

Supplementary Materials

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Tom Hähnel^{1,2*}, Tamara Raschka^{1,3} Stefano Sapienza^{4,5}, Jochen Klucken^{4,5,6}, Enrico Glaab⁴, Jean-Christophe Corvol⁷, Björn H. Falkenburger^{2,8}, Holger Fröhlich^{1,3}

1. Department of Bioinformatics, Fraunhofer Institute for Algorithms and Scientific Computing (SCAI), Sankt Augustin, Germany
2. Department of Neurology, Medical Faculty and University Hospital Carl Gustav Carus, TUD Dresden University of Technology, Dresden, Germany
3. Bonn-Aachen International Center for IT, University of Bonn, Bonn, Germany
4. Biomedical Data Science, Luxembourg Centre for Systems Biomedicine (LCSB), University of Luxembourg, Esch-sur-Alzette, Luxembourg
5. Luxembourg Institute of Health (LIH), Strassen, Luxembourg
6. Centre Hospitalier de Luxembourg (CHL), Luxembourg
7. Sorbonne Université, Paris Brain Institute – ICM, Inserm, CNRS, Assistance Publique Hôpitaux de Paris, Pitié-Salpêtrière Hospital, Department of Neurology, Paris, France
8. German Center for Neurodegenerative Diseases (DZNE), Tatzberg 41, 01307 Dresden, Germany

Corresponding author:

Dr. med. Tom Hähnel
Department of Bioinformatics
Fraunhofer Institute for Algorithms and Scientific Computing (SCAI)
Schloss Birlinghoven 1
53757 Sankt Augustin, Germany
Phone: +49 (0)351 458 11880
Email: tom.haehnel@scai-extern.fraunhofer.de

Running title: Parkinson's Disease Progression Subtypes

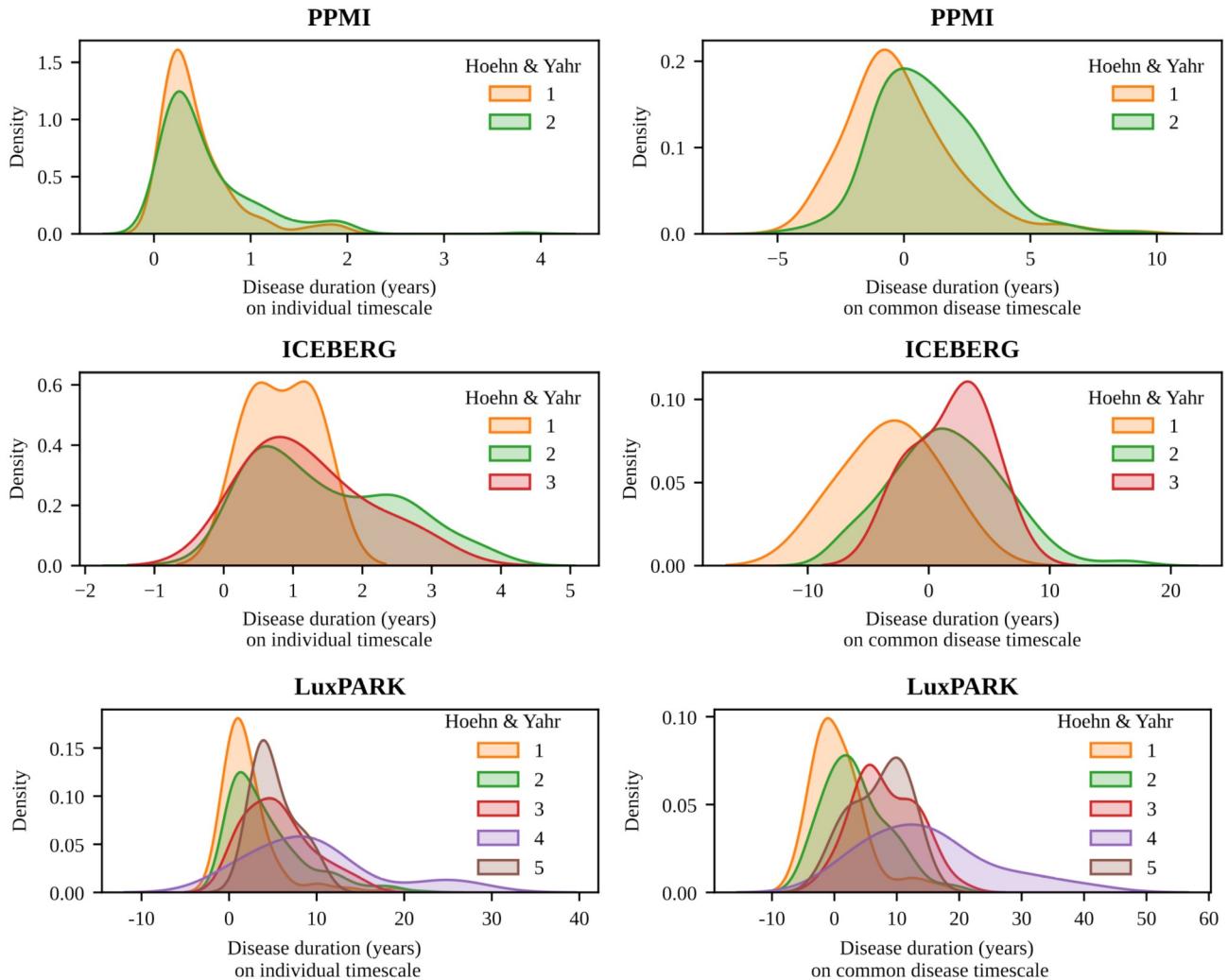
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Table of Contents

Supplementary Figures and Tables.....	3
Forest plots for symptom domain progression (in cohort).....	31
Forest plots for symptom domain progression (cross-cohort validation).....	32
Forest plots for symptom domain baseline associations (in cohort).....	33
Forest plots for symptom domain baseline associations (cross-cohort validation).....	34
ICEBERG study group.....	35
NCER-PD/LuxPARK consortium.....	36

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Supplementary Figures and Tables



Supplementary Figure 1: Effect of time-aligning PwPD on distributions of H&Y stages

The H&Y distributions from PPMI, ICEBERG and LuxPARK at baseline are depicted. On the left side, H&Y stages are plotted against the original time scale. On the right side, H&Y stages are plotted against the common timescale calculated from the LTJMM.

Abbreviations: H&Y: Hoehn&Yahr, LTJMM: latent time joint mixed-effects model

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Study and parameter	Fast-progressing subtype	Slow-progressing subtype	p-value
Age (years)			
PPMI	67.6	62.0	<0.0001
ICEBERG	64.0	63.7	0.86
LuxPARK	70.1	66.8	<0.0001
Age at onset (years)			
PPMI	67.1	61.4	<0.0001
ICEBERG	62.5	61.4	0.86
LuxPARK	67.0	60.5	<0.0001
Disease duration (years)			
PPMI	0.3	0.3	0.86
ICEBERG	1.3	1.2	0.86
LuxPARK	2.8	3.0	0.44
Sex (% male)			
PPMI	73.0 %	65.4 %	0.38
ICEBERG	71.4 %	58.9 %	0.38
LuxPARK	73.2 %	65.4 %	0.21

Supplementary Table 1: Demographic differences between progression subtypes

PwPD baseline characteristics for fast-progressing and slow-progressing subtypes for the three cohorts PPMI, ICEBERG and LuxPARK. For sex, percentage of male PwPD is shown. For other characteristics, median values are reported. Corresponding p-values were corrected for multiple testing using Benjamini-Hochberg procedure.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Symptom domain	Outcome	Definition/calculation of the outcome
Anxiety	NMSQ Anxiety	NMSQ item 17
	HADS anxiety	HADS anxiety sub-score
	STA	STA sum score
	PDQ39 Anxiety	PDQ39 item 21
	UPDRS I Anxiety	UPDRS I item 4
Apathy	DAS	DAS sum score
	SAS	SAS sum score
	UPDRS I Apathy	UPDRS I item 5
Autonomic symptoms	NMSQ Autonomic	NMSQ sum of items 4, 5, 6, 7, 8, 9, 19, 20, 28
	SCOPA-AUT	SCOPA sum score
	UPDRS I Autonomic	UPDRS I sum of items 10, 11, 12
Attention	NMSQ Attention	NMSQ item 15
	Letter Number Sequencing	Letter Number Sequencing score
	Digit Span	Digit Span Score: sum of forward scores and backward scores
	MATTIS Attention	MATTIS attention sub-score
	MOCA Attention	MoCA sum of: digits, letters, subtraction points
	MMSE Attention	MMSE attention sub-score
	PDQ39 Attention	PDQ39 item 31
	SIQCODE Attention	Short IQCODE score item 11
Conceptualization	MATTIS Conceptualization	MATTIS conceptualization sub-score
	MOCA Abstraction	MoCA abstraction sub-score
	FAB Conceptualization	FAB item 1
Language	Boston Naming Test	Boston Naming Test sum score
	MOCA Language + Naming	MoCA sum of items: naming, repeat and verbal fluency task
	VFT phonematic F	phonematic VFT F total word count
	VFT phonematic S	phonematic VFT S total word count
	VFT semantic animal	semantic VFT animal total word count
	VFT semantic sum	semantic VFT total word count (sum of tasks colors, fruits, towns, animals)
	VFT semantic supermarket	semantic VFT supermarket total word count
	MMSE Language	MMSE language sub-score
Memory	FAB VFT	FAB lexical fluency item
	NMSQ Memory	NMSQ item 12
	CERAD Words DR	CERAD word count immediate recall
	CERAD Words IR	CERAD word count delayed recall
	CERAD Words Recognition	CERAD recognition (number of correct, Yes + No)
	Hopkins Verbal Learning Test DR	Hopkins Verbal Learning Test delayed recall
	Hopkins Verbal Learning Test IR	Hopkins Verbal Learning Test immediate recall
	MOCA Orientation + Memory	MoCA sum of: memory (uncued only), orientation
	MATTIS Memory	MATTIS memory sub-score
	MMSE Memory	MMSE sum of: orientation (location + time), words memorization
Overall Cognition	SIQCODE Memory	Short IQCODE score sum of items 1, 2, 3, 4, 5, 6, 7
	PDQ39 Memory	PDQ39 item 32
	MATTIS	MATTIS sum score
	MMSE	MMSE sum score
	MoCA	MoCA sum score
Overall Cognition	SIQCODE	Short IQCODE score sum score
	FAB	FAB sum score

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Symptom domain	Outcome	Definition/calculation of the outcome
	PDQ39 Cognition	PDQ39 sum of items 31, 32
	UPDRS I Cognition	UPDRS I item 1
	NMSQ Cognition	NMSQ sum of items 12, 15
Visu-executive function	MMSE Construction	MMSE item 30
	Judgment Line Orientation	Judgment of Line Orientation sum score
	Symbol Digit Modalities	Symbol Digital Modalities sum score
	Stroop Errors	Stroop test number of errors
	Stroop Time	Stroop test required time
	Trailmaking A	Trail Making Test A time
	Trailmaking B	Trail Making Test B time
	MATTIS Initiation + Construction	MATTIS sum of: sub-score initiation, sub-score construction
	FAB 3-6	FAB sum of items 3, 4, 5, 6
	MOCA Visuospatial/Executive	MoCA visuospatial/executive sub-score
Depression	BDI	BDI sum score
	GDS	GDS sum score
	HADS depression	HADS depression sub-score
	PDQ39 Depression	PDQ39 sum of items 17, 18, 19, 20, 22
	NMSQ Depression	NMSQ sum of items 13, 16
Fatigue	UPDRS I Depression	UPDRS 1 item 3
	UPDRS I Fatigue	UPDRS 1 item 13
Hallucinations	NMSQ Hallucination	NMSQ sum of items 14, 30
	UPDRS I Hallucinations	UPDRS 1 item 2
Impulsivity	QUIP	QUIP sum score
	QUIP-RS	QUIPRS sum score
Motor symptoms (overall)	PDQ39 ADL	PDQ39 ADL sub-score
	Pegboard	PEGBoard sum of: average of left hand, right hand and both hands
	UPDRS II	UPDRS II sum score
	UPDRS III off	UPDRS III sum score (OFF only)
	UPDRS III on	UPDRS III sum score (ON only)
	UPDRS IV	UPDRS IV sum score
Non motor symptoms (overall)	NMSQ	NMSQ sum score
	UPDRS I	UPDRS I sum score
Overall disease severity	UPDRS I-III on	UPDRS I, II, III sum (ON only)
	UPDRS I-III off	UPDRS I, II, III sum (OFF only)
	FAQ	FAQ sum score
	PDQ39	PDQ39 sum score
	SEADL	SEADL score
	H&Y	Hoehn & Yahr
	CGIS	CGI-S score
	NMSQ Pain	NMSQ item 10
	PDQ39 Pain	PDQ39 sum of items 37, 38
	UPDRS I Pain	UPDRS 1 item 9
Axial & PIGD symptoms	UPDRS III axial off	UPDRS III axial score (OFF only)
	UPDRS III axial on	UPDRS III axial score (ON only)
	FOGAC	FOGAC sum score
	FOGQ	FOGQ sum score

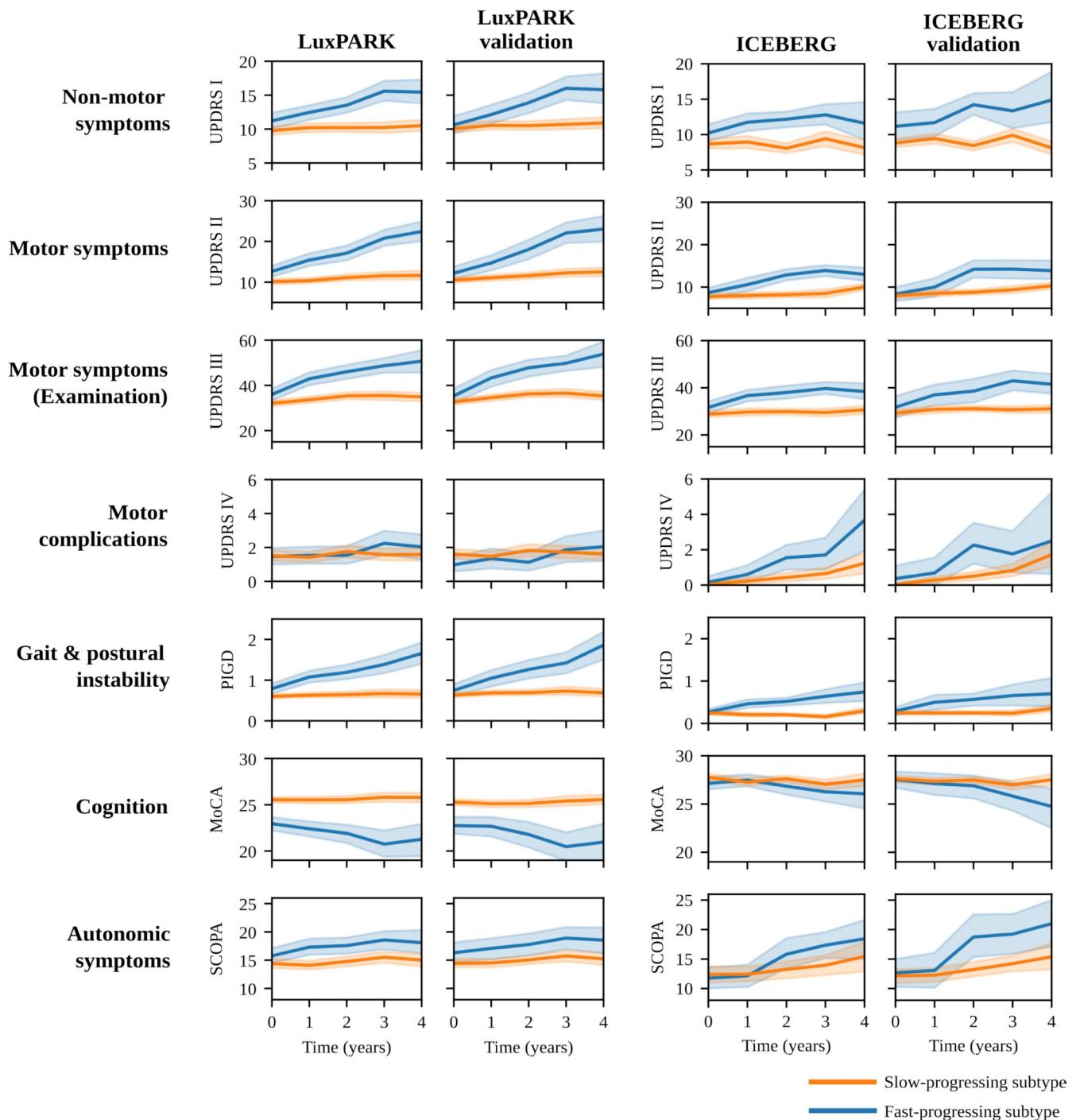
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Symptom domain	Outcome	Definition/calculation of the outcome
	GABS Examination	GABS sum of items 8-24
	GABS Questionnaire	GABS sum of items 1-7
	NFOGQ	NFOGQ sum score
	PDQ39 Mobility	PDQ39 mobility sub-score
	PIGD off	PIGD score (OFF only)
	PIGD on	PIGD score (ON only)
	TUG	Timed Up and Go time
Sleep (general)	ESS	ESS sum score
	PDSS	PDSS sum score
	UPDRS I Sleep	UPDRS I sum of items 7, 8
	NMSQ Sleep	NMSQ sub of items 22, 23
RBD Sleep	RBD-HK	RBD-HK sum score
	RBD-SQ	RBD-SQ sum score
	NMSQ RBD	NMSQ sum of items 24, 25
Smell	NMSQ Smell	NMSQ item 2
	Sniffin Test	Sniffin Test score
	UPSIT	UPSIT sum score
Tremor	TD off	TD score (OFF only)
	TD on	TD score (ON only)

Supplementary Table 2: Construction of symptom domains

Abbreviations: BDI: Beck Depression Inventory, CERAD: Consortium to Establish a Registry for Alzheimer's Disease, CGIS: Clinical Global Impression-Severity, DAS: Dimensional Apathy Scale, ESS: Epworth Sleepiness Scale, FAB: Frontal Assessment Battery, FAQ: Functional Activities Questionnaire, FOGAC: Freezing of Gait AC, FOGQ: Freezing of Gait Questionnaire, GABS: Clinical Gait and Balance Scale, GDS: Geriatric Depression Scale, H&Y: Hoehn & Yahr scale, HADS: Hospital Anxiety and Depression Scale, MATTIS: Mattis Dementia Rating Scale, MMSE: Mini Mental Status Examination, MOCA: Montreal Cognitive Assessment, NFOGQ: New Freezing of Gait Questionnaire, NMSQ: Non-Motor Symptoms Questionnaire, PDQ39: Parkinson's Disease Questionnaire-39, PDSS: Parkinson's Disease Sleep Scale, PIGD: Postural Instability and Gait Disorder score, QUIP: Questionnaire for Impulsive-Compulsive Disorders, QUIP-RS: QUIP-Rating Scale, RBD-HK: REM Sleep Behavior Disorder Questionnaire-Hong Kong, RBD-SQ: REM Sleep Behavior Disorder Screening Questionnaire, SAS: Starkstein Apathy Scale, SCOPA-AUT: Scales for Outcomes in Parkinson's Disease-Autonomic Dysfunction, SEADL: Schwab and England Activities of Daily Living Scale, SIQCD: Short Informant Questionnaire on Cognitive Decline in the Elderly, STA: State-Trait Anxiety Inventory, TD: Tremor Dominance Score, TUG: Timed Up and Go, UPDRS: MDS-Unified Parkinson's Disease Rating Scale, UPSIT: University of Pennsylvania Smell Identification Test, VFT: Verbal Fluency Task

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

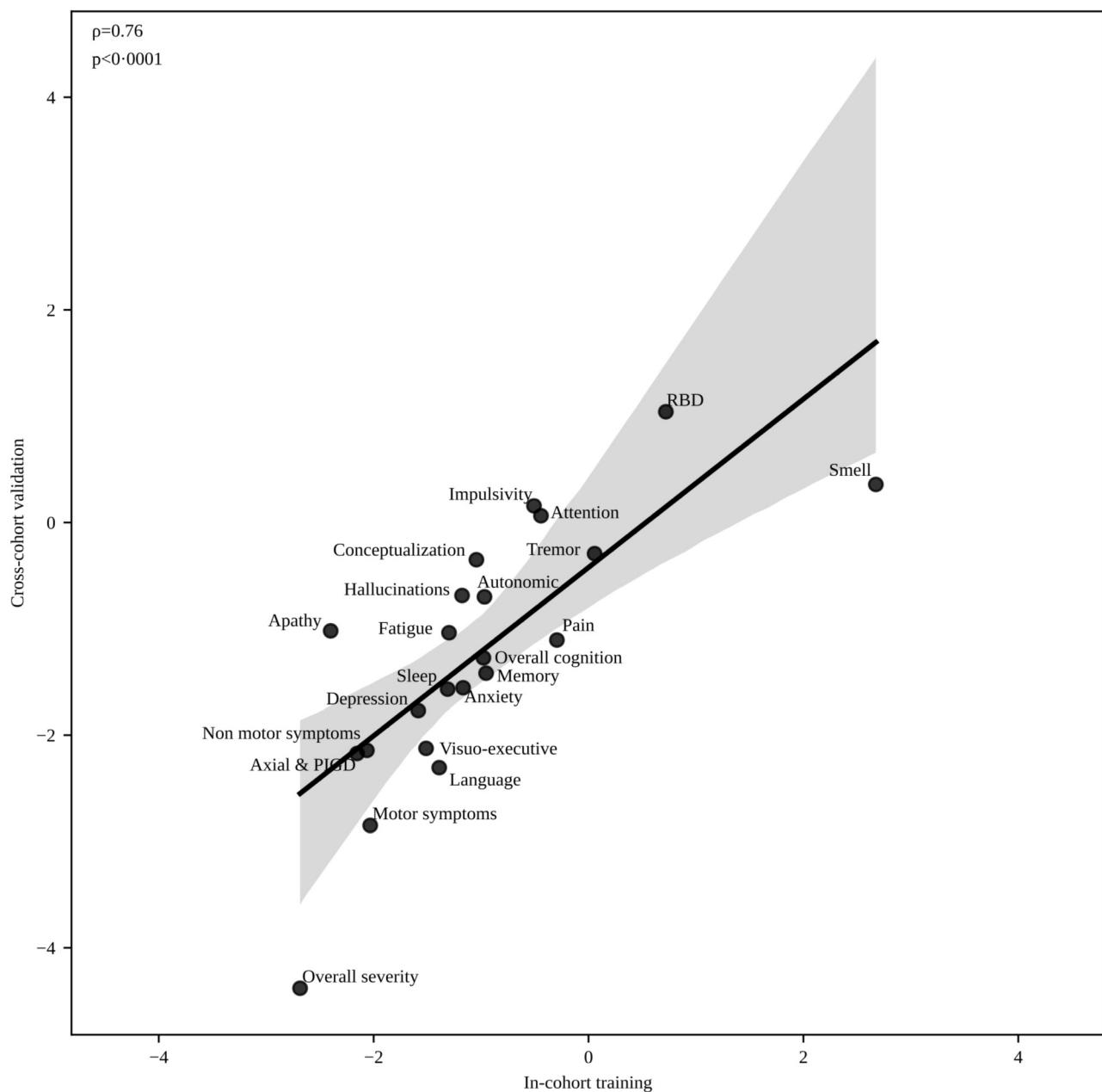


Supplementary Figure 2: Progression trajectories of subtypes for motor and non-motor symptoms (validation)

Progression of motor symptoms (UPDRS II/III/IV, PIGD) and non-motor symptoms (UPDRS I, MoCA, SCOPA) for the slow-progressing subtype (orange) and fast-progressing subtype (blue) for the ICEBERG and LuxPARK cohort. The in-cohort training results and the cross-cohort validation results (models trained on PPMI) are shown side by side. Mean and 95% confidence interval for each subtype are shown.

Abbreviations: MoCA: Montreal Cognitive Assessment, PIGD: Postural Instability and Gait Dysfunction score, SCOPA: Scales for Outcomes in Parkinson's Disease-Autonomic Dysfunction, UPDRS: Unified Parkinson's Disease Rating Scale.

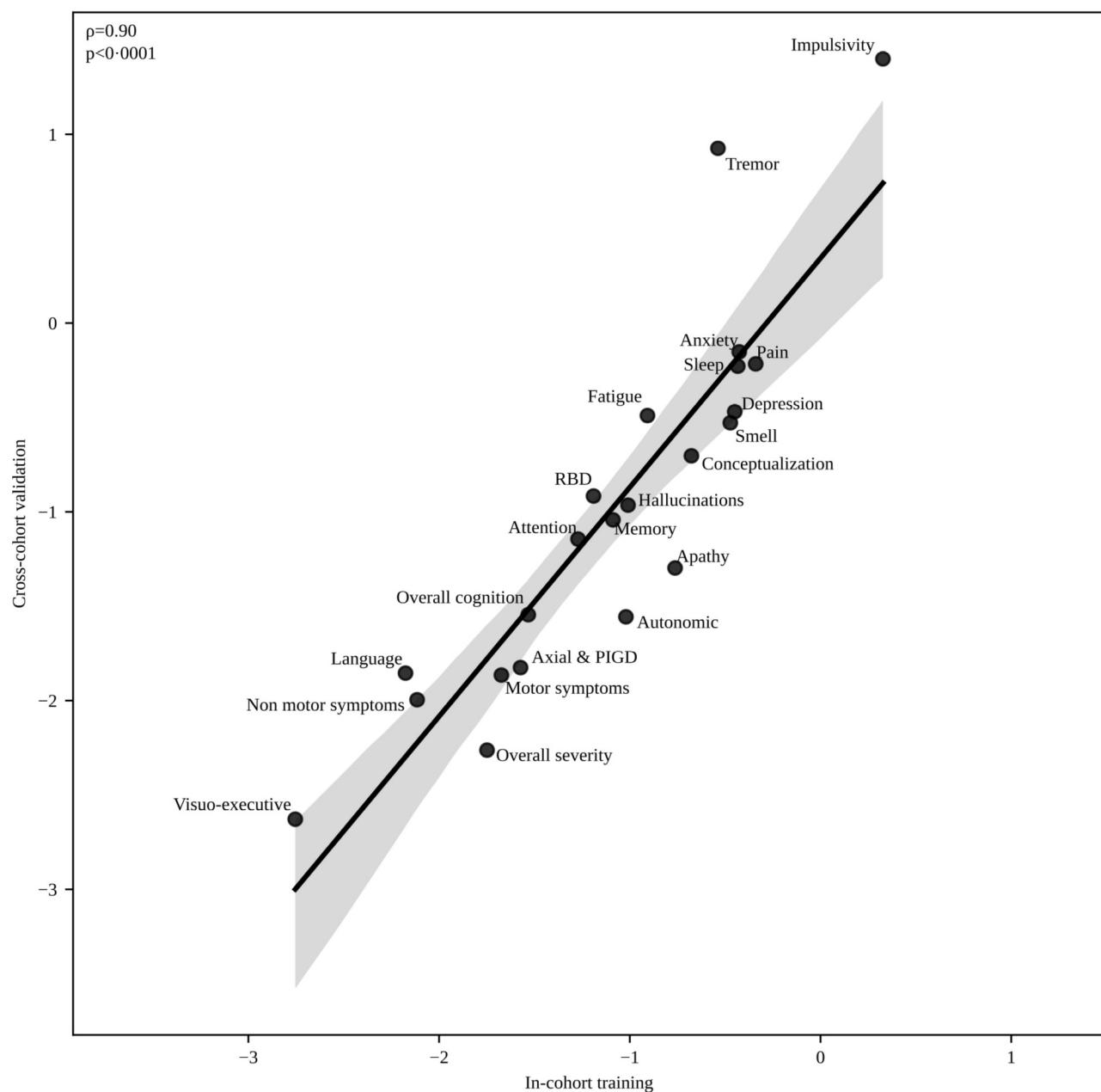
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 3: Symptom domain progression rate validation

The figure depicts the correlation of standardized mean differences (SMDs) of progression rates calculated for each symptom domain using the in-cohort training approach and the cross-cohort validation approach (i.e. models trained on PPMI). The 95% confidence interval of the regression line is depicted in gray. The Pearson correlation coefficient with corresponding p-value is shown.

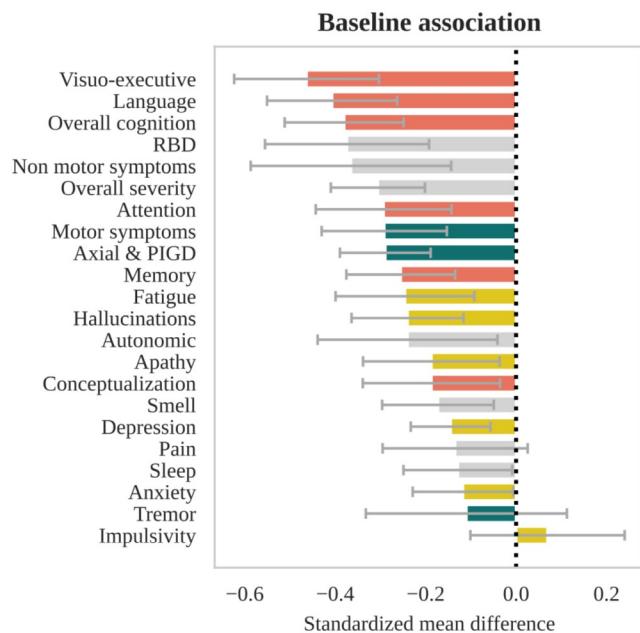
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 4: Symptom domain baseline associations validation

The figure depicts the correlation of average regression coefficients for baseline outcomes calculated for each symptom domain using the in-cohort training approach and the cross-cohort validation approach (i.e. models trained on PPMI). The 95% confidence interval of the regression line is depicted in gray. The Pearson correlation coefficient with corresponding p -value is shown.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

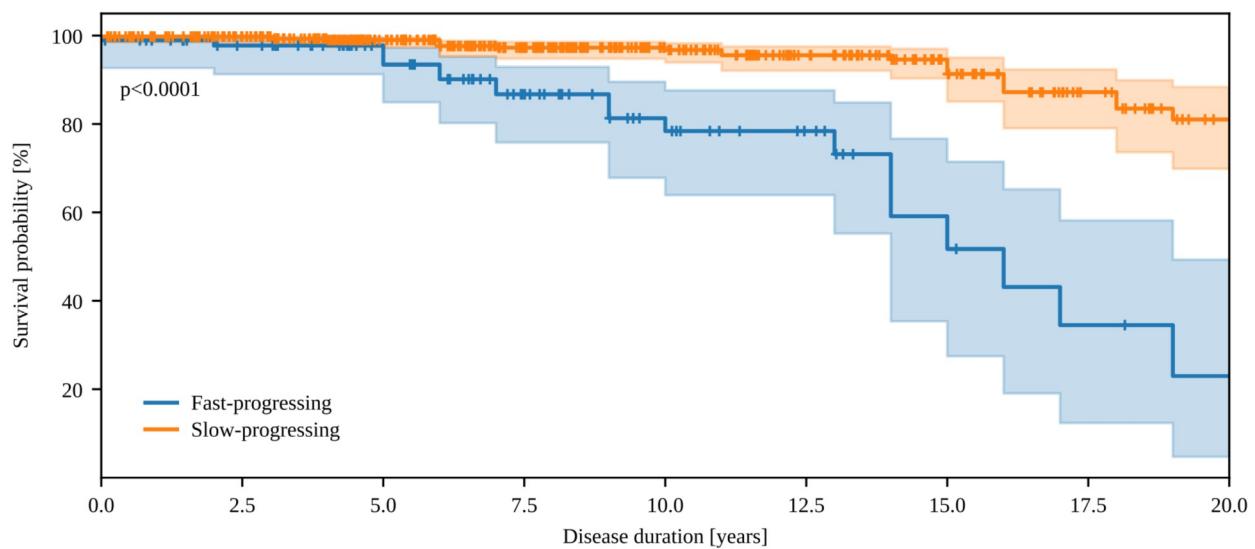


Supplementary Figure 5: Direct comparison of baseline characteristics between progression subtypes

Standardized mean differences (SMD) were calculated for symptom domains at baseline between subtypes. In contrast to Fig. 2C in the main manuscript, baseline outcomes were compared directly without a correction for differences in disease duration. Negative values indicate that more severe symptoms at baseline are associated with the faster subtype. 95% confidence intervals are shown and were corrected for multiple testing.

Abbreviations: PIGD: Postural Instability and Gait Dysfunction score, RBD: REM behavior sleep disorder

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



	At risk	526	466	366	272	188	133	83	48	29
Censored	33	90	186	271	351	404	446	475	491	
Events	2	5	9	18	22	24	32	38	41	

Supplementary Figure 6: Survival curves (validation)

Kaplan-Meier estimator for survival probability on the common disease timescale for fast-progressing (blue) and slow-progressing (orange) PwPD in LuxPARK. Right-censored observations are indicated by a small vertical tick. The corresponding p-value for the subtype covariate from the cox proportional hazard model is reported. 95% confidence intervals are shown. The analysis was done using the PPMI-trained model as cross-cohort validation.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

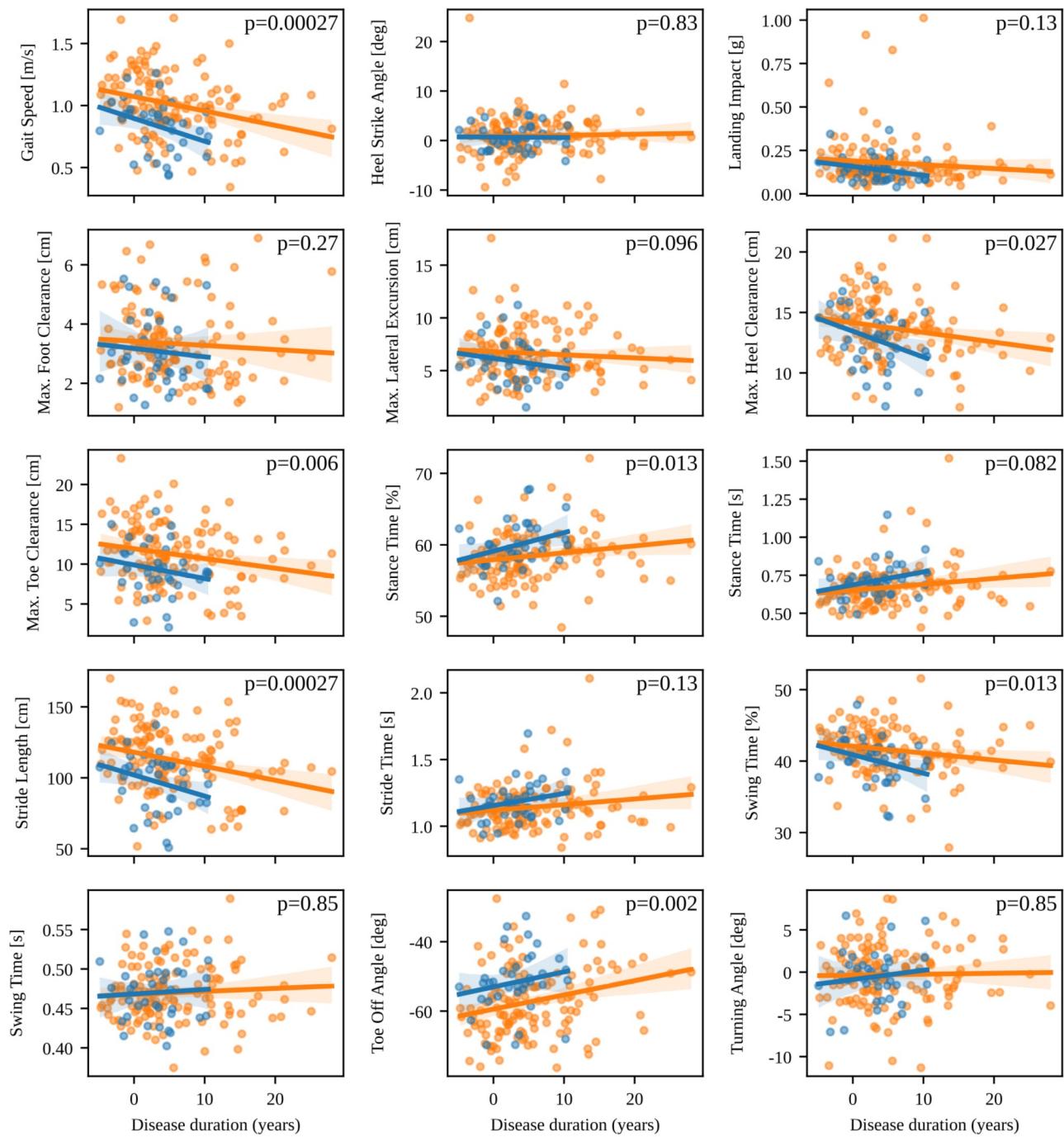
Gait parameter	Unit	Description
Gait speed	m/s	The average walking speed.
Heel strike angle	degree	The angle between the toes and the surface when the foot lands.
Landing impact	g	The maximum vertical acceleration during landing of the foot.
Max. foot clearance	cm	The maximum elevation of the foot from the ground during the swing phase.
Max. heel clearance	cm	The maximum elevation of the heel from the ground during the swing phase.
Max. toe clearance	cm	The maximum elevation of the toe from the ground during the swing phase.
Max. lateral excursion	cm	The maximum lateral deviation of the foot in the swing phase, measured from an imaginary line between the foot's position at start and end of the swing phase.
Stance time (absolute)	s	Duration from initial contact of the foot with the surface until start of next swing phase of the foot.
Stance time (relative)	%	Proportion of stance time divided by the total duration of the stride.
Stride length	cm	The length of one stride.
Stride time	s	Sum of stance time and swing time.
Swing time (absolute)	s	Duration from start of swing until next foot contact with the surface.
Swing time (relative)	%	Proportion of swing time divided by the total duration of the stride.
Toe off angle	degree	The angle between the heel and the surface at the beginning of the swing phase.
Turning angle	degree	The angle between the direction of the last swing phase (imaginary line between foot position at the beginning and end of the swing phase) and the orientation of the foot in the next stance phase.

Supplementary Table 3: Description of digital gait biomarkers.

Gait parameters were calculated as mean of all straight steps from the Timed Up and Go task. Turning steps were excluded from the calculation.

