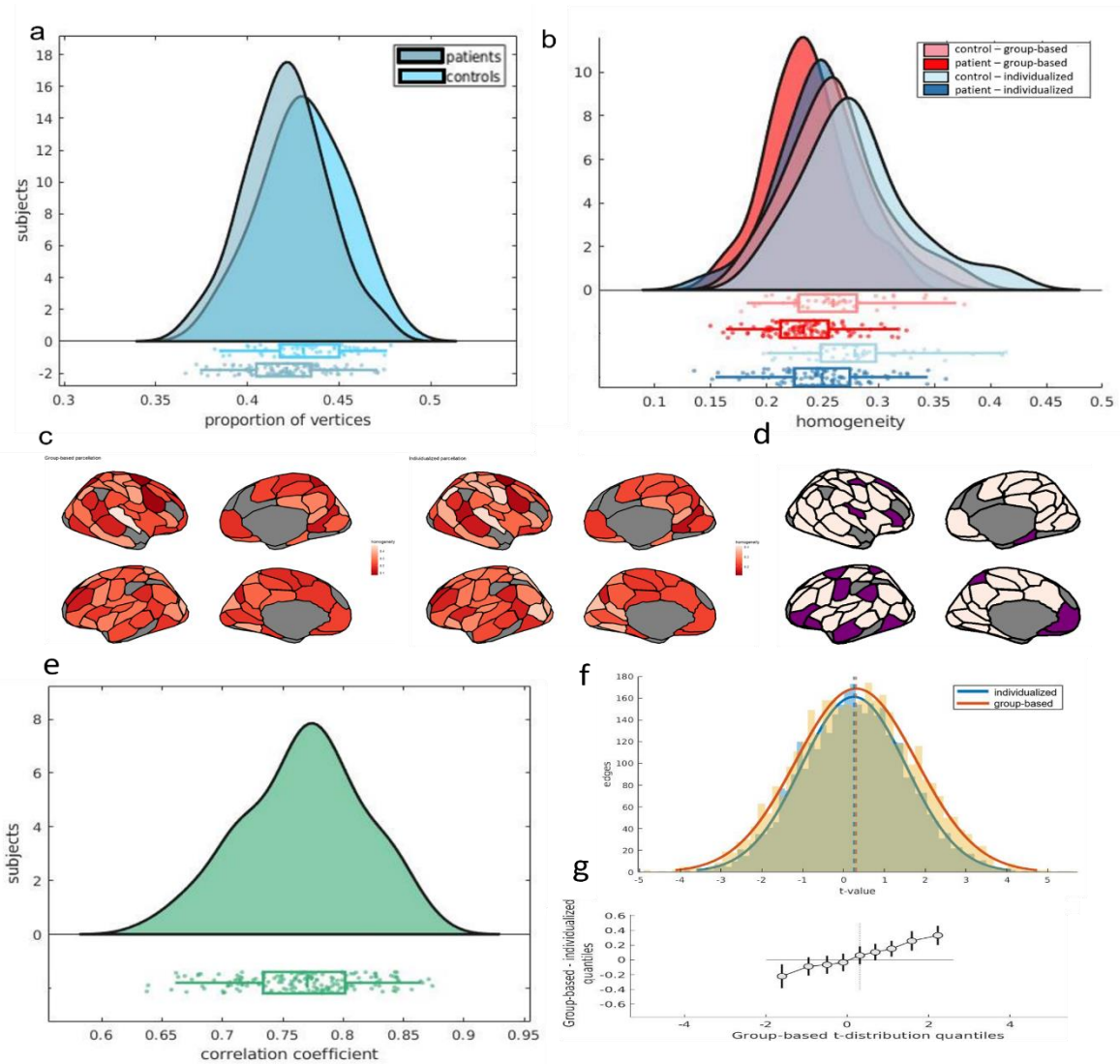


# 1 Supplementary Materials

## 2 Spatial and functional properties of group-based vs individualized 3 parcellation



4

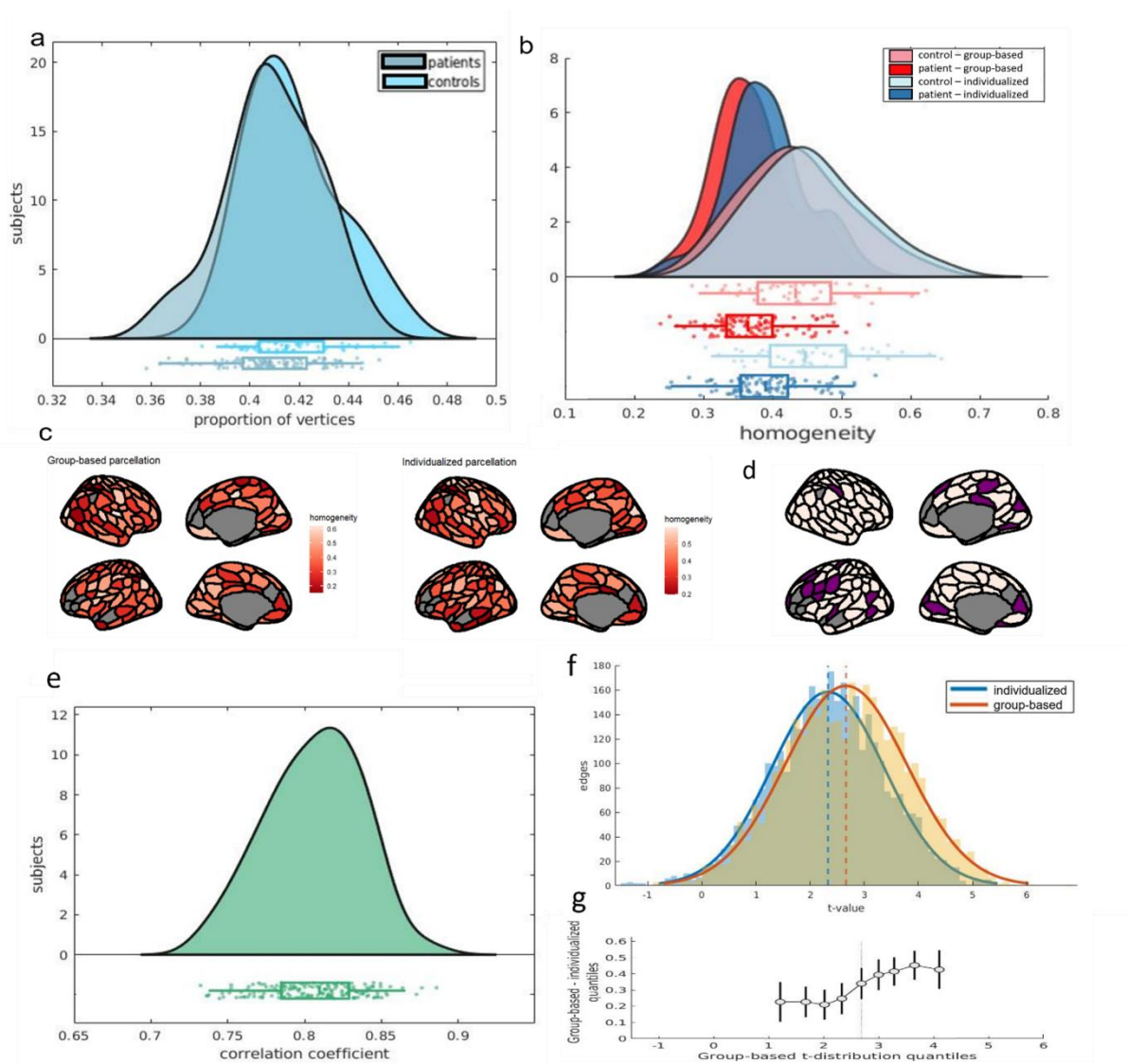
### 5 **Figure 1 - Spatial and functional properties of group-based vs individualized parcellation,**

