

**Supplementary Material for “Brain resting state is disrupted in chronic back pain patients” (Tagliazucchi et al.)**

In Table S1 the location of seeds with high connectivity (hubs) is shown, together with their MNI152 atlas coordinates, AAL atlas region name, RSN's membership and abbreviation used throughout the paper.

Figure S1 shows average normalized degree distributions for all RSN's and link density  $\delta = 0.05$ . The degree of the selected seeds is located over the degree distributions.

Figure S2 illustrates the robustness of seed location for changes in the link density ( $\delta$ ) of the functional connectivity networks. Seed location in RSN5 is shown for  $\delta = 0.01, 0.05, 0.1, 0.5$ . Similar results are obtained when other RSN's are considered.

In Figure S3 the location of seeds in RSN5 and RSN6 obtained for 3 different subpopulations (group 1, group 2, group 1 + 2) is shown.

In Figure S4 the pairwise correlation between BOLD signal from three seeds in the DMN (where the correlation balance is broken in CBP) and different ROIs is shown for healthy controls and CBP patients. These ROIs include the insular cortices (increased functional connectivity in CBP), middle frontal gyrus (decreased functional connectivity in CBP) and two control sites (precuneus and inferior parietal cortex).

In figure S5 maps of seed based correlation are shown (in z-scores) for the three seeds located in the DMN.

In Figure S6 the mean quadratic distance (D) between the triggered average at the insular cortices and the seed (ORBmid, ANG.R, ANG.L) is shown for healthy subjects and CBP patients, as a function of the triggering threshold (in s.d.). The distance D is defined as the sum of the differences of the squares between both time series at each time point, averaged by the length of the series.

The triggered averaging procedure is shown in Figure S7. This procedure is illustrated with real data from a normal subject and the same data with randomized phases. This randomization provide for a null hypothesis of observing the same correlation by chance. For that the signals were Fourier transformed, their phases randomized and Inverse transformed. In that way the transformed signal preserved their frequency spectrum but their phase relation was destroyed. Figure S8 shows the triggered averages between ORBmid, ANG.R, ANG.L, Insula R, Insula L for BOLD signal with randomized phases.

In Figure S9 the triggered average computed using seeds in 7 regions (ORBmid, ANG.R, ANG.L, PCUN.R, IPC.R, Insula R, Insula L) is shown. Threshold was set to 1 s.d.

Coordinates	Region	Abbreviation	Independent Components
(2,-82,20)	Cuneus	CUN	RSN1
(30,-90,16)	Middle Occipital Gyrus	MOG.R	RSN2
(-26,-90,16)	Middle Occipital Gyrus	MOG.L	RSN2
(2,6,44)	Median Cingulate and Paracingulate Gyri	DCG	RSN3, RSN6, RSN7
(-54,2,-8)	Superior Temporal Gyrus	STG.L(1)	RSN3, RSN6
(8,2,-4)	Superior Temporal Gyrus	STG.R(1)	RSN3, RSN6, RSN7
(62,-22,16)	Superior Temporal Gyrus	STG.L(2)	RSN3
(-58,-22,8)	Superior Temporal Gyrus	STG.R(2)	RSN3
(-2,-14,48)	Supplementary Motor Area	SMA	RSN4
(-38,-14,52)	Postcentral Gyrus	PoCG.L	RSN4
(50,-14,52)	Postcentral Gyrus	PoCG.R	RSN4
(2,54,-8)	Middle Frontal Gyrus, Orbital Part	ORBmid	RSN5
(2,-62,44)	Precuneus	PCUN	RSN5
(50,-66,28)	Angular Gyrus	ANG.R	RSN5
(-46,-70,28)	Angular Gyrus	ANG.L	RSN5
(34,46,20)	Middle Frontal Gyrus	MFG.R(1)	RSN6, RSN7
(-34,42,20)	Middle Frontal Gyrus	MFG.L	RSN6
(10,-42,28)	Precuneus	PCUN.R(1)	RSN6, RSN7
(58,-38,28)	Supramarginal Gyrus	SMG.R	RSN6
(-58,-42,28)	Supramarginal Gyrus	SMG.L	RSN6
(10,-68,52)	Precuneus	PCUN.R(2)	RSN7
(38,-2,60)	Middle Frontal Gyrus	MFG.R(2)	RSN7
(54,-62,-8)	Inferior Temporal Gyrus	ITG.R	RSN7, RSN8
(38,-66,48)	Inferior Parietal Cortex	IPC.R	RSN7
(-6,-70,56)	Precuneus	PCUN.L	RSN8
(-54,-62,-16)	Inferior Temporal Gyrus	ITG.L	RSN8
(-30,-6,64)	Superior Frontal Gyrus	SFG.L	RSN8

Table S1: MNI152 atlas coordinates, regions, abbreviations and RSN's membership for all the 27 high connectivity seeds (hubs)

