

1 **Sex-specific age-related changes in glymphatic function assessed by resting-state functional**
2 **magnetic resonance imaging**

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4 Feng Han¹, Xufu Liu¹, Yifan Yang¹, Xiao Liu^{1,2} *

5 **Affiliations:**

6 ¹ Department of Biomedical Engineering, The Pennsylvania State University, PA, USA;

7 ² Institute for Computational and Data Sciences, The Pennsylvania State University, PA, USA

8 *Correspondence to: xxl213@psu.edu

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10

11 **Summary**

12

13 The glymphatic system that clears out brain wastes, such as amyloid- β ($A\beta$) and tau, through
14 cerebrospinal fluid (CSF) flow may play an important role in aging and dementias. However, a
15 lack of non-invasive tools to assess the glymphatic function in humans hindered the understanding
16 of the glymphatic changes in healthy aging. The global infra-slow (<0.1 Hz) brain activity
17 measured by the global mean resting-state fMRI signal (gBOLD) was recently found to be coupled
18 by large CSF movements. This coupling has been used to measure the glymphatic process and
19 found to correlate with various pathologies of Alzheimer's disease (AD), including $A\beta$ pathology.
20 Using resting-state fMRI data from a large group of 719 healthy aging participants, we examined
21 the sex-specific changes of the gBOLD-CSF coupling, as a measure of glymphatic function, over
22 a wide age range between 36-100 years old. We found that this coupling index remains stable
23 before around age 55 and then starts to decline afterward, particularly in females. Menopause may
24 contribute to the accelerated decline in females.

25

26 **Keywords**

27 Healthy aging humans; glymphatic function; cerebrospinal fluid (CSF) flow; global brain
28 activity; gender-effect; sleep quality; menopause.

29

30 **Introduction**

31

32 Aging is the leading risk factor for cognitive decline and neurodegenerative disorders that are often
33 associated with excessive accumulation of misfolded proteins, including the amyloid- β and tau, in
34 the brain (Hou et al., 2019; Mawuenyega et al., 2010; Peng et al., 2016). Recent studies suggested
35 the aggregation of toxic proteins could be partly attributed to impaired glymphatic clearance at
36 advancing ages (Benveniste et al., 2019; Boland et al., 2018; Jessen et al., 2015). The glymphatic
37 system, as “glia-lymphatic system”, constitutes a pathway for brain waste clearance in the central
38 nervous system (Iliff et al., 2012; Jessen et al., 2015). In this clearance pathway, cerebrospinal
39 fluid (CSF) moves from the periarterial space, facilitated by aquaporin-4 (AQP4) channels in
40 astroglial endfeet, into the interstitial space to wash out interstitial solutes, including A β and tau,
41 into the perivenous space surrounding deep-draining veins (Jessen et al., 2015; Tarasoff-Conway
42 et al., 2015). The paravascular CSF recirculation and interstitial solute efflux have been found to
43 decrease in aged mice due to widespread loss of perivascular AQP4 polarization and reduced
44 pulsatility of intracortical arterioles (Kress et al., 2014). In humans, the clearance along the
45 glymphatic pathway and downstream meningeal lymphatic vessels, measured by contrast-agent
46 MRI, decreased and delayed in older patients as compared with younger ones (Zhou et al., 2020).
47 However, the invasive nature of these imaging tools has hindered a large-scale study of glymphatic
48 function in healthy aging subjects. As a result, it remains unclear how the glymphatic function
49 changes in aging, which is vital to understanding the mechanisms of age-related neurodegenerative
50 disorders and cognitive decline.

51

52 Global infra-slow (< 0.1 Hz) brain activity measured by resting-state fMRI (rsfMRI) was recently
53 linked to the glymphatic function (Kiviniemi et al., 2016) and used to quantify its changes in
54 Alzheimer's disease (AD) (Han et al., 2021b) and Parkinson's disease (PD) patients (Han et al.,
55 2021a). Increasing evidence suggested the brain exhibits highly structured, brain-wide infra-slow
56 (< 0.1 Hz) activity during the resting state (Gu et al., 2021; Liu et al., 2021; Raut et al., 2021;
57 Thompson et al., 2014). This global brain activity is evident in neural signals of distinct scales,
58 ranging from single neuron recordings to whole-brain fMRI, and closely related to transient
59 arousal modulations (Gu et al., 2021; Liu et al., 2021). The fMRI measure of this activity, i.e., the
60 global mean rsfMRI blood-oxygenation-level-dependent (gBOLD) signal, is coupled by large CSF
61 movements (Fultz et al., 2019) and astroglial calcium waves (Wang et al., 2018), suggesting its
62 potential link to the glymphatic function. The gBOLD is greatly enhanced during sleep (Fukunaga
63 et al., 2006; Larson-Prior et al., 2009; Olbrich et al., 2009), in accordance with the sleep-enhanced
64 nature of the glymphatic function (Xie et al., 2013). In contrast, arterial and respiratory pulsations,
65 which had been traditionally regarded as the main glymphatic drivers (Iliff et al., 2013; Yamada
66 et al., 2013), actually lack of this attribute with the decreased amplitude during sleep (Boudreau et
67 al., 2013; Douglas et al., 1982; Snyder et al., 1964). For all these reasons, the strength of gBOLD-
68 CSF coupling has been proposed as a surrogate measure of the glymphatic function and found to
69 correlate with various AD pathologies and cognitive decline in PD (Han et al., 2021b, 2021a).
70 Recently, the disengagement of gBOLD from the default mode network (DMN) regions were
71 found to account for early, preferential $A\beta$ accumulation in these higher-order brain areas in the
72 early stage of $A\beta$ pathology (Han et al., 2022). In these early studies, the gBOLD-CSF coupling
73 also was found to correlate significantly with age and sex (Han et al., 2021b, 2021a), but the related
74 findings were limited by narrow age ranges and complicated by the inclusion of patient data.

75

76 The fMRI-based glymphatic measurement, together with the widely available rsfMRI data,
77 provides us a unique opportunity to study the change of the glymphatic function over a wider age
78 range and in a larger population of healthy aging subjects. In this study, we used rsfMRI data of
79 719 healthy aging subjects in the Human Connectome Project Aging (HCP-A) (Harms et al., 2018)
80 to study the age-related changes in glymphatic function in a sex-specific way. We found that the
81 fMRI-based glymphatic measure remained relatively stable within the range of age 36-54 and then
82 started to decrease around age mid-50s. Compared with males, females showed a larger and more
83 abrupt decline of the glymphatic function at this transitioning point. In addition, menopause may
84 lead to an accelerated glymphatic decline in females.

