As stated in the main text, the present data differed in several ways from those of our previous study of striatal FC (Di Martino et al., 2008). For example, the two studies utilized entirely different participant samples, different magnets of different field strengths, and different scanning parameters.

Regardless of these differences, the patterns of positive and negative functional connectivity observed for the placebo condition were remarkably consistent with those previously observed by Di Martino et al. Nonetheless, several differences in the patterns of connectivity are notable. Specifically, because Di Martino et al. examined the connectivity of the six seeds within a single group, they analyzed FC using a single model, and orthogonalized the time series of each seed with respect to that of all the other seeds. This approach aims to detect the pattern of FC unique to each seed among a set of seeds (see also Margulies et al., 2007).

Entering multiple seed time series in a single model yields the pattern of correlation for each seed time series, controlling for the other seed time series. Use of such a model is less suitable for the examination of group- or condition-related effects, however because the nature or degree of the signal removed by orthogonalization could differ between groups or conditions. In the present study, we thus analyzed the FC of each seed within its own model. As expected, we observed increased overlap among the patterns of FC associated with each of the seeds than previously observed by Di Martino et al. However, when we examined the FC of all six right hemisphere seeds in a single model with orthogonalization, for the placebo condition, there was a greater similarity between the present results and those of Di Martino et al. (Figure S5).