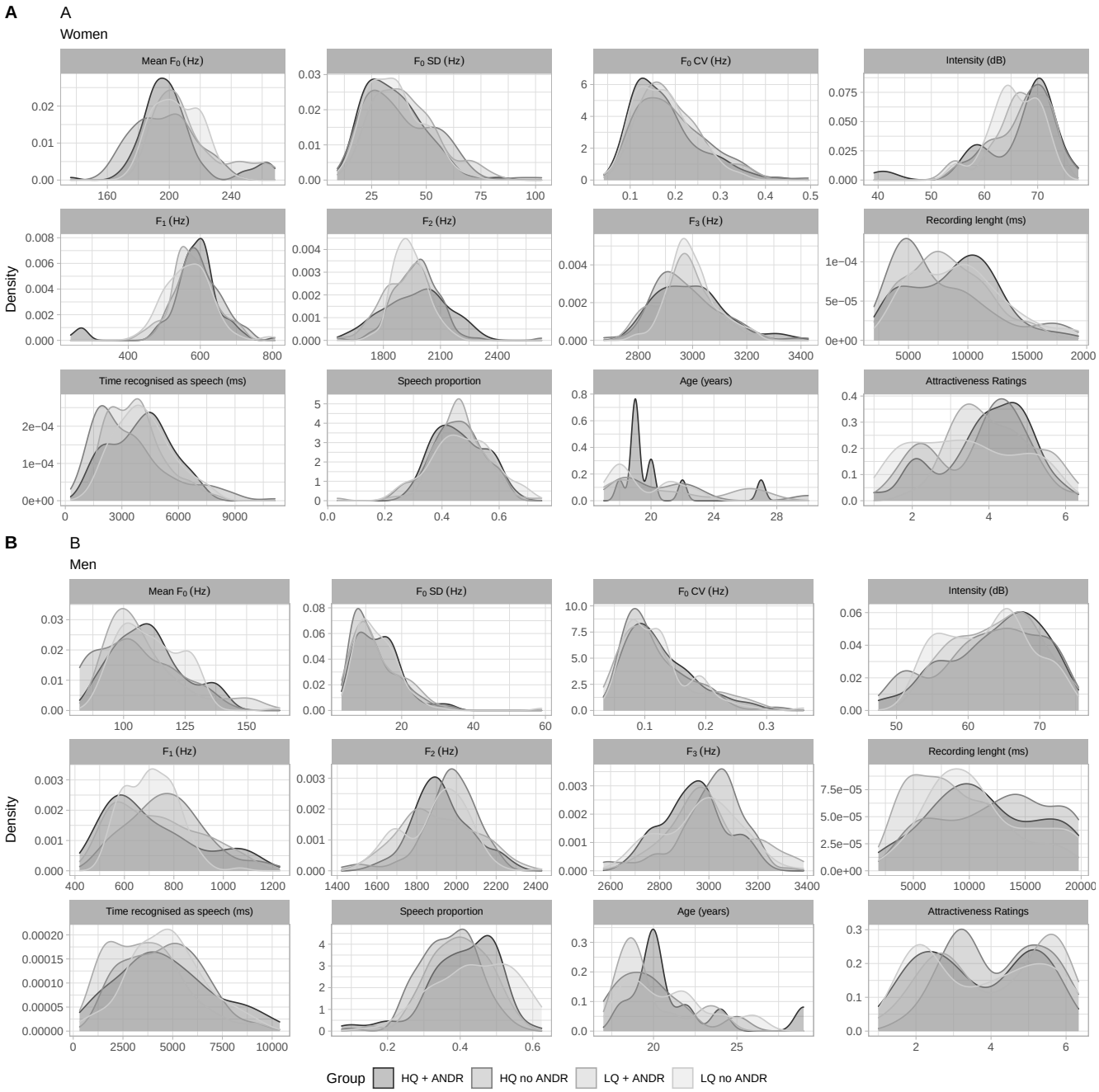

Figure 2. Distribution of all measured variables by sex and group. (A) Women. (B) Men. Vertical lines represent the mean for each group. Detailed descriptives are found in Table S1 for women, and Table S2 for men.

2.2.4 Correlations

2.2.4.1 Table S3 All participants.

```
corAll <- corstarsl(db[, c(10:12, 15, 19:20, 23)])
rownames(corAll) <- varnames[c(1:3, 6, 10:12)]
colnamescor <- c("Mean $F_{0}$ (Hz)",
                 "$F_{0}$ SD (Hz)",
                 "$F_{0}$ CV (Hz)",
                 "Intensity (dB)",
                 "Recording\nlenght (ms)",
```

```
                "Time recognised\nas speech (ms)")
kable(corAll,
      booktabs = TRUE,
      align = "c",
      digits = 2,
      caption = "\\textbf{Table S3.} Correlations between measured variables
      for all participants",
      col.names = linebreak(colnamescor,
                            align = "c"),
      escape = FALSE) %>%
    kable_styling(latex_options = c("HOLD_position", "scale_down")) %>%
    footnote(
      general = "*$p$ < 0.05, **$p$ < 0.01, ***$p$ < 0.001",
      threeparttable = TRUE,
      escape = FALSE)
```

Table S3. Correlations between measured variables for all participants

	Mean F_0 (Hz)	F_0 SD (Hz)	F_0 CV (Hz)	Intensity (dB)	Recording lenght (ms)	Time recognised as speech (ms)
Mean F_0 (Hz)						
F_0 SD (Hz)	0.74***					
F_0 CV (Hz)	0.41***	0.89***				
Intensity (dB)	0.29***	0.31***	0.27***			
Recording lenght (ms)	-0.29***	-0.22***	-0.12***	-0.10**		
Time recognised as speech (ms)	-0.15***	-0.12***	-0.07*	0.03	0.86***	
Attractiveness Ratings	-0.02	0.08*	0.12***	0.08*	-0.06	-0.08*

Note:
*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$

2.2.4.2 Table S4 Women.

```
corF <- corstarsl(WomD[, c(10:12, 15, 19:20, 23)])
rownames(corF) <- varnames[c(1:3, 6, 10:12)]
colnames(corF) <- varnames[c(1:3, 6, 10:11)]
kable(corF,
      booktabs = TRUE,
      align = "c",
      digits = 2,
      caption = "\\textbf{Table S4.} Correlations between measured variables for women",
      col.names = linebreak(colnamescor,
                            align = "c"),
      escape = FALSE) %>%
    kable_styling(latex_options = c("HOLD_position", "scale_down")) %>%
    footnote(
      general = "*$p$ < 0.05, **$p$ < 0.01, ***$p$ < 0.001",
      threeparttable = TRUE,
      escape = FALSE)
```

Table S4. Correlations between measured variables for women

	Mean F_0 (Hz)	F_0 SD (Hz)	F_0 CV (Hz)	Intensity (dB)	Recording lenght (ms)	Time recognised as speech (ms)
Mean F_0 (Hz)						
F_0 SD (Hz)	0.18***					
F_0 CV (Hz)	-0.08	0.96***				
Intensity (dB)	0.17***	0.23***	0.18***			
Recording lenght (ms)	-0.05	-0.06	-0.06	0.02		
Time recognised as speech (ms)	-0.01	-0.03	-0.04	0.06	0.89***	
Attractiveness Ratings	0.01	0.21***	0.22***	0.11*	-0.04	-0.01

Note:
*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$

2.2.4.3 Table S5 Men.

```
corM <- corstarsl(MenD[, c(10:12, 15, 19:20, 23)])
rownames(corM) <- varnames[c(1:3, 6, 10:12)]
colnames(corM) <- varnames[c(1:3, 6, 10:11)]
kable(corM,
      booktabs = TRUE,
      align = "c",
      digits = 2,
      caption = "\\textbf{Table S5.} Correlations between measured variables for men",
      col.names = linebreak(colnamescor,
                            align = "c"),
      escape = FALSE) %>%
    kable_styling(latex_options = c("HOLD_position", "scale_down")) %>%
    footnote(
      general = "*$p$ < 0.05, **$p$ < 0.01, ***$p$ < 0.001",
      threeparttable = TRUE,
      escape = FALSE)
```

Table S5. Correlations between measured variables for men

	Mean F_0 (Hz)	F_0 SD (Hz)	F_0 CV (Hz)	Intensity (dB)	Recording lenght (ms)	Time recognised as speech (ms)
Mean F_0 (Hz)						
F_0 SD (Hz)	0.37***					
F_0 CV (Hz)	0.07	0.94***				
Intensity (dB)	0.20***	0.22***	0.19***			
Recording lenght (ms)	-0.18***	-0.01	0.06	-0.08		
Time recognised as speech (ms)	-0.07	-0.01	0.03	0.08	0.84***	
Attractiveness Ratings	0.09*	0.12**	0.10*	0.07	-0.09	-0.14**

Note:
*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$

2.3 Time recognised as speech

There were interesting differences between the length of the recordings, and the time recognised as speech (time in which the Praat algorithms, produced an F_0 value).

2.3.1 Figure 3. Time recognised as speech and Recoding Length

2.3.1.1 Colour version Online version.

```
#Correlation Recoding Length and Time recognised as speech
Fig3A <- ggplot(db,
                aes(x = Recording_length,
                    y = Voice_length,
                    colour = Sex)) +
  stat_smooth(method = 'lm') +
  geom_point(alpha = 0.5) +
  xlab("Recoding Length (ms)") +
  ylab("Time recognised as speech (ms)") +
  theme(legend.position = "none") +
  xlim(0, 20000) +
  ylim(0, 12000) +
  geom_rug(alpha = 0.5) +
  stat_cor(aes(label = paste(..rr.label..,
                             cut(..p..,
                                 breaks = c(-Inf,
                                            0.0001,
                                            0.001,
                                            0.01,
                                            0.05,
                                            Inf),
                                 labels = c("'****'",
                                            "'***'",
                                            "'**'",
                                            "'*'",
                                            "'n.s.'")),
                             sep = "~")),
           label.x.npc = "left",
           label.y.npc = "top",
           color = "black") +
  scale_color_brewer(palette = "Set1") +
  facet_wrap(~Sex)

#Time recognised as speech by Stimuli Attractiveness and Sex
t.time <- db %>%
  group_by(Sex) %>%
  pairwise_t_test(Voice_length ~ Session)
t.time$p.signif[t.time$p.signif == "ns"] <- NA

Fig3B <- ggplot(db,
                aes(x = Session,
                   y = Voice_length,
                   color = Sex)) +
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_point(alpha = 0.2,
             position = position_jitterdodge(jitter.width = 0.2,
                                             dodge.width = 1)) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               aes(group = Sex),
               color = "black",
               position = position_dodge(1)) +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
```

```
               width=0.1,
               aes(group = Sex),
               color = "black",
               position = position_dodge(1)) +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            aes(group = Sex),
            position = position_dodge(1),
            color = "black",
            linetype = 3) +
  labs(y = "Time recognised as speech (ms)",
       x = "Session") +
  stat_pvalue_manual(t.time,
                     label = "p.signif",
                     y.position = 11000,
                     tip.length = 0) +
  theme(legend.position = "none") +
  scale_color_brewer(palette = "Set1") +
  labs(fill = "Stimuli_Attractiveness")

##Time recognised as speech by Sex
t.Prop <- db %>%
  t_test(Prop ~ Sex) %>%
  adjust_pvalue() %>%
  add_significance("p.adj")
t.Prop$p.adj.signif[t.Prop$p.adj.signif == "ns"] <- NA

Fig3C <- ggviolin(db,
                  x = "Sex",
                  y = "Prop",
                  color = "Sex") +
  geom_jitter(aes(color = Sex),
              alpha = 0.2,
              width = 0.1) +
  theme_gray() +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               color = "black") +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.1,
               color = "black") +
  stat_pvalue_manual(t.Prop,
                     label = "p.adj.signif",
                     y.position = 0.84,
                     tip.length = 0) +
  ylab("Proportion of time \n recognised as speech") +
  scale_color_brewer(palette = "Set1") +
  theme(legend.position = "none")

#Fig 3 COMPLETE
Fig3 <- ggarrange(Fig3A,
                  ggarrange(Fig3B,
                            Fig3C,
```

```
                        ncol = 2,
                        labels = c("B", "C")),
                nrow = 2, labels = "A",
                common.legend = TRUE,
                legend = "bottom")

Fig3
```

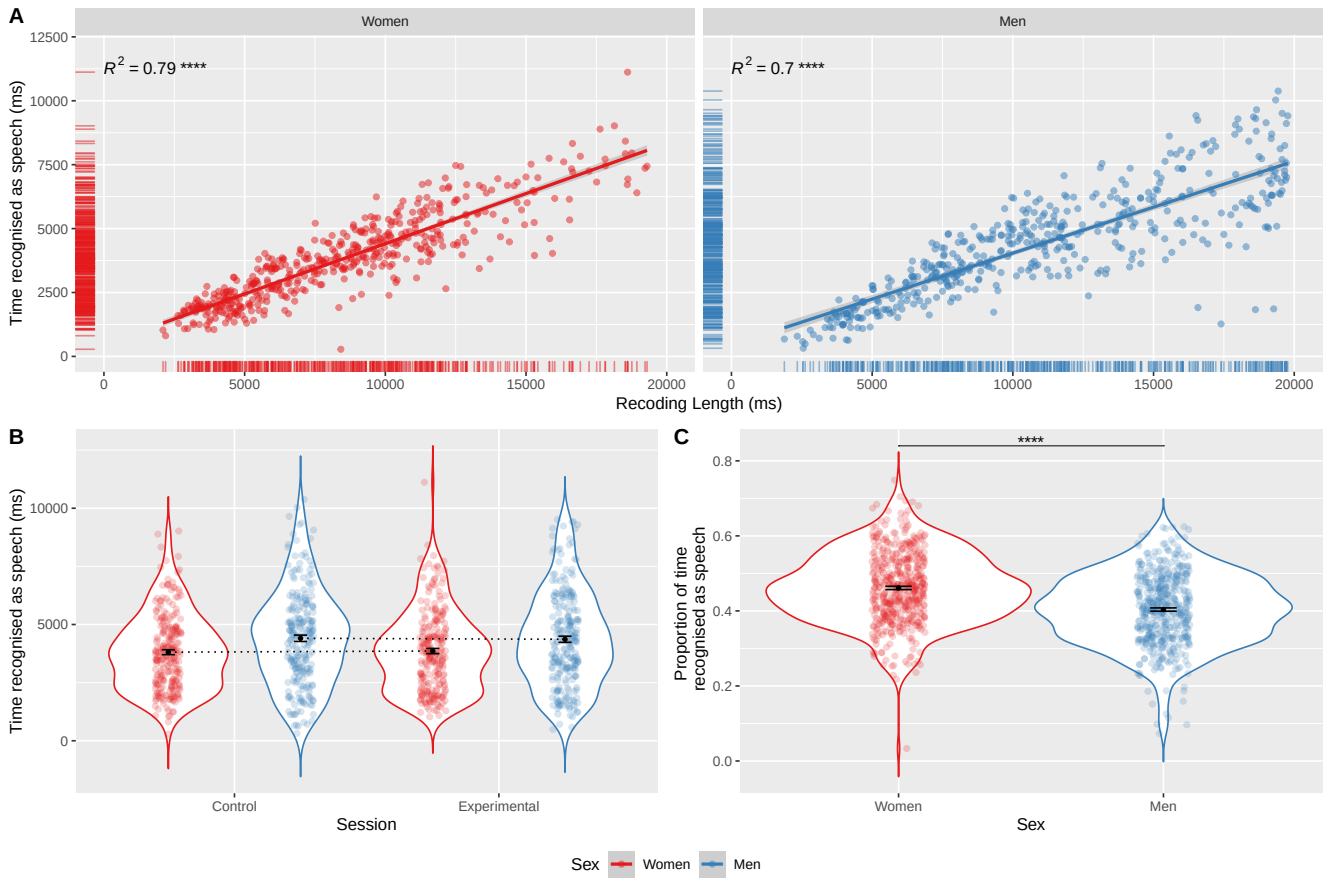

Figure 3. Differences in time recognised as speech and recoding length. (A) Correlation between time recognised as speech and recoding length. (B) Within-subject differences in time recognised as speech in responses to attractive and unattractive stimuli. (C) Proportion of time recognised as speech by sex. Comparisons between men and women were performed using *t*-tests: **** $p < 0.0001$.