85

86 **Results**

87

88 **Nonlinear age trajectory of the gBOLD-CSF coupling**

89

90 We used rsfMRI data of 719 healthy subjects (403 females) from the HCP-A project with age
91 ranging from 36 to 100. Following previous procedures (Fultz et al., 2019; Han et al., 2021b,
92 2021a), we obtained the whole-brain gBOLD signal from the gray matter regions and the bottom-
93 slice CSF signal around the bottom of the cerebellum to measure CSF movements via MR inflow
94 effects (Fultz et al., 2019; Gao et al., 1996; Gao and Liu, 2012) (**Fig. S1A and S1B**). Consistent
95 with the previous studies, the averaged cross-correlation function of the two signals displayed a
96 biphasic pattern with a negative peak ($r = -0.33$) at the +3.2 sec lag (**Fig. S1C**). The gBOLD-CSF
97 correlation at this +3.2 sec time lag was then computed for individual subjects to quantify their

98 coupling and thus the glymphatic function. The gBOLD-CSF coupling was then averaged within
99 10 equal-size groups of subjects at different ages, and the resulting age-related trend displayed a
100 clear non-linear trajectory: it remains relatively stable between ages 36 to 54 and then begins to
101 decline at around 55 years old (i.e., yrs) (**Fig. 1A**). We then divided the entire cohort into younger
102 and older groups according to the age boundary (53.9 yrs) between the fourth and fifth groups,
103 which had the largest drop among pairs of consecutive groups. The gBOLD-CSF coupling is not
104 correlated ($r = -3.7 \times 10^{-3}$, $p = 0.95$) with age in the younger group whereas this correlation is
105 significant ($r = 0.14$, $p = 3.9 \times 10^{-3}$) in the older group (**Fig. 1B**).

106
107 We examined potential factors mediating this age-coupling association. Neither the coupling index
108 nor age was significantly correlated with the total Pittsburgh Sleep Quality Index (PSQI) score,
109 but they were similarly correlated with a few PSQI items, including sleep medication, trouble
110 sleeping, and sleep hours. Nevertheless, the age-related changes in the gBOLD-CSF coupling
111 remain largely unchanged with adjusting for these sleep-related measurements (**Fig. 2**). Likewise,
112 the age trajectory of the gBOLD-CSF remained similar with controlling for other non-sleep factors,
113 including the head motion assessed by mean framewise displacement (FD) (**Fig. S2**), the brain
114 volume (**Fig. S3**), and the CSF volume (mainly from the ventricles) (**Fig. S4**), even though these
115 factors showed a significant dependence on age (all $p < 3.9 \times 10^{-7}$ for linear regression).

116

117 **Sex-specific differences in age-related changes**

118

119 The gBOLD-CSF coupling is different between females and males. The mean gBOLD-CSF
120 strength is significantly ($p = 7.9 \times 10^{-6}$, two-sample t-test) weaker in females than males (**Fig. 3A**),

121 consistent with the previous finding in an AD cohort (Han et al., 2021b). The age trajectories of
122 the coupling index are different for the two groups. The gBOLD–CSF coupling decreases more
123 evidently and abruptly with aging in the females, particularly around 55 yrs, whereas the males
124 showed a more gradual and steady age-related changes (**Fig. 3B**).

125
126 We further tested whether and how the gBOLD-CSF coupling is affected by menopause, which
127 often occurs before age 55. This analysis was focused on the age range of 36-55, which includes
128 both post-menopause and other females. The menopause status had no significant effects on the
129 gBOLD-CSF coupling strength for two subgroups of subjects of similar ages (both $p > 0.13$; two
130 sample t-test). However, it showed a marginally significant ($p = 0.061$) interaction with age on the
131 coupling strength. Consistent with this result, the gBOLD-CSF coupling in the postmenopausal
132 females appeared to decline earlier in the age mid-40s (**Fig. 3C**), making the drop around age 55
133 less abrupt and significant ($p = 0.058$). The result suggests the potential effect of the menopause
134 to accelerate the decline of the fMRI-based glymphatic measure.

135

136 **Discussion**

137

138 Here we study the sex-specific age-related change in the glymphatic function in a large healthy
139 aging population based on the gBOLD-CSF coupling measured by rsfMRI. We showed that the
140 gBOLD-CSF coupling changes with age in a non-linear way: it remains relatively stable from 36
141 yrs to 54 yrs and then begins to decrease afterwards. Importantly, the decrease at age mid-50s is
142 larger and more abrupt in females than in males.

143

144 Converging evidence has suggested a link between the glymphatic function and the resting-state
145 global brain activity, often measured by the gBOLD signal of rsfMRI. The gBOLD, once regarded
146 as noise, measured a brain-wide, low-frequency (< 0.1 Hz) activity linked to transient arousal
147 modulations, which also has been observed in monkey electrocorticography (ECoG) (Liu et al.,
148 2015, 2018) and mice spiking data as highly structured patterns (Liu et al., 2021). The low-
149 frequency rsfMRI signals were first linked to the glymphatic function due to their potential link to
150 CSF dynamics and vasomotor waves (Kiviniemi et al., 2016). It was found later that it is the global
151 component of rsfMRI, i.e., gBOLD, that is coupled to CSF movements in a sleep-dependent way
152 (Fukunaga et al., 2006; Fultz et al., 2019; Helakari et al., 2022; Larson-Prior et al., 2009; Olbrich
153 et al., 2009). The sleep dependency makes it more suitable for driving the sleep-dependent
154 glymphatic clearance (Holth et al., 2019; Xie et al., 2013), as compared with the cardiac and
155 respiratory pulsations that are actually suppressed during sleep (Baust and Bohnert, 1969;
156 Boudreau et al., 2013; Douglas et al., 1982; Guazzi and Zanchetti, 1965; Snyder et al., 1964).
157 Nevertheless, the gBOLD is not independent from these physiological drivers but shows strong
158 correlations with the low-frequency modulation of cardiac and respiratory functions (Birn et al.,
159 2006; Chang et al., 2009; Gu et al., 2020; Özbay et al., 2019, 2018; Power et al., 2018). Consistent
160 with these human findings of strong low-frequency physiological modulation, a recent mice study
161 demonstrated very strong arterial constrictions/dilations during sleep in the same frequency range
162 (<0.1 Hz) (Turner et al., 2020). Such low-frequency vessel modulations were coupled by pupil
163 size changes suggestive of transient arousal modulations (Turner et al., 2022), similar to the global
164 brain activity measured by gBOLD (Liu et al., 2021, 2018; Pais-Roldán et al., 2020; Turchi et al.,
165 2018). Animal research also suggested that the gBOLD is coupled by large calcium signals of
166 astrocytes (Pais-Roldán et al., 2020), and the AQP4 channels on the endfeet of these cells are a

