Supplementary Table 1. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HMAT atlas-derived primary motor area mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.180	0.033	<0.0001	0.0002	0.0003
CII	-0.249	0.066	<0.0001	0.0002	0.0002
CIV	-0.259	0.072	<0.0001	0.0002	0.0002
MitoD	-0.227	0.054	<0.0001	0.0002	0.0003
MRC	-0.280	0.085	<0.0001	0.0002	0.0003
TRC	-0.275	0.082	<0.0001	0.0002	0.0003
R2*					
CI	-0.027	<0.001	<0.0001	0.0002	0.0003
CII	-0.048	0.002	<0.0001	0.0002	0.0003
CIV	-0.033	0.001	<0.0001	0.0002	0.0004
MitoD	-0.029	<0.001	<0.0001	0.0002	0.0002
MRC	-0.019	<0.001	<0.0001	0.0002	0.0003
TRC	-0.039	0.001	<0.0001	0.0002	0.0003
Proton density					
CI	0.205	0.044	<0.0001	0.0002	0.0003
CII	0.245	0.064	<0.0001	0.0002	0.0003
CIV	0.266	0.076	<0.0001	0.0002	0.0002
MitoD	0.229	0.055	<0.0001	0.0002	0.0003
MRC	0.318	0.112	<0.0001	0.0002	0.0002
TRC	0.291	0.096	<0.0001	0.0002	0.0003
MTsat					
CI	-0.064	0.004	<0.0001	0.0002	0.0003
CII	-0.069	0.005	<0.0001	0.0002	0.0003
CIV	-0.082	0.007	<0.0001	0.0002	0.0003
MitoD	-0.038	0.001	<0.0001	0.0002	0.0003
MRC	-0.092	0.008	<0.0001	0.0002	0.0004
TRC	-0.084	0.007	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 60,176 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 2. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HMAT atlas-derived dorsal premotor cortex mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.345	0.135	<0.0001	0.0002	0.0003
CII	-0.320	0.114	<0.0001	0.0002	0.0003
CIV	-0.377	0.165	<0.0001	0.0002	0.0003
MitoD	-0.362	0.151	<0.0001	0.0002	0.0003
MRC	-0.326	0.119	<0.0001	0.0002	0.0003
TRC	-0.362	0.154	<0.0001	0.0002	0.0003
R2*					
CI	-0.112	0.013	<0.0001	0.0002	0.0003
CII	-0.101	0.010	<0.0001	0.0002	0.0003
CIV	-0.123	0.015	<0.0001	0.0002	0.0004
MitoD	-0.131	0.017	<0.0001	0.0002	0.0003
MRC	-0.077	0.006	<0.0001	0.0002	0.0003
TRC	-0.107	0.012	<0.0001	0.0002	0.0003
Proton density					
CI	0.217	0.049	<0.0001	0.0002	0.0003
CII	0.201	0.042	<0.0001	0.0002	0.0003
CIV	0.245	0.064	<0.0001	0.0002	0.0002
MitoD	0.193	0.039	<0.0001	0.0002	0.0003
MRC	0.290	0.092	<0.0001	0.0002	0.0002
TRC	0.261	0.073	<0.0001	0.0002	0.0003
MTsat					
CI	-0.123	0.015	<0.0001	0.0002	0.0003
CII	-0.092	0.008	<0.0001	0.0002	0.0003
CIV	-0.125	0.016	<0.0001	0.0002	0.0003
MitoD	-0.111	0.012	<0.0001	0.0002	0.0003
MRC	-0.095	0.009	<0.0001	0.0002	0.0004
TRC	-0.113	0.013	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 52,792 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 3. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HMAT atlas-derived presupplementary motor cortex mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.142	0.020	<0.0001	0.0002	0.0003
CII	-0.130	0.017	<0.0001	0.0002	0.0003
CIV	-0.209	0.046	<0.0001	0.0002	0.0002
MitoD	-0.222	0.052	<0.0001	0.0002	0.0003
MRC	-0.119	0.014	<0.0001	0.0002	0.0003
TRC	-0.196	0.040	<0.0001	0.0002	0.0003
R2*					
CI	-0.104	0.011	<0.0001	0.0002	0.0003
CII	-0.101	0.010	<0.0001	0.0002	0.0003
CIV	-0.160	0.026	<0.0001	0.0002	0.0004
MitoD	-0.201	0.042	<0.0001	0.0002	0.0002
MRC	-0.076	0.006	<0.0001	0.0002	0.0004
TRC	-0.145	0.021	<0.0001	0.0002	0.0003
Proton density					
CI	0.013	<0.001	0.0747	0.3631	0.3994
CII	-0.037	0.001	<0.0001	0.0002	0.0003
CIV	-0.076	0.006	<0.0001	0.0002	0.0002
MitoD	-0.038	0.001	<0.0001	0.0002	0.0004
MRC	0.031	0.001	<0.0001	0.0002	0.0002
TRC	-0.062	0.004	<0.0001	0.0002	0.0002
MTsat					
CI	-0.053	0.003	<0.0001	0.0002	0.0003
CII	-0.195	0.039	<0.0001	0.0002	0.0003