Abbreviations: max: maximum, min: minimum

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

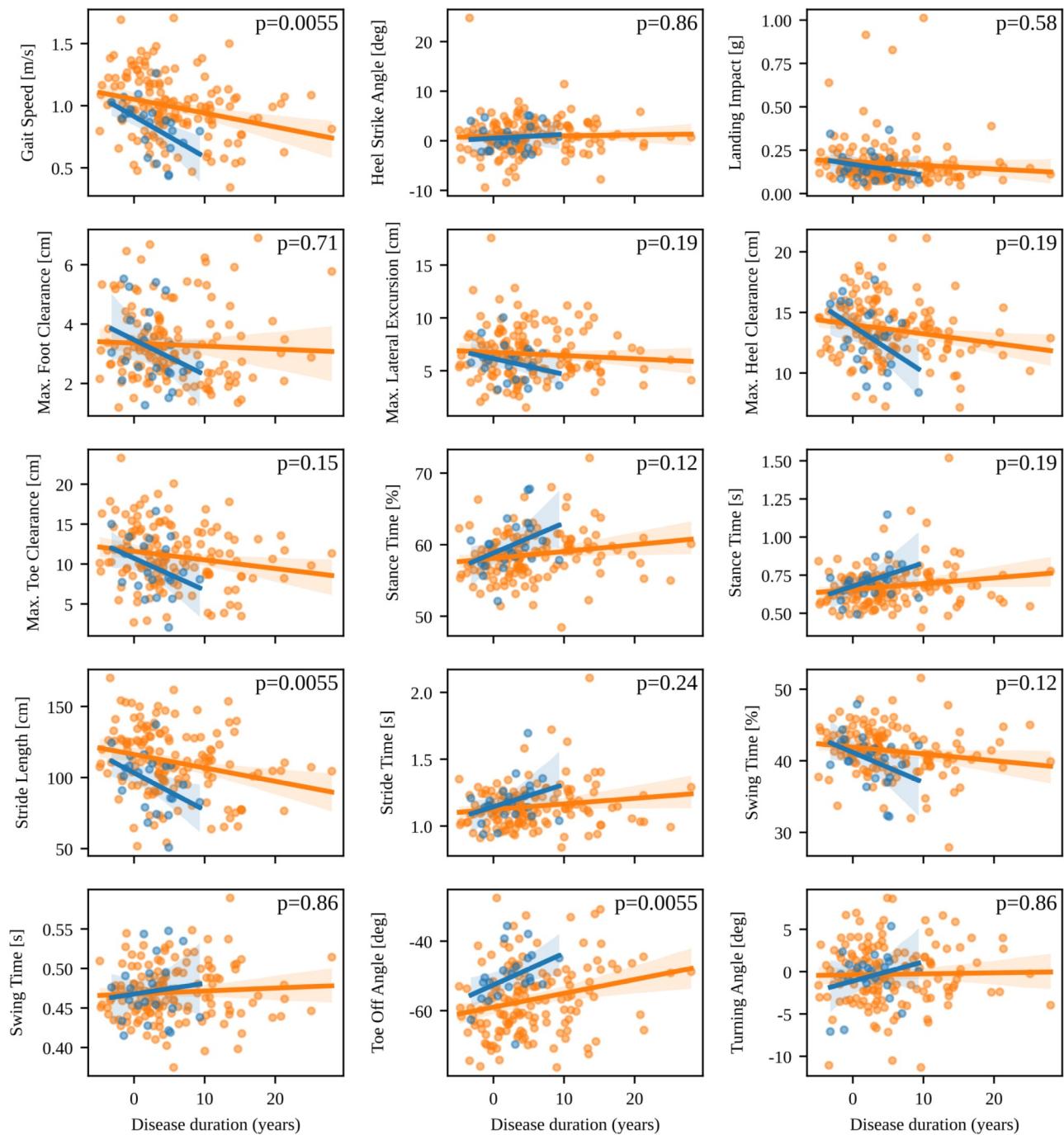


Supplementary Figure 7: Digital gait biomarkers

Correlation of all digital gait markers with disease duration on the common disease timescale for fast-progressing (blue) and slow-progressing (orange) PwPD. The corresponding p-values from the ANCOVA analyses are shown and were corrected for multiple testing. 95% confidence intervals are depicted.

Abbreviations: deg: degree.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

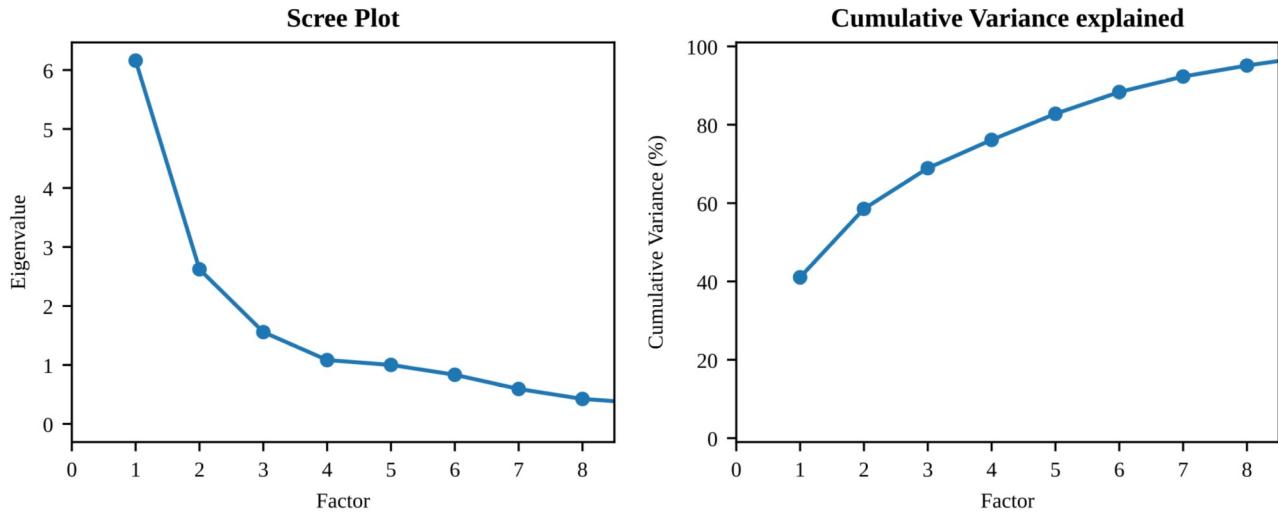


Supplementary Figure 8: Digital gait biomarkers (validation)

Correlation of all digital gait markers with disease duration on the common disease timescale for fast-progressing (blue) and slow-progressing (orange) PwPD. The corresponding p-values from the ANCOVA analyses are shown and were corrected for multiple testing. 95% confidence intervals are shown. The analysis was done using the PPMI-trained model as cross-cohort validation.

Abbreviations: deg: degree.

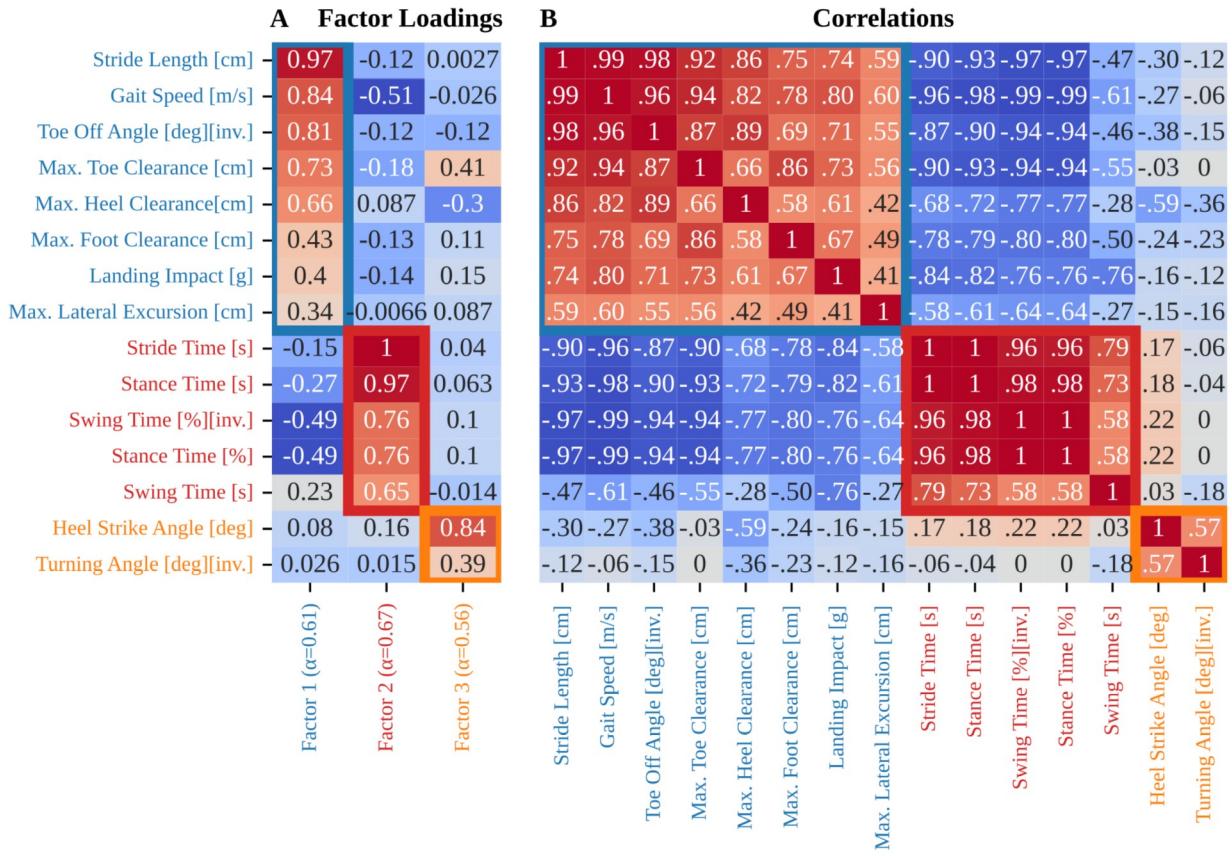
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 9: Scree plot and variance explained for exploratory factor analysis of digital gait parameters

An exploratory factor analysis was performed using the LuxPARK gait data. The figure shows the Eigenvalues (left) and cumulative variance explained (right) depending on the chosen number of factors. Based on the Scree-Plot, we decided to use three factors.

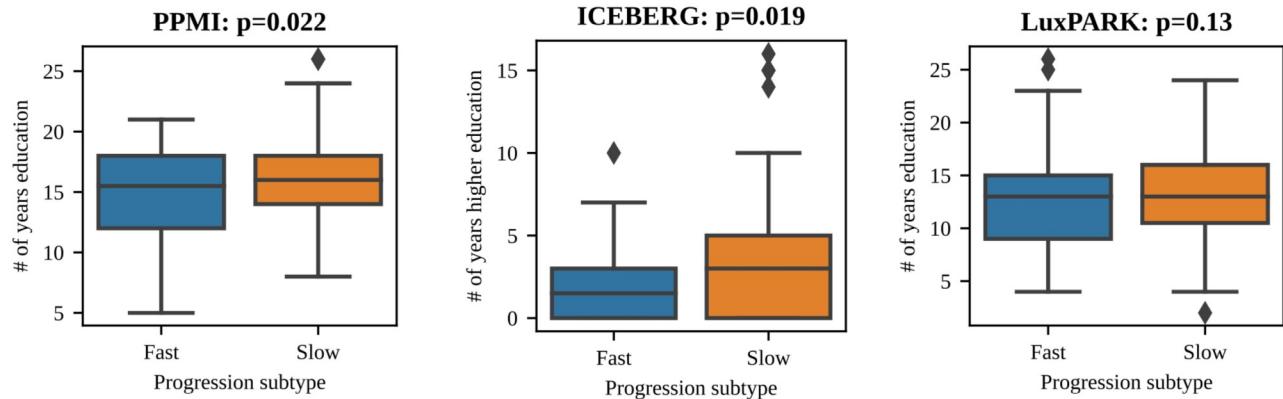
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 10: Factor analysis and correlation matrix for digital gait data

A: Factor loadings for all gait features and the three factors. The choice of three factors was derived from the scree plot displayed in Supplementary Figure 9. The gait features which are mostly determined by the same factor are surrounded by a colored rectangle. The features Toe Off Angle, Swing Time, Turning Angle (marked by “[inv.]”) had been inverted to enforce positive factor loadings for better visualization and for the calculation of Cronbach's alpha, which is displayed below each column. The first factor primarily encompassed the spatial sequence of the step, including measures of length and height of the step. In contrast, the second factor was based on the timing of the stance and stride phases of the steps. The third factor incorporated two angles, i.e., the heel strike angle and turning angle. **B:** Correlation heatmap between gait features sorted by the loadings of each factor. Gait features belonging to the same factor are surrounded by a colored rectangle.

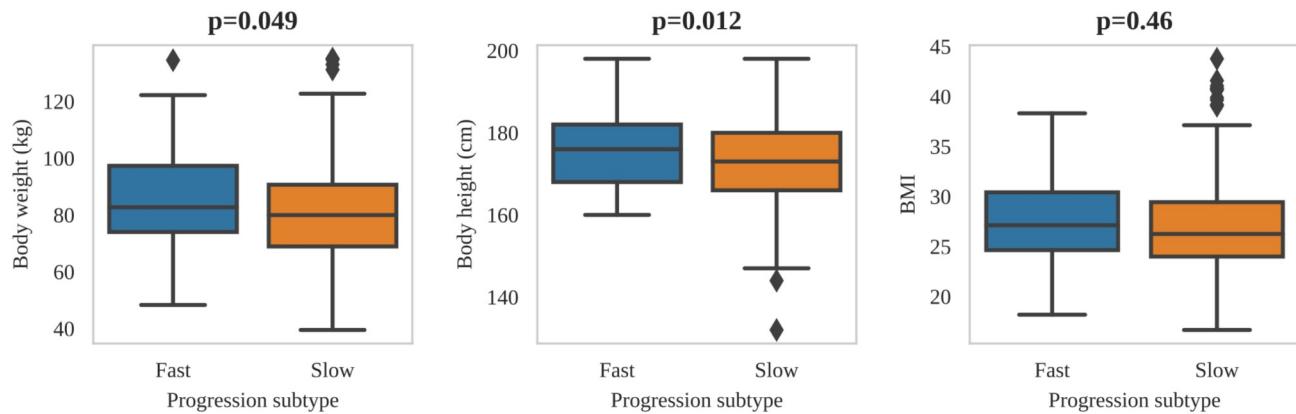
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 11: Association of PD progression subtypes with educational level

Comparison of education levels between both progression subtypes, i.e., number of education years (PPMI, LuxPARK) and number of years with higher education (ICEBERG). Correction for multiple testing was performed using Benjamini-Hochberg procedure. The boxplots are displayed with a median line, box borders representing the interquartile range (IQR), whiskers extending to 1.5 times the IQR, and outliers depicted as diamonds beyond the whiskers.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 12: Association of PD progression subtypes with body weight, body height and body mass index
 All analyzes were performed for PPMI. P-values were corrected for age and sex. Correction for multiple testing was performed using Benjamini-Hochberg procedure. The boxplots are displayed with a median line, box borders representing the interquartile range (IQR), whiskers extending to 1.5 times the IQR, and outliers depicted as diamonds beyond the whiskers.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Blood pressure parameter	p-value (uncorrected)	p-value (corrected for multiple testing)
Systolic blood pressure (supine)	0.45	0.68
Diastolic blood pressure (supine)	0.62	0.74
Systolic blood pressure (standing)	0.44	0.68
Diastolic blood pressure (standing)	0.24	0.68
Systolic blood pressure drop (supine - standing)	0.96	0.96
Diastolic blood pressure drop (supine - standing)	0.38	0.68

Supplementary Table 4: Association of PD progression subtypes with blood pressure

All analyzes were performed for PPMI. P-values were corrected for age and sex. Correction for multiple testing was performed using Benjamini-Hochberg procedure.

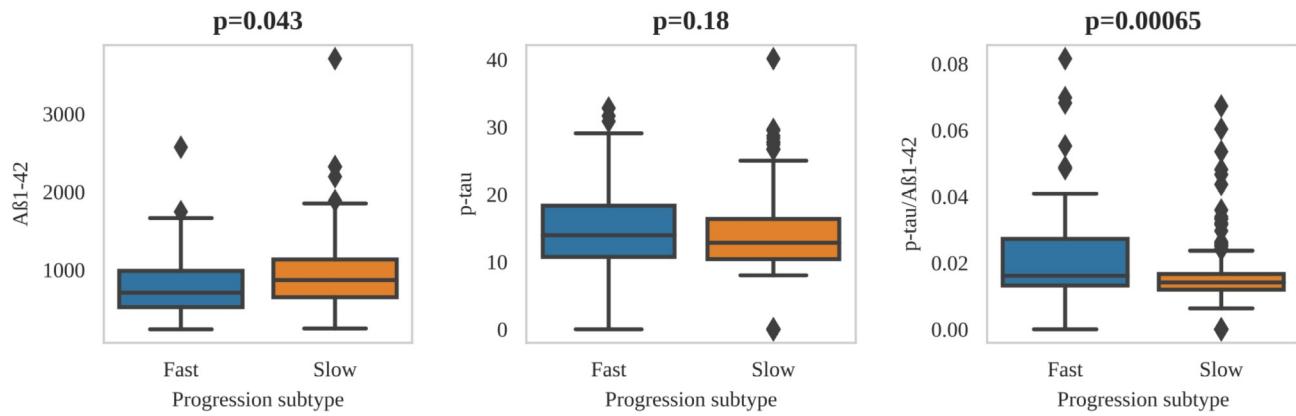
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Comorbidity group	p-value (uncorrected)	p-value (corrected for multiple testing)
Pulmonary	0.033	0.26
Ophthalmological	0.035	0.26
Metabolic/Endocrine	0.16	0.81
Dermatological	0.26	0.87
Psychiatric	0.46	0.87
Cardiovascular	0.47	0.87
Musculoskeletal	0.48	0.87
Allergy/immunologic	0.56	0.87
Other	0.67	0.87
Gastrointestinal	0.68	0.87
Gynecological/Urologic	0.71	0.87
Renal	0.75	0.87
Hemato/Lymphatic	0.75	0.87
ENT	0.86	0.92
Hepatobiliary	0.96	0.96

Supplementary Table 5: Association of PD progression subtypes with diagnoses groups

All analyzes were performed for PPMI. P-values were corrected for age and sex. Correction for multiple testing was performed using Benjamini-Hochberg procedure.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 13: Association of PD progression subtypes with Alzheimer's disease pathology cerebrospinal fluid biomarkers

All analyzes were performed for PPMI. P-values were corrected for age and sex. Correction for multiple testing was performed using Benjamini-Hochberg procedure. The boxplots are displayed with a median line, box borders representing the interquartile range (IQR), whiskers extending to 1.5 times the IQR, and outliers depicted as diamonds beyond the whiskers.

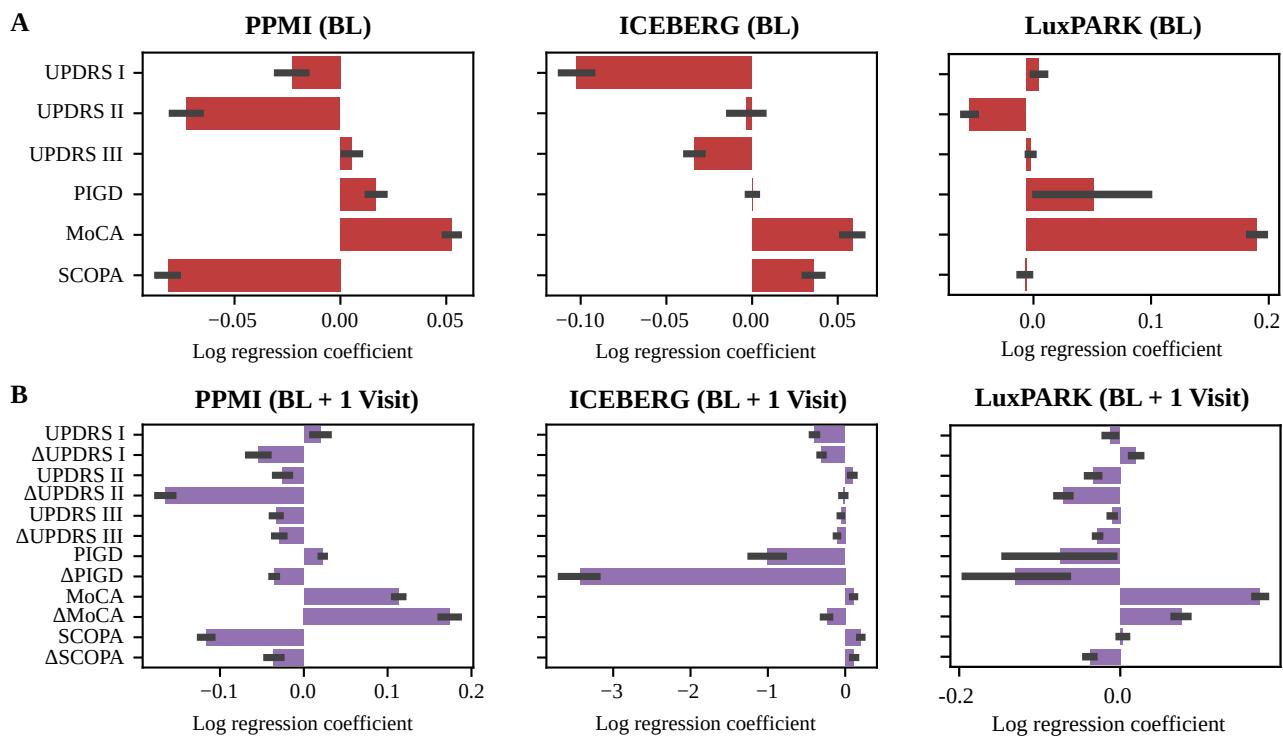
Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Comedication group	p-value (uncorrected)	p-value (corrected for multiple testing)
Calcium Channel Blockers	0.18	0.95
Beta Antagonists	0.31	0.95
NSARs (without ASS)	0.44	0.95
NSAR	0.53	0.95
Ibuprofen	0.63	0.95
Statins	0.73	0.95
ASS	0.83	0.95
Contraceptives	1.0	1.0

Supplementary Table 6: Association of PD progression subtypes with specific medications.

All analyzes were performed for PPMI. P-values were corrected for age and sex. Correction for multiple testing was performed using Benjamini-Hochberg procedure.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

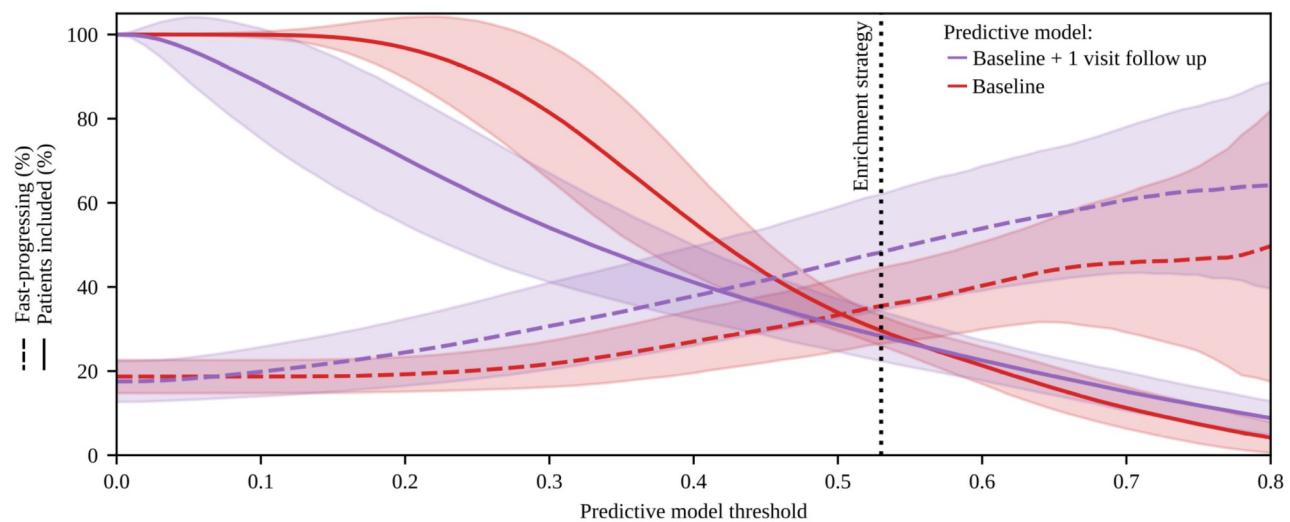


Supplementary Figure 14: Coefficients of logistic regression models for subtype predictions

Logistic regression coefficients with 95% confidence interval using baseline data (**A**, red) or baseline data with one follow up visit (**B**, purple) from the predictive logistic regression model are shown. Higher outcome scores together with positive coefficients influence the prediction towards the slow-progressing subtype and towards the fast-progressing subtype if coefficients are negative.

Abbreviations: BL: Baseline, Δ : Difference from first visit to baseline, MoCA: Montreal Cognitive Assessment, PIGD: Postural Instability and Gait Dysfunction score, SCOPA: Scales for Outcomes in Parkinson's Disease-Autonomic Dysfunction, UPDRS: Unified Parkinson's Disease Rating Scale.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 15: Trade-off between enriching fast-progressing PwPD and number of eligible PwPD

Depending on the chosen threshold applied to the logistic predictive model, the percentage of fast-progressing PwPD (dashed lines) and the percentage of PwPD being still eligible for study inclusion (solid lines) changes. Curves are displayed for the predictive model using baseline data (red) and the predictive model using data from baseline and one follow-up visit (purple). The vertical dotted line indicates the threshold of the predictive model, where still 30% of PwPD are eligible for study inclusion and a 47% enrichment of fast-progressing PwPD is achieved using the predictive model based on baseline data and one follow-up visit. 95% confidence intervals are depicted.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

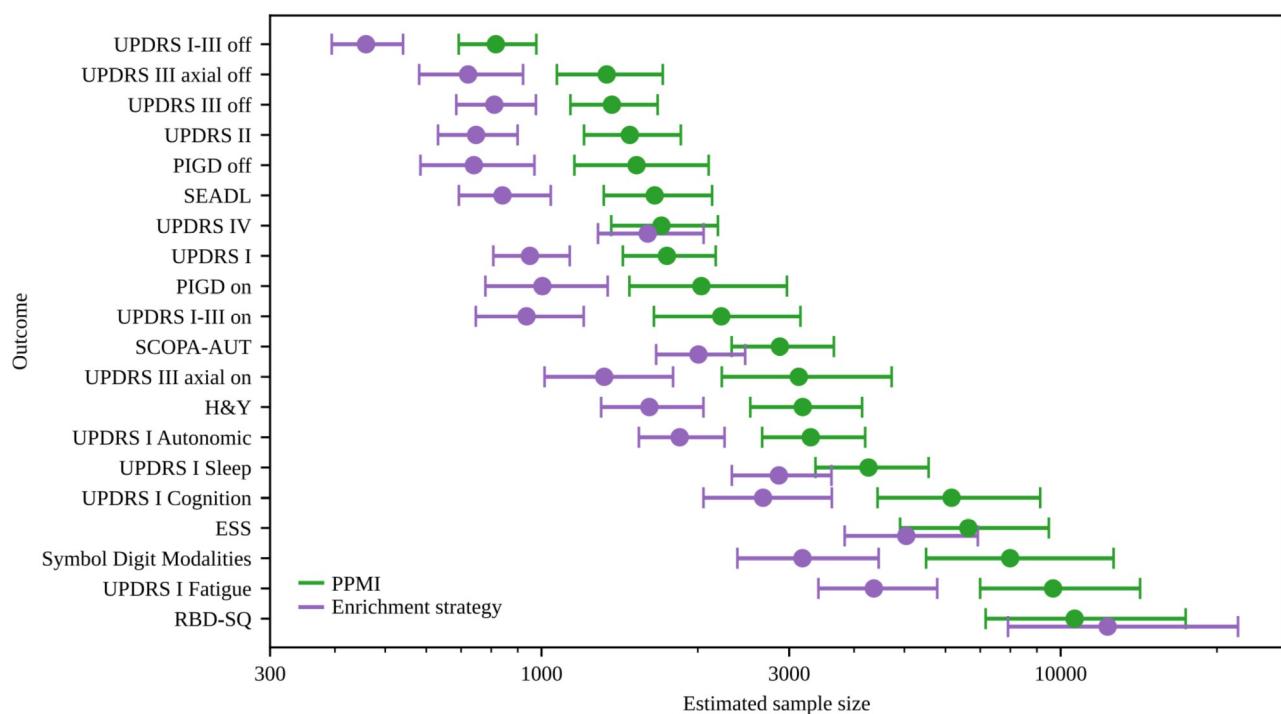
% fast-progressing PwPD	PPMI	ICEBERG	LuxPARK
No enrichment	18 %	27 %	26 %
BL enrichment (in-cohort)	36 %	43 %	47 %
BL+FU enrichment (in-cohort)	47 %	65 %	53 %
BL enrichment (cross-cohort)	-	27 %	38 %
BL+FU enrichment (cross-cohort)	-	38 %	41 %

Supplementary Table 7:Enrichment of fast-progressing PwPD using different predictive models

Predictive models were based on baseline data (BL) or baseline with one follow up visit (BL+FU). Models were trained on the same data set (in-cohort), or PPMI and cross-validated on ICEBERG/LuxPARK (cross-cohort). Using the predictive models and an appropriate threshold for the three cohorts (PPMI, ICEBERG, LuxPARK), the reported fractions of fast-progressing PwPD can be achieved in a study cohort by still allowing inclusion of 30% of all PwPD. The “No enrichment” row reports the fraction of fast-progressing in the original cohorts without applying any enrichment strategy.

Abbreviations: BL: baseline, FU: follow up

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis



Supplementary Figure 16: Subtype enrichment for sample size reduction in clinical trials using different outcomes

Required sample sizes for a clinical trial depending on the clinical score used as primary outcome in the trial. The required sample sizes calculated using the default PPMI cohort are shown in green. The required sample sizes using the enrichment strategy from Fig. 5A are shown in purple. Mean estimate and 95% confidence intervals are shown. Sample sizes were calculated for all outcomes listed in Supplementary Table 2 and assessed in PPMI. From these outcomes, only the 20 outcomes with lowest required sample sizes are shown. The estimated sample size is shown on a logarithmic axis.

Abbreviations: ESS: Epworth Sleepiness Scale, H&Y: Hoehn & Yahr, PIGD: Postural Instability and Gait Disorder score, RBD-SQ: REM Sleep Behavior Disorder Screening Questionnaire, SCOPA-AUT: Scales for Outcomes in Parkinson's Disease-Autonomic Dysfunction, SEADL: Schwab and England Activities of Daily Living Scale, UPDRS: Unified Parkinson's Disease Rating Scale.

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

% sample size reduction	PPMI	ICEBERG	LuxPARK
BL (in-cohort)	30 %	32 %	44 %
BL+FU (in-cohort)	43 %	56 %	52 %
BL (cross-cohort)	-	0 %	28 %
BL+FU (cross-cohort)	-	36 %	34 %

Supplementary Table 8: Sample size reduction in a simulated clinical trial using different predictive models for enrichment of fast-progressing PwPD

Predictive models were based on baseline data (BL) or baseline with one follow up visit (BL+FU). Models were trained on the same data set (in-cohort) or PPMI and cross-validated on ICEBERG/LuxPARK (cross-cohort). Using the predictive models and an appropriate threshold to the three cohorts (PPMI, ICEBERG, LuxPARK), the reported sample size reductions can be achieved by still allowing inclusion of 30% of all PwPD.

Abbreviations: BL: baseline, FU: follow up

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

	PPMI	ICEBERG	LuxPARK
number of clusters	2	2	2
learning rate	0.0001	0.001	0.0001
batch size	16	32	16
number of nodes (first hidden layer)	64	32	32
number of nodes (second hidden layer)	1	1	2

Supplementary Table 9: Results of VaDER hyperparameter optimization for PPMI, ICEBERG and LuxPARK

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Model	Parameter	Grid values	Baseline PPMI / ICEBERG / LuxPARK	Baseline + FU PPMI / ICEBERG / LuxPARK
Logistic regression	Lambda	0.001, 0.01, 0.1, 1, 10, 100, 1000	0.01 / 0.01 / 100	0.01 / 10 / 10
Random Forest	Bootstrap	True, False	True / True / True	True / True / True
	Maximum depth	10, 20, 30, 40	40 / 20 / 20	20 / 10 / 10
	Minimum samples per leaf	1, 2, 4	4 / 1 / 1	4 / 2 / 1
	Minimum samples per split	2, 5, 10	10 / 5 / 10	10 / 10 / 10
	Number of Estimators	200, 600, 800, 1000, 1200, 1400, 1600, 1800, 2000	800 / 1400 / 1800	1800 / 2000 / 200
XGBoost	Minimum Child Weight	1, 5, 10	10 / 1 / 1	5 / 1 / 5
	Gamma	0.5, 1, 1.5, 2, 5	2 / 0.5 / 5	0.5 / 1.5 / 1.5
	Subsample	0.6, 0.8, 1.0	0.8 / 0.6 / 0.8	0.8 / 0.6 / 1.0
	Colsample by tree	0.6, 0.8, 1.0	0.8 / 0.6 / 0.6	0.6 / 1.0 / 1.0
	Maximum Depth	3, 4, 5	4 / 4 / 3	4 / 3 / 3

Supplementary Table 10: Predictive model hyperparameter optimization

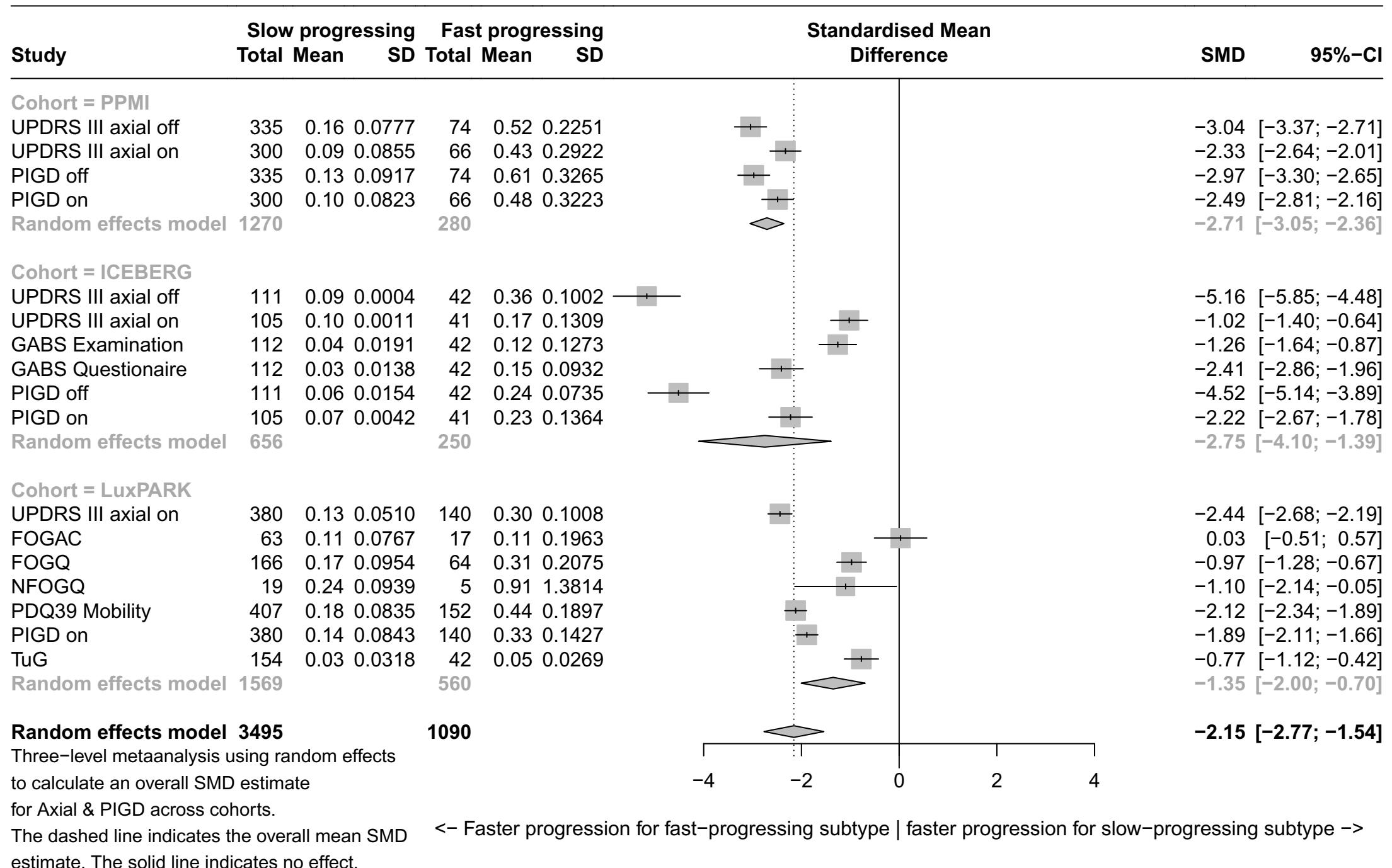
Hyperparameter space used for hyperparameter optimization. For Logistic regression, L2 penalization and hyperparameter grid search was used. For Random Forest and XGBoost, randomized hyperparameter search with 50 samples was used. Repeated stratified k-fold cross validation was performed using 5 splits and 20 repeats. Results of hyperparameter training for the baseline-only and baseline with one visit follow-up models are presented.