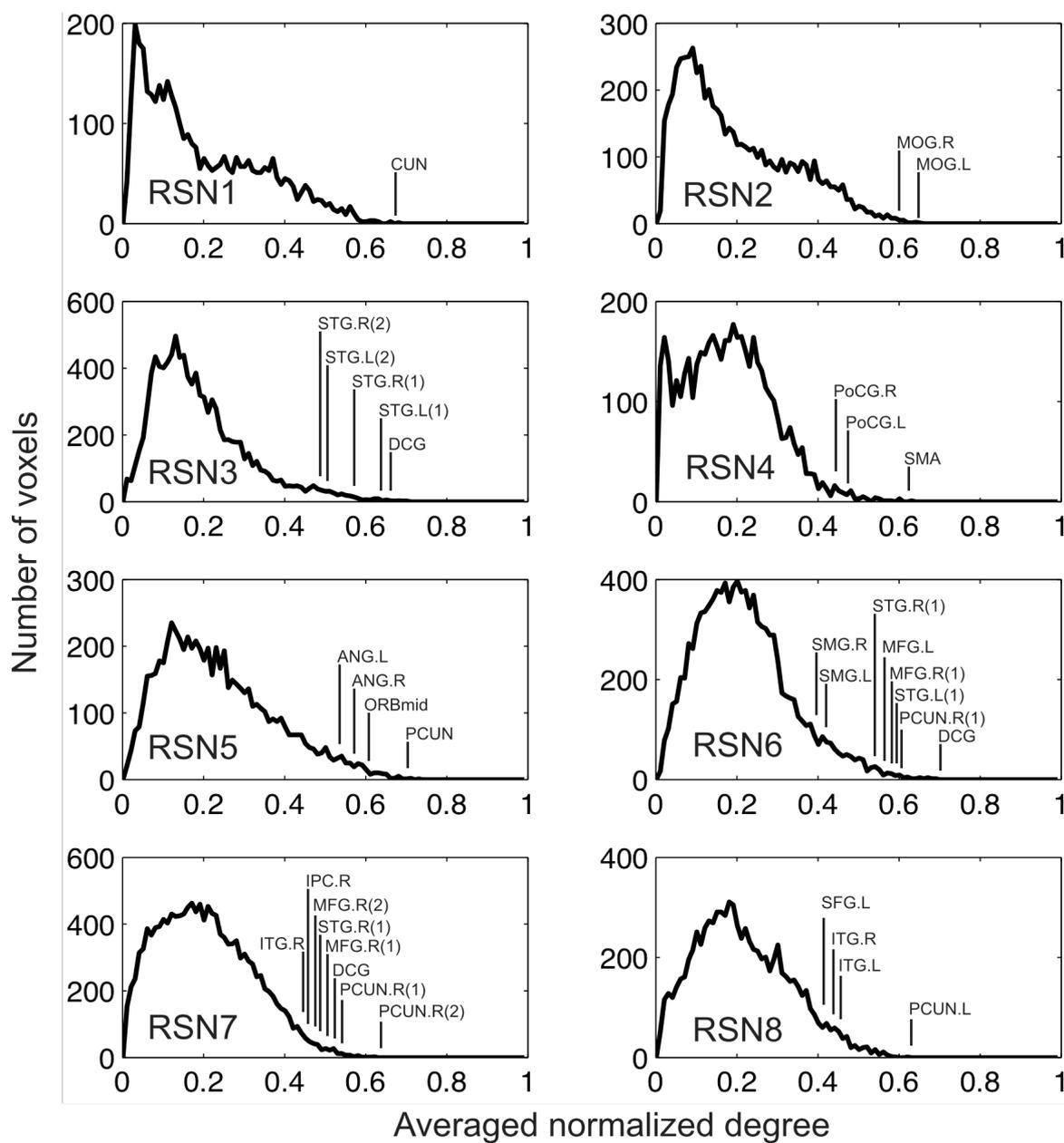


Figure S1: Average normalized degree distributions for all RSN's and  $\delta = 0.05$ . Degree of the seeds is indicated above the curve.