CIV	-0.162	0.027	<0.0001	0.0002	0.0003
MitoD	-0.163	0.027	<0.0001	0.0002	0.0003
MRC	-0.198	0.040	<0.0001	0.0002	0.0004
TRC	-0.162	0.027	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 17,468 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 4. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HMAT atlas-derived primary somatosensory cortex mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.083	0.007	<0.0001	0.0002	0.0003
CII	-0.038	0.001	<0.0001	0.0002	0.0003
CIV	-0.096	0.009	<0.0001	0.0002	0.0002
MitoD	-0.050	0.002	<0.0001	0.0002	0.0003
MRC	-0.087	0.007	<0.0001	0.0002	0.0003
TRC	-0.090	0.008	<0.0001	0.0002	0.0003
R2*					
CI	0.006	<0.001	0.2134	0.7552	0.9230
CII	0.100	0.010	<0.0001	0.0002	0.0003
CIV	0.089	0.008	<0.0001	0.0002	0.0004
MitoD	0.101	0.010	<0.0001	0.0002	0.0002
MRC	0.082	0.007	<0.0001	0.0002	0.0003
TRC	0.092	0.009	<0.0001	0.0002	0.0003
Proton density					
CI	0.124	0.016	<0.0001	0.0002	0.0003
CII	0.177	0.032	<0.0001	0.0002	0.0003
CIV	0.206	0.044	<0.0001	0.0002	0.0002
MitoD	0.135	0.018	<0.0001	0.0002	0.0003
MRC	0.243	0.063	<0.0001	0.0002	0.0002
TRC	0.223	0.052	<0.0001	0.0002	0.0003
MTsat					
CI	0.031	<0.001	<0.0001	0.0002	0.0003
CII	0.159	0.026	<0.0001	0.0002	0.0003
CIV	0.116	0.014	<0.0001	0.0002	0.0003
MitoD	0.144	0.021	<0.0001	0.0002	0.0003
MRC	0.136	0.019	<0.0001	0.0002	0.0004
TRC	0.135	0.018	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 34,304 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 5. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HMAT atlas-derived supplementary motor cortex mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	<0.001	<0.001	0.9936	1.0000	1.0000
CII	0.070	0.005	<0.0001	0.0002	0.0003
CIV	-0.060	0.004	<0.0001	0.0002	0.0002
MitoD	-0.016	<0.001	0.0179	0.1002	0.1225
MRC	0.041	0.002	<0.0001	0.0002	0.0003
TRC	-0.045	0.002	<0.0001	0.0002	0.0003
R2*					
CI	-0.028	<0.001	<0.0001	0.0002	0.0003
CII	0.070	0.005	<0.0001	0.0002	0.0003
CIV	-0.059	0.003	<0.0001	0.0002	0.0004
MitoD	-0.054	0.003	<0.0001	0.0002	0.0002
MRC	0.084	0.007	<0.0001	0.0002	0.0003
TRC	-0.037	0.001	<0.0001	0.0002	0.0003
Proton density					
CI	0.180	0.034	<0.0001	0.0002	0.0003
CII	0.108	0.012	<0.0001	0.0002	0.0003
CIV	0.141	0.020	<0.0001	0.0002	0.0002
MitoD	0.132	0.017	<0.0001	0.0002	0.0003
MRC	0.226	0.051	<0.0001	0.0002	0.0002
TRC	0.169	0.029	<0.0001	0.0002	0.0003
MTsat					
CI	-0.003	<0.001	0.6212	0.9972	1.0000
CII	-0.065	0.004	<0.0001	0.0002	0.0003
CIV	-0.081	0.007	<0.0001	0.0002	0.0003
MitoD	-0.044	0.002	<0.0001	0.0002	0.0003
MRC	-0.052	0.003	<0.0001	0.0002	0.0004
TRC	-0.074	0.005	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 21,712 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 6. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HMAT atlas-derived ventral premotor cortex mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.045	0.002	<0.0001	0.0002	0.0003
CII	0.007	<0.001	0.1326	0.5691	0.6902
CIV	-0.030	<0.001	<0.0001	0.0002	0.0002
MitoD	-0.016	<0.001	0.0004	0.0020	0.0027
MRC	-0.009	<0.001	0.0481	0.2556	0.2812
TRC	-0.029	<0.001	<0.0001	0.0002	0.0003
R2*					
CI	-0.025	<0.001	<0.0001	0.0002	0.0003
CII	0.005	<0.001	0.2869	0.8688	1.0000
CIV	-0.011	<0.001	0.0203	0.1174	0.1435
MitoD	0.022	<0.001	<0.0001	0.0002	0.0002
MRC	-0.025	<0.001	<0.0001	0.0002	0.0003
TRC	-0.018	<0.001	<0.0001	0.0002	0.0003
Proton density					
CI	0.178	0.033	<0.0001	0.0002	0.0003
CII	0.178	0.033	<0.0001	0.0002	0.0003
CIV	0.177	0.032	<0.0001	0.0002	0.0002
