

# Genome-wide association meta-analysis of expressive and receptive vocabulary from infancy to early childhood

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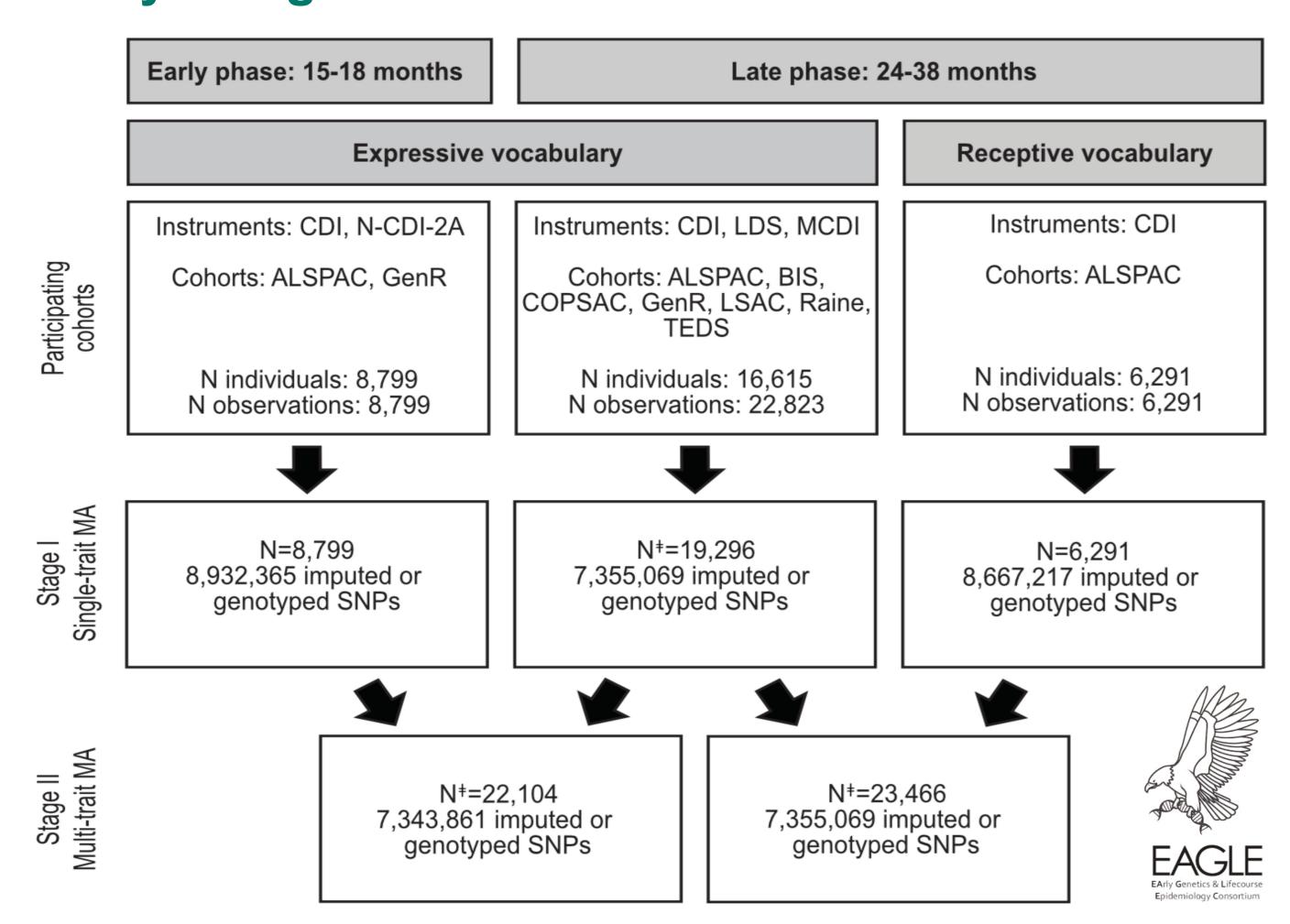
#### In a nutshell - we aimed to ...

(i) identify genome-wide association signals for early vocabulary, (ii) elucidate the underlying genetic architecture and (iii) characterise polygenic links with later-life cognitive, behavioral and health outcomes.

