



*<http://www.brainactivityatlas.org>*

## **The Brain Activity Atlas for HCP FFA**

Face-selective regions on the fusiform gyrus (FG), or "Fusiform Face Areas (FFAs)", were defined as either mFus-faces/FFA-2 or pFus-faces/FFA-1 for each of 1053 participants from Human Connectome Project Young Adult (HCP-YA, S1200 data release, 2017) by taking both individual cortical landmarks (OTS: occipito-temporal sulcus; CoS: collateral sulcus; MFS: mid-fusiform sulcus) and face-selective activation clusters (faces versus others,  $Z > 1.65$ ,  $p < 0.05$ , uncorrected) into account. At least one face-selective region was identifiable in every hemisphere in each participant and 95.44% of hemispheres had two face-selective regions on the FG. The spatial organization of FG face-selective regions could be categorized into one of three different types, or topological groups, in a given hemisphere: separate, continuous, or single.

This dataset contains all individual FFAs, their probabilistic maps and maximum probability maps (MPMs), and group IDs for each hemisphere (see "Details for files" section). Even more, we split the strip-like fusiform face complex (FFC) in the HCP MMP Atlas (Glasser et al., 2016) into two parts (i.e., pFus-faces/FFA-1 and mFus-faces/FFA-2), which are also provided in the dataset. All maps are provided in both 32k\_fs\_LR and fsaverage spaces. If you use these maps in your publication, please cite: <https://www.biorxiv.org/content/10.1101/2022.04.08.487562v1>

## **MRI acquisition**

The HCP-YA MRI data were acquired on the HCP's custom 3T Siemens Skyra

scanner using a 32-channel head coil. T1-weighted (T1w) images were acquired using the 3D MPRAGE sequence (TR = 2400 ms, TE = 2.14 ms, voxel size = 0.7 mm isotropic, iPAT = 2). T2-weighted (T2w) images were acquired using the 3D SPACE sequence (TR = 3200 ms, TE = 565 ms, voxel size = 0.7 mm isotropic, iPAT = 2). Functional data were acquired using gradient-echo EPI sequence (TR = 720 ms, TE = 33.1 ms, isotropic voxel size = 2 mm, MB = 8). More details of the HCP-YA MRI acquisition can be found in elsewhere (Barch et al., 2013; Glasser et al., 2013; Smith et al., 2013; Sotiropoulos et al., 2013; Uğurbil et al., 2013).

## **Functional localizer**

Face-selective regions were localized using a working memory task in which four stimulus types (faces, places, tools and body parts) were presented in separate blocks (Barch et al., 2013). The localizer consists of two runs, and each run contains eight task blocks (10 trials of 2.5 s each, for 25 s) and 4 fixation blocks (15 s each). Within each run, half of the task blocks use a 2-back working memory task and the other half use a 0-back working memory task. A 2.5 s cue indicated the task type at the start of the block. For each trial, the stimulus is presented 2 s, followed by a 500 ms inter-trial interval (ITI).

## **MRI processing**

The MRI data of HCP-YA were preprocessed with the HCP minimal preprocessing pipelines (Glasser et al., 2013). The T1w and T2w images were used to i) reconstruct individual cortical surfaces, ii) estimate the T1w/T2w ratio (which is a measure of tissue contrast enhancement that is a proxy for myelination), and iii) cortical thickness. The individual surfaces and related maps were further registered to the standard fsLR surface via the multimodal surface matching (MSM) algorithm (Glasser et al., 2016; Robinson et al., 2014). All functional images from individual participants were motion corrected, temporally filtered (highpass filter, cutoff = 2000 s for rfMRI data and 200 s for tfMRI data), spatially denoised via the ICA+FIX

approach (for rfMRI only), and registered to the standard CIFTI grayordinate fsLR space using the MSM algorithm. The preprocessed task fMRI data were entered into a general linear model (GLM) to estimate fMRI activity at each vertex/voxel in each run with FSL (FMRIB's Software Library, [www.fmrib.ox.ac.uk/fsl](http://www.fmrib.ox.ac.uk/fsl)) (Barch et al., 2013). The boxcar convolved with a double gamma hemodynamic response function, and its temporal derivative was used to model the BOLD responses. Linear contrasts were computed to estimate effects of interest (e.g., faces vs. others). Fixed-effects analyses were conducted to estimate the average effects across runs within each participant.