MitoD	0.177	0.032	<0.0001	0.0002	0.0003
MRC	0.195	0.040	<0.0001	0.0002	0.0002
TRC	0.190	0.037	<0.0001	0.0002	0.0003
MTsat					
CI	-0.033	0.001	<0.0001	0.0002	0.0003
CII	0.025	<0.001	<0.0001	0.0002	0.0003
CIV	-0.035	0.001	<0.0001	0.0002	0.0003
MitoD	0.005	<0.001	0.2658	0.8414	1.0000
MRC	-0.012	<0.001	0.0108	0.0650	0.1021
TRC	-0.033	0.001	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 46,704 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 7. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived putamen mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.282	0.086	<0.0001	0.0002	0.0003
CII	-0.301	0.101	<0.0001	0.0002	0.0003
CIV	-0.254	0.069	<0.0001	0.0002	0.0002
MitoD	-0.358	0.146	<0.0001	0.0002	0.0003
MRC	-0.248	0.065	<0.0001	0.0002	0.0003
TRC	-0.237	0.060	<0.0001	0.0002	0.0003
R2*					
CI	0.137	0.019	<0.0001	0.0002	0.0003
CII	0.143	0.021	<0.0001	0.0002	0.0003
CIV	0.100	0.011	<0.0001	0.0002	0.0004
MitoD	0.156	0.025	<0.0001	0.0002	0.0002
MRC	0.109	0.012	<0.0001	0.0002	0.0003
TRC	0.125	0.015	<0.0001	0.0002	0.0003
Proton density					
CI	0.024	0.001	0.0028	0.0163	0.0224
CII	-0.019	<0.001	0.0257	0.1505	0.1948
CIV	0.050	0.003	<0.0001	0.0002	0.0002
MitoD	0.001	<0.001	0.8683	1.0000	1.0000
MRC	0.052	0.002	<0.0001	0.0002	0.0002
TRC	0.033	0.001	<0.0001	0.0002	0.0003
MTsat					
CI	0.158	0.025	<0.0001	0.0002	0.0003
CII	0.176	0.032	<0.0001	0.0002	0.0003
CIV	0.160	0.027	<0.0001	0.0002	0.0003
MitoD	0.097	0.010	<0.0001	0.0002	0.0003
MRC	0.145	0.022	<0.0001	0.0002	0.0004
TRC	0.168	0.028	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 14,838 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 8. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived nucleus accumbens mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.204	0.043	<0.0001	0.0002	0.0003
CII	-0.283	0.087	<0.0001	0.0002	0.0003
CIV	-0.282	0.086	<0.0001	0.0002	0.0002
MitoD	-0.337	0.127	<0.0001	0.0002	0.0003
MRC	-0.292	0.093	<0.0001	0.0002	0.0003
TRC	-0.254	0.067	<0.0001	0.0002	0.0003
R2*					
CI	-0.270	0.078	<0.0001	0.0002	0.0003
CII	-0.367	0.155	<0.0001	0.0002	0.0003
CIV	-0.284	0.088	<0.0001	0.0002	0.0004
MitoD	-0.461	0.271	<0.0001	0.0002	0.0002
MRC	-0.250	0.067	<0.0001	0.0002	0.0003
TRC	-0.256	0.070	<0.0001	0.0002	0.0003
Proton density					
CI	0.082	0.007	0.0034	0.0187	0.0242
CII	0.135	0.018	<0.0001	0.0002	0.0003
CIV	0.268	0.077	<0.0001	0.0002	0.0002
MitoD	0.135	0.018	<0.0001	0.0002	0.0003
MRC	0.288	0.091	<0.0001	0.0002	0.0002
TRC	0.249	0.067	<0.0001	0.0002	0.0003
MTsat					
CI	0.310	0.107	<0.0001	0.0002	0.0003
CII	0.187	0.037	<0.0001	0.0002	0.0003
CIV	-0.082	0.006	0.0035	0.0239	0.0309
MitoD	0.119	0.014	<0.0001	0.0002	0.0003
MRC	-0.014	0.001	0.6054	0.9966	0.9992
TRC	-0.018	0.001	0.5058	0.9852	0.9966

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 1,281 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 9. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived red nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.114	0.014	0.0001	0.0010	0.0015
CII	0.168	0.028	<0.0001	0.0002	0.0003
CIV	0.145	0.022	<0.0001	0.0002	0.0002
MitoD	0.238	0.060	<0.0001	0.0002	0.0003
MRC	0.132	0.017	<0.0001	0.0002	0.0003
TRC	0.105	0.011	0.0004	0.0033	0.0045
R2*					
CI	0.173	0.031	<0.0001	0.0002	0.0003
CII	0.202	0.042	<0.0001	0.0002	0.0003
CIV	0.104	0.011	0.0005	0.0029	0.0049
MitoD	0.196	0.040	<0.0001	0.0002	0.0002
MRC	0.136	0.019	<0.0001	0.0002	0.0003
TRC	0.133	0.017	<0.0001	0.0002	0.0003