167 key player of the glymphatic system (Iliff et al., 2012; Jessen et al., 2015). To date, the key
168 evidence linking the gBOLD to the glymphatic function came from a human study showing that
169 the gBOLD is coupled to large CSF movements (Fultz et al., 2019). Based on this, the gBOLD-
170 CSF coupling was used to quantify glymphatic function and found correlated with various
171 pathologies of AD and cognitive decline in PD (Han et al., 2021b, 2021a). The preferential
172 reduction of gBOLD signal in the higher-order default mode network was found to account for
173 early, preferential β -amyloid accumulations in the same regions at the early stage of AD (Han et
174 al., 2022). All these findings established the foundation for using the gBOLD-CSF coupling to
175 measure the glymphatic function. But a direct proof of their relationship would need future
176 experiments capable of recording brain signals across distinct spatial and temporal scales. It is also
177 worth noting that the debate is ongoing regarding specific components of glymphatic theory, e.g.,
178 the convective flow in the interstitial space and the involvement of AQP4 channels in the process
179 (Abbott et al., 2018; Hladky and Barrand, 2022). Nevertheless, a consensus view is reached
180 regarding the existence of periarterial CSF flow (Mestre et al., 2018) and its role in waste clearance
181 (van Veluw et al., 2020), which is more related to the gBOLD-CSF coupling in the present study.
182
183 Brain aging affects the glymphatic function. The CSF inflow of larger tracers or macromolecules
184 decreased up to 85% in old wild-type mice as compared to young counterpart (Da Mesquita et al.,
185 2018; Nedergaard and Goldman, 2020). The decreased glymphatic flow in aged mice has been
186 partly attributed to dysregulation of astroglial water transport due to the widespread loss of AQP4
187 polarization (Kress et al., 2014), the decline of CSF pressure (Fleischman et al., 2012), and the
188 changes of CSF secretion and protein content (Chen et al., 2009). Arterial wall stiffening and
189 associated reduction of arterial pulsatility (Zieman et al., 2005) may also account for age-related

190 glymphatic reduction (Iliff et al., 2013). Human studies of glymphatic function remain sparse (Eide
191 et al., 2018; Zhou et al., 2020). Previous studies using the gBOLD-CSF coupling found a consistent
192 association between the age and glymphatic function, but only in patients of relatively old ages
193 (Han et al., 2021a, 2021b). A retrospective study combined contrast-agent MRI data from various
194 patient groups to study the glymphatic function and its change with age (Zhou et al., 2020). Despite
195 different methodologies and patient cohorts from the present study, a similar age trajectory was
196 observed for the glymphatic function: it remains stable before 50 yrs and then begins to decline
197 since then (Zhou et al., 2020). The age-related glymphatic changes could be critical for the aging-
198 related risk for neurodegenerative diseases (Hou et al., 2019). The glymphatic dysfunction may
199 result in inadequate clearance and thus accumulation of toxic proteins, such as A β and tau, and
200 thereby increase the vulnerability to developing cognitive impairments and neurodegenerative
201 diseases (Jessen et al., 2015; Tarasoff-Conway et al., 2015). Epidemiologic research suggested the
202 late-onset AD, the most common AD variant, starts around the mid-60s with the prevalence
203 doubled every 5 years afterwards (Qiu et al., 2009). But the pathophysiological process, including
204 the accumulation of aggregated A β , could begin more than a decade before the dementia (Jack et
205 al., 2013; Sperling et al., 2014). Together, these findings suggested a timeline consistent with our
206 finding that the glymphatic function begins to decrease at age mid-50s.

207

208 The female sex is another leading risk factor for developing AD (Mielke et al., 2014). It has been
209 found a significantly weaker glymphatic function, as measured by gBOLD-CSF coupling strength,
210 in females than in males (Han et al., 2021b). Here we confirmed the finding with a much larger
211 dataset from healthy populations. Importantly, we further showed that the glymphatic function had
212 different age trajectories in the two groups with the females displaying a larger and more abrupt

213 decline at around 55 yrs. In fact, women indeed show larger and faster cognitive declines than men
214 with aging (Levine et al., 2021; Nooyens et al., 2022). Together with increasing evidence that links
215 the glymphatic dysfunction and cognitive impairments (Da Mesquita et al., 2018; Iliff et al., 2014;
216 Zou et al., 2019), the sex-specific glymphatic change with aging may provide a possible
217 explanation for the sex differences in age-related cognitive decline. The menopause and associated
218 hormone loss have been suggested to contribute to cognitive decline in females (Brown and
219 Gervais, 2020; Hachul et al., 2015). Our result is not inconsistent with this notion by showing a
220 marginally significant ($p = 0.061$) interaction between age and menopause on the coupling metrics.
221 Among the females of age 36-55, the post-menopausal group appeared to show a decline of
222 gBOLD-CSF coupling with age, which is absent in the non-menopause group. A limited sample
223 size and information related to menopause could partially account for statistical non-significance.
224 But the finding should warrant future studies looking into the menopause effects on the glymphatic
225 function with a refined design and/or augmented dataset.