6 **based on s100 GSR. a** The proportion of vertices changed for controls ( $M(SD) =$   
7  $0.431(0.023)$ ) and for patients ( $M(SD) = 0.421(0.022)$ ). There were slightly more vertices  
8 relabelled in controls than in patients  $t(165) = 2.448, p = 0.0077$  95% $CI = [0.003, 0.017]$ .

9 **b** The distribution of homogeneity scores per subject. Mean homogeneity for the group

10 parcellation in controls was 0.261 ( $SD = 0.04$ ), and 0.281 ( $SD = 0.05$ ) for the individualized  
11 parcellation. In patients, the mean homogeneity for the group parcellation was 0.235 ( $SD =$   
12  $0.04$ ) and 0.250 ( $SD = 0.04$ ) for the individualized parcellation. A two-way mixed ANOVA  
13 revealed that mean homogeneity was higher for the individualized parcellation ( $F(148) =$   
14  $234.91, p < 0.0001$ ) and higher in controls compared to patients ( $F(148) = 15.72, p =$   
15  $0.0001$ ), with an interaction between parcellation type and diagnosis ( $F(148) = 4.68, p =$   
16  $0.032$ ). Panel **c** shows homogeneity scores for every parcel for group-based and individualized  
17 parcellation. Light colored parcels in **d** represent parcels showing significant difference in  
18 homogeneity scores, between parcellation approaches, for  $p_{FDR} < 0.05$ . Homogeneity is  
19 displayed in inflated surfaces with the group-based parcellation. **e** The distribution of the  
20 Pearson's coefficient of correlation comparing FC matrices derived from group-based and  
21 individualized parcellation. Matrices were positively correlated and ranged between 0.637 and  
22 0.874 (median = 0.770). **f** Distributions of  $t$ -values quantifying FC differences between patients  
23 and controls at each edge and for individualized parcellation ( $M(SD) = 0.253(1.28)$ ) and for  
24 group-based parcellation ( $M(SD) = 0.310(1.48)$ ). The difference between the individualized  
25 and group-based parcellations were statistically significant, according to a Wilcoxon Sign Rank  
26 Test ( $Z = 3.471, p < 0.0001$ ). **g** Shift function for the two  $t$ -distributions. Each circle  
27 represents the difference between each decile of both distributions, as a function of the deciles  
28 in group-based distribution and the bars represent the 95% boot-strap confidence interval  
29 associated with the difference.

30



31

32 **Figure 2 - Spatial and functional properties of group-based vs individualized parcellation,**

33 **based on s200. a** The proportion of vertices changed for controls ( $M(SD) =$

34  $0.418(0.019)$ ) and for patients ( $M(SD) = 0.409(0.020)$ ). There were slightly more vertices

35 relabelled in controls than in patients  $t(163) = 2.448, p = 0.0078$  95%CI = [0.002, 0.015].

36 **b** The distribution of homogeneity scores per subject. Mean homogeneity for the group

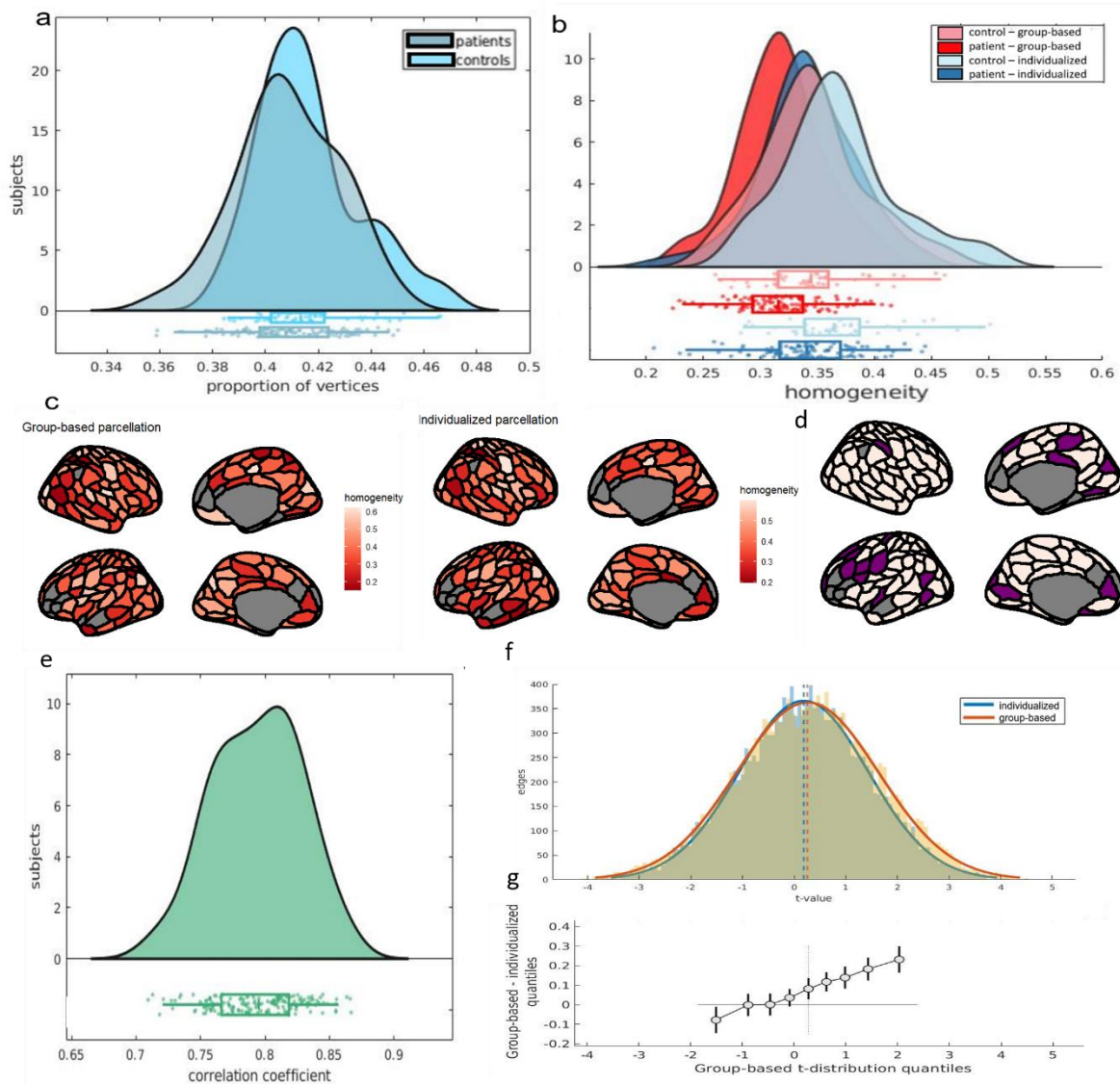
37 parcellation in controls was 0.434 ( $SD = 0.08$ ), and 0.454 ( $SD = 0.08$ ) for the individualized