### **Manual definition of pFus-faces/FFA-1 and mFus-faces/FFA-2**

Face-selective regions on the lateral fusiform gyrus (FG) were manually delineated for each hemisphere and each participant based on individual, thresholded ( $Z > 1.65$ ,  $p < 0.05$ , uncorrected) face-selective activation maps (faces versus others). From this thresholded map, face-selective regions were labeled as either mFus-faces/FFA-2 or pFus-faces/FFA-1 based on previously published criteria differentiating the cortical location of the two regions relative to sulci within and surrounding the FG.

Specifically, mFus-faces/FFA-2 is coupled with the anterior tip of the mid-fusiform sulcus (MFS) whereas pFus-faces/FFA-1 is located on the posterior aspect of the FG, extending into the occipito-temporal sulcus (Weiner, 2019; Weiner et al., 2014). To define each region, we implemented a three-pronged approach. First, author X.C. labeled each region manually on the individual thresholded face-selective map with a customized software (FreeROI, <https://github.com/BNUCNL/FreeROI>). Second, author Z.Z. checked the regions and refined them together with X.C. Third, author K.S.W. finalized the regions.

### **Probabilistic maps and MPMs**

A probabilistic map was created for each fusiform face-selective region to characterize the likelihood that a given vertex belongs to that region across all

participants on whom the region had been identified. Besides, a MPM was constructed to summarize the probabilistic maps of all regions into one map. Specifically, we assigned each vertex to the region to which the vertex had the highest probability of belonging. Thus, the MPM defined the most likely areas to which each vertex belonged. The vertices with a maximum probability smaller than a specific threshold were considered to not belong to either region. We provided the MPM with four thresholds: 0%, 10%, 25%, and 50%.

### **Three topological groups**

Overall, we categorized the spatial organization of mFus-faces/FFA-2 and pFus-faces/FFA-1 into three types, or topological groups: separate, continuous, and single. The “separate” group consisted of two cortically distinct face-selective regions in a given hemisphere that were separated by a cortical gap. The “continuous” group consisted of two regions that were identifiable and contiguous, but could be separated based on previously proposed anatomical criteria based on cortical folding (Weiner, 2019; Weiner et al., 2014). The “single” group consisted of one region in which either mFus-faces/FFA-2 or pFus-faces/FFA-1, but not both, was identifiable in a given hemisphere.

### **Split the HCP FFC**

Based on the probabilistic maps we created, the HCP FFC was split into pFus-faces/FFA-1 and mFus-faces/FFA-2 by assigning each of its vertices to the region to which the vertex had the highest probability of belonging.

### **Key, name, and rgba color of each FFA**

<pre>key2name = {   0: '???',   1: 'R_pFus-faces',   2: 'R_mFus-faces',   3: 'L_pFus-faces',   4: 'L_mFus-faces' }</pre>	<pre>key2rgba = {   0: (1.0, 1.0, 1.0, 0.0),   1: (0.0, 1.0, 0.0, 1.0),   2: (0.0, 0.0, 1.0, 1.0),   3: (0.0, 1.0, 0.0, 1.0),   4: (0.0, 0.0, 1.0, 1.0) }</pre>
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## Details for files

- ***subject\_id.txt*** includes 1053 subjects' IDs (one per line).
- ***group\_id.csv*** includes two columns named as left hemisphere (lh) and right hemisphere (rh) respectively. The values are group IDs of each of 2106 hemispheres. 0 means “single” group; 1 means “continuous” group; 2 means “separate” group.

## 32k\_fs\_LR space

- ***HCP-YA\_FFA-indiv.32k\_fs\_LR.dlabel.nii*** includes individual FFAs and subject IDs of 1053 participants, as well as the key, name, and rgba color of each FFA.
- ***HCP-YA\_FFA-prob.32k\_fs\_LR.dscalar.nii*** includes probabilistic maps of FFAs.
- ***HCP-YA\_FFA-MPM\_thr-0.32k\_fs\_LR.dlabel.nii*,**  
***HCP-YA\_FFA-MPM\_thr-10.32k\_fs\_LR.dlabel.nii*,**  
***HCP-YA\_FFA-MPM\_thr-25.32k\_fs\_LR.dlabel.nii*,** and  
***HCP-YA\_FFA-MPM\_thr-50.32k\_fs\_LR.dlabel.nii*** include the MPM with the threshold as 0%, 10%, 25%, and 50% respectively, as well as the key, name, and rgba color of each FFA.
- ***HCP-YA\_FFA-split.32k\_fs\_LR.dlabel.nii*** includes pFus-faces/FFA-1 and mFus-faces/FFA-2 split from the area “FFC” of the HCP MMP atlas, as well as the key, name, and rgba color of each FFA.