2.3.1.2 Greyscale version

Print version.

```
#Correlation Recoding Length and Time recognised as speech
Fig3Abw <- Fig3A +
  scale_color_grey(start = 0,
                   end = 0.4) +
  scale_fill_grey(start = 0,
                  end = 0.4) +
  theme_light() +
  facet_wrap(~Sex) +
  theme(strip.text.x = element_text(color = "black"))

#Time recognised as speech by Stimuli Attractiveness and Sex
```

```
Fig3Bbw <- Fig3B +
  scale_color_grey(start = 0,
                   end = 0.4) +
  scale_fill_grey(start = 0,
                   end = 0.4) +
  theme_light()

##Time recognised as speech by Sex
Fig3Cbw <- Fig3C +
  scale_color_grey(start = 0,
                   end = 0.4) +
  scale_fill_grey(start = 0,
                   end = 0.4) +
  theme(legend.position = "none") +
  theme_light()

#Fig 3 COMPLETE
Fig3bw <- ggarrange(Fig3Abw,
                    ggarrange(Fig3Bbw,
                              Fig3Cbw,
                              ncol = 2,
                              labels = c("B", "C"),
                              common.legend = TRUE,
                              legend = "none"),
                    nrow = 2, labels = "A",
                    common.legend = TRUE,
                    legend = "bottom")

Fig3bw
```

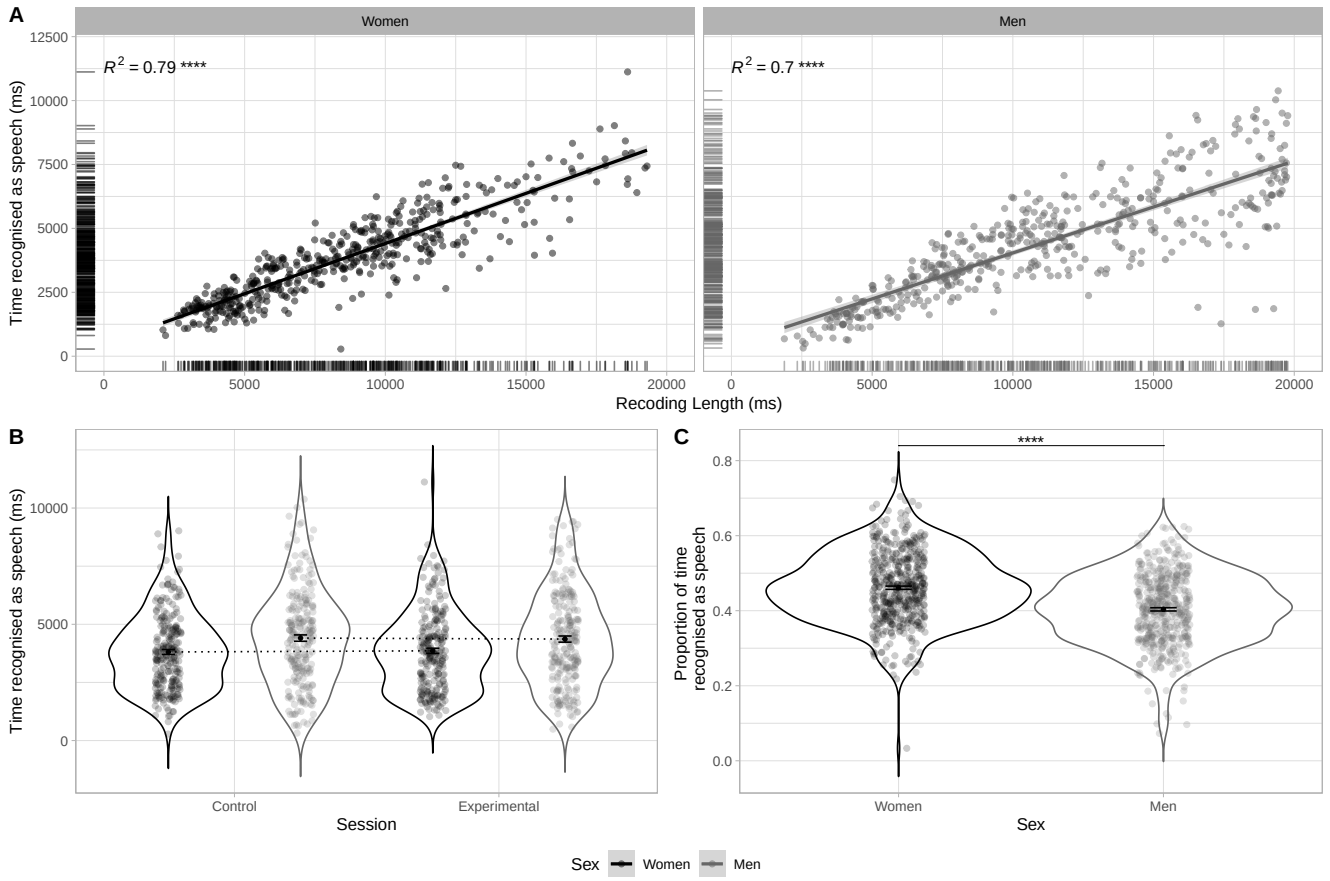

Figure 3. Differences in time recognised as speech and recoding length. (A) Correlation between time recognised as speech and recoding length. (B) Within-subject differences in time recognised as speech in responses to attractive and unattractive stimuli. (C) Proportion of time recognised as speech by sex. Comparisons between men and women were performed using *t*-tests: **** $p < 0.0001$.

2.4 Models of measured variables

Separate models were created for each dependent variable (**Mean F_0**, **F_0 SD**, **F_0 CV**, **Mean intensity**, and **Attractiveness ratings**). Following the experimental design, and because we were interested in the effects of the presence of body odour, for all models we only included the main effect of `Session` (control, experimental), as well as all its possible interactions with `Sex` (women, men), `Odour_Quality` (HQ, LQ), `ANDR` (added, not added), and `Stimuli_Attractiveness` (attractive, unattractive), were included as fixed factors. `Session` was also included as random factors, with correlated random slopes and intercepts for each participant. No other main effects were tested.

2.4.1 Mean F_0

2.4.1.1 Model fitting

Linear Mixed Model (LMM) fitting.

```
m.Mean_F0 <- lmer(Mean_F0 ~
                    Session *
                    Stimuli_Attractiveness *
                    Sex * Odour_Quality *
                    ANDR +
                    (1 + Session | Subject),
            REML = FALSE,
            data = db)
```

2.4.1.1.1 Figure S1. Diagnostics Diagnostics included residual distribution, homoscedasticity, and linearity in each fixed factor.

```
FigS1 <- modDiag(m.Mean_F0)
FigS1
```

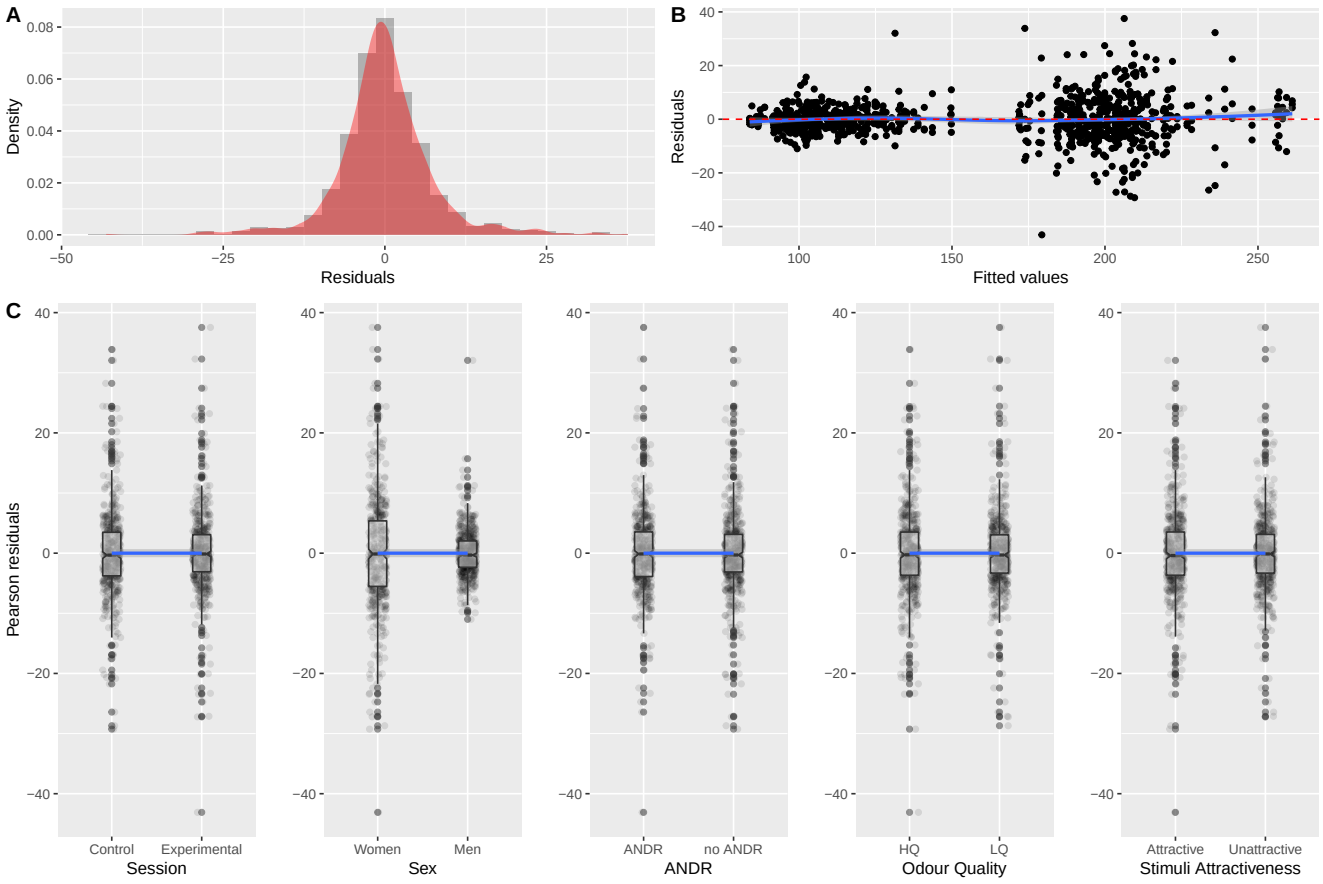

Figure S1. Mean F_0 model diagnostics. (A) Residual distribution. (B) Homoscedasticity (constant variance of residuals); the amount and distance of points above and below the blue line is randomly spread. (C) Linearity in each (single term) fixed factor. ANDR = Androstadienone; For odour quality, HQ = high quality, and LQ = low quality.

2.4.1.1.2 Table S6. Mean F_0 model ANOVA-type table including Sum of squares, degrees of freedom, F and p values, for all main effects and interactions.

```
lmeSig(m.Mean_F0, "\\textbf{Table S6.} Mean $F_{0}$ model")
```

Table S6. Mean F_0 model

	Sum of Squares	*df*	*F*	*p*
S	91.34	1 — 79.11	1.44	0.234
SA	1416.84	1 — 791.28	22.36	**<0.0001**
Sex	48119.25	1 — 80.1	759.31	**<0.0001**
OQ	159.90	1 — 80.1	2.52	0.116
ANDR	73.39	1 — 80.1	1.16	0.285
S × SA	63.82	1 — 791.28	1.01	0.316
S × Sex	227.90	1 — 79.11	3.60	0.062
SA × Sex	119.68	1 — 791.28	1.89	0.17
S × OQ	53.64	1 — 79.11	0.85	0.36
SA × OQ	551.76	1 — 791.28	8.71	**0.003**
Sex × OQ	56.55	1 — 80.1	0.89	0.348
S × ANDR	29.18	1 — 79.11	0.46	0.499
SA × ANDR	48.31	1 — 791.28	0.76	0.383
Sex × ANDR	27.79	1 — 80.1	0.44	0.51
OQ × ANDR	13.14	1 — 80.1	0.21	0.65
S × SA × Sex	140.26	1 — 791.28	2.21	0.137
S × SA × OQ	8.54	1 — 791.28	0.13	0.714
S × Sex × OQ	49.00	1 — 79.11	0.77	0.382
SA × Sex × OQ	537.57	1 — 791.28	8.48	**0.004**
S × SA × ANDR	4.86	1 — 791.28	0.08	0.782
S × Sex × ANDR	87.98	1 — 79.11	1.39	0.242
SA × Sex × ANDR	3.59	1 — 791.28	0.06	0.812
S × OQ × ANDR	33.24	1 — 79.11	0.52	0.471
SA × OQ × ANDR	275.71	1 — 791.28	4.35	**0.037**
Sex × OQ × ANDR	24.38	1 — 80.1	0.38	0.537
S × SA × Sex × OQ	0.46	1 — 791.28	0.01	0.932
S × SA × Sex × ANDR	36.43	1 — 791.28	0.57	0.449
S × SA × OQ × ANDR	0.28	1 — 791.28	0.00	0.947
S × Sex × OQ × ANDR	141.06	1 — 79.11	2.23	0.14
SA × Sex × OQ × ANDR	0.05	1 — 791.28	0.00	0.977
S × SA × Sex × OQ × ANDR	119.10	1 — 791.28	1.88	0.171

Note:
S = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality, low quality); ANDR = androstadienone (added, not added); SA = stimuli attractiveness (attractive, unattractive).

2.4.1.2 Figure S2. Mean F_0 Modulation Figure of all effects, including pairwise comparisons between control and experimental sessions, for each group, sex, and stimuli attractiveness category.

```
#Pairwise comparisons, adjusting the p values for multiple comparisons
emmsF0 <- emmeans(m.Mean_F0, ~
                    Session |
                    Odour_Quality:ANDR:Stimuli_Attractiveness:Sex,
                  lmer.df = "satterthwaite")
t.Mean_F0 <- contr.stars(emmsF0)

#Figure
FigS2 <- ggplot(db,
                aes(x = Session,
                    y = Mean_F0,
```

```
                    color = Stimuli_Attractiveness))+
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_point(alpha = 0.4,
             position = position_jitterdodge(jitter.width = 0.2,
                                             dodge.width = 1)) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            aes(group = Stimuli_Attractiveness),
            position = position_dodge(1),
            color = "black",
            linetype = 3) +
  labs(y = expression(paste("Mean F"[0], " (Hz)")),
       color = "Stimuli Attractiveness") +
  facet_grid(Sex ~ Odour_Quality + ANDR,
             scales = "free",
             switch = "y") +
  stat_pvalue_manual(t.Mean_F0,
                     label = "p.signif",
                     y.position = rep(c(290, 298, 170, 175),
                                      each = 4),
                     tip.length = 0,
                     position = position_dodge(width = 2),
                     color = "Stimuli_Attractiveness") +
  theme(legend.position = "bottom")
FigS2
```

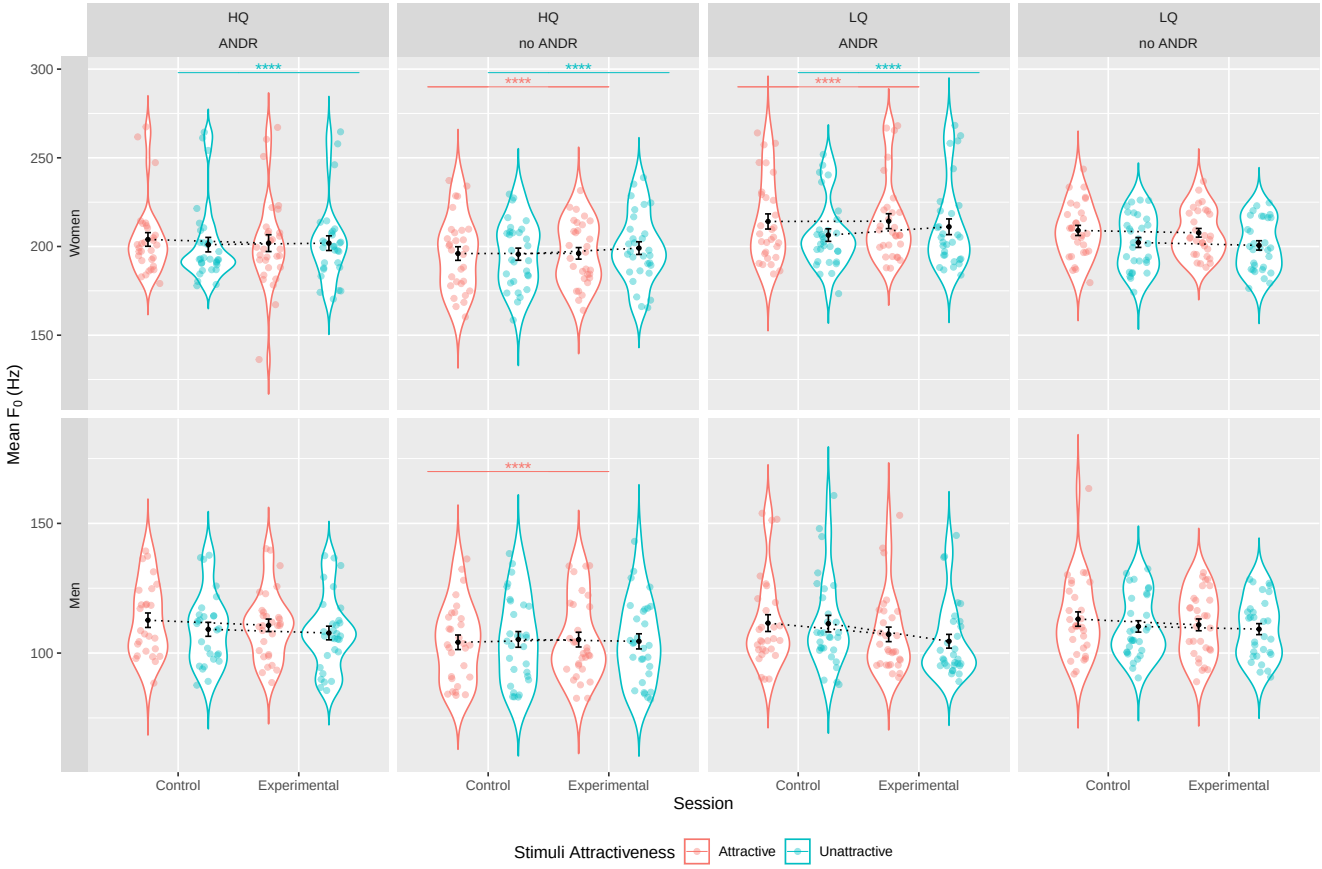

Figure S2. Modulation in Mean F_0. Kernel density (violin) plots and actual (jittered) data points for each group, and sex (top row = women; bottom row = men) , by session (control, experimental), and stimuli attractiveness (red = attractive; blue = unattractive). Black bars represent means ± SEM. Black, dashed lines represent the within-subject change between sessions. Significant effects of session for each group, sex, and stimuli attractiveness category (pairwise contrasts using `emmeans`), are represented with coloured lines and stars: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$,**** $p < 0.0001$.