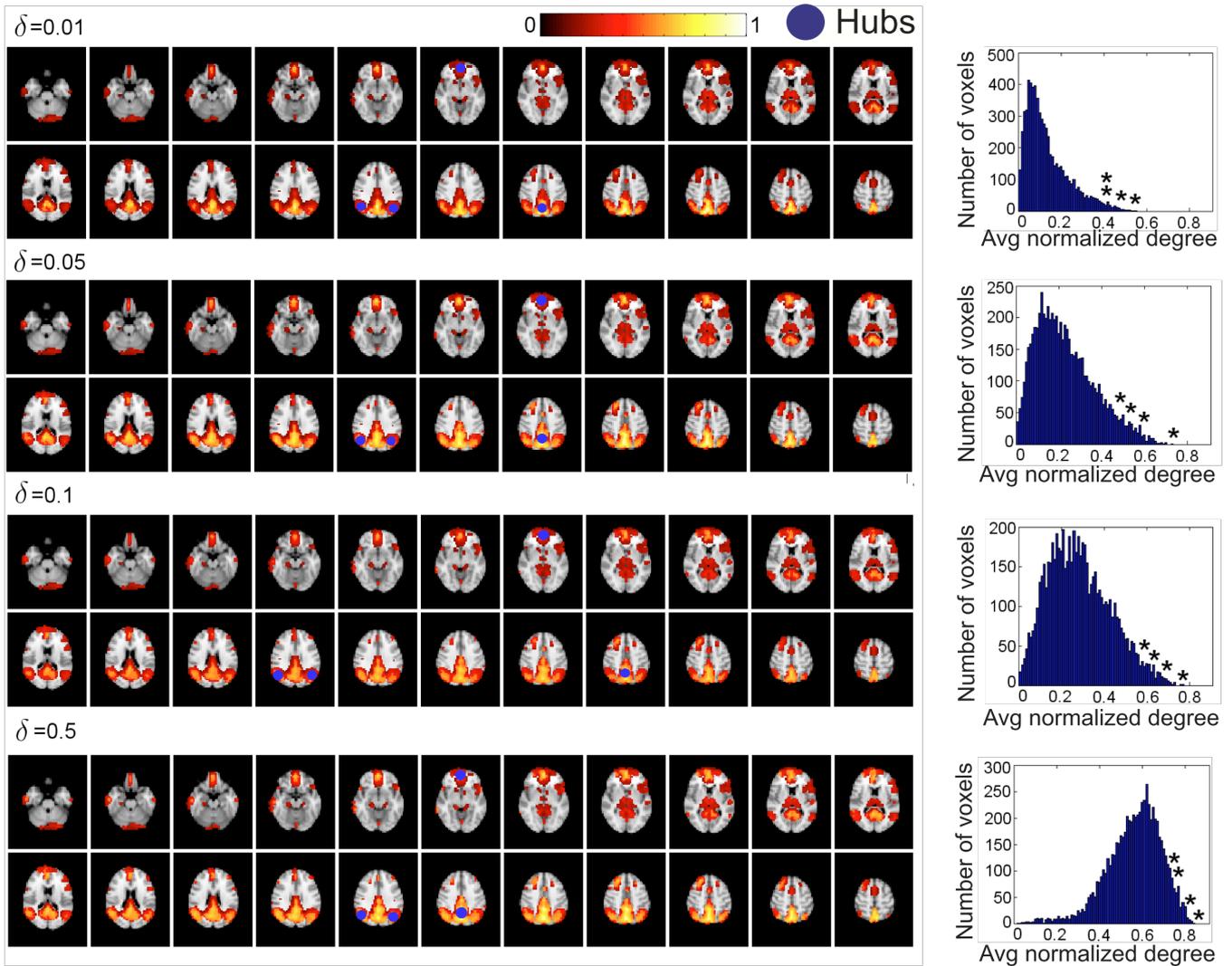


Figure S2: Left: Location of selected high connectivity seeds in RSN5, obtained for link density of  $\delta = 0.01, 0.05, 0.1, 0.5$ . Right: Average normalized degree distributions