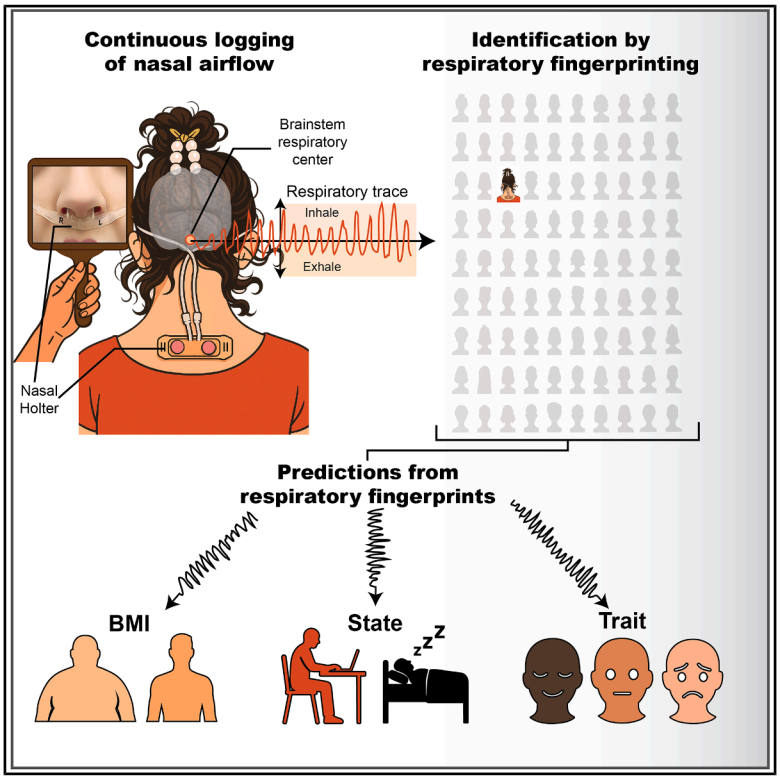
Article

Current Biology

Humans have nasal respiratory fingerprints

Graphical abstract



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In brief

By treating nasal airflow as a 24-h time series, Soroka et al. find that individuals have a unique respiratory pattern—a nasal respiratory fingerprint—that remains stable over time. This fingerprint predicts various aspects of physiology, mood, and cognition, making for a novel, informative marker in health and disease.

Highlights

- Humans have individually unique nasal respiratory patterns
- Human nasal respiratory fingerprints reflect the brain drivers of respiration
- Human nasal respiratory fingerprints predict physiological markers such as BMI
- Human nasal respiratory fingerprints predict mood and cognition

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Humans have nasal respiratory fingerprints

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SUMMARY

Long-term respiratory patterns are generated by remarkably complex brain networks. Because brains are unique, we hypothesized that their dependent respiratory patterns may be similarly unique. To test this hypothesis, we developed a wearable device that precisely measures and logs nasal airflow in each nostril separately for up to 24-h periods. We found that we could identify members of a 97-participant cohort at a remarkable 96.8% accuracy from nasal airflow patterns alone. In other words, humans have individual nasal airflow fingerprints. Moreover, in test-retest experiments, we found that these individual fingerprints remain stable over extended periods of time, such that individual identification by nasal airflow fingerprints was on par with or better than voice recognition. Finally, we find that the high sensitivity of these fingerprints provides significant indications on both physiological states, such as levels of arousal and body-mass index, and cognitive traits, such as levels of anxiety, levels of depression, and behavioral tendencies. We conclude that long-term patterns of nasal airflow reflect the brain drivers of respiration, are individually unique, and have significant implications for health, emotion, and cognition.

INTRODUCTION

Breathing may seem like a simple process; we coordinate it effortlessly and rarely pay it much attention. Yet, breathing is in fact controlled by a remarkably complex and extensive brain network that acts as a respiratory pace-maker, governing autonomic respiratory patterns in accordance with physiological homeostatic needs, while allowing for volitional takeover of respiration in response to behavioral needs.[1,2] The key components of this network lie within the brainstem in the medullary pre-Bötzinger complex.[2,3] Although rhythmic bursts of pre-Bötzinger activity can drive inhalation regardless of external input, its activity is constantly modulated by information from chemoreceptors and mechanoreceptors from throughout the respiratory system.[3,4] This modulation depends on a vast brain network, consisting of additional medullary mechanisms,[5] pontine mechanisms,[6] and several cortical and subcortical structures all involved in both the voluntary and involuntary control of respiration.[7,8] This extensive respiratory-brain structural and functional network[9] implies that if we could very precisely characterize respiration over extended time, we could deduce meaningful information on its ensemble activity. Furthermore, because brains are unique,[10] precise characterizations of their internally generated long-term respiratory patterns may also be unique. Given all this, to test the hypothesis that humans have unique respiratory fingerprints and that such fingerprints may be informative on brain output, we developed a small, wearable respiratory logger and precisely measured nasal respiration continuously for 24 h in 100 healthy participants.

RESULTS

Humans have individual respiratory fingerprints

We used a miniature wearable device (STAR Methods) (Figure 1) to measure nasal airflow in 100 participants (52F, mean age = 26.33 ± 3.61 years, range = 18–35 years) who each wore the device for 24 h continuously, with 42 participants returning for a second 24-h session (mean inter-test interval = 3.5 months, range = 5 days to 23 months). Participants logged basic daily activity using a dedicated cell phone application and completed several questionnaires that we routinely obtain from experimental participants (STAR Methods). Because data were corrupted in three of these sessions, we proceeded to analyze 97 participants.

To directly test our hypothesis that humans can be identified by their respiratory pattern, we parametrized the data using BreathMetrics, a previously published method that extracts 24 parameters from the respiratory trace[11] (Figure 2A). We divided the raw data of 97 participants to time series of 5 min (with no overlap) and analyzed data from wake and sleep separately (mean length wake intervals = 15.3 ± 1.54 h, mean length sleep intervals = 7.84 ± 1.33 h). Using the first 65% of data for training and the rest for testing, a neural network classifier, winner takes all (see STAR Methods), obtained 90.7% individual identification during wake (24 respiratory features, chance = 1.03%, 88 hits from 97 participants, binomial p = 1.9e−163, Cohen's h = 2.32, confidence interval [CI] = [0.9, 0.91]) (Figures 2B–2D) and 64.95% during sleep (63 hits from 97 participants, p = 7.8e−100, Cohen's h = 1.67, CI = [0.64, 0.65]) (Figures 2B and 2C). The poorer performance during sleep may reflect genuinely