2.4.2 F_0 SD

2.4.2.1 Model fitting Linear Mixed Model (LMM) fitting.

```
m.F0_SD <- lmer(F0_SD ~
                  Session *
                  Stimuli_Attractiveness *
                  Sex * Odour_Quality *
                  ANDR +
                  (1 + Session | Subject),
          REML = FALSE,
          data = db)
```

2.4.2.1.1 Figure S3. Diagnostics Diagnostics included residual distribution, homoscedasticity, and linearity in each fixed factor.

```
FigS3 <- modDiag(m.F0_SD)
FigS3
```

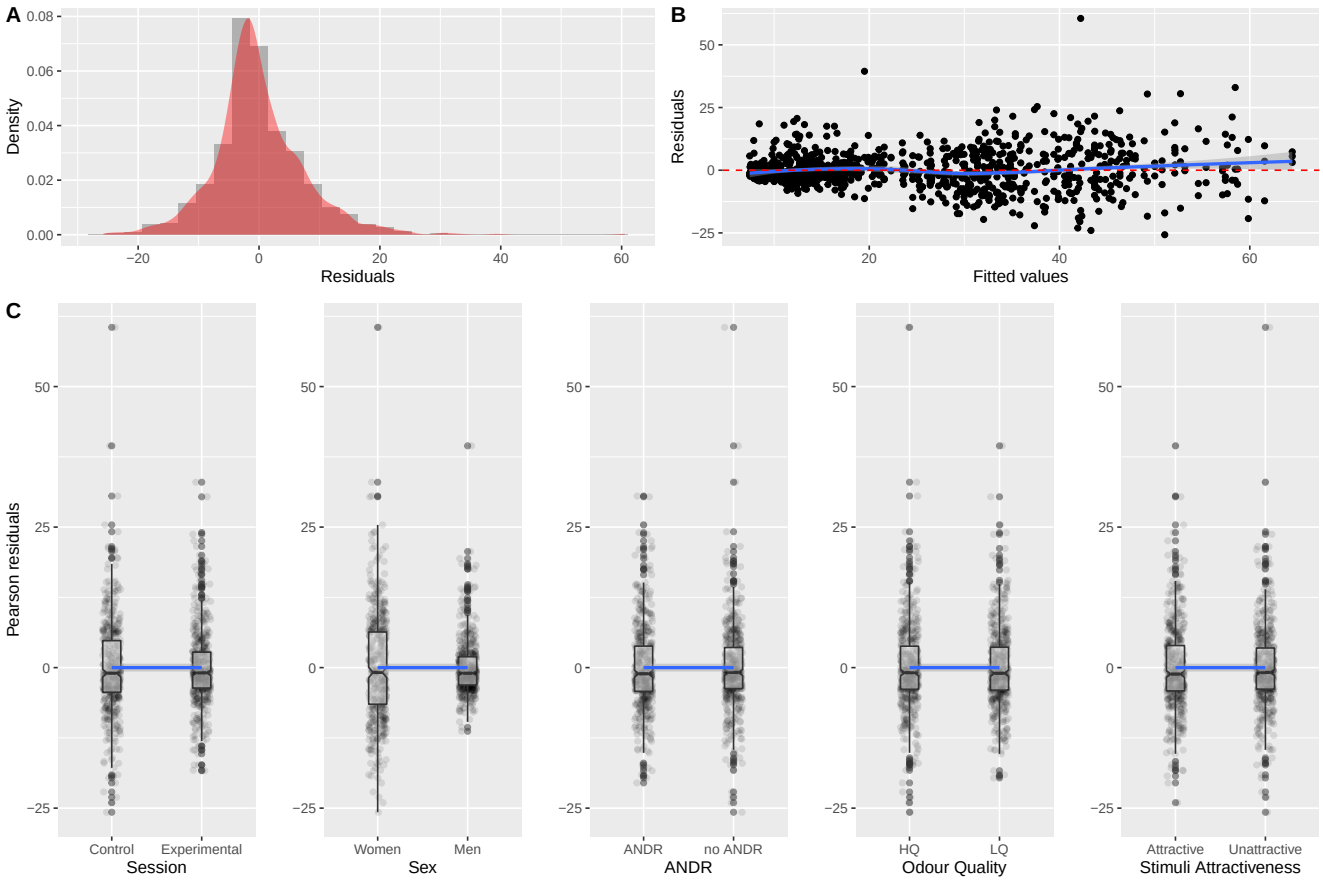

Figure S3. F_0 SD model diagnostics. (A) Residual distribution. (B) Homoscedasticity (constant variance of residuals); the amount and distance of points above and below the blue line is randomly spread. (C) Linearity in each (single term) fixed factor. ANDR = Androstadienone; For odour quality, HQ = high quality, and LQ = low quality.

2.4.2.1.2 Table S7. F_0 SD model ANOVA-type table including Sum of squares, degrees of freedom, F and p values, for all main effects and interactions.

```
lmeSig(m.F0_SD, "\\textbf{Table S7.} $F_{0}$ SD model")
```

Table S7. F_0 SD model

	Sum of Squares	*df*	*F*	*p*
S	268.35	1 — 80.13	3.97	**0.05**
SA	1294.04	1 — 791.83	19.14	**<0.0001**
Sex	14858.75	1 — 80.28	219.78	**<0.0001**
OQ	7.92	1 — 80.28	0.12	0.733
ANDR	5.93	1 — 80.28	0.09	0.768
S × SA	121.28	1 — 791.83	1.79	0.181
S × Sex	36.51	1 — 80.13	0.54	0.465
SA × Sex	305.36	1 — 791.83	4.52	**0.034**
S × OQ	0.83	1 — 80.13	0.01	0.912
SA × OQ	5.58	1 — 791.83	0.08	0.774
Sex × OQ	6.20	1 — 80.28	0.09	0.763
S × ANDR	80.19	1 — 80.13	1.19	0.279
SA × ANDR	9.24	1 — 791.83	0.14	0.712
Sex × ANDR	0.30	1 — 80.28	0.00	0.947
OQ × ANDR	64.82	1 — 80.28	0.96	0.33
S × SA × Sex	5.62	1 — 791.83	0.08	0.773
S × SA × OQ	15.46	1 — 791.83	0.23	0.633
S × Sex × OQ	89.15	1 — 80.13	1.32	0.254
SA × Sex × OQ	110.78	1 — 791.83	1.64	0.201
S × SA × ANDR	65.84	1 — 791.83	0.97	0.324
S × Sex × ANDR	105.77	1 — 80.13	1.56	0.215
SA × Sex × ANDR	7.81	1 — 791.83	0.12	0.734
S × OQ × ANDR	132.92	1 — 80.13	1.97	0.165
SA × OQ × ANDR	541.79	1 — 791.83	8.01	**0.005**
Sex × OQ × ANDR	145.88	1 — 80.28	2.16	0.146
S × SA × Sex × OQ	2.99	1 — 791.83	0.04	0.833
S × SA × Sex × ANDR	13.16	1 — 791.83	0.19	0.659
S × SA × OQ × ANDR	86.37	1 — 791.83	1.28	0.259
S × Sex × OQ × ANDR	91.82	1 — 80.13	1.36	0.247
SA × Sex × OQ × ANDR	179.53	1 — 791.83	2.66	0.104
S × SA × Sex × OQ × ANDR	0.30	1 — 791.83	0.00	0.947

Note:
S = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality, low quality); ANDR = androstadienone (added, not added); SA = stimuli attractiveness (attractive, unattractive).

2.4.2.2 Figure S4. F_0 SD Modulation Figure of all effects, including pairwise comparisons between control and experimental sessions, for each group, sex, and stimuli attractiveness category.

```
#Pairwise comparisons, adjusting the p values for multiple comparisons
emmsF0_SD <- emmeans(m.F0_SD, ~
                     Session |
                     Odour_Quality:ANDR:Stimuli_Attractiveness:Sex,
                   lmer.df = "satterthwaite")
t.F0_SD <- contr.stars(emmsF0_SD)

#Figure
FigS4 <- ggplot(db,
       aes(x = Session,
           y = F0_SD,
```

```
          color = Stimuli_Attractiveness))+
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_point(alpha = 0.4,
             position = position_jitterdodge(jitter.width = 0.2,
                                             dodge.width = 1)) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            aes(group = Stimuli_Attractiveness),
            position = position_dodge(1),
            color = "black",
            linetype = 3) +
  labs(y = expression(paste("F"[0], " SD (Hz)")),
       color = "Stimuli Attractiveness") +
  facet_grid(Sex ~ Odour_Quality + ANDR,
             scales = "free",
             switch = "y") +
  stat_pvalue_manual(t.F0_SD,
                     label = "p.signif",
                     y.position = rep(c(100, 105, 48, 45),
                                      each = 4),
                     tip.length = 0,
                     position = position_dodge(width = 2),
                     color = "Stimuli_Attractiveness") +
  theme(legend.position = "bottom")
FigS4
```

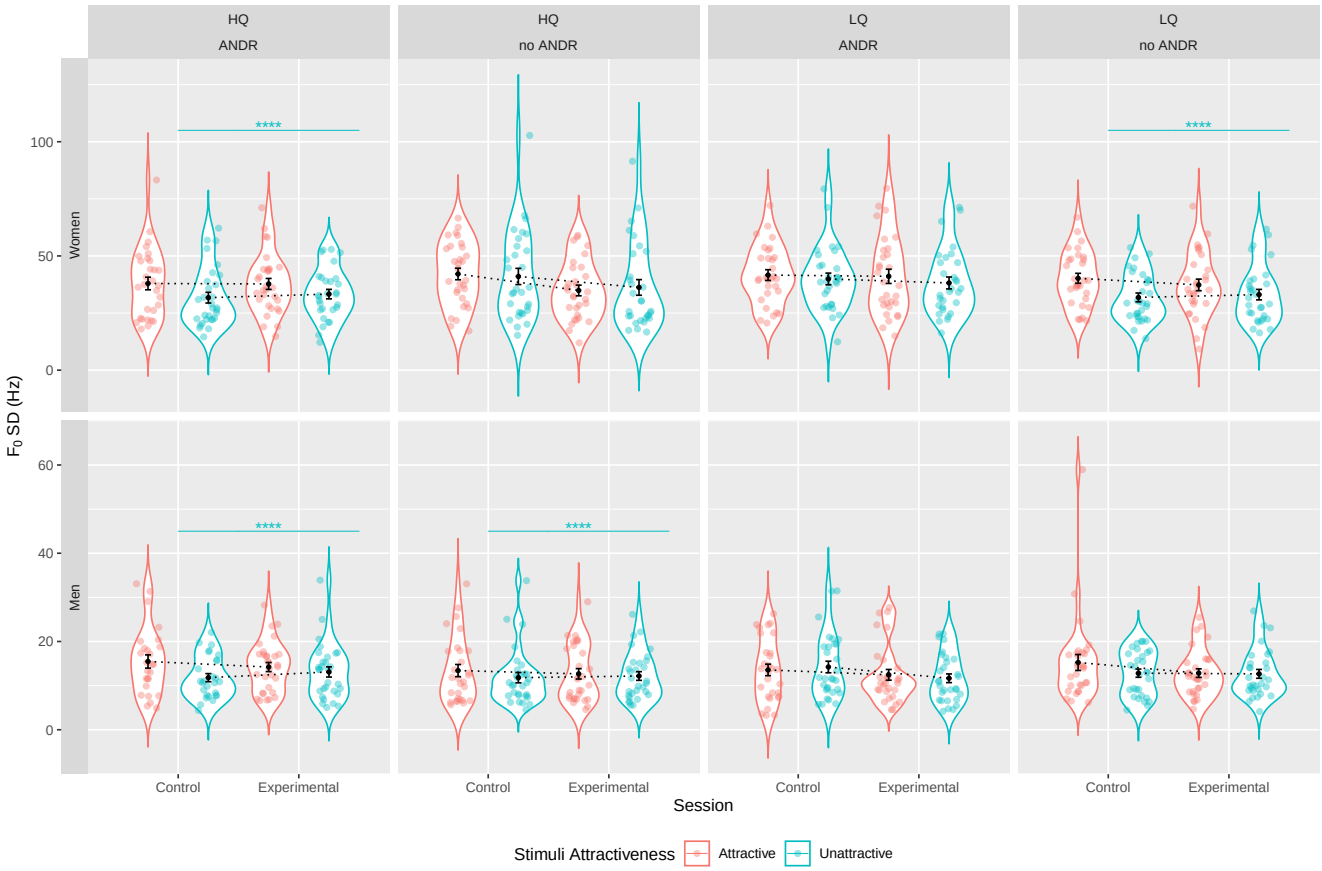

Figure S4. Modulation in F_0 SD. Kernel density (violin) plots and actual (jittered) data points for each group, and sex (top row = women; bottom row = men) , by session (control, experimental), and stimuli attractiveness (red = attractive; blue = unattractive). Black bars represent means ± SEM. Black, dashed lines represent the within-subject change between sessions. Significant effects of session for each group, sex, and stimuli attractiveness category (pairwise contrasts using `emmeans`), are represented with coloured lines and stars: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$,**** $p < 0.0001$.

2.4.3 F_0 CV

2.4.3.1 Model fitting

Linear Mixed Model (LMM) fitting.

```
m.F0_CV <- lmer(F0_CV ~
                    Session *
                    Stimuli_Attractiveness *
                    Sex * Odour_Quality *
                    ANDR +
                    (1 + Session | Subject),
                REML = FALSE,
                data = db)
```

2.4.3.1.1 Figure S5. Diagnostics

Diagnostics included residual distribution, homoscedasticity, and linearity in each fixed factor.

```
FigS5 <- modDiag(m.F0_CV)
FigS5
```

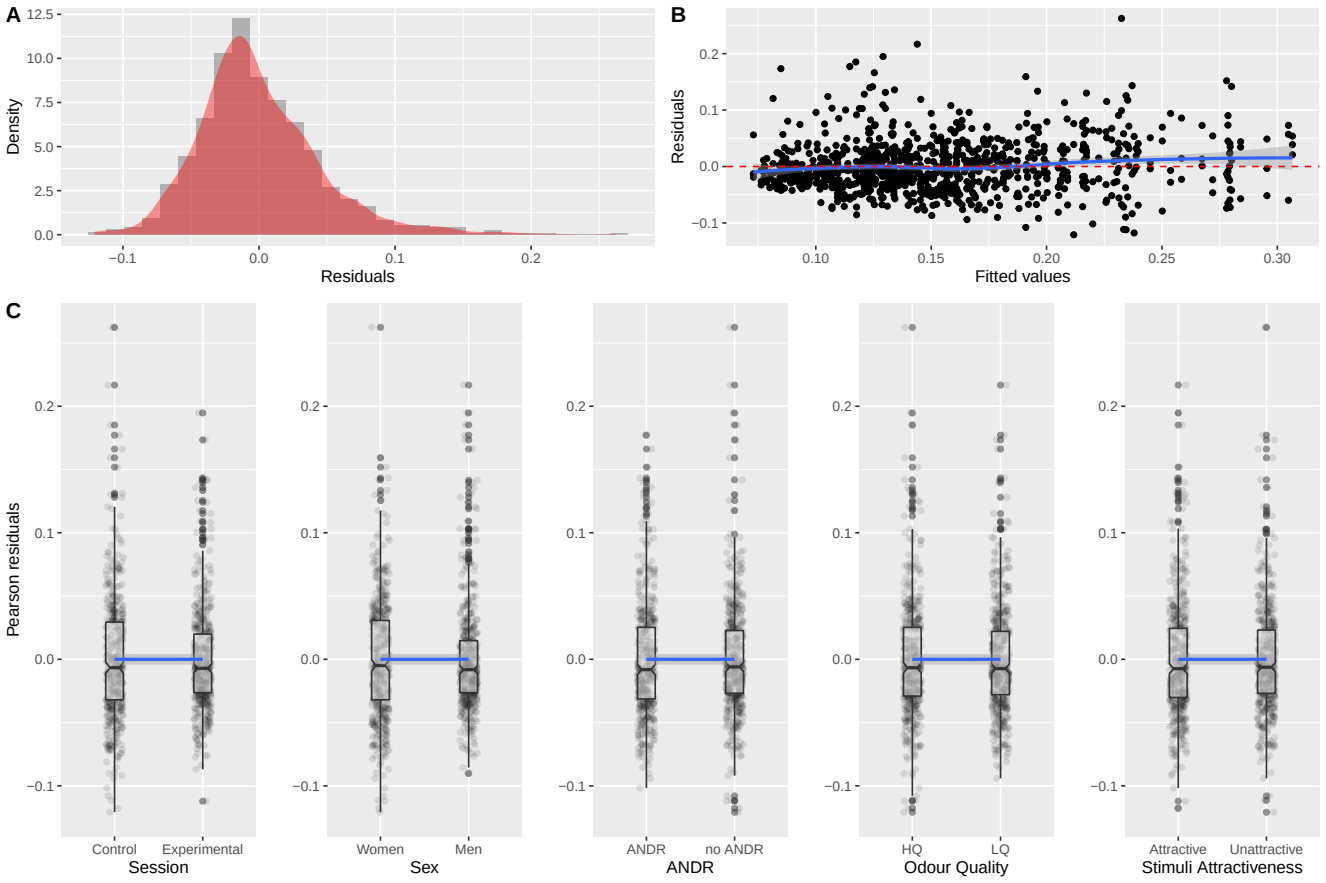

Figure S5. F_0 CV model diagnostics. (A) Residual distribution. (B) Homoscedasticity (constant variance of residuals); the amount and distance of points above and below the blue line is randomly spread. (C) Linearity in each (single term) fixed factor. ANDR = Androstadienone; For odour quality, HQ = high quality, and LQ = low quality.