226
227 Sleep quality appeared not to be a major contributor to the age-related glymphatic changes. The
228 gBOLD-CSF coupling and age are similarly correlated with a few sleep measures, including the
229 frequency of using sleep medication and the sleep troubles in the month prior to the experiments.
230 However, the age-related changes in the gBOLD-CSF coupling remained largely unchanged after
231 adjusting for these sleep measures. Nevertheless, the change in sleep architecture might be related
232 to the sex difference seen in the age-related glymphatic changes. The age and sex are known to
233 have a strong interaction effect on the composition of sleep stages. Aging in males is associated
234 with a significant increase of light sleep (stages 1&2) but decrease in slow wave sleep (SWS: sleep
235 stages 3&4), whereas this age-related change is absent in women (Mander et al., 2017; Redline et

236 al., 2004). It is known that the glymphatic function increases during sleep and anesthesia featuring
237 strong slow wave activity (SWA) (Hablitz et al., 2019; Ju et al., 2017; Xie et al., 2013), and one
238 would thus expect an improved glymphatic clearance with a higher percentage of SWS. The
239 empirical evidence, however, suggested an opposite by showing higher SWS is associated with
240 lower CSF A β 42 level (Varga et al., 2016), which is an early indicator of preclinical AD and often
241 accompanied by cortical A β accumulation (Jack et al., 2013; Palmqvist et al., 2017). The paradox
242 might be explained by an observation about the gBOLD and its coupling with CSF flow. They
243 were more specifically related to ultra-slow (0.6-1 Hz) component of SWA (often related to K-
244 complexes) (Özbay et al., 2019) and phasic changes of SWA power (Fultz et al., 2019; Gu et al.,
245 2022), which could be stronger during the light sleep than SWS. Indeed, the SWA was found to
246 decrease in subjects with more cortical A β and poorer memory consolidation (Mander et al., 2015;
247 Winer et al., 2020), as well as AD patients (De Gennaro et al., 2017), but the reduction was specific
248 to its ultra-slow component (0.6-1 Hz) with the delta-band (1-4 Hz) power showing opposite
249 changes. Based on all these findings, it is possible that the age-related increase in the percentage
250 of light sleep in males may help to offset some age-related decline in glymphatic function and thus
251 lead to its slow deterioration as compared with females. However, the test of this hypothesis would
252 have to be left for future studies, particularly those with assessment of subjects' sleep architecture.

253

254 **STAR Methods**

255

256 **Participants and study data**

257 This study included 719 healthy human subjects (36~100 yrs; 403 females) who have participated
258 in all 4 sessions of rsfMRI scanning in the HCP-A project

259 (<https://www.humanconnectome.org/study/hcp-lifespan-aging>). For these subjects, we also used
260 their T1-weighted structural MRI imaging and demographic data, such as the age, sex, and the
261 menstrual cycle of females. These “typical aging” subjects were healthy for their age without
262 identified pathological causes of cognitive declines, such as stroke or clinical dementia
263 (Bookheimer et al., 2019). All participants provided written informed consent, and investigators
264 at each HCP-A participating site obtained ethical approval from the corresponding institutional
265 review board (IRB).

266
267 The use of de-identified data from the HCP-A and the sharing of analysis results have been
268 reviewed and approved by the Pennsylvania State University IRB (IRB#: STUDY00008766) and
269 also strictly followed the National Institute of Mental Health (NIMH) Data Archive-data use
270 certification (DUC).

271

272

273 **Image acquisition and preprocessing**

274 The rsfMRI data were acquired at 3T MR scanners (Siemens Medical Solutions; Siemens,
275 Erlangen, Germany) with a matched protocol (Harms et al., 2018) across four acquisition sites
276 including Washington University St. Louis, University of Minnesota, Massachusetts General
277 Hospital, and University of California, Los Angeles (researchers in Oxford University dedicating
278 to the data analysis). For each subject, 4 sessions of rsfMRI (including the anterior to posterior
279 phase encoding (PE) from Day1, i.e., AP1, as well as PA1, AP2, and PA2) were followed by one
280 T1-weighted structural MRI session (MPRAGE sequence, echo time (TE)= 1.8/3.6/5.4/7.2 ms
281 [multi-echo], repetition time (TR) = 2,500 ms, field of view (FOV) = 256 × 256 mm², 320 × 300

282 matrix, number of slices = 208, voxel size = $0.8 \times 0.8 \times 0.8 \text{ mm}^3$, flip angle = 8°) (Harms et al.,
283 2018). The T1-weighted MRI served to provide the whole brain and CSF volume information and
284 was used for the anatomical segmentation and registration. For rsfMRI acquisition, 488 fMRI
285 volumes were collected with a multiband gradient-recalled (GRE) echo-planar image (EPI)
286 sequence (TR/TE=800/37 ms, flip angle= 52° , FOV = 208 mm, 104×90 matrices, 72 oblique axial
287 slices, 2 mm isotropic voxels, multiband acceleration factor of 8).

288

289 We referred to the previous study (Han et al., 2021b) in preprocessing the rsfMRI data using the
290 FSL (version 5.0.9; <https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/FSL>) (Smith et al., 2004) and AFNI
291 (version 16.3.05; <https://afni.nimh.nih.gov/>) (Cox, 1996). The general fMRI preprocessing
292 procedures included motion correction, skull stripping, spatial smoothing (full width at half
293 maximum (FWHM) = 4mm), temporal filtering (bandpass, approximately 0.01 to 0.1 Hz), and the
294 co-registration of each fMRI volume to corresponding T1-weighted structural MRI and then to the
295 152-brain Montreal Neurological Institute (MNI-152) space. The motion parameters were not
296 regressed out to avoid attenuating the gBOLD signal (Gu et al., 2020; Han et al., 2021b). The
297 preprocessing of structural images was performed using FSL. Processing steps included spatial
298 normalization and skull stripping.

299

300 **Extract gBOLD and the CSF inflow signals and compute their coupling**

301

302 We followed the previous studies (Han et al., 2021b, 2021a) to extract the gBOLD signal and CSF
303 inflow signal. We defined the mask of the gray matter regions based on the Harvard-Oxford
304 cortical and subcortical structural atlases (<https://neurovault.org/collections/262/>). We then

305 transformed the gray-matter mask from the MNI-152 space back to the original space of each
306 session to avoid spatial blurring from the registration process (Fultz et al., 2019), and spatially
307 averaged the Z-normalized gray-matter rsfMRI signals to obtain the gBOLD signal. Following the
308 previous study (Han et al., 2021b), the CSF inflow signal was extracted from the CSF region at
309 the bottom edge of fMRI, with a similar voxel number of CSF ROI for all subjects/sessions (see
310 an example in **Fig. S1A**). We extracted the CSF ROI from the preprocessed fMRI signal at the
311 original individual space referring to the corresponding CSF region below the bottom of the
312 cerebellum from the high-resolution T1-weighted MRI (see an exemplary time-series of gBOLD
313 and bottom CSF fMRI in **Fig. S1B**).