Proton density					
CI	-0.039	0.015	0.1959	0.7378	0.7729
CII	-0.034	0.012	0.2481	0.8248	0.8641
CIV	0.015	0.002	0.6381	0.9986	1.0000
MitoD	0.041	0.017	0.1815	0.7086	0.9170
MRC	-0.022	0.005	0.4830	0.9815	0.9980
TRC	-0.043	0.001	0.1593	0.6534	0.7187
MTsat					
CI	0.013	<0.001	0.6646	0.9994	1.0000
CII	0.082	0.007	0.0061	0.0372	0.0545
CIV	0.112	0.013	0.0127	0.0012	0.0016
MitoD	0.159	0.026	<0.0001	0.0002	0.0003
MRC	0.074	0.005	0.0055	0.0818	0.1200
TRC	0.037	0.001	0.0014	0.7814	0.9048

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 1,101 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 10. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived substantia nigra mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.176	0.016	0.0002	0.0019	0.0026
CII	0.273	0.119	<0.0001	0.0002	0.0003
CIV	0.131	0.016	0.0004	0.0023	0.0028
MitoD	0.161	0.093	<0.0001	0.0002	0.0003
MRC	0.074	0.007	0.0151	0.0927	0.1133
TRC	0.168	0.008	0.0073	0.0481	0.0588
R2*					
CI	0.168	0.028	<0.0001	0.0002	0.0003
CII	0.234	0.058	<0.0001	0.0002	0.0003
CIV	0.036	0.001	0.1651	0.6460	0.6768
MitoD	0.052	0.003	0.0456	0.2325	0.2842
MRC	0.052	0.003	0.0442	0.2267	0.2771
TRC	0.106	0.011	<0.0001	0.0002	0.0003
Proton density					
CI	0.236	0.059	<0.0001	0.0002	0.0003
CII	0.292	0.093	<0.0001	0.0002	0.0003
CIV	0.153	0.024	<0.0001	0.0002	0.0002
MitoD	0.154	0.024	<0.0001	0.0002	0.0004
MRC	0.125	0.016	<0.0001	0.0002	0.0002
TRC	0.204	0.043	<0.0001	0.0002	0.0003
MTsat					
CI	0.147	0.022	<0.0001	0.0002	0.0003
CII	0.272	0.080	<0.0001	0.0002	0.0003
CIV	0.104	0.011	<0.0001	0.0002	0.0003
MitoD	0.141	0.020	<0.0001	0.0002	0.0003
MRC	0.044	0.002	0.0846	0.3961	0.5126
TRC	0.147	0.022	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 1,499 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 11. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived caudate nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.131	0.018	<0.0001	0.0002	0.0003
CII	-0.201	0.042	<0.0001	0.0002	0.0003
CIV	-0.101	0.010	<0.0001	0.0002	0.0002
MitoD	-0.163	0.027	<0.0001	0.0002	0.0003
MRC	-0.187	0.036	<0.0001	0.0002	0.0003
TRC	-0.125	0.016	<0.0001	0.0002	0.0003
R2*					
CI	0.097	0.009	<0.0001	0.0002	0.0003
CII	-0.010	<0.001	0.0243	0.8172	1.0000
CIV	0.143	0.021	<0.0001	0.0002	0.0004
MitoD	0.107	0.011	<0.0001	0.0002	0.0002
MRC	0.019	<0.001	0.0264	0.1465	0.1896
TRC	0.109	0.012	<0.0001	0.0002	0.0003
Proton density					
CI	0.248	0.066	<0.0001	0.0002	0.0003
CII	0.370	0.158	<0.0001	0.0002	0.0003
CIV	0.240	0.061	<0.0001	0.0002	0.0003
MitoD	0.131	0.017	<0.0001	0.0002	0.0003
MRC	0.279	0.084	<0.0001	0.0002	0.0002
TRC	0.299	0.098	<0.0001	0.0002	0.0003
MTsat					
CI	-0.303	0.101	<0.0001	0.0002	0.0003
CII	-0.350	0.140	<0.0001	0.0002	0.0003
CIV	-0.271	0.079	<0.0001	0.0002	0.0003
MitoD	-0.249	0.066	<0.0001	0.0002	0.0003
MRC	-0.374	0.162	<0.0001	0.0002	0.0004
TRC	-0.274	0.081	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 13,224 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 12. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived globus pallidus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.176	0.032	<0.0001	0.0002	0.0003
CII	-0.261	0.073	<0.0001	0.0002	0.0003
CIV	-0.165	0.028	<0.0001	0.0002	0.0002
MitoD	-0.195	0.039	<0.0001	0.0002	0.0003
MRC	-0.108	0.012	<0.0001	0.0002	0.0003
TRC	-0.187	0.036	<0.0001	0.0002	0.0003
R2*					
CI	0.015	<0.001	0.2586	0.8282	0.9589
CII	-0.004	<0.001	0.7779	1.0000	1.0000
CIV	-0.038	0.001	0.0049	0.0268	0.0393