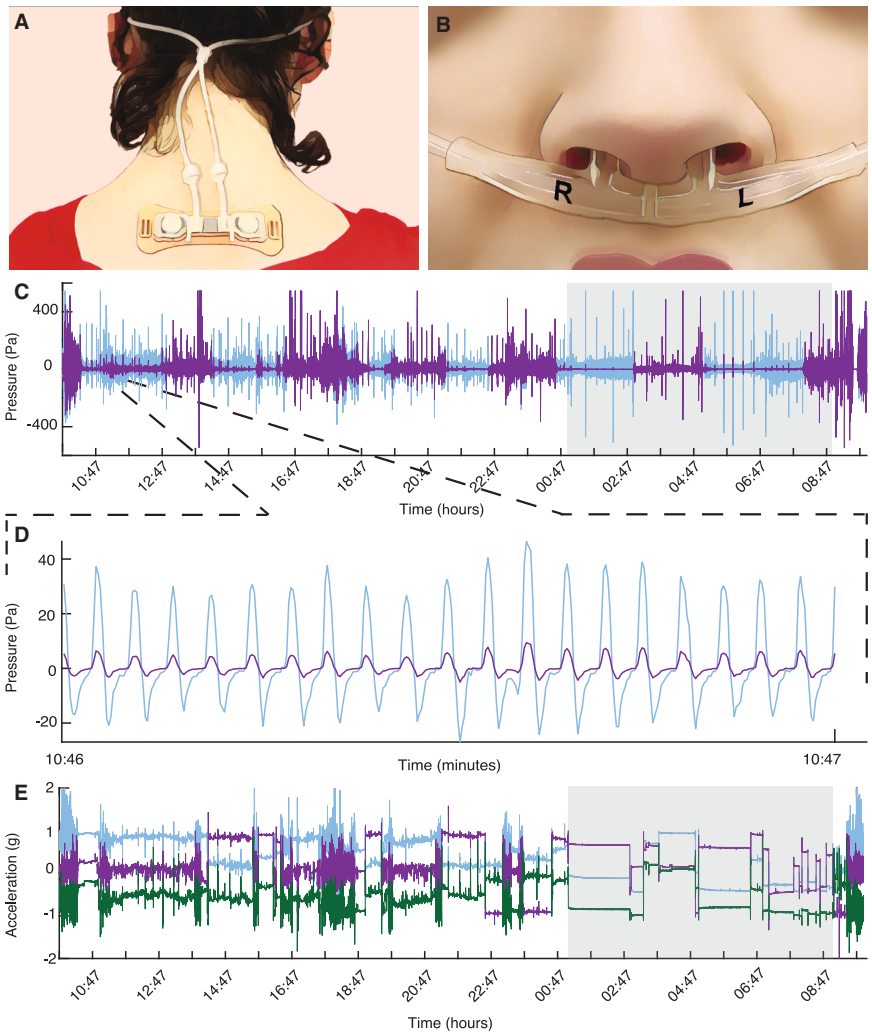

Figure 1. Logging nasal airflow over extended periods of time

(A) Placement of the silicone-encased device pasted on the nape of the neck.

(B) The nasal cannula with separate lines for left and right nostrils.

(C) 24 h of raw flow data, right nostril in purple and left nostril in light blue, sleep shaded in gray.

(D) A zoom into 1 min of the respiratory data, showing right nostril in purple and left nostril in light blue. The difference between nostrils reflects the nasal cycle.

(E) Concomitant data from the three-dimensional position/motion sensor.

See also Figures S1 and S5.

reduced specificity in sleep vs. wake or it may merely reflect reduced power due to the shorter duration of sleep vs. wake periods. To address this, we capped the wake data of each participant to match the duration of their sleep and reconducted the analysis. We observe 82.47% individual identification during capped wake (80 hits from 97 participants, binomial p = 7.87e−100, Cohen's h = 1.6, CI = [0.61, 0.626]), which remains significantly better than sleep (X^2 = 11.9, p = 0.0006) (we nevertheless remain cautious regarding this "wake advantage," as detailed in the discussion). To further gauge the impact of recording duration, we reconducted the same analysis scheme using shorter and shorter time bins. Remembering that by chance we would expect to identify about one person, we find that using only 1 h of wake recording we can still identify 28.87% of participants (28 hits from 97 participants, p = 2.1e−32, Cohen's h = 0.93, CI = [0.28, 0.3]), and from 1 h of sleep we identify 43.3% of participants (42 hits from 97 participants, p = 2.3e−62, Cohen's h = 1.3, CI = [0.46, 0.47]) (Figures 2B and 2C).

In sum, we can effectively identify members of our cohort from nasal airflow alone. One may note, however, that activity impacts respiratory patterns, so perhaps we are merely identifying individuals based on their levels of activity. To address this, we independently analyzed the data obtained from the 3-degrees-of-freedom position sensor within the device. We observed that although we could identify individuals at a significant 37% accuracy, this remains overwhelmingly inferior to identification by nasal airflow (Figure S1).

To allow extrapolation from our sample to the population, we repeated the analysis, this time randomly selecting only 20 participants for the analysis (chance = 5%), and repeated the process 100 times for wake and sleep separately. During wake, we obtained 93.78% ± 5.35% individual identification. We repeated this analysis on 40, 60, and 80 participants, obtaining 90.41% ± 3.1%, 89.56% ± 2.5%, and 90.82% ± 1.7%, respectively (chance = 5%, 2.5%, 1.67%, and 1.25%, all binomial p < 6.5e−22, all effect sizes > 2.18) (Figures 2E and 2F). During sleep, we obtained 79.66% ± 7.22% identification accuracy, and on 40, 60, and 80 participants identification accuracy decreased to 74.72 ± 4.3, 72.64 ± 3.37, and 71.29 ± 2.08 accuracy, respectively (chance = 5%, 2.5%, 1.67%, and 1.25%, all binomial p < 3.7e−16, all effect sizes > 1.76) (Figure 2E). In other words, we conclude that individual identification capability is not limited to our cohort alone.

The above analyses used 24 features. To ask post hoc how many of these features were necessary for such performance, we applied two supervised feature selection approaches, the maximum relevance minimum redundancy (MRMR[12]) algorithm, and neighbor components analysis (NCA[13]). We applied these algorithms to avoid the 620 septillion (24!) reanalyses necessary for testing all possible BreathMetrics feature combinations. We observe that performance improves as parameters are added up to ∼20 parameters (Figure 2G). According to MRMR, the most relevant features for this identification task were inhale volume and inhale duty cycle. Yet, using these parameters alone, we obtained only 18.6% identification accuracy (Figure S2). The 4 irrelevant parameters by MRMR were exhale duty cycle, percent of breaths with inhale pause, coefficient of

