

Study of the Mechanism of Action of *Blarcamesine* (ANAVEX®2-73): Whole Blood Transcriptomics Analysis (RNAseq) Identifies Treatment Impact on Compensatory Pathways by Restoring Key Neurodegenerative Pathways Functionality, including Alzheimer's and Parkinson's Disease Pathways

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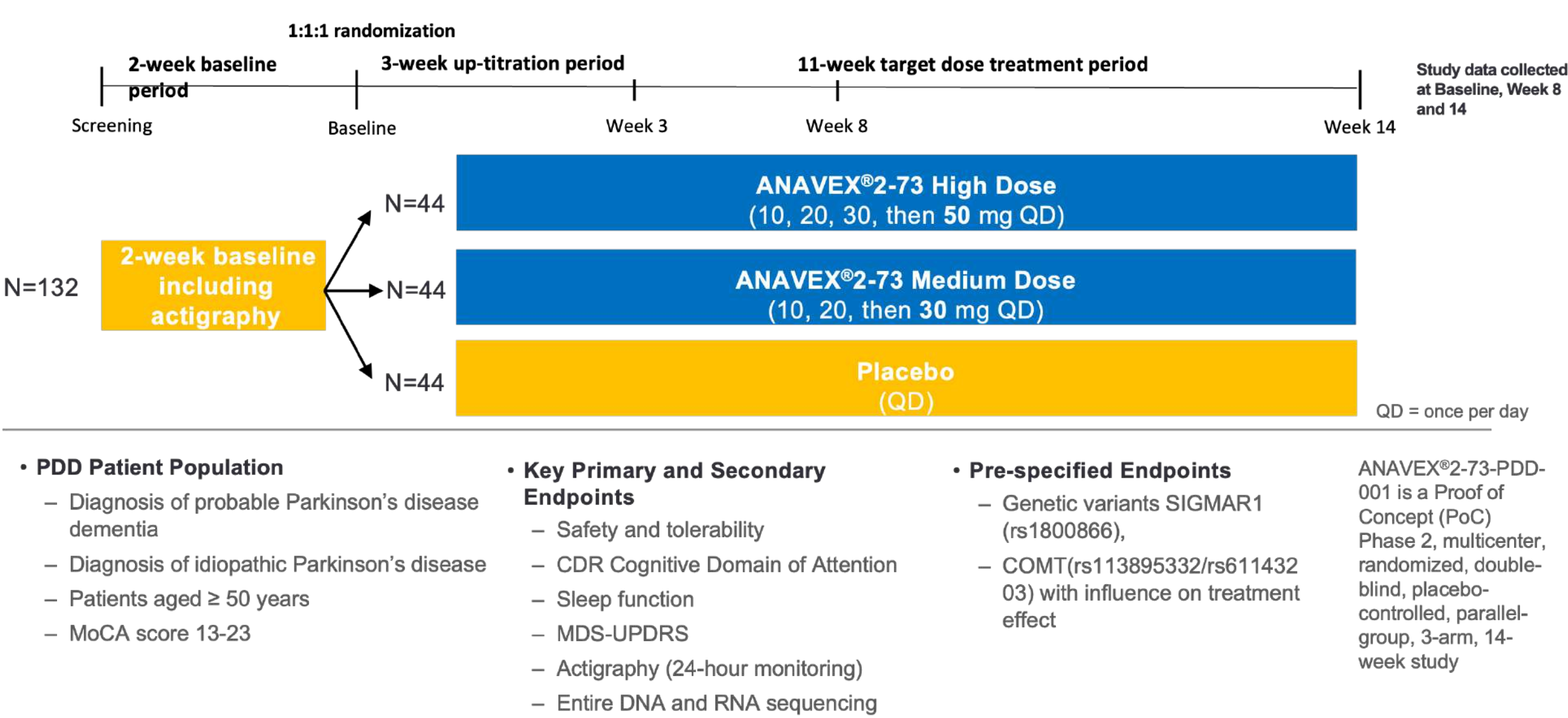
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Overview

- ANAVEX®2-73 (*blarcamesine*) is a Sigma-1 receptor (SIGMAR1) agonist that mechanistically focuses on a new target relevant to Alzheimer's disease, Parkinson's disease and other neurological diseases
- SIGMAR1 activation is a compensatory mechanism to chronic CNS diseases
- The direct occupancy of ANAVEX®2-73 at SIGMAR1 has been established previously using quantitative PET scan
- Full genomic analysis of ANAVEX®2-73-PDD-001 Phase 2 study in patients with Parkinson's Disease Dementia (PDD) assessed biomarkers of response exploring potential for a Precision Medicine approach
- The overall goal of this study is to specify the ANAVEX®2-73 response pathways by identifying the most differentially expressed genes and characterizing the pathways involved