314

315 The cross-correlation function was calculated on the extracted gBOLD signal and the CSF inflow
316 signal for each fMRI session from each individual subject. The cross-correlation function
317 quantified the Pearson's correlation at different time lags. We first averaged all the cross-
318 correlation functions from the 4 individual fMRI sessions (AP1, PA1, AP2, and PA2) for each
319 subject, and further averaged the functions across all subjects (**Fig. S1C**). Referring to the previous
320 studies (Han et al., 2021b, 2021a), we quantified the gBOLD–CSF coupling with the session-mean
321 cross-correlation at the lag of +3.2 seconds, where the negative peak of the subject-mean cross-
322 correlation located, for each subject.

323

324 **The relationship between the gBOLD–CSF coupling and age**

325

326 To access the association between the gBOLD–CSF coupling and age, we first divided all the
327 subjects into 10 sub-groups with different ages (based on the deciles), and further calculated and

328 compared the mean gBOLD–CSF coupling for each sub-group. Moreover, all the subjects were
329 separated into the younger (age < 53.9 yrs) and older (age ≥ 53.9 yrs) groups. The linear regression
330 was used to evaluate the association between the ages and the coupling measures for the subjects
331 in each sub-group.

332

333 Several sensitivity analyses were then performed to test whether the age-coupling association
334 would be driven by the various sleep quality measures (i.e., PSQI measures), the brain volume, as
335 well as the CSF volume. We included the total PSQI score, as well as 4 different PSQI items,
336 which were selected due to their strong dependence ($p < 0.05$ for linear regression or ordinal
337 regression) with the coupling measures or age, covering the components/aspects of sleep
338 medication, trouble sleeping, and sleep hours in the sensitivity test. In the test, each of these PSQI
339 measures was first linked to the coupling measures and age, and then regressed out from the
340 coupling measures to further examine the age-coupling associations studied in **Fig. 1**. Similar age-
341 coupling association tests were applied on the whole brain volume and CSF volume, respectively.
342 The whole brain volume was accessed by the volume number of all brain regions excluding the
343 CSF area from the T1-weight MRI, where the CSF regions mainly from all the ventricles were
344 extracted to quantify the CSF volume. To test whether the head motion would drive the age-
345 coupling association, we adjusted the gBOLD-CSF coupling for the head motion from each
346 rsfMRI acquisition, which was quantified by the session-mean framewise displacement (FD),
347 following the previous study (Han et al., 2021b) and replicated the analysis in **Fig. 1**. The FD was
348 calculated as the sum of the absolute value of all 6 translational and rotational realignment
349 parameters derived from the preprocessing (Power et al., 2012). We did not use motion-censoring

350 methods (Power et al., 2014, 2012) to avoid the influence from the cross-correlation of the
351 concatenated timeseries of gBOLD and CSF fMRI signals.

352

353 **Sex-specific coupling changes with aging**

354

355 We further compared the gBOLD–CSF coupling strength between the male and female subjects,
356 as well as the respective trajectory of coupling changing with aging. First, we compared the
357 coupling measures between sexes with a two-sample t-test. Second, we divided the males or
358 females into 7 sub-groups (one group per 10 years; starting from 36~45 yrs, i.e., $36 \leq \text{age} < 46$),
359 respectively, and compared the coupling measures across these sub-groups.

360

361 To examine whether the menopause would affect the tendency of the coupling measure changing
362 with aging, we separated all the females into the “post-menopause” and “other females” groups
363 (based on the measure of “whether having no period for 12 months” in the “menstrual cycle” data),
364 divided the “other females” into two stages of the “36~45 yrs” and “46~55 yrs”, and compared the
365 coupling measures between the two stages. Similarly, we also selected the same age range/sub-
366 groups for the post-menopausal subjects and contrasted the corresponding coupling measures
367 between the two sub-groups, as well as compared the coupling across the “post-menopause” and
368 “other females” subjects for each age-stage. Furthermore, we applied the same grouping metric on
369 the “post-menopause” subjects as the entire group of females above, i.e., 7 groups with an age
370 duration of 10 years (from 36~45 yrs), and then replicated the analyses for whole females to
371 observe the trajectory of the coupling changing with aging.

372

373 **Statistical analysis**

374

375 The present study used the two-sample t-test for the group comparison of continuous variables,
376 including the coupling difference of neighboring groups and that between males and females. The
377 linear regression was applied to estimate the association between age and gBOLD–CSF coupling
378 for the younger group and older group, respectively. The ordinal regression was used for responses
379 with natural ordering among categories (i.e., the association between the coupling measure or age
380 and these PSQI measures). The cross-correlation function was used to evaluate the relationship
381 between the gBOLD signal and CSF inflow signal at different time lags. We also tested the
382 interaction effects of age and menopause on the coupling measure. In the study, Pearson’s
383 correlation was employed to assess the inter-subject associations between different variables. A
384 p-value less than 0.05 was considered statistical significance.

385

386 **Acknowledgements**

387

388 The HCP-A dataset reported in this study was supported by grants U01AG052564 and
389 U01AG052564-S1 and by the 14 NIH Institutes and Centers that support the NIH Blueprint for
390 Neuroscience Research, by the McDonnell Center for Systems Neuroscience at Washington
391 University, by the Office of the Provost at Washington University, and by the University of
392 Minnesota Medical School. We gratefully acknowledge the efforts of all the individuals who have
393 contributed to the project.

394

395 Data and/or research tools used in the preparation of this manuscript were obtained from the
396 National Institute of Mental Health (NIMH) Data Archive (NDA). NDA is a collaborative
397 informatics system created by the National Institutes of Health to provide a national resource to
398 support and accelerate research in mental health. Dataset identifier(s): 10.15154/1528735. This
399 manuscript reflects the views of the authors and may not reflect the opinions or views of the NIH
400 or of the Submitters submitting original data to NDA.