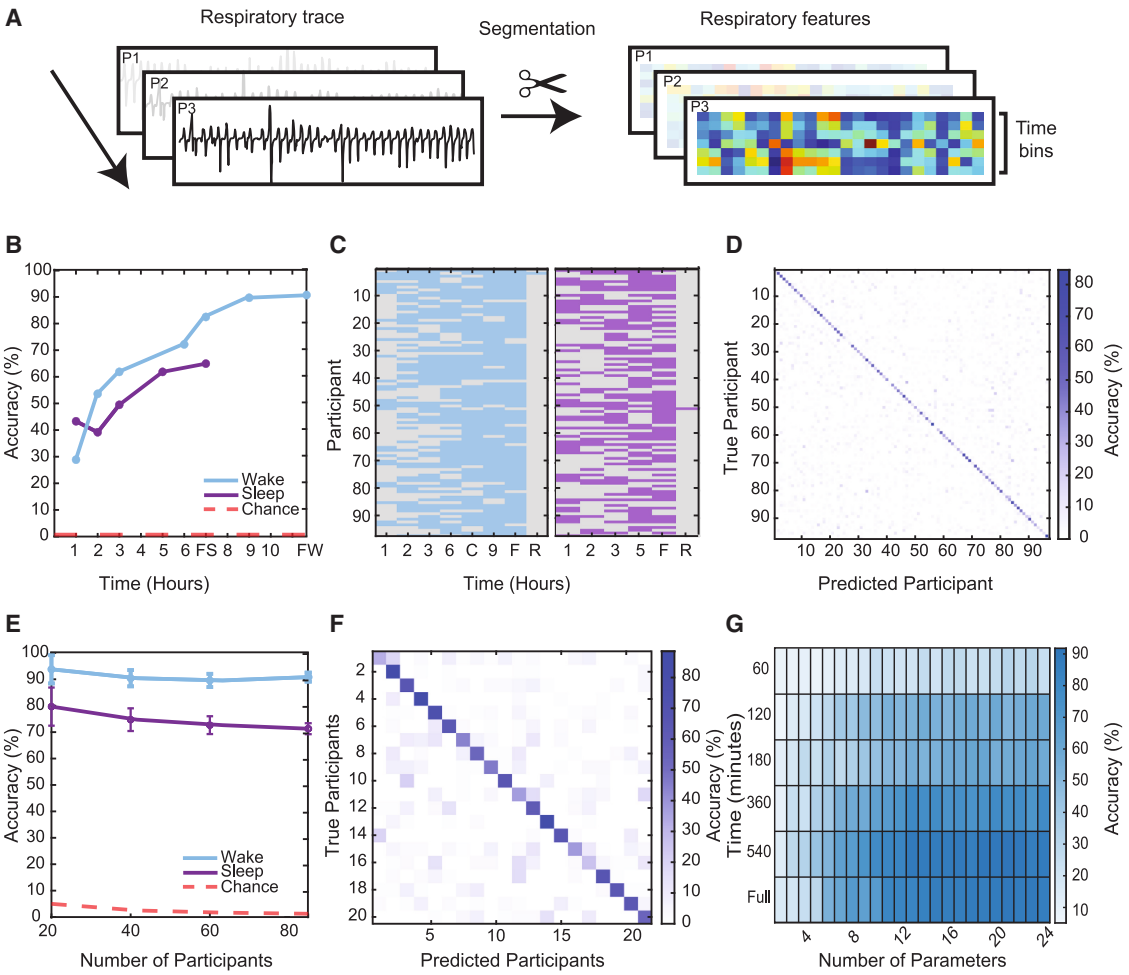

Figure 2. Humans can be positively identified by patterns of nasal airflow

(A) Raw 24 h respiratory traces divided into time series of 5 min and parametrized using BreathMetrics.

(B–D) Identification accuracy (%), $n = 97$. (B) Identification accuracy in wake (light blue) and in sleep (purple) as a function of recording duration. Chance denoted by the dashed red line, $n = 97$. FS, full sleep time; FW, full wake time. (C) Identification accuracy in wake (light blue) and in sleep (purple) as a function of recording duration. C, capped wake time; F, full time; R, random labels. (D) Confusion matrix (true vs. predicted labels) for full wake time. As the blue is darker, the accuracy is higher, $n = 97$.

(E) Average identification accuracy of 100 iterations as a function of number of participants. Wake in light blue, sleep in purple. Error bars are standard deviation. Chance denoted by the dashed red line, $n = 97$.

(F) An example confusion matrix (1 from 100) for random selection of 20 participants for full wake time. As the blue is darker, the accuracy is higher.

(G) Identification accuracy as a function of number of features (1–24) and time (1 h to full day). Features are added from the most to the least important according to the MRMR algorithm.

See also Figures S1 and S2.

variance (COV) exhale duty cycle, and COV inhale pause duty cycle. The NCA algorithm highlighted four parameters as the most relevant features: inhale and exhale duration and inhale and exhale volume COV. Yet, using these parameters alone we obtained only 25.77% identification accuracy (Figure S2). The 4 irrelevant parameters by NCA were peak inspiratory flow value, tidal volume, and the percent of breaths with inhale or exhale pause. Taken together, these analyses show that although some features were more informative than others, performance was not carried by a limited feature set, and a large number of features (~20) are necessary for accurate respiratory fingerprints.

Respiratory fingerprints remain stable over time

Next, we asked whether these unique respiratory characteristics are stable over time. 42 participants came back for a second 24-h session (mean interval between recordings = 3.57 ± 0.17 months, range = 5 days to 23.5 months). To estimate stability, we trained only on day 1 data and tested only on day 2 data (Figure 3A). Using all waking hours, we identify a person on day 2 with mean accuracy of 95.24% (chance = 1/42, success = 40/42, binomial p = 9.6e−63, Cohen's h = 2.4, CI = [0.94, 0.96]) (Figures 3B–3D). Using all sleeping hours, we identify at 71.43%, (chance = 1/42, success = 30/42, binomial p = 1.6−39, Cohen's h = 1.9, CI = [0.7, 0.73]) (Figures 3B and 3C).

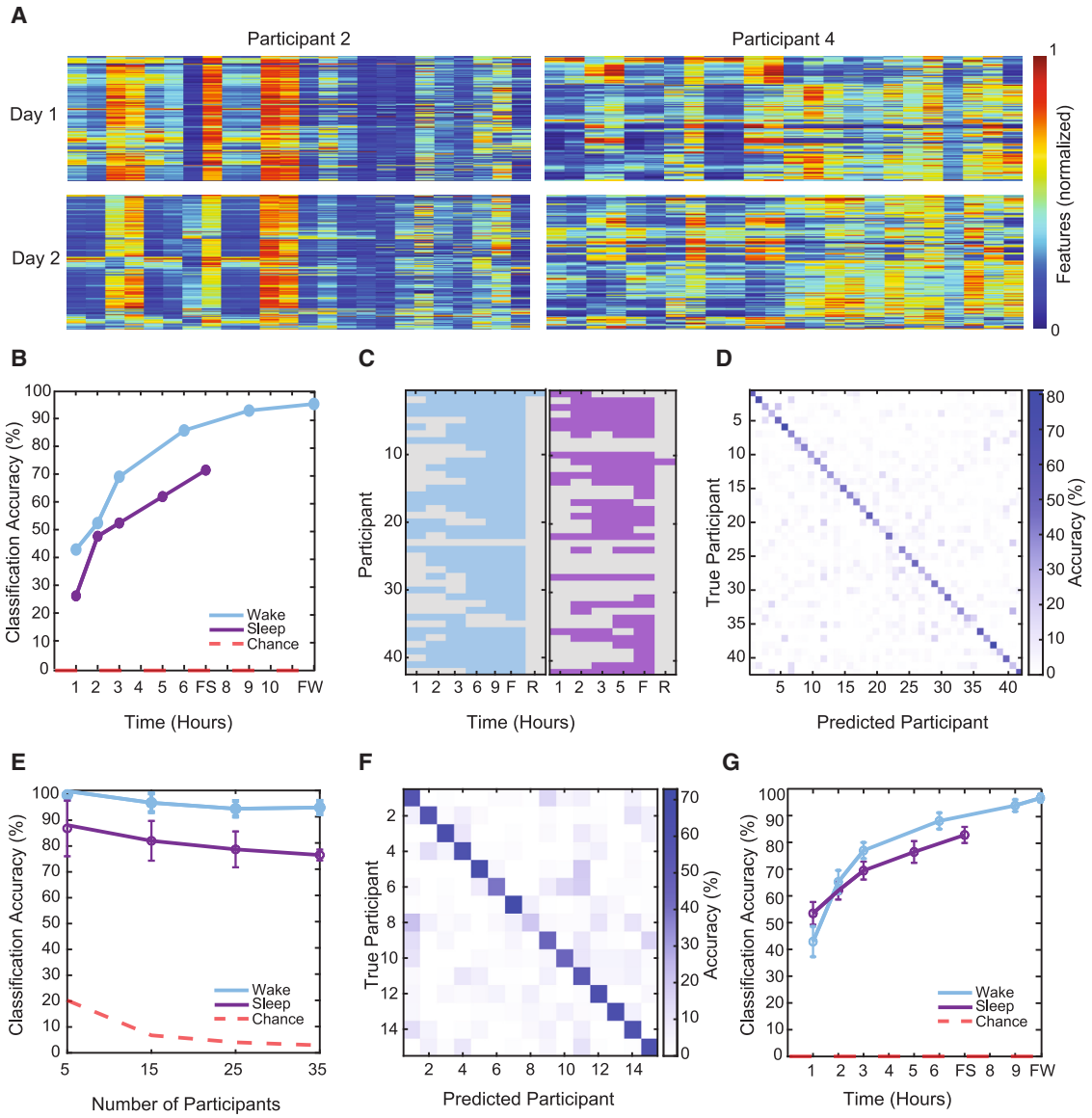

Figure 3. Nasal respiratory fingerprints remain stable over time

(A) Examples of day 1 and day 2 fingerprints in 2 participants who look like themselves over time but nothing like each other.