MitoD	0.012	<0.001	0.3608	0.9344	0.9999
MRC	-0.020	<0.001	0.1295	0.5584	0.5950
TRC	-0.026	<0.001	0.0564	0.2847	0.3296
Proton density					
CI	-0.025	<0.001	0.0670	0.3363	0.3894
CII	-0.156	0.025	<0.0001	0.0002	0.0003
CIV	0.081	0.007	<0.0001	0.0002	0.0002
MitoD	0.004	<0.001	0.7585	0.9996	1.0000
MRC	0.098	0.010	<0.0001	0.0002	0.0002
TRC	0.036	0.001	0.0079	0.0432	0.0559
MTsat					
CI	0.017	<0.001	0.2214	0.7782	1.0000
CII	-0.005	<0.001	0.6909	0.9992	0.9992
CIV	0.119	0.014	<0.0001	0.0002	0.0003
MitoD	-0.004	<0.001	0.7600	0.9994	1.0000
MRC	0.118	0.014	<0.0001	0.0002	0.0004
TRC	0.101	0.010	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 5,361 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 13. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived ventral pallidum mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.174	0.031	<0.0001	0.0002	0.0003
CII	-0.235	0.058	<0.0001	0.0002	0.0003
CIV	-0.230	0.056	<0.0001	0.0002	0.0002
MitoD	-0.217	0.050	<0.0001	0.0002	0.0003
MRC	-0.205	0.044	<0.0001	0.0002	0.0003
TRC	-0.186	0.036	<0.0001	0.0002	0.0003
R2*					
CI	-0.080	0.006	0.0619	0.3211	0.4155
CII	-0.132	0.018	0.0020	0.0126	0.0185
CIV	-0.194	0.039	<0.0001	0.0002	0.0004
MitoD	-0.207	0.045	<0.0001	0.0002	0.0002
MRC	-0.106	0.011	0.0135	0.0748	0.1028
TRC	-0.154	0.024	0.0003	0.0038	0.0052
Proton density					
CI	0.113	0.013	0.0080	0.0436	0.0533
CII	0.060	0.004	0.1606	0.6507	0.7534
CIV	0.122	0.015	0.0042	0.0248	0.0303
MitoD	0.119	0.014	0.0055	0.0310	0.0426
MRC	0.107	0.011	0.0128	0.0668	0.0816
TRC	0.082	0.007	0.0561	0.2741	0.3350
MTsat					
CI	-0.024	<0.001	0.5753	0.9936	1.0000
CII	-0.074	0.005	0.0858	0.4151	0.4885
CIV	-0.006	<0.001	0.8899	1.0000	1.0000
MitoD	-0.003	<0.001	0.9356	1.0000	1.0000
MRC	-0.055	0.003	0.2018	0.7428	0.9079
TRC	-0.048	0.002	0.2608	0.8356	0.9386

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 8,266 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 14. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived habenular nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.127	0.016	0.0303	0.1663	0.1925
CII	0.007	<0.001	0.9036	1.0000	1.0000
CIV	0.096	0.009	0.1020	0.4697	0.5464
MitoD	0.230	0.056	0.0000	0.0005	0.0007
MRC	0.090	0.008	0.1251	0.5466	0.5613
TRC	0.077	0.006	0.1932	0.7232	0.8374
R2*					
CI	-0.045	0.002	0.4407	0.9691	1.0000
CII	-0.049	0.003	0.4024	0.9548	1.0000
CIV	-0.184	0.036	0.0016	0.0093	0.0146
MitoD	-0.088	0.007	0.1394	0.6026	0.6977
MRC	-0.202	0.043	0.0006	0.0039	0.0061
TRC	-0.172	0.031	0.0037	0.0205	0.0265
Proton density					
CI	-0.205	0.044	0.0005	0.0038	0.0056
CII	0.002	<0.001	0.9729	1.0000	1.0000
CIV	0.094	0.091	0.1097	0.5028	0.5531
MitoD	0.017	0.003	0.7702	1.0000	1.0000
MRC	0.039	0.015	0.5058	0.9855	0.9980
TRC	0.057	0.004	0.3299	0.9121	0.9555
MTsat					
CI	-0.017	<0.001	0.7686	0.9998	1.0000
CII	-0.054	0.002	0.3660	0.9333	0.9919
CIV	0.109	0.012	0.0632	0.3165	0.3481
MitoD	0.049	0.002	0.4107	0.9565	1.0000
MRC	0.121	0.014	0.0396	0.2087	0.2870
TRC	0.096	0.009	0.1018	0.4623	0.5650

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 228 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 15. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived dentate nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.107	0.012	<0.0001	0.0002	0.0003
CII	0.048	0.002	0.0158	0.0949	0.1228
CIV	0.030	<0.001	0.1339	0.5832	0.6111
MitoD	0.052	0.002	0.0089	0.0595	0.0770
MRC	0.046	0.002	0.0208	0.1205	0.1395
TRC	0.023	<0.001	0.2438	0.8142	0.8530