38 parcellation. In patients, the mean homogeneity for the group parcellation was 0.371 ( $SD =$

39 0.06) and 0.392 ( $SD = 0.06$ ) for the individualized parcellation. A two-way mixed ANOVA

40 revealed that mean homogeneity was higher for the individualized parcellation ( $F(148) =$

41 901.60,  $p < 0.0001$ ) and higher in controls compared to patients ( $F(148) = 29.33, p <$   
42  $0.0001$ ), with no interaction between parcellation type and diagnosis ( $F(148) = 0.708, p =$   
43  $0.402$ ). Panel **c** shows homogeneity scores for every parcel for group-based and individualized  
44 parcellation. Light colored parcels in **d** represent parcels showing significant difference in  
45 homogeneity scores, between parcellation approaches, for  $p_{FDR} < 0.05$ . Homogeneity is  
46 displayed in inflated surfaces with the group-based parcellation. **e** The distribution of the  
47 Pearson's coefficient of correlation comparing FC matrices derived from group-based and  
48 individualized parcellation. Matrices were positively correlated and ranged between 0.732 and  
49 0.886 (median = 0.810). **f** Distributions of  $t$ -values quantifying FC differences between patients  
50 and controls at each edge and for individualized parcellation ( $M(SD) = 2.330(1.04)$ ) and for  
51 group-based parcellation ( $M(SD) = 2.663(1.13)$ ). The difference between the individualized  
52 and group-based parcellations were statistically significant, according to a Wilcoxon Sign Rank  
53 Test ( $Z = 24.053, p < 0.0001$ ). **g** Shift function for the two  $t$ -distributions. Each circle  
54 represents the difference between each decile of both distributions, as a function of the deciles  
55 in group-based distribution and the bars represent the 95% boot-strap confidence interval  
56 associated with the difference.



57

58 **Figure 3 - Spatial and functional properties of group-based vs individualized parcellation,**

59 **based on s200 GSR. a** The proportion of vertices changed for controls ( $M(SD) =$

60  $0.416(0.019)$ ) and for patients ( $M(SD) = 0.409(0.019)$ ). There were slightly more vertices

61 relabelled in controls than in patients  $t(163) = 2.479, p = 0.0071$  95%CI = [0.001, 0.014].

62 **b** The distribution of homogeneity scores per subject. Mean homogeneity for the group

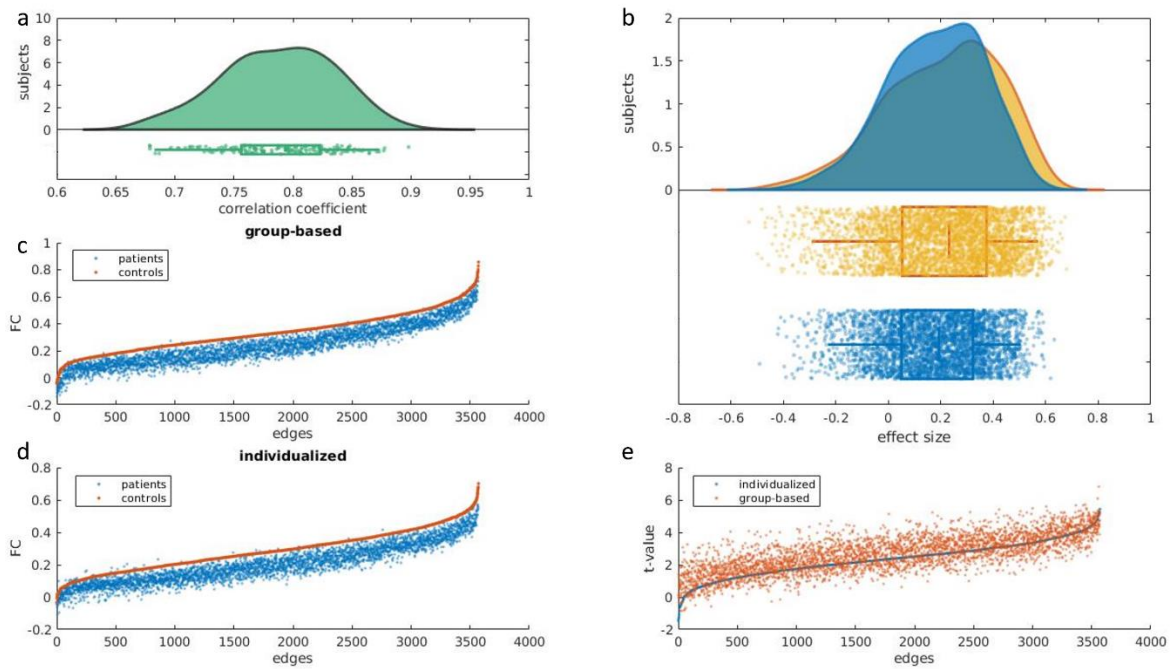
63 parcellation in controls was 0.346 ( $SD = 0.05$ ), and 0.370 ( $SD = 0.05$ ) for the individualized

64 parcellation. In patients, the mean homogeneity for the group parcellation was 0.318 ( $SD =$

65 0.04) and 0.341 ( $SD = 0.04$ ) for the individualized parcellation. A two-way mixed ANOVA

66 revealed that mean homogeneity was higher for the individualized parcellation ( $F(148) =$

67 1040.06,  $p < 0.0001$ ) and higher in controls compared to patients ( $F(148) = 14.35, p =$   
68  $0.0002$ ), with no interaction between parcellation type and diagnosis ( $F(148) = 0.246, p =$   
69  $0.621$ ). Panel **c** shows homogeneity scores for every parcel for group-based and individualized  
70 parcellation. Light colored parcels in **d** represent parcels showing significant difference in  
71 homogeneity scores, between parcellation approaches, for  $p_{FDR} < 0.05$ . Homogeneity is  
72 displayed in inflated surfaces with the group-based parcellation. **e** The distribution of the  
73 Pearson's coefficient of correlation comparing FC matrices derived from group-based and  
74 individualized parcellation. Matrices were positively correlated and ranged between 0.710 and  
75 0.867 (Median = 0.795). **f** Distributions of  $t$ -values quantifying FC differences between  
76 patients and controls at each edge and for individualized parcellation ( $M(SD) = 0.184(1.25)$ )  
77 and for group-based parcellation ( $M(SD) = 0.261(1.37)$ ). The difference between the  
78 individualized and group-based parcellations were statistically significant, according to a  
79 Wilcoxon Sign Rank Test ( $Z = 10.581, p < 0.0001$ ). **g** Shift function for the two  $t$ -  
80 distributions. Each circle represents the difference between each decile of both distributions,  
81 as a function of the deciles in group-based distribution and the bars represent the 95% boot-  
82 strap confidence interval associated with the difference.