(B–D) Identification accuracy over time, $n = 42$. (B) Identification accuracy over time, in wake (light blue) and in sleep (purple), as a function of recording duration. Chance denoted by the dashed red line, $n = 42$. FS, full sleep time; FW, full wake time. (C) Identification accuracy over time, in wake (light blue) and in sleep (purple), as a function of recording duration, $n = 42$. F, full time; R, random labels. (D) Confusion matrix (true vs. predicted labels) for full wake time (day 1 as training, day 2 as testing). As the blue is darker, the accuracy is higher, $n = 42$.

(E) Average identification accuracy of 100 iterations as a function of number of participants. Wake in light blue, sleep in purple. Error bars are standard deviation. Chance denoted by the dashed red line, $n = 42$.

(F) An example confusion matrix (1 from 100) for random selection of 20 participants for full wake time. As the blue is darker, the accuracy is higher.

(G) Identification accuracy in wake (light blue) and in sleep (purple) as a function of recording duration using HCTSA parameters. Error bars are standard deviation. Chance denoted by the dashed red line. FS, full sleep time; FW, full wake time.

See also Table S1.

Moreover, using only 1 h for training and 1 h for testing on data from wake obtained 42.86% (chance = 1/42, success = 18/42, binomial $p = 1.2e{-}18$, Cohen's h = 1.12, CI = [0.41, 0.45]) and 26.19% accuracy using data from sleep (chance = 1/42, success = 11/42, binomial $p = 2.8e{-}09$, Cohen's h = 0.77, CI = [0.25, 0.28]) (Figures 3B and 3C). Here, again, to extrapolate the results to the population, we randomly selected 100 times 5, 15, 25, and 35 participants from our sample. The obtained identification rates were 99.76% ± 1.78%, 95.32% ± 3.56%, 93.04% ± 2.99%, and 93.5% ± 2.57% for 5, 15, 25, and 35 participants, respectively (chance = 20%, 6.67%, 4%, and 2.86%, respectively, all binomial $p < 4.8e{-}16$, all effect sizes > 2.01)

(Figures 3E and 3F). During sleep we obtained 86.8% ± 10.75%, 80.8% ± 7.6%, 77.6% ± 6.84%, and 75.4% ± 2.06% (chance = 20%, 6.67%, 4%, and 2.86%, respectively, all binomial $p < 9.8e{-}59$, all effect sizes > 1.44) (Figure 3E). In sum, we can identify people by their individual respiratory fingerprints even across significant periods of time, ranging from months to nearly 2 years, and this ability goes beyond our cohort alone.

All the above were achieved using 24 respiratory parameters identified in BreathMetrics.[11] To further probe our approach of treating the airflow trace as a timeline rather than a series of independent events (breaths), we used the highly comparative time-series-analysis tool (HCTSA),[14] which computes 7,729 features per time series. Unlike BreathMetrics, which was developed for analyzing breath, HCTSA is a non-specific time-series tool. To avoid overfitting, we divided the data into training and testing sets (50%-50%). We optimized parameters on half of the data and tested on the other half, choosing each time 94 (square root of training matrix) among 7,729 features. As this half is chosen randomly, we repeated this process 30 times. We observed a mean of 96.81% ± 1.62% identification accuracy (Figure 3G) (chance = 1/48 = 2.08%, success = 45-48/48, $p < 3.6e{-}72$, Cohen's h = 2.5, CI = [0.95, 0.98]) (the parameters that generated optimal performance are in Table S1). Once again, in a post hoc analysis, we plot performance as a function of the number of features used and find that accuracy plateaus at ~100 features. Moreover, by plotting feature sets together (Figure S2), we observe that the 24 BreathMetrics parameters perform better than the optimal 24 parameters taken from the time-series tool but that using ~100 parameters makes for a marginally better overall result (96.81% vs. 90.7%, $X^2 = 2.6$, $p = 0.1$). To conclude all this, we state that humans can be identified by their nasal respiratory patterns at near-biometric-level accuracy.

Respiratory fingerprints reflect state and trait

Respiratory patterns are clearly linked to aspects of physiology. For example, respiratory patterns have been linked to arousal, whereby tidal volume and minute ventilation fall during sleep[15,16] and the power of the laterality index (LI), namely the extent of asymmetry in nasal airflow across nostrils, increases.[17] To ask whether we see these phenomena in our data, we first used the position/motion sensor to determine wake and sleep times (this measure is indeed tightly linked to the app-generated self-reported times of sleep and wake, r = 0.83, $p < 7.9e{-}16$, see STAR Methods) and then compared between the mean respiratory values in these two states. Consistent with the literature, we observed significantly reduced tidal volume (mean wake = 0.22 ± 0.1 L, mean sleep = 0.17 ± 0.086 L, t(96) = 6, $p = 3.63e{-}0.8$, Cohen's d′ = 0.52) (Figure 4A), significantly reduced minute ventilation (mean wake = 0.0777 ± 0.03 L/min, mean sleep = 0.057 ± 0.024 L/min, t(96) = 8.3, $p = 8.03e{-}13$, Cohen's d′ = 0.77) (Figure 4B), and significantly higher LI power during sleep (mean wake LI power = 0.36 ± 0.14, mean sleep LI power = 0.82 ± 0.12, t(96) = 28, $p = 9.37e{-}48$, Cohen's d′ = 3.56) (Figure 4C). Given the extent of these differences, we tested whether we could classify sleep and wake using the respiratory data alone. We applied the multi-cluster unsupervised feature selection (MCFS) tool[18] and entered the top five features (breathing rate and its covariance, inhale and exhale duty cycle, and the variance of LI power) into a linear classifier, which classified sleep and wake at 100% accuracy (Figure 4D). If we use only 5 min of data, we still obtain 94.33% classification (all $p < 1.1e{-}41$).

Whereas sleep-wake is a dynamic process, respiratory patterns have also been linked to less dynamic physiological features such as body-mass index (BMI).[19] To ask whether BMI is reflected in our measures, we tested for correlations between BMI scores and respiratory parameters. Significant correlations (corrected for multiple comparisons) emerged between BMI score and tidal volume during sleep (Spearman R = 0.36, adjusted $p = 0.041$) (Figure 4F) and exhale volume during sleep (Spearman R = 0.34, adjusted $p = 0.048$) (Figure S3). This link between respiration and BMI may merely reflect the added metabolic needs of added mass, with no necessary relation to brain pace-makers of respiration. To address this, we reconducted the above analysis using only respiratory measures related to the nasal cycle. Overall inhale volume remains constant across the nasal cycle,[20] and the fluctuating asymmetry reflects autonomic aspects of respiratory brain drivers alone. Using only nasal cycle parameters during both wake and sleep (see STAR Methods), we predict BMI at Spearman R = 0.31, $p = 0.018$, CI = [0.1, 0.49] (Figure 4G). This implies that the neural dynamics in brain drivers of respiration are related to BMI.

Beyond aspects of physiology, respiratory patterns have been linked to various aspects of cognition and emotion, but this link has emerged, as far as we know, in the extremes associated with pathology. For example, altered respiratory patterns are associated with clinical depression,[21] clinical anxiety,[22] and with the neurodevelopmental pathology of autism.[23] To ask whether the sensitivity of respiratory fingerprints can inform on these traits in a typical healthy population, we tested for associations between the long-term recordings of nasal airflow and the outcomes of three standard questionnaires our participants completed: the Beck depression inventory[24] and the trait anxiety (TA) questionnaire,[25] which were completed by 84 participants, and the autism quotient (AQ) questionnaire[26] completed by 86 participants.