of RSN5 for the same values of  $\delta$ . Degree of the selected seeds is indicated with an asterisk (\*) above the distribution curve.

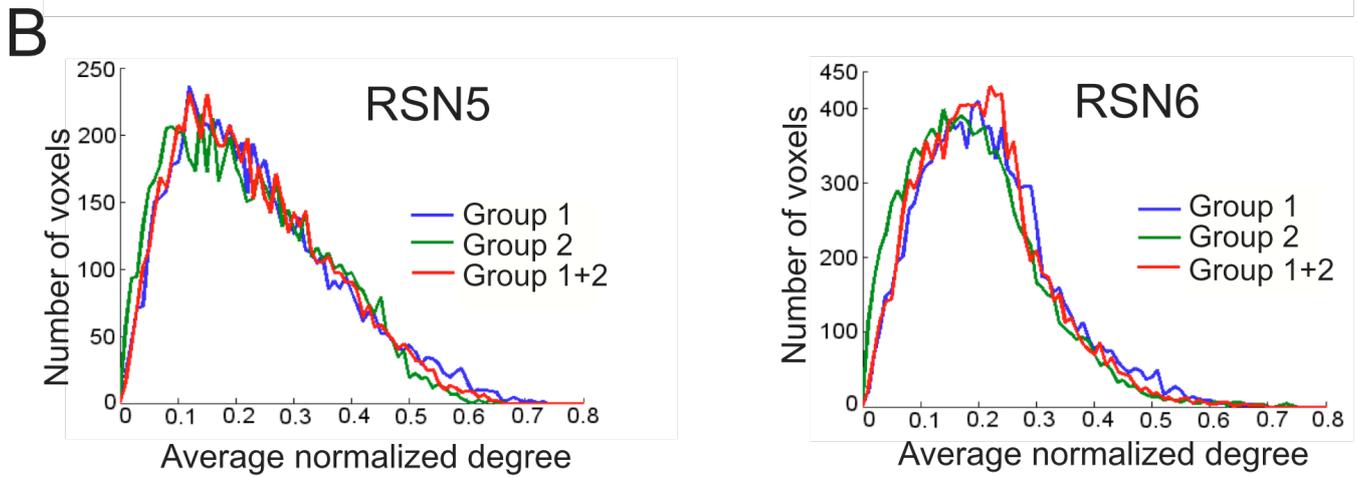
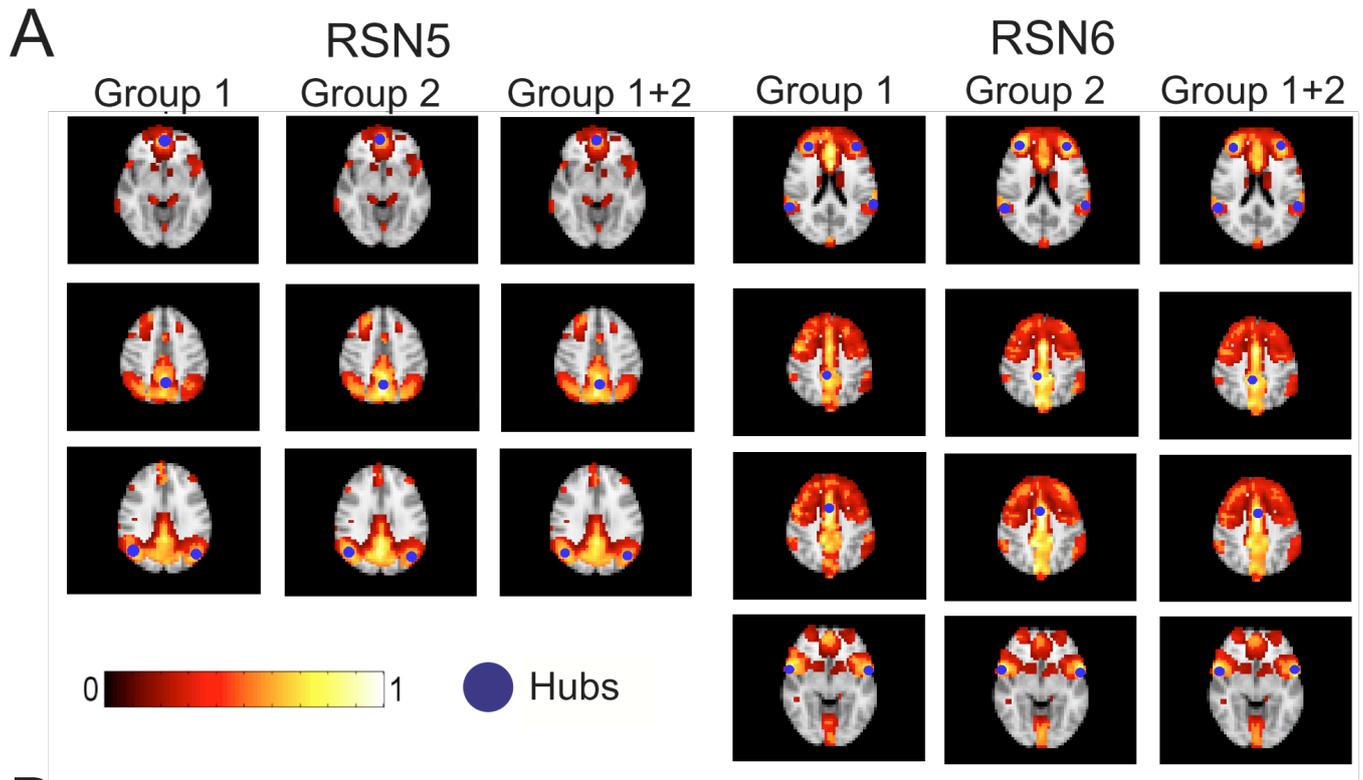


