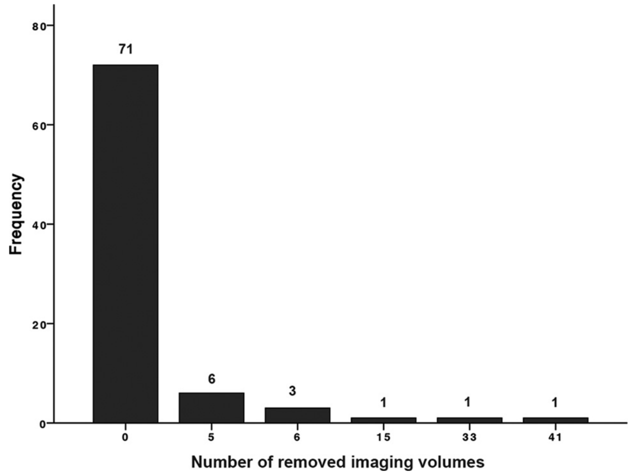
On-line Table: Brain regions with significant differences in binarized DC maps between patients with T2DM and healthy controls[a]

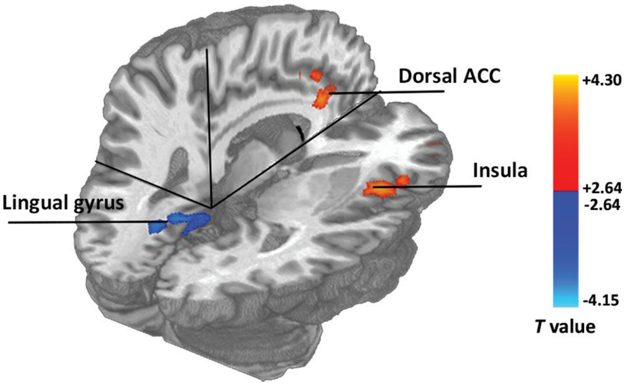
Brain Regions	MNI			Voxels	Peak *t*-Value
	X	Y	Z		
RAI	+42	+15	+0	40	+4.09
dACC	+6	+30	+24	32	+3.92
L lingual gyrus	−15	−51	−3	33	−3.60

Note:—MNI indicates Montreal Neurological Institute; RAI, right anterior insula; L, left.

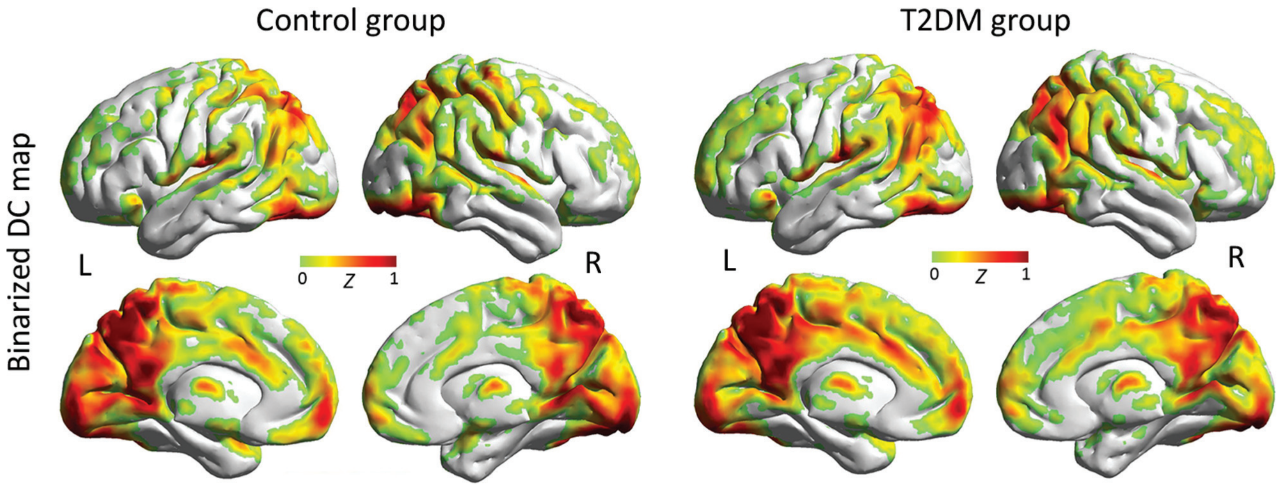
[a] Comparisons were performed at $P < .05$, corrected by AlphaSim multiple comparisons. X, y, and z are coordinates of primary peak locations in the MNI space. Positive *t*-values are T2DM > control subjects. Negative *t*-values are T2DM < control subjects.



ON-LINE FIG 1. The distribution of the number of removed imaging volumes among all the participants. In most of our participants ($n = 71$), no imaging volume was removed. The largest number of removed volumes was 41 ($n = 1$). Therefore, the scrubbing procedure implemented in our study was acceptable and did not have much effect on the overall statistical power of the DC calculation.



ON-LINE FIG 3. Group differences of binarized DC maps between patients with T2DM and healthy controls ($P < .05$, AlphaSim-corrected). Patients with T2DM show a significantly decreased value (cool color) in the left lingual gyrus and increased values (warm color) in the dACC and the right anterior insula, similar to the weighted DC results. The color scale denotes the *t*-value.



ON-LINE FIG 2. Spatial distribution of binarized DC maps in patients with T2DM and healthy controls ($P < .05$, family-wise error–corrected). The binarized DC map shows a spatial distribution similar to that of the weighted map. Standardized DC values are significantly higher in the posterior cingulate, visual cortex, medial prefrontal cortex, insula, and thalamus than the global mean values in both groups. R indicates right; L, left.