2.4.3.1.2 Table S8. F_0 CV model ANOVA-type table including Sum of squares, degrees of freedom, F and p values, for all main effects and interactions.

```
lmeSig(m.F0_CV, "\\textbf{Table S8.} $F_{0}$ CV model")
```

Table S8. F_0 CV model

	Sum of Squares	*df*	*F*	*p*
S	0.01	1 — 79.94	2.66	0.107
SA	0.03	1 — 791.68	13.33	**<0.001**
Sex	0.12	1 — 80.29	48.95	**<0.0001**
OQ	0.00	1 — 80.29	0.04	0.842
ANDR	0.00	1 — 80.29	0.00	0.953
S × SA	0.00	1 — 791.68	1.14	0.286
S × Sex	0.00	1 — 79.94	0.38	0.539
SA × Sex	0.00	1 — 791.68	1.20	0.275
S × OQ	0.00	1 — 79.94	0.05	0.831
SA × OQ	0.00	1 — 791.68	0.70	0.402
Sex × OQ	0.00	1 — 80.29	0.02	0.886
S × ANDR	0.00	1 — 79.94	0.95	0.334
SA × ANDR	0.00	1 — 791.68	0.06	0.805
Sex × ANDR	0.00	1 — 80.29	0.05	0.821
OQ × ANDR	0.00	1 — 80.29	0.55	0.46
S × SA × Sex	0.00	1 — 791.68	0.06	0.812
S × SA × OQ	0.00	1 — 791.68	0.28	0.594
S × Sex × OQ	0.00	1 — 79.94	1.32	0.253
SA × Sex × OQ	0.00	1 — 791.68	0.94	0.332
S × SA × ANDR	0.00	1 — 791.68	1.16	0.282
S × Sex × ANDR	0.00	1 — 79.94	1.20	0.276
SA × Sex × ANDR	0.00	1 — 791.68	0.04	0.849
S × OQ × ANDR	0.01	1 — 79.94	2.16	0.146
SA × OQ × ANDR	0.01	1 — 791.68	5.60	**0.018**
Sex × OQ × ANDR	0.00	1 — 80.29	1.37	0.246
S × SA × Sex × OQ	0.00	1 — 791.68	0.47	0.494
S × SA × Sex × ANDR	0.00	1 — 791.68	0.13	0.715
S × SA × OQ × ANDR	0.00	1 — 791.68	1.50	0.22
S × Sex × OQ × ANDR	0.00	1 — 79.94	1.33	0.252
SA × Sex × OQ × ANDR	0.00	1 — 791.68	1.11	0.293
S × SA × Sex × OQ × ANDR	0.00	1 — 791.68	0.01	0.933

Note:
S = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality, low quality); ANDR = androstadienone (added, not added); SA = stimuli attractiveness (attractive, unattractive).

2.4.3.2 Figure S6. F_0 CV Modulation Figure of all effects, including pairwise comparisons between control and experimental sessions, for each group, sex, and stimuli attractiveness category.

```
#Pairwise comparisons, adjusting the p values for multiple comparisons
emmsF0_CV <- emmeans(m.F0_CV, ~
                   Session |
                   Odour_Quality:ANDR:Stimuli_Attractiveness:Sex,
                 lmer.df = "satterthwaite")
t.F0_CV <- contr.stars(emmsF0_CV)

#Figure
FigS6 <- ggplot(db,
       aes(x = Session,
           y = F0_CV,
```

```
          color = Stimuli_Attractiveness))+
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_point(alpha = 0.4,
             position = position_jitterdodge(jitter.width = 0.2,
                                             dodge.width = 1)) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            aes(group = Stimuli_Attractiveness),
            position = position_dodge(1),
            color = "black",
            linetype = 3) +
  labs(y = expression(paste("F"[0], " CV (Hz)")),
       color = "Stimuli Attractiveness") +
  facet_grid(Sex ~ Odour_Quality + ANDR,
             scales = "free",
             switch = "y") +
  stat_pvalue_manual(t.F0_CV,
                     label = "p.signif",
                     y.position = rep(c(0.62, 0.66, 0.40, 0.43),
                                      each = 4),
                     tip.length = 0,
                     position = position_dodge(width = 2),
                     color = "Stimuli_Attractiveness") +
  theme(legend.position = "bottom")
FigS6
```

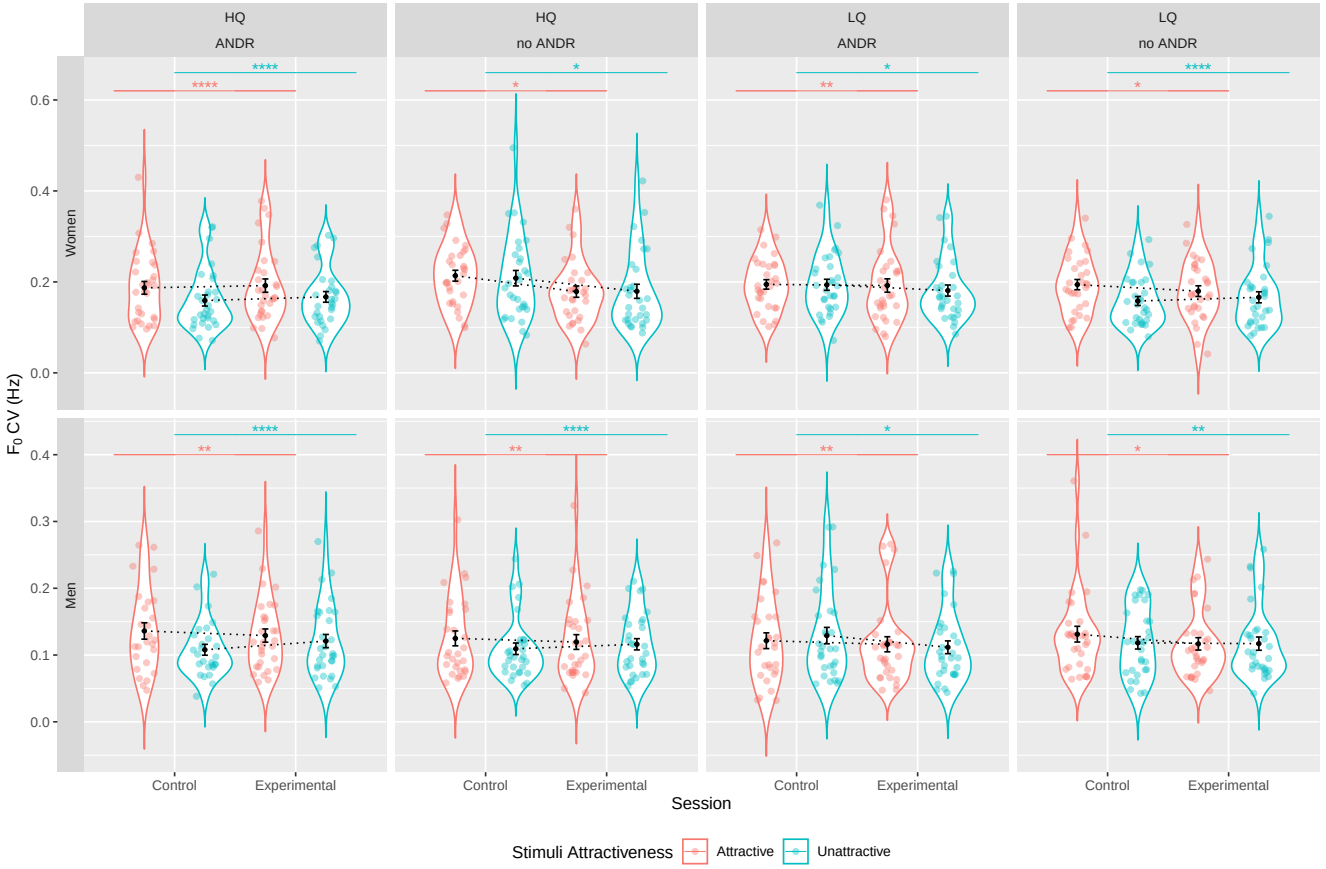

Figure S6. Modulation in F_0 CV. Kernel density (violin) plots and actual (jittered) data points for each group, and sex (top row = women; bottom row = men) , by session (control, experimental), and stimuli attractiveness (red = attractive; blue = unattractive). Black bars represent means ± SEM. Black, dashed lines represent the within-subject change between sessions. Significant effects of session for each group, sex, and stimuli attractiveness category (pairwise contrasts using `emmeans`), are represented with coloured lines and stars: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$,**** $p < 0.0001$.

2.4.4 Mean intensity

2.4.4.1 Model fitting Linear Mixed Model (LMM) fitting.

```
m.Int <- lmer(Intensity ~
                    Session *
                    Stimuli_Attractiveness *
                    Sex * Odour_Quality *
                    ANDR +
                    (1 + Session | Subject),
              REML = FALSE,
              data = db)
m.Int <- update(m.Int,
                control = lmerControl(optimizer = "bobyqa",
                                      optCtrl = list(maxfun=2e5)))
```

Because this model failed to converge, we fitted the model forcing `bobyqa` optimizer for both phases, and a large number of evaluations (following the recommendations found here). This fixed initial the converge issues.

2.4.4.1.1 Figure S7. Diagnostics Diagnostics included residual distribution, homoscedasticity, and linearity in each fixed factor.

```
FigS7 <- modDiag(m.Int)
FigS7
```

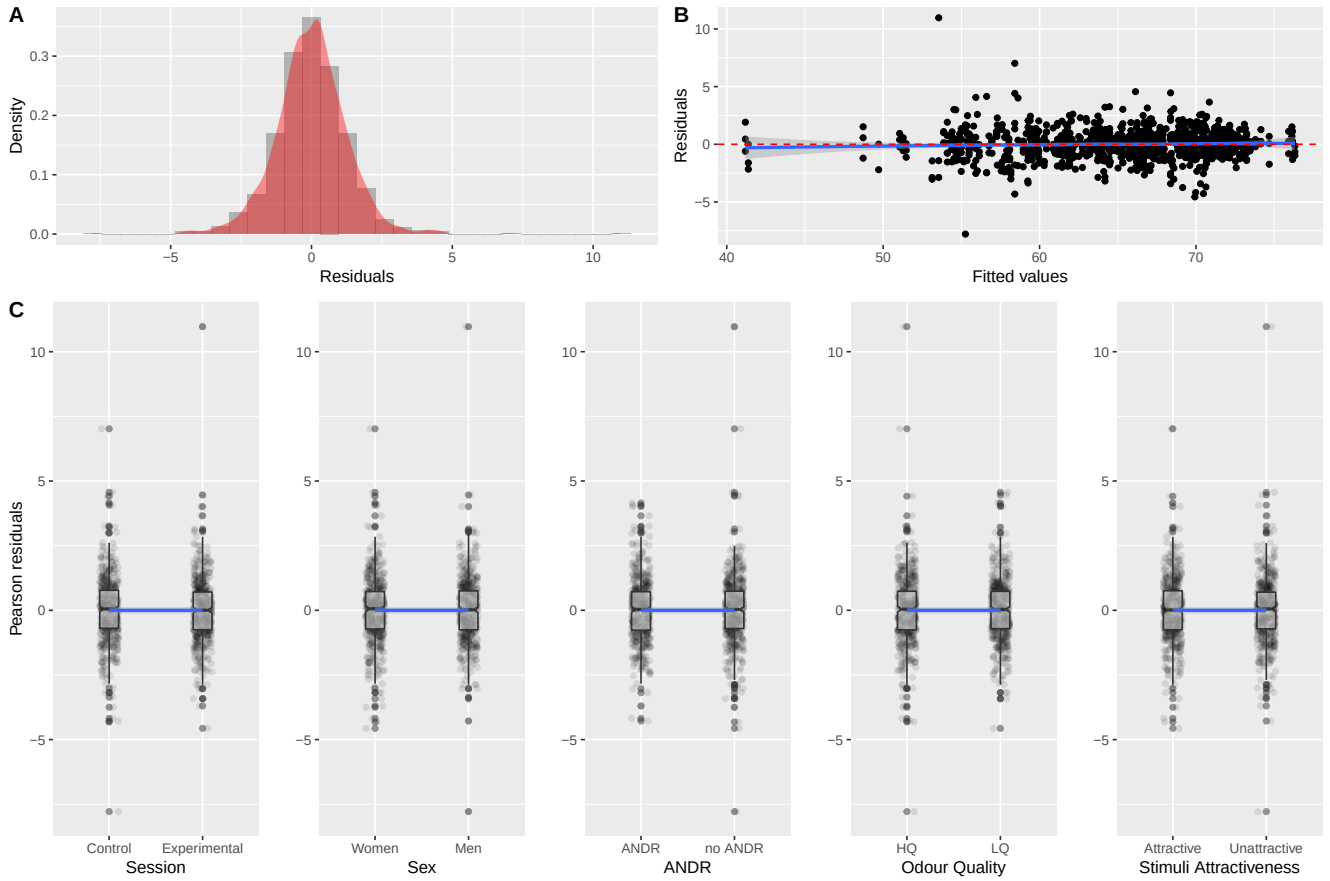

Figure S7. Intensity model diagnostics. (A) Residual distribution. (B) Homoscedasticity (constant variance of residuals); the amount and distance of points above and below the blue line is randomly spread. (C) Linearity in each (single term) fixed factor. ANDR = Androstadienone; For odour quality, HQ = high quality, and LQ = low quality.

2.4.4.1.2 Table S9. Intensity model ANOVA-type table including Sum of squares, degrees of freedom, F and p values, for all main effects and interactions.

```
lmeSig(m.Int, "\\textbf{Table S9.} Mean intensity model")
```

Table S9. Mean intensity model

	Sum of Squares	*df*	*F*	*p*
S	0.24	1 — 79.66	0.11	0.736
SA	5.67	1 — 790.97	2.71	0.1
Sex	14.41	1 — 80.19	6.88	**0.01**
OQ	0.22	1 — 80.19	0.10	0.749
ANDR	0.46	1 — 80.19	0.22	0.642
S × SA	2.36	1 — 790.97	1.13	0.288
S × Sex	0.04	1 — 79.66	0.02	0.891
SA × Sex	2.23	1 — 790.97	1.06	0.303
S × OQ	0.37	1 — 79.66	0.17	0.677
SA × OQ	0.92	1 — 790.97	0.44	0.507
Sex × OQ	0.06	1 — 80.19	0.03	0.863
S × ANDR	0.86	1 — 79.66	0.41	0.524
SA × ANDR	3.02	1 — 790.97	1.44	0.23
Sex × ANDR	0.33	1 — 80.19	0.16	0.694
OQ × ANDR	0.70	1 — 80.19	0.33	0.564
S × SA × Sex	0.02	1 — 790.97	0.01	0.929
S × SA × OQ	0.53	1 — 790.97	0.25	0.617
S × Sex × OQ	0.07	1 — 79.66	0.03	0.856
SA × Sex × OQ	3.47	1 — 790.97	1.66	0.198
S × SA × ANDR	0.15	1 — 790.97	0.07	0.788
S × Sex × ANDR	0.73	1 — 79.66	0.35	0.557
SA × Sex × ANDR	7.35	1 — 790.97	3.51	0.061
S × OQ × ANDR	3.00	1 — 79.66	1.44	0.234
SA × OQ × ANDR	0.14	1 — 790.97	0.06	0.799
Sex × OQ × ANDR	0.27	1 — 80.19	0.13	0.72
S × SA × Sex × OQ	3.11	1 — 790.97	1.49	0.223
S × SA × Sex × ANDR	0.76	1 — 790.97	0.37	0.546
S × SA × OQ × ANDR	0.98	1 — 790.97	0.47	0.493
S × Sex × OQ × ANDR	0.07	1 — 79.66	0.04	0.851
SA × Sex × OQ × ANDR	4.66	1 — 790.97	2.23	0.136
S × SA × Sex × OQ × ANDR	3.61	1 — 790.97	1.72	0.19

Note:
S = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality, low quality); ANDR = androstadienone (added, not added); SA = stimuli attractiveness (attractive, unattractive).

