

Supplementary material

Supplementary Table 1: Brain regions showing significant FC differences in 1×3 ANOVA within the investigated striatal functional networks at $p < 0.001$ -*FWE_c* cut-off threshold.

Network	Contrast	Anatomical region	MNI (x,y,z)	Cluster size (# voxels)	Z-value	T-value	<i>P_{corr}</i> -value
Striatal network	LRRK2 NM-MC > NM-NC	L caudate	-8, 2 24	75	4.53	4.88	0.02
	LRRK2 NM-MC > GBA-NMC	R thalamus	10 -10 16	70	3.6	3.78	0.02

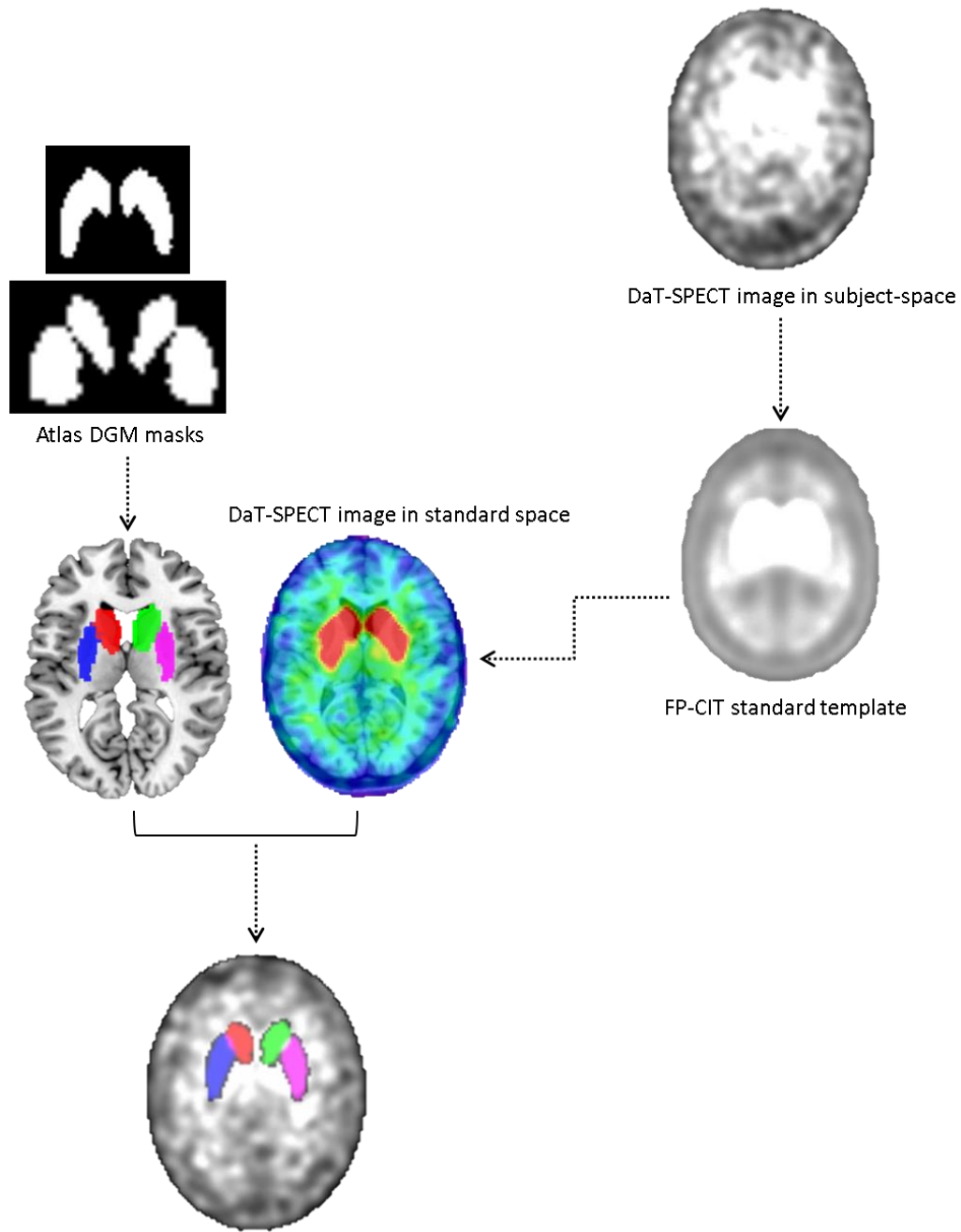
FC = functional connectivity, MNI: Montreal Neurological Institute, R = right, L = left.