### *fsaverage space*

- ***HCP-YA\_FFA-indiv.164k\_fsavg\_LR.dlabel.nii*** includes individual FFAs and subject IDs of 1053 participants, as well as the key, name, and rgba color of each FFA.
- ***HCP-YA\_FFA-prob.164k\_fsavg\_LR.dscalar.nii*** includes probabilistic maps of FFAs.
- ***HCP-YA\_FFA-MPM\_thr-0.164k\_fsavg\_LR.dlabel.nii***,  
***HCP-YA\_FFA-MPM\_thr-10.164k\_fsavg\_LR.dlabel.nii***,  
***HCP-YA\_FFA-MPM\_thr-25.164k\_fsavg\_LR.dlabel.nii***, and  
***HCP-YA\_FFA-MPM\_thr-50.164k\_fsavg\_LR.dlabel.nii*** include the MPM with the threshold as 0%, 10%, 25%, and 50% respectively, as well as the key, name, and rgba color of each FFA.
- ***HCP-YA\_FFA-split.164k\_fsavg\_LR.dlabel.nii*** includes pFus-faces/FFA-1 and mFus-faces/FFA-2 split from the area “FFC” of the HCP MMP atlas, as well as the key, name, and rgba color of each FFA.

## Figures

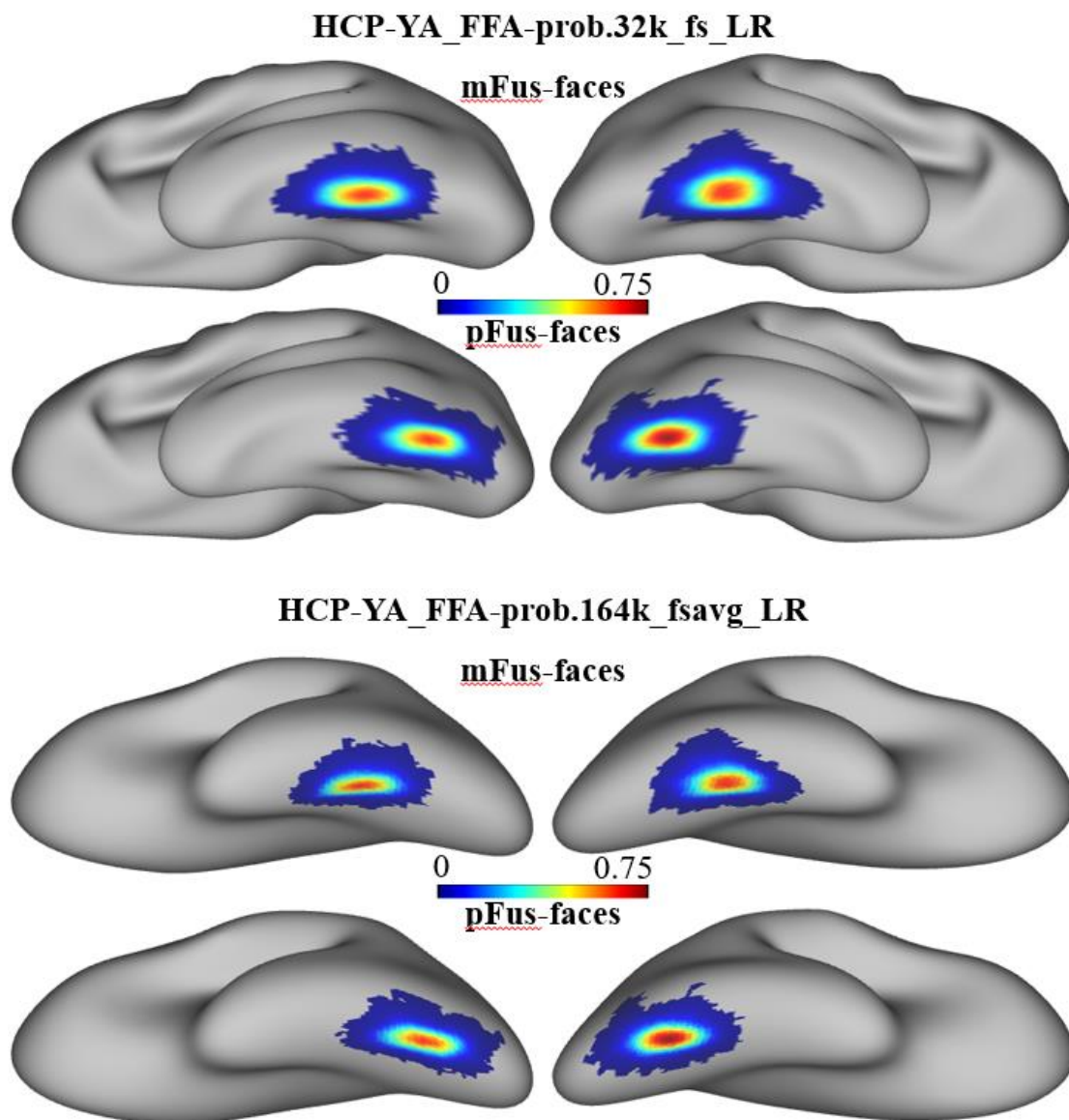


Figure 1. Probabilistic maps in 32k\_fs\_LR (top) and fsaverage (bottom) spaces.

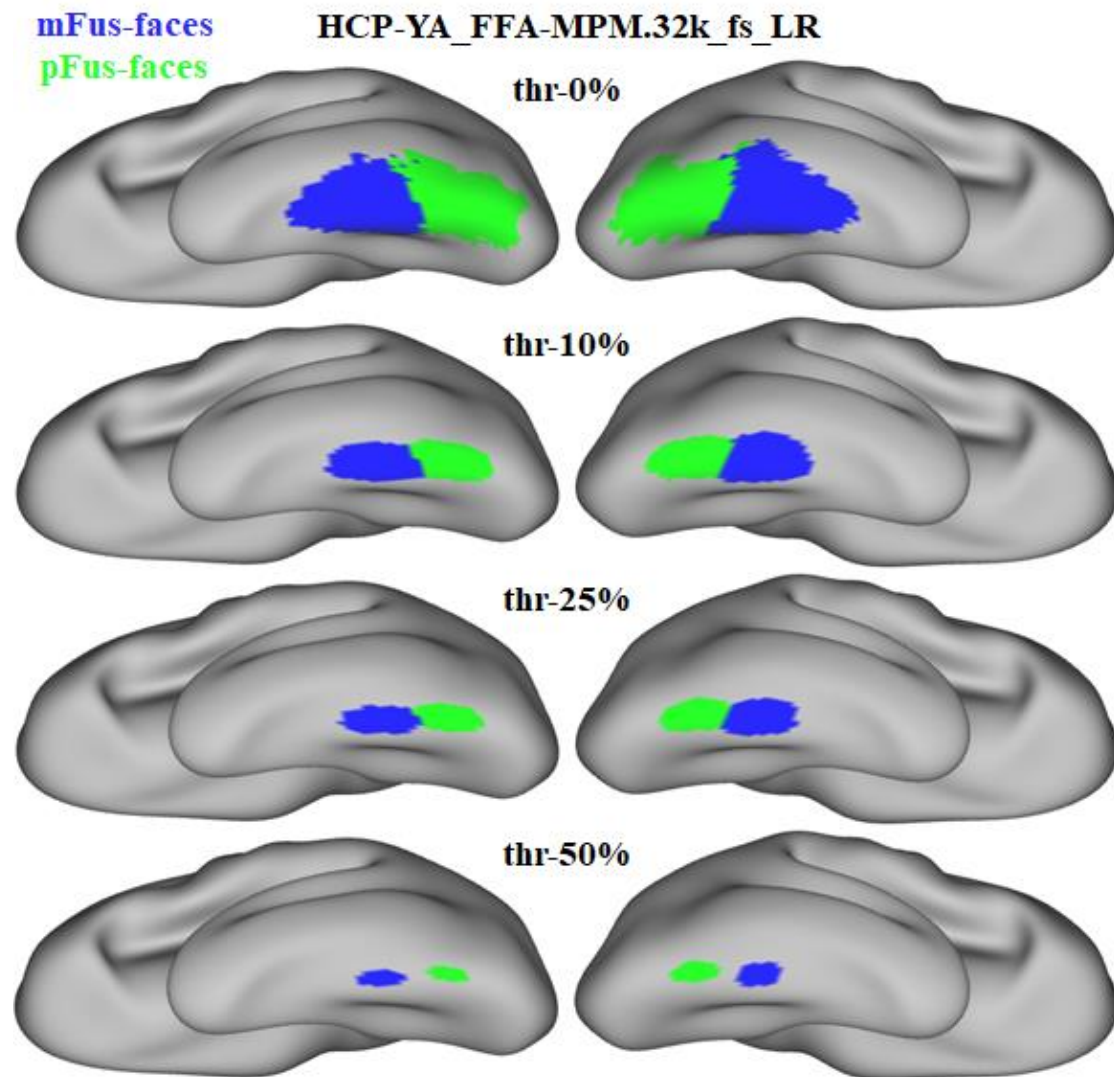


Figure 2. Maximum probability maps with thresholds as 0%, 10%, 25%, and 50% in 32k\_fs\_LR space.