#### Background

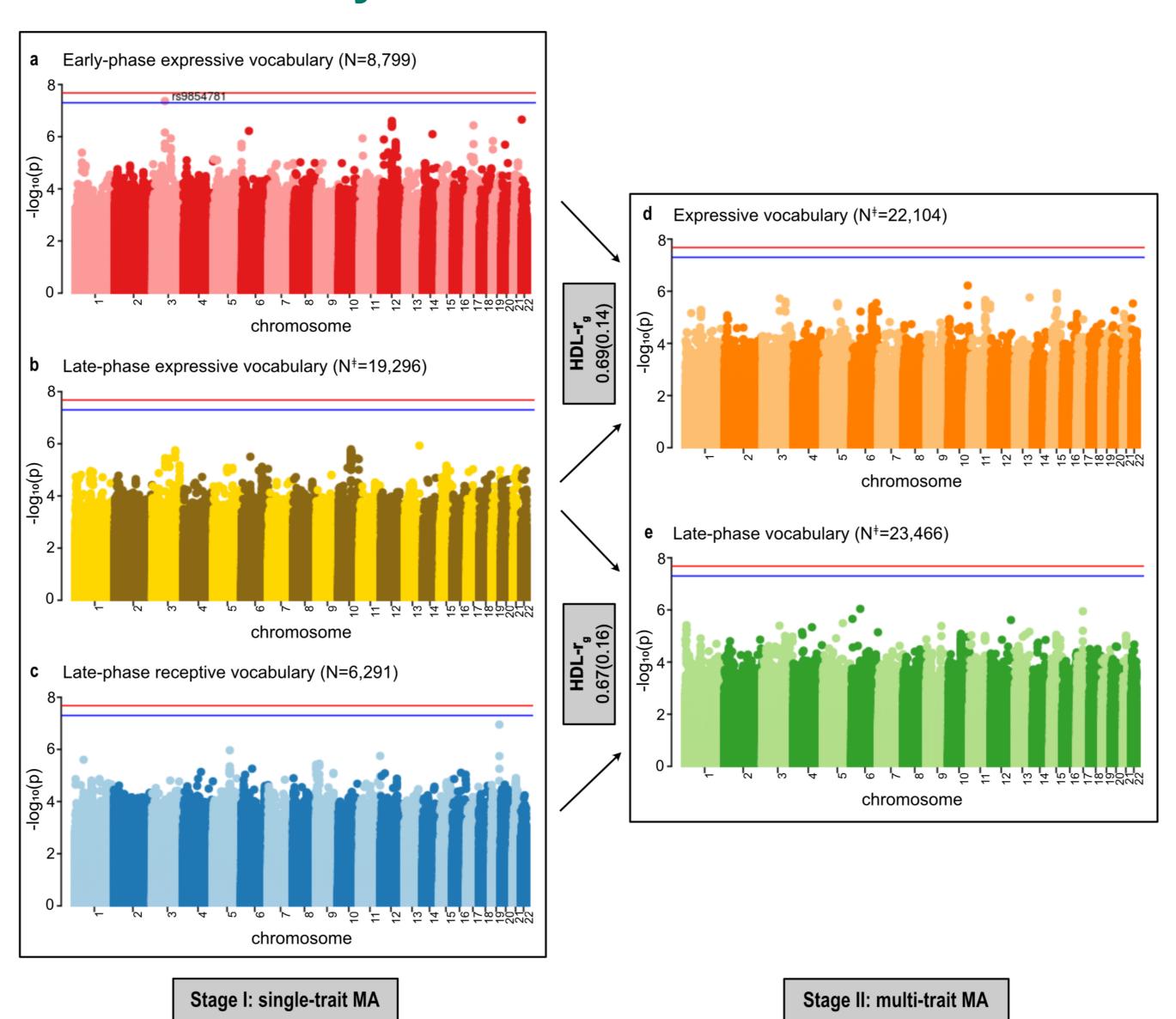
The genetic architectures underlying expressive and receptive vocabulary in early life are complex and little characterised. Here, we present the largest metagenome-wide association study (meta-GWAS) of early vocabulary (15-38 months) till date, based on 37,913 observations and 17,298 individuals, within the Early Genetics and Life Course Epidemiology (EAGLE) Consortium.

#### Study design



Expressive and/or receptive vocabulary was assessed using parent questionnaires in children of European descent from seven independent population-based or community-based cohorts. Meta-GWASs were performed for early-phase expressive vocabulary, late-phase expressive vocabulary, and late-phase receptive vocabulary using METAL as part of stage I. To increase statistical power, multi-trait SNP-vocabulary associations were examined by combining genetically related vocabulary traits using MTAG as part of stage II.  $\ddagger$  Estimated sample size based on the increase in mean  $\chi^2$  statistic using MTAG. Abbreviations: CDI, Communicative Development Inventory; LDS, Language Development Survey; MA, meta-analysis; SNP, Single-Nucleotide Polymorphism

## **SNP-vocabulary associations**



Single-trait (stage I) and multi-trait (stage II) SNP-vocabulary associations were assessed using METAL and MTAG, respectively. No SNP-vocabulary associations passed the adjusted threshold (red line, P<2.1x10<sup>-8</sup>). rs9854781 was associated with early-phase expressive vocabulary at the unadjusted genome-wide significance threshold (blue line, P<5x10<sup>-8</sup>). Genetic correlations among single-trait vocabulary summary statistics were derived with HDL.  $\pm$  Estimated sample size based on the increase in mean  $\chi^2$  statistic using MTAG. Abbreviations: HDL, High-Density Llkelihood; MA, meta-analysis.