401

402 **Funding:**

403

404 This work is supported by funding from the following:

405 National Institutes of Health grant RF1 MH123247-01 (Xiao Liu);

406 National Institutes of Health grant R01 NS113889 (Xiao Liu).

407

408 **Author contributions:**

409

410 Conceptualization: Feng Han, Xiao Liu

411 Methodology: Feng Han, Xiao Liu

412 Investigation: Feng Han, Xufu Liu, Yifan Yang, Xiao Liu

413 Visualization: Feng Han, Yifan Yang, Xiao Liu

414 Funding acquisition: Xiao Liu

415 Project administration: Xiao Liu

416 Supervision: Xiao Liu

417 Writing – original draft: Feng Han, Xiao Liu

418 Writing – review & editing: Feng Han, Xufu Liu, Yifan Yang, Xiao Liu

419

420 **Competing Interests:**

421

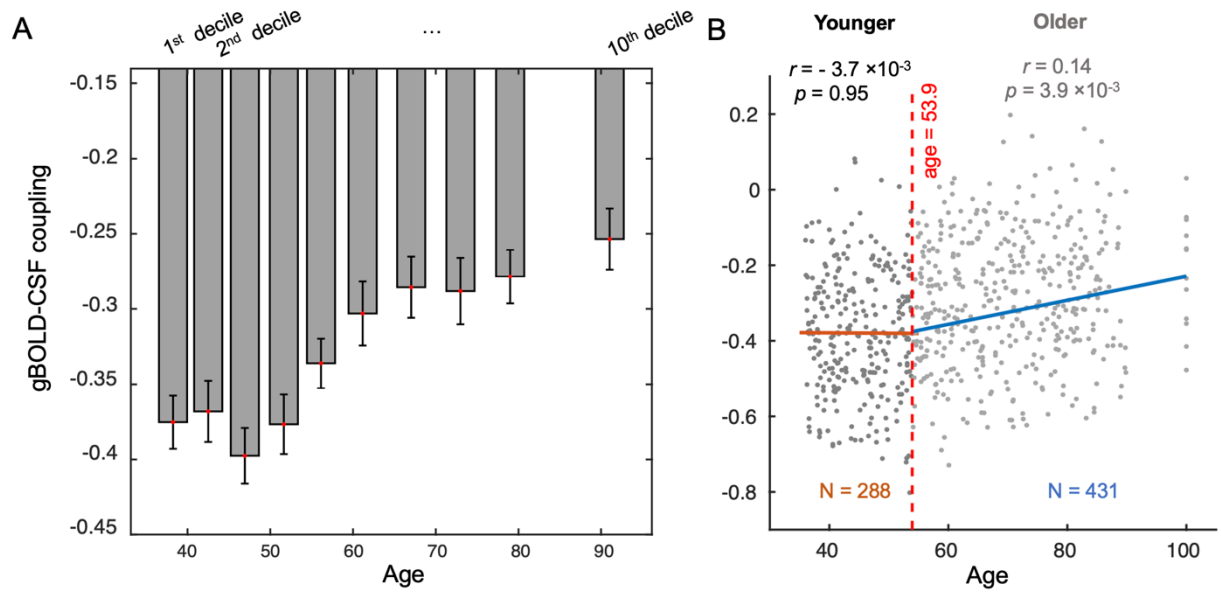
422 The authors report no financial interests or potential conflicts of interest.

423

424 **Data and Materials Availability:**

425

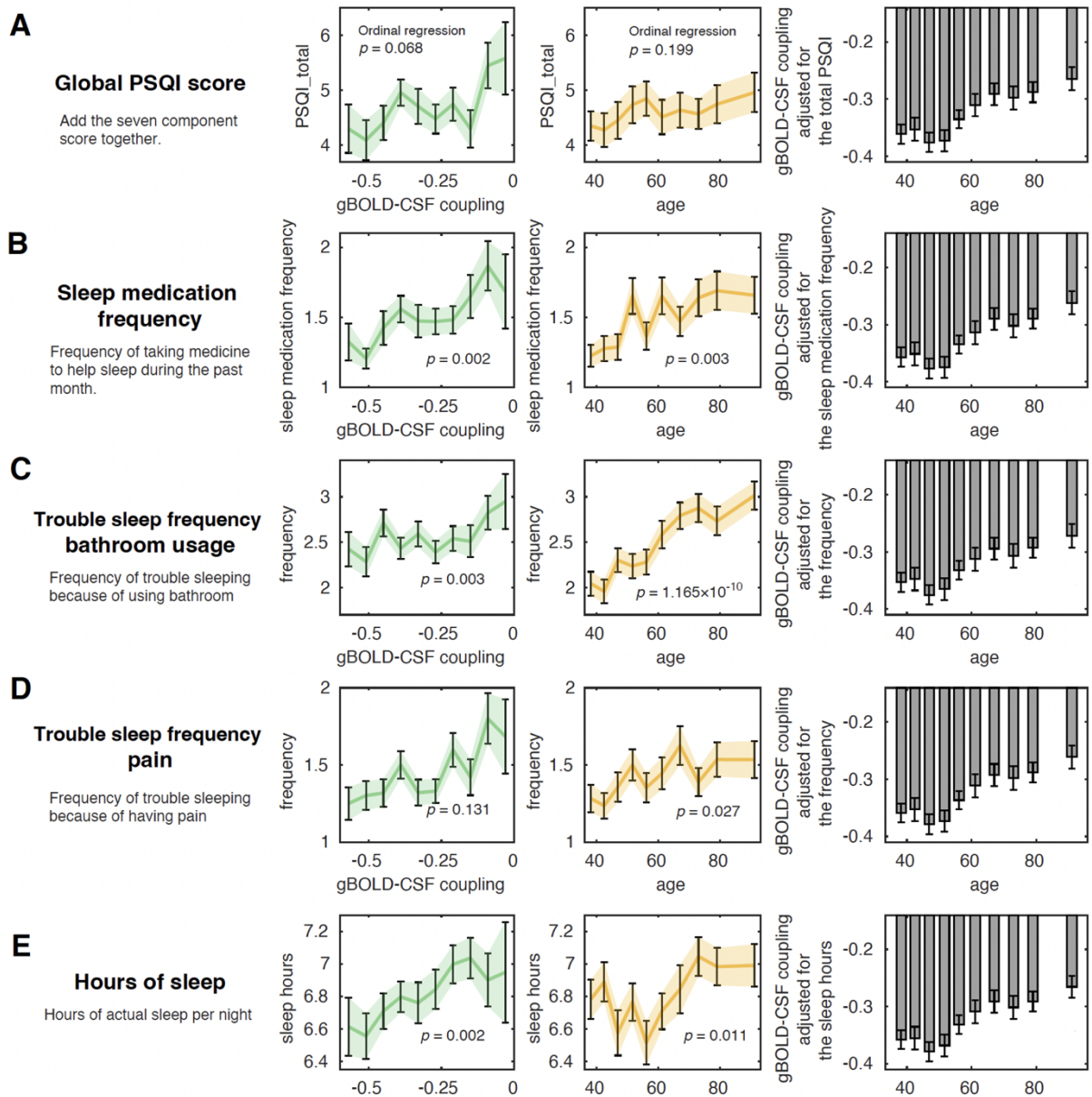
426 The multimodal data, including subject characteristics, structural MRI, and rsfMRI are all publicly
427 available at the NDA website upon the approval of the data use application
428 (<https://nda.nih.gov/get/access-data.html>). All the code used in the present study are available from
429 the corresponding author upon request.