84

85 **Figure 4 – Correlation between FC matrices derived from different parcellation**  
 86 **approaches, based on the s100 atlas.** Panel a shows the distribution and boxplot of  
 87 correlations between FC matrices derived using group-based and individualized parcellations  
 88 for each individual. Panel b shows the effect size (Cohen's  $d$ ) of the FC differences between  
 89 patients and controls at every edge, as observed using both parcellation approaches. Panels c  
 90 and d show the average FC for every edge for patients and controls, ordered by controls FC  
 91 values. Panel e shows the t-values associated with patients and controls FC differences, ordered  
 92 by the individualized parcellation t-values.

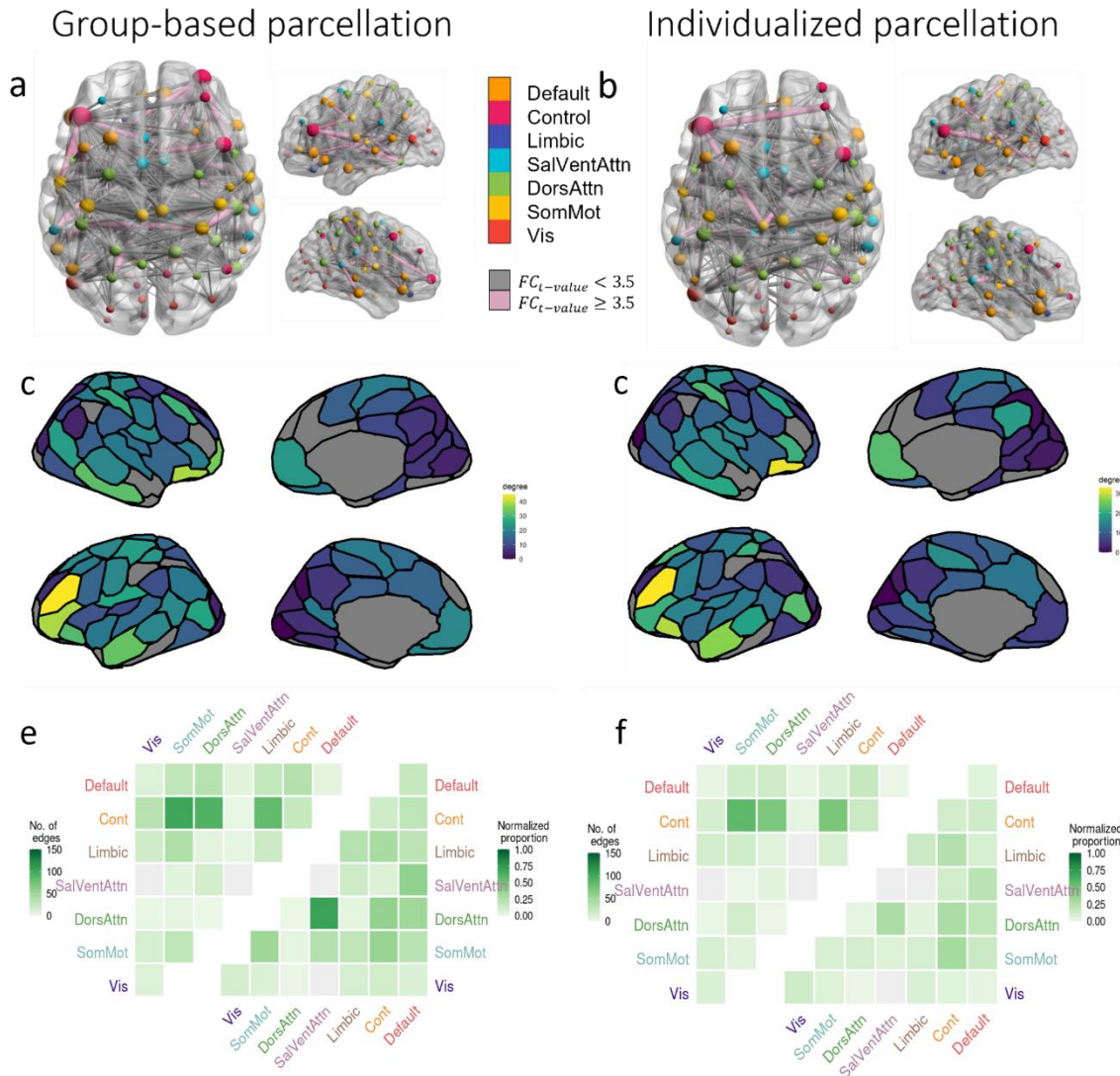
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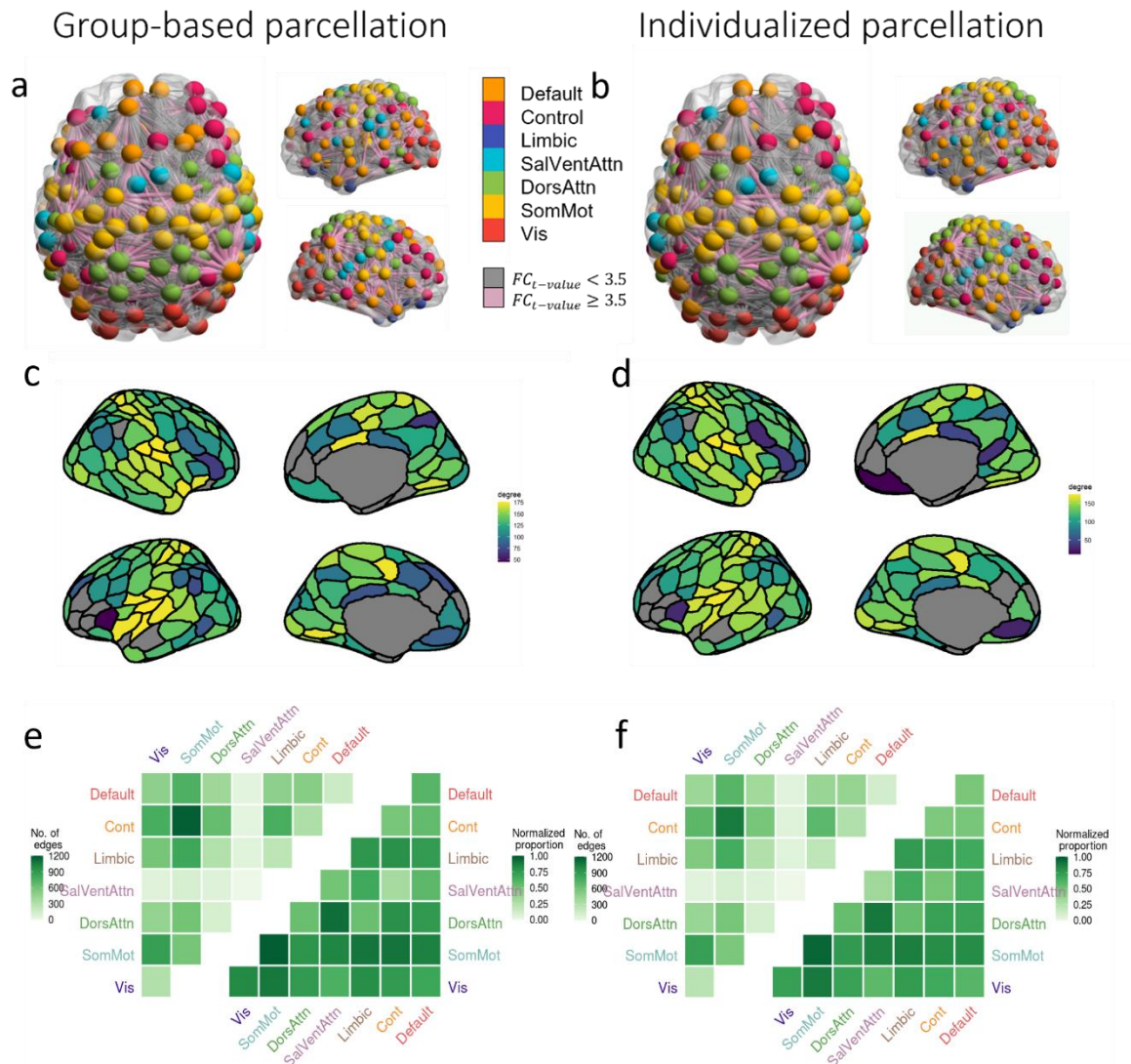
98 **Thresholded group differences in FC according to parcellation method**