2.4.4.2 Figure S8. Mean Intensity Modulation Figure of all effects, including pairwise comparisons between control and experimental sessions, for each group, sex, and stimuli attractiveness category.

```
#Pairwise comparisons, adjusting the p values for multiple comparisons
emmsInt <- emmeans(m.Int, ~
                     Session |
                     Odour_Quality:ANDR:Stimuli_Attractiveness:Sex,
                   lmer.df = "satterthwaite")
t.Int <- contr.stars(emmsInt)

#Figure
FigS8 <- ggplot(db,
       aes(x = Session,
           y = Intensity,
```

```
          color = Stimuli_Attractiveness))+
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_point(alpha = 0.4,
             position = position_jitterdodge(jitter.width = 0.2,
                                             dodge.width = 1)) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            aes(group = Stimuli_Attractiveness),
            position = position_dodge(1),
            color = "black",
            linetype = 3) +
  labs(y = "Mean Intensity (dB)",
       color = "Stimuli Attractiveness") +
  facet_grid(Sex ~ Odour_Quality + ANDR,
             scales = "free",
             switch = "y") +
  stat_pvalue_manual(t.Int,
                     label = "p.signif",
                     y.position = rep(c(90, 93, 85, 88),
                                      each = 4),
                     tip.length = 0,
                     position = position_dodge(width = 2),
                     color = "Stimuli_Attractiveness") +
  theme(legend.position = "bottom")
FigS8
```

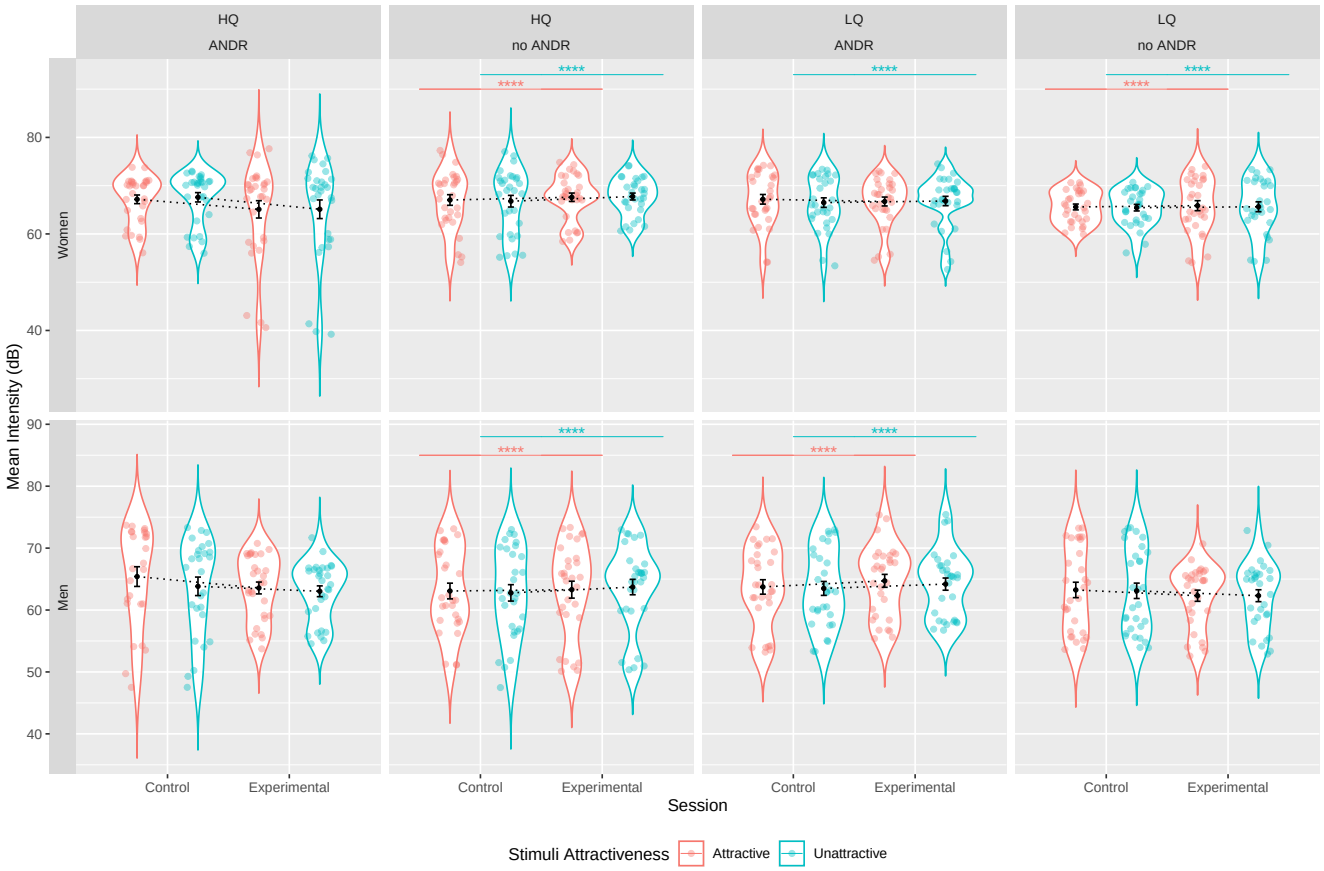

Figure S8. Modulation in mean Intensity. Kernel density (violin) plots and actual (jittered) data points for each group, and sex (top row = women; bottom row = men) , by session (control, experimental), and stimuli attractiveness (red = attractive; blue = unattractive). Black bars represent means ± SEM. Black, dashed lines represent the within-subject change between sessions. Significant effects of session for each group, sex, and stimuli attractiveness category (pairwise contrasts using `emmeans`), are represented with coloured lines and stars: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$,**** $p < 0.0001$.

2.4.5 Attractiveness ratings

2.4.5.1 Model fitting

Linear Mixed Model (LMM) fitting.

```
m.Att <- lmer(AttractivenessRatings ~
                Session *
                Stimuli_Attractiveness *
                Sex * Odour_Quality *
                ANDR +
                (1 + Session | Subject),
              REML = FALSE,
              data = db)
```

2.4.5.1.1 Figure S9. Diagnostics

Diagnostics included residual distribution, homoscedasticity, and linearity in each fixed factor.

```
FigS9 <- modDiag(m.Att)
FigS9
```

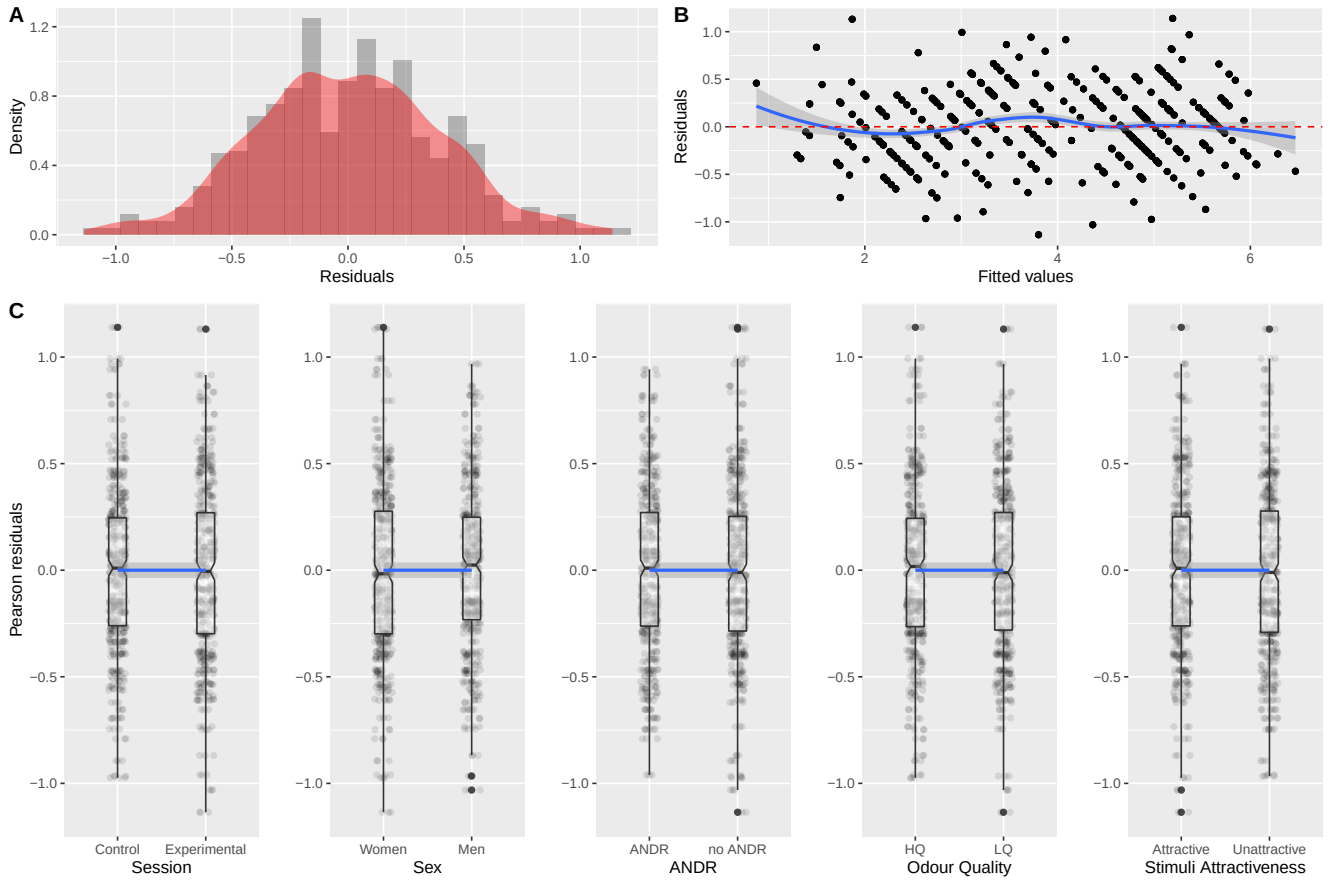

Figure S9. Attractiveness ratings model diagnostics. (A) Residual distribution. (B) Homoscedasticity (constant variance of residuals); the amount and distance of points above and below the blue line is randomly spread. (C) Linearity in each (single term) fixed factor. ANDR = Androstadienone; For odour quality, HQ = high quality, and LQ = low quality.

2.4.5.1.2 Table S10. Attractiveness ratings model ANOVA-type table including Sum of squares, degrees of freedom, F and p values, for all main effects and interactions.

```
lmeSig(m.Att, "\\textbf{Table S10.} Attractiveness ratings model")
```

Table S10. Attractiveness ratings model

	Sum of Squares	*df*	*F*	*p*
S	0.00	1 — 79.84	0.02	0.887
SA	1083.66	1 — 791.01	5677.98	**<0.0001**
Sex	0.15	1 — 80.25	0.81	0.371
OQ	0.03	1 — 80.25	0.16	0.691
ANDR	0.42	1 — 80.25	2.21	0.141
S × SA	0.00	1 — 791.01	0.00	0.956
S × Sex	0.35	1 — 79.84	1.83	0.18
SA × Sex	47.46	1 — 791.01	248.65	**<0.0001**
S × OQ	0.15	1 — 79.84	0.77	0.383
SA × OQ	9.61	1 — 791.01	50.33	**<0.0001**
Sex × OQ	0.01	1 — 80.25	0.04	0.837
S × ANDR	0.01	1 — 79.84	0.06	0.812
SA × ANDR	2.67	1 — 791.01	13.97	**<0.001**
Sex × ANDR	0.95	1 — 80.25	4.99	**0.028**
OQ × ANDR	1.57	1 — 80.25	8.22	**0.005**
S × SA × Sex	0.40	1 — 791.01	2.12	0.146
S × SA × OQ	0.10	1 — 791.01	0.54	0.465
S × Sex × OQ	0.19	1 — 79.84	0.98	0.325
SA × Sex × OQ	0.02	1 — 791.01	0.08	0.771
S × SA × ANDR	1.67	1 — 791.01	8.77	**0.003**
S × Sex × ANDR	0.33	1 — 79.84	1.74	0.191
SA × Sex × ANDR	9.03	1 — 791.01	47.31	**<0.0001**
S × OQ × ANDR	0.09	1 — 79.84	0.46	0.501
SA × OQ × ANDR	0.04	1 — 791.01	0.21	0.643
Sex × OQ × ANDR	0.07	1 — 80.25	0.39	0.535
S × SA × Sex × OQ	0.18	1 — 791.01	0.97	0.326
S × SA × Sex × ANDR	0.05	1 — 791.01	0.27	0.603
S × SA × OQ × ANDR	0.01	1 — 791.01	0.05	0.819
S × Sex × OQ × ANDR	0.59	1 — 79.84	3.08	0.083
SA × Sex × OQ × ANDR	2.26	1 — 791.01	11.85	**<0.001**
S × SA × Sex × OQ × ANDR	0.40	1 — 791.01	2.09	0.149

Note:
S = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality, low quality); ANDR = androstadienone (added, not added); SA = stimuli attractiveness (attractive, unattractive).

2.4.5.2 Figure S10. Odour effects on attractiveness ratings Figure of all effects, including pairwise comparisons between control and experimental sessions, for each group, sex, and stimuli attractiveness category.

```
#Pairwise comparisons, adjusting the p values for multiple comparisons
emmsAtt <- emmeans(m.Att, ~
                     Session |
                     Odour_Quality:ANDR:Stimuli_Attractiveness:Sex,
                   lmer.df = "satterthwaite")
t.Att <- contr.stars(emmsAtt)

#Figure
FigS10 <- ggplot(db,
       aes(x = Session,
           y = AttractivenessRatings,
```

```
          color = Stimuli_Attractiveness))+
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_point(alpha = 0.4,
             position = position_jitterdodge(jitter.width = 0.2,
                                             dodge.width = 1)) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            aes(group = Stimuli_Attractiveness),
            position = position_dodge(1),
            color = "black",
            linetype = 3) +
  labs(y = "Attractiveness ratings",
       color = "Stimuli Attractiveness") +
  facet_grid(Sex ~ Odour_Quality + ANDR,
             scales = "free",
             switch = "y") +
  stat_pvalue_manual(t.Att,
                     label = "p.signif",
                     y.position = rep(c(7.4, 7.7, 7.2, 7.5),
                                      each = 4),
                     tip.length = 0,
                     position = position_dodge(width = 2),
                     color = "Stimuli_Attractiveness") +
  theme(legend.position = "bottom")
FigS10
```

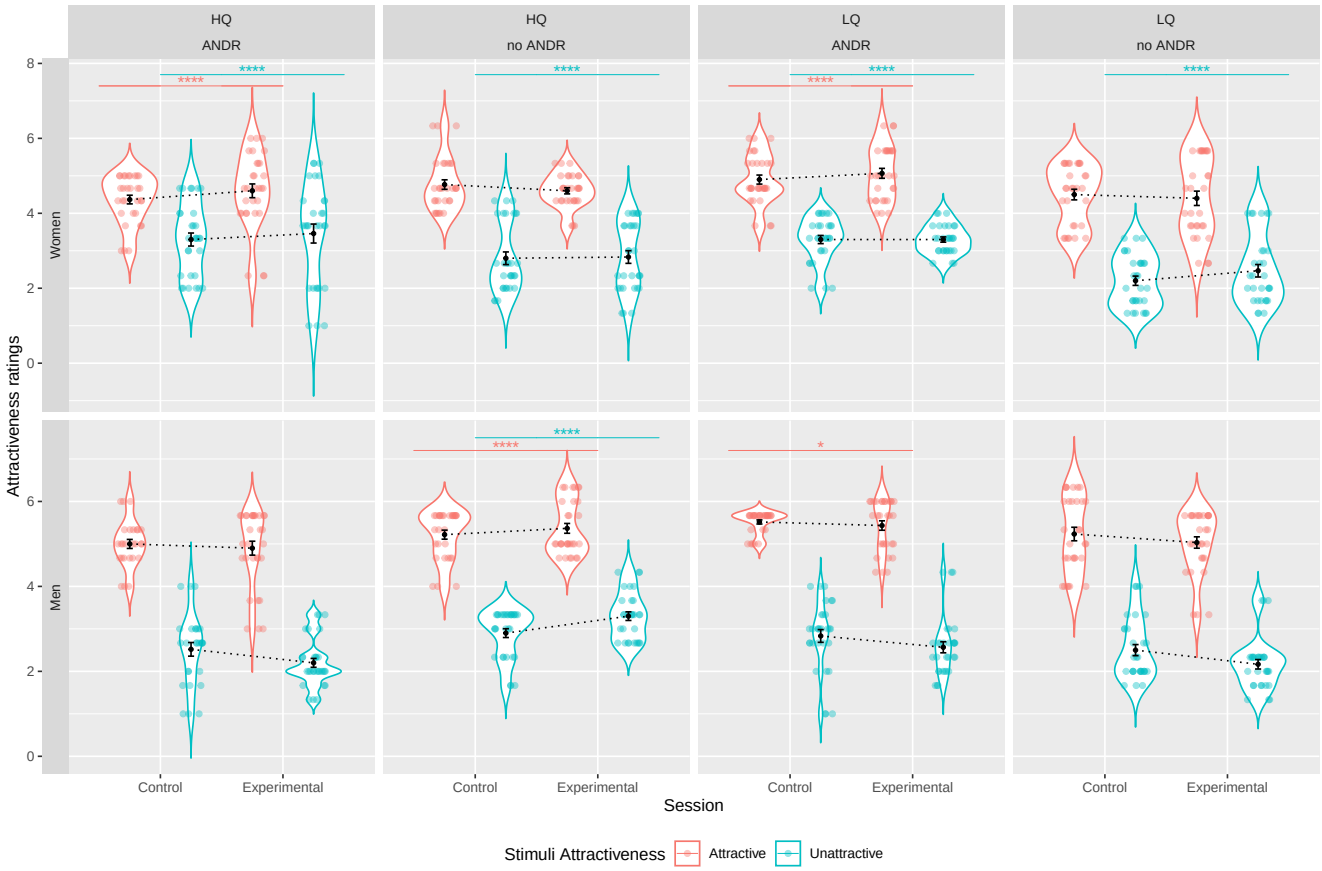

Figure S10. Modulation in attractiveness ratings. Kernel density (violin) plots and actual (jittered) data points for each group, and sex (top row = women; bottom row = men) , by session (control, experimental), and stimuli attractiveness (red = attractive; blue = unattractive). Black bars represent means ± SEM. Black, dashed lines represent the within-subject change between sessions. Significant effects of session for each group, sex, and stimuli attractiveness category (pairwise contrasts using `emmeans`), are represented with coloured lines and stars: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$,**** $p < 0.0001$.