430

431 **Fig. 1 The change of gBOLD–CSF coupling with age.** (A) The gBOLD–CSF coupling remains
432 relatively stable before age mid-50s and then begins to decrease since then. The entire cohort was
433 grouped into 10 subgroups of equal size. Each error bar represents one standard error of the mean.
434 (B) The gBOLD-CSF coupling was significantly correlated with age for the group of subjects over
435 53.9 yrs ($r = 0.14$, $p = 3.9 \times 10^{-3}$; gray dots at the right), but not so ($r = -3.7 \times 10^{-3}$, $p = 0.95$; black
436 dots at the left) for the younger group. Each dot represents one subject.

437



438

439 **Fig. 2 The age-related changes in gBOLD-CSF coupling remain similar with controlling for**

440 **sleep measures.** The gBOLD-CSF coupling (left) and age (middle) are similarly correlated with

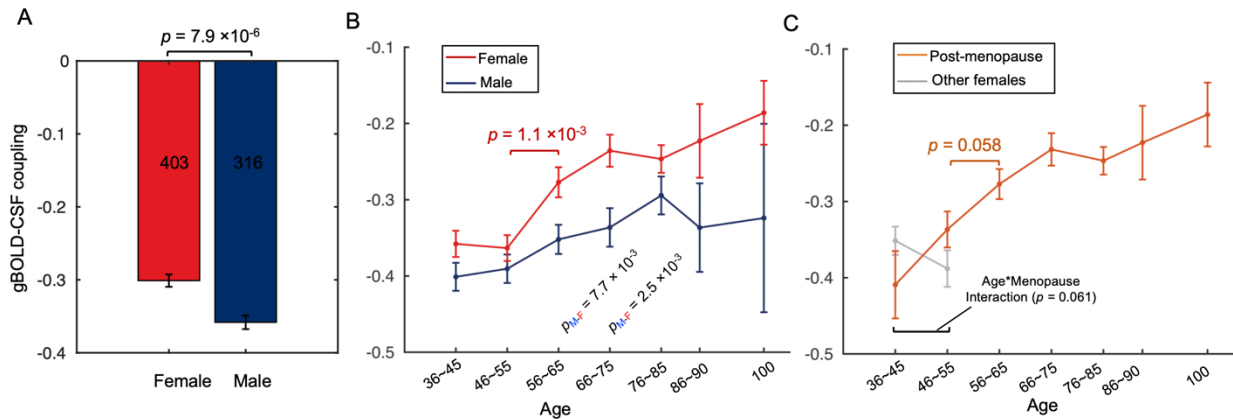
441 a few sleep-related measurements in PSQI, including the sleep medication frequency (2nd row),

442 the frequency of bathroom-use during sleep-time (3rd row), the frequency of having pain during

443 sleep-time (4th row), and sleep hours (5th row), but not the total PSQI score (1st row). However, the

444 age-related changes in gBOLD-CSF coupling remain similar with adjusting for these PSQI
445 measures (right). Each dot represents one subject, and error bars represent the standard error of the
446 mean.
447

448



449

450 **Fig. 3 The age-coupling association showed distinct patterns between males and females. (A)**

451 The gBOLD-CSF coupling is significantly weaker in females (red) than in males (blue) ($p =$

452 7.9×10^{-6} , two-sample t-test). (B) The age-related changes of the gBOLD-CSF coupling were

453 summarized separately for the females and males and showed different patterns of trajectory:

454 gBOLD-CSF coupling in the females showed a steep decline around 55 yrs ($p = 1.1 \times 10^{-3}$ for two

455 consecutive subgroups around that age), in contrast to the slow and gradual decreases in the males.

456 (C) The gBOLD-CSF coupling trends in the “Post-menopause” and “Other females” groups. All

457 females above age 55 are post-menopause. Within the age range of 36-55, the menopause status

458 and age showed a marginally significant ($p = 0.061$) interaction effect on the gBOLD-CSF

459 coupling. The coupling index started to decrease early at age mid-40s and thus its reduction around

460 age mid-50s is less significant ($p = 0.058$) as compared with the entire female group.

461

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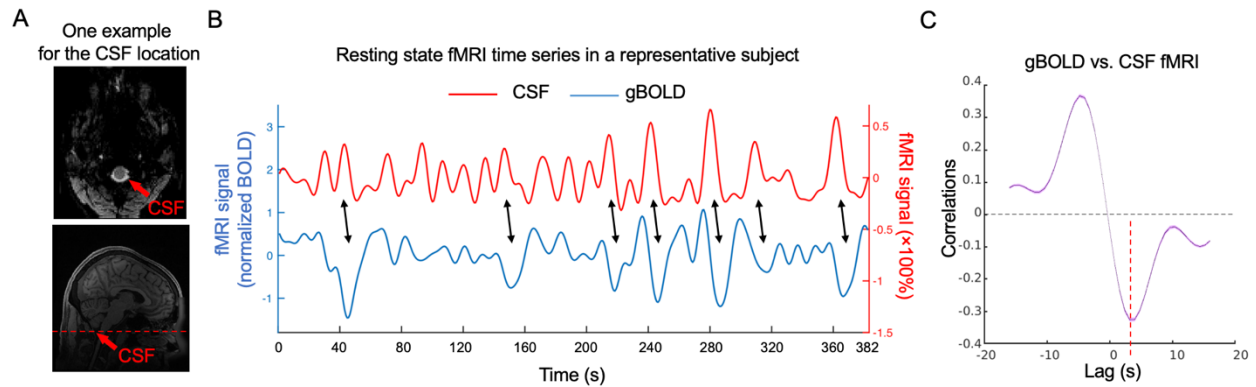
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Supplementary Materials