100 **Figure 5 – Edge-level regional and network-level case-control FC differences according**  
 101 **to parcellation type, based on s100 GSR.** The NBS identified a single connected component  
 102 as showing significant FC differences between groups using both the (a) group-based ( $p = 0$ )  
 103 and (b) individualized parcellations ( $p = 0.0002$ ). The group-based component (a and c)  
 104 comprises 676 edges and the individualized component (b and d) comprises 484 edges. Panels



105 **a** and **b** show the specific edges comprising the NBS components obtained with the group-  
106 based and individualized parcellations, respectively, with nodes colored according to network  
107 affiliation and sized by degree. Edges are sized by strength of dysconnectivity. Edges  
108 associated with a t-value  $< 3.5$  are represented by grey lines and those associated with a t-value  
109  $\geq 3.5$  are represented in pink. The images were created using the software BrainNet Viewer  
110 (Xia et al., 2013). Panels **a**, **c** and **e** are based on group parcellation. Panels **c** and **d** show the  
111 degree of each region in the NBS component for the group and individualized parcellations,  
112 respectively. Edges are represented by grey lines. The upper triangle of each matrix in panels  
113 **e** and **f** shows the total number of NBS component edges (raw counts) falling within and  
114 between seven canonical networks. The lower triangles show the same data normalized for  
115 network size (normalized counts). Vis – visual network; SomMot – somatomotor network;  
116 DorsAttn – dorsal attention network; SalVentAttn – salience/ventral attention network; Cont –  
117 control network; Default – Default Mode Network.



118

119 **Figure 6 – Edge-level regional and network-level case-control FC differences according**

120 **to parcellation type, based on s200.** The NBS identified a single connected component as

121 showing significant FC differences between groups using both the (a) group-based

122 ( $p = 0$ ; i. e., no null value exceeded the observed estimate) and (b) individualized

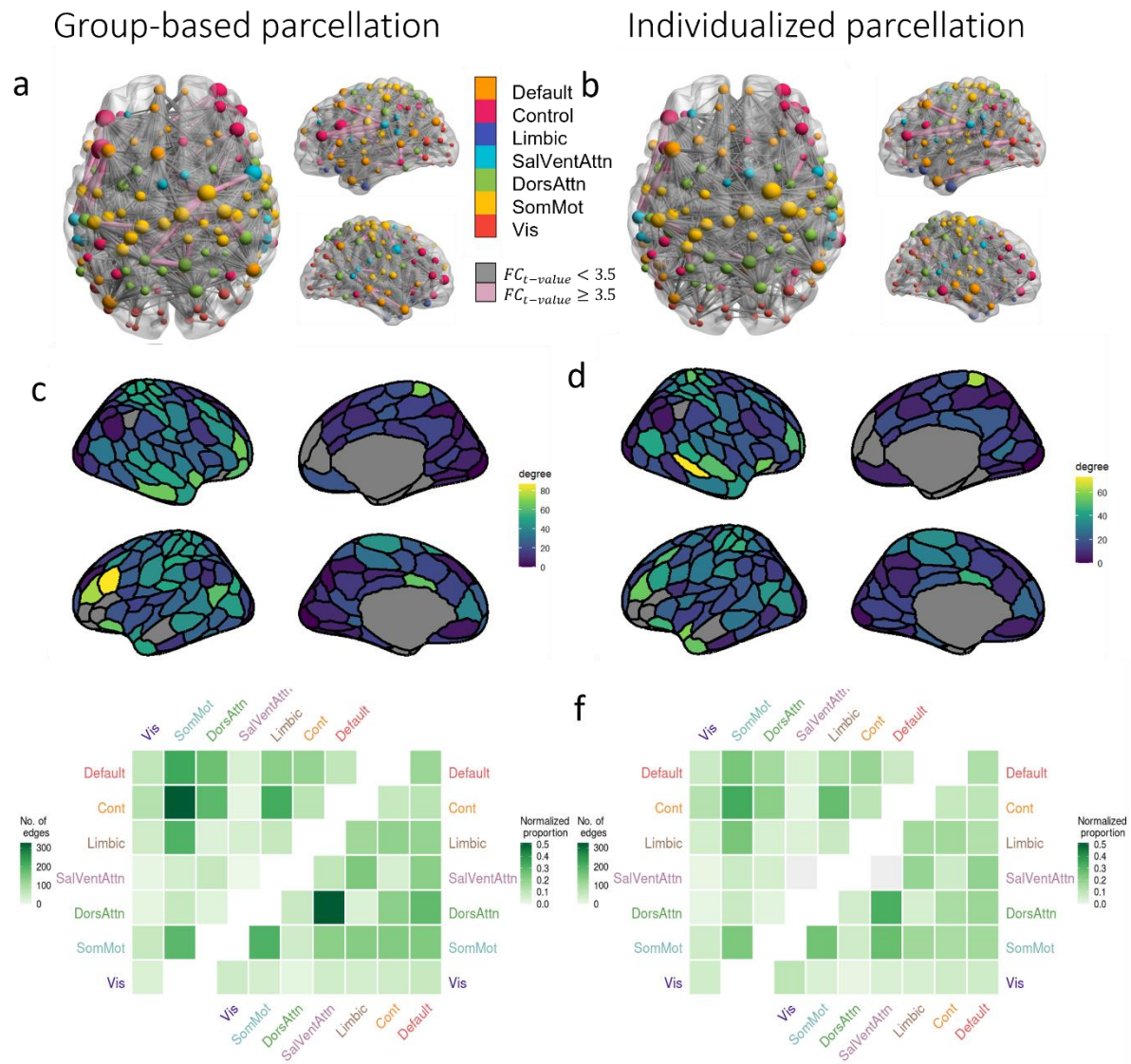
123 parcellations ( $p = 0$ ). The group-based component (a and c) comprises 11,927 edges and the