R2*					
CI	0.002	<0.001	0.8939	1.0000	1.0000
CII	-0.011	0.001	0.5562	0.9932	1.0000
CIV	-0.050	0.002	0.0123	0.0747	0.0967
MitoD	0.008	<0.001	0.6891	0.9990	0.9990
MRC	-0.030	<0.001	0.1280	0.5680	0.5950
TRC	-0.032	0.001	0.1069	0.4993	0.5426
Proton density					
CI	0.134	0.018	<0.0001	0.0002	0.0003
CII	0.150	0.023	<0.0001	0.0002	0.0003
CIV	0.002	<0.001	0.9076	1.0000	1.0000
MitoD	-0.087	0.007	<0.0001	0.0003	0.0005
MRC	0.102	0.010	<0.0001	0.0002	0.0004
TRC	0.063	0.004	0.0014	0.0083	0.0137
MTsat					
CI	-0.020	<0.001	0.3060	0.8932	1.0000
CII	0.046	0.003	0.0199	0.1103	0.1517
CIV	-0.052	0.002	0.0086	0.0539	0.0624
MitoD	-0.009	<0.001	0.6305	0.9988	1.0000
MRC	0.015	<0.001	0.4411	0.9722	0.9966
TRC	-0.008	<0.001	0.6723	0.9992	0.9992

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 2,485 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 16. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived subthalamic nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.038	0.001	0.3649	0.9316	0.9760
CII	-0.035	0.001	0.4155	0.9604	1.0000
CIV	0.134	0.018	0.0015	0.0074	0.0086
MitoD	0.046	0.002	0.2827	0.8604	0.9014
MRC	0.104	0.011	0.0143	0.0810	0.1048
TRC	0.037	0.001	0.3879	0.9470	0.9470
R2*					
CI	-0.021	<0.001	0.6240	0.9970	0.9970
CII	-0.072	0.005	0.0903	0.4377	0.5068
CIV	-0.034	0.001	0.4214	0.9604	0.9990
MitoD	-0.113	0.013	0.0078	0.0422	0.0580
MRC	-0.022	<0.001	0.6018	0.9958	1.0000
TRC	-0.041	0.002	0.3321	0.9096	0.9970
Proton density					
CI	-0.041	0.002	0.3305	0.9082	0.9082
CII	-0.055	0.003	0.1967	0.7294	0.8023
CIV	0.116	0.014	0.0060	0.0310	0.0359
MitoD	0.011	<0.001	0.7899	1.0000	1.0000
MRC	0.092	0.008	0.0305	0.1665	0.1928
TRC	0.031	0.001	0.4597	0.9742	0.9742
MTsat					
CI	0.008	<0.001	0.8487	1.0000	1.0000
CII	0.036	0.001	0.3887	0.9468	0.9919
CIV	0.174	0.031	<0.0001	0.0004	0.0006
MitoD	0.102	0.010	0.0166	0.0904	0.1243
MRC	0.170	0.030	<0.0001	0.0004	0.0008
TRC	0.096	0.009	0.0231	0.1192	0.1639

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 555 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 17. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived thalamus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.085	0.007	<0.0001	0.0002	0.0003
CII	0.102	0.010	<0.0001	0.0002	0.0003
CIV	0.123	0.015	<0.0001	0.0002	0.0002
MitoD	0.060	0.036	<0.0001	0.0002	0.0003
MRC	0.102	0.010	<0.0001	0.0002	0.0004
TRC	0.011	0.013	<0.0001	0.0002	0.0003
R2*					
CI	0.020	<0.001	0.0047	0.0344	0.0458
CII	0.004	<0.001	0.6000	0.9932	1.0000
CIV	-0.049	0.002	<0.0001	0.0002	0.0002
MitoD	-0.081	0.006	<0.0001	0.0002	0.0003
MRC	0.008	<0.001	0.2358	0.8038	0.9125
TRC	0.004	<0.001	0.5570	0.9890	1.0000
Proton density					
CI	-0.054	0.002	<0.0001	0.0002	0.0003
CII	-0.181	0.034	<0.0001	0.0002	0.0003
CIV	-0.001	<0.001	0.9604	1.0000	1.0000
MitoD	-0.187	0.036	<0.0001	0.0002	0.0003
MRC	-0.007	<0.001	0.0305	0.1665	0.1987
TRC	-0.012	<0.001	0.0991	0.4607	0.6123
MTsat					
CI	-0.236	0.059	<0.0001	0.0002	0.0003
CII	-0.300	0.099	<0.0001	0.0002	0.0003
CIV	-0.046	0.002	<0.0001	0.0002	0.0002
MitoD	-0.329	0.121	<0.0001	0.0002	0.0003
MRC	-0.165	0.028	<0.0001	0.0002	0.0004
TRC	-0.115	0.013	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 19,809 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 18. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived intralaminar thalamic nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.166	0.028	<0.0001	0.0002	0.0003
CII	0.140	0.020	<0.0001	0.0002	0.0003