To first test for an overall relationship between respiratory measures and these cognitive measures, we conducted a canonical correlation analysis (CCA) between all respiratory parameters (the BreathMetrics measures in wake and sleep) and all cognitive parameters (Beck, TA, and AQ). The analysis was conducted in the cohort of 80 participants who completed all three tests. The analysis revealed a strong multivariate association between respiratory patterns and cognition (canonical correlation coefficient $[r_1] = 0.87$, Wilks' $\lambda = 0.031$, $\chi^2(144) = 184.55$, $p = 0.013$) (Figure 5A). We further asked whether this link was retained in all three measures and observed significant correlations for each measure alone (Beck, r = 0.46, $p = 1.439e{-}05$ TA, r = 0.32, $p = 4.054e{-}03$, AQ, r = -0.26, $p = 0.021$) (Figure 5B).

Given this overall outcome, we now further explored the link between patterns of breathing and each independent measure. Given our typical healthy, relatively young cohort, we recorded overall low Beck scores (range 0–20, mean = 4.94, SD = 5.46). To initially screen for relevant respiratory parameters, we

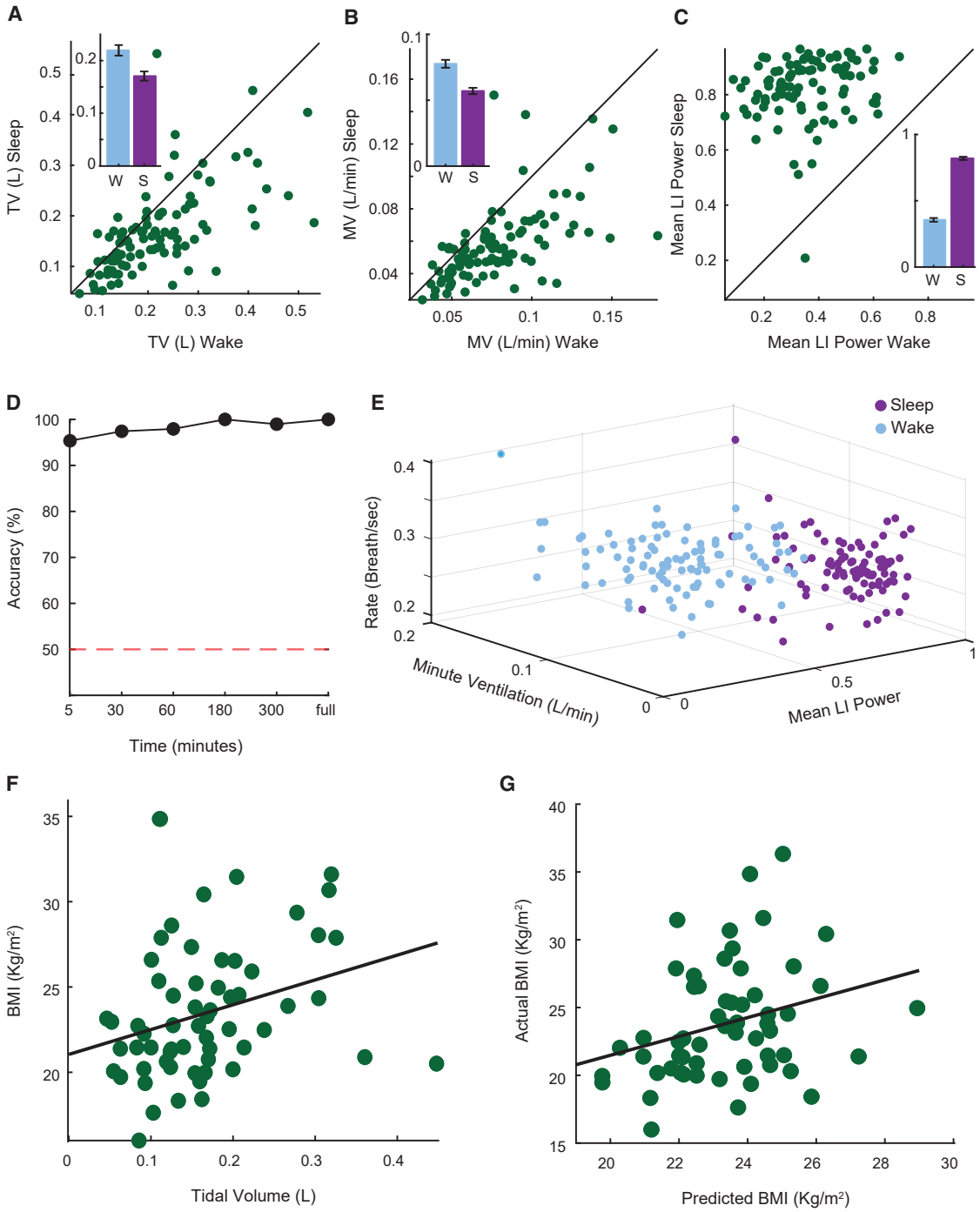

Figure 4. Respiratory fingerprints reflect state

(A) Tidal volume (TV) in wake and sleep.

(B) Minute ventilation (MV) in wake and sleep.

(C) Mean LI power in wake and sleep.

In (A)–(C) each dot is a participant (n = 97), and the diagonal is the unit slope-line ($x = y$). Thus, data under the line are greater in wake, and data above the line are greater in sleep. The inlay contains the same data in bar-graph form, error bars reflect standard error.

(D) Classification accuracy as a function of recording duration (n = 97).

(E) Three-dimensional classification plot, each dot is a participant (n = 97), sleep in purple and wake in light blue.

(F) Relation of BMI to tidal volume during sleep (n = 62).

(G) Prediction of BMI using nasal cycle parameters alone (n = 62).

See also Figure S3.