124 individualized component (b and d) comprises 11,149 edges. Panels a and b show the specific

125 edges comprising the NBS components obtained with the group-based and individualized

126 parcellations, respectively, with nodes colored according to network affiliation and sized by

127 degree. Edges are sized by strength of dysconnectivity. Edges associated with a t-value < 3.5  
128 are represented by grey lines and those associated with a t-value  $\geq 3.5$  are represented in pink.  
129 The images were created using the software BrainNet Viewer (Xia et al., 2013). Panels **a**, **c**  
130 and **e** are based on group parcellation. Panels **c** and **d** show the degree of each region in the  
131 NBS component for the group and individualized parcellations, respectively. Edges are  
132 represented by grey lines. The upper triangle of each matrix in panels **e** and **f** shows the total  
133 number of NBS component edges (raw counts) falling within and between seven canonical  
134 networks. The lower triangles show the same data normalized for network size (normalized  
135 counts). Vis – visual network; SomMot – somatomotor network; DorsAttn – dorsal attention  
136 network; SalVentAttn – salience/ventral attention network; Cont – control network; Default –  
137 Default Mode Network.



138

139 **Figure 7 – Edge-level regional and network-level case-control FC differences according**

140 **to parcellation type, based on s200 GSR.** The NBS identified a single connected component

141 as showing significant FC differences between groups using both the (a) group-based ( $p =$

142 0.001) and (b) individualized parcellations ( $p = 0.0014$ ). The group-based component (a and

143 c) comprises 2,481 edges and the individualized component (b and d) comprises 1,882 edges.

144 Panels a and b show the specific edges comprising the NBS components obtained with the

145 group-based and individualized parcellations, respectively, with nodes colored according to

146 network affiliation and sized by degree. Edges are sized by strength of dysconnectivity. Edges

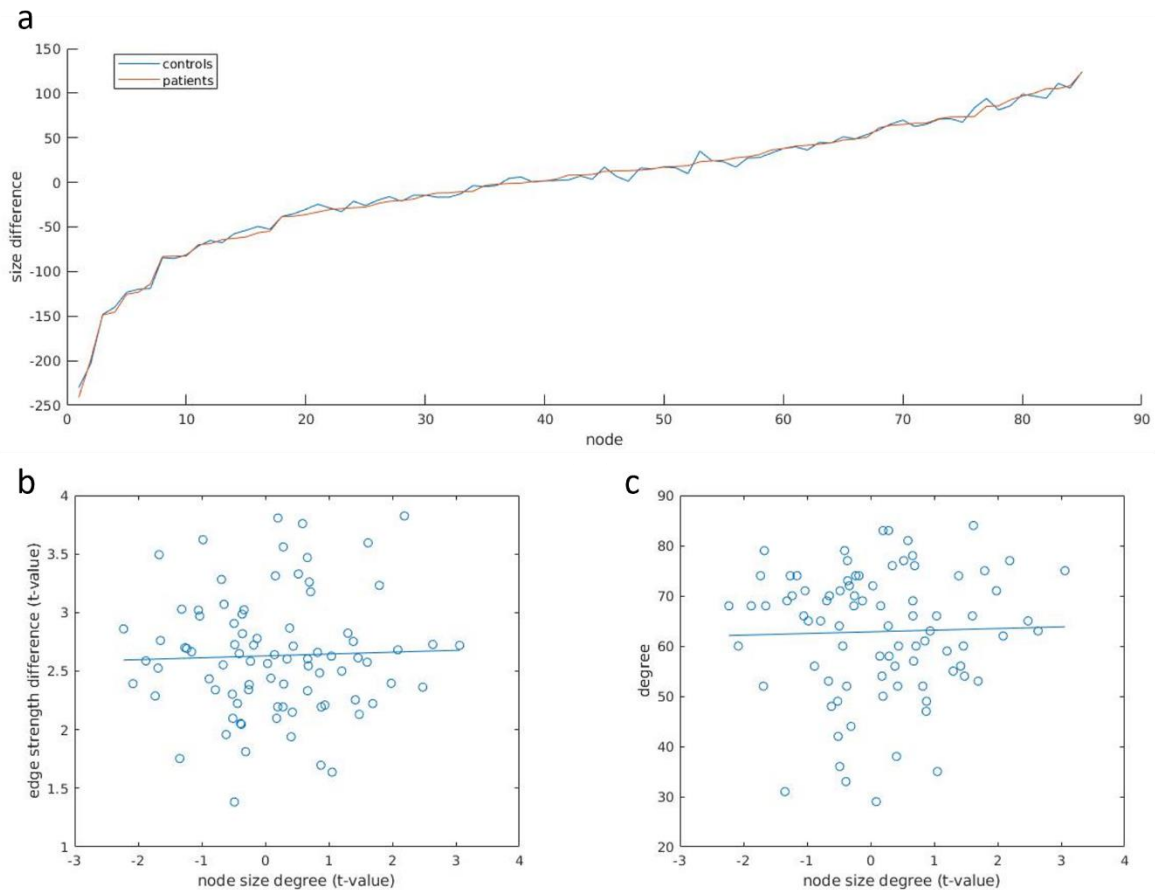
147 associated with a t-value  $< 3.5$  are represented by grey lines and those associated with a t-value  
148  $\geq 3.5$  are represented in pink. The images were created using the software BrainNet Viewer  
149 (Xia et al., 2013). Panels **a**, **c** and **e** are based on group parcellation. Panels **c** and **d** show the  
150 degree of each region in the NBS component for the group and individualized parcellations,  
151 respectively. Edges are represented by grey lines. The upper triangle of each matrix in panels  
152 **e** and **f** shows the total number of NBS component edges (raw counts) falling within and  
153 between seven canonical networks. The lower triangles show the same data normalized for  
154 network size (normalized counts). Vis – visual network; SomMot – somatomotor network;  
155 DorsAttn – dorsal attention network; SalVentAttn – salience/ventral attention network; Cont –  
156 control network; Default – Default Mode Network.