Figure S3: A. Location of hubs in RSN5 and RSN6 for 3 different subpopulations (group 1, group 2, group 1 + 2). B. Average normalized degree distributions of both RSN's for the 3 different groups.

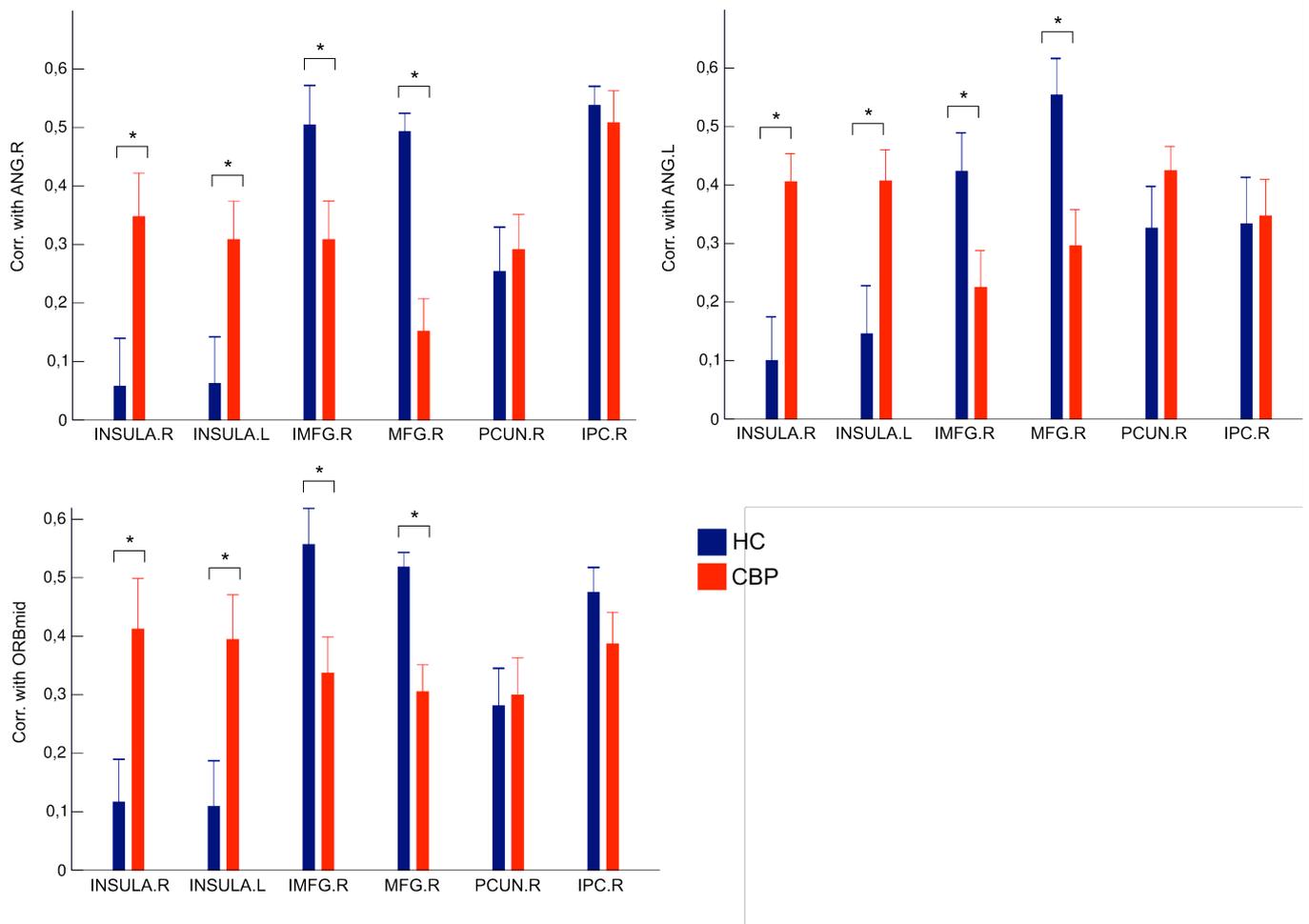


Figure S4: Pairwise correlation between BOLD signal at seeds in DMN (ANG.R, ANG.L, and ORBmid) and the insular cortices, middle frontal gyrus (MFG) and two control sites (PCUN.R, IPC.R). Asterisks (\*) indicate t-test significant differences ( $p < 0.05$ )

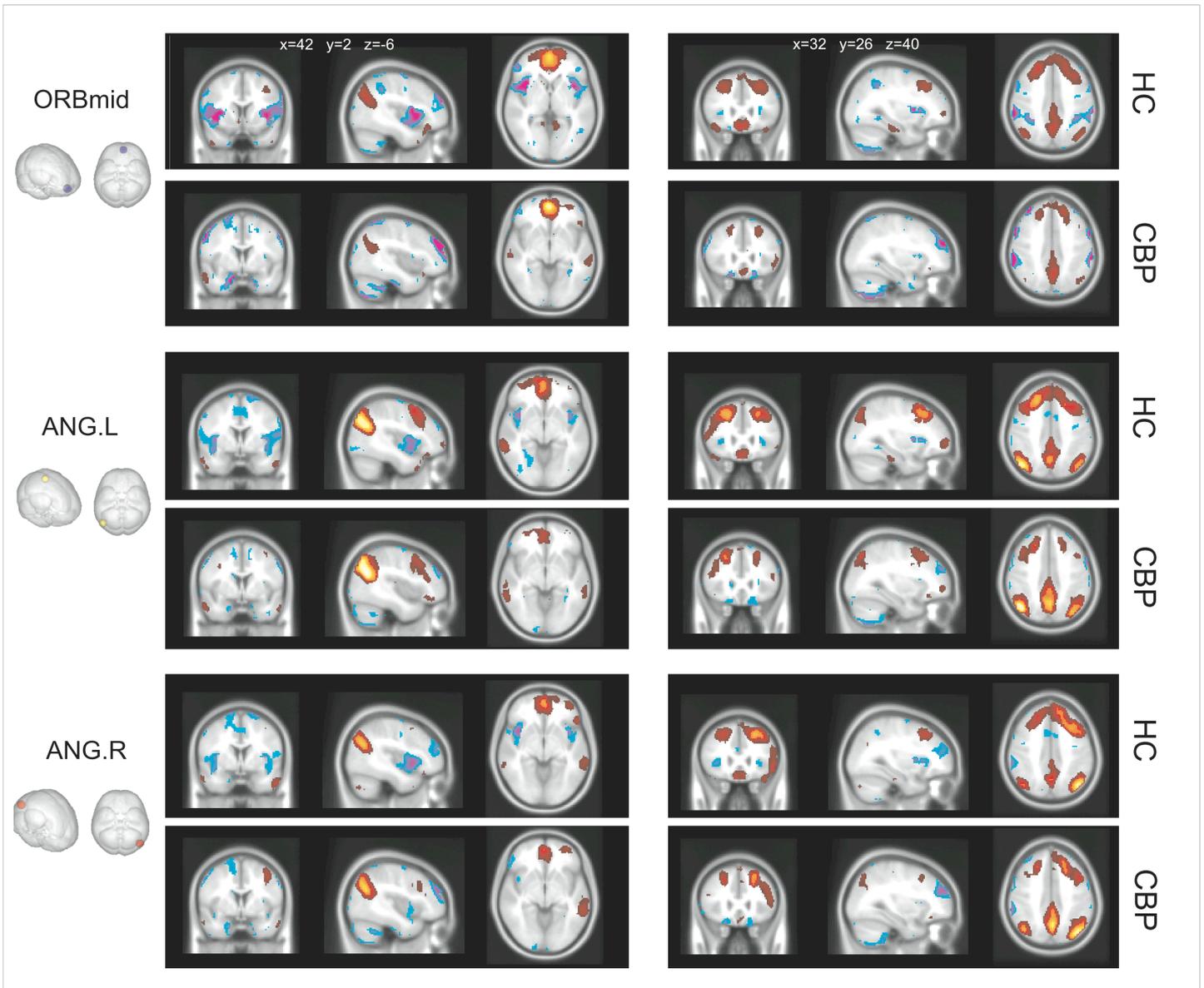


Figure S5: Value of linear correlation of all grey matter voxels with three seeds located at the DMN (thresholded at  $z = 2$ ) for healthy controls (HC) and CBP patients.