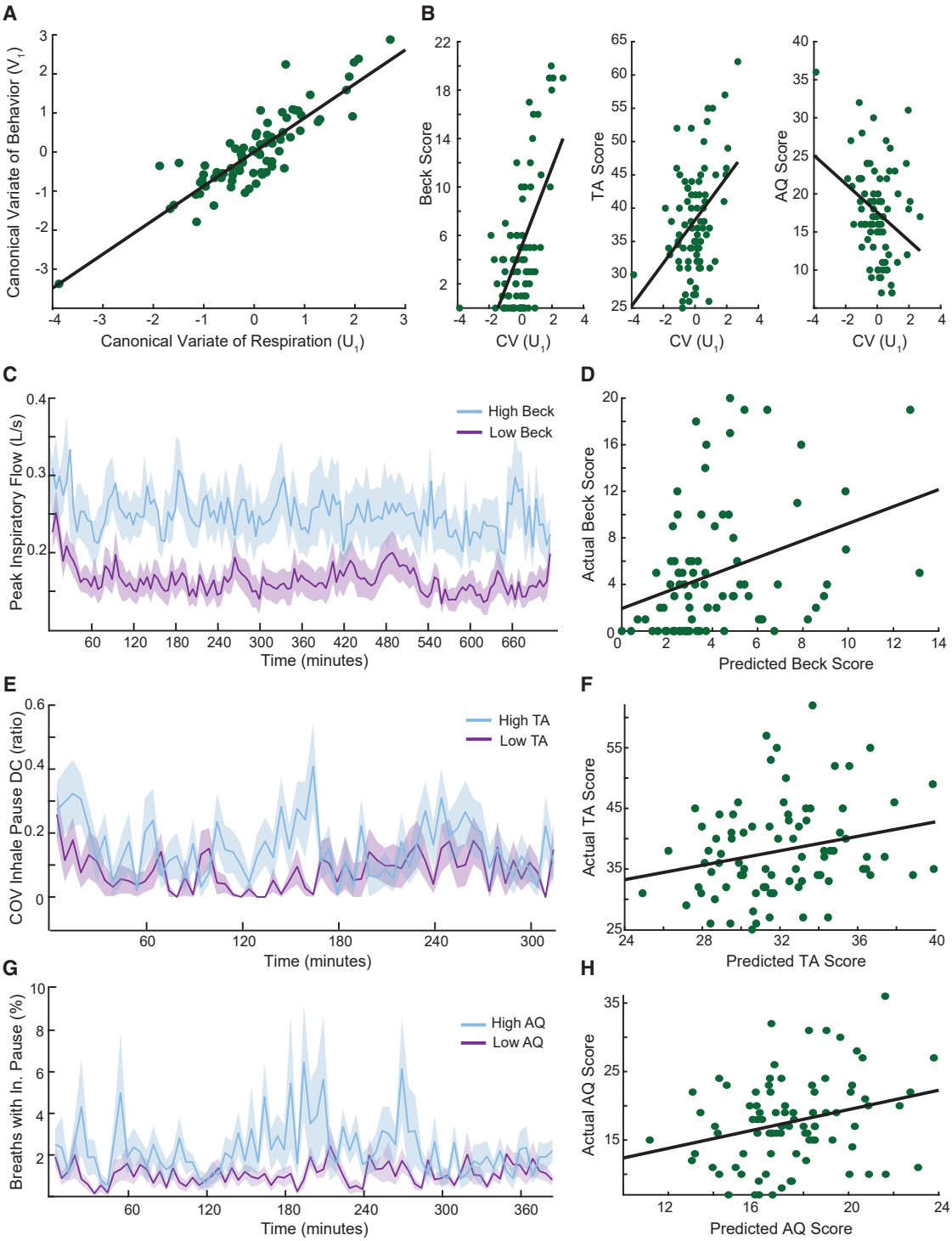

Figure 5. Respiratory fingerprints reflect trait

(A) Canonical correlation analysis (CCA) showing multivariate relationship between respiratory parameters and behavioral traits. *x* axis is the first canonical variate from the respiratory dataset (U_1). *y* axis is the first canonical variate from behavioral data (V_1)(*n* = 80).

(B) Spearman correlations between the first canonical variate (CV) from the respiratory dataset (U_1) and individual behavioral traits: Beck, TA, and AQ (*n* = 80).

(C) Differences in average peak inspiratory flow value during wake in participants with high (*n* = 16) vs. low Beck score (*n* = 21) as a function of time. High Beck score in light blue, low in purple. Standard errors are shaded.

(D) Correlation between predicted and actual Beck score (*n* = 84).

(legend continued on next page)

compared the low-scoring 15th percentile of scores (all Beck = 0, $n = 21$) to the high-scoring 15th percentile of scores (Beck range = 10–20, $n = 16$) for each parameter using an ANOVA with correction for multiple comparisons. We observed significant differences in average peak inspiratory flow value in wake that increased in higher Beck (mean low Beck = 0.17 ± 0.11 [L/s] mean high Beck = 0.25±0.16 [L/s], ($F(1, 6749) = 10.71$, adjusted $p = 0.026$, $\eta 2 = 0.46$, CI = [0.03, 0.14]) (Figure 5C) and in the duty cycle of exhale pause in wake that also increased in higher Beck (mean low Beck = 0.28 ± 0.13 [ratio] mean high Beck = 0.33 ± 0.21 [ratio], ($F(1, 6790) = 8.61$, adjusted $p = 0.04$, $\eta 2 = 0.12$, CI = [0.018, 0.09]) (Figure S4A). In other words, participants with lower and higher Beck scores (but all of them without clinical depression) have significant differences in respiratory patterns. Moreover, if we average each parameter across time and build a predictor (see STAR Methods), we can predict Beck scores of typical healthy individuals from respiratory features alone at Spearman R = 0.35, $p = 0.002$, and CI = [0.16, 0.54] (Figure 5D). Finally, to ask whether Beck scores can be estimated from the nasal cycle alone, we replicated the above analysis using only nasal cycle features but failed to identify a link.

Our cohort also had low TA scores (range 25–62, mean = 38.02, SD = 7.77). We again compared the low-scoring 15th percentile of scores (TA range = 25–31, $n = 16$) to the high-scoring 15th percentile of scores (TA range = 45–62, $n = 16$) in each parameter. We observe that participants with higher TA score have significantly shorter inhales during sleep (mean low TA = 1.5 ± 0.42 s, mean high TA = 1.4 ± 0.16 s, ($F(1, 3179) = 9.8$, adjusted $p = 0.021$, $\eta 2 = 0.14$, CI = [−0.2, −0.05]) (Figure S4B) and increased COV of inhale pause duty cycle during sleep (mean low TA = 0.15 ± 0.32 [ratio] mean high TA = 0.21 ± 0.38 [ratio], ($F(1, 3203) = 9.926$, adjusted $p = 0.039$, $\eta 2 = 0.03$, CI = [0.02, 0.1]) (Figure 5E). Moreover, if we build a predictor (see STAR Methods), we can predict TA score from respiratory features at R = 0.32, $p = 0.0032$, CI = [0.03, 0.44] (Figure 5F). Finally, to ask whether TA scores can be estimated from the nasal cycle alone, we replicated the above analysis using only nasal cycle features. We again compared the low- and high-scoring 15th percentiles (using 30-min blocks). We observe that participants with lower TA scores have significantly higher nostril correlation during sleep (mean low TA = 0.65 ± 0.35 (R), mean high TA = 0.47 ± 0.45 s, ($F(1, 318) = 8.68$, adjusted $p = 0.02$, $\eta 2 = 0.27$, CI = [−0.3, −0.06]) (Figure S4C). Using only nasal cycle parameters during both wake and sleep (see STAR Methods) we predict TA score at R = 0.28, $p = 0.015$, CI = [0.07, 0.47] (Figure S4D).

Finally, our typical cohort also had overall low AQ scores (range 7–36, mean= 17.64, SD = 6.26). To again screen for relevant respiratory parameters, we again compare the low-scoring 15th percentile of scores (AQ range = 7-10, $n = 14$) to the high-scoring 15th percentile of scores (AQ range = 24–36, $n = 13$). We observed significant differences in inhale pause duration in wake that increased with higher AQ score (mean low AQ = 1.2 ± 0.58 s, mean high AQ = 1.4 ± 0.65 s, ($F(1, 4942) = 9.63$, adjusted $p = 0.046$, $\eta 2 = 0.09$, CI = [0.06, 0.27]) (Figure S4E), COV of inhale pause duty cycle in sleep (mean low AQ = 0.16 ± 0.32 [ratio], mean high AQ = 0.24 ± 0.39 [ratio], ($F(1, 2741) = 14$, adjusted $p = 0.0045$, $\eta 2 = 0.03$, CI = [0.04, 0.13]) (Figure S4F), and in the percent of breaths with inhale pause in sleep, which also increased with AQ score (mean low AQ = 1.7% ± 3.6%, mean high AQ = 3.2% ± 7.2%, ($F(1, 2741) = 9.23$, adjusted $p = 0.029$, $\eta 2 = 0.07$ CI = [0.49, 2.26]) (Figure 5G). In other words, participants with lower and higher AQ scores (but all of them without autism) have significant differences in respiratory patterns. Moreover, if we build a predictor (see STAR Methods) we can predict AQ score from respiratory features at R = 0.28, $p = 0.01$, CI = [0.07, 0.46]) (Figure 5H). Finally, to ask whether AQ scores can be estimated from the nasal cycle alone, we replicated the above analysis using only nasal cycle features. We observe that participants with lower AQ score have significantly higher variance in LI power during wake (mean low AQ = 0.116 ± 0.07 [SD], mean high AQ = 0.118 ± 0.06 s, ($F(1, 774) = 8.17$, adjusted $p = 0.0175$, $\eta 2 = 0.01$, CI = 0.006, 0.04]) (Figure S4G) but failed to predict AQ score from NC parameters alone (Figure S4H). In sum, we are able to make powerful population-level statements on levels of depression, anxiety, and behavioral traits, as well as modest but significant individual predictions, all from long-term nasal respiratory patterns alone.