CIV	0.203	0.043	<0.0001	0.0002	0.0002
MitoD	0.023	<0.001	0.1391	0.5867	0.6454
MRC	0.194	0.039	<0.0001	0.0002	0.0003
TRC	0.204	0.043	<0.0001	0.0002	0.0003
R2*					
CI	-0.059	0.003	<0.0001	0.0004	0.0005
CII	-0.120	0.015	<0.0001	0.0002	0.0003
CIV	0.028	<0.001	0.0434	0.2375	0.2612
MitoD	-0.190	0.037	<0.0001	0.0002	0.0002
MRC	0.073	0.005	<0.0001	0.0002	0.0004
TRC	0.061	0.004	<0.0001	0.0002	0.0003
Proton density					
CI	0.414	0.207	<0.0001	0.0002	0.0003
CII	0.412	0.204	<0.0001	0.0002	0.0003
CIV	0.185	0.035	<0.0001	0.0002	0.0002
MitoD	0.196	0.040	<0.0001	0.0002	0.0003
MRC	0.410	0.203	<0.0001	0.0002	0.0002
TRC	0.298	0.097	<0.0001	0.0002	0.0003
MTsat					
CI	-0.017	<0.001	0.2916	0.8730	1.0000
CII	-0.104	0.011	<0.0001	0.0002	0.0003
CIV	0.108	0.012	<0.0001	0.0002	0.0003
MitoD	-0.260	0.072	<0.0001	0.0002	0.0003
MRC	0.047	0.002	0.0028	0.0172	0.0291
TRC	0.120	0.014	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 3,980 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 19. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived thalamic posterior nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.040	0.002	0.0032	0.0196	0.0239
CII	-0.022	<0.001	0.1119	0.5043	0.6163
CIV	0.156	0.025	<0.0001	0.0002	0.0002
MitoD	-0.024	<0.001	0.0818	0.3991	0.4621
MRC	0.107	0.011	<0.0001	0.0002	0.0003
TRC	0.139	0.020	<0.0001	0.0002	0.0003
R2*					
CI	-0.080	0.007	<0.0001	0.0002	0.0003
CII	-0.060	0.004	<0.0001	0.0002	0.0003
CIV	-0.178	0.033	<0.0001	0.0002	0.0004
MitoD	-0.095	0.009	<0.0001	0.0002	0.0002
MRC	-0.159	0.026	<0.0001	0.0002	0.0003
TRC	-0.159	0.026	<0.0001	0.0002	0.0003
Proton density					
CI	-0.117	0.053	<0.0001	0.0002	0.0003
CII	-0.192	0.004	<0.0001	0.0002	0.0003
CIV	-0.001	0.056	<0.0001	0.0002	0.0002
MitoD	-0.195	0.041	<0.0001	0.0002	0.0003
MRC	-0.045	0.078	<0.0001	0.0002	0.0002
TRC	-0.025	0.078	<0.0001	0.0002	0.0003
MTsat					
CI	0.113	0.014	<0.0001	0.0002	0.0003
CII	-0.027	0.038	<0.0001	0.0002	0.0003
CIV	0.230	<0.001	0.9189	1.0000	1.0000
MitoD	-0.264	0.040	<0.0001	0.0002	0.0003
MRC	0.214	0.002	0.0010	0.0076	0.0139
TRC	0.224	<0.001	0.0704	0.3519	0.4554

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 5,340 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 20. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived thalamic ventral nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	-0.013	<0.001	0.2259	0.7764	0.8530
CII	0.086	0.007	<0.0001	0.0002	0.0003
CIV	0.070	0.005	<0.0001	0.0002	0.0003
MitoD	0.103	0.011	<0.0001	0.0002	0.0002
MRC	-0.008	<0.001	0.4730	0.9794	1.0000
TRC	0.033	0.001	0.0023	0.0112	0.1449
R2*					
CI	0.132	0.018	<0.0001	0.0002	0.0003
CII	0.089	0.008	<0.0001	0.0002	0.0003
CIV	0.005	<0.001	0.6298	0.9970	0.9970
MitoD	-0.058	0.003	<0.0001	0.0002	0.0002
MRC	0.094	0.009	<0.0001	0.0002	0.0003
TRC	0.096	0.009	<0.0001	0.0002	0.0003
Proton density					
CI	-0.168	0.029	<0.0001	0.0002	0.0003
CII	-0.237	0.059	<0.0001	0.0002	0.0003
CIV	-0.132	0.018	<0.0001	0.0002	0.0002
MitoD	-0.035	0.001	0.0015	0.0102	0.0149
MRC	-0.157	0.025	<0.0001	0.0002	0.0003
TRC	-0.175	0.032	<0.0001	0.0002	0.0003
MTsat					
CI	-0.324	0.117	<0.0001	0.0002	0.0003
CII	-0.277	0.083	<0.0001	0.0002	0.0003
CIV	-0.147	0.022	<0.0001	0.0002	0.0003
MitoD	-0.093	0.009	<0.0001	0.0002	0.0003
MRC	-0.277	0.083	<0.0001	0.0002	0.0004
TRC	-0.252	0.068	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 8,260 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 21. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived anterior thalamic nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.033	0.001	0.3072	0.8874	0.9760