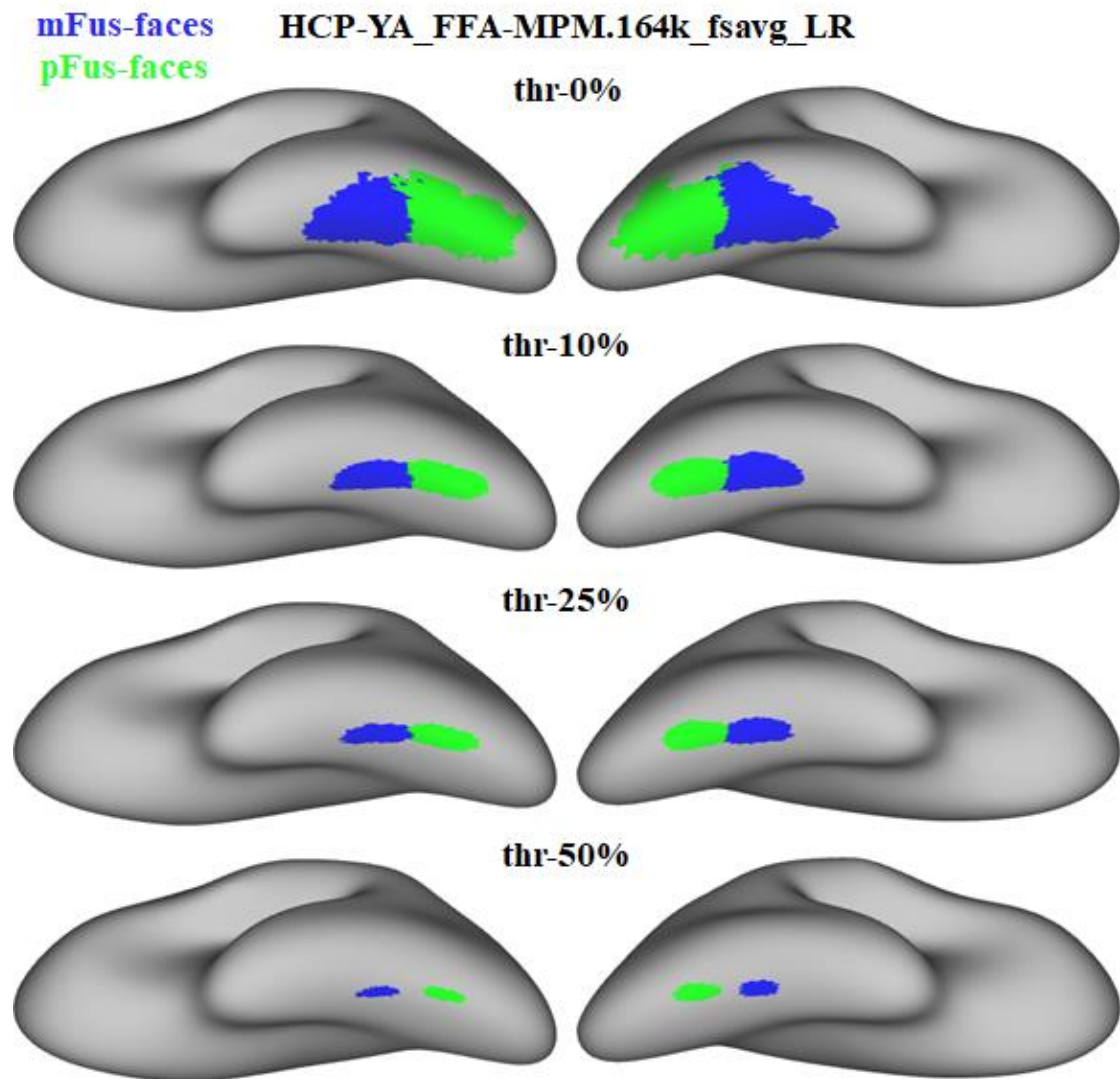


Figure 3. Maximum probability maps with thresholds as 0%, 10%, 25%, and 50% in fsaverage space.