DISCUSSION

Respiration is typically measured across short durations to assess pulmonary function. This has led to a host of measures that indicate on lung and airway anatomy and integrity.[27] Here, however, we measured respiratory patterns over extended periods of time, treating respiration as a timeline. This provides instead an indication on the pattern generated by the neural drivers of respiration. We hypothesized that such a measure may uncover individually specific nasal respiratory fingerprints. This possibility had been previously considered,[28–30] and the current development of a wearable logger allowed us to address it directly using 24-h recordings. Consistent with this hypothesis, we could identify 96.8% of participants using patterns of nasal airflow alone. Moreover, these patterns remained individually specific across the nearly 2 years that we tested, an outcome on-par or better than voice recognition.[31] Although identification accuracy was higher for wake than for sleep, we treat this particular result with caution. This is because the overall sleep data were occasionally disrupted by the cannula displacing from the nostril during sleep. Indeed, we see that in the sub-analyses where we used very restricted durations, e.g., 1 h of wake vs. 1 h of sleep, sleep results were then stronger than wake. Thus,

(E) Differences in the coefficient of variance inhale pause duty cycle during sleep, in participants with high ($n = 16$) vs. low ($n = 16$) TA score as a function of time. High TA score in light blue, low in purple. Standard errors are shaded.
(F) Correlation between predicted and actual TA score ($n = 84$).
(G) Differences in the percent of breaths with inhale pause during sleep in participants with high AQ score ($n = 13$) vs. low AQ score ($n = 14$) as a function of time. High AQ score in light blue, low in purple. Standard errors are shaded.
(H) Correlation between actual and predicted AQ score ($n = 86$).
See also Figure S4 and Table S2.

the overall advantage of wake over sleep in identification performance may reflect methodological limitations (see STAR Methods), and, in any case, both were remarkably strong. Because this specificity was far stronger than we had anticipated, we further asked whether nasal airflow over time could indicate on the varied information that we routinely collect from our experimental participants. We found that we could obtain, from nasal airflow alone, significant estimates on information ranging from levels of arousal, to BMI, and to measures of mood, anxiety, and behavioral traits. We acknowledge that a portion of the specificity and information we obtain may reflect underlying respiratory neuroanatomy, but the long-term temporal dynamics, such as the highly meaningful inhale and exhale pause values, and, particularly, all nasal cycle measures, more likely reflect the combined output of brain respiratory networks. Taken together, all this implies that respiratory nasal airflow over time provides for a measure that may be highly informative on health, emotion, and cognition.

Our method and recordings focused on nasal rather than oral airflow. There are several lines of evidence implying that nasal over oral airflow is indeed a privileged indicator on brain respiratory efferents and afferents.[9] In terms of information the nose sends to the brain, a host of intra-nasal sensory systems transmit airflow information, including the olfactory[32] and trigeminal[33] nerves, allowing nasal airflow to drive patterns of brain activity.[34,35] In turn, in terms of information the brain sends to the nose, it controls airflow asymmetry through the nasal cycle,[17] and it precisely times nasal airflow (sniffs) to coordinate information-processing in olfaction[36] and beyond.[37] We have previously hypothesized that through evolution, this functional aspect of olfaction propagated across sensory and cognitive systems to generate a ''sniffing brain,'' where information is more effectively processed on inhale vs. exhale across sensory domains.[38] Consistent with this notion in humans (see Tort et al.[9] for comprehensive review across species), phase of nasal airflow has been linked to neural excitability,[39–45] related to memory consolidation[46] and retrieval[47] (but see Thunell et al.[48]), quality of mental imagery,[49,50] discrimination of facial fear,[47] pupil size,[51] and visuospatial processing.[38] Whereas correlation of mental activity with respiratory phase does not alone imply causality, several studies combine to in fact demonstrate a profound direct influence of nasal airflow on patterns of neural activity.[34,35,52] Our observation here of individual identification by patterns of nasal airflow is consistent with this framework and implies that such long-term measurements of nasal airflow may be informative in all these areas of research.

Although our approach and method have methodological limitations (see STAR Methods), we end in concluding that measuring nasal airflow over time provides remarkably informative data, allowing for biometric-level personal identification and for the estimation of various measures of physiology and cognition.[3] The latter is consistent with the high levels of depression and anxiety seen in patients with respiratory disorders[53] and the improved mood and cognition through respiratory modifications.[54] We think this approach of measuring long-term nasal airflow patterns may provide insight into diseases of all kinds, particularly those involving the neural drivers of respiration. Therefore, we envision application of respiratory fingerprints across various areas of medicine[55] and basic research.[56]

RESOURCE AVAILABILITY

Lead contact

Requests for further information and resources should be directed to and will be fulfilled by the lead contact, Noam Sobel (noam.sobel@weizmann.ac.il).

Materials availability

This study did not generate new unique reagents.

Data and code availability

- All data have been deposited at https://github.com/TimnaSoroka/identification_paper and are publicly available as of the date of publication.
- All original code has been deposited at https://github.com/TimnaSoroka/identification_paper and is publicly available as of the date of publication.
- Any additional information required to reanalyze the data reported in this paper is available from the lead contact upon request.

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AUTHOR CONTRIBUTIONS

Developed concepts, T.S. and N.S.; developed the device, A.W. and N.S.; wrote software, D.H.; collected data, T.S. and T.W.; analyzed data, T.S., A.R., K.S., and L.G.; wrote the first draft, T.S. and N.S.; edited the final draft, T.S., A.R., K.S., D.H., A.W., L.G., T.W., O.P., and N.S.

DECLARATION OF INTERESTS

The Weizmann Institute of Science has applied, in the names of all authors, for patents on diagnosing several diseases from patterns of nasal airflow. Co-authors K.S., D.H., A.W., and N.S. hold the patent for the Nasal Holter, a measurement device used in this study. N.S. is the founder of; K.S., D.H., A.W., and O.P. are shareholders of; and O.P. is a paid consultant for Sniff Logic LTD, a company further developing the device. Sniff Logic LTD was formed after the data for this study were collected; it had no financial link to this study and was not involved in it in any way.

STAR★METHODS

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SUPPLEMENTAL INFORMATION

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STAR★METHODS

KEY RESOURCES TABLE

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Deposited data		
Airflow and motion data	This paper	https://github.com/TimnaSoroka/identification_paper
Software and algorithms		
matlab R2023a	MathWorks	https://www.mathworks.com/
HCTSA	Fulcher and Jones[14]	https://github.com/benfulcher/hctsa
BreathMetrics	Noto et al.[11]	https://github.com/zelanolab/breathmetrics

EXPERIMENTAL MODEL AND STUDY PARTICIPANT DETAILS

Participants

We studied 100 participants (52F, mean age = 26.33±3.61 years, range = 18-35 years), who all provided written informed consented to procedures approved by the Weizmann institute IRB committee. All of them reported breathing mainly through their nose, with no history of nose surgeries, no known sleep disorders and normal sense of smell. Subsets of participants completed a demographics questionnaire, the Trait Anxiety Questionnaire (TA)[25] (n = 84), the Autism Spectrum Quotient (AQ)[26] questionnaire (n = 86), and the Beck Depression Inventory questionnaire[24] (n = 84). Three participants were excluded from all analyses due to technical recording problems.

Experimental model

Participants wore the device for 24 consecutive hours, and reported their basic activities during that time. 42 participants completed the experiment twice.