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159

160 **The effects of variation in parcel size**



161

162 **Figure 8 – Changes in parcels size and its correlation to node degree and edge**

163 **dysconnectivity, based on s100. a** The average difference in size of every region between

164 individualized and group-based parcellation for patients and controls. Size is measured in terms

165 of vertices and the change reported is the average size difference for controls and patients.

166 Positive numbers correspond to the node being larger in individualized parcellation. There was

167 no difference in parcel size changes between groups ( $p = 0.889$ ) Panel b shows the node size

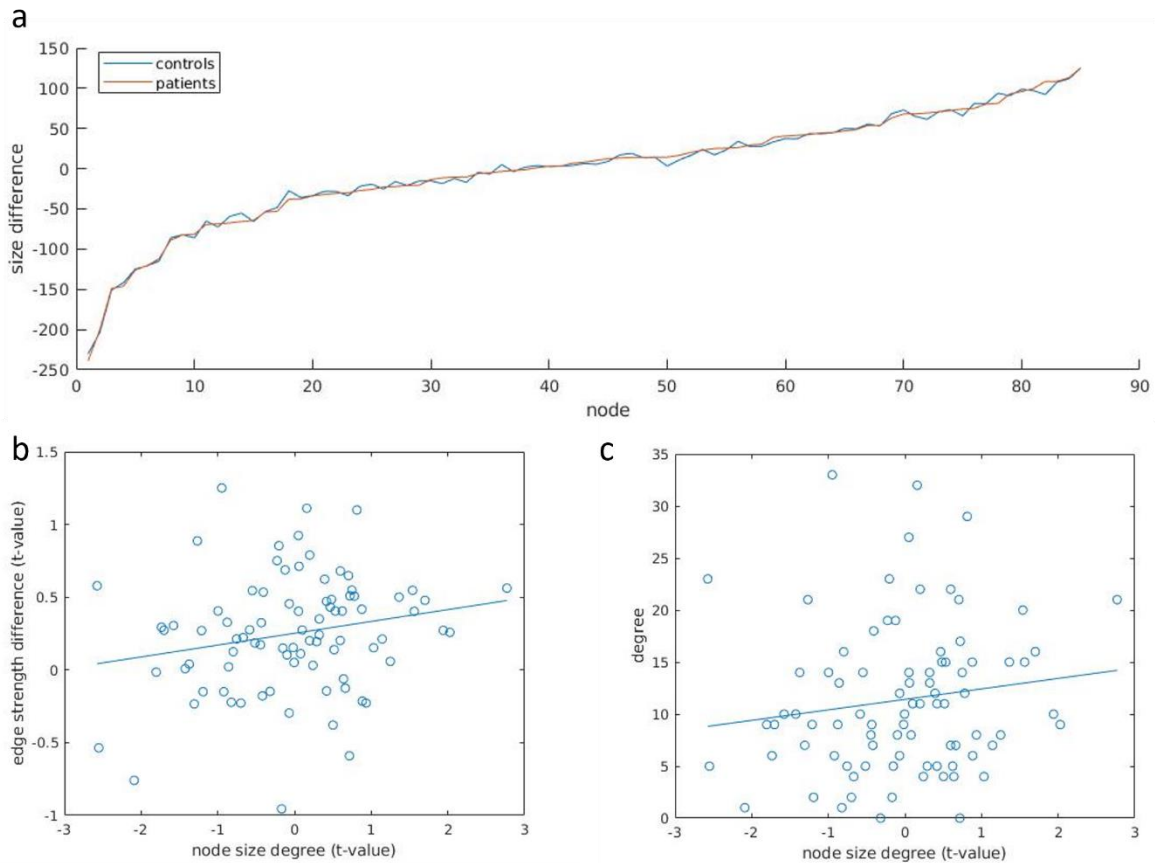
168 difference and average edge dysconnectivity for every region (blue dots) and the correlation

169 between both (blue line) for individualized parcellation. Panel c shows the node size difference

170 and node degree for every node (blue dots) and the correlation between both (blue line) for

171 individualized parcellation. Correlation is given by the Spearman's coefficient.

172



173

174 **Figure 9 – Changes in parcels size and its correlation to node degree and edge**

175 **dysconnectivity, based on s100 GSR. a** The average difference in size of every region

176 between individualized and group-based parcellation for patients and controls. Size is

177 measured in terms of vertices and the change reported is the average size difference for controls

178 and patients. Positive numbers correspond to the node being larger in individualized

179 parcellation. There was no difference in parcel size changes between groups ( $p = 0.990$ ).

180 Panel b shows the node size difference and average edge dysconnectivity for every region (blue

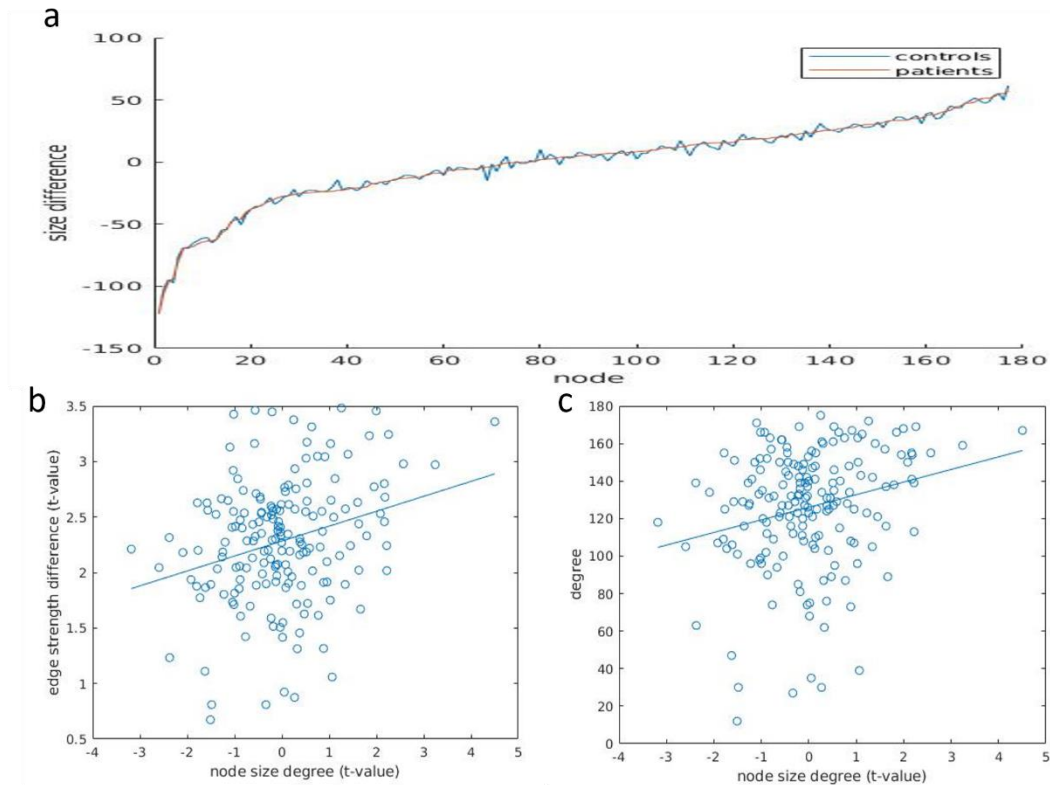
181 dots) and the correlation ( $r = 0.202, p = 0.064$ ) between both (blue line) for individualized

