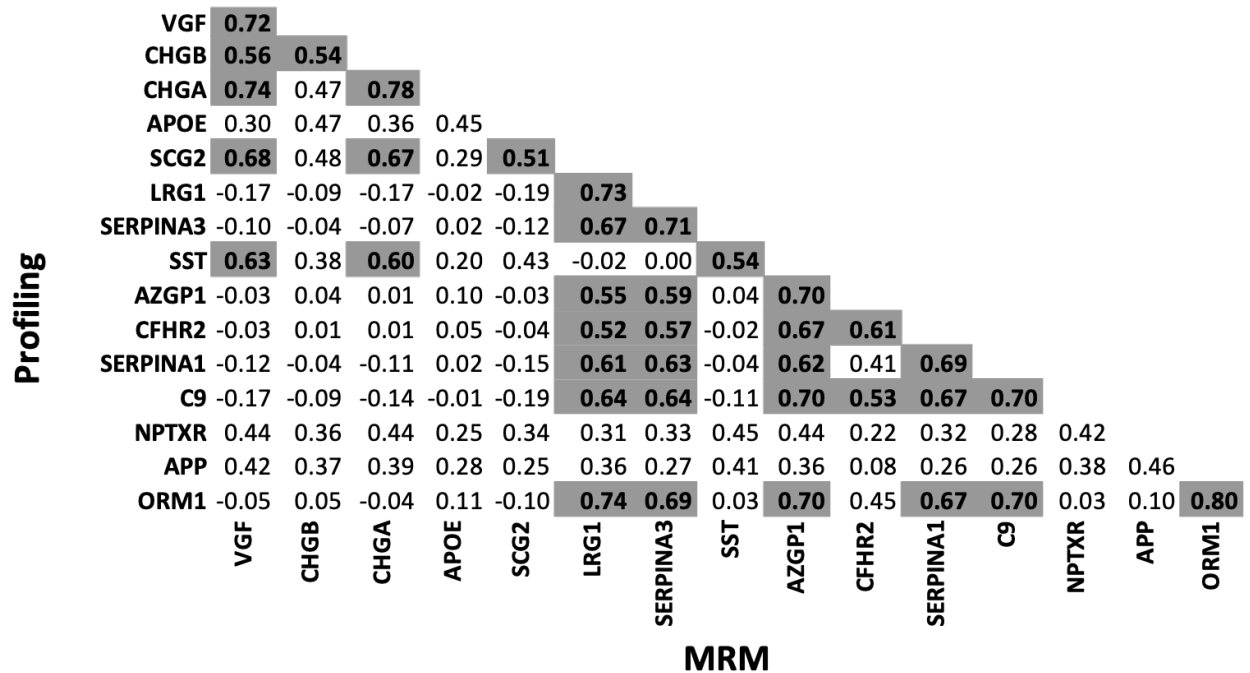# Supplementary Material

Alterations in Self-Aggregating Neuropeptides in Cerebrospinal Fluid of Patients with Parkinsonian Disorders

Profiling (Y-axis) / MRM (X-axis):

Profiling	VGF	CHGB	CHGA	APOE	SCG2	LRG1	SERPINA3	SST	AZGP1	CFHR2	SERPINA1	C9	NPTXR	APP	ORM1
VGF	0.72														
CHGB	0.56	0.54													
CHGA	0.74	0.47	0.78												
APOE	0.30	0.47	0.36	0.45											
SCG2	0.68	0.48	0.67	0.29	0.51										
LRG1	-0.17	-0.09	-0.17	-0.02	-0.19	0.73									
SERPINA3	-0.10	-0.04	-0.07	0.02	-0.12	0.67	0.71								
SST	0.63	0.38	0.60	0.20	0.43	-0.02	0.00	0.54							
AZGP1	-0.03	0.04	0.01	0.10	-0.03	0.55	0.59	0.04	0.70						
CFHR2	-0.03	0.01	0.01	0.05	-0.04	0.52	0.57	-0.02	0.67	0.61					
SERPINA1	-0.12	-0.04	-0.11	0.02	-0.15	0.61	0.63	-0.04	0.62	0.41	0.69				
C9	-0.17	-0.09	-0.14	-0.01	-0.19	0.64	0.64	-0.11	0.70	0.53	0.67	0.70			
NPTXR	0.44	0.36	0.44	0.25	0.34	0.31	0.33	0.45	0.44	0.22	0.32	0.28	0.42		
APP	0.42	0.37	0.39	0.28	0.25	0.36	0.27	0.41	0.36	0.08	0.26	0.26	0.38	0.46	
ORM1	-0.05	0.05	-0.04	0.11	-0.10	0.74	0.69	0.03	0.70	0.45	0.67	0.70	0.03	0.10	0.80

Supplementary Figure 1. Pearson correlation matrix of significant candidates as measured in all individual samples. The matrix allows comparison of the quantification of proteins (as measured by multiple peptides in profiling) and single peptides as selected for validation in MRM. Y-axis lists proteins quantified in profiling and x-axis list protein name as measured by single peptide in MRM. Higher correlations are also detected between proteins with similar molecular functions: the dense core vesicle proteins and neuropeptides, CHGA, SCG2, VGF, SST; or the inflammatory markers, C9, ORM1, AZGP1, LRG1. Coefficient factors of correlation are highlighted when they are higher than 0.5.