CII	0.078	0.006	0.0148	0.0834	0.1147
CIV	0.016	<0.001	0.6131	0.9968	0.9968
MitoD	-0.003	<0.001	0.9230	1.0000	1.0000
MRC	0.049	0.002	0.1266	0.5613	0.5613
TRC	0.105	0.011	0.0011	0.0064	0.0082
R2*					
CI	0.132	0.018	<0.0001	0.0002	0.0003
CII	0.136	0.019	<0.0001	0.0002	0.0003
CIV	0.072	0.005	0.0237	0.1298	0.1503
MitoD	0.162	0.027	<0.0001	0.0002	0.0002
MRC	0.084	0.007	0.0090	0.0500	0.0733
TRC	0.064	0.004	0.0481	0.2525	0.3086
Proton density					
CI	0.144	0.021	<0.0001	0.0002	0.0003
CII	0.069	0.005	0.0308	0.1626	0.1987
CIV	0.154	0.024	<0.0001	0.0002	0.0003
MitoD	0.015	<0.001	0.6381	0.9980	1.0000
MRC	0.159	0.026	<0.0001	0.0002	0.0003
TRC	0.135	0.019	<0.0001	0.0002	0.0003
MTsat					
CI	-0.055	0.003	0.0888	0.4219	0.0003
CII	0.087	0.008	0.0066	0.0408	0.4885
CIV	<0.001	<0.001	0.9904	1.0000	0.0499
MitoD	-0.140	0.020	<0.0001	0.0002	1.0000
MRC	0.032	0.001	0.3261	0.9048	0.9966
TRC	0.116	0.014	0.0003	0.0008	0.0012

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 965 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.

Supplementary Table 22. Voxel-wise spatial correlation between Parkinson's disease-related differences derived from multiparametric mapping and the six mitochondrial brain atlases features across the HybraPD atlas-derived medial thalamic nucleus mask.

	r	Cohen's f^2	p_{uncorr}	p_{perm}	p_{FDR}
R1					
CI	0.259	0.072	<0.0001	0.0002	0.0003
CII	0.225	0.054	<0.0001	0.0002	0.0003
CIV	0.175	0.032	<0.0001	0.0002	0.0002
MitoD	0.091	0.008	<0.0001	0.0002	0.0003
MRC	0.238	0.060	<0.0001	0.0002	0.0003
TRC	0.192	0.038	<0.0001	0.0002	0.0003
R2*					
CI	-0.060	0.004	0.0001	0.0004	0.0003
CII	-0.031	0.001	0.0506	0.2691	0.3700
CIV	-0.082	0.007	<0.0001	0.0002	0.0004
MitoD	-0.126	0.016	<0.0001	0.0002	0.0002
MRC	0.022	<0.001	0.1579	0.6369	0.6369
TRC	-0.015	<0.001	0.3450	0.9214	0.9652
Proton density					
CI	0.225	0.053	<0.0001	0.0002	0.0003
CII	0.063	0.004	<0.0001	0.0002	0.0003
CIV	0.229	0.056	<0.0001	0.0002	0.0002
MitoD	-0.198	0.041	<0.0001	0.0002	0.0003
MRC	0.269	0.078	<0.0001	0.0002	0.0002
TRC	0.270	0.078	<0.0001	0.0002	0.0003
MTsat					
CI	0.113	0.013	<0.0001	0.0002	0.0003
CII	-0.027	<0.001	0.0502	0.2697	0.3490
CIV	0.230	0.056	<0.0001	0.0002	0.0003
MitoD	-0.264	0.075	<0.0001	0.0002	0.0003
MRC	0.214	0.048	<0.0001	0.0002	0.0004
TRC	0.224	0.053	<0.0001	0.0002	0.0003

We assessed the group differences in R1, R2*, proton density, and MTsat using t-maps containing PwPD > HCs values and six mitochondrial feature maps: CI, CII, CIV, MitoD, MRC, and TRC. After masking for finite values, n = 5,110 voxels were included in the analysis. For each type of analysis, we report nominal, permutation-derived, and false discovery rate (FDR)-adjusted p-values. CI, CII, CIV: mitochondrial electron transport chain protein complexes I, II, and IV. Cohen's f^2: standardized effect size measure. HCs: healthy controls. MitoD: mitochondrial density. MTsat: magnetic transfer saturation. MRC: mitochondrial respiration capacity. PwPD: patients with Parkinson's disease. p_{FDR}: false-discovery rate-adjusted p-value. p_{perm}: non-parametric p-value derived from permutation testing. p_{uncorr}: nominal p-value. r: correlation coefficient. R^2: coefficient of determination. R1: longitudinal relaxation rate. R2*: effective transverse relaxation rate. TRC: tissue respiration capacity.