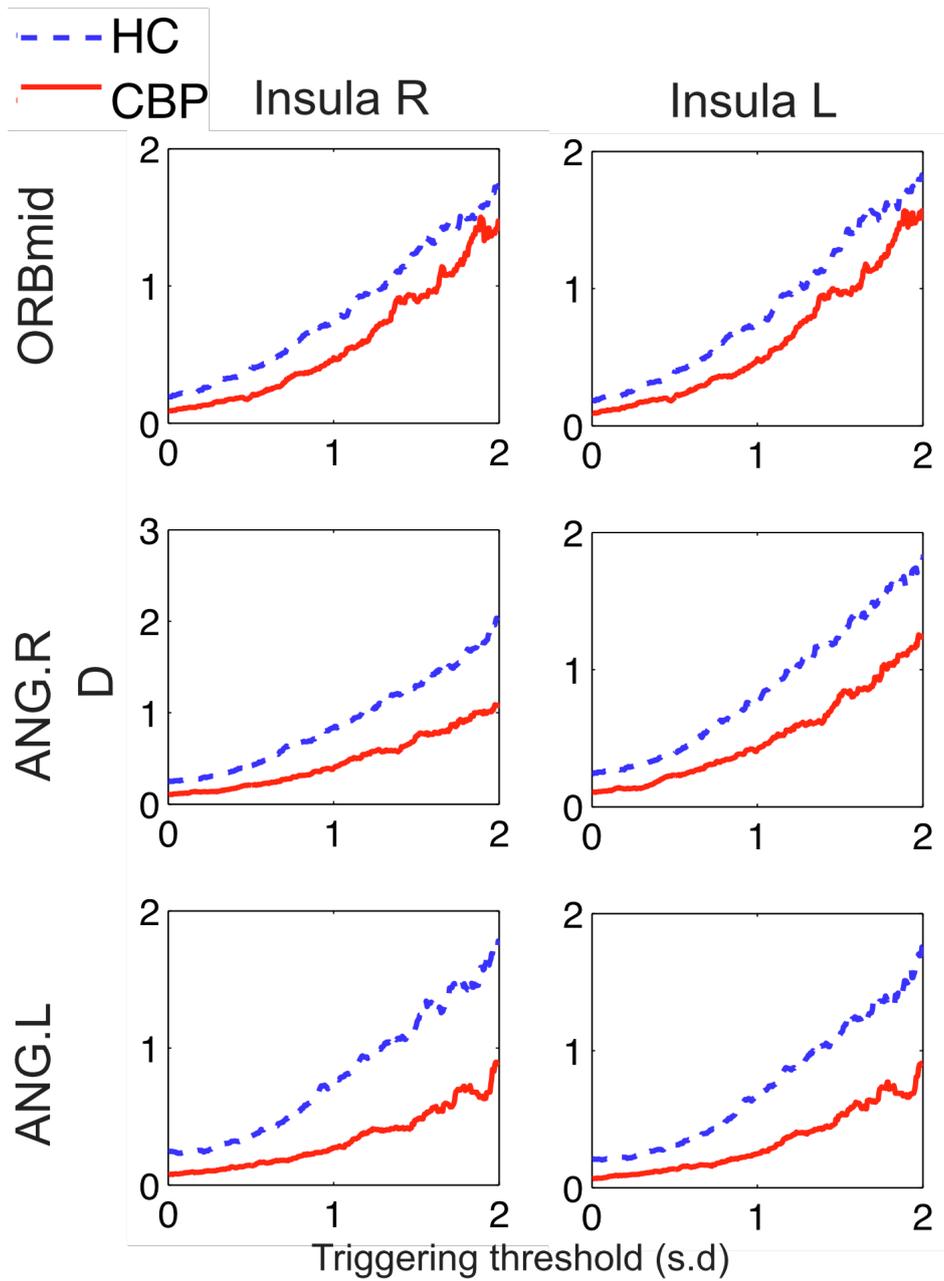


Figure S6: Mean quadratic distance (D) between the triggered average at the insular cortices and the seed (ORBmid, ANG.R, ANG.L) is shown for healthy controls (HC) and patients (CBP).