Abbreviations: FU: follow up

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Forest plots for symptom domain progression (in cohort)

Forest plot for progression characteristics of symptom domain Axial & PIGD



Forest plot for progression characteristics of symptom domain Depression

Study

	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = LuxPARK									
BDI	406	0.04	0.0176	149	0.14	0.0358	-0.10	-4.19	[-4.50; -3.88]
NMSQ Depression	408	1.04	0.5080	152	2.15	0.2609	-1.11	-2.43	[-2.67; -2.20]
PDQ39 Depression	407	0.06	0.0499	152	0.18	0.0605	-0.12	-2.31	[-2.54; -2.08]
UPDRS I Depression	408	0.84	0.1665	153	1.53	0.4505	-0.70	-2.51	[-2.75; -2.28]
Random effects model	1629			606				-2.86	[-3.72; -1.99]
Cohort = PPMI									
GDS	324	0.05	0.1681	73	0.35	0.1441	-0.30	-1.78	[-2.06; -1.50]
UPDRS I Depression	335	1.16	1.4484	74	2.83	2.1275	-1.67	-1.04	[-1.31; -0.78]
Random effects model	659			147				-1.41	[-2.13; -0.69]
Cohort = ICEBERG									
HADS depression	112	0.10	0.0186	42	0.16	0.0578	-0.06	-1.60	[-1.99; -1.20]
NMSQ Depression	112	2.00	0.4071	42	1.42	1.4046	0.58	0.72	[0.35; 1.08]
UPDRS I Depression	112	1.54	0.5269	42	0.83	1.2172	-0.71	0.91	[0.54; 1.28]
Random effects model	336			126				0.01	[-1.56; 1.59]
Random effects model	2624			879				-1.58	[-2.64; -0.53]
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Depression across cohorts. The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.									
<- Faster progression for fast-progressing subtype faster progression for slow-progressing subtype ->									

Forest plot for progression characteristics of symptom domain Overall severity

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG									
CGIS	112	1.07	0.0666	42	2.39	0.8408		-2.99	[-3.48; -2.50]
H&Y	112	-0.40	0.3209	42	0.57	0.1069		-3.45	[-3.97; -2.92]
SEADL	112	0.05	0.0260	42	0.13	0.1255		-1.17	[-1.55; -0.79]
UPDRS I-III off	111	0.14	0.0092	42	0.30	0.0654		-4.65	[-5.28; -4.01]
UPDRS I-III on	105	0.11	0.0103	41	0.23	0.0362		-5.75	[-6.51; -4.99]
Random effects model	552			209				-3.58	[-5.10; -2.06]
Cohort = LuxPARK									
FAQ	354	0.09	0.0549	124	0.30	0.1342		-2.47	[-2.73; -2.22]
H&Y	408	2.37	1.5849	153	2.93	2.3835		-0.31	[-0.49; -0.12]
PDQ39	403	0.10	0.0470	149	0.28	0.1213		-2.33	[-2.56; -2.10]
UPDRS I-III on	377	0.14	0.0350	138	0.34	0.1151		-2.99	[-3.26; -2.72]
Random effects model	1542			564				-2.02	[-3.18; -0.86]
Cohort = PPMI									
H&Y	335	4.88	1.8738	74	4.44	3.7381		0.19	[-0.06; 0.44]
SEADL	335	0.14	0.0788	74	0.58	0.2890		-3.09	[-3.42; -2.76]
UPDRS I-III off	335	0.26	0.1092	74	0.64	0.1259		-3.38	[-3.72; -3.04]
UPDRS I-III on	300	0.11	0.0952	66	0.46	0.2094		-2.77	[-3.10; -2.44]
Random effects model	1305			288				-2.26	[-3.88; -0.63]
Random effects model	3399			1061				-2.68	[-3.55; -1.82]

Three-level metaanalysis using random effects

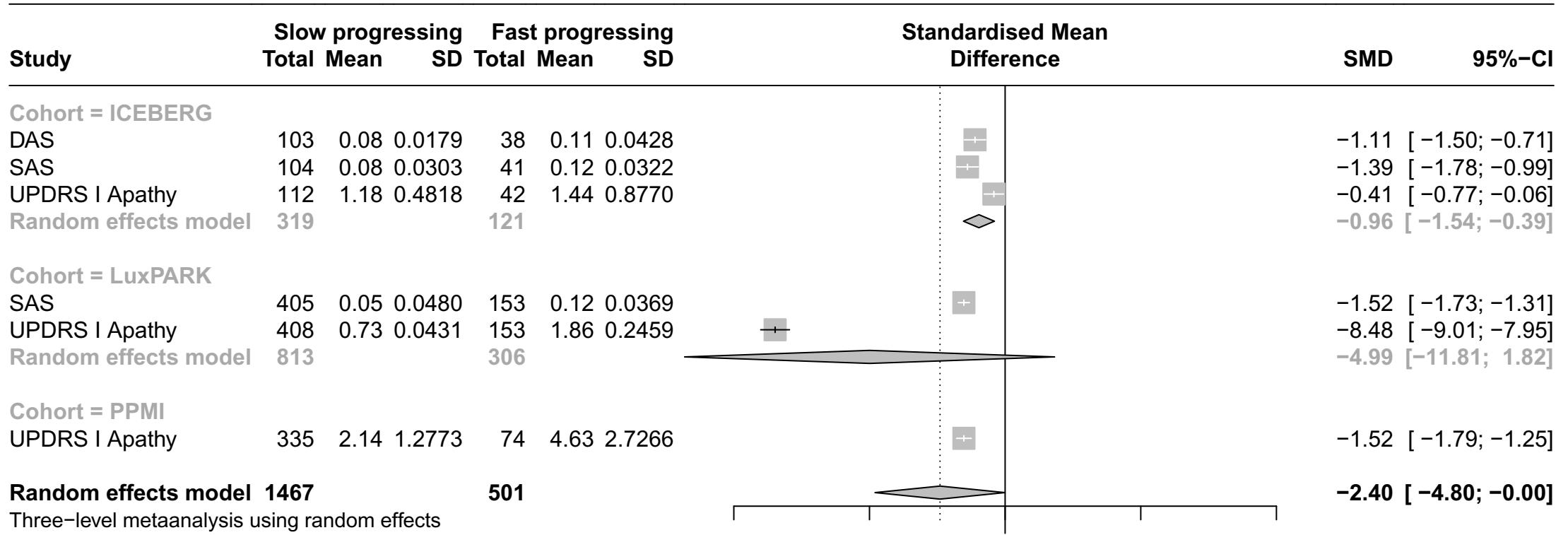
to calculate an overall SMD estimate

for Overall severity across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Apathy



Three-level metaanalysis using random effects
to calculate an overall SMD estimate
for Apathy across cohorts.

The dashed line indicates the overall mean SMD
estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Sleep

Study

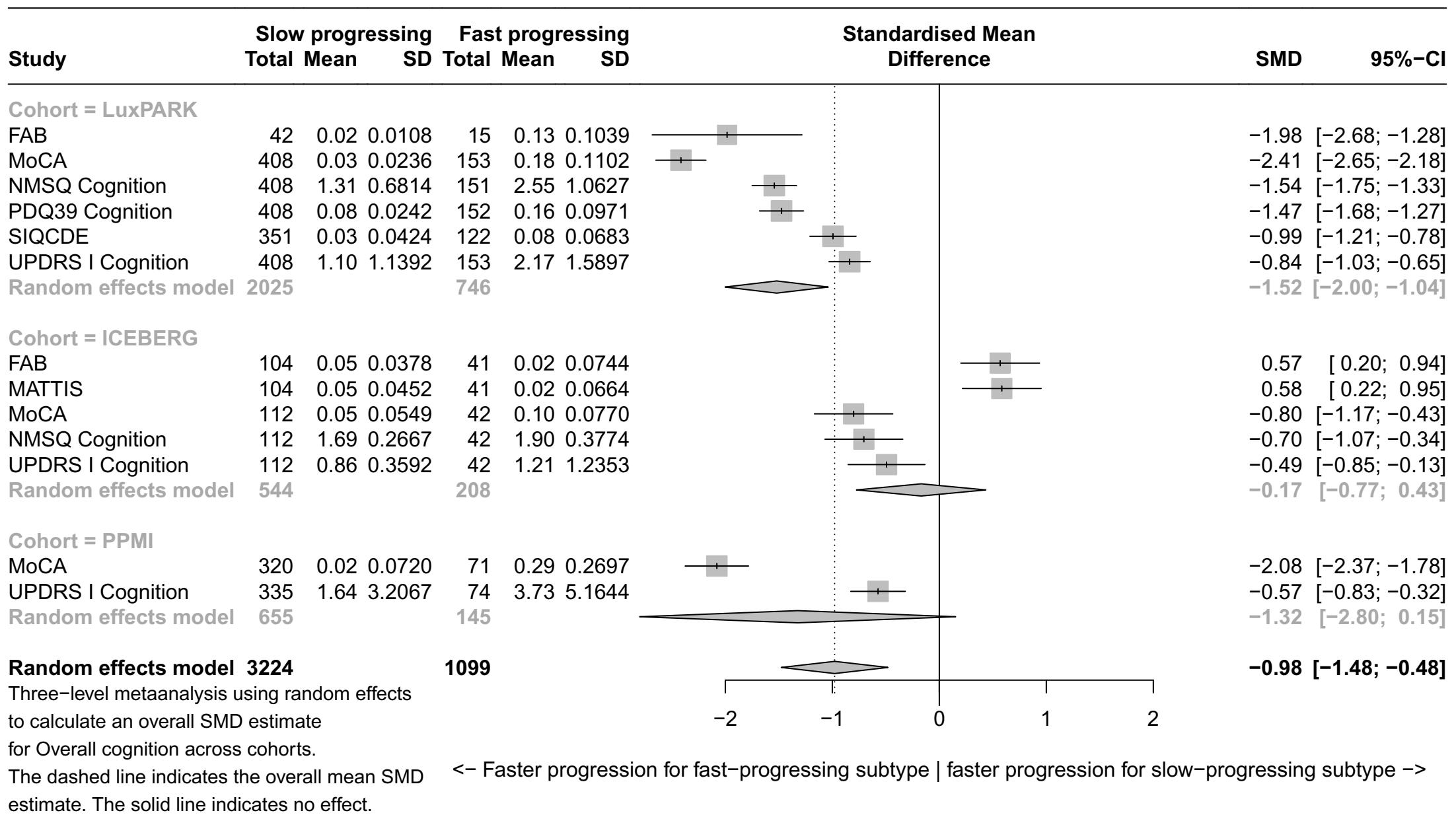
	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = PPMI									
ESS	324	0.15	0.1390	73	0.28	0.1024	-0.13	-1.00	[-1.26; -0.73]
UPDRS I Sleep	335	0.25	0.1857	74	0.48	0.2186	-0.23	-1.18	[-1.44; -0.92]
Random effects model	659			147			-0.13	-1.09	[-1.28; -0.90]
Cohort = ICEBERG									
ESS	111	0.15	0.1219	41	0.22	0.0565	-0.07	-0.67	[-1.04; -0.31]
NMSQ Sleep	112	1.08	0.5661	42	2.25	0.1739	-1.17	-2.37	[-2.81; -1.92]
UPDRS I Sleep	112	0.07	0.0314	42	0.13	0.0082	-0.06	-2.22	[-2.66; -1.79]
Random effects model	335			125			-0.13	-1.75	[-2.82; -0.68]
Cohort = LuxPARK									
NMSQ Sleep	408	0.64	0.0903	152	0.83	0.5505	-0.19	-0.61	[-0.80; -0.42]
PDSS	406	0.10	0.0189	152	0.13	0.0379	-0.03	-1.29	[-1.49; -1.09]
UPDRS I Sleep	408	0.09	0.0213	153	0.13	0.0592	-0.04	-1.29	[-1.49; -1.09]
Random effects model	1222			457			-0.04	-1.06	[-1.51; -0.62]
Random effects model 2216		729						-1.31	[-1.75; -0.88]

Three-level metaanalysis using random effects to calculate an overall SMD estimate for Sleep across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Overall cognition



Forest plot for progression characteristics of symptom domain Conceptualization

The forest plot displays the Standardised Mean Difference (SMD) for each study and model, comparing slow progressing vs fast progressing subtypes. The x-axis represents the SMD, ranging from -3 to 3. A vertical dashed line at 0 indicates no effect. A solid horizontal line at approximately -0.85 indicates the overall mean SMD estimate.

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = LuxPARK									
FAB Conceptualization	43	-1.31	0.2084	16	-2.15	1.9839		0.80	[0.21; 1.40]
MOCA Abstraction	408	0.16	0.2392	153	0.43	0.1078		-1.29	[-1.49; -1.09]
Random effects model	451			169				-0.26	[-2.31; 1.79]
Cohort = ICEBERG									
FAB Conceptualization	104	0.97	1.5829	41	0.87	0.2338		0.08	[-0.28; 0.44]
MATTIS Conceptualization	104	0.00	0.0741	41	0.05	0.0337		-0.74	[-1.11; -0.37]
MOCA Abstraction	112	0.53	0.6543	42	1.72	0.5240		-1.90	[-2.31; -1.48]
Random effects model	320			124				-0.85	[-1.97; 0.27]
Cohort = PPMI									
MOCA Abstraction	320	-1.90	0.9625	71	1.57	1.5654		-3.16	[-3.50; -2.82]
Random effects model	1091			364				-1.04	[-2.17; 0.08]

Three-level metaanalysis using random effects to calculate an overall SMD estimate for Conceptualization across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Visuo–executive

The forest plot displays the results of a meta-analysis comparing slow progressing and fast progressing groups across three cohorts. The y-axis represents the Standardised Mean Difference (SMD), ranging from -2.00 to 1.00. The x-axis shows the study categories: ICEBERG, LuxPARK, and PPMI. Individual study estimates are shown as grey squares with horizontal error bars representing the 95% confidence interval. A diamond at the bottom of each column represents the random effects model estimate. The overall SMD and 95% CI are also provided.

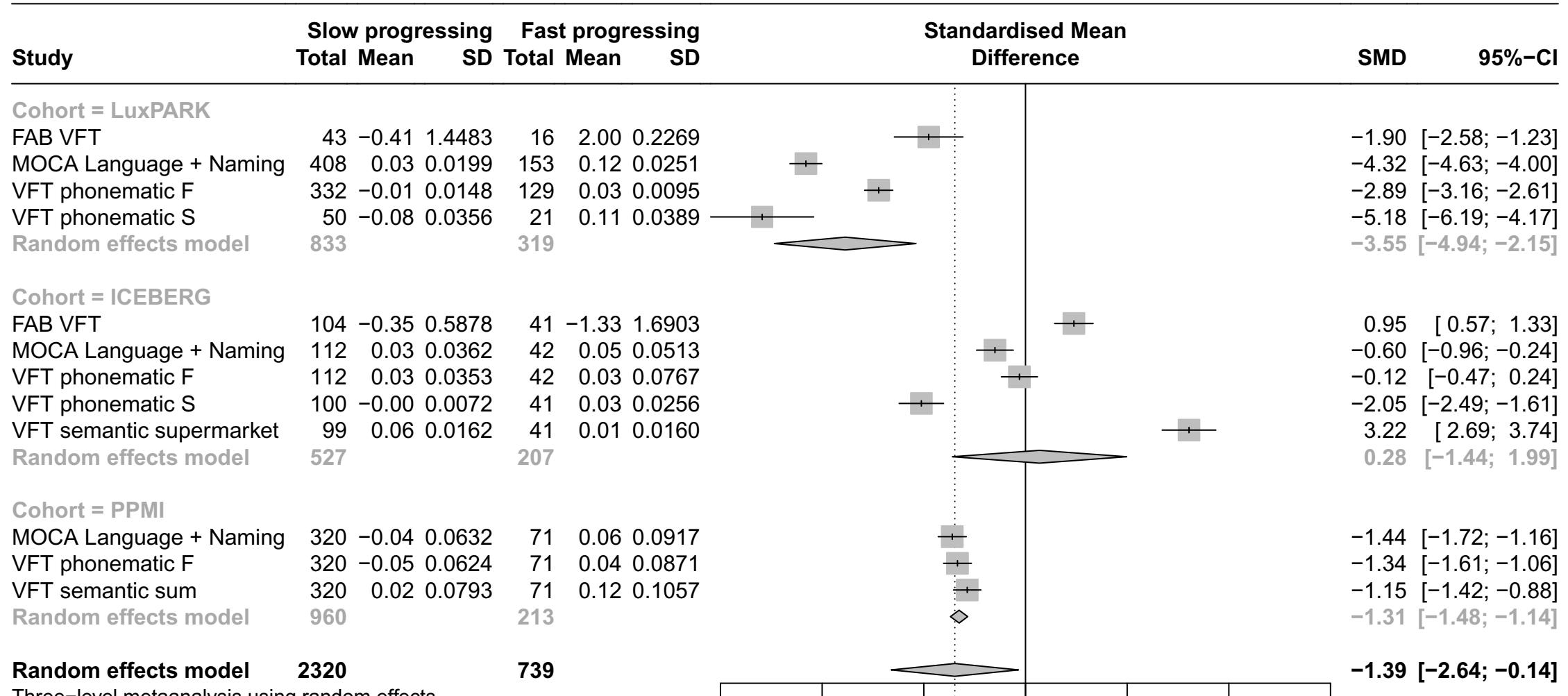
Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG									
FAB 3-6	104	0.06	0.0473	41	0.02	0.1003		0.64	[0.27; 1.01]
MATTIS Initiation + Construction	104	0.04	0.0456	41	0.03	0.0611		0.33	[-0.03; 0.69]
MOCA Visuospatial/Executive	112	0.81	0.5368	42	1.37	0.1911		-1.20	[-1.58; -0.82]
Random effects model	320			124				-0.08	[-1.19; 1.04]
Cohort = LuxPARK									
FAB 3-6	42	0.07	0.0238	15	0.09	0.0408		-0.74	[-1.34; -0.13]
MOCA Visuospatial/Executive	408	0.86	0.0973	153	2.12	0.3547		-6.23	[-6.64; -5.82]
Trailmaking A	392	0.02	0.0225	134	0.07	0.0747		-1.17	[-1.38; -0.96]
Trailmaking B	357	0.04	0.0371	99	0.09	0.0523		-1.20	[-1.44; -0.97]
Random effects model	1199			401				-2.34	[-4.89; 0.22]
Cohort = PPMI									
Judgement Line Orientation	320	0.04	0.0357	71	0.17	0.1483		-1.84	[-2.13; -1.55]
MOCA Visuospatial/Executive	320	0.77	1.2703	71	4.01	2.9805		-1.89	[-2.18; -1.60]
Symbol Digit Modalities	320	0.05	0.0727	71	0.21	0.1285		-1.81	[-2.10; -1.52]
Random effects model	960			213				-1.85	[-2.02; -1.68]
Random effects model	2479			738				-1.51	[-2.67; -0.35]

Three-level metaanalysis using random effects
to calculate an overall SMD estimate
for Visuo-executive across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Language



Three-level metaanalysis using random effects to calculate an overall SMD estimate for Language across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Anxiety

Study

	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG									
HADS anxiety	112	0.02	0.0221	42	0.08	0.0598		-1.76	[-2.16; -1.35]
NMSQ Anxiety	111	1.38	0.8609	42	1.29	1.9033		0.07	[-0.29; 0.42]
UPDRS I Anxiety	112	0.90	0.0762	42	0.84	1.9574		0.06	[-0.29; 0.42]
Random effects model	335			126				-0.54	[-1.73; 0.65]
Cohort = LuxPARK									
NMSQ Anxiety	408	1.08	0.3337	151	1.74	0.3269		-2.00	[-2.22; -1.77]
PDQ39 Anxiety	408	1.03	0.3142	153	1.67	0.5120		-1.70	[-1.91; -1.49]
UPDRS I Anxiety	408	0.64	0.1651	153	1.25	1.1298		-1.01	[-1.20; -0.81]
Random effects model	1224			457				-1.57	[-2.14; -0.99]
Cohort = PPMI									
STA	323	0.02	0.1127	72	0.23	0.0952		-1.94	[-2.23; -1.65]
UPDRS I Anxiety	335	1.05	2.2489	74	3.37	2.2233		-1.04	[-1.30; -0.77]
Random effects model	658			146				-1.48	[-2.37; -0.60]
Random effects model	2217			729				-1.17	[-1.75; -0.59]

Three-level metaanalysis using random effects to calculate an overall SMD estimate for Anxiety across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Memory

The forest plot displays the standardized mean difference (SMD) for memory tests across three cohorts. The x-axis represents the SMD, ranging from -1.0 to 1.0. The y-axis lists the memory tests. Each test is represented by a grey square indicating the mean difference, a horizontal line representing the 95% confidence interval, and a diamond representing the random effects model estimate.

Study	Slow progressing				Fast progressing				Standardised Mean Difference		SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD						
Cohort = PPMI												
Hopkins Verbal Learning Test DR	320	0.01	0.0245	71	-0.00	0.0144						0.59 [0.33; 0.85]
Hopkins Verbal Learning Test IR	320	0.04	0.0872	71	0.17	0.1296						-1.32 [-1.60; -1.05]
MOCA Orientation + Memory	320	-0.01	0.0912	71	0.21	0.1801						-1.97 [-2.26; -1.68]
Random effects model	960			213								-0.90 [-2.41; 0.61]
Cohort = ICEBERG												
MATTIS Memory	104	0.07	0.0605	41	0.08	0.0382						-0.21 [-0.57; 0.16]
MOCA Orientation + Memory	112	0.02	0.0179	42	0.03	0.0961						-0.37 [-0.72; -0.01]
NMSQ Memory	111	1.19	1.4812	42	2.28	1.4312						-0.74 [-1.10; -0.37]
Random effects model	327			125								-0.44 [-0.74; -0.13]
Cohort = LuxPARK												
MOCA Orientation + Memory	408	0.01	0.0204	153	0.11	0.0920						-2.05 [-2.27; -1.83]
NMSQ Memory	408	1.13	0.0606	151	2.30	1.2830						-1.75 [-1.96; -1.53]
PDQ39 Memory	408	0.74	0.2966	152	1.58	1.5416						-1.01 [-1.20; -0.81]
SIQCDE Memory	352	0.03	0.0459	122	0.07	0.0527						-0.68 [-0.89; -0.47]
Random effects model	1576			578								-1.37 [-1.99; -0.75]
Random effects model	2863			916								-0.95 [-1.48; -0.43]

Three-level metaanalysis using random effects
to calculate an overall SMD estimate
for Memory across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Attention

The forest plot displays the Standardised Mean Difference (SMD) for attention measures across three cohorts: PPMI, ICEBERG, and LuxPARK. Individual study data points are shown as grey squares with horizontal error bars representing 95% CIs. A vertical dotted line at SMD = 0 indicates no difference. A horizontal diamond represents the random effects model summary estimate, with its own 95% CI.

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = PPMI									
Letter Number Sequencing	56	0.03	0.1650	5	-0.04	0.0202		0.40	[-0.52; 1.31]
MOCA Attention	320	1.33	0.7561	71	3.97	2.4125		-2.15	[-2.44; -1.85]
Random effects model	376			76				-0.91	[-3.40; 1.58]
Cohort = ICEBERG									
MATTIS Attention	104	0.00	0.0367	41	-0.02	0.0090		0.71	[0.34; 1.08]
MOCA Attention	112	0.52	0.2299	42	0.94	0.5589		-1.18	[-1.56; -0.80]
NMSQ Attention	111	2.20	0.0771	42	1.79	0.1678		3.71	[3.16; 4.26]
Random effects model	327			125				1.07	[-1.71; 3.86]
Cohort = LuxPARK									
MOCA Attention	408	0.58	0.3055	153	1.52	0.5164		-2.49	[-2.73; -2.25]
NMSQ Attention	408	1.47	1.1380	152	2.09	0.1286		-0.63	[-0.82; -0.44]
PDQ39 Attention	408	1.34	0.2652	153	1.77	0.4815		-1.29	[-1.49; -1.09]
SIQCDE Attention	353	0.49	0.3458	122	1.00	0.8884		-0.94	[-1.15; -0.72]
Random effects model	1577			580				-1.34	[-2.13; -0.54]
Random effects model	2280			781				-0.44	[-1.66; 0.77]

Three-level metaanalysis using random effects
to calculate an overall SMD estimate
for Attention across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Non motor symptoms

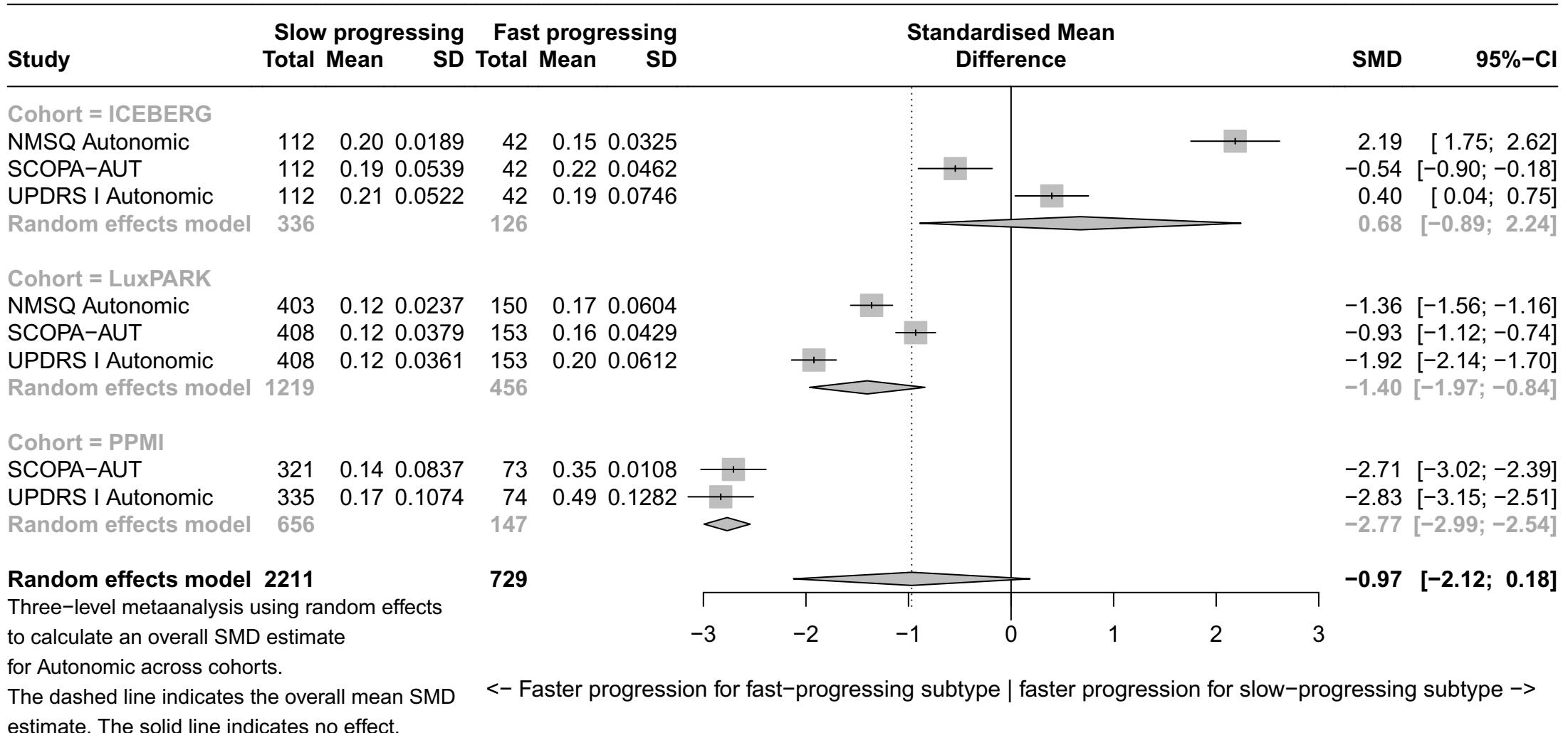
Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = LuxPARK									
NMSQ	402	0.11	0.0262	148	0.20	0.0522	-0.09	-2.75	[-3.00; -2.50]
UPDRS I	408	0.10	0.0268	153	0.22	0.0835	-0.12	-2.41	[-2.64; -2.17]
Random effects model	810			301			-0.21	-2.58	[-2.91; -2.24]
Cohort = ICEBERG									
NMSQ	111	0.20	0.0447	42	0.22	0.0016	-0.02	-0.50	[-0.86; -0.14]
UPDRS I	112	0.14	0.0182	42	0.19	0.0535	-0.05	-1.66	[-2.06; -1.25]
Random effects model	223			84			-0.07	-1.07	[-2.21; 0.06]
Cohort = PPMI									
UPDRS I	335	0.19	0.1170	74	0.55	0.1480	-0.36	-2.97	[-3.30; -2.65]
Random effects model 1368		459					-2.06	-2.06	[-2.94; -1.19]

Three-level metaanalysis using random effects to calculate an overall SMD estimate for Non motor symptoms across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Autonomic



Forest plot for progression characteristics of symptom domain Hallucinations

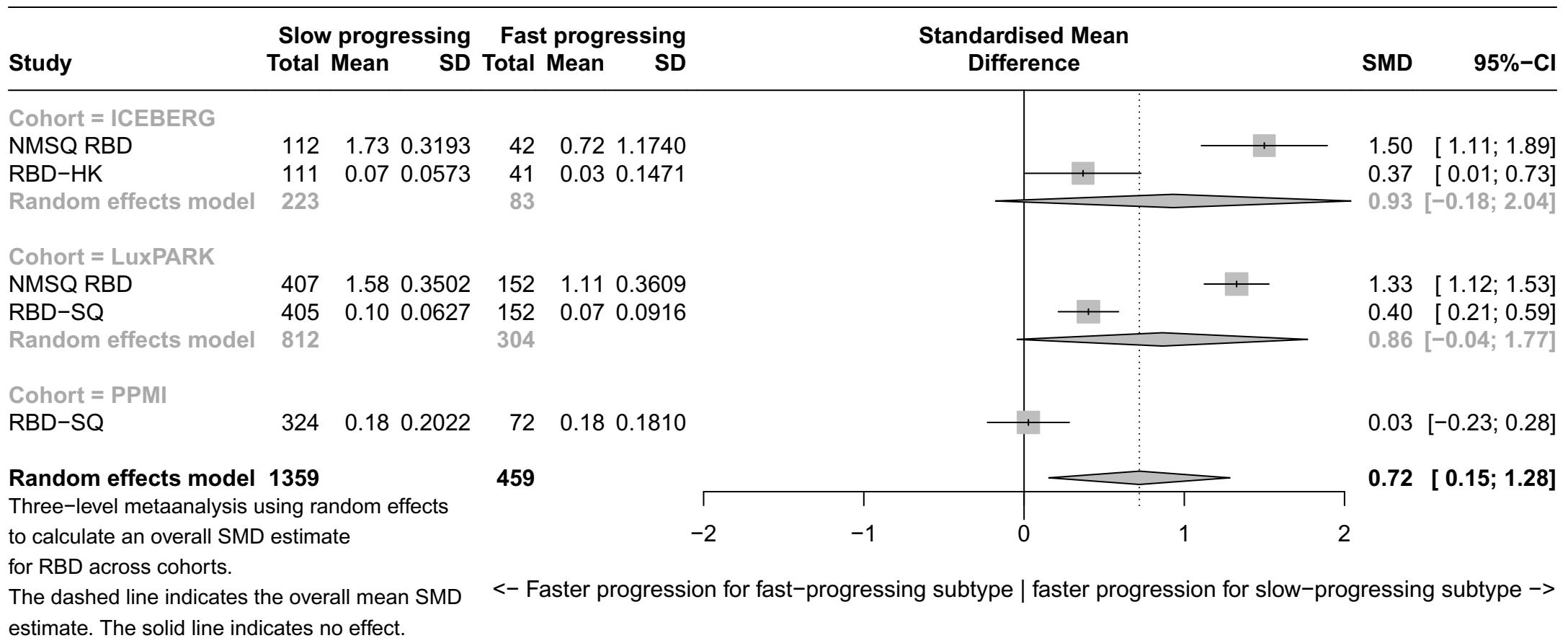
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Hallucinations across cohorts

The dashed line indicates the overall mean S estimate. The solid line indicates no effect.

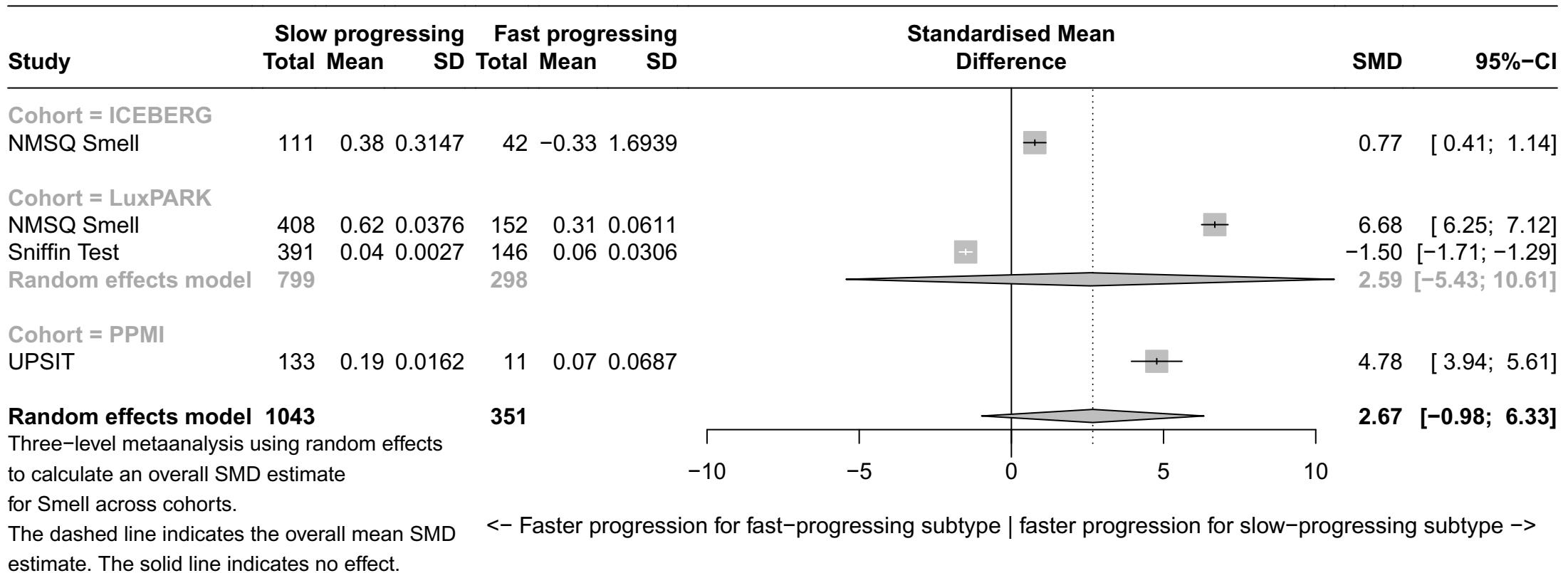
<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Pain

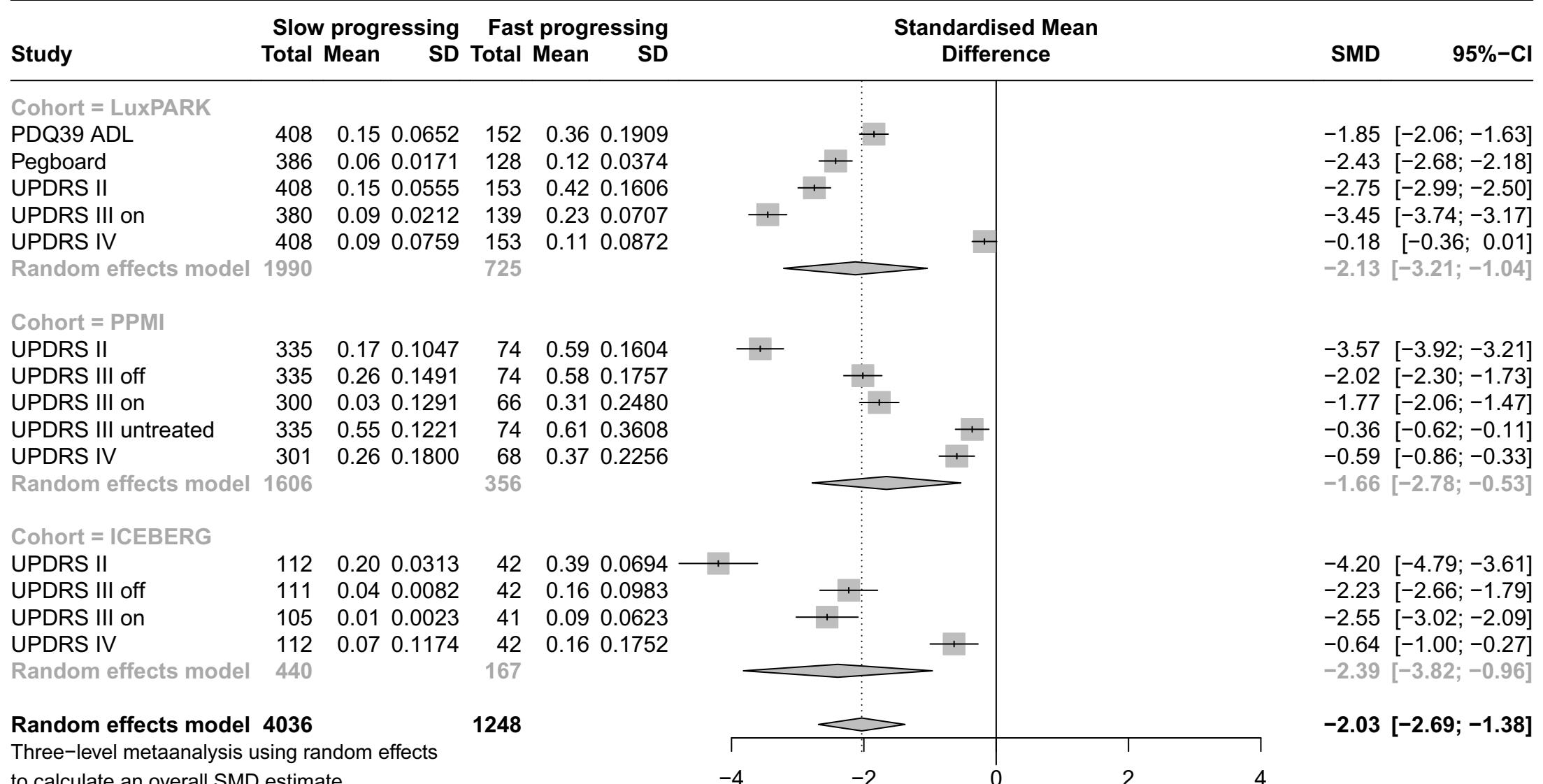
Forest plot for progression characteristics of symptom domain RBD



Forest plot for progression characteristics of symptom domain Smell



Forest plot for progression characteristics of symptom domain Motor symptoms



Three-level metaanalysis using random effects to calculate an overall SMD estimate for Motor symptoms across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Impulsivity

Forest plot showing Standardised Mean Difference (SMD) for Slow vs Fast progressing subtypes across three cohorts:

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = PPMI									
QUIP	324	0.04	0.0547	72	0.07	0.1027	-0.41	[-0.67; -0.16]	
Cohort = ICEBERG									
QUIP-RS	112	0.04	0.0690	42	0.09	0.0820	-0.67	[-1.03; -0.31]	
Random effects model	436			114			-0.51	[-0.75; -0.27]	

Three-level metaanalysis using random effects to calculate an overall SMD estimate for Impulsivity across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Forest plots for symptom domain progression (cross-cohort validation)

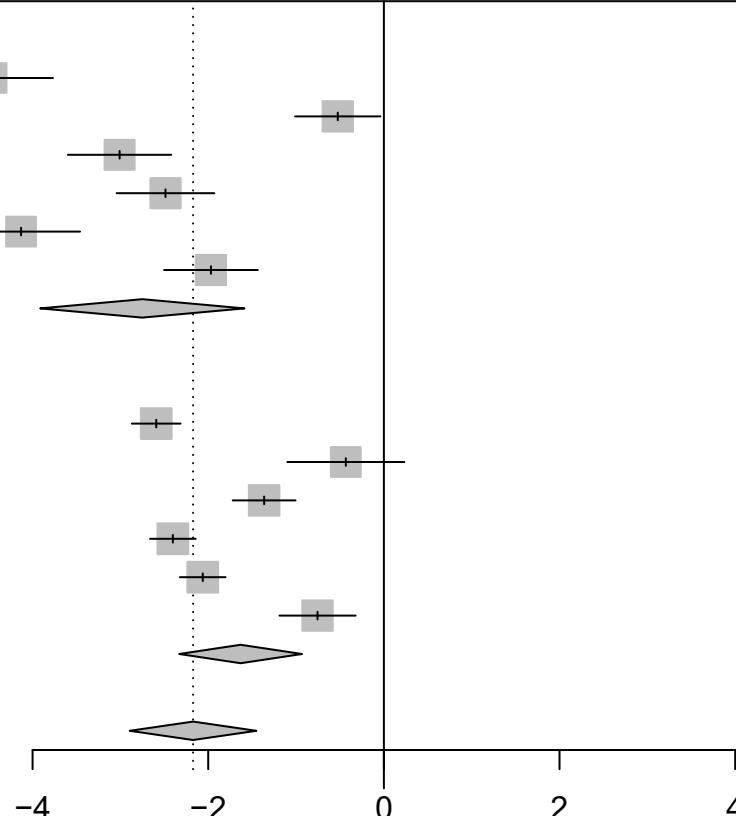
Forest plot for progression characteristics of symptom domain Axial & PIGD (validation)