ANAVEX®2-73 PoC Phase 2 PDD Study Design

A Phase 2 trial to Assess the Safety, Tolerability and Efficacy of ANAVEX®2-73 (*blarcamesine*) Oral Capsules in the Treatment of Parkinson's Disease Dementia

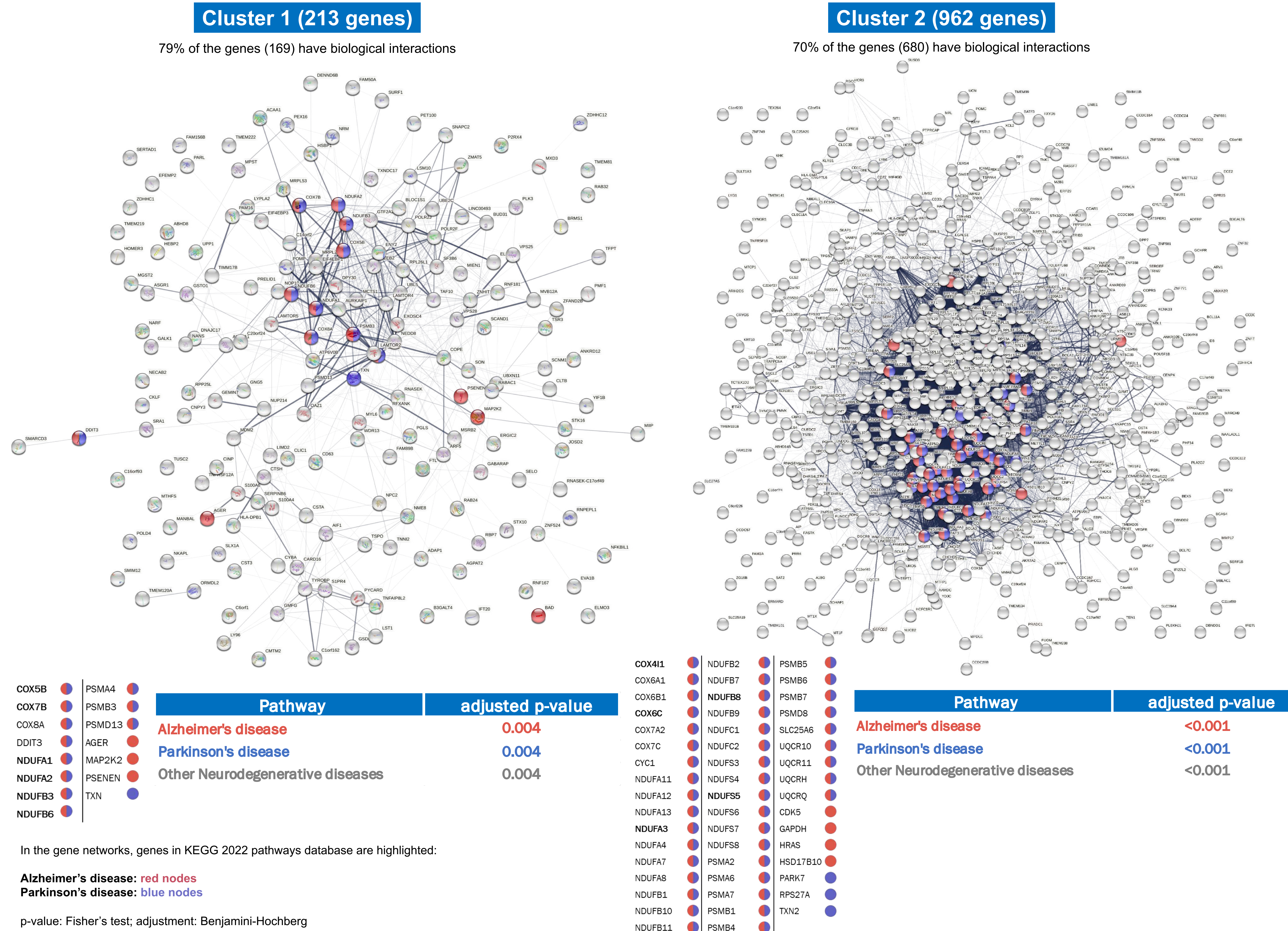


Data description

- Whole blood transcriptomics analysis (RNAseq) of patients with Parkinson's disease dementia was performed for the ANAVEX®2-73-PDD-001 study at two timepoints: Baseline and Week 14 (end of trial)
- All available RNA samples with RIN≥4¹ (130 samples) were analyzed
- The expression of 14,150 genes at these two timepoints were analyzed from both placebo and ANAVEX®2-73 treated patients