2.4.6 Table 1. All models

```
t.1 <- lmeSigFin(m.Mean_F0)
t.2 <- lmeSigFin(m.F0_SD)
t.3 <- lmeSigFin(m.F0_CV)
t.4 <- lmeSigFin(m.Int)
t.5 <- lmeSigFin(m.Att)

#Select only rows containing the main effect or interactions with Session,
#and only the columns containing F and p values.
m.Tab <- cbind(t.1[,3:4],
               t.2[,3:4],
               t.3[,3:4],
               t.4[,3:4],
               t.5[,3:4])
m.Tab <- m.Tab[c(1,6:7,9,12,16:18,20:21,23,26:29,31),]
kable(m.Tab,
      digits = 2,
      caption = "\\textbf{Table 1.} Anova-type table for all models,
including only main effects and interactions with Session",
```

```
    align = "c",
    booktabs = TRUE,
    escape = FALSE) %>%
  kable_styling(latex_options = c("HOLD_position", "scale_down")) %>%
  footnote(general = "S = Session (control, experimental);
  Sex = participants sex (women, men);
  OQ = odour quality (high quality, low quality);
  ANDR = androstadienone (added, not added);
  SA = stimuli attractiveness (attractive, unattractive).
  For all results, including all main effects, $df$ and Sums of Squares,
  see Tables S6 to S10.",
           threeparttable = TRUE,
           escape = FALSE) %>%
  add_header_above(c(" " = 1,
                     "Mean $F_{0}$" = 2,
                     "$F_{0}$ SD" = 2,
                     "$F_{0}$ CV" = 2,
                     "Intensity" = 2,
                     "Attractiveness ratings" = 2),
                   escape = FALSE)
```

Table 1. Anova-type table for all models, including only main effects and interactions with Session

	Mean F_0		F_0 SD		F_0 CV		Intensity		Attractiveness ratings	
	F	*p*	*F*	*p*	*F*	*p*	*F*	*p*	*F*	*p*
S	1.44	0.234	3.97	**0.05**	2.66	0.107	0.11	0.736	0.02	0.887
S × SA	1.01	0.316	1.79	0.181	1.14	0.286	1.13	0.288	0.00	0.956
S × Sex	3.60	0.062	0.54	0.465	0.38	0.539	0.02	0.891	1.83	0.18
S × OQ	0.85	0.36	0.01	0.912	0.05	0.831	0.17	0.677	0.77	0.383
S × ANDR	0.46	0.499	1.19	0.279	0.95	0.334	0.41	0.524	0.06	0.812
S × SA × Sex	2.21	0.137	0.08	0.773	0.06	0.812	0.01	0.929	2.12	0.146
S × SA × OQ	0.13	0.714	0.23	0.633	0.28	0.594	0.25	0.617	0.54	0.465
S × Sex × OQ	0.77	0.382	1.32	0.254	1.32	0.253	0.03	0.856	0.98	0.325
S × SA × ANDR	0.08	0.782	0.97	0.324	1.16	0.282	0.07	0.788	8.77	**0.003**
S × Sex × ANDR	1.39	0.242	1.56	0.215	1.20	0.276	0.35	0.557	1.74	0.191
S × OQ × ANDR	0.52	0.471	1.97	0.165	2.16	0.146	1.44	0.234	0.46	0.501
S × SA × Sex × OQ	0.01	0.932	0.04	0.833	0.47	0.494	1.49	0.223	0.97	0.326
S × SA × Sex × ANDR	0.57	0.449	0.19	0.659	0.13	0.715	0.37	0.546	0.27	0.603
S × SA × OQ × ANDR	0.00	0.947	1.28	0.259	1.50	0.22	0.47	0.493	0.05	0.819
S × Sex × OQ × ANDR	2.23	0.14	1.36	0.247	1.33	0.252	0.04	0.851	3.08	0.083
S × SA × Sex × OQ × ANDR	1.88	0.171	0.00	0.947	0.01	0.933	1.72	0.19	2.09	0.149

Note:
S = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality, low quality); ANDR = androstadienone (added, not added); SA = stimuli attractiveness (attractive, unattractive). For all results, including all main effects, *df* and Sums of Squares, see Tables S6 to S10.

2.4.7 Figure 4. Session effects and interactions

2.4.7.1 Colour version Online version.

```
#Figure 4A F0_SD (Session main effect)
emmsF0_SD <- emmeans(m.F0_SD,
                     ~ Session,
                     lmer.df = "satterthwaite")
tt.F0_SD <- contr.stars(emmsF0_SD)
```

```
#Figure
Fig4A <- ggplot(augment(m.F0_SD),
                aes(x = Session,
                    y = F0_SD))+
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_jitter(alpha = 0.4,
              width = 0.2) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               color = "black") +
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.2,
               color = "black") +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            color = "black",
            linetype = 3,
            aes(group=1)) +
  labs(y = expression(paste("F"[0], " SD (Hz)")),
       subtitle = expression(paste("Session effects on F"[0],
                                   " SD (Hz)"))) +
  stat_pvalue_manual(tt.F0_SD,
                     label = "p.signif",
                     y.position = 120,
                     tip.length = 0) +
  theme(legend.position = "bottom")

#Figure 4B AttractivenessRatings (Session:Stimuli_Attractiveness:ANDR interaction)
emmsAtt2 <- emmeans(m.Att,
                    ~ Session |
                      ANDR:Stimuli_Attractiveness,
                    lmer.df = "satterthwaite")
tt.Att <- contr.stars(emmsAtt2)

#Figure
Fig4B <- ggplot(augment(m.Att),
                aes(x = Session,
                    y = AttractivenessRatings,
                    color = Stimuli_Attractiveness))+
  geom_violin(position = position_dodge(1),
              trim = FALSE) +
  geom_point(alpha = 0.4,
             position = position_jitterdodge(jitter.width = 0.2,
                                             jitter.height = 0.1,
                                             dodge.width = 1)) +
  stat_summary(fun.y = "mean",
               geom = "point",
               size = 1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
```

```
  stat_summary(fun.data = data.summary,
               geom = "errorbar",
               width=0.1,
               aes(group = Stimuli_Attractiveness),
               color = "black",
               position = position_dodge(1)) +
  geom_line(stat = "smooth",
            method = "lm",
            se = FALSE,
            color = "black",
            linetype = 3,
            aes(group = Stimuli_Attractiveness),
            position = position_dodge(1)) +
  labs(y = "Attractiveness ratings",
       subtitle = "Session effects on attractiveness ratings",
       color = "Stimuli attractiveness") +
  stat_pvalue_manual(tt.Att,
                     label = "p.signif",
                     y.position = rep(c(7.5, 8),
                                      each = 2),
                     tip.length = 0,
                     position = position_dodge(width = 2),
                     color = "Stimuli_Attractiveness") +
  facet_wrap(~ ANDR) +
  theme(legend.position = "bottom")


Fig4 <- ggarrange(Fig4A,
                  Fig4B,
                  labels = "AUTO",
                  nrow = 1,
                  widths = c(1, 2))
Fig4
```

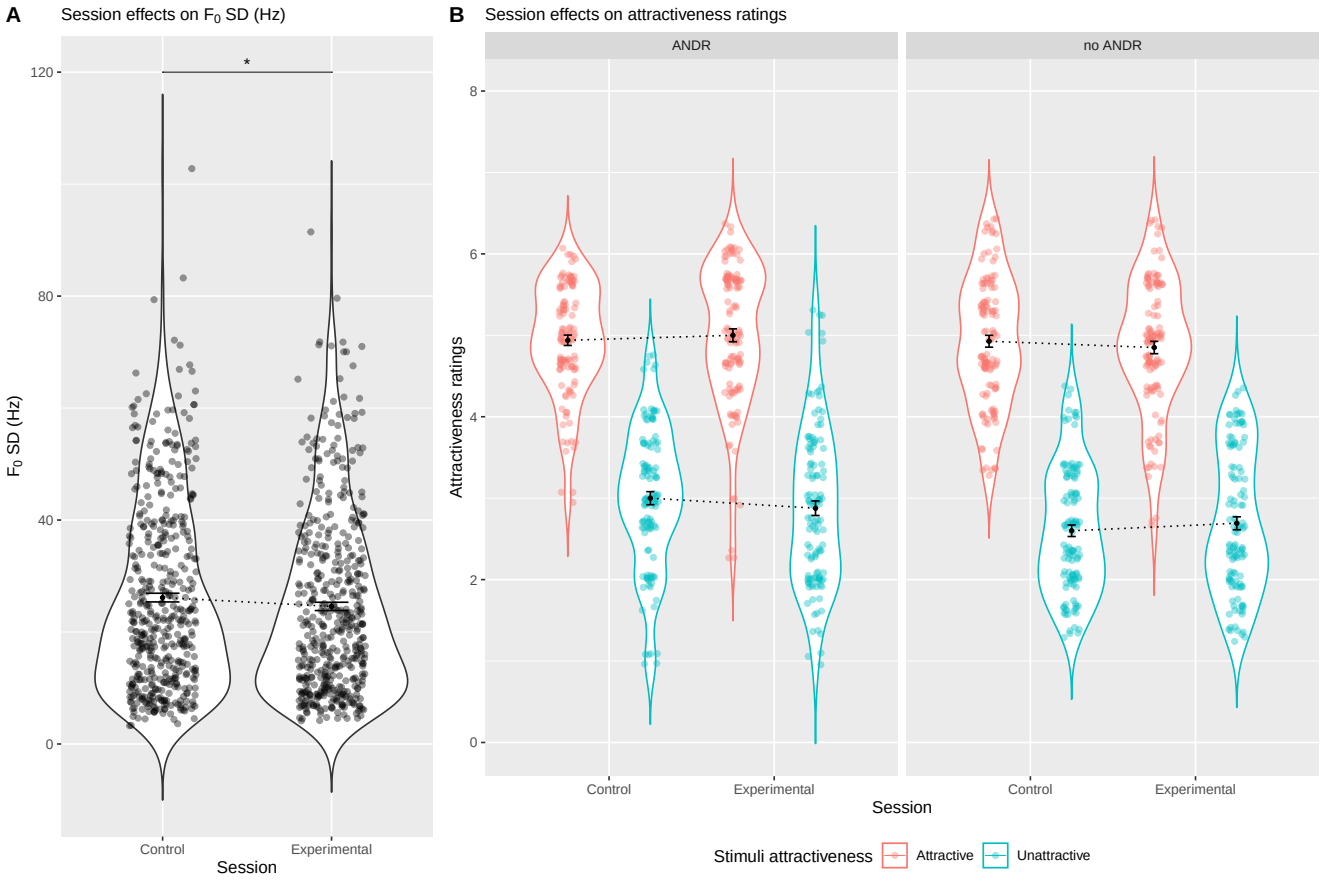

Figure 4. Significant Session effects and interactions. (A) Main effect of Session for F_0 SD. (B) Interactions between Session, Stimuli Attractiveness and ANDR for Attractiveness ratings. The black line represents the general within-subject change between sessions (pairwise contrasts using `emmeans`). Significant effects of session are represented with lines and stars: * $p < 0.05$.

2.4.7.2 Greyscale version

Print version.

```
#Figure 4A F0_SD (Session main effect)
Fig4Abw <- Fig4A +
  theme_light()

#Figure 4B AttractivenessRatings (Session:Stimuli_Attractiveness:ANDR interaction)
Fig4Bbw <- Fig4B +
  scale_color_grey(start = 0,
                   end = 0.4) +
  theme_light() +
  theme(legend.position = "bottom") +
  theme(strip.text.x = element_text(color = "black"))


Fig4bw <- ggarrange(Fig4Abw,
                    Fig4Bbw,
                    labels = "AUTO",
                    nrow = 1,
                    widths = c(1, 2))
Fig4bw
```

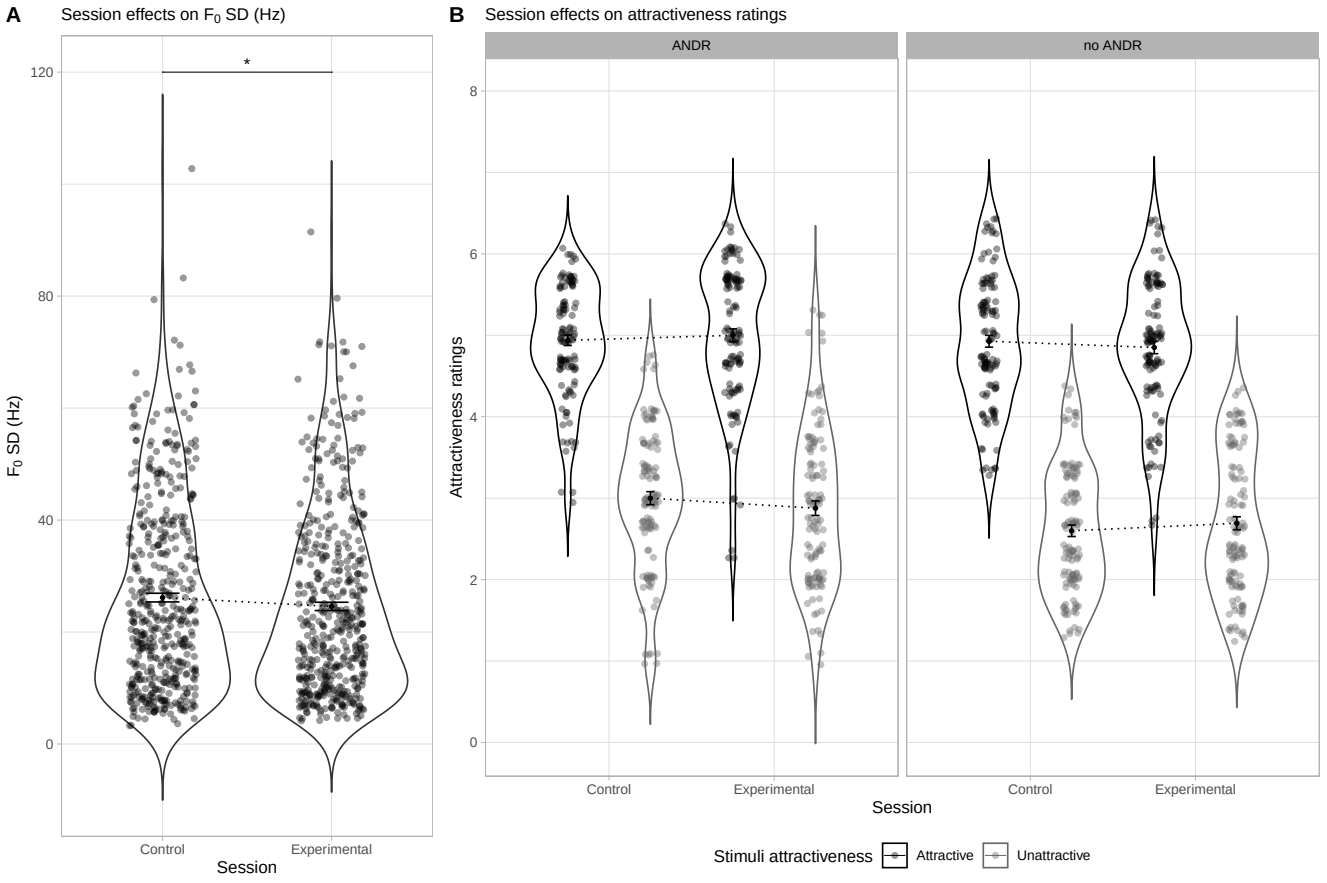

Figure 4. Significant Session effects and interactions. (A) Main effect of Session for F_0 SD. (B) Interactions between Session, Stimuli Attractiveness and ANDR for Attractiveness ratings. The black line represents the general within-subject change between sessions (pairwise contrasts using `emmeans`). Significant effects of session are represented with lines and stars: * $p < 0.05$.

2.5 Models to predict attractiveness ratings

To test whether the acoustic characteristics of the participants' voices predicted the attractiveness ratings they gave to each stimulus, in each session, we fitted mixed linear regressions using `Sex`, `Mean_F0`, `F0_CV`, (mean) `Intensity`, `Odour_Quality` and `ANDR`, as well as the interactions between `Sex` and `Mean_F0`, `Sex` and `F0_CV`, and `Sex` and `Intensity` were included as fixed predictors. The interaction between participant ID (`Subject`) and `Session` was entered as a random intercept factor, to account for the two times that each participant rated and responded to each stimulus (one in each session), and avoid pseudoreplication. Although it would be ideal to allow random slopes for the acoustic variables for each `Subject:Session` interaction, these models failed to converge in all cases, with all optimizers.

We included F_0 CV and not F_0 SD, for three reasons: first, given that both are measures of F_0 variability, they are highly correlated (see tables S3 to S5). Second, unlike F_0 SD, F_0 CV is not significantly correlated with mean F_0 in women (Table S4), or men (Table S5). And third, we preferred F_0 CV given that it is a better representation of the perceptual variability, as it takes into account the mean F_0 of each recording.

This initial model was then reduced to include only the most relevant acoustic variables: mean F_0, and F_0 CV. Initial and Final models were then compared using the Akaike information criterion (AIC) and Akaike weights ($w_i(AIC)$).