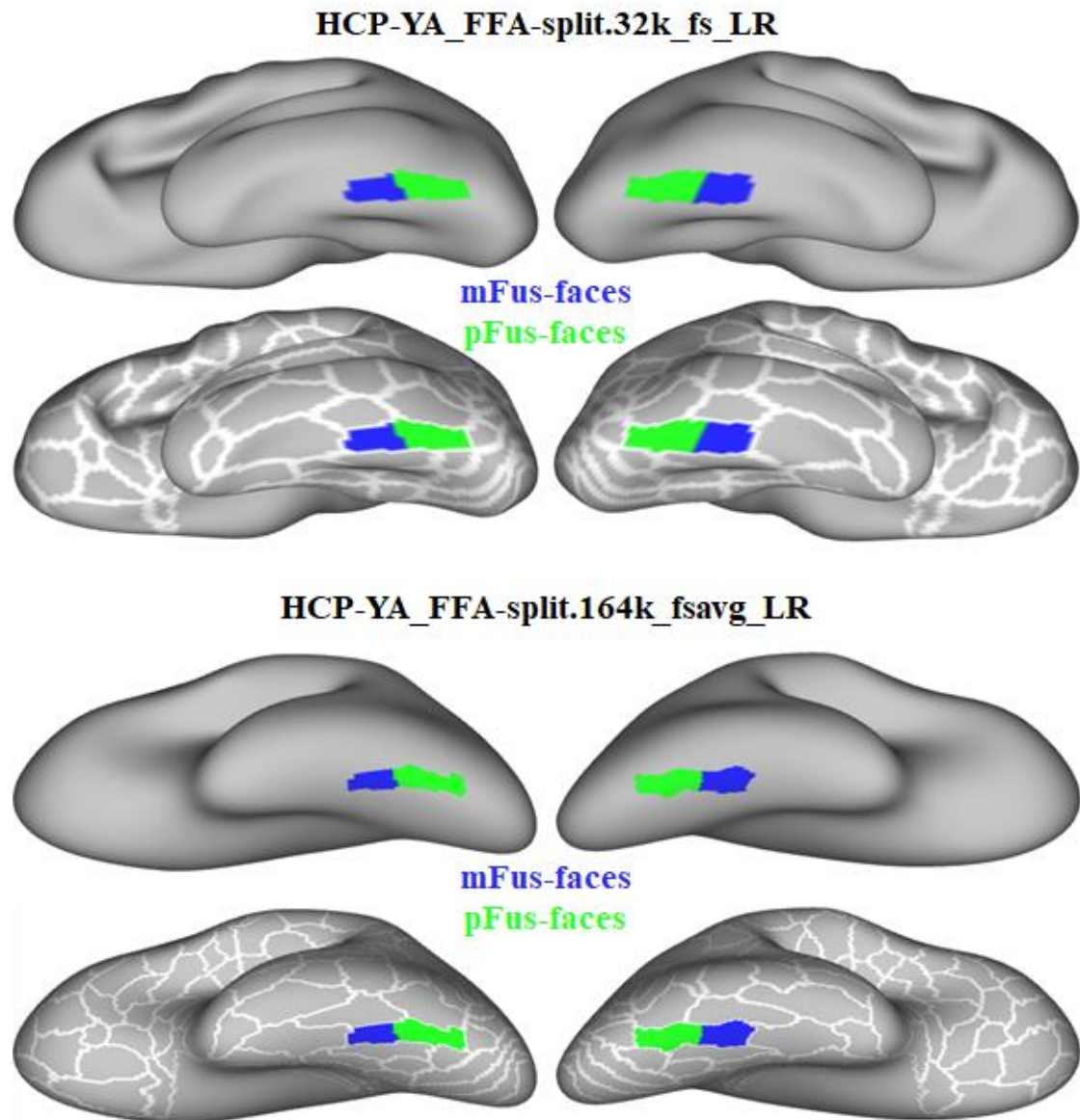


Figure 4. pFus-faces/FFA-1 (green) and mFus-faces/FFA-2 (blue) split from the HCP FFC in 32k\_fs\_LR (top) and fsaverage (bottom) spaces. White lines are outlines of areas in the HCP MMP Atlas.