¹ RIN = RNA integrity number

In the two clusters of genes impacted by ANAVEX®2-73, over 70% of the genes are known to have biological interactions. Pathway enrichment analysis revealed that multiple neurodegenerative pathways, including Alzheimer's disease and Parkinson's disease were significantly (adjusted p-value < 0.005) enriched for these genes



Expression levels of dysregulated neurodegenerative genes were restored by the therapeutic effect of ANAVEX®2-73

- Both identified clusters are up-regulated for treated patients compared to placebo: Cluster 2 eigengene expression was significantly increased for patients treated with ANAVEX®2-73 high oral dose compared to placebo (p = 0.021)
- These genes are known to be down-regulated in the pathology of both Alzheimer's disease^{1,2} and Parkinson's disease^{3,4}

¹ Liang WS, Reiman EM, Valla J, et al. Alzheimer's disease is associated with reduced expression of energy metabolism genes in posterior cingulate neurons. *Proc Natl Acad Sci U S A*. 2008;105(11):4441-4446. doi:10.1073/pnas.0709259105
² Lannon K, Keohane A, Pidsley R, et al. Mitochondrial genes are altered in blood early in Alzheimer's disease. *Neurobiol Aging*. 2017;53:36-47. doi:10.1016/j.neurobiolaging.2016.12.029
³ Hauser MA, Li YJ, Xu H, et al. Expression profiling of substantia nigra in Parkinson disease, progressive supranuclear palsy, and frontotemporal dementia with parkinsonism. *Arch Neurol*. 2005;62(6):917-921. doi:10.1001/archneur.62.6.917
⁴ Hendrickx DM, Glaab E. Comparative transcriptome analysis of Parkinson's disease and Hutchinson-Gilford progeria syndrome reveals shared susceptible cellular network processes. *BMC Med Genomics*. 2020;13(1):114. Published 2020 Aug 18. doi:10.1186/s12920-020-00761-6

Key results

- Randomized, placebo-controlled clinical trial in 132 patients with Parkinson's disease dementia (PDD) included prespecified biomarkers of response as well as Whole Exome Sequencing DNA data and full RNA exome expression data collection. This study demonstrated dose-dependent, statistically significant improvement of dementia assessment, Quality of Episodic Memory with ANAVEX®2-73 (p=0.003) as well as significant improvement of Parkinson's assessment, MDS-UPDRS Total score (p=0.034) for patients treated with ANAVEX®2-73 high oral dose once daily during 14-week trial
- ANAVEX®2-73 transcriptomics analysis (RNAseq), identified a gene network that is differentially expressed in Parkinson's disease dementia (PDD) patients treated with ANAVEX®2-73 compared to placebo after 14 weeks of treatment
- Biological relevance of this gene network was assessed through pathway analysis and confirmed the impact of ANAVEX®2-73 treatment on pathways involved in neurodegenerative diseases, especially Alzheimer's disease and Parkinson's disease
- While genes are down-regulated in Alzheimer's disease and Parkinson's disease, ANAVEX®2-73 singularly impacted expression levels of these genes in multiple pathways by countering the pathological down-regulation of genes in both Alzheimer's (p<0.005) and Parkinson's disease (p<0.005) and other degenerative diseases (p<0.005) and these may represent additional potential biomarkers of disease pathology and response