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG (validation)									
UPDRS III axial off	134	0.12	0.0154	19	0.54	0.2700	-4.47	[-5.16; -3.77]	
UPDRS III axial on	127	0.13	0.0067	19	0.16	0.1915	-0.53	[-1.01; -0.04]	
GABS Examination	135	0.05	0.0213	19	0.27	0.2062	-3.01	[-3.60; -2.42]	
GABS Questionnaire	135	0.04	0.0637	19	0.32	0.2745	-2.49	[-3.04; -1.93]	
PIGD off	134	0.09	0.0457	19	0.37	0.1549	-4.13	[-4.80; -3.46]	
PIGD on	127	0.09	0.0434	19	0.23	0.1583	-1.97	[-2.50; -1.44]	
Random effects model	792			114			-2.75	[-3.91; -1.59]	
Cohort = LuxPARK (validation)									
UPDRS III axial on	430	0.15	0.0629	90	0.34	0.1203	-2.59	[-2.87; -2.31]	
FOGAC	70	0.09	0.0702	10	0.15	0.3365	-0.43	[-1.10; 0.23]	
FOGQ	188	0.18	0.1030	42	0.43	0.3730	-1.36	[-1.72; -1.01]	
PDQ39 Mobility	461	0.21	0.1023	98	0.51	0.2099	-2.40	[-2.66; -2.14]	
PIGD on	430	0.15	0.0996	90	0.39	0.1639	-2.06	[-2.32; -1.80]	
TuG	172	0.03	0.0320	24	0.07	0.1145	-0.76	[-1.19; -0.32]	
Random effects model	1751			354			-1.63	[-2.33; -0.93]	
Random effects model 2543		468					-2.17	[-2.89; -1.45]	

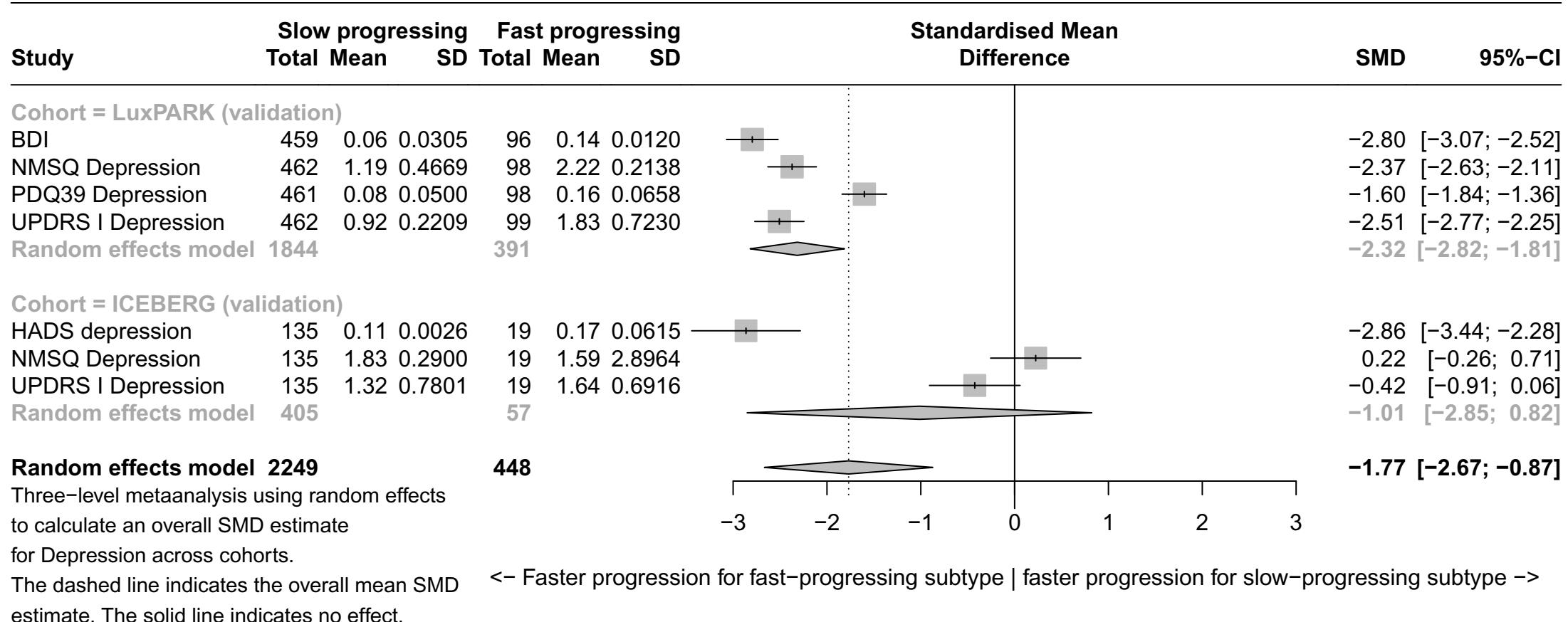
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Axial & PIGD across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->



Forest plot for progression characteristics of symptom domain Depression (validation)



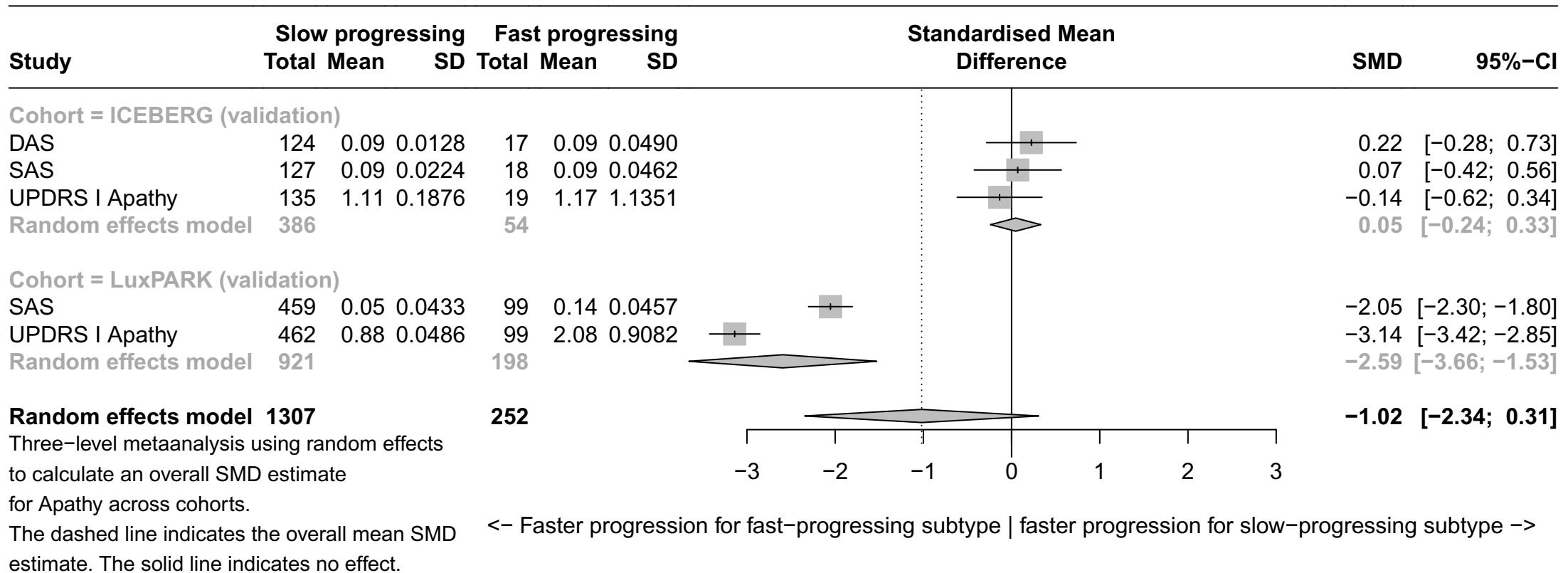
Forest plot for progression characteristics of symptom domain Overall severity (validation)

The forest plot displays the Standardised Mean Difference (SMD) for slow progressing versus fast progressing cohorts across three validation cohorts. The x-axis represents the SMD, ranging from -10 to 10. The y-axis lists the studies and cohorts. Each study is represented by a grey diamond indicating the SMD and its 95% confidence interval. A vertical dotted line at SMD = 0 serves as a reference. The plot shows a clear trend where SMD values decrease from ICEBERG to LuxPARK, and further in the Random effects model.

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG (validation)									
CGIS	135	1.40	0.2906	19	2.38	1.5224	-	-1.65	[-2.16; -1.13]
H&Y	135	-0.47	0.0485	19	0.81	0.6415	-	-5.68	[-6.49; -4.88]
SEADL	135	0.06	0.0267	19	0.20	0.1218	-	-2.84	[-3.42; -2.26]
UPDRS I-III off	134	0.17	0.0261	19	0.61	0.1236	-	-8.93	[-10.05; -7.81]
UPDRS I-III on	127	0.14	0.0236	19	0.43	0.0561	-	-9.86	[-11.11; -8.62]
Random effects model	666			95				-5.76	[-8.93; -2.60]
Cohort = LuxPARK (validation)									
FAQ	399	0.11	0.0810	79	0.33	0.1342	-	-2.39	[-2.68; -2.11]
H&Y	462	2.74	0.5202	99	4.83	1.2833	-	-2.92	[-3.20; -2.64]
PDQ39	456	0.12	0.0548	96	0.32	0.1556	-	-2.38	[-2.64; -2.12]
UPDRS I-III on	426	0.16	0.0502	89	0.40	0.1484	-	-3.14	[-3.44; -2.84]
Random effects model	1743			363				-2.70	[-3.08; -2.33]
Random effects model	2409			458				-4.38	[-6.33; -2.43]

Three-level metaanalysis using random effects
to calculate an overall SMD estimate
for Overall severity across cohorts.
The dashed line indicates the overall mean SMD
estimate. The solid line indicates no effect. <- P

Forest plot for progression characteristics of symptom domain Apathy (validation)



Forest plot for progression characteristics of symptom domain Sleep (validation)

The figure is a forest plot with 'Study' on the y-axis and 'SMD' on the x-axis. The x-axis ranges from -4 to 4, with a vertical dashed line at 0 representing the overall mean SMD estimate. Individual study estimates are shown as grey squares with error bars for SD, and a diamond represents the random effects model estimate. A solid horizontal line at SMD = 0 indicates no effect.

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG (validation)									
ESS	133	0.17	0.1063	19	0.16	0.0548	+0.09	[−0.39; 0.58]	
NMSQ Sleep	135	1.21	0.2211	19	3.35	1.1076	-4.89	[−5.62; −4.16]	
UPDRS I Sleep	135	0.08	0.0224	19	0.15	0.0255	-3.05	[−3.64; −2.45]	
Random effects model	403			57			-2.60	[−5.46; 0.25]	
Cohort = LuxPARK (validation)									
NMSQ Sleep	462	0.68	0.0575	98	0.76	0.3560	-0.53	[−0.75; −0.31]	
PDSS	460	0.11	0.0237	98	0.12	0.0355	-0.51	[−0.73; −0.29]	
UPDRS I Sleep	462	0.10	0.0325	99	0.12	0.0353	-0.64	[−0.86; −0.42]	
Random effects model	1384			295			-0.56	[−0.69; −0.43]	
Random effects model 1787		352					-1.57	[−3.11; −0.03]	
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Sleep across cohorts.									
The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.									
<– Faster progression for fast-progressing subtype faster progression for slow-progressing subtype –>									

Forest plot for progression characteristics of symptom domain Overall cognition (validation)

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = LuxPARK (validation)									
FAB	48	0.03	0.0435	9	0.23	0.2836		-1.69	[-2.47; -0.91]
MoCA	462	0.04	0.0278	99	0.21	0.1602		-2.31	[-2.57; -2.06]
NMSQ Cognition	462	1.36	0.5848	97	3.17	1.3498		-2.34	[-2.60; -2.08]
PDQ39 Cognition	461	0.08	0.0310	99	0.18	0.1010		-1.95	[-2.19; -1.70]
SIQCDE	396	0.04	0.0408	77	0.10	0.0812		-1.16	[-1.42; -0.91]
UPDRS I Cognition	462	1.21	0.1909	99	3.13	1.2061		-3.58	[-3.88; -3.28]
Random effects model	2291			480				-2.18	[-2.85; -1.52]
Cohort = ICEBERG (validation)									
FAB	127	0.05	0.0383	18	0.01	0.0697		1.03	[0.53; 1.54]
MATTIS	127	0.04	0.0346	18	0.07	0.0661		-0.71	[-1.22; -0.21]
MoCA	135	0.05	0.0503	19	0.15	0.0817		-1.80	[-2.33; -1.28]
NMSQ Cognition	135	1.85	0.4908	19	1.30	1.3777		0.83	[0.34; 1.32]
UPDRS I Cognition	135	0.87	0.8917	19	1.09	1.5180		-0.22	[-0.70; 0.26]
Random effects model	659			93				-0.17	[-1.19; 0.85]
Random effects model	2950			573				-1.27	[-2.10; -0.44]

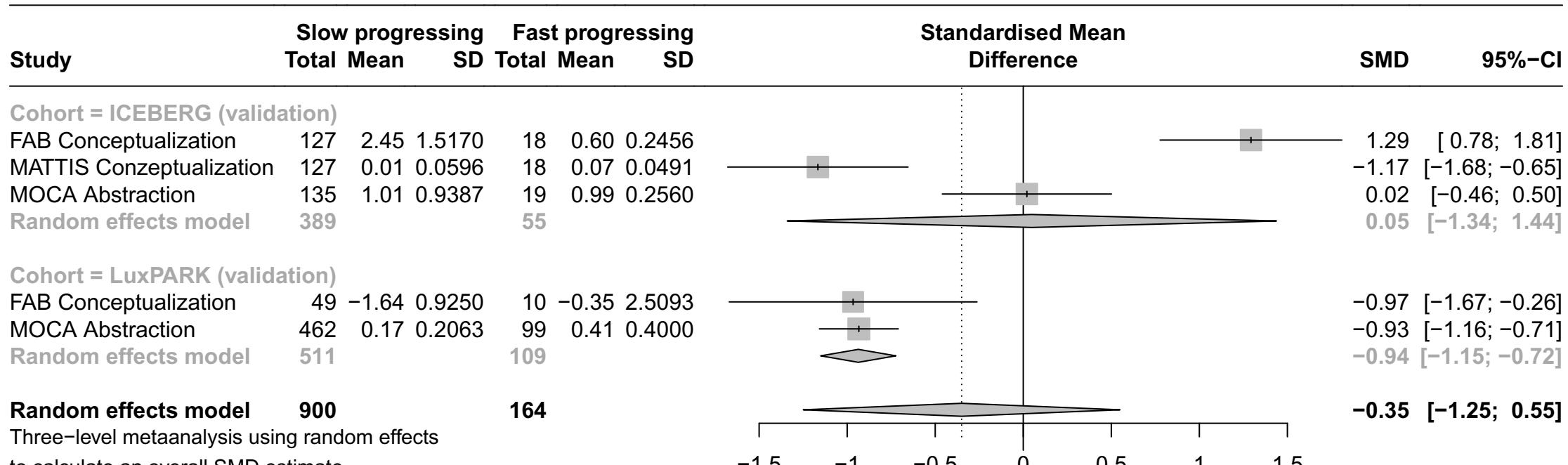
Three-level metaanalysis using random effects
to calculate an overall SMD estimate
for Overall cognition across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->



Forest plot for progression characteristics of symptom domain Conceptualization (validation)



Three-level metaanalysis using random effects

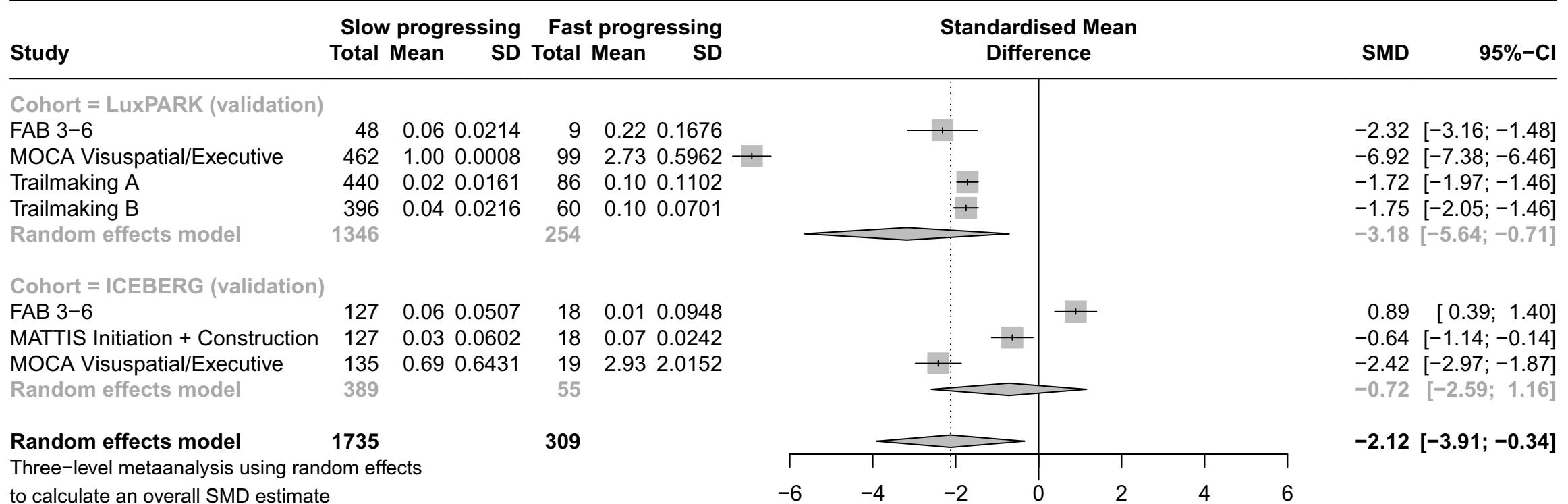
to calculate an overall SMD estimate

for Conceptualization across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Visuo-executive (validation)



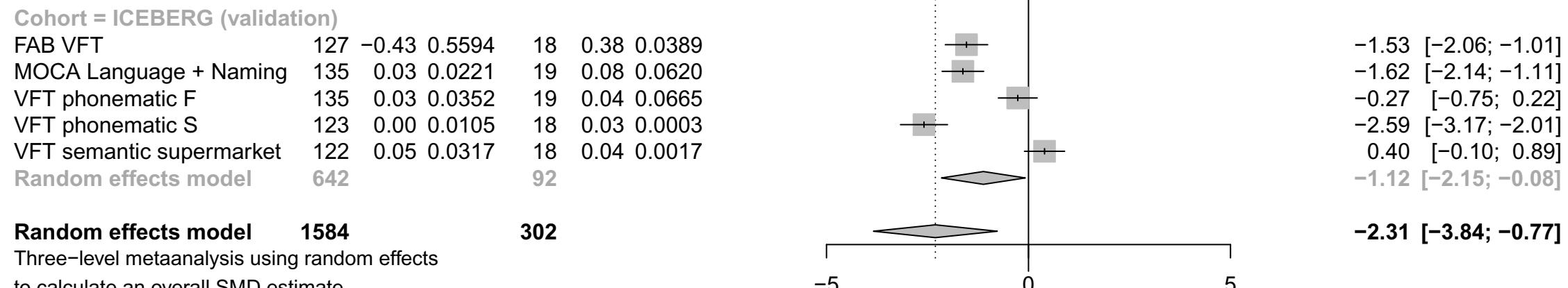
Three-level metaanalysis using random effects
to calculate an overall SMD estimate
for Visuo-executive across cohorts.
The dashed line indicates the overall mean SMD
estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Language (validation)

Detailed description: This forest plot displays the results of a meta-analysis comparing cognitive test scores between slow-progressing and fast-progressing groups. The y-axis represents the Standardised Mean Difference (SMD). Individual study estimates are shown as grey squares with horizontal error bars representing 95% CIs. A vertical dotted line at SMD = 0 indicates no difference. A horizontal line represents the random effects model estimate. The x-axis labels include the study names and their sample sizes.

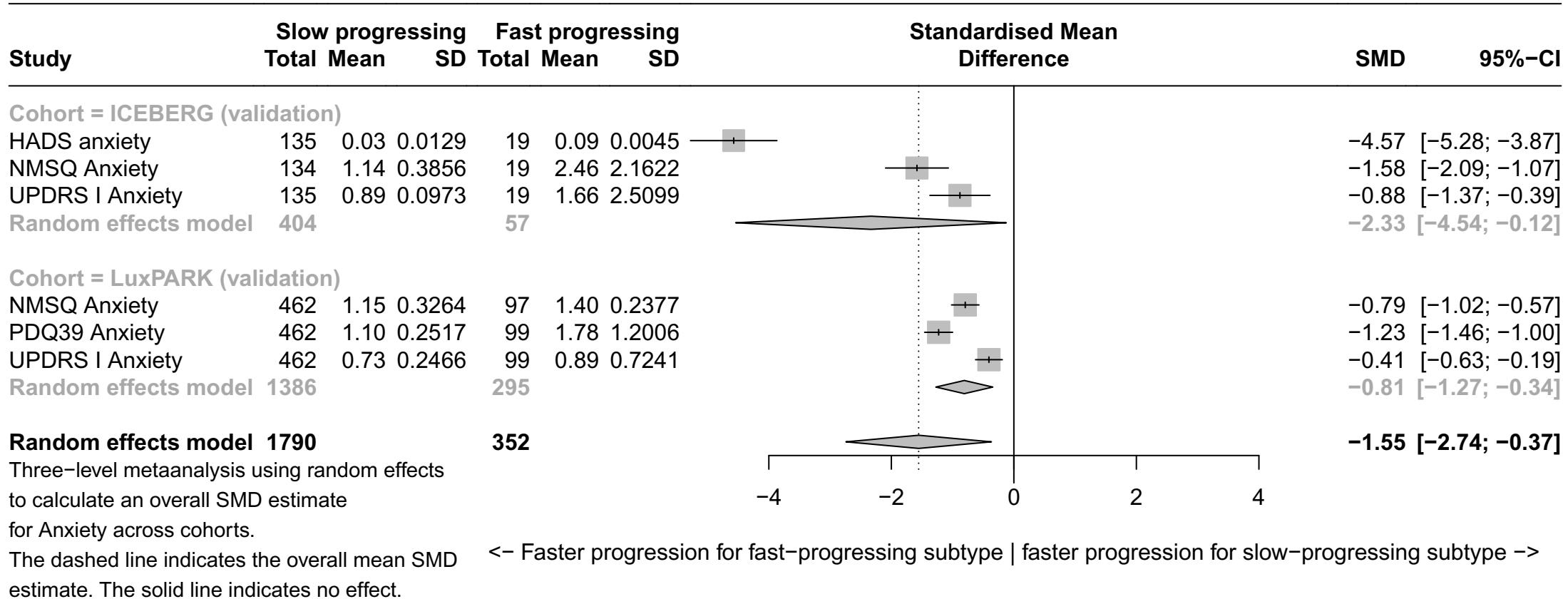
Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = LuxPARK (validation)									
FAB VFT	49	0.61	2.3727	10	2.27	1.7866	-0.71	[−1.41; −0.02]	
MOCA Language + Naming	462	0.04	0.0173	99	0.18	0.0729	-4.19	[−4.52; −3.86]	
VFT phonematic F	374	-0.00	0.0089	87	0.06	0.0011	-7.27	[−7.80; −6.75]	
VFT phonematic S	57	-0.02	0.0422	14	0.17	0.1257	-2.94	[−3.71; −2.18]	
Random effects model	942			210			-3.79	[−6.47; −1.11]	



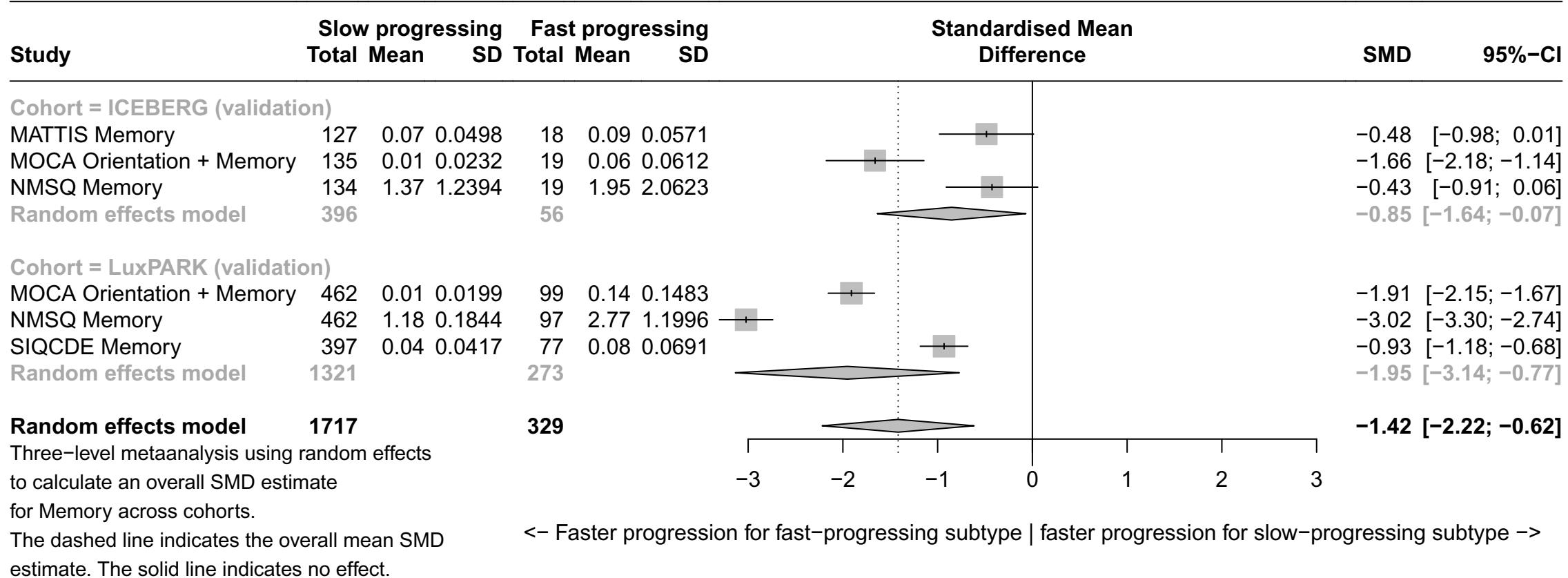
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Language across cohorts.

The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

Forest plot for progression characteristics of symptom domain Anxiety (validation)



Forest plot for progression characteristics of symptom domain Memory (validation)



Forest plot for progression characteristics of symptom domain Attention (validation)

The forest plot displays the standardized mean difference (SMD) for attention measures between slow and fast progressing cohorts. The x-axis represents the SMD, ranging from -1.00 to 2.00. Each study is represented by a grey square indicating the mean difference, with a horizontal line representing the 95% confidence interval. A vertical dotted line at SMD = 0 serves as a reference. The plot includes a diamond representing the random effects model estimate.

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG (validation)									
MATTIS Attention	127	0.01	0.0320	18	-0.07	0.0070		2.63	[2.05; 3.21]
MOCA Attention	135	0.63	0.1829	19	1.40	1.5398		-1.37	[-1.88; -0.87]
NMSQ Attention	134	2.26	0.0973	19	0.47	0.8163		6.02	[5.18; 6.85]
Random effects model	396			56				2.41	[-1.77; 6.60]
Cohort = LuxPARK (validation)									
MOCA Attention	462	0.67	0.2059	99	2.00	0.8758		-3.22	[-3.50; -2.93]
NMSQ Attention	462	1.53	0.9835	98	2.55	0.6917		-1.07	[-1.30; -0.85]
PDQ39 Attention	462	1.41	0.1286	99	1.88	0.9219		-1.17	[-1.40; -0.94]
SIQCDE Attention	398	0.58	0.4896	77	1.30	0.8721		-1.26	[-1.52; -1.00]
Random effects model	1784			373				-1.68	[-2.68; -0.67]

Random effects model 2180

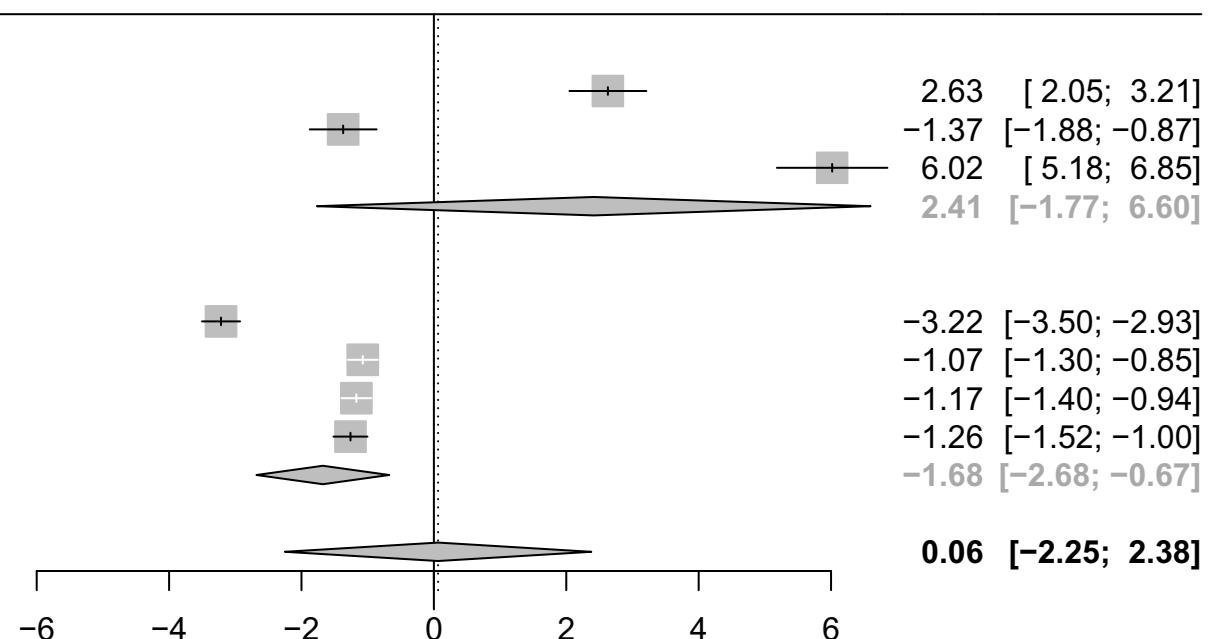
Three-level metaanalysis using random effect

to calculate an overall SMD estimate

for Attention across cohorts.

The dashed line indicates the overall mean SMD

estimate. The solid line indicates no effect



`<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->`

Forest plot for progression characteristics of symptom domain Non motor symptoms (validation)

The forest plot displays the Standardised Mean Difference (SMD) for non-motor symptoms between slow-progressing and fast-progressing subtypes across three cohorts. The x-axis represents the SMD, ranging from -4 to 4. A vertical dashed line at SMD = 0 indicates no effect. A solid horizontal line represents the overall mean SMD estimate.

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = ICEBERG (validation)									
NMSQ	134	0.20	0.0347	19	0.22	0.0014	-0.69 [-1.18; -0.20]		
UPDRS I	135	0.14	0.0230	19	0.23	0.0397	-3.28 [-3.89; -2.67]		
Random effects model	269			38			-1.98 [-4.52; 0.56]		
Cohort = LuxPARK (validation)									
NMSQ	455	0.12	0.0300	95	0.21	0.0641	-2.42 [-2.68; -2.16]		
UPDRS I	462	0.12	0.0412	99	0.24	0.0886	-2.20 [-2.46; -1.95]		
Random effects model	917			194			-2.31 [-2.52; -2.10]		
Random effects model	1186			232			-2.14 [-3.17; -1.11]		
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Non motor symptoms across cohorts.									
The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.									

← Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype →

Forest plot for progression characteristics of symptom domain Autonomic (validation)

Forest plot for progression characteristics of symptom domain Hallucinations (validation)

Slow progressing **Fast progressing**

Study	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = LuxPARK (validation)									
NMSQ Hallucination	462	1.67	0.2022	98	1.81	1.0142		-0.30	[-0.52; -0.09]
UPDRS I Hallucinations	462	1.31	0.2786	99	1.38	0.8747		-0.16	[-0.38; 0.06]
Random effects model	924			197				-0.23	[-0.39; -0.08]
Cohort = ICEBERG (validation)									
NMSQ Hallucination	135	0.93	0.9204	19	1.38	0.7406		-0.50	[-0.99; -0.02]
UPDRS I Hallucinations	135	1.03	2.0070	19	8.38	9.9115		-1.88	[-2.40; -1.35]
Random effects model	270			38				-1.19	[-2.53; 0.16]
Random effects model 1194	235							-0.69	[-1.44; 0.06]
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Hallucinations across cohorts.									
The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.									

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

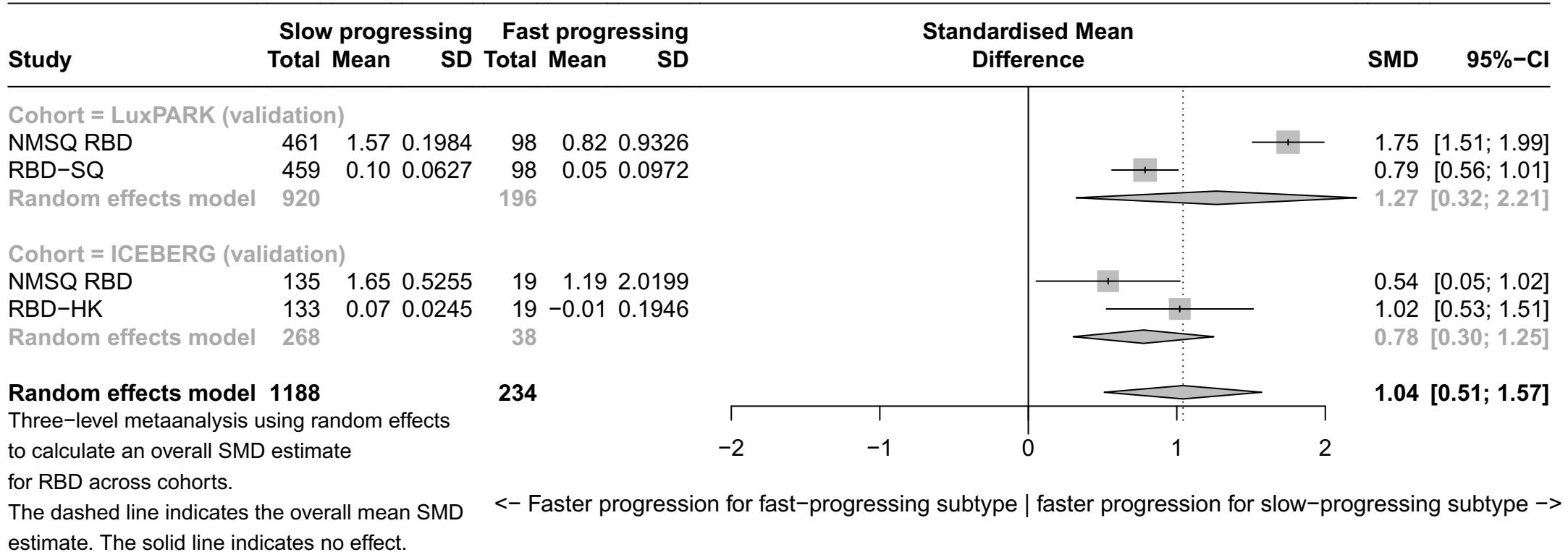
Forest plot for progression characteristics of symptom domain Pain (validation)

Study	Slow progressing				Fast progressing				Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD					
Cohort = LuxPARK (validation)											
NMSQ Pain	462	0.79	0.0950	98	1.35	0.0765	+			-6.03	[-6.45; -5.62]
PDQ39 Pain	461	0.11	0.0314	99	0.12	0.0169	+			-0.29	[-0.51; -0.08]
UPDRS I Pain	462	1.17	0.2438	99	1.69	0.8251	+			-1.26	[-1.49; -1.03]
Random effects model	1385			296						-2.53	[-6.00; 0.95]
Cohort = ICEBERG (validation)											
NMSQ Pain	134	0.68	0.3044	19	0.81	0.4887	+			-0.39	[-0.88; 0.09]
UPDRS I Pain	135	1.06	0.1449	19	0.69	0.1723	+			2.47	[1.92; 3.03]
Random effects model	269			38						1.04	[-1.77; 3.85]
Random effects model 1654											
Three-level metaanalysis using random effects to calculate an overall SMD estimate for Pain across cohorts.				334						-1.11	[-3.81; 1.60]

Three-level metaanalysis using random effects to calculate an overall SMD estimate for Pain across cohorts.
The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain RBD (validation)



Forest plot for progression characteristics of symptom domain Smell (validation)

Study

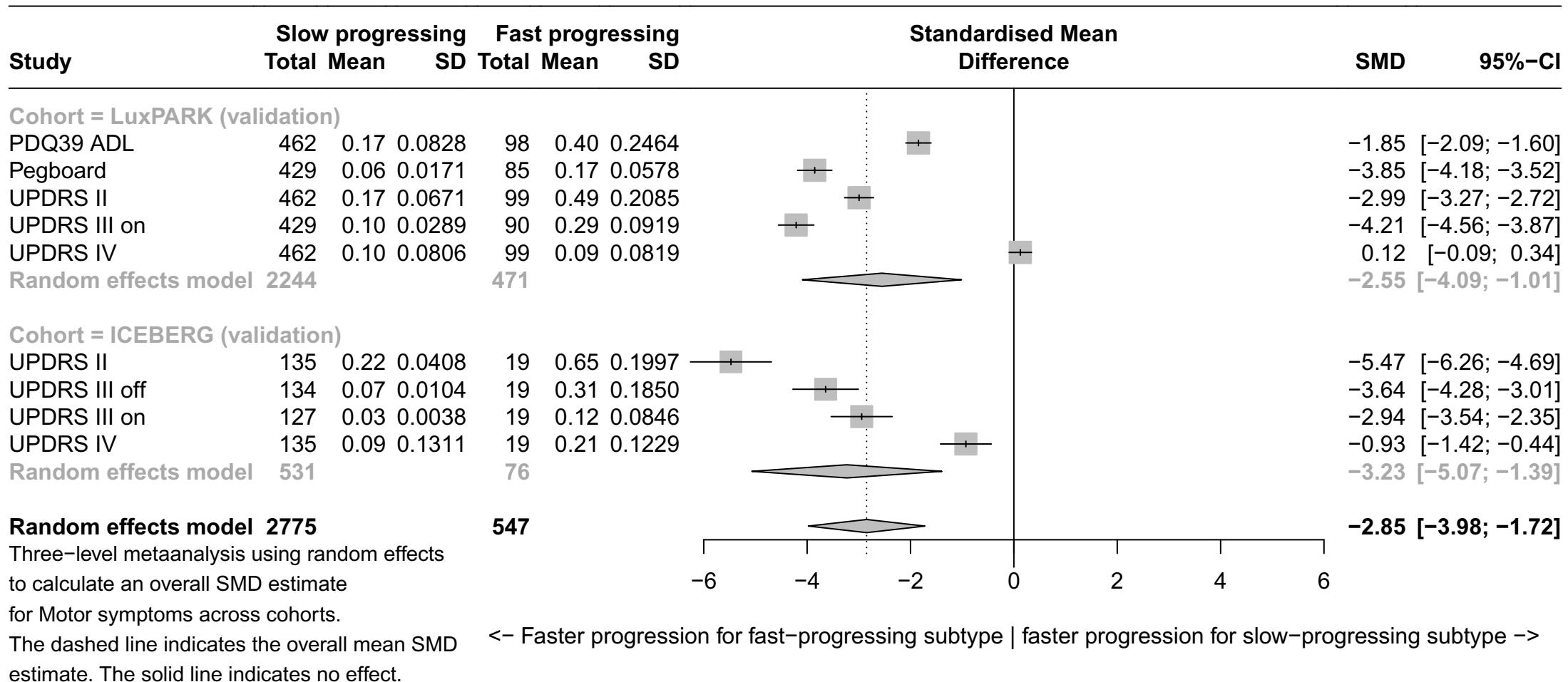
	Slow progressing			Fast progressing			Standardised Mean Difference	SMD	95%-CI
	Total	Mean	SD	Total	Mean	SD			
Cohort = LuxPARK (validation)									
NMSQ Smell	462	0.58	0.0529	98	0.19	0.7260		1.28	[1.05; 1.51]
Sniffin Test	443	0.04	0.0063	94	0.08	0.0285		-2.79	[-3.07; -2.51]
Random effects model	905			192				-0.75	[-4.75; 3.24]
Cohort = ICEBERG (validation)									
NMSQ Smell	134	0.58	0.2972	19	-1.47	2.1280		2.60	[2.04; 3.16]
Random effects model 1039	211							0.36	[-2.82; 3.54]

Three-level metaanalysis using random effects to calculate an overall SMD estimate for Smell across cohorts.