Supplementary Table 2: Demographic and clinical characteristics of converters to definite PD at baseline.

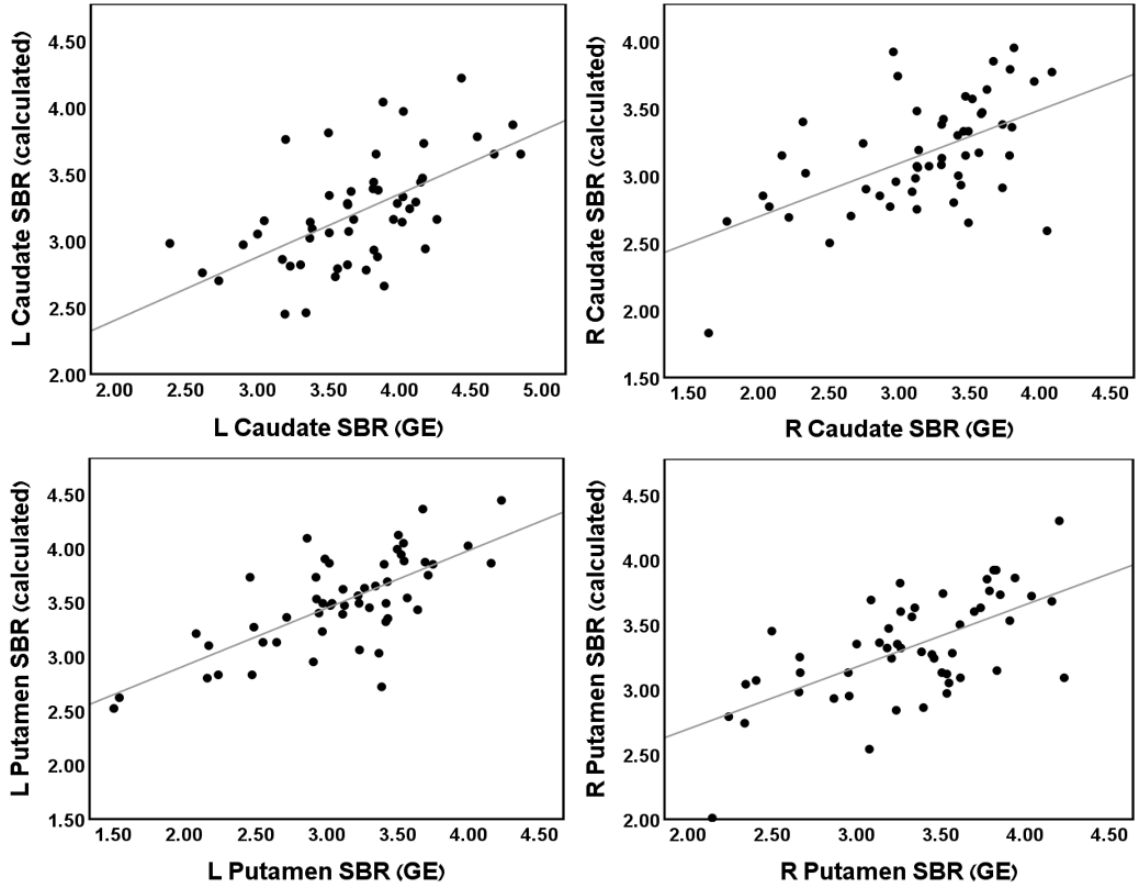
	Converter 1	Converter 2	Converter 3
Age	65	47	63
Gender	Male	Male	Female
Genetic status	GBA (N3705)	GBA(IVS-2)	LRRK2
UPDRS-III	0	4	0
UPDRS- Total	11	12	2
MOCA	28	29	25
LR at baseline	95.07	90.96	20.78

LR:likelihood ratio, UPDRS: Unified Parkinson's disease rating scale, MOCA: Montreal cognitive assessment. LR: likelihood ratio.

Figures



Supplementary Figure 1: Schematic depiction of the DaTscan processing steps.



Supplementary Figure 2: The agreement between the SBR values achieved using two methods. Scatter plots demonstrate the agreement between the calculated SBR values within the striatal regions of interest (ROIs) obtained from both the clinical imaging software (GE, and the described method in the methods section).