METHOD DETAILS

Device

We developed a wearable spirometry micro-logger (6.3*1.2 cm, ∼22 gr) with two highly sensitive pressure/flow sensors (SDP31, Sensirion, Stäfa, Switzerland), one for each nostril (Figure 1). The device, we call the Nasal Holter, is technically identical to a device we previously described in detail,[17] yet here we miniaturized it by incorporating all elements within a flexible printed circuit. The device is powered by two 675-size replaceable hearing-aid batteries, has on-board memory (64MB), 3-axes acceleration sensor, and Bluetooth connectivity. The device is pasted to the nape of the neck using medical double-sided adhesive tape (Figure 1), and linked to the nostrils by a cannula with separate left and right nostril lines. The device allows for recording and storage of 24 continuous hours at 6Hz. Given ongoing respiration at ∼0.25Hz, this ∼24-fold sampling rate, combined with the exquisite sensitivity of the sensors, provides detection of minute perturbations in airflow, making for an ecologically relevant logger.

The pressure sensors provide an inherently highly accurate temporal trace. This allows high-precision determination of temporal dynamics such as inhalation onset, offset, duration, curve-shape, and associated statistics of temporal variability. By contrast, the absolute air flow-rate estimations (in milliliters per second) and associated volume estimations (in liters), such as inhale or exhale volume, are derived measures with reduced accuracy. Moreover, such volume measures are influenced by individual aspects such as the ratio of cannula diameter to naris diameter, and by transient events such as the movement of the cannula within the naris. In order to estimate the accuracy of volumetric measures with this device, we measured 10 intervals for 2.7±2.3 minutes using a set-up that put the Nasal Holter and a verified spirometer (AD Instruments. Human Respiratory Kit PTK10) in line. A previous study that used such an inline setup to estimate volumetric accuracy from cannula pressure signals used a linear fit between the square root of the pressure signal and the verified spirometer signal.[57] Doing the same and using a leave one out scheme to predict the verified device from our device, we observe that the root mean square error (RMSE) was = 0.087±0.034L, reflecting 93.04±2.88% accuracy for our device in volumetrics. If we in fact don't square root the signal, we observed slightly better performance at 0.0592±0.03L, reflecting 95.38±2.31% accuracy. Whereas this approach treats the entire respiratory waveform, we wanted to gain further insight to the accuracy of inhale and exhale measures separately. We therefore calculated inhale and exhale flow-rates for both signals, and again using a leave one out scheme, predicted flow values. We observe that the RMSE in estimated flow-rate was = 0.004±0.004L/s, reflecting 95.6±7.37% accuracy (Figure S5A). The error in estimated exhale volume was 0.074±0.041 L, reflecting 90.6±4.35% accuracy (Figure S5B), and the error in estimated inhale volume was 0.079±0.073 L, reflecting 87.2±21.5% accuracy (Figure S5C). In other

words, whereas our device provides exquisite temporal airflow dynamics, it is at ~90% accuracy for absolute measures of flow-rate and volume.

Methodological limitations

Our methods have limitations we would like to acknowledge. First, as detailed directly above, a method relying on a nasal cannula rather than a face-mask has limited accuracy in volumetrics. Thus, whereas our temporal measures are extremely accurate, our estimation of absolute true values of flow and volume can be off by between 5% and 15%. Also, although our selected temporal resolution of 6Hz is sufficient for extracting most potential patterns of interest, for optimal characterization of the respiratory trace we would increase this to 25Hz.[58] This was not an oversight, but rather a power-constraint. We wanted to maintain a miniature lightweight device for wearability, and therefore opted for hearing-aid batteries. The power consumption at 25Hz depletes these batteries within 8 hours. Thus, here we opted for longer recordings at reduced sampling rates. A third limitation of our method for real-world settings is in its aesthetics, or rather lack thereof. Using our approach may be limited by the willingness of participants to wear a nasal cannula for extended periods of time, as a nasal cannula has the "look of disease". Although our paid volunteers did this willingly, this may nevertheless pose a limitation in some settings. On this front, it is noteworthy that performance remains strong using sleep data. This may serve to mitigate the latter concern, as the aesthetic consideration is typically reduced in the privacy of sleep. In turn, a sleep-related limitation is that the nasal prongs occasionally slipped out of the nostrils during sleep. This can be corrected in the future by adding adhesive strips. Finally, although the advantages of nasal over oral airflow as an indicator on neural drivers of respiration was discussed above, in some instances concurrent information on oral flow may be an advantage, and that was not available here.

QUANTIFICATION AND STATISTICAL ANALYSIS

Data preprocessing

Data were first divided into wake and sleep intervals per each participant, according to the accelerometer (15 minutes after laying down). The self-reported and data-drived timings were significantly correlated (Pearson r = 0.83, Figure S5D). Four participants had corrupted acceleration sensor data. In these participants we used the self-reported time instead. Reported naps during the day were removed. Wake intervals shorter than one hour were removed.

Respiratory parameters

The data were divided into 5-minute consecutive blocks (with no overlap). For all parameters with per-breath values in BreathMetrics, such as volume, flow, and duration, we use the mean value per the 5-minute block. For measures without per-breath values, such as coefficient of variance, etc., we calculated the feature across the 5-minute block. For the identification task we initially used the 24 BreathMetrics parameters.[11] As the toolbox is provided for higher sampling rates (>20Hz), we did not use it in native form, but rather calculated the parameters ourselves. Next, we added parameters using the Highly Comparative Time Series Analysis tool (HCTSA),[14] which computes 7729 features per timeseries. These features are general timeseries features, not optimized for respiration.

Nasal cycle analysis

Whereas the above were calculated on the summated left and right-nostril signals, we also calculated 4 Nasal Cycle parameters according to previously published methods[17]: mean LI, LI power, nostril correlation and cycle periodicity. These values were obtained separately for wake and sleep, and in cases where we wanted to observe them over time, they were parsed to 30-minute bins. Cycle periodicity was estimated by average interval length when calculated across all wake/ sleep intervals, and as the variance of LI when calculated in bins.

Feature selection

To avoid classification overfitting, we decreased our set of parameters to no more than a square root of the length of the training set. This determined 94 parameters from 7729 in HCTSA. Optimization was by 10000 random repetitions, choosing each time 3 parameters and using them for classification (linear classifier, 5-fold cross validation). Then, we chose the most prominent parameters from the best classification results (top 10%).

Respiratory fingerprints

To test the fingerprint hypothesis, we first prepared a per-participant matrix containing all wake or sleep data divided into 5-minutes blocks (97 participants, average 15.3h wake (920 minutes)-> 920/5*97 rows in a matrix). For classification using the 24 BreathMetrics parameters we first removed sparse rows (more than half nans) and extreme rows (differ by more than 5 standard deviations). Classification accuracy was calculated using the "fitcnet" classifier in Matlab. The model trains a neural network with one hidden layer of 300 neurons using Rectified Linear Unit (ReLU) activation. It standardizes the input data, does not apply any regularization, allows up to 1000 training iterations, and uses the specified class labels for classification. After running the model, we applied 5-fold cross validation. Next, we used a "winner takes all scheme" to convert all identification scores to binary "succeeded or not". Success = The highest number of predictions were for the true participant, fail = The highest number of predictions were not for the true participant.

Behavioral trait prediction

To compare high and low scores in Beck, TA and AQ we used mixed effect ANOVAs with high or low score as fixed effects and time and subject ID as random effects. To predict trait values from respiratory data we used a leave-one-out approach. To maintain independent feature selection, we identified the features separately on each iteration (i.e., without the tested participant in feature selection). We used all features with significant correlation values ($p < 0.05$, uncorrected), and in cases where we had less than 5 such features, we did not conduct feature-selection

Statistical analysis and exclusions

All analyses were done using MATLAB (R2023a). Significance in all classification tasks was assessed using binomial distribution probability. Respiration blocks with less than 5 breaths per minute or with more than 40 breaths per minute were assumed to reflect technical errors such as displacement of the cannula, and were therefore excluded. Spearman correlations between questionnaire scores and respiratory parameters were calculated when the assumption of normality was rejected. Outliers were defined as values exceeding ±2.5 standard deviations for approximately normally distributed variables, and as the extreme 2% for skewed variables. All P-values are two sided.