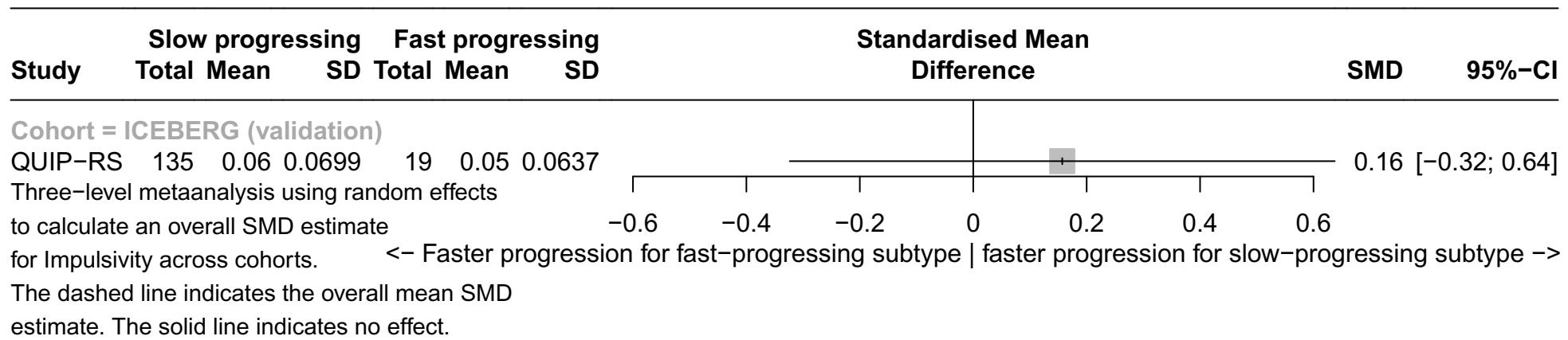
The dashed line indicates the overall mean SMD estimate. The solid line indicates no effect.

<- Faster progression for fast-progressing subtype | faster progression for slow-progressing subtype ->

Forest plot for progression characteristics of symptom domain Motor symptoms (validation)



Forest plot for progression characteristics of symptom domain Impulsivity (validation)



Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Forest plots for symptom domain baseline associations (in cohort)

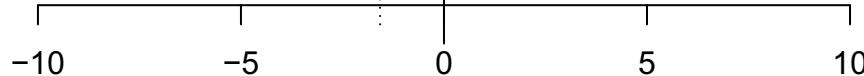
Forest plot for baseline characteristics of symptom domain Axial & PIGD

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = PPMI						
UPDRS III axial off	409	-1.97	19.1667		-1.97	[-3.83; -0.12]
PIGD off	408	-0.20	18.6873		-0.20	[-2.01; 1.61]
Random effects model	817				-1.08	[-2.81; 0.66]
Cohort = ICEBERG						
UPDRS III axial off	154	-0.38	11.4575		-0.38	[-2.18; 1.43]
UPDRS III axial on	131	0.90	10.2805		0.90	[-0.86; 2.66]
GABS Examination	153	-1.39	12.5291		-1.39	[-3.38; 0.59]
GABS Questionnaire	153	-2.39	13.8401		-2.39	[-4.58; -0.19]
PIGD off	154	0.13	10.0528		0.13	[-1.46; 1.71]
PIGD on	131	0.31	9.7995		0.31	[-1.37; 1.99]
Random effects model	876				-0.32	[-1.17; 0.53]
Cohort = LuxPARK						
UPDRS III axial on	470	-3.63	15.2257		-3.63	[-5.01; -2.26]
FOGAC	128	-6.42	27.4149		-6.42	[-11.17; -1.67]
FOGQ	201	-2.79	13.2743		-2.79	[-4.63; -0.96]
NFOGQ	36	-3.52	10.2342		-3.52	[-6.87; -0.18]
PDQ39 Mobility	545	-2.24	11.3523		-2.24	[-3.20; -1.29]
PIGD on	468	-2.58	14.2520		-2.58	[-3.87; -1.29]
TuG	140	-0.62	25.2455		-0.62	[-4.81; 3.56]
Random effects model	1988				-2.74	[-3.37; -2.11]
Random effects model	3681				-1.57	[-2.39; -0.76]

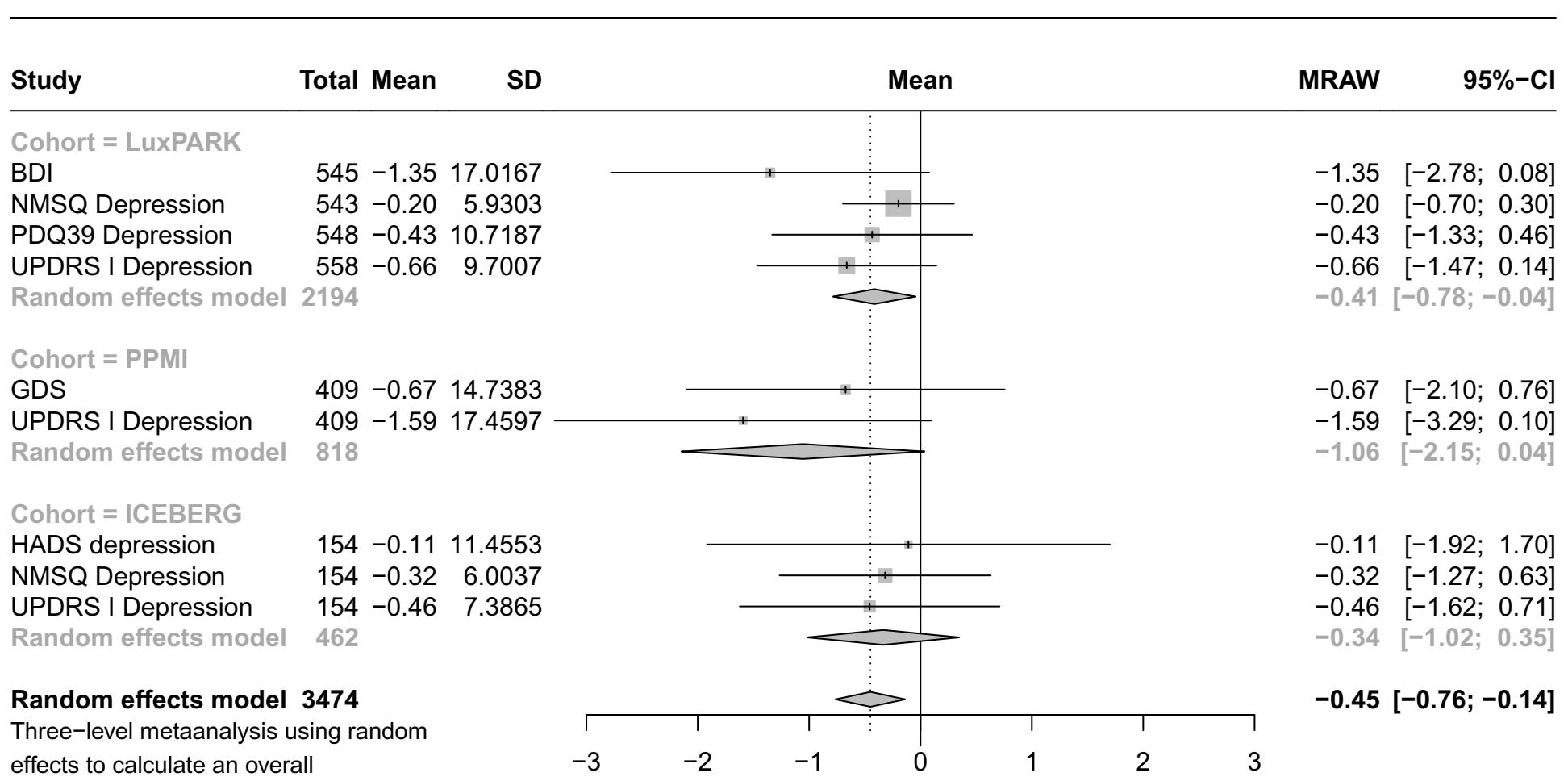
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Axial & PIGD across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->



Forest plot for baseline characteristics of symptom domain Depression



<- Associated with fast-progressing type | associated with slow-progressing type ->

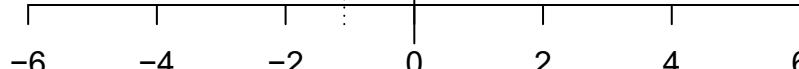
Forest plot for baseline characteristics of symptom domain Memory

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = LuxPARK						
CERAD Words DR	212	-0.99	9.7183			-0.99 [-2.30; 0.31]
CERAD Words IR	216	-1.63	12.8291			-1.63 [-3.35; 0.08]
CERAD Words Recognition	217	0.59	18.0617			0.59 [-1.81; 2.99]
MOCA Orientation + Memory	559	-2.54	12.4261			-2.54 [-3.57; -1.51]
NMSQ Memory	545	-0.39	4.6017			-0.39 [-0.77; 0.00]
PDQ39 Memory	549	-0.90	8.6625			-0.90 [-1.62; -0.17]
SIQCDE Memory	234	-1.96	18.3043			-1.96 [-4.30; 0.39]
Random effects model	2532					-1.12 [-1.83; -0.40]
Cohort = PPMI						
Hopkins Verbal Learning Test DR	407	-4.56	25.5606			-4.56 [-7.05; -2.08]
Hopkins Verbal Learning Test IR	408	-2.53	14.5925			-2.53 [-3.95; -1.11]
MOCA Orientation + Memory	409	-0.95	12.3831			-0.95 [-2.15; 0.25]
Random effects model	1224					-2.44 [-4.35; -0.54]
Cohort = ICEBERG						
MATTIS Memory	154	-0.29	9.4798			-0.29 [-1.79; 1.20]
MMSE Memory	154	-0.57	7.2104			-0.57 [-1.71; 0.57]
MOCA Orientation + Memory	154	0.17	10.2795			0.17 [-1.46; 1.79]
NMSQ Memory	152	-0.61	4.8031			-0.61 [-1.37; 0.16]
Random effects model	614					-0.47 [-1.02; 0.08]
Random effects model	4370					-1.09 [-1.61; -0.57]

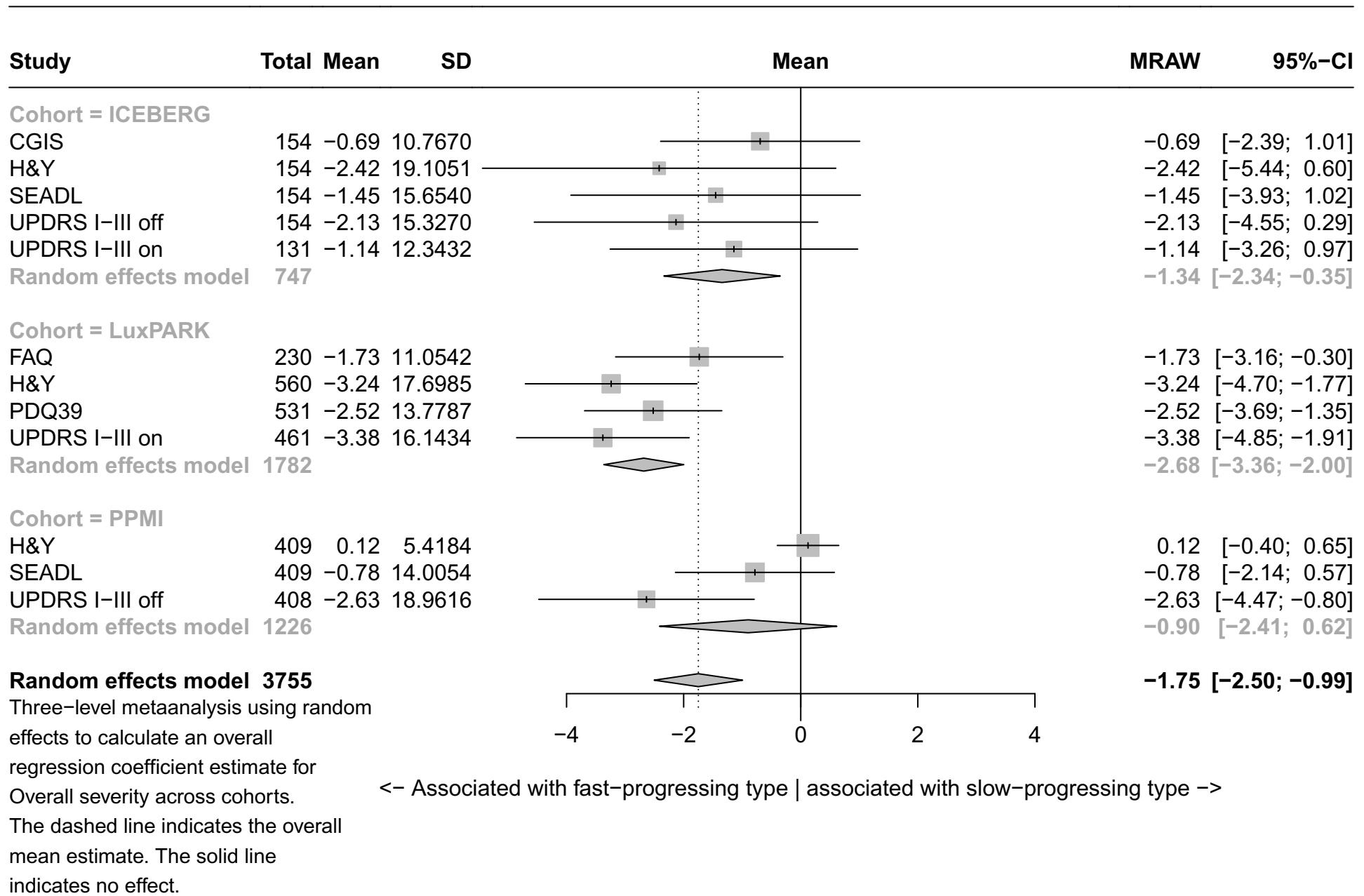
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Memory across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

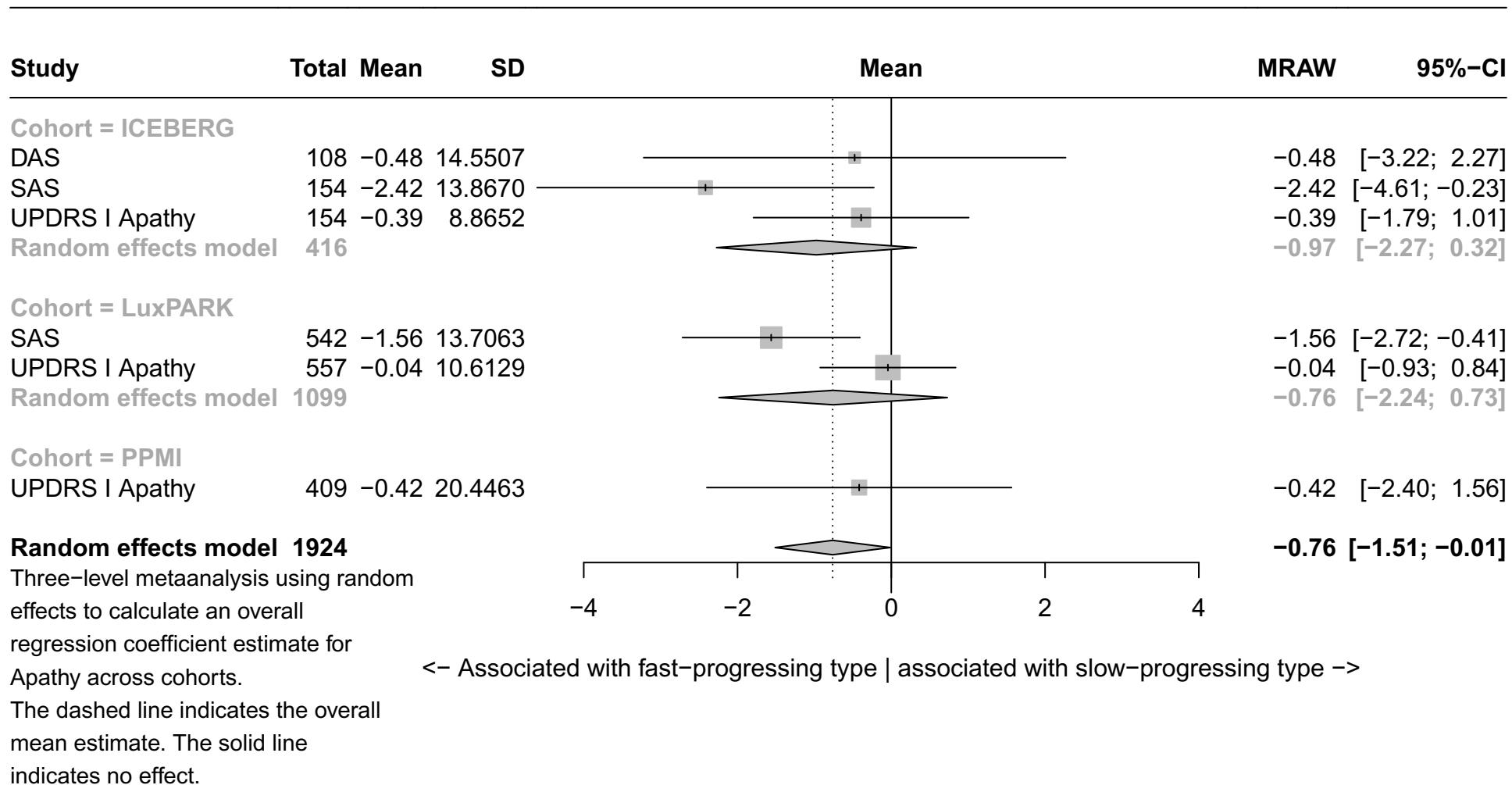
<- Associated with fast-progressing type | associated with slow-progressing type ->



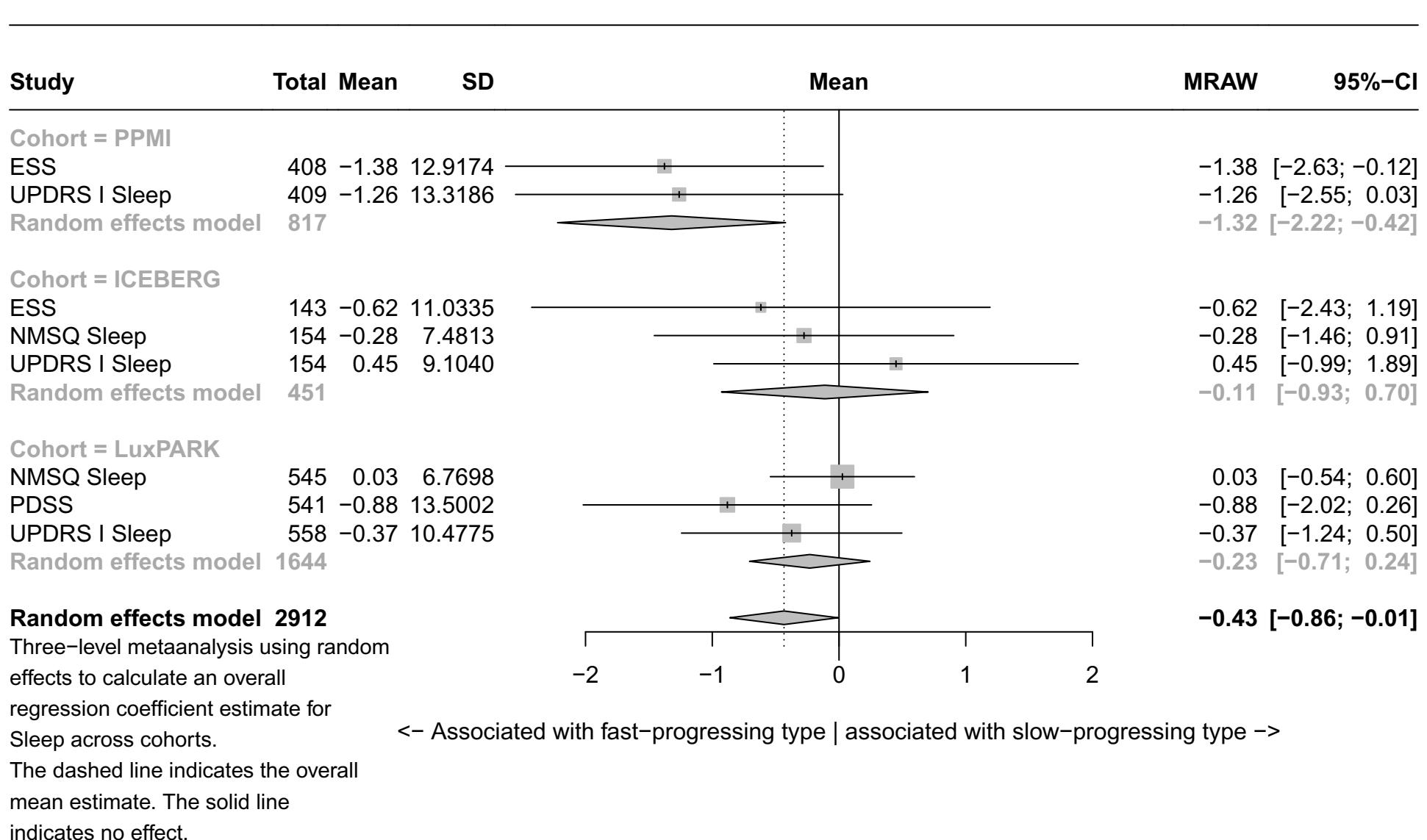
Forest plot for baseline characteristics of symptom domain Overall severity



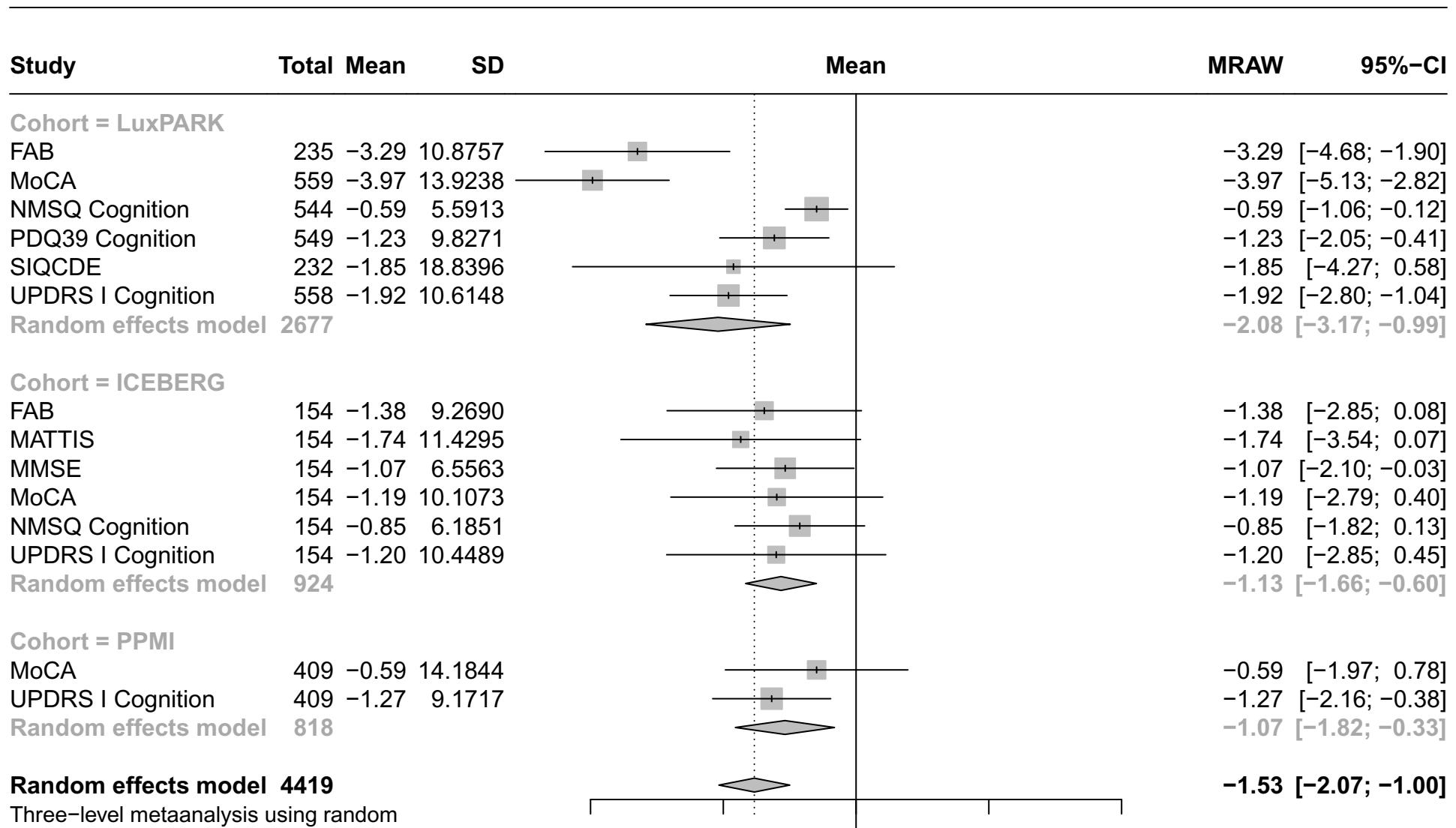
Forest plot for baseline characteristics of symptom domain Apathy



Forest plot for baseline characteristics of symptom domain Sleep

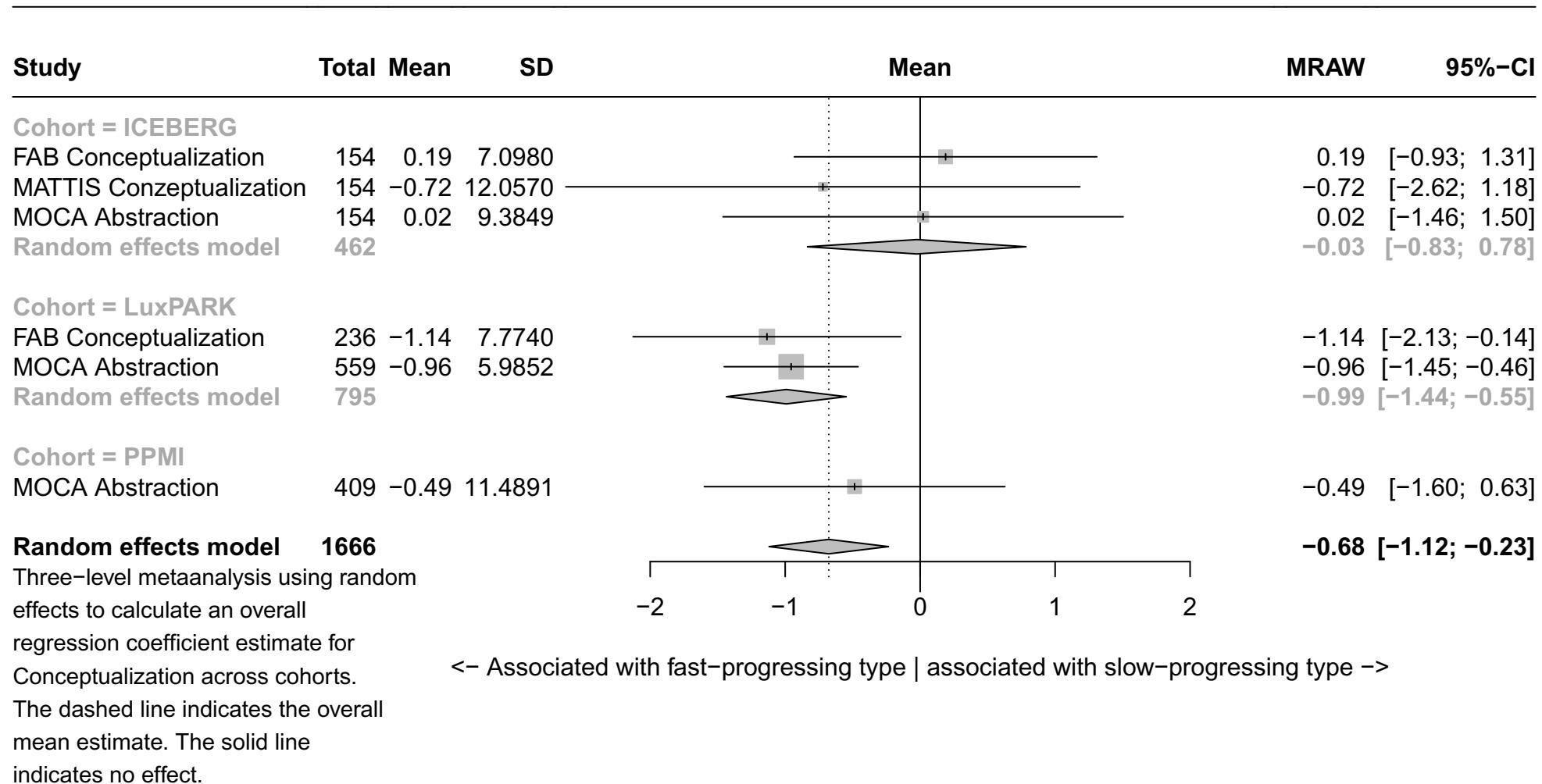


Forest plot for baseline characteristics of symptom domain Overall cognition



<- Associated with fast-progressing type | associated with slow-progressing type ->

Forest plot for baseline characteristics of symptom domain Conceptualization



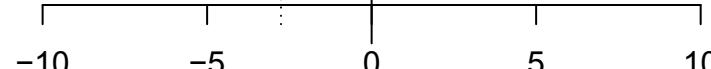
Forest plot for baseline characteristics of symptom domain Visuo–executive

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = ICEBERG						
FAB 3–6	154	-1.18	9.2951			-1.18 [-2.65; 0.29]
MATTIS Initiation + Construction	154	-1.16	11.8424			-1.16 [-3.03; 0.71]
MMSE Construction	154	-2.06	15.8255			-2.06 [-4.56; 0.44]
MOCA Visuospatial/Executive	154	-1.15	7.7696			-1.15 [-2.38; 0.08]
Random effects model	616					-1.25 [-2.05; -0.46]
Cohort = LuxPARK						
FAB 3–6	235	-3.08	10.8871			-3.08 [-4.47; -1.69]
Judgement Line Orientation	214	-2.53	11.8539			-2.53 [-4.12; -0.94]
MOCA Visuospatial/Executive	560	-2.36	9.4592			-2.36 [-3.15; -1.58]
Stroop Errors	208	-7.66	45.0379			-7.66 [-13.78; -1.54]
Stroop Time	208	-3.35	15.9332			-3.35 [-5.51; -1.18]
Trailmaking A	549	-6.75	26.6864			-6.75 [-8.98; -4.51]
Trailmaking B	480	-5.51	18.8538			-5.51 [-7.20; -3.83]
Random effects model	2454					-3.94 [-5.30; -2.59]
Cohort = PPMI						
Judgement Line Orientation	408	-1.19	11.5763			-1.19 [-2.31; -0.07]
MOCA Visuospatial/Executive	409	-0.50	12.3462			-0.50 [-1.69; 0.70]
Symbol Digit Modalities	408	-5.02	21.9826			-5.02 [-7.15; -2.89]
Random effects model	1225					-2.10 [-4.71; 0.52]
Random effects model	4295					-2.75 [-3.77; -1.74]

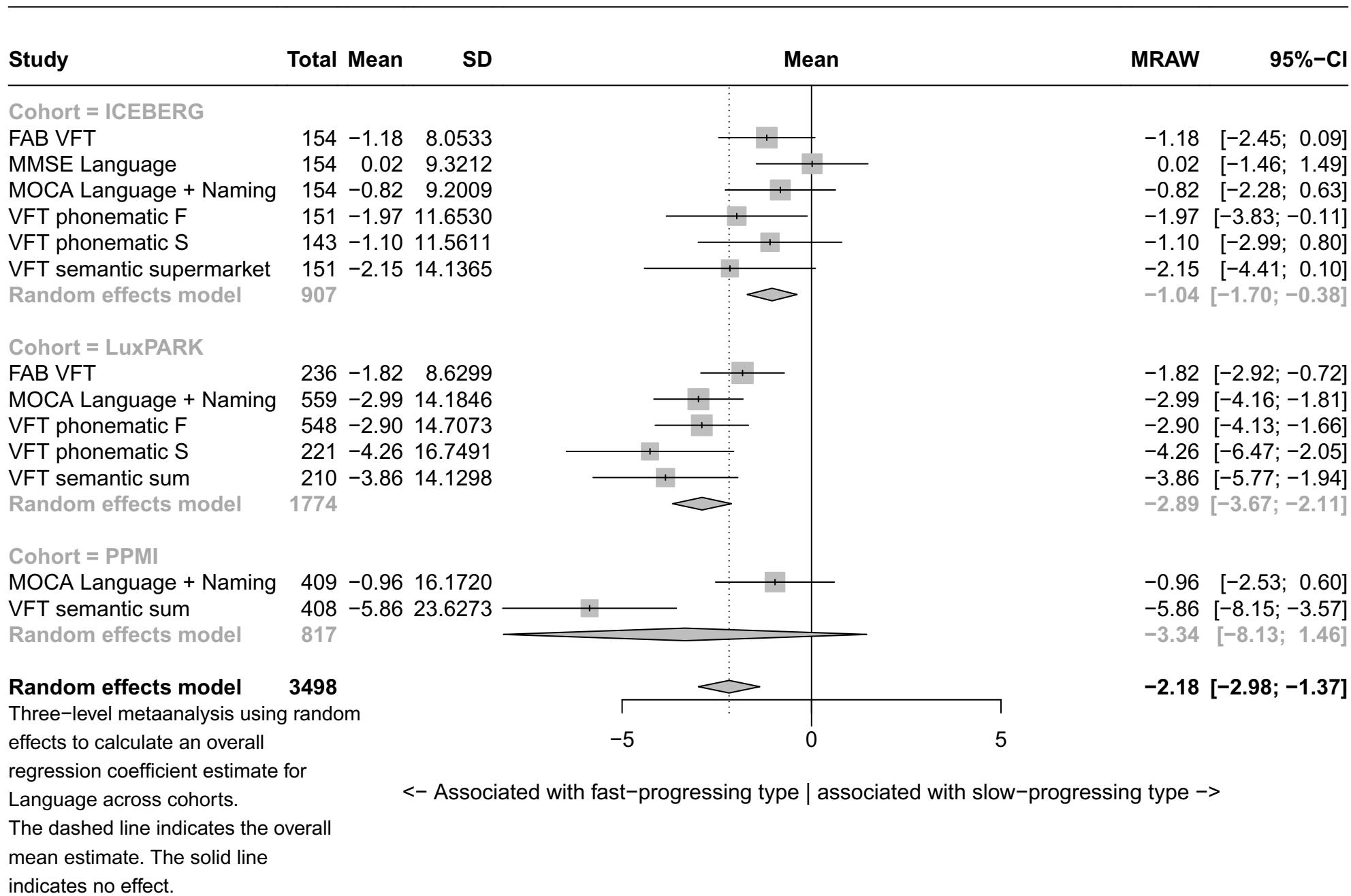
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Visuo–executive across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

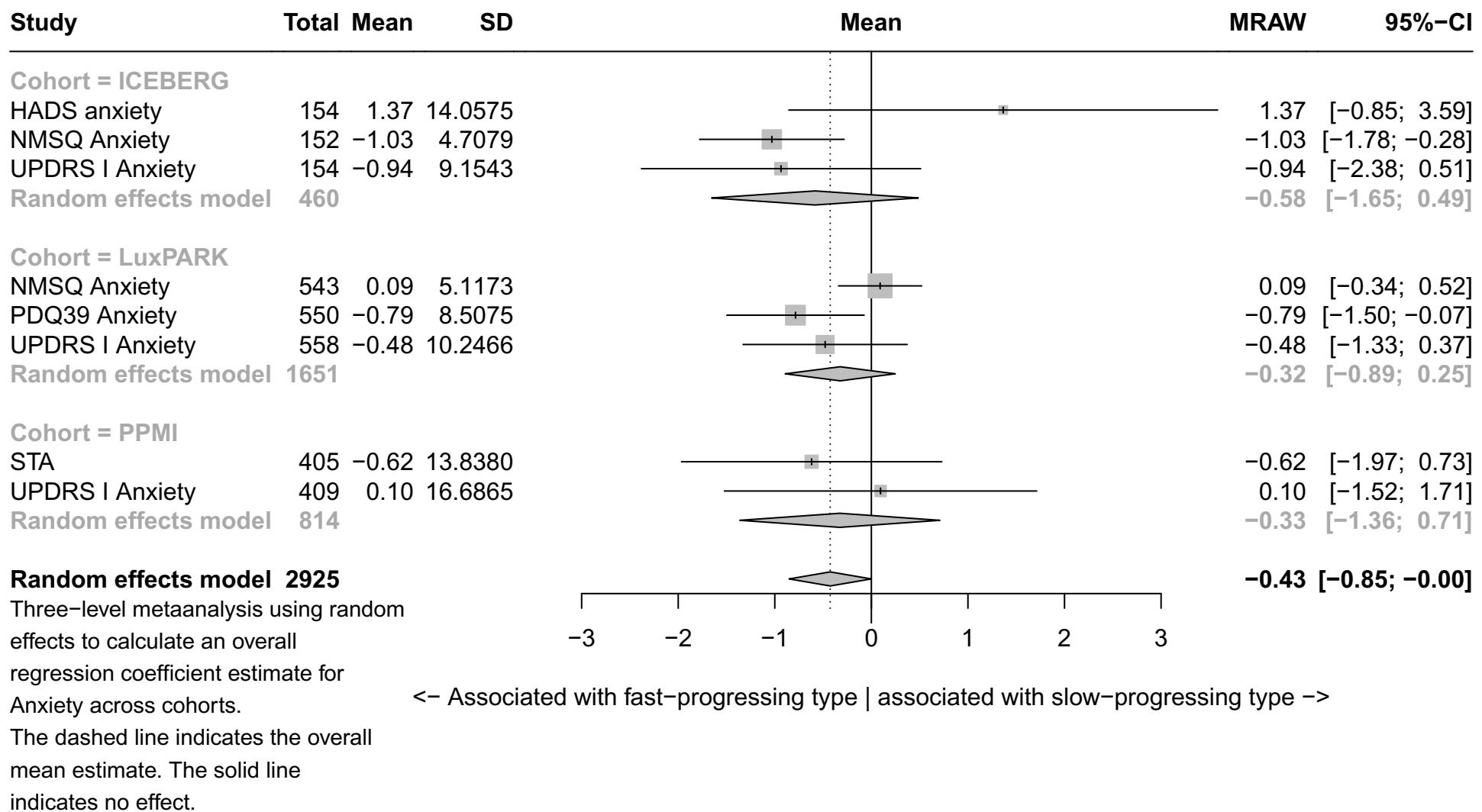
<– Associated with fast–progressing type | associated with slow–progressing type –>