2.5.1 Initial Model

2.5.1.1 Model fitting Linear Mixed Model (LMM) fitting.

```
m1 <- lmer(AttractivenessRatings ~
             Sex +
             Mean_F0 +
             F0_CV +
             Min_F0 +
             Intensity +
             Mean_F0:Sex +
             F0_CV:Sex +
             Min_F0:Sex +
             Intensity:Sex +
             Odour_Quality +
             ANDR +
             (1 | Subject:Session),
           data = db)
```

2.5.1.1.1 Table S11. Initial model regression table Regression-type table including estimates, standard errors, degrees of freedom, as well as t and p values for each term.

```
rnames <- c("(Intercept)",
            "Sex (men)",
            "Mean $F_{0}$ (Hz)",
            "$F_{0}$ CV (Hz)",
            "Min $F_{0}$ (Hz)",
            "Intensity (dB)",
            "OQ(LQ)",
            "ANDR (no ANDR)",
            "Sex (men)  $\\times$ Mean $F_{0}$ (Hz)",
            "Sex (men)  $\\times$ $F_{0}$ CV (Hz)",
            "Sex (men)  $\\times$ Min $F_{0}$ (Hz)",
            "Sex (men)  $\\times$ Intensity (dB)")

s1 <- as.data.frame(summary(m1)$coefficients)
s1 <- summasig(s1, 5)
row.names(s1) <- rnames
kable(s1,
      align = "c",
      digits = 2,
      caption = "\\textbf{Table S11.} Initial model summary",
      col.names = c("Estimate",
                    "Std. Error",
                    "$df$",
                    "$t$",
                    "$p$"),
      booktabs = TRUE,
      escape = FALSE) %>%
  kable_styling(latex_options = "HOLD_position") %>%
  footnote(general = paste0("$R^2_{marginal}$ = ",
                            round(r.squaredGLMM(m1)[1], 2),
                            ", $R^2_{conditional}$ = ",
                            round(r.squaredGLMM(m1)[2], 2),
                            ". Cond. = Session (control, experimental);
                            Sex = participants sex (women, men);
                            OQ = odour quality (high quality = HQ, low quality = LQ);
                            ANDR = androstadienone (added, not added);
                            Control session, HQ body odour, and added ANDR were used as
                            reference for categorical predictors.
```

```
                        Women were used as reference category for Sex.
                        Significant effects are in bold."),
          threeparttable = TRUE,
          escape = FALSE)
```

Table S11. Initial model summary

	Estimate	Std. Error	*df*	*t*	*p*
(Intercept)	1.48	1.04	235.38	1.42	0.156
Sex (men)	0.66	1.45	255.92	0.46	0.649
Mean F_0 (Hz)	0.00	0.00	342.24	0.32	0.745
F_0 CV (Hz)	3.81	0.96	621.35	3.95	**0.0001**
Min F_0 (Hz)	0.00	0.00	914.23	1.75	0.08
Intensity (dB)	0.01	0.01	177.95	1.10	0.274
OQ(LQ)	-0.06	0.11	146.10	-0.54	0.59
ANDR (no ANDR)	-0.16	0.11	144.64	-1.49	0.138
Sex (men) × Mean F_0 (Hz)	0.01	0.01	270.24	1.39	0.165
Sex (men) × F_0 CV (Hz)	-1.76	1.54	744.41	-1.15	0.252
Sex (men) × Min F_0 (Hz)	-0.01	0.01	883.39	-0.76	0.45
Sex (men) × Intensity (dB)	-0.01	0.02	184.99	-0.28	0.776

Note:
$R^2_{marginal} = 0.04$, $R^2_{conditional} = 0.14$. Cond. = Session (control, experimental); Sex = participants sex (women, men); OQ = odour quality (high quality = HQ, low quality = LQ); ANDR = androstadienone (added, not added); Control session, HQ body odour, and added ANDR were used as reference for categorical predictors. Women were used as reference category for Sex. Significant effects are in bold.

2.5.2 Intermediate Model

2.5.2.1 Model fitting Linear Mixed Model (LMM) fitting.

```
m2 <- lmer(AttractivenessRatings ~
             Sex +
             Mean_F0 +
             F0_CV +
             Min_F0 +
             Mean_F0:Sex +
             F0_CV:Sex +
             Min_F0:Sex +
             (1 | Subject:Session),
           REML = FALSE,
           data = db)
```

2.5.2.1.1 Table S12. Intermediate model regression table Regression-type table including estimates, standard errors, degrees of freedom, as well as *t* and *p* values for each term.

```
s2 <- as.data.frame(summary(m2)$coefficients)
s2 <- summasig(s2, 5)
row.names(s2) <- rnames[c(1:5,9:11)]
kable(s2,
      align = "c",
      digits = 2,
      caption = "\\textbf{Table S12.} Intermediate model summary",
      col.names = c("Estimate",
```

```
                    "Std. Error",
                    "$df$",
                    "$t$",
                    "$p$"),
      booktabs = TRUE,
      escape = FALSE) %>%
  kable_styling(latex_options = "HOLD_position") %>%
  footnote(general = paste0("$R^2_{marginal}$ = ",
                            round(r.squaredGLMM(m2)[1], 2),
                            ", $R^2_{conditional}$ = ",
                            round(r.squaredGLMM(m2)[2], 2),
                            ". Women were used as reference category for Sex.
                            Significant effects are in bold."),
           threeparttable = TRUE,
           escape = FALSE)
```

Table S12. Intermediate model summary

	Estimate	Std. Error	*df*	*t*	*p*
(Intercept)	2.11	0.74	368.12	2.85	**0.005**
Sex (men)	0.47	0.99	354.29	0.47	0.637
Mean F_0 (Hz)	0.00	0.00	341.83	0.60	0.548
F_0 CV (Hz)	3.99	0.95	622.27	4.22	**0.0001**
Min F_0 (Hz)	0.00	0.00	920.94	1.72	0.085
Sex (men) × Mean F_0 (Hz)	0.01	0.01	264.86	1.50	0.136
Sex (men) × F_0 CV (Hz)	-1.84	1.52	751.39	-1.21	0.225
Sex (men) × Min F_0 (Hz)	-0.01	0.01	851.00	-0.94	0.348

Note:
$R^2_{marginal}$ = 0.04, $R^2_{conditional}$ = 0.13. Women were used as reference category for Sex. Significant effects are in bold.

2.5.3 Final Model

2.5.3.1 Model fitting Linear Mixed Model (LMM) fitting.

```
m3 <- lmer(AttractivenessRatings ~
             Sex +
             Mean_F0 +
             F0_CV +
             (1 | Subject:Session),
           REML = FALSE,
           data = db)
```

2.5.3.1.1 Table S13. Final model regression table Regression-type table including estimates, standard errors, degrees of freedom, as well as t and p values for each term.

```
s3 <- as.data.frame(summary(m3)$coefficients)
s3 <- summasig(s3, 5)
row.names(s3) <- rnames[c(1:4)]
kable(s3,
      align = "c",
      digits = 2,
      caption = "\\textbf{Table S13.} Final model summary",
      col.names = c("Estimate",
                    "Std. Error",
```

```
                    "$df$",
                    "$t$",
                    "$p$"),
      booktabs = TRUE,
      escape = FALSE) %>%
  kable_styling(latex_options = "HOLD_position") %>%
  footnote(general = paste0("$R^2_{marginal}$ = ",
                            round(r.squaredGLMM(m3)[1], 2),
                            ", $R^2_{conditional}$ = ",
                            round(r.squaredGLMM(m3)[2], 2),
                            ". Women were used as reference category for Sex.
                            Significant effects are in bold."),
           threeparttable = TRUE,
           escape = FALSE)
```

Table S13. Final model summary

	Estimate	Std. Error	*df*	*t*	*p*
(Intercept)	2.02	0.59	299.83	3.42	**0.001**
Sex (men)	0.87	0.29	267.00	2.98	**0.003**
Mean F_0 (Hz)	0.01	0.00	274.69	2.10	**0.037**
F_0 CV (Hz)	3.18	0.72	714.50	4.39	**0.0001**

Note:
$R^2_{marginal} = 0.03$, $R^2_{conditional} = 0.13$. Women were used as reference category for Sex. Significant effects are in bold.

2.5.3.2 Table S14. Model comparison and selection Comparison of the Initial, Intermediate and Final models by AIC and Akaike weights.

```
# Calculate AIC
aict <- AICtab(m1, m2, m3,
               weights = TRUE,
               base = TRUE)
class(aict) <- "data.frame"
tabS14 <- aict
tabS14$weight <- format(round(tabS14$weight, 4),
                        nsmall = 4,
                        scientific = FALSE)
row.names(tabS14) <- c("Final",
                       "Intermediate",
                       "Initial")
# Formatted table
kable(tabS14,
      booktabs = TRUE,
      digits = 4,
      align = c("l", "c", "c", "c", "c"),
      caption = "\\textbf{Table S14.} Information criteria for the Initial,
      Intermediate and Final models",
      col.names = c("$AIC$",
                    "$\\Delta AIC$",
                    "$df$",
                    "$w_{i}(AIC)$"),
      escape = FALSE) %>%
  kable_styling(latex_options = "HOLD_position") %>%
  footnote(general = paste0("The Final Model is close to ",
```

```
                        round(aict[1,4]/aict[2,4], 2),
                        " times more likely to be the best model
                        compared to the Intermediate Model, and about ",
                        format(round(aict[1,4]/aict[3,4], 12),
                               big.mark = ",", scientific = FALSE),
                        " times compared to Initial Model (the Intermediate Model,
                        was around ",
                        format(round(aict[2,4]/aict[3,4], 12),
                               big.mark = ",", scientific = FALSE),
                        " times more likely compared to the Initial Model).
                        For a detailed description of values,
                        see the \\\\href{https://www.shorturl.at/iGIKT}{ICtab}
                        function documentation."),
          threeparttable = TRUE,
          escape = FALSE)
```

Table S14. Information criteria for the Initial, Intermediate and Final models

	AIC	ΔAIC	*df*	$w_i(AIC)$
Final	3246.879	0.0000	6	0.7896
Intermediate	3249.524	2.6445	10	0.2104
Initial	3311.105	64.2260	14	0.0000

Note:
The Final Model is close to 3.75 times more likely to be the best model compared to the Intermediate Model, and about 88,408,423,407,662 times compared to Initial Model (the Intermediate Model, was around 23,563,747,209,244 times more likely compared to the Initial Model). For a detailed description of values, see the ICtab function documentation.

2.5.3.3 Final model diagnostic

2.5.3.3.1 Figure S11. Final model diagnostics. Once a Final model was chosen, diagnostics (residual distribution, homoscedasticity, and linearity in each fixed factor) were performed.

```
lmerDiag(m3, db)
```

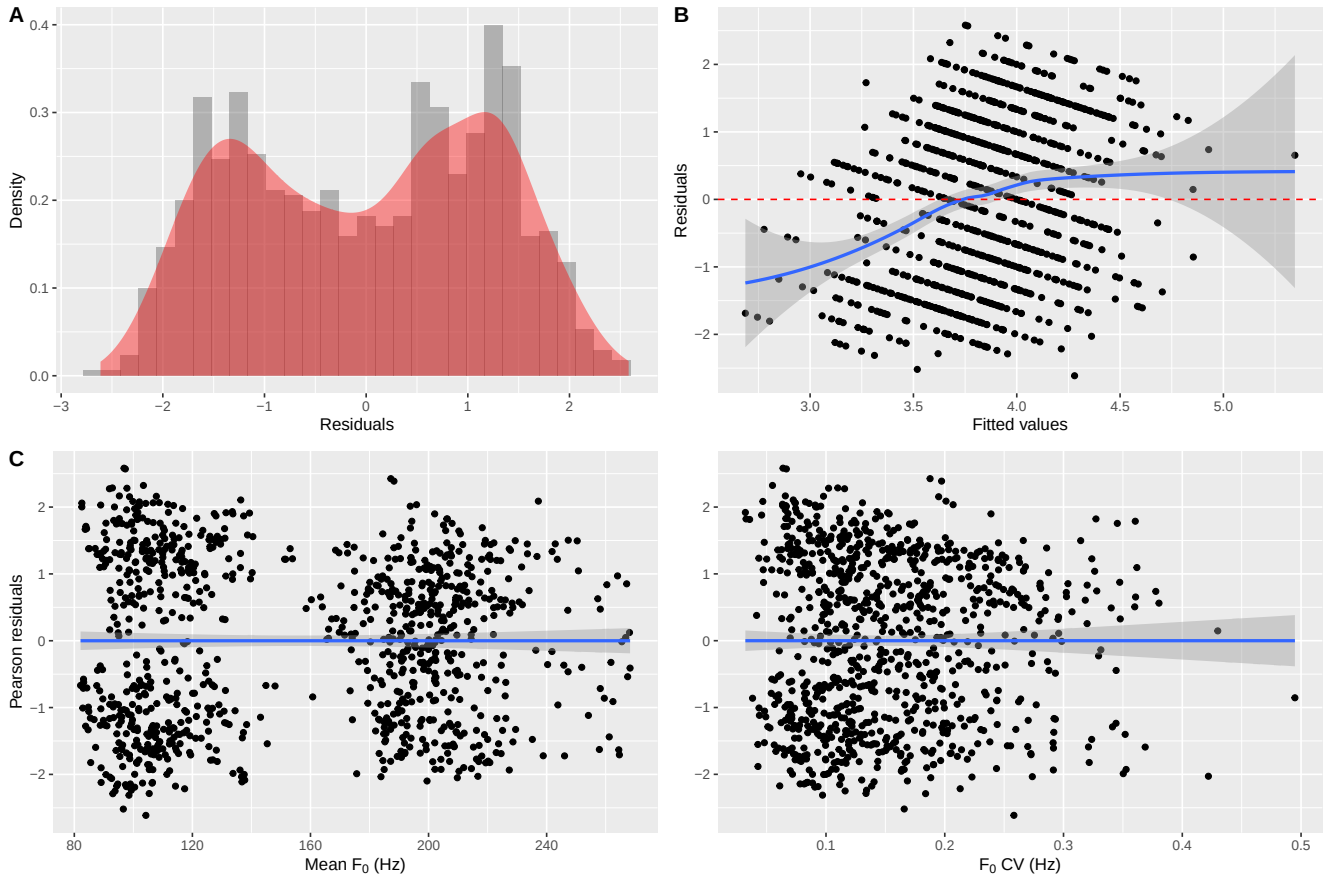

Figure S11. Final model diagnostics. (A) Residual distribution. (B) Homoscedasticity (constant variance of residuals); the amount and distance of points above and below the blue line is randomly spread. (C) Linearity in each fixed factor.

2.5.3.3.2 Table S15. Final model distribution family. As shown in Fig. S11A, the residual distribution of the Final model was highly bimodal. To test whether a different distribution family was more appropriate (i.e. fitting a generalised, instead of a general, mixed linear model), we checked the probability of the model for each distribution family, using the `check_distribution` function, from the `performance` package.

```
#Calculate probabilities for each distribution family
m3dist <- check_distribution(m3)

#Select only distribution families with at leat a 2% probability
m3dist <- as.data.frame(subset(m3dist, m3dist$p_Residuals > 0.02 | m3dist$p_Response > 0.02))

#Transform probabilities to percentages
m3dist$p_Residuals <- paste0(round(m3dist$p_Residuals*100, 2), "\\%")
m3dist$p_Response <- paste0(round(m3dist$p_Response*100, 2), "\\%")

#Format distribution names
m3dist$Distribution <- c("Beta-binomial",
                         "Binomial",
                         "Gamma",
                         "Normal",
                         "Poisson",
                         "Weibull")

#Bold highest probability
```

```
m3dist[4, 1] <- cell_spec(m3dist[4, 1], "latex", bold = TRUE)

# Formatted table
kable(m3dist,
      booktabs = TRUE,
      align = c("l", "c", "c"),
      row.names = FALSE,
      caption = "\\textbf{Table S15.} Distributional family for the Final model",
      col.names = c("Family",
                    "Residuals",
                    "Response"),
      escape = FALSE) %>%
  add_header_above(c(" " = 1,
                     "Probability for each distribution" = 2)) %>%
  row_spec(4, background = "#c4c4c4") %>%
  kable_styling(latex_options = "HOLD_position") %>%
  footnote(general = "Only families with at least one probability higher than
  2\\\\% are shown, but a total of 17 distribution families were tested by the function.",
           threeparttable = TRUE,
           escape = FALSE)
```

Table S15. Distributional family for the Final model

	Probability for each distribution	
Family	Residuals	Response
Beta-binomial	0%	31.25%
Binomial	0%	50%
Gamma	3.12%	0%
Normal	87.5%	0%
Poisson	0%	15.62%
Weibull	9.38%	3.12%

Note:
Only families with at least one probability higher than 2% are shown, but a total of 17 distribution families were tested by the function.