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Fig. S1 to S4 for multiple supplementary figures

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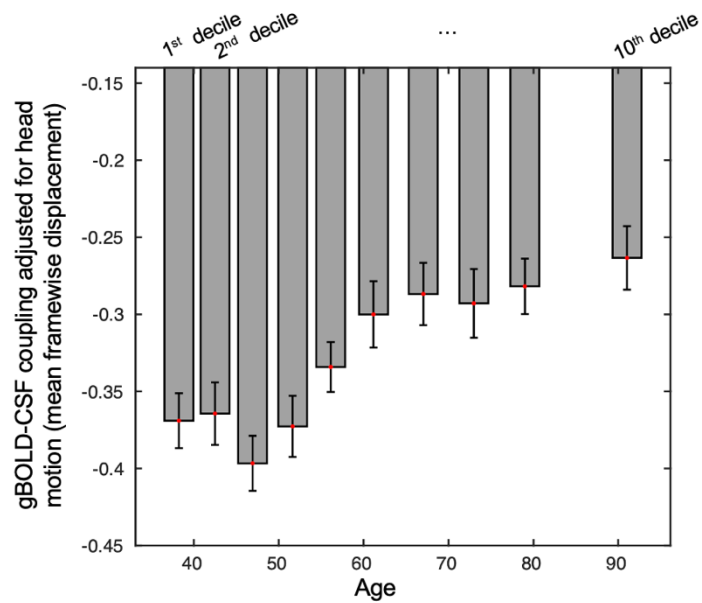
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769 **Fig. S1 gBOLD is coupled with CSF changes in HCP-Aging data. (A) Top:** CSF region at
770 bottom fMRI slice shown in an example subject; **Bottom:** location of bottom rsfMRI slice marked
771 in corresponding structural MRI (dashed line). **(B)** gBOLD (blue) and CSF (red) rsfMRI signals
772 showed a coupled change (black arrows) from a representative example. **(C)** Averaged cross-
773 correlation function between gBOLD and CSF across 719 subjects. The red dashed line marks the
774 time lag (+3.2-sec) where the negative peak of the mean cross-correlation occurs. The shaded
775 regions represent the area within one standard error of the mean.

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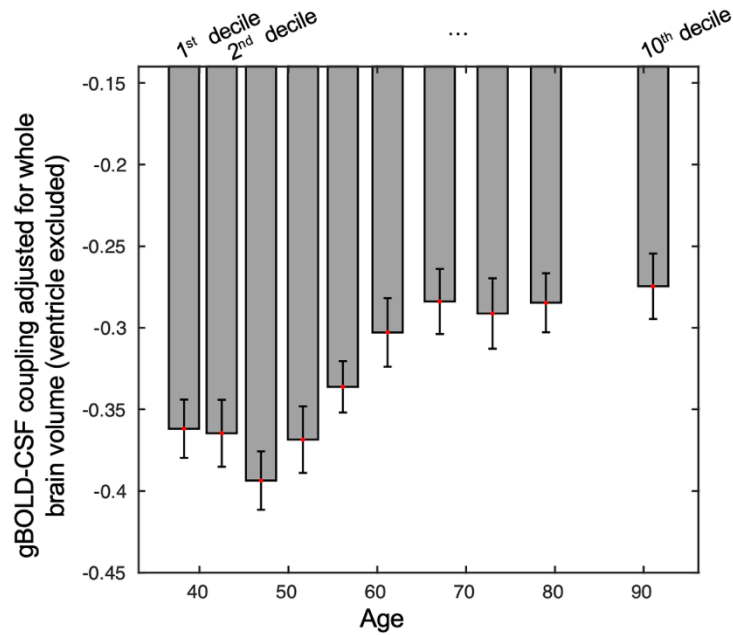


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779 **Fig. S2 The age-coupling association was not affected by head motion during fMRI**
780 **acquisition.** Similar results as **Fig.1** were found when the mean FD was regressed out from the
781 gBOLD-CSF coupling for each rsfMRI session.

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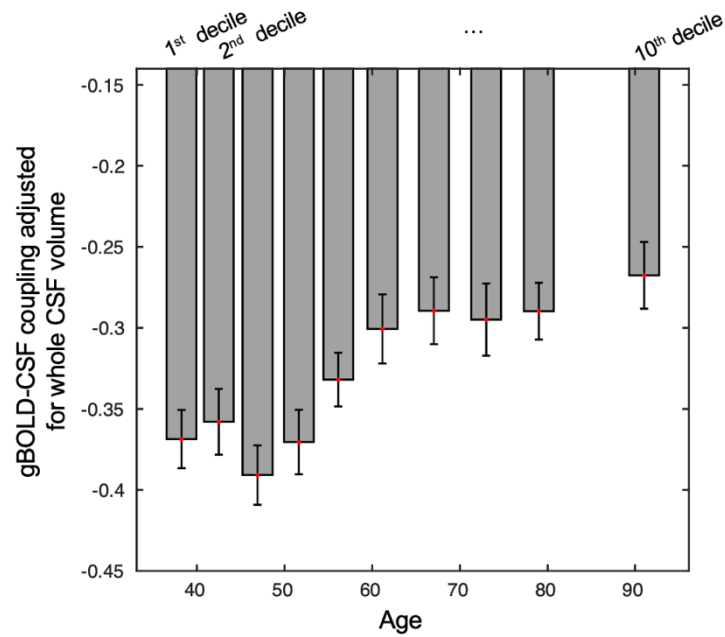


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785 **Fig. S3 The age-coupling association was not dominant by the whole brain volume.** Consistent
786 results as **Fig.1** were found when we regressed out the whole brain volume (ventricles excluded)
787 from the gBOLD-CSF coupling for each rsfMRI session.

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791 **Fig. S4 The age-coupling association was not affected by the whole CSF volume.** Similar
792 results as **Fig.1** were found when the volume of the whole CSF area was regressed out from the
793 gBOLD-CSF coupling for each rsfMRI session.