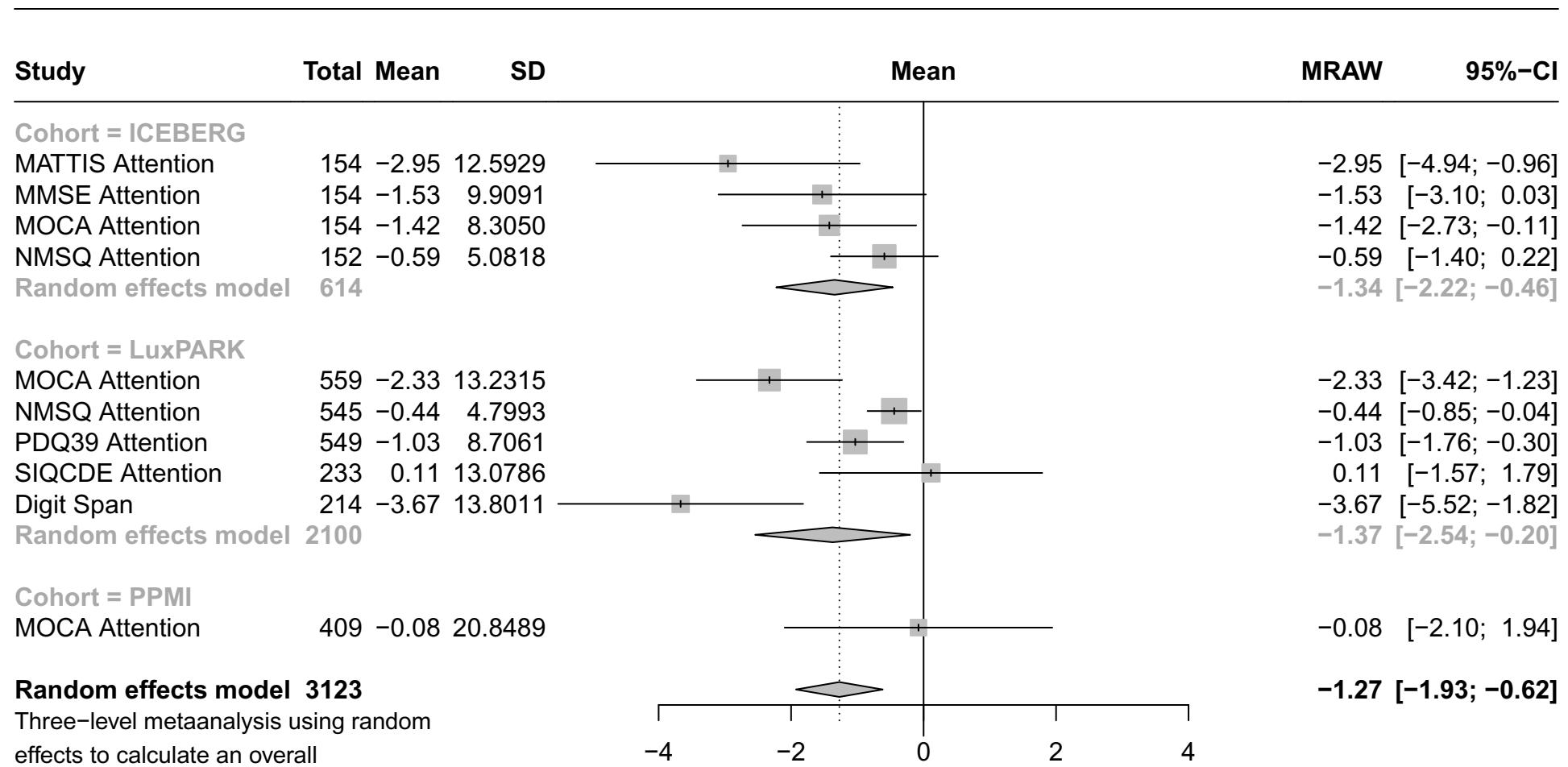
Forest plot for baseline characteristics of symptom domain Language



Forest plot for baseline characteristics of symptom domain Anxiety



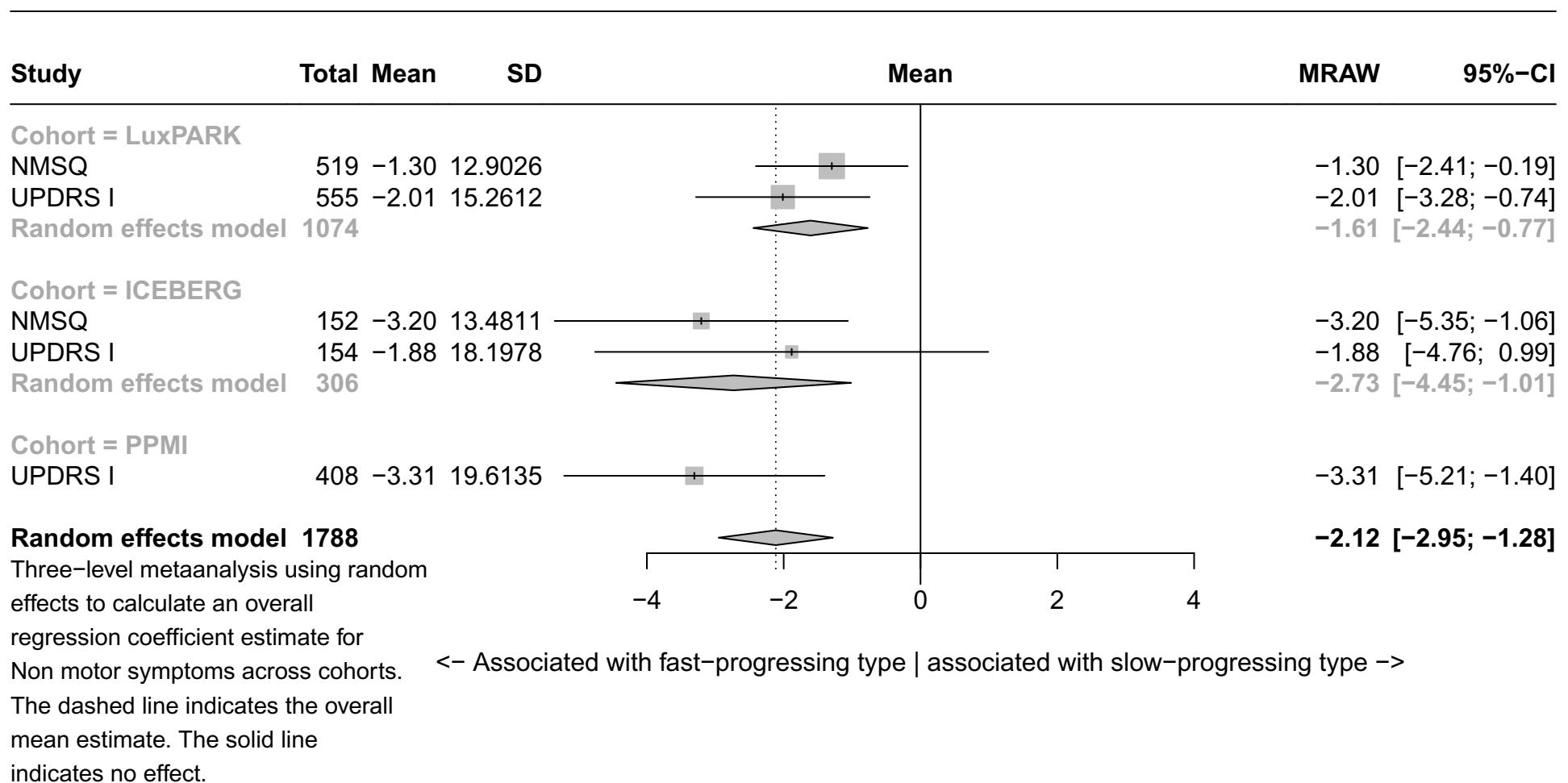
Forest plot for baseline characteristics of symptom domain Attention



The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->

Forest plot for baseline characteristics of symptom domain Non motor symptoms

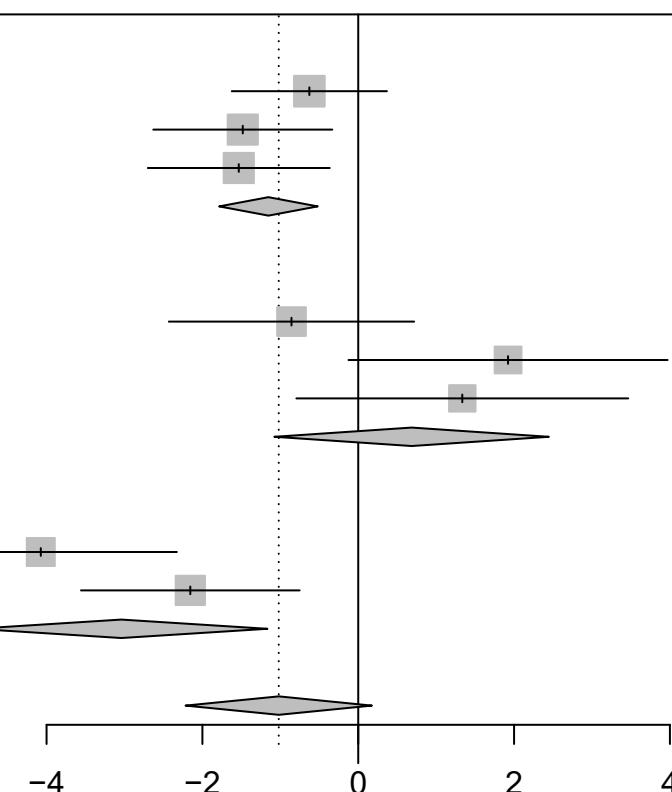


Forest plot for baseline characteristics of symptom domain Autonomic

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = LuxPARK						
NMSQ Autonomic	525	-0.63	11.64	12	-0.63	[-1.62; 0.37]
SCOPA-AUT	547	-1.48	13.70	72	-1.48	[-2.63; -0.33]
UPDRS I Autonomic	558	-1.53	14.06	69	-1.53	[-2.70; -0.37]
Random effects model	1630				-1.15	[-1.78; -0.52]
Cohort = ICEBERG						
NMSQ Autonomic	154	-0.86	9.96	77	-0.86	[-2.43; 0.72]
SCOPA-AUT	153	1.92	12.92	48	1.92	[-0.13; 3.97]
UPDRS I Autonomic	154	1.34	13.48	33	1.34	[-0.79; 3.47]
Random effects model	461				0.69	[-1.08; 2.45]

Cohort = PPMI

SCOPA-AUT 398 -4.07 17.7790
UPDRS I Autonomic 409 -2.16 14.4778
Random effects model **807**



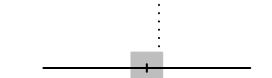
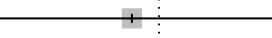
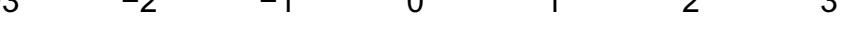
Random effects model 2898

Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Autonomic across cohorts

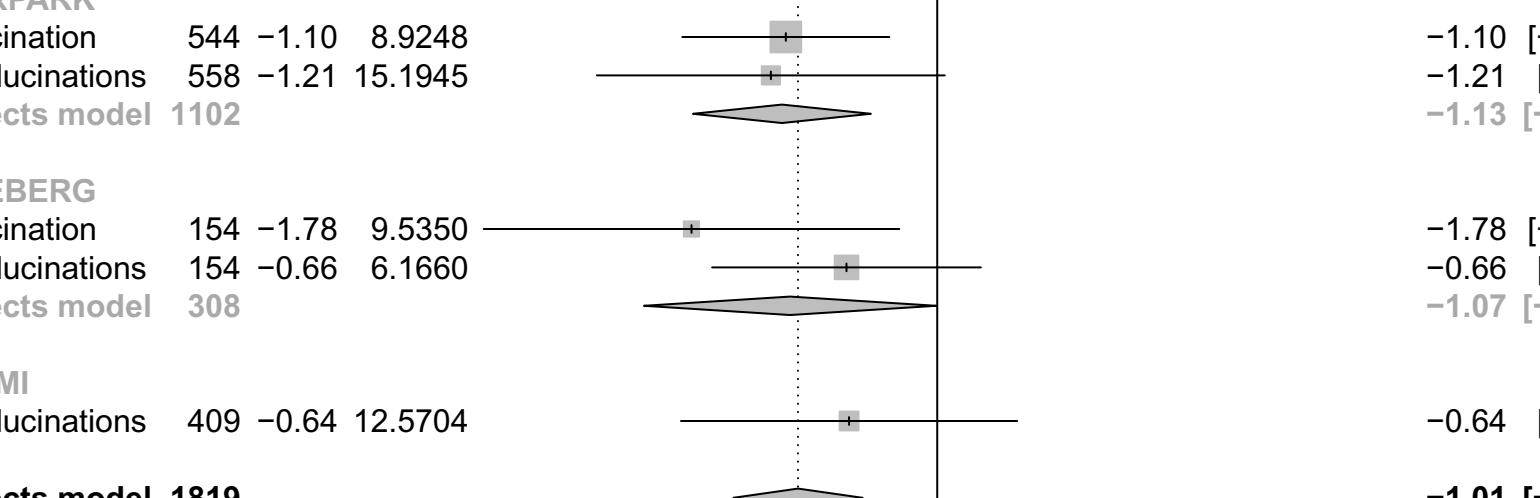
The dashed line indicates the overall mean estimate. The solid line indicates no effect.

`<- Associated with fast-progressing type | associated with slow-progressing type ->`

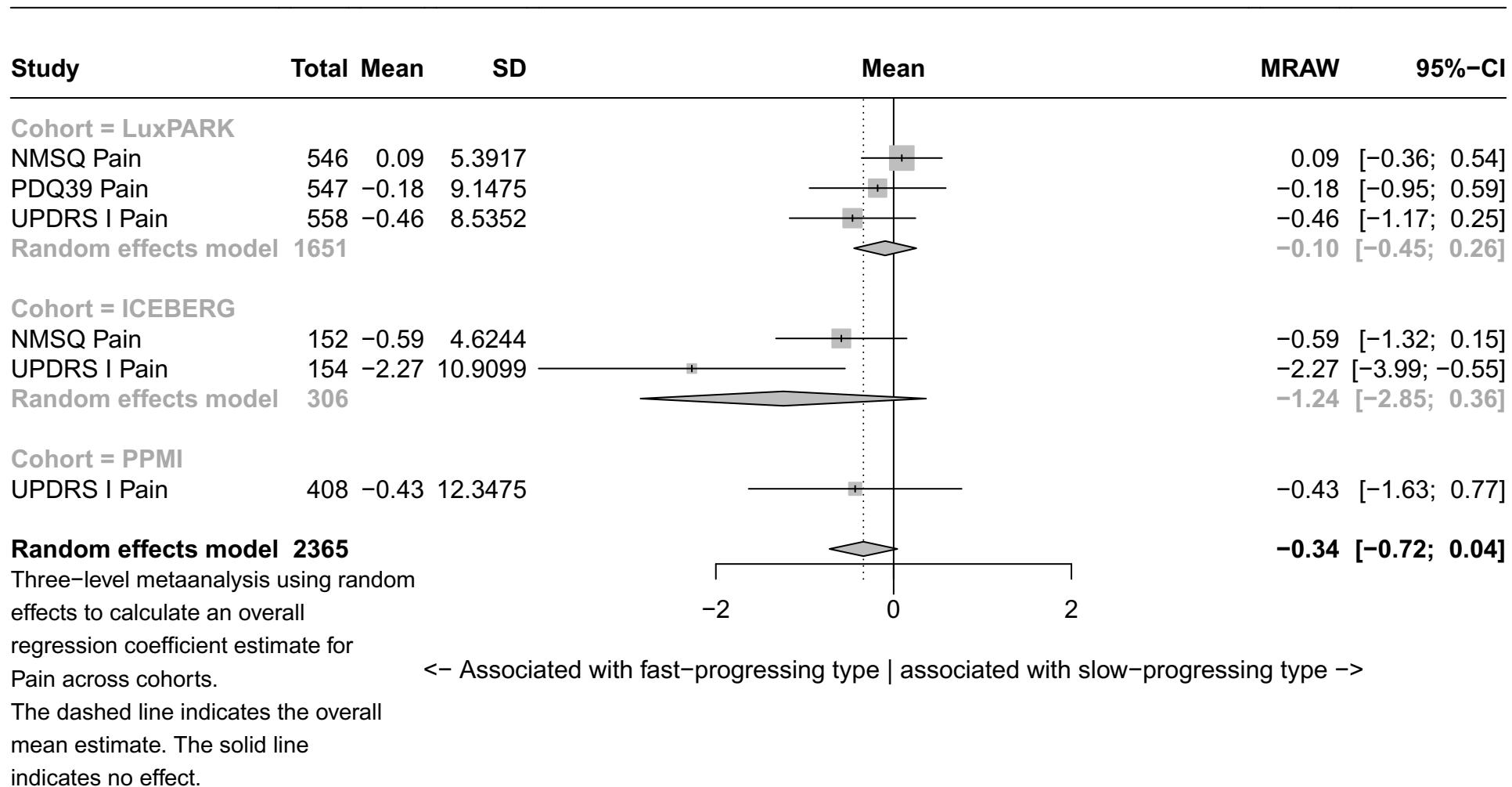
Forest plot for baseline characteristics of symptom domain Hallucinations

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = LuxPARK						
NMSQ Hallucination	544	-1.10	8.9248		-1.10	[-1.85; -0.35]
UPDRS I Hallucinations	558	-1.21	15.1945		-1.21	[-2.47; 0.06]
Random effects model	1102				-1.13	[-1.77; -0.48]
Cohort = ICEBERG						
NMSQ Hallucination	154	-1.78	9.5350		-1.78	[-3.29; -0.27]
UPDRS I Hallucinations	154	-0.66	6.1660		-0.66	[-1.63; 0.32]
Random effects model	308				-1.07	[-2.13; -0.01]
Cohort = PPMI						
UPDRS I Hallucinations	409	-0.64	12.5704		-0.64	[-1.86; 0.58]
Random effects model	1819				-1.01	[-1.48; -0.54]
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Hallucinations across cohorts.						
The dashed line indicates the overall mean estimate. The solid line indicates no effect.						

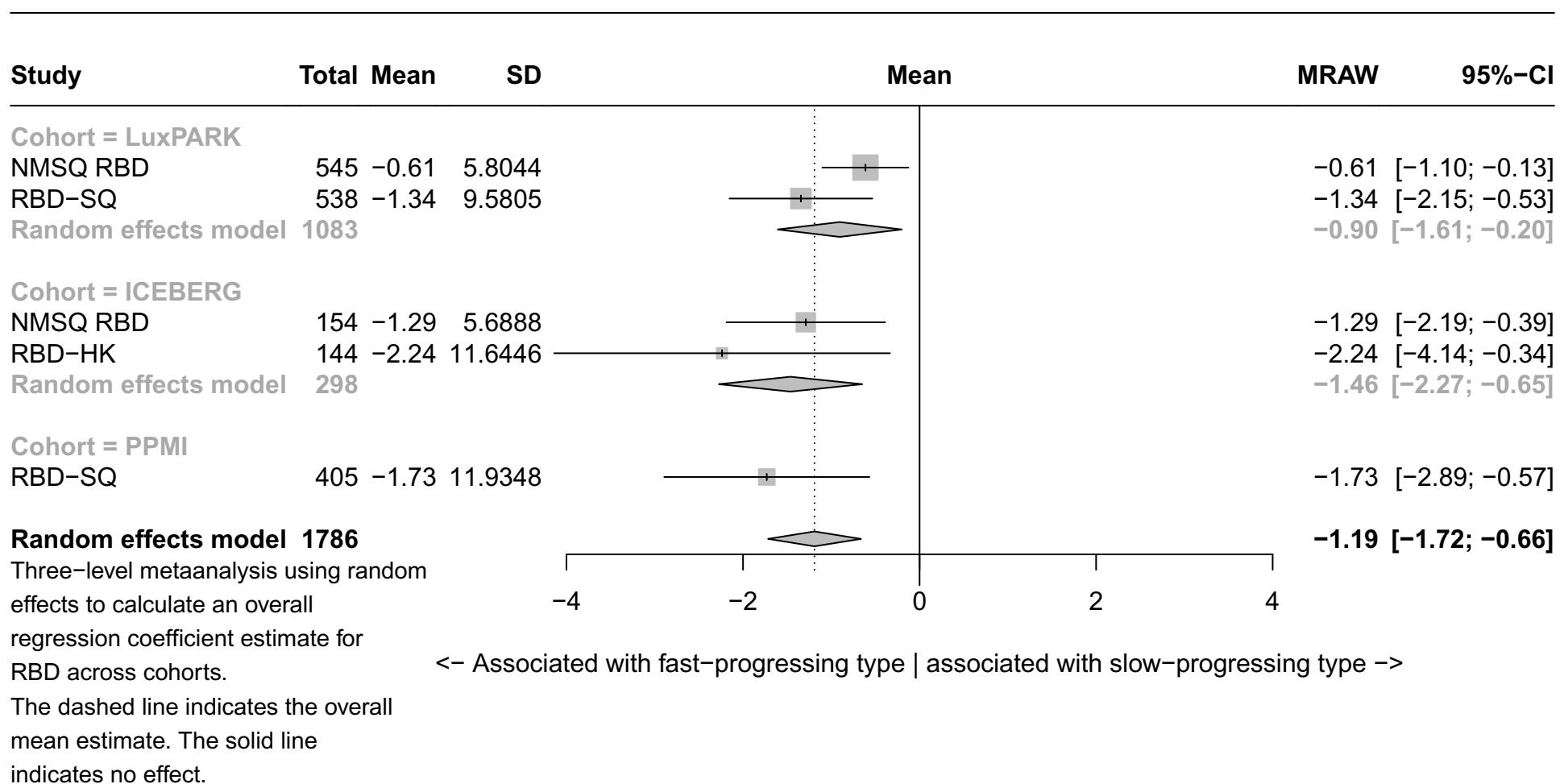
← Associated with fast-progressing type | associated with slow-progressing type →



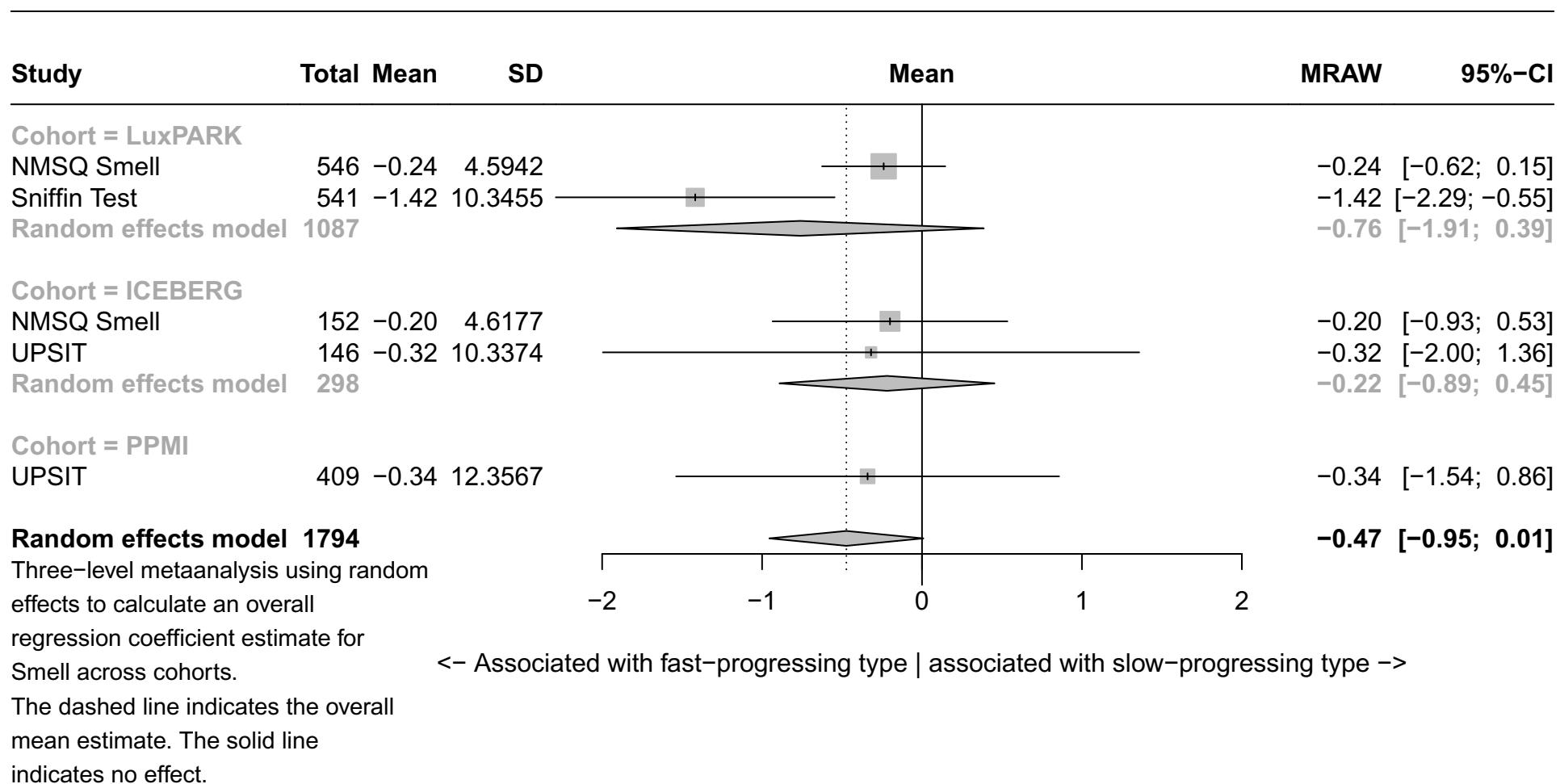
Forest plot for baseline characteristics of symptom domain Pain



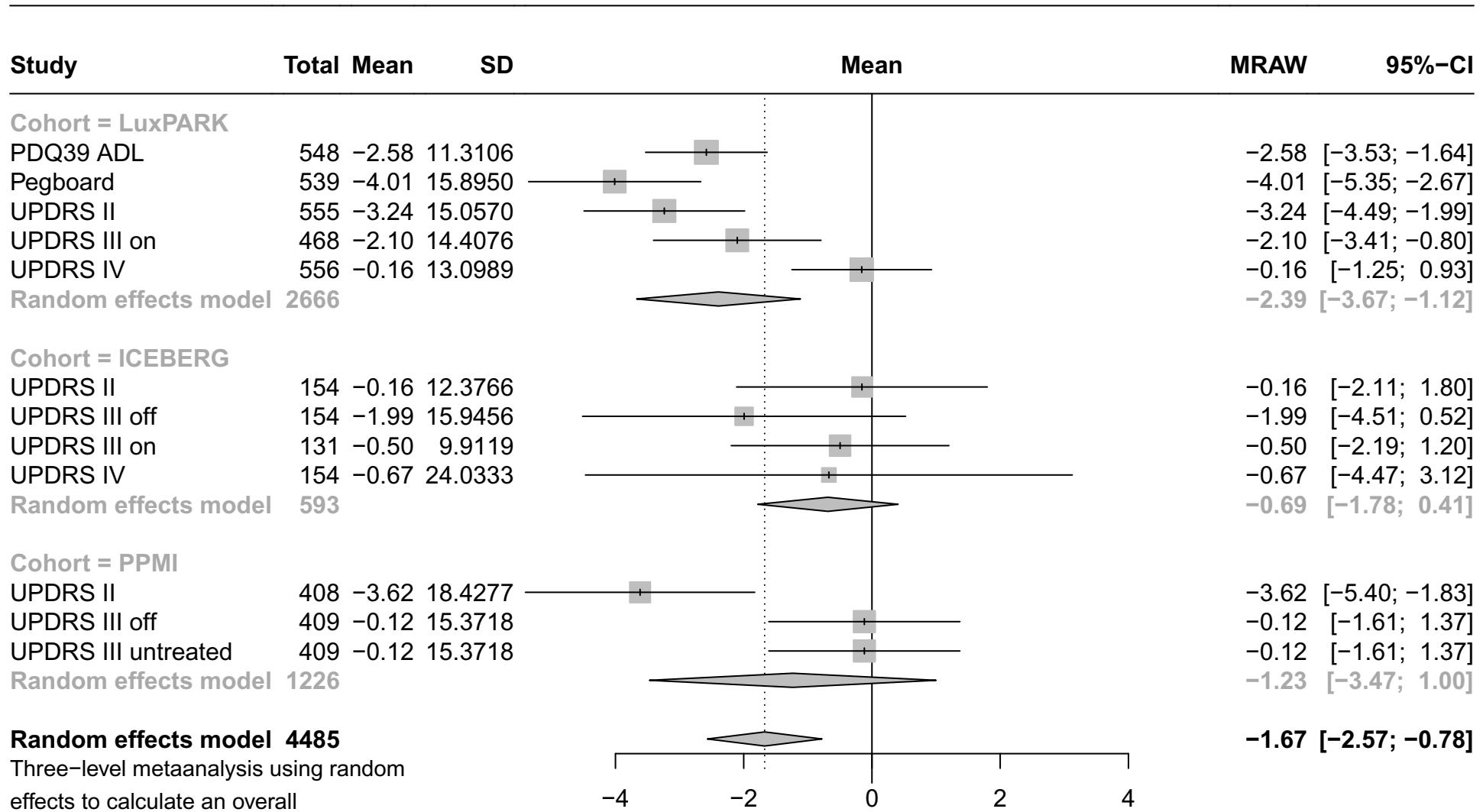
Forest plot for baseline characteristics of symptom domain RBD



Forest plot for baseline characteristics of symptom domain Smell



Forest plot for baseline characteristics of symptom domain Motor symptoms

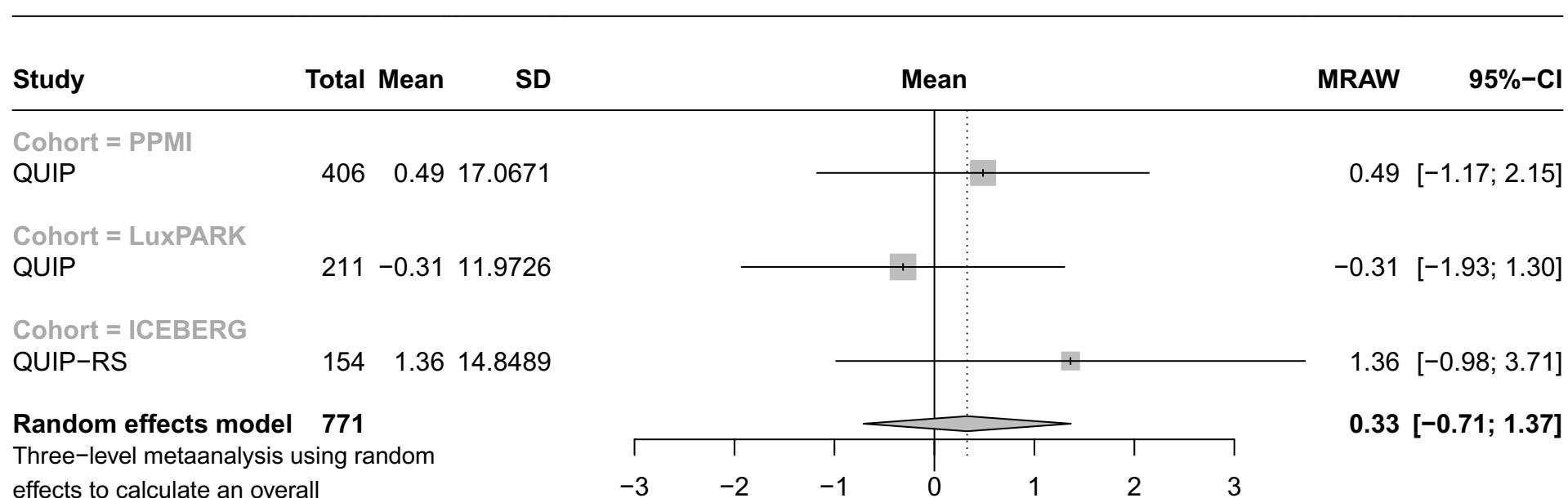


Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Motor symptoms across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->

Forest plot for baseline characteristics of symptom domain Impulsivity

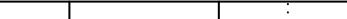
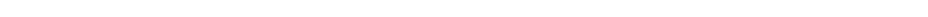
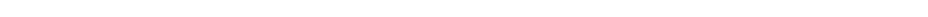
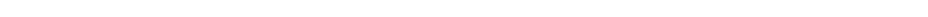
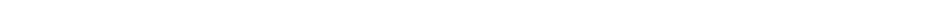
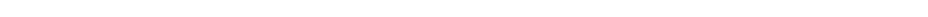
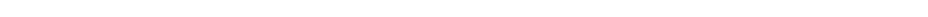


Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Impulsivity across cohorts.