2.5.3.4 Table 2. Final model regression table (with bootstrap 95% CI) Although the most probable family distribution for the Final model was a normal one (87.5%; Table S15), it still differed (see Fig. S11A) and was highly bimodal, even when separate models were fitted for women and men (not included here). Because of this, we calculated bootstrap confidence intervals for the model estimates, using the `confint.merMod` function, from the `lme4` package.

```
set.seed(101)
m3CI <- confint(m3,
                parm = c(3,4,5,6),
                method = "boot",
                nsim = 1000,
                boot.type = "perc")

s4 <- as.data.frame(summary(m3)$coefficients)
s4 <- summasig(s4, 5)
s4 <- cbind(s4, m3CI)
s4 <- s4[c(1,6:7,2:5)]
row.names(s4) <- rnames[c(1:4)]
```

```
kable(s4,
      align = "c",
      digits = 2,
      caption = "\\textbf{Table 2.} Final model summary (with bootstrap 95\\% CI)",
      col.names = c("Estimate",
                    "Lower 95\\% CI",
                    "Upper 95\\% CI",
                    "Std. Error",
                    "$df$",
                    "$t$",
                    "$p$"),
      booktabs = TRUE,
      escape = FALSE) %>%
  kable_styling(latex_options = "HOLD_position") %>%
  footnote(general = paste0("$R^2_{marginal}$ = ",
                            round(r.squaredGLMM(m3)[1], 2),
                            ", $R^2_{conditional}$ = ",
                            round(r.squaredGLMM(m3)[2], 2),
                            ". Confidence intervals were calculated as the 2.5 and 97.5
                            percentiles from bootstrap (1000 simulations).
                            Women were used as reference category for Sex.
                            Significant effects are in bold."),
           threeparttable = TRUE,
           escape = FALSE)
```

Table 2. Final model summary (with bootstrap 95% CI)

	Estimate	Lower 95% CI	Upper 95% CI	Std. Error	*df*	*t*	*p*
(Intercept)	2.02	0.83	3.09	0.59	299.83	3.42	**0.001**
Sex (men)	0.87	0.33	1.47	0.29	267.00	2.98	**0.003**
Mean F_0 (Hz)	0.01	0.00	0.01	0.00	274.69	2.10	**0.037**
F_0 CV (Hz)	3.18	1.86	4.61	0.72	714.50	4.39	**0.0001**

Note:
$R^2_{marginal}$ = 0.03, $R^2_{conditional}$ = 0.13. Confidence intervals were calculated as the 2.5 and 97.5 percentiles from bootstrap (1000 simulations). Women were used as reference category for Sex. Significant effects are in bold.

2.5.4 Figure 5. Voice predictor slopes

2.5.4.1 Colour version Online version.

```
Fig5A <- ggplot(fortify.merMod(m3),
                aes(x = Mean_F0,
                    y = predict(m3),
                    colour = Group)) +
  geom_line(stat="smooth",
            method = "lm",
            aes(lty=Group,
                group = Subject)) +
  geom_point(alpha = 0.2) +
  geom_rug(aes(colour = Group),
           position = "jitter",
           alpha = 0.3) +
  geom_smooth(method = "lm",
              colour = "black") +
```

```
  labs(x = expression(paste("Mean F"[0],
                            " (Hz)")),
       y = "Attractiveness ratings (predicted)",
       subtitle = expression(paste("Mean F"[0],
                                   " (Hz)"))) +
  facet_wrap(~ Sex, scales = "free_x")

Fig5B <- ggplot(fortify.merMod(m3),
                aes(x = F0_CV,
                    y = predict(m3),
                    colour = Group)) +
  geom_line(stat="smooth",
            method = "lm",
            aes(lty=Group,
                group = Subject)) +
  geom_point(alpha = 0.2) +
  geom_rug(aes(colour = Group),
           position = "jitter",
           alpha = 0.3) +
  geom_smooth(method = "lm",
              colour = "black") +
  labs(x = expression(paste("F"[0],
                            " CV (Hz)")),
       y = "Attractiveness ratings (predicted)",
       subtitle = expression(paste("F"[0],
                                   " CV (Hz)")))  +
  facet_wrap(~ Sex, scales = "free_x")

Fig5 <- ggarrange(Fig5A,
                  Fig5B,
                  common.legend = TRUE,
                  legend = "bottom",
                  labels = "AUTO",
                  nrow = 2)
Fig5
```

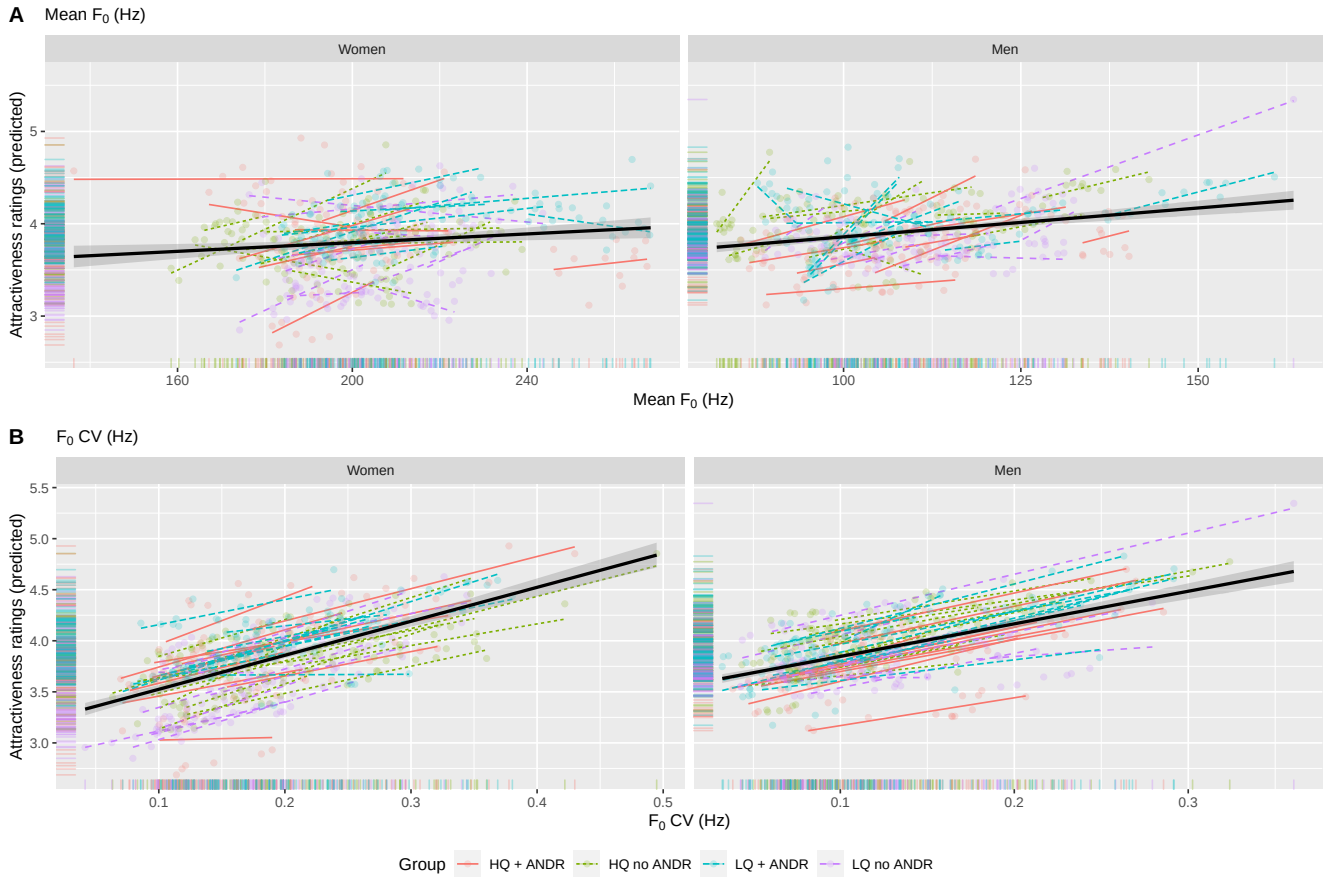

Figure 5. Single term voice predictor slopes. Slope of coefficients for each (single term) fixed predictor, against predicted attractiveness ratings for the Final Model (linear relationship between each model term and predicted response), for women (left) and men (right). (A) Mean F_0. (B) F_0 CV. Coloured lines represent the slope for each participant, according to their group. The black line represents the general effect.

2.5.4.2 Greyscale version

Print version.

```
Fig5Abw <- Fig5A +
  scale_color_grey(start = 0,
                   end = 0.4) +
  theme_light() +
  theme(legend.position = "bottom") +
  theme(strip.text.x = element_text(color = "black"))


Fig5Bbw <- Fig5B +
  scale_color_grey(start = 0,
                   end = 0.4) +
  theme_light() +
  theme(legend.position = "bottom") +
  theme(strip.text.x = element_text(color = "black"))

Fig5bw <- ggarrange(Fig5Abw,
                    Fig5Bbw,
                    common.legend = TRUE,
                    legend = "bottom",
                    labels = "AUTO",
                    nrow = 2)
```

```
Fig5bw
```

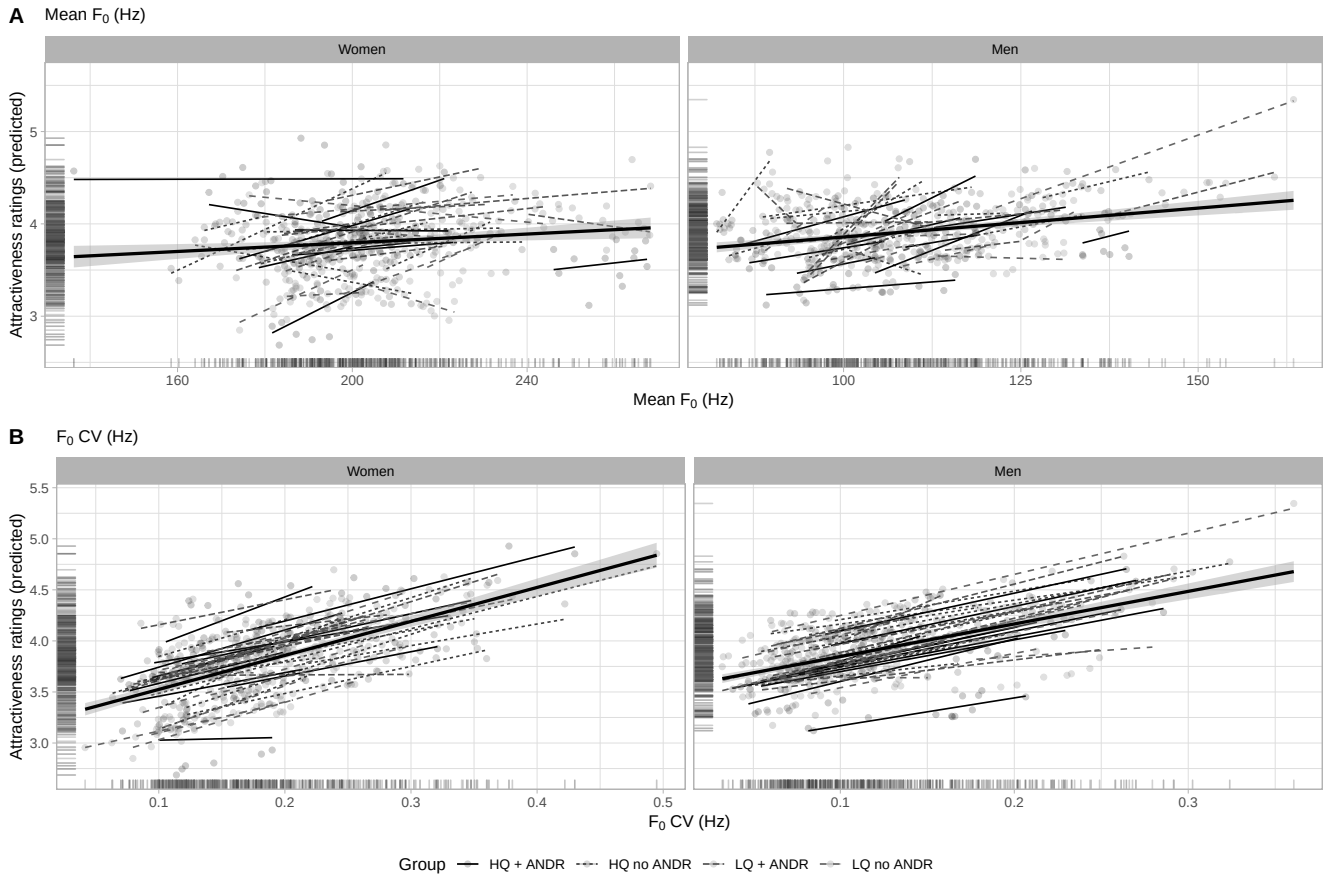

Figure 5. Single term voice predictor slopes. Slope of coefficients for each (single term) fixed predictor, against predicted attractiveness ratings for the Final Model (linear relationship between each model term and predicted response), for women (left) and men (right). (A) Mean F_0. (B) F_0 CV. Dashed lines represent the slope for each participant, according to their group. The thick black line represents the general effect.

3 References

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4 Session info (for reproducibility)

```
library(pander)
pander(sessionInfo(), locale = FALSE)
```

R version 4.0.0 (2020-04-24)

Platform: x86_64-w64-mingw32/x64 (64-bit)

attached base packages: *stats4*, *stats*, *graphics*, *grDevices*, *utils*, *datasets*, *methods* and *base*

other attached packages: *pander(v.0.6.3)*, *Hmisc(v.4.4-0)*, *Formula(v.1.2-3)*, *survival(v.3.1-12)*, *lattice(v.0.20-41)*, *MuMIn(v.1.43.17)*, *broom(v.0.5.6)*, *performance(v.0.4.6)*, *bbmle(v.1.0.23.1)*, *sciplot(v.1.2-0)*, *rstatix(v.0.5.0)*, *osfr(v.0.2.8)*, *emmeans(v.1.4.6)*, *lmerTest(v.3.1-2)*, *lme4(v.1.1-23)*, *Matrix(v.1.2-18)*, *psych(v.1.9.12.31)*, *car(v.3.0-8)*, *carData(v.3.0-3)*, *lemon(v.0.4.4)*, *data.table(v.1.12.8)*, *kableExtra(v.1.1.0)*, *xtable(v.1.8-4)*, *gridExtra(v.2.3)*, *ggpubr(v.0.3.0)*, *plyr(v.1.8.6)*, *forcats(v.0.5.0)*, *stringr(v.1.4.0)*, *dplyr(v.1.0.0)*, *purrr(v.0.3.4)*, *readr(v.1.3.1)*, *tidyr(v.1.1.0)*, *tibble(v.3.0.1)*, *ggplot2(v.3.3.1)*, *tidyverse(v.1.3.0)* and *knitr(v.1.28)*

loaded via a namespace (and not attached): *readxl(v.1.3.1)*, *backports(v.1.1.7)*, *splines(v.4.0.0)*, *TH.data(v.1.0-10)*, *urltools(v.1.7.3)*, *digest(v.0.6.25)*, *htmltools(v.0.4.0)*, *fansi(v.0.4.1)*, *magrittr(v.1.5)*, *checkmate(v.2.0.0)*, *memoise(v.1.1.0)*, *cluster(v.2.1.0)*, *openxlsx(v.4.1.5)*, *modelr(v.0.1.8)*, *sandwich(v.2.5-1)*, *bdsmatrix(v.1.3-4)*, *jpeg(v.0.1-8.1)*, *colorspace(v.1.4-1)*, *rvest(v.0.3.5)*, *haven(v.2.2.0)*, *xfun(v.0.14)*, *crayon(v.1.3.4)*, *jsonlite(v.1.6.1)*, *zoo(v.1.8-8)*, *glue(v.1.4.1)*, *gtable(v.0.3.0)*, *webshot(v.0.5.2)*, *abind(v.1.4-5)*, *scales(v.1.1.1)*, *mvtnorm(v.1.1-0)*, *DBI(v.1.1.0)*, *Rcpp(v.1.0.4.6)*, *viridisLite(v.0.3.0)*, *htmlTable(v.1.13.3)*, *foreign(v.0.8-78)*, *htmlwidgets(v.1.5.1)*, *httr(v.1.4.1)*, *RColorBrewer(v.1.1-2)*, *acepack(v.1.4.1)*, *ellipsis(v.0.3.1)*, *pkgconfig(v.2.0.3)*, *farver(v.2.0.3)*, *nnet(v.7.3-13)*, *dbplyr(v.1.4.3)*, *crul(v.0.9.0)*, *tidyselect(v.1.1.0)*, *labeling(v.0.3)*, *rlang(v.0.4.6)*, *reshape2(v.1.4.4)*, *munsell(v.0.5.0)*, *cellranger(v.1.1.0)*, *tools(v.4.0.0)*, *cli(v.2.0.2)*, *generics(v.0.0.2)*, *evaluate(v.0.14)*, *yaml(v.2.2.1)*, *fs(v.1.4.1)*, *zip(v.2.0.4)*, *randomForest(v.4.6-14)*, *nlme(v.3.1-147)*, *xml2(v.1.3.2)*, *compiler(v.4.0.0)*, *rstudioapi(v.0.11)*, *curl(v.4.3)*, *png(v.0.1-7)*, *ggsignif(v.0.6.0)*, *reprex(v.0.3.0)*, *statmod(v.1.4.34)*, *stringi(v.1.4.6)*, *highr(v.0.8)*, *nloptr(v.1.2.2.1)*, *vctrs(v.0.3.1)*, *pillar(v.1.4.4)*, *lifecycle(v.0.2.0)*, *triebeard(v.0.3.0)*, *estimability(v.1.3)*, *cowplot(v.1.0.0)*, *insight(v.0.8.4)*, *R6(v.2.4.1)*, *latticeExtra(v.0.6-29)*, *rio(v.0.5.16)*, *codetools(v.0.2-16)*, *boot(v.1.3-24)*, *MASS(v.7.3-51.5)*, *assertthat(v.0.2.1)*, *withr(v.2.2.0)*, *httpcode(v.0.3.0)*, *mnormt(v.1.5-7)*, *multcomp(v.1.4-13)*, *mgcv(v.1.8-31)*, *bayestestR(v.0.6.0)*, *parallel(v.4.0.0)*, *hms(v.0.5.3)*, *grid(v.4.0.0)*, *rpart(v.4.1-15)*, *coda(v.0.19-3)*, *minqa(v.1.2.4)*, *rmarkdown(v.2.1)*, *numDeriv(v.2016.8-1.1)*, *lubridate(v.1.7.8)* and *base64enc(v.0.1-3)*