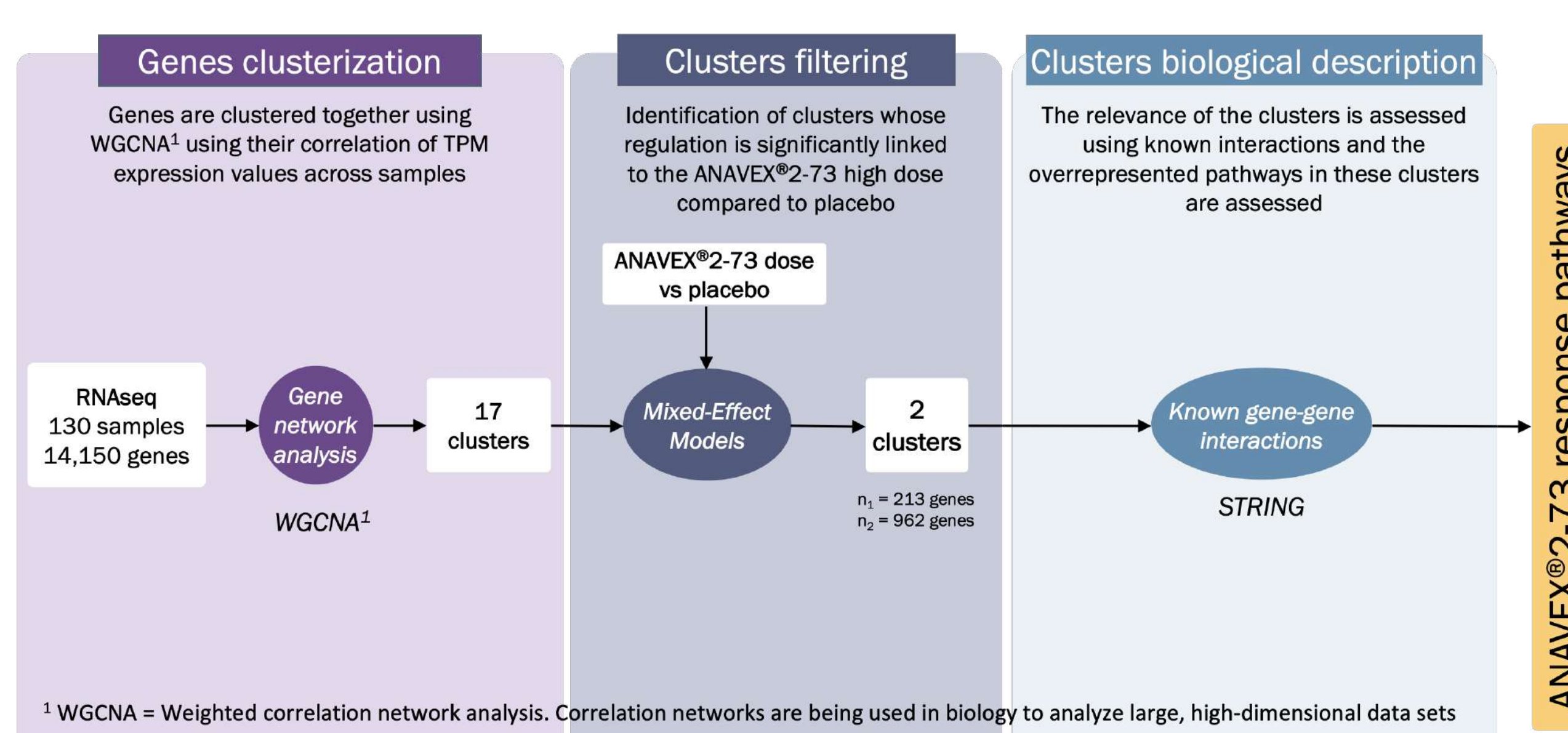
Conclusion

- These findings will facilitate contextualization of upcoming readout of ANAVEX®2-73 Phase 2b/3 Alzheimer's disease clinical trial
- Findings further support pivotal studies in Parkinson's disease and Parkinson's disease dementia
- These findings also enable the translational identification of additional potential therapeutic indications for ANAVEX®2-73

References

Hempel et al, *Alzheimer's Dement*, 2020
 Reyes et al, *Sci Rep*. 2021
 Hauser et al, *Arch Neurol*, 2005
 Hendricks et al, *BMC Med Genomics*, 2020
 WGCNA: Langfelder & Horvath, *BMC Bioinformatics*, 2008
 STRING: Szklarczyk et al, *NAR*, 2021
 KEGG: Kanehisa & Goto, *NAR*, 2000

Multi-disciplinary method to identify ANAVEX®2-73 genes response pathways



Genes clusterization

- Genes were clustered together using WGCNA¹, starting from their correlation of TPM² expression values across samples: WGCNA created 17 clusters (size: 13 to 11,190 genes)
- The cluster's eigengene³ was used as summary of expression level of the cluster

Clusters filtering

- For each cluster, the eigengene is used as target variable of a linear mixed effect model with 3 covariates: Dose, patient, and timepoint
- Clusters without significant (Dunnett's test) contrasts between treated and placebo across all timepoints are filtered out
- The ratio between cluster size and number of pathways was calculated and the top 2 clusters were eventually retained

Clusters biological description

- For each cluster, functional interactions between the genes of the cluster were assessed using the STRING database (Edge score >0.150; no text mining edges)
- Genes that have no interaction with any other genes of the cluster were discarded, which led to a reduced cluster
- Pathway enrichment analysis was performed on these reduced clusters. False Discovery Rate (FDR)⁴ with adjustment for multiple testing (Benjamini-Hochberg procedure) was used to characterize pathway overrepresentation

¹ WGCNA = Weighted correlation network analysis. Correlation networks are being used in biology to analyze large, high-dimensional data sets
² TPM = Transcript per million. TPM value represents a relative expression level that should be comparable between samples
³ Eigengene = One of a set of a genes matrix that tabulates the mRNA or gene expression of the genes across the samples
⁴ FDR = False Discovery Rate: adjustment for multiple testing with the Benjamini-Hochberg procedure