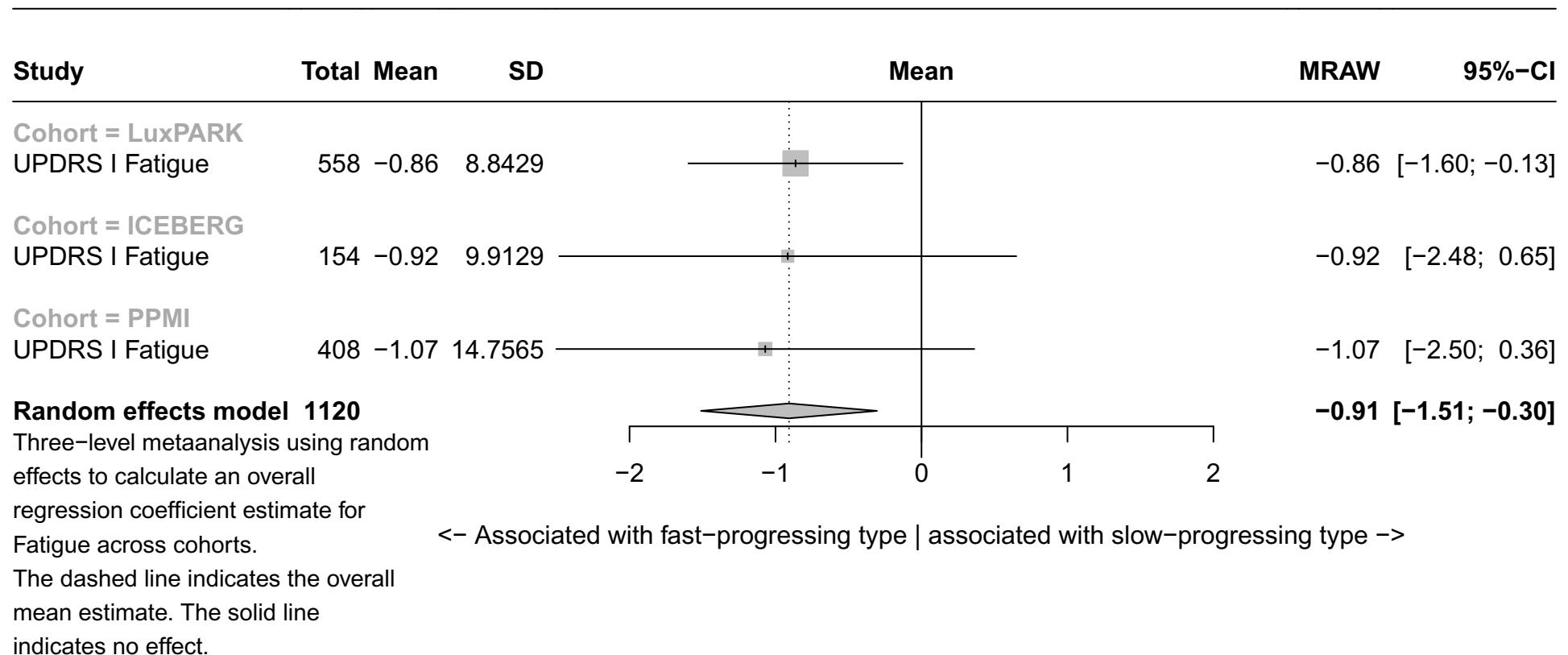
The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->

Forest plot for baseline characteristics of symptom domain Tremor

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = ICEBERG						
TD off	154	-1.40	10.3429		-1.40	[-3.04; 0.23]
TD on	131	-1.16	9.1063		-1.16	[-2.71; 0.40]
Random effects model	285				-1.27	[-2.40; -0.14]
Cohort = PPMI						
TD off	408	-0.77	14.8601		-0.77	[-2.21; 0.68]
Cohort = LuxPARK						
TD on	470	0.72	12.3080		0.72	[-0.39; 1.83]
Random effects model 1163					-0.54	[-1.57; 0.50]
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Tremor across cohorts.						
The dashed line indicates the overall mean estimate. The solid line indicates no effect.						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
						
				<img alt="Forest plot scale from -3 to 3 with dashed line at 0 and		

Forest plot for baseline characteristics of symptom domain Fatigue



Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

Forest plots for symptom domain baseline associations (cross-cohort validation)

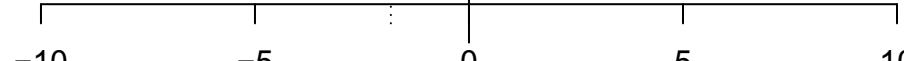
Forest plot for baseline characteristics of symptom domain Axial & PIGD (validation)

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = ICEBERG (validation)						
UPDRS III axial off	154	-0.98	15.4066		-0.98	[-3.41; 1.46]
UPDRS III axial on	131	0.24	13.1173		0.24	[-2.01; 2.48]
GABS Examination	153	-0.80	16.1203		-0.80	[-3.36; 1.75]
GABS Questionnaire	153	-1.21	15.6229		-1.21	[-3.69; 1.26]
PIGD off	154	-0.27	13.3111		-0.27	[-2.37; 1.83]
PIGD on	131	0.41	12.9408		0.41	[-1.80; 2.63]
Random effects model	876				-0.37	[-1.32; 0.57]
Cohort = LuxPARK (validation)						
UPDRS III axial on	470	-3.77	16.9217		-3.77	[-5.30; -2.24]
FOGAC	128	-5.80	27.1058		-5.80	[-10.50; -1.11]
FOGQ	201	-2.84	15.0671		-2.84	[-4.92; -0.75]
NFOGQ	36	-5.66	15.1159		-5.66	[-10.60; -0.72]
PDQ39 Mobility	545	-2.20	12.8964		-2.20	[-3.28; -1.12]
PIGD on	468	-2.78	16.2694		-2.78	[-4.25; -1.31]
TuG	140	-1.15	25.7075		-1.15	[-5.41; 3.11]
Random effects model	1988				-2.87	[-3.62; -2.12]
Random effects model 2864					-1.83	[-2.70; -0.95]

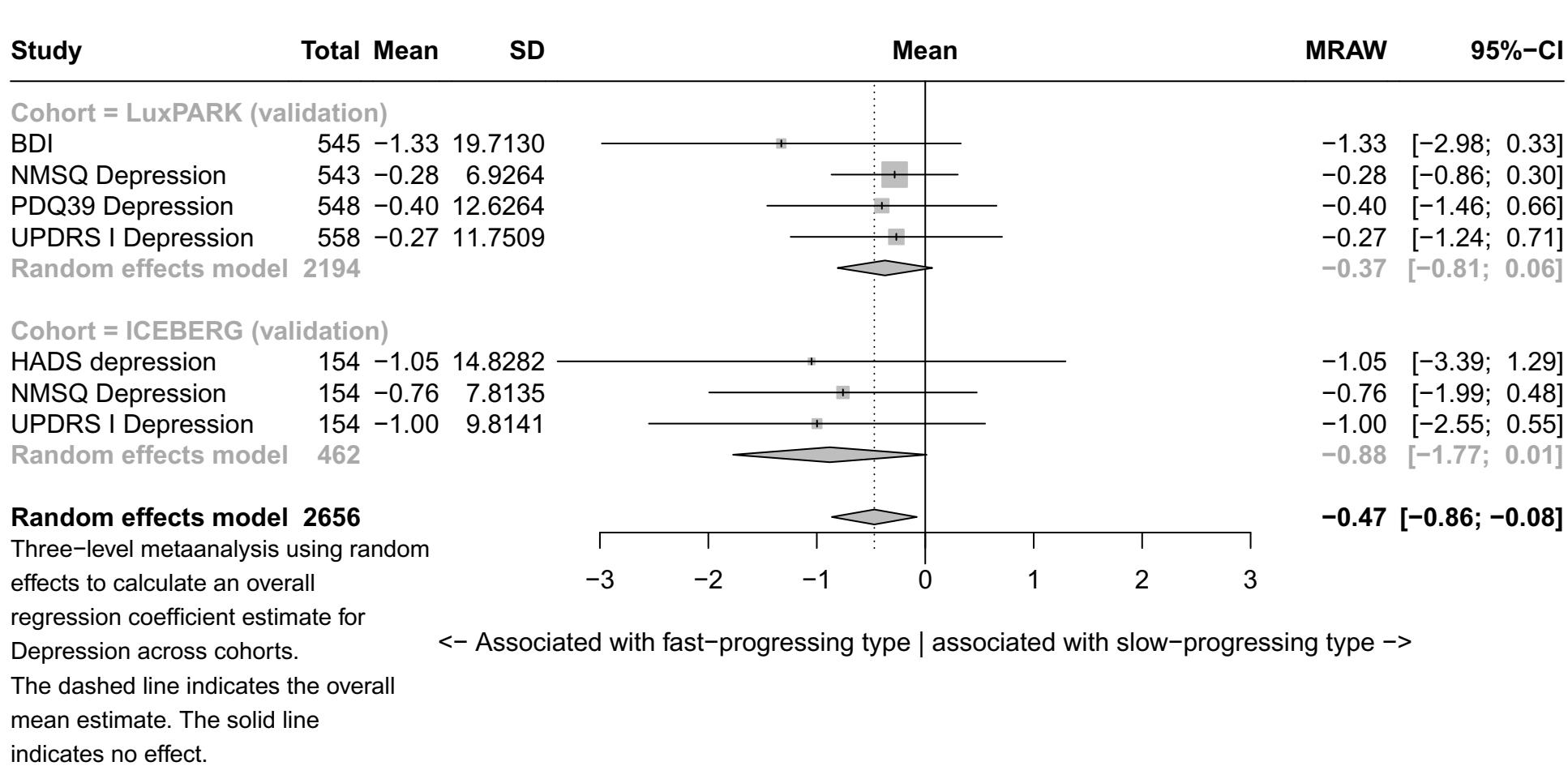
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Axial & PIGD across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->



Forest plot for baseline characteristics of symptom domain Depression (validation)



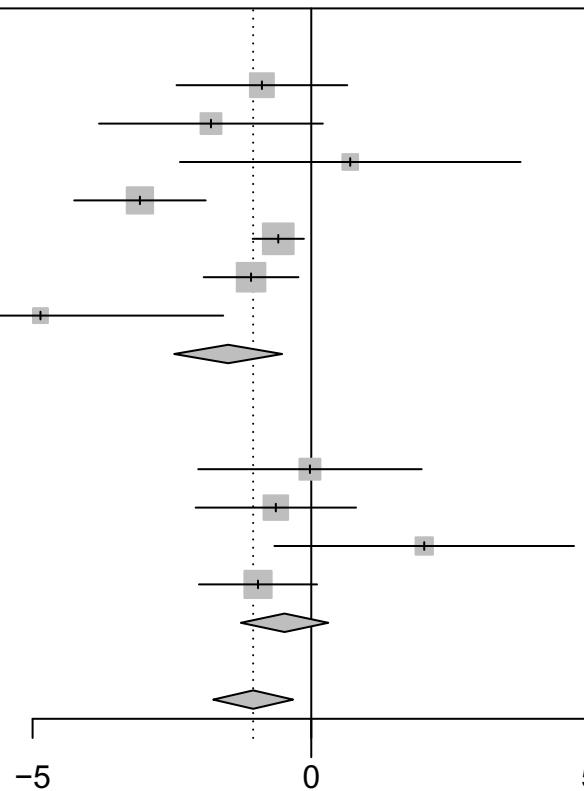
Forest plot for baseline characteristics of symptom domain Memory (validation)

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = LuxPARK (validation)						
CERAD Words DR	212	-0.89	11.3786			-0.89 [-2.42; 0.65]
CERAD Words IR	216	-1.80	15.0581			-1.80 [-3.81; 0.21]
CERAD Words Recognition	217	0.70	22.9648			0.70 [-2.36; 3.75]
MOCA Orientation + Memory	559	-3.07	14.2284			-3.07 [-4.25; -1.89]
NMSQ Memory	545	-0.59	5.4772			-0.59 [-1.05; -0.13]
PDQ39 Memory	549	-1.08	10.1624			-1.08 [-1.93; -0.23]
SIQCDE Memory	234	-4.86	25.5950			-4.86 [-8.14; -1.58]
Random effects model	2532					-1.49 [-2.46; -0.52]
Cohort = ICEBERG (validation)						
MATTIS Memory	154	-0.02	12.6948			-0.02 [-2.03; 1.98]
MMSE Memory	154	-0.64	9.1126			-0.64 [-2.08; 0.80]
MOCA Orientation + Memory	154	2.03	17.0214			2.03 [-0.66; 4.72]
NMSQ Memory	152	-0.96	6.6616			-0.96 [-2.01; 0.10]
Random effects model	614					-0.48 [-1.26; 0.31]
Random effects model	3146					-1.04 [-1.76; -0.33]

Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Memory across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->



Forest plot for baseline characteristics of symptom domain Overall severity (validation)

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = ICEBERG (validation)						
CGIS	154	-0.40	14.2454		-0.40	[-2.65; 1.85]
H&Y	154	-2.83	21.5373		-2.83	[-6.23; 0.57]
SEADL	154	-2.45	21.8125		-2.45	[-5.90; 0.99]
UPDRS I-III off	154	-1.80	19.8928		-1.80	[-4.94; 1.34]
UPDRS I-III on	131	-0.49	15.9447		-0.49	[-3.22; 2.24]
Random effects model	747				-1.29	[-2.58; -0.00]

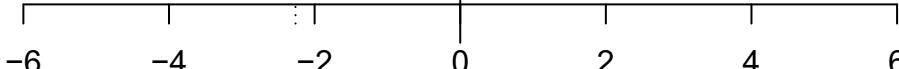
Cohort = LuxPARK (validation)						
FAQ	230	-1.50	12.7248		-1.50	[-3.14; 0.15]
H&Y	560	-3.31	19.4615		-3.31	[-4.92; -1.70]
PDQ39	531	-2.49	15.7021		-2.49	[-3.82; -1.15]
UPDRS I-III on	461	-3.59	18.3575		-3.59	[-5.27; -1.92]
Random effects model	1782				-2.70	[-3.54; -1.86]

Random effects model 2529

Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Overall severity across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->



-2.26 [-3.05; -1.48]

Forest plot for baseline characteristics of symptom domain Apathy (validation)

The forest plot displays the mean effect sizes and 95% confidence intervals for three outcome measures (DAS, SAS, UPDRS I Apathy) across three study groups: ICEBERG validation, LuxPARK validation, and a Random effects model. The y-axis represents the mean effect size, and the x-axis represents the study group. Individual study estimates are shown as grey squares with horizontal error bars for the 95% CI. A vertical dotted line at zero indicates no effect. The random effects model estimate is shown as a diamond representing the weighted average of all studies.

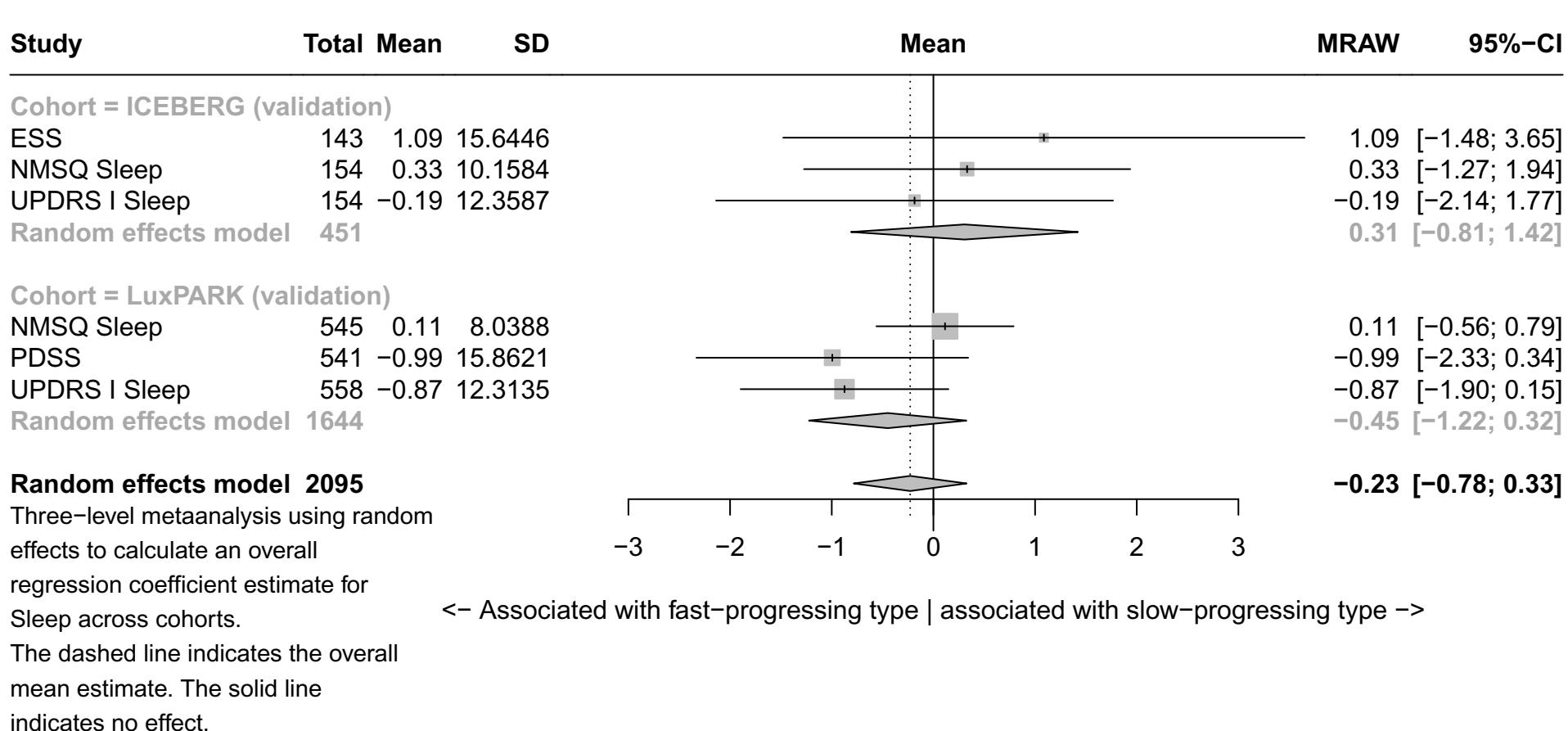
Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = ICEBERG (validation)						
DAS	108	-0.09	20.9958			-0.09 [-4.05; 3.87]
SAS	154	-4.30	18.2740			-4.30 [-7.18; -1.41]
UPDRS I Apathy	154	-1.40	10.8177			-1.40 [-3.11; 0.31]
Random effects model	416					-2.02 [-4.15; 0.11]
Cohort = LuxPARK (validation)						
SAS	542	-1.81	15.7765			-1.81 [-3.14; -0.48]
UPDRS I Apathy	557	0.43	13.4736			0.43 [-0.69; 1.55]
Random effects model	1099					-0.66 [-2.85; 1.53]
Random effects model	1515					-1.30 [-2.78; 0.18]

Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Apathy across cohorts.

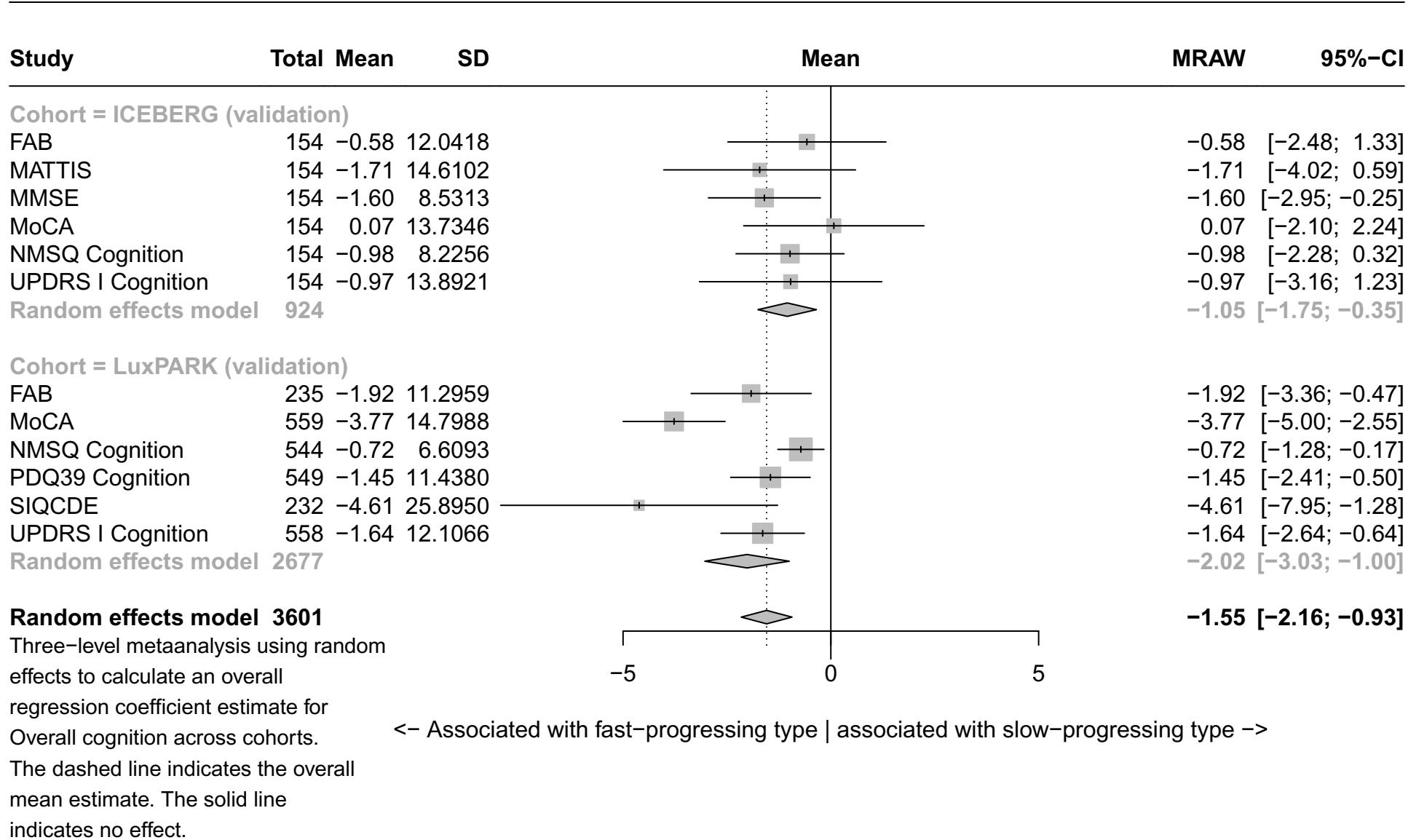
The dashed line indicates the overall mean estimate. The solid line indicates no effect.

<- Associated with fast-progressing type | associated with slow-progressing type ->

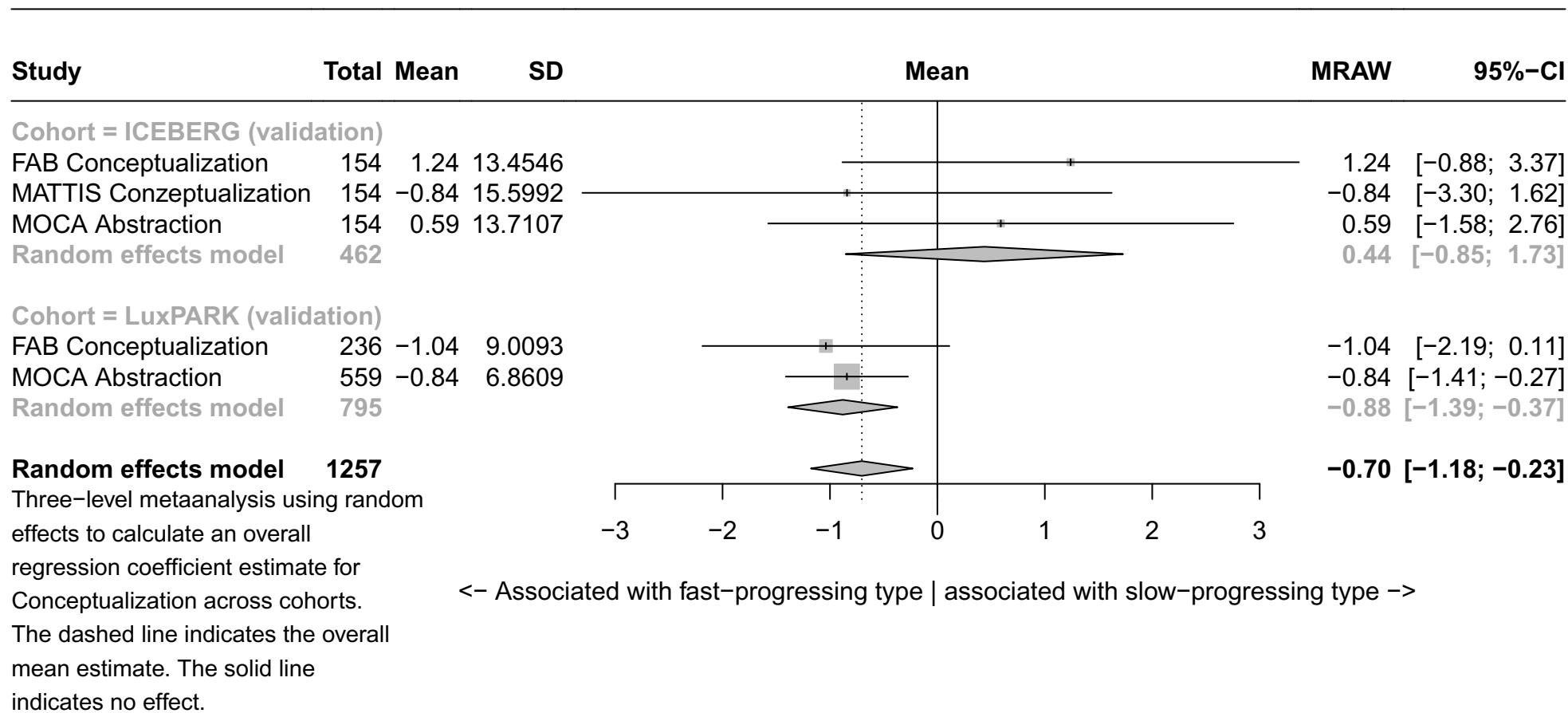
Forest plot for baseline characteristics of symptom domain Sleep (validation)



Forest plot for baseline characteristics of symptom domain Overall cognition (validation)



Forest plot for baseline characteristics of symptom domain Conceptualization (validation)

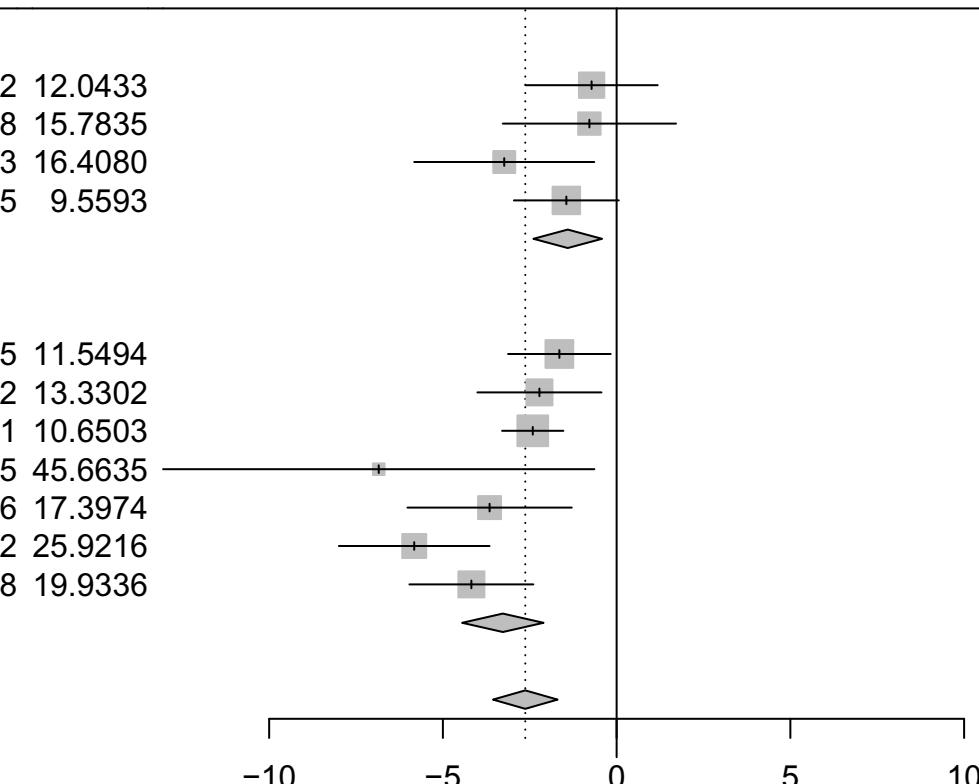


Forest plot for baseline characteristics of symptom domain Visuo–executive (validation)

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = ICEBERG (validation)						
FAB 3–6	154	-0.72	12.0433			-0.72 [-2.62; 1.18]
MATTIS Initiation + Construction	154	-0.78	15.7835			-0.78 [-3.28; 1.71]
MMSE Construction	154	-3.23	16.4080			-3.23 [-5.83; -0.64]
MOCA Visuospatial/Executive	154	-1.45	9.5593			-1.45 [-2.96; 0.06]
Random effects model	616					-1.41 [-2.39; -0.42]
Cohort = LuxPARK (validation)						
FAB 3–6	235	-1.65	11.5494			-1.65 [-3.12; -0.17]
Judgement Line Orientation	214	-2.22	13.3302			-2.22 [-4.01; -0.44]
MOCA Visuospatial/Executive	560	-2.41	10.6503			-2.41 [-3.30; -1.53]
Stroop Errors	208	-6.85	45.6635			-6.85 [-13.05; -0.64]
Stroop Time	208	-3.66	17.3974			-3.66 [-6.02; -1.29]
Trailmaking A	549	-5.82	25.9216			-5.82 [-7.99; -3.66]
Trailmaking B	480	-4.18	19.9336			-4.18 [-5.96; -2.40]
Random effects model	2454					-3.27 [-4.45; -2.10]
Random effects model	3070					-2.63 [-3.56; -1.70]

Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Visuo–executive across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.



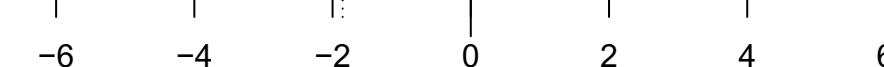
<– Associated with fast–progressing type | associated with slow–progressing type –>

Forest plot for baseline characteristics of symptom domain Language (validation)

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = ICEBERG (validation)						
FAB VFT	154	-0.55	10.5285			-0.55 [-2.21; 1.11]
MMSE Language	154	-0.48	11.9227			-0.48 [-2.36; 1.41]
MOCA Language + Naming	154	-0.84	11.6445			-0.84 [-2.68; 1.00]
VFT phonematic F	151	-1.39	15.1994			-1.39 [-3.81; 1.03]
VFT phonematic S	143	-0.53	15.4382			-0.53 [-3.06; 2.00]
VFT semantic supermarket	151	-2.42	19.5949			-2.42 [-5.55; 0.70]
Random effects model	907					-0.84 [-1.70; 0.01]
Cohort = LuxPARK (validation)						
FAB VFT	236	-1.28	10.0470			-1.28 [-2.56; 0.00]
MOCA Language + Naming	559	-2.63	15.7566			-2.63 [-3.94; -1.32]
VFT phonematic F	548	-3.19	17.7775			-3.19 [-4.67; -1.70]
VFT phonematic S	221	-3.32	19.1413			-3.32 [-5.84; -0.79]
VFT semantic sum	210	-4.27	16.9366			-4.27 [-6.56; -1.98]
Random effects model	1774					-2.70 [-3.70; -1.71]
Random effects model	2681					-1.85 [-2.62; -1.09]

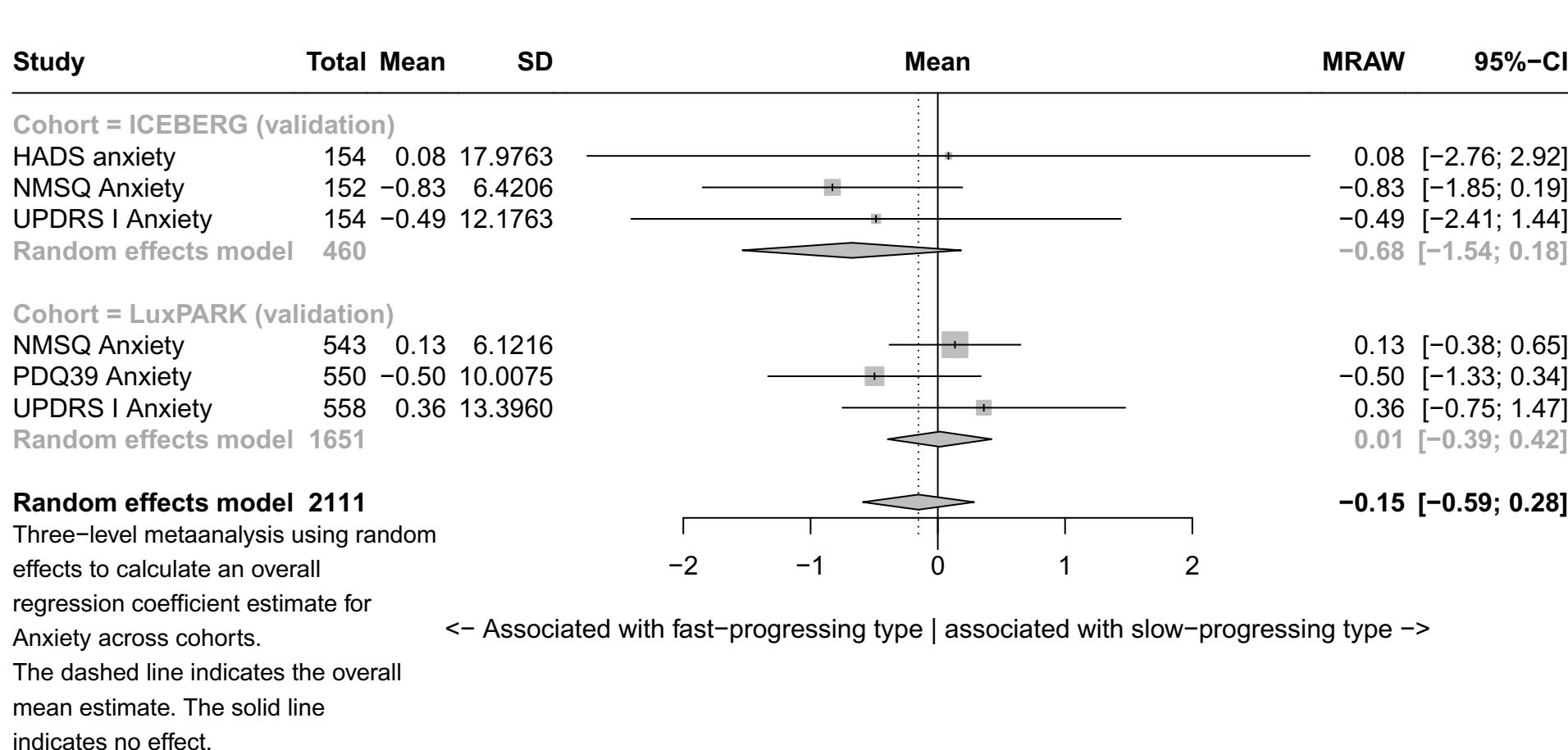
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Language across cohorts.

The dashed line indicates the overall mean estimate. The solid line indicates no effect.

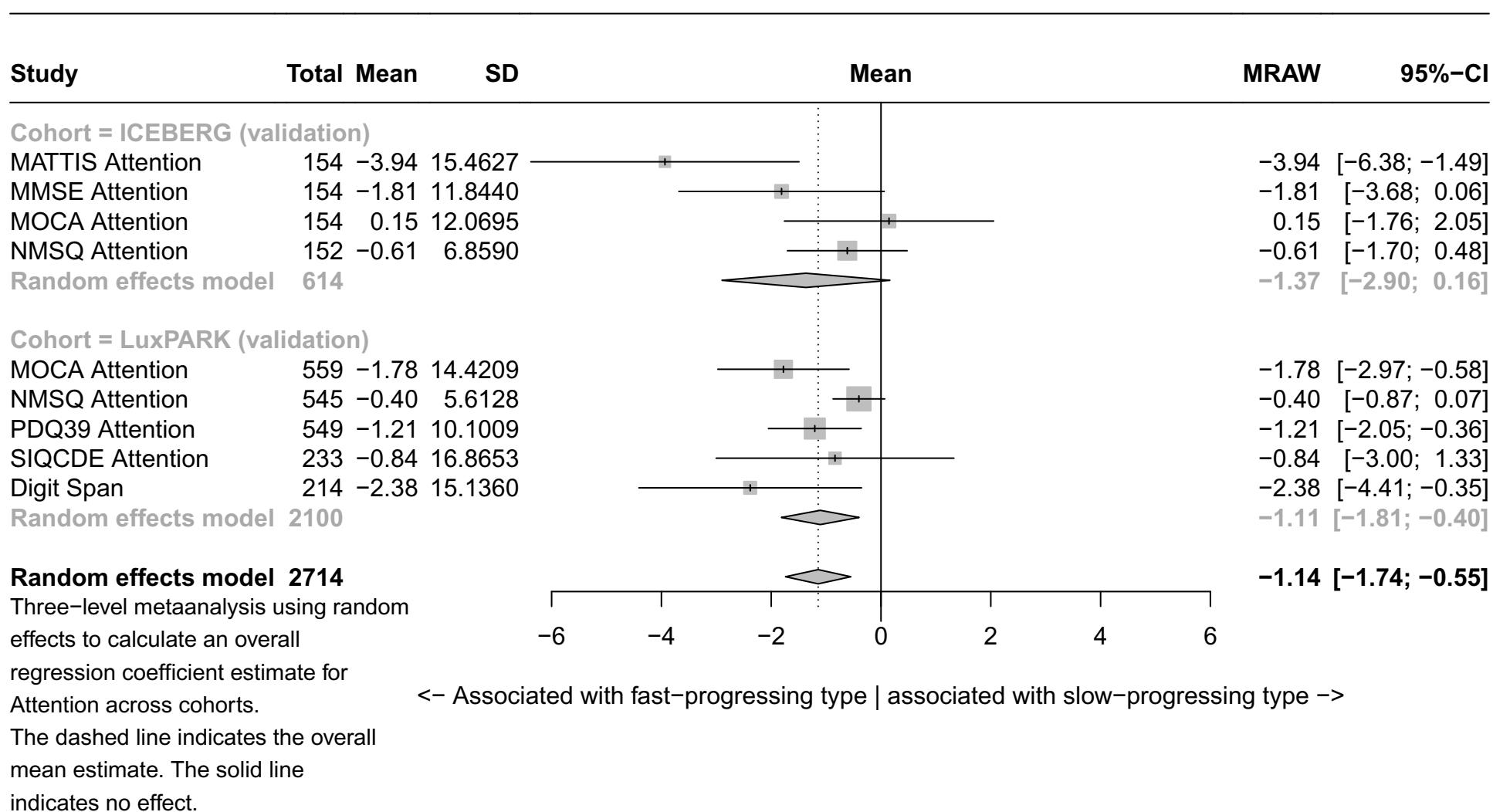


<- Associated with fast-progressing type | associated with slow-progressing type ->

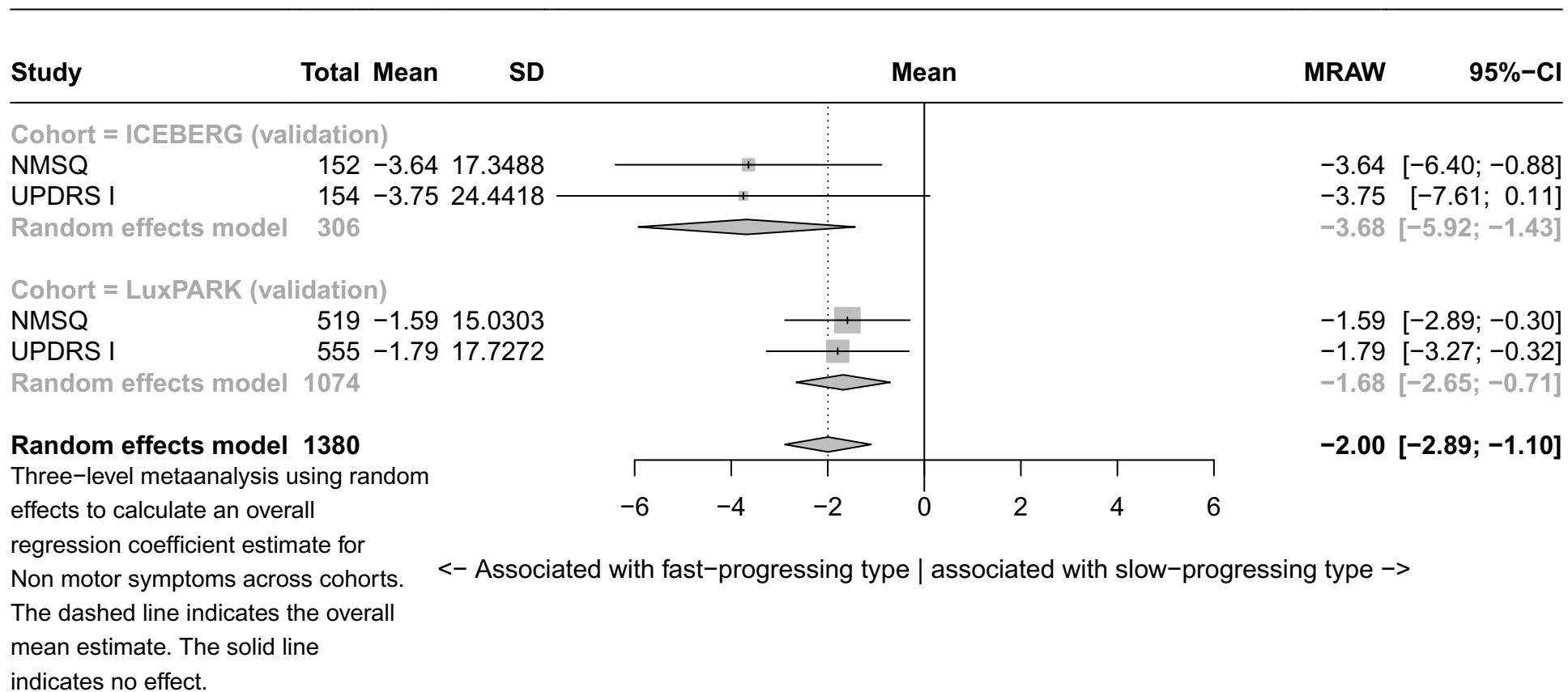
Forest plot for baseline characteristics of symptom domain Anxiety (validation)