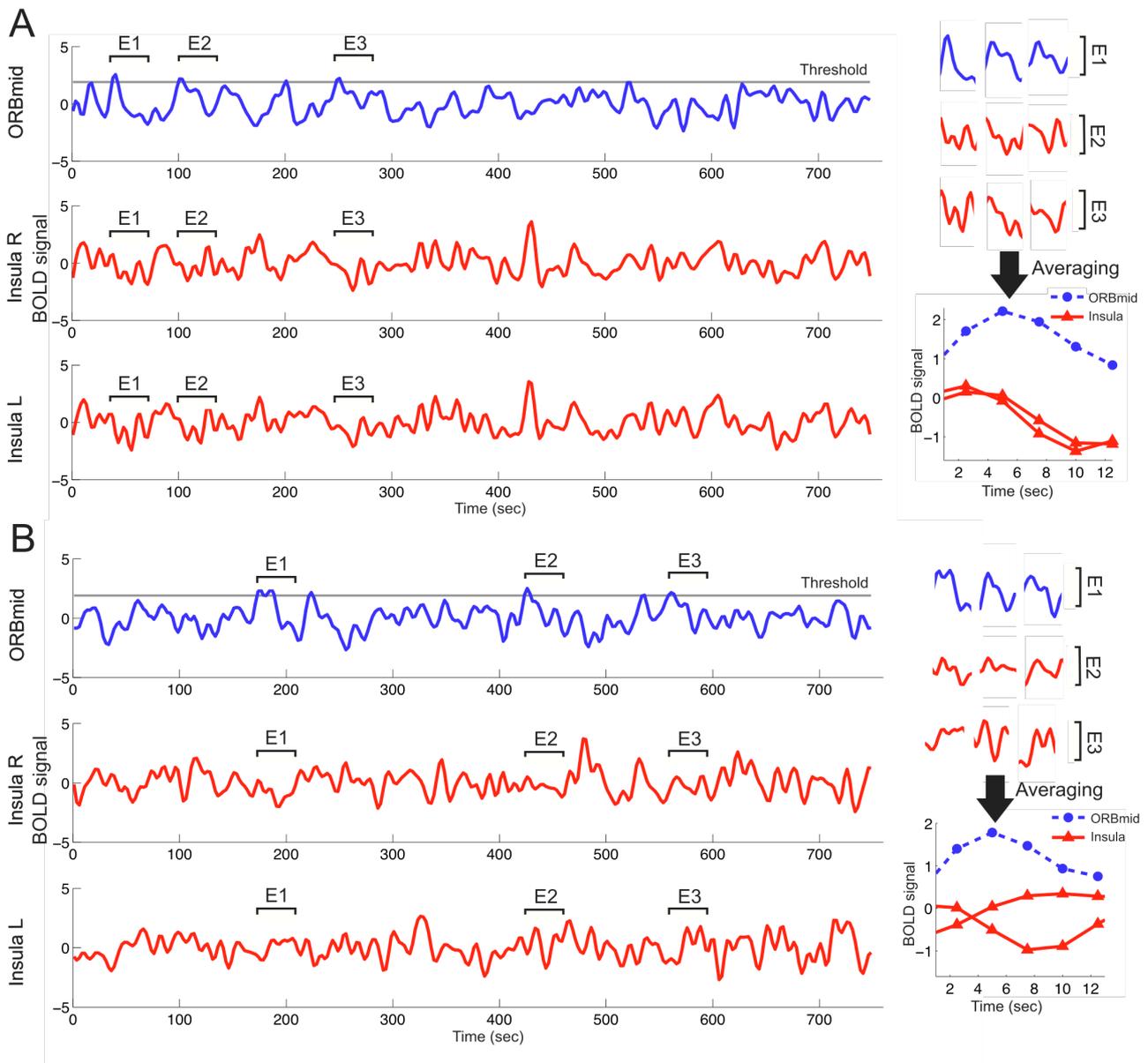


Figure S7: Procedure to construct triggered averages.

A. Whenever the BOLD signal at the seed (ORBmid) crosses an arbitrary threshold, an event is defined (in this example, events are E1, E2 and E3) and the signal is extracted over a time window after the onset of the event, both at the seed and the insular cortices. The extracted time series are then averaged.

B. The procedure when applied to a data with the same spectral properties as in A but with their phases randomized using Fourier transform.