182 parcellation. Panel c shows the node size difference and node degree for every node (blue dots)

183 and the correlation ( $r = 0.164, p = 0.133$ ) between both (blue line) for individualized

184 parcellation. Correlation is given by the Spearman's coefficient.

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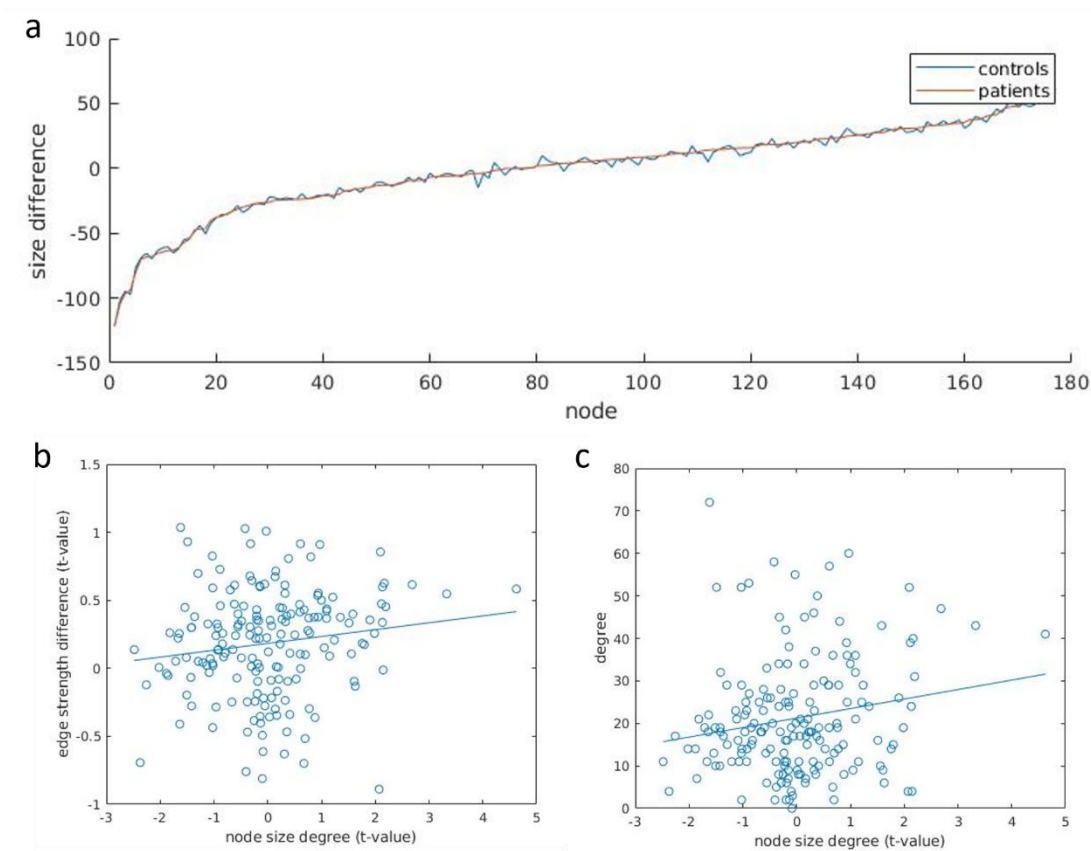


186

187 **Figure 10 - Changes in parcels size and its correlation to node degree and edge**  
 188 **dysconnectivity, based on s200. a** The average difference in size of every region between  
 189 individualized and group-based parcellation for patients and controls. Size is measured in terms  
 190 of vertices and the change reported is the average size difference for controls and patients.  
 191 Positive numbers correspond to the node being larger in individualized parcellation. There was  
 192 no difference in parcel size changes between groups, according to permutation testing  
 193 ( $p = 0.550$ ). The second region of the somatomotor network of the left hemisphere showed  
 194 significant difference in change in size ( $p_{FDR} = 0.035$ ), with controls having a greater size  
 195 difference between parcellations. Panel **b** shows the node size difference and average edge  
 196 dysconnectivity for every region (blue dots) and the correlation ( $r = 0.213, p =$   
 197  $0.004$ ) between both (blue line) for individualized parcellation. Panel **c** shows the node size  
 198 difference and node degree for every node (blue dots) and the correlation ( $r = 0.215, p =$



199 0.004) between both (blue line) for individualized parcellation. Correlation is given by the  
200 Spearman's coefficient.



201

202

203 **Figure 11 – Changes in parcels size and its correlation to node degree and edge**

204 **dysconnectivity, based on s200 GSR. a** The average difference in size of every region

205 between individualized and group-based parcellation for patients and controls. Size is

206 measured in terms of vertices and the change reported is the average size difference for controls

207 and patients. Positive numbers correspond to the node being larger in individualized

208 parcellation. There was no difference in parcel size changes between groups ( $p = 0.981$ ).

209 Panel **b** shows the node size difference and average edge dysconnectivity for every region (blue

210 dots) and the correlation ( $r = 0.160, p = 0.034$ ) between both (blue line) for individualized

211 parcellation. Panel **c** shows the node size difference and node degree for every node (blue dots)

212 and the correlation ( $r = 0.152, p = 0.043$ ) between both (blue line) for individualized  
213 parcellation. Correlation is given by the Spearman's coefficient.

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223 Reference:

224 Xia, M., Wang, J., & He, Y. (2013). BrainNet Viewer: A Network Visualization Tool for  
225 Human Brain Connectomics. *PLOS ONE*, 8(7), e68910.

226 <https://doi.org/10.1371/journal.pone.0068910>

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