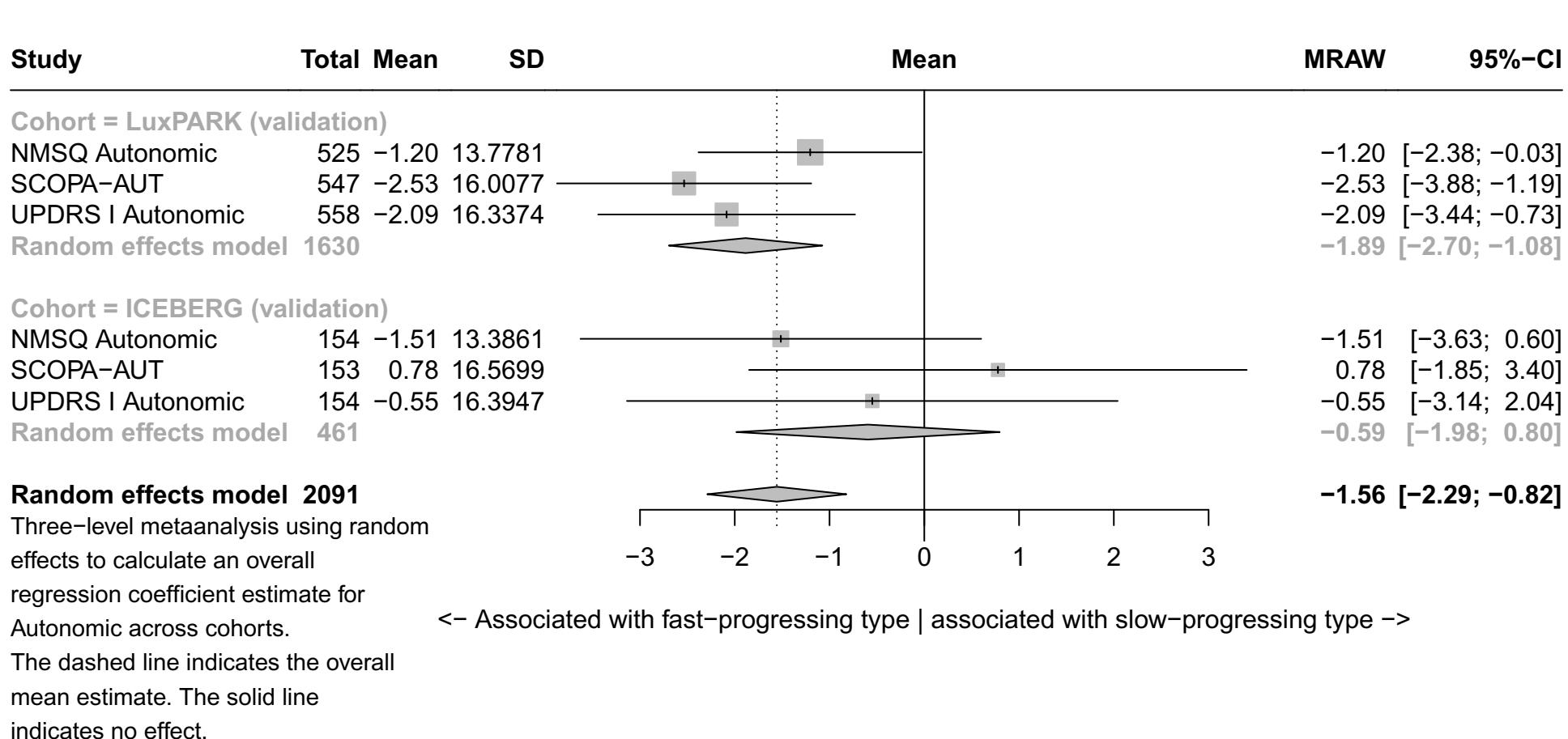
Forest plot for baseline characteristics of symptom domain Attention (validation)



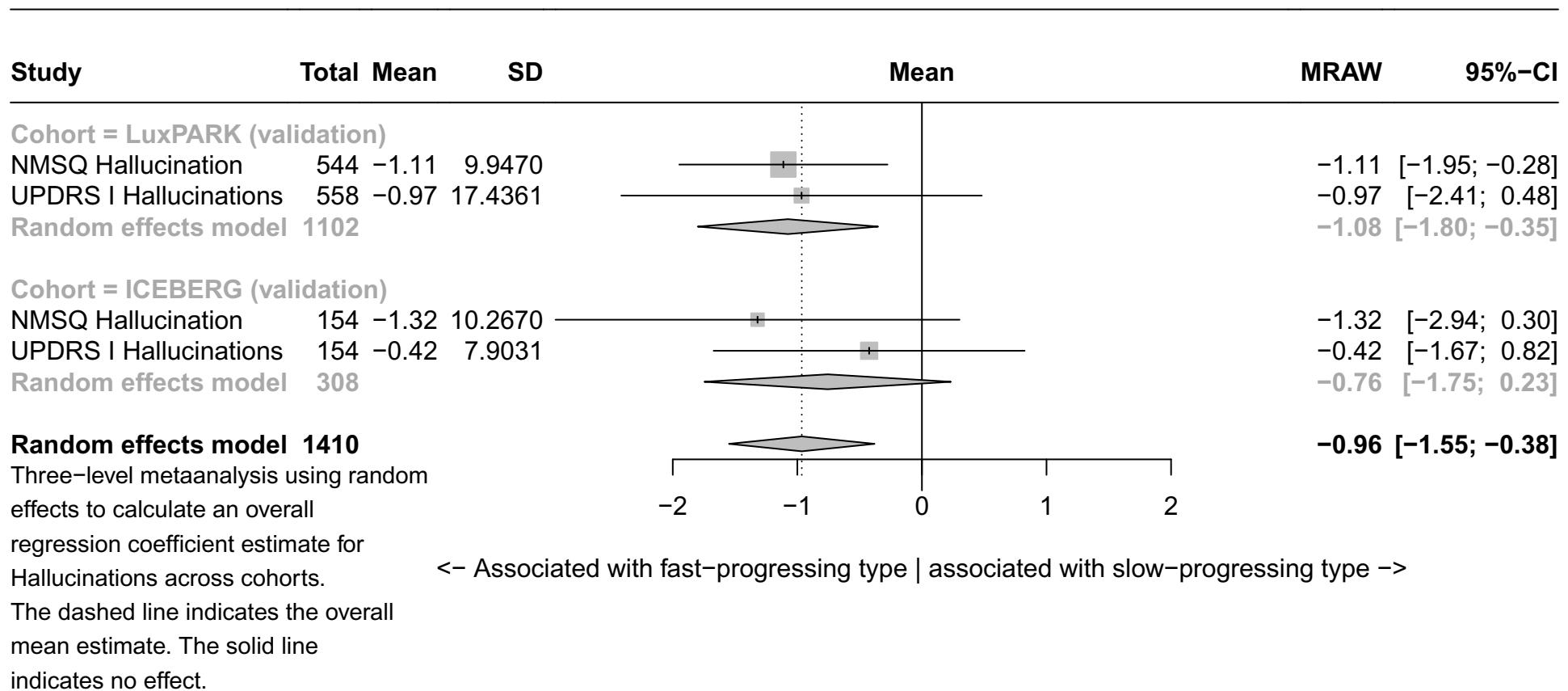
Forest plot for baseline characteristics of symptom domain Non motor symptoms (validation)



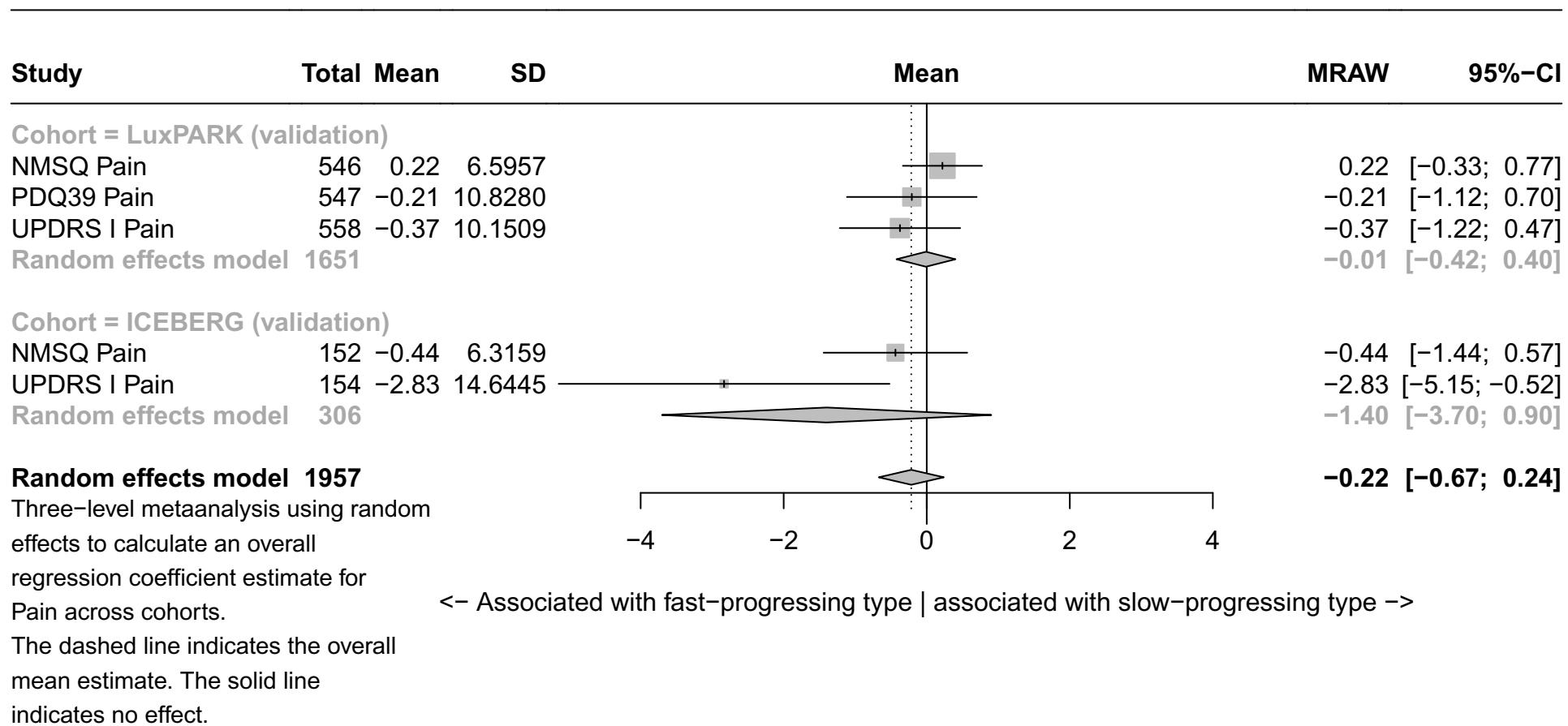
Forest plot for baseline characteristics of symptom domain Autonomic (validation)



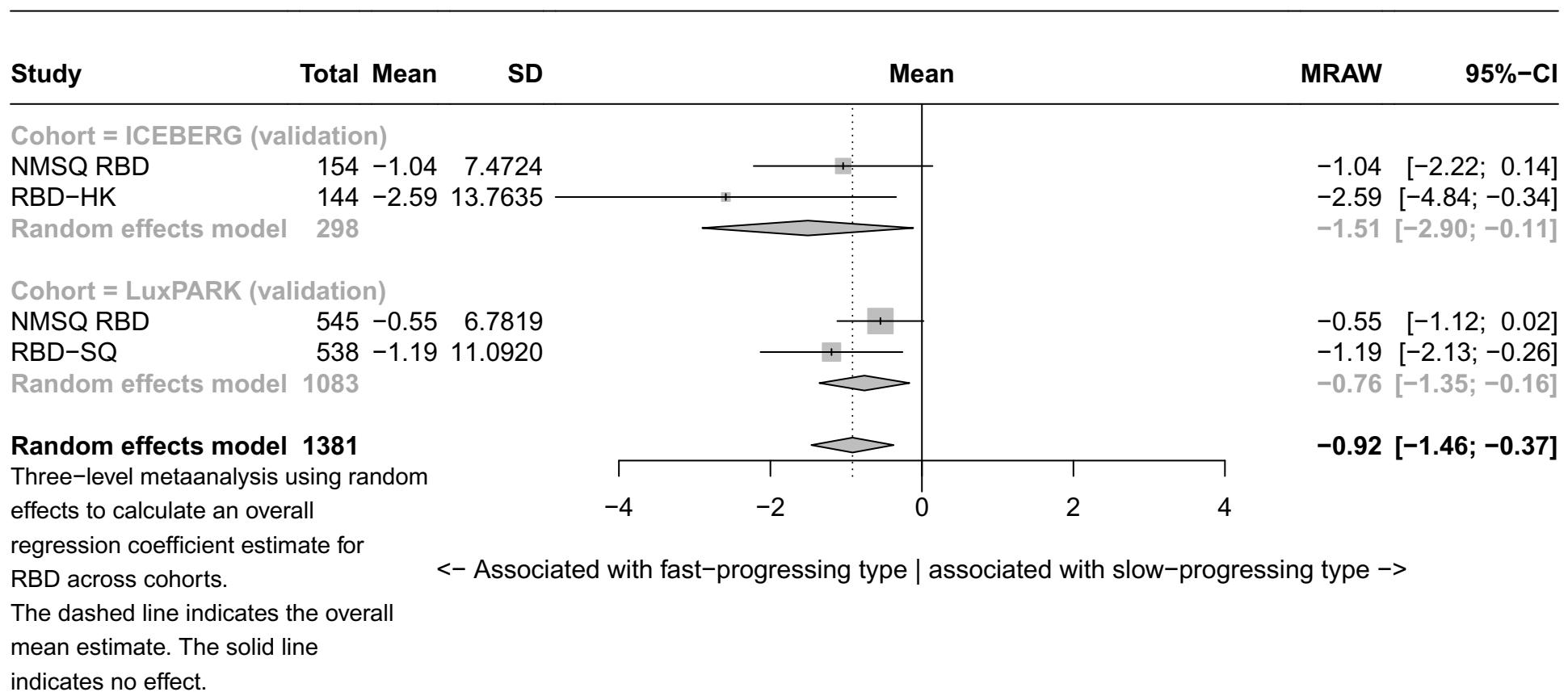
Forest plot for baseline characteristics of symptom domain Hallucinations (validation)



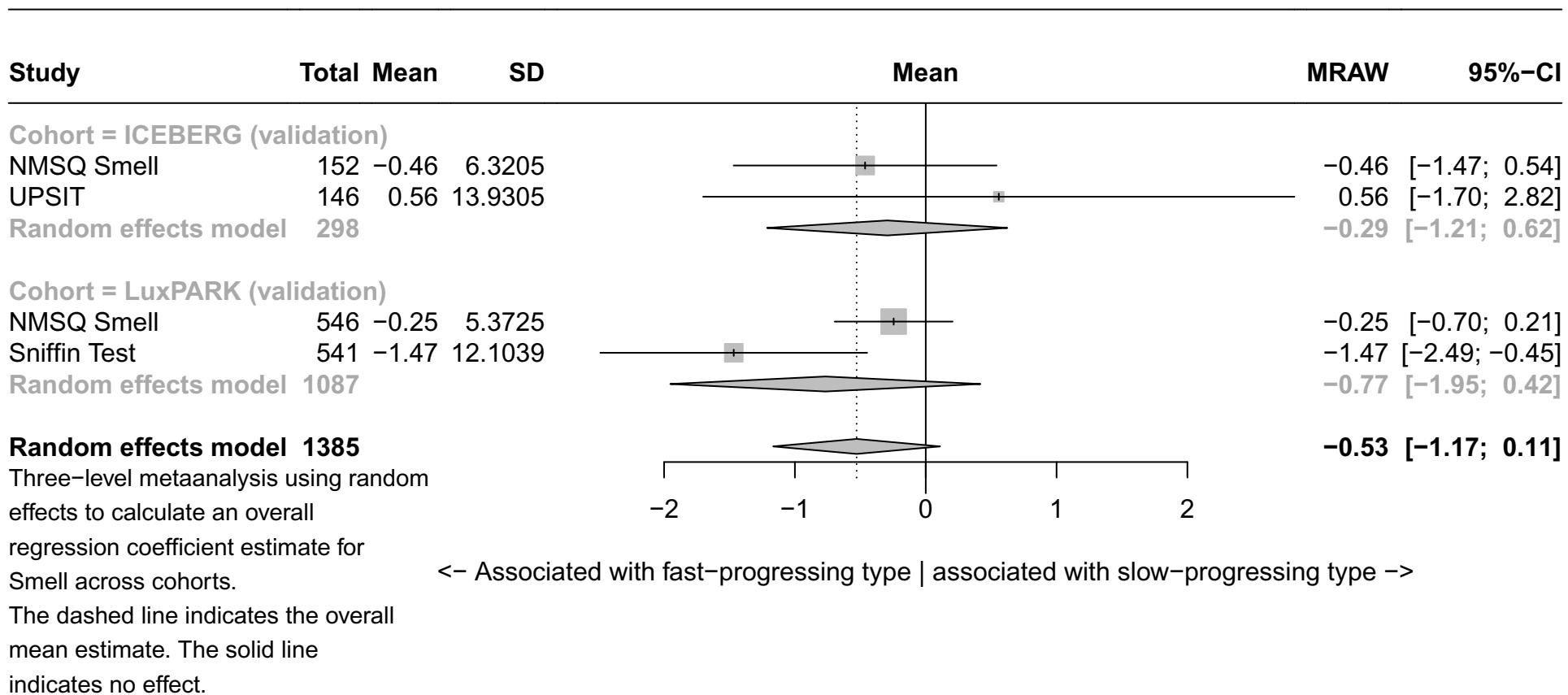
Forest plot for baseline characteristics of symptom domain Pain (validation)



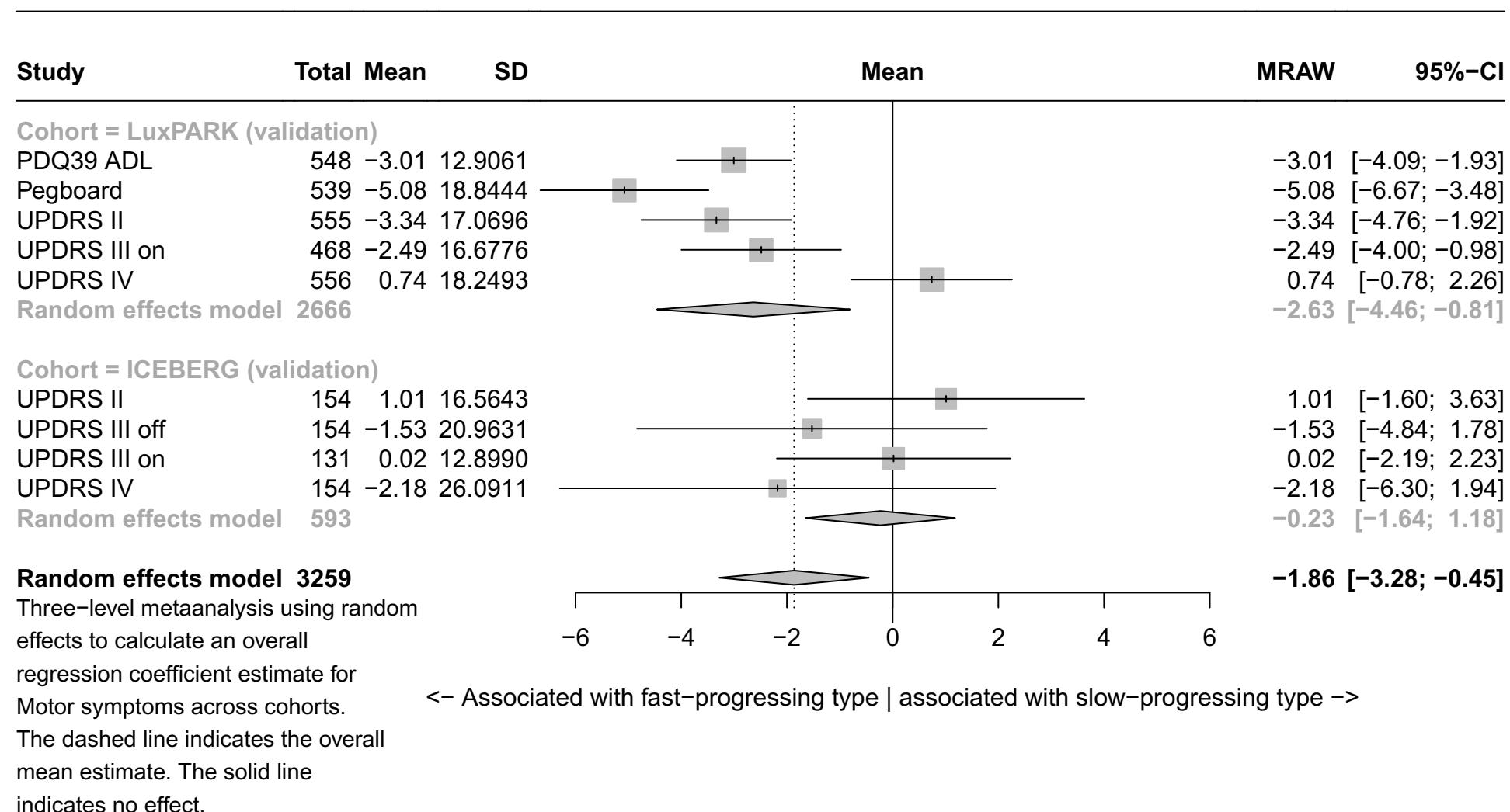
Forest plot for baseline characteristics of symptom domain RBD (validation)



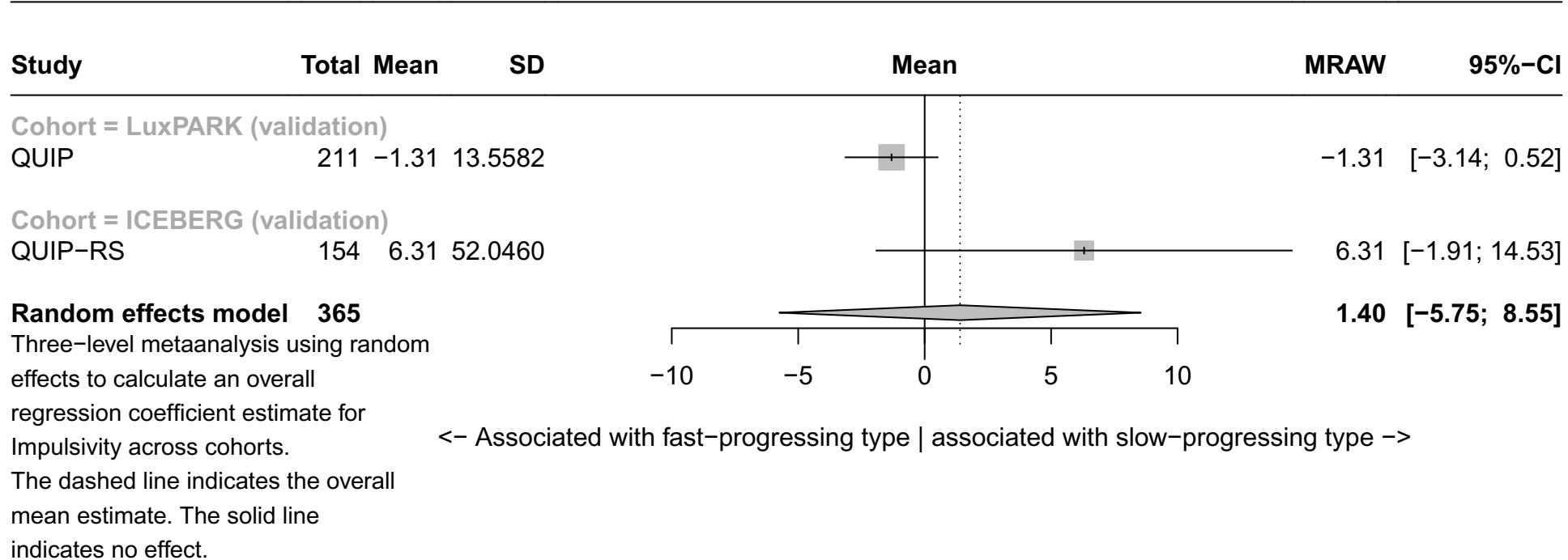
Forest plot for baseline characteristics of symptom domain Smell (validation)



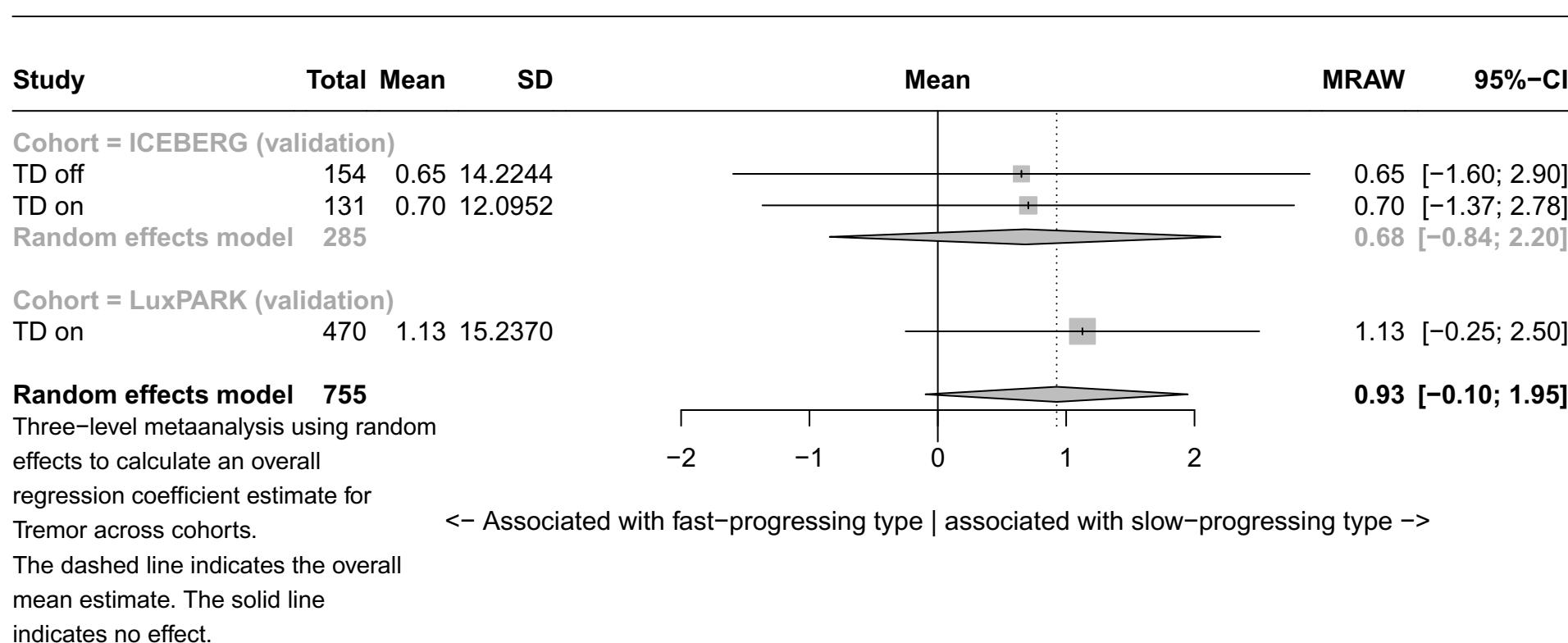
Forest plot for baseline characteristics of symptom domain Motor symptoms (validation)



Forest plot for baseline characteristics of symptom domain Impulsivity (validation)



Forest plot for baseline characteristics of symptom domain Tremor (validation)



Forest plot for baseline characteristics of symptom domain Fatigue (validation)

Study	Total	Mean	SD	Mean	MRAW	95%-CI
Cohort = LuxPARK (validation)						
UPDRS I Fatigue	558	-0.47	10.5204			-0.47 [-1.35; 0.40]
Cohort = ICEBERG (validation)						
UPDRS I Fatigue	154	-0.59	13.2677			-0.59 [-2.68; 1.51]
Random effects model	712					-0.49 [-1.30; 0.32]
Three-level metaanalysis using random effects to calculate an overall regression coefficient estimate for Fatigue across cohorts.						
The dashed line indicates the overall mean estimate. The solid line indicates no effect.						
				<- Associated with fast-progressing type associated with slow-progressing type ->		

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

ICEBERG study group

Steering committee: Marie Vidailhet, MD, PhD, (Pitié-Salpêtrière Hospital, Paris, principal investigator of ICEBERG), Jean-Christophe Corvol, MD, PhD (Pitié-Salpêtrière Hospital, Paris, scientific lead), Isabelle Arnulf, MD, PhD (Pitié-Salpêtrière Hospital, Paris, member of the steering committee), Stéphane Lehericy, MD, PhD (Pitié-Salpêtrière Hospital, Paris, member of the steering committee);

Clinical data: Marie Vidailhet, MD, PhD, (Pitié-Salpêtrière Hospital, Paris, coordination), Graziella Mangone, MD, PhD (Pitié-Salpêtrière Hospital, Paris, co-coordination), Jean-Christophe Corvol, MD, PhD (Pitié-Salpêtrière Hospital, Paris), Isabelle Arnulf, MD, PhD (Pitié-Salpêtrière Hospital, Paris), Sara Sambin, MD (Pitié-Salpêtrière Hospital, Paris), Poornima Menon, MD (Pitié-Salpêtrière Hospital, Paris), Jonas Ihle, MD (Pitié-Salpêtrière Hospital, Paris), Caroline Weill, MD, (Pitié-Salpêtrière Hospital, Paris), David Grabli, MD, PhD (Pitié-Salpêtrière Hospital, Paris); Florence Cormier-Dequaire, MD (Pitié-Salpêtrière Hospital, Paris); Louise Laure Mariani, MD, PhD (Pitié-Salpêtrière Hospital, Paris), Bertrand Degos, MD, PhD (Avicenne Hospital, Bobigny);

Neuropsychological data: Richard Levy, MD (Pitié-Salpêtrière Hospital, Paris, coordination), Fanny Pineau, MS (Pitié-Salpêtrière Hospital, Paris, neuropsychologist), Julie Socha, MS (Pitié-Salpêtrière Hospital, Paris, neuropsychologist), Eve Benchetrit, MS (La Timone Hospital, Marseille, neuropsychologist), Virginie Czernecki, MS (Pitié-Salpêtrière Hospital, Paris, neuropsychologist), Marie-Alexandrine, MS (Pitié-Salpêtrière Hospital, Paris, neuropsychologist);

Eye movement: Sophie Rivaud-Pechoux, PhD (ICM, Paris, coordination); Elodie Hainque, MD, PhD (Pitié-Salpêtrière Hospital, Paris);

Sleep assessment: Isabelle Arnulf, MD, PhD (Pitié-Salpêtrière Hospital, Paris, coordination), Smaranda Leu Semenescu, MD (Pitié-Salpêtrière Hospital, Paris), Pauline Dodet, MD (Pitié-Salpêtrière Hospital, Paris);

Genetic data: Jean-Christophe Corvol, MD, PhD (Pitié-Salpêtrière Hospital, Paris, coordination), Graziella Mangone, MD, PhD (Pitié-Salpêtrière Hospital, Paris, co-coordination), Samir Bekadar, MS (Pitié-Salpêtrière Hospital, Paris, biostatistician), Alexis Brice, MD (ICM, Pitié-Salpêtrière Hospital, Paris), Suzanne Lesage, PhD (INSERM, ICM, Paris, genetic analyses);

Metabolomics: Fanny Mochel, MD, PhD (Pitié-Salpêtrière Hospital, Paris, coordination), Farid Ichou, PhD (ICAN, Pitié-Salpêtrière Hospital, Paris), Vincent Perlberg, PhD, Pierre and Marie Curie University), Benoit Colsch, PhD (CEA, Saclay), Arthur Tenenhaus, PhD (Supelec, Gif-sur-Yvette, data integration);

Brain MRI data: Stéphane Lehericy, MD, PhD (Pitié-Salpêtrière Hospital, Paris, coordination), Rahul Gaurav, MS, (Pitié-Salpêtrière Hospital, Paris, data analysis), Nadya Pyatigorskaya, MD, PhD, (Pitié-Salpêtrière Hospital, Paris, data analysis); Lydia Yahia-Cherif, PhD (ICM, Paris, Biostatistics), Romain Valabregue, PhD (ICM, Paris, data analysis), Cécile Galléa, PhD (ICM, Paris);

Datscan imaging data: Marie-Odile Habert, MCU-PH (Pitié-Salpêtrière Hospital, Paris, coordination);

Voice recording: Dijana Petrovska, PhD (Telecom Sud Paris, Evry, coordination), Laetitia Jeancolas, MS (Telecom Sud Paris, Evry);

Study management: Alizé Chalançon (Pitié-Salpêtrière Hospital, Paris, Project manager), Carole Dongmo-Kenfack (Pitié-Salpêtrière Hospital, Paris, clinical research assistant); Christelle Laganot (Pitié-Salpêtrière Hospital, Paris, clinical research assistant), Valentine Maheo (Pitié-Salpêtrière Hospital, Paris, clinical research assistant), Manon Gomes (Pitié-Salpêtrière Hospital, Paris, clinical research assistant)

Study sponsoring: The ICEBERG Study was funded by the Programme d'investissements d'avenir (ANR-10-IAIHU-06), the Paris Institute of Neurosciences – IHU (IAIHU-06), the Agence Nationale de la Recherche (ANR-11-INBS-0006), and Électricité de France (Fondation d'Entreprise EDF).

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

NCER-PD/LuxPARK consortium

We would like to thank all participants of the Luxembourg Parkinson's Study for their important support to our research. Furthermore, we acknowledge the joint effort of the National Centre of Excellence in Research on Parkinson's Disease (NCER-PD) Consortium members from the partner institutions Luxembourg Centre for Systems Biomedicine, Luxembourg Institute of Health, Centre Hospitalier de Luxembourg, and Laboratoire National de Santé generally contributing to the Luxembourg Parkinson's Study as listed below:

Geeta ACHARYA², Gloria AGUAYO², Myriam ALEXANDRE², Muhammad ALI¹, Wim AMMERLANN², Giuseppe ARENA¹, Rudi BALLING¹, Michele BASSIS¹, Katy BEAUMONT², Regina BECKER¹, Camille BELLORA², Guy BERCHEM³, Daniela BERG¹¹, Alexandre BISDORFF⁵, Ibrahim BOUSSAAD¹, Kathrin BROCKMANN¹¹, Jessica CALMES², Lorieza CASTILLO², Gessica CONTESOTTO², Nico DIEDERICH³, Rene DONDELINGER⁵, Daniela ESTEVES², Guy FAGHERAZZI², Jean-Yves FERRAND², Manon GANTENBEIN², Thomas GASSE¹¹, Piotr GAWRON¹, Soumyabrata GHOSH¹, Marijus GIRAITIS^{2,3}, Enrico GLAAB¹, Elisa GÓMEZ DE LOPE¹, Jérôme GRAAS², Mariella GRAZIANO¹⁷, Valentin GROUES¹, Anne GRÜNEWALD¹, Wei GU¹, Gaël HAMMOT², Anne-Marie HANFF^{2,20,21}, Linda HANSEN^{1,3}, Michael HENEKA¹, Estelle HENRY², Sylvia HERBRINK⁶, Sascha HERZINGER¹, Michael HEYMANN², Michele HU⁸, Alexander HUNDT², Nadine JACOBY¹⁸, Jacek JAROSLAW LEBIODA¹, Yohan JAROSZ¹, Sonja JÓNSDÓTTIR², Quentin KLOPFENSTEIN¹, Jochen KLUCKEN^{1,2,3}, Rejko KRÜGER^{1,2,3}, Pauline LAMBERT², Zied LANDOULSI¹, Roseline LENTZ⁷, Inga LIEPELT¹¹, Robert LISZKA¹⁴, Laura LONGHINO³, Victoria LORENTZ², Paula Cristina LUPU², Tainá M. MARQUES¹, Clare MACKAY¹⁰, Walter MAETZLER¹⁵, Katrin MARCUS¹³, Guilherme MARQUES², Patricia MARTINS CONDE¹, Patrick MAY¹, Deborah MCINTYRE², Chouaib MEDIOUNI², Francoise MEISCH¹, Myriam MENSTER², Maura MINELLI², Michel MITTELBRONN^{1,4}, Brit MOLLENHAUER¹², Friedrich MÜHLSCHLEGEL⁴, Romain NATI³, Ulf NEHRBASS², Sarah NICKELS¹, Beatrice NICOLAI³, Jean-Paul NICOLAY¹⁹, Fozia NOOR², Marek OSTASZEWSKI¹, Clarissa P. C. GOMES¹, Sinthuja PACHCHEK¹, Claire PAULY^{1,3}, Laure PAULY^{2,20}, Lukas PAVELKA^{1,3}, Magali PERQUIN², Nancy E. RAMIA¹, Rosalina RAMOS LIMA², Armin RAUSCHENBERGER¹, Rajesh RAWAL¹, Dheeraj REDDY BOBBILI¹, Kirsten ROOMP¹, Eduardo ROSALES², Isabel ROSETY¹, Estelle SANDT², Stefano SAPIENZA¹, Venkata SATAGOPAM¹, Margaux SCHMITT², Sabine SCHMITZ¹, Reinhard SCHNEIDER¹, Jens SCHWAMBORN¹, Amir SHARIFY², Ekaterina SOBOLEVA¹, Kate SOKOLOWSKA², Hermann THIEN², Elodie THIRY³, Rebecca TING JIIN LOO¹, Christophe TREFOIS¹, Johanna TROUET², Olena TSURKALENKO², Michel VAILLANT², Mesele VALENTI², Gilles VAN CUTSEM^{1,3}, Carlos VEGA¹, Liliana VILAS BOAS³, Maharshi VYAS¹, Richard WADE-MARTINS⁹, Paul WILMES¹, Evi WOLLSCHEID-LENGELING¹, Gelani ZELIMKHANOV³

1. Luxembourg Centre for Systems Biomedicine, University of Luxembourg, Esch-sur-Alzette, Luxembourg
2. Luxembourg Institute of Health, Strassen, Luxembourg
3. Centre Hospitalier de Luxembourg, Strassen, Luxembourg
4. Laboratoire National de Santé, Dudelange, Luxembourg
5. Centre Hospitalier Emile Mayrisch, Esch-sur-Alzette, Luxembourg
6. Centre Hospitalier du Nord, Ettelbrück, Luxembourg
7. Parkinson Luxembourg Association, Leudelange, Luxembourg
8. Oxford Parkinson's Disease Centre, Nuffield Department of Clinical Neurosciences, University of Oxford, Oxford, UK
9. Oxford Parkinson's Disease Centre, Department of Physiology, Anatomy and Genetics, University of Oxford, South Parks Road, Oxford, UK
10. Oxford Centre for Human Brain Activity, Wellcome Centre for Integrative Neuroimaging, Department of Psychiatry, University of Oxford, Oxford, UK
11. Center of Neurology and Hertie Institute for Clinical Brain Research, Department of Neurodegenerative Diseases, University Hospital Tübingen, Germany
12. Paracelsus-Elena-Klinik, Kassel, Germany
13. Ruhr-University of Bochum, Bochum, Germany
14. Westpfalz-Klinikum GmbH, Kaiserslautern, Germany
15. Department of Neurology, University Medical Center Schleswig-Holstein, Kiel, Germany

Progression subtypes in Parkinson's disease identified by a data driven multi cohort analysis

16. Department of Neurology Philipps, University Marburg, Marburg, Germany
17. Association of Physiotherapists in Parkinson's Disease Europe, Esch-sur-Alzette, Luxembourg
18. Private practice, Ettelbruck, Luxembourg
19. Private practice, Luxembourg, Luxembourg
20. Faculty of Science, Technology and Medicine, University of Luxembourg, Esch-sur-Alzette, Luxembourg
21. Department of Epidemiology, CAPHRI School for Public Health and Primary Care, Maastricht University Medical Centre+, Maastricht, the Netherlands