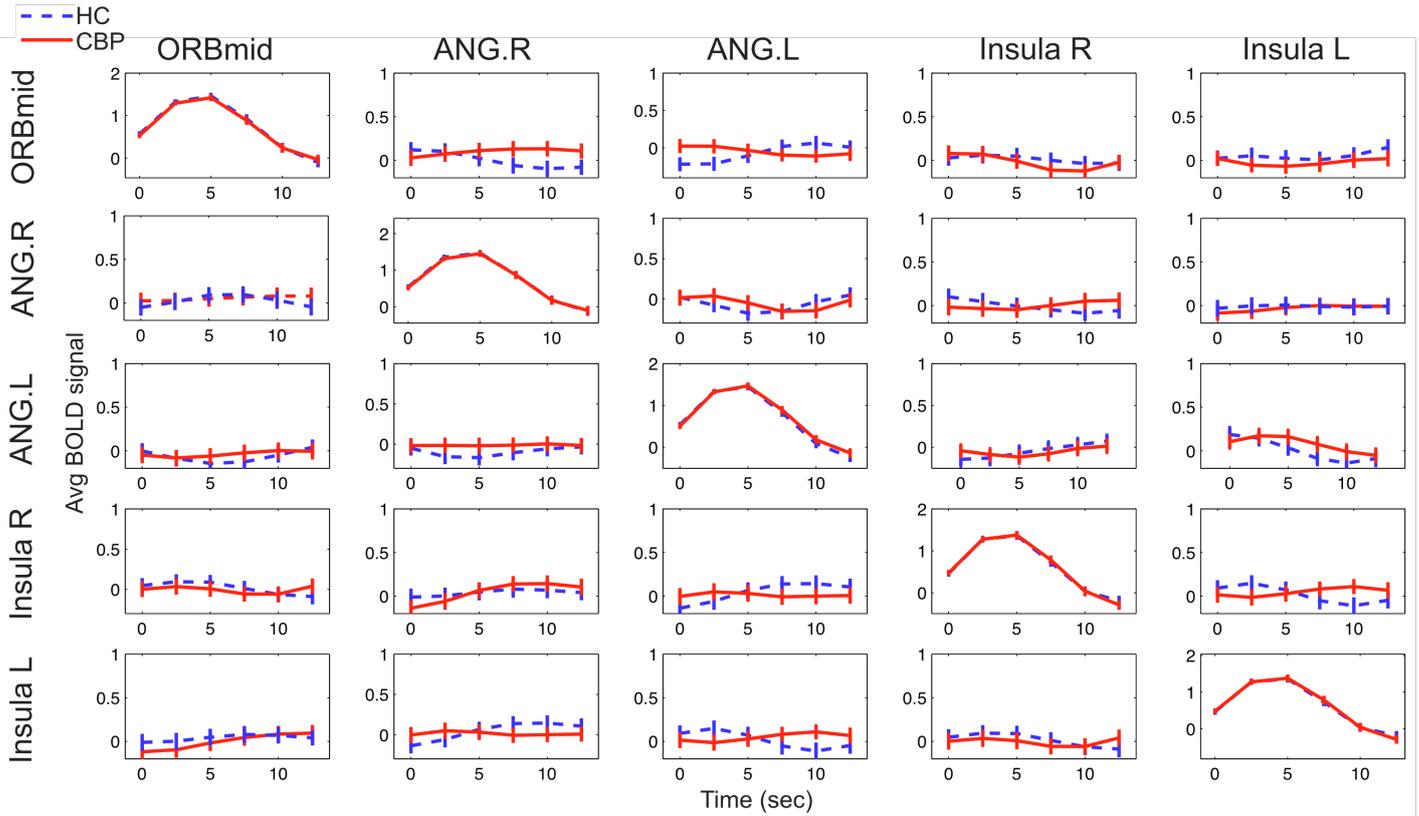


Figure S8: Triggered averages between five different seeds for BOLD signal with randomized phases. Columns define which signal is triggered to define the events and rows correspond to the average extracted from the signal at the different regions after the onset of the events. For example, the panel located at boxes (2,1) is the average of ANG.R when signal at ORBmid is used to trigger the average. Threshold was set to 1 s.d. Results are shown for healthy controls (HC) and patients (CBP). Notice that as expected in all cases except those in the diagonal the average is null.

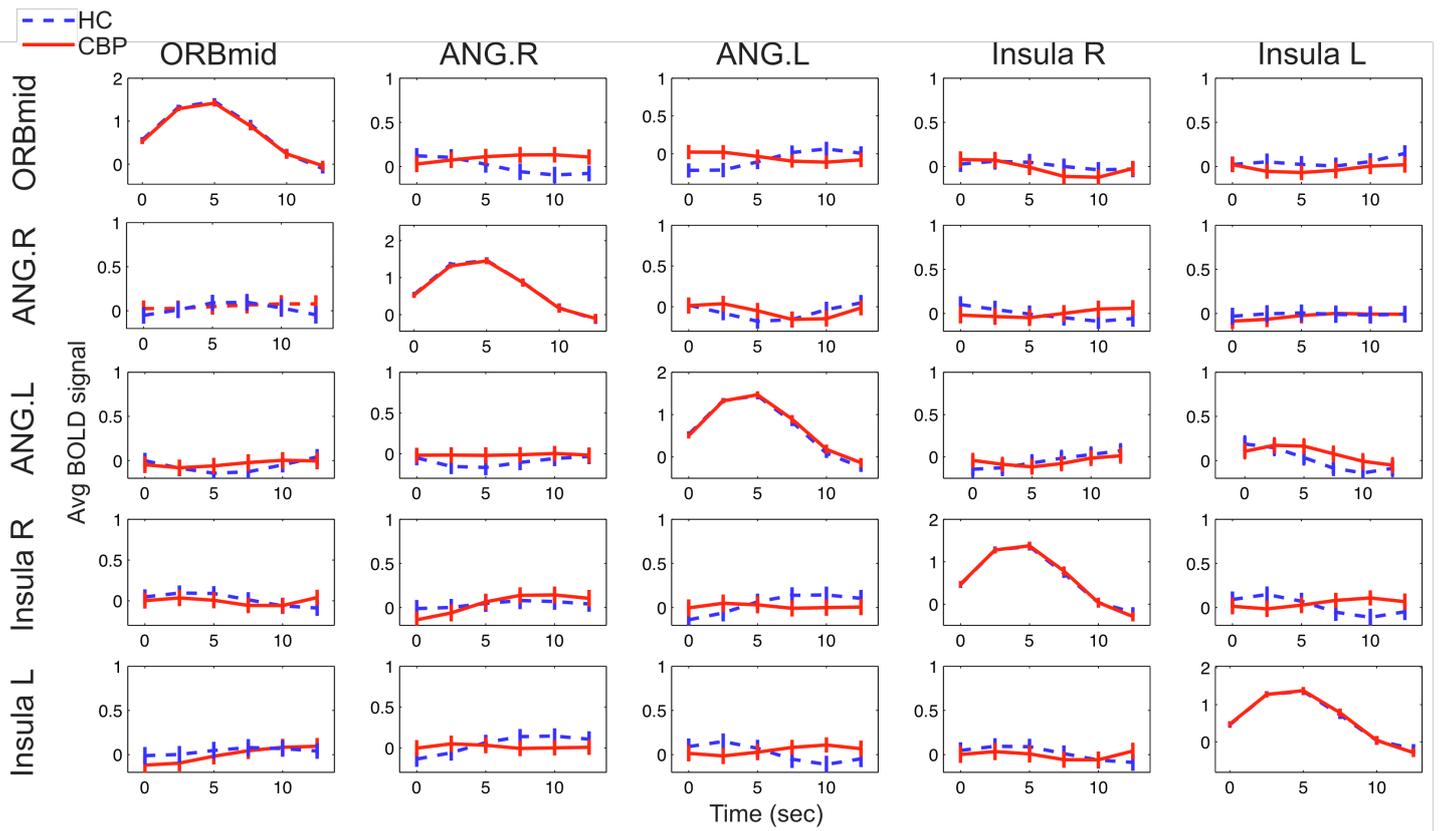


Figure S9: Triggered averages between 7 different seeds. Columns define which signal is triggered to define the events and rows are the average over the signals extracted at the different regions after the onset of the events. Threshold was set to 1 s.d.. Results are shown for healthy controls (HC) and patients (CBP).