## **SNP-heritability of early vocabulary**

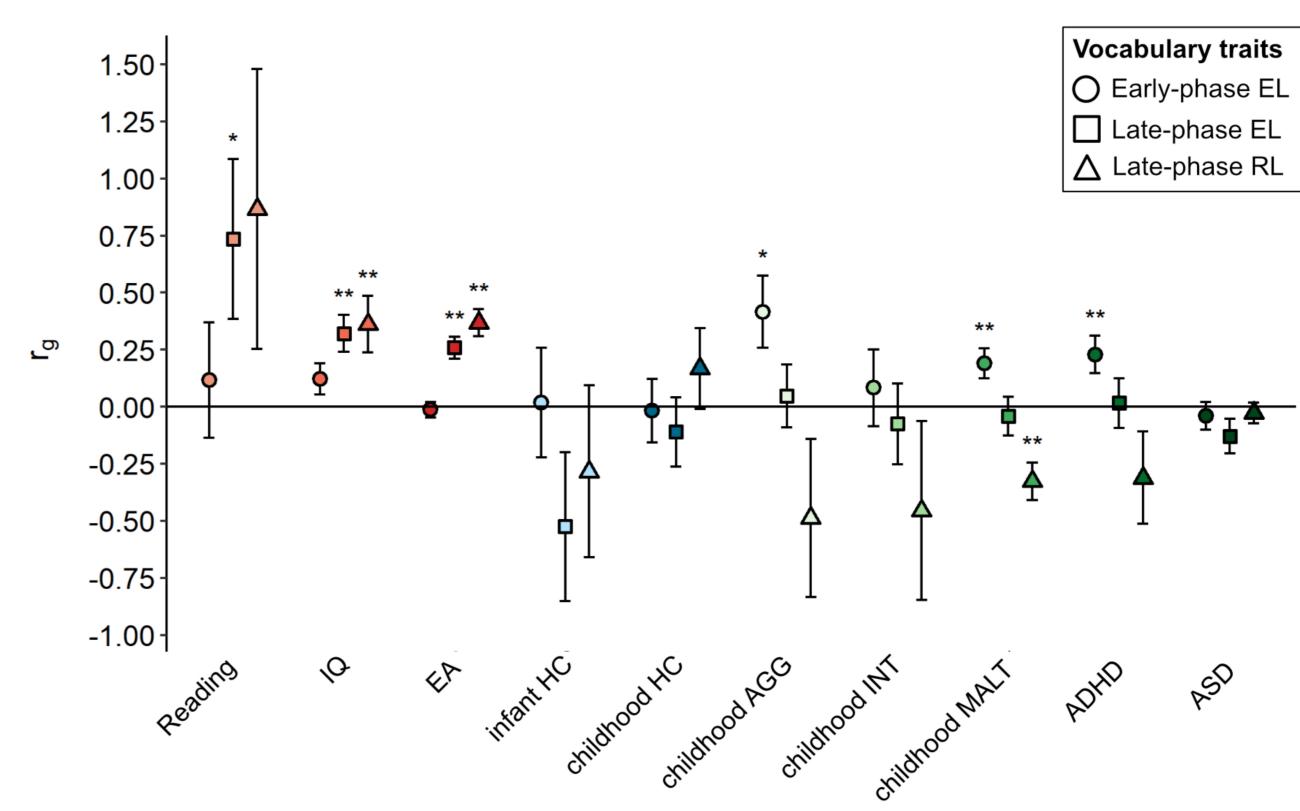
Analysis	Trait	SNP-h <sup>2</sup> (SE)	Z-score	Р	N
Stage I: single-trait MA	Early-phase EV	0.24(0.02)	8.64	<1x10 <sup>-10</sup>	8,799
	Late-phase EV	0.08(0.01)	5.53	3x10 <sup>-8</sup>	19,296 <sup>‡</sup>
	Late-phase RV	0.20(0.04)	5.21	2x10 <sup>-7</sup>	6,291
Stage II: multi-trait MA	EV	0.10(0.01)	6.91	<1x10 <sup>-10</sup>	22,104 <sup>‡</sup>
	Late-phase vocabulary	0.07(0.01)	5.00	5x10 <sup>-7</sup>	23,466 <sup>‡</sup>

SNP-heritability (SNP-h²), corresponding standard error (SE) and P-value were estimated with High-Density Likelihood (HDL) software using a HapMap3 reference panel. SNP-h² Z-scores were calculated by dividing SNP-h² by its standard error.  $\pm$  Estimated sample size based on the increase in mean  $\chi^2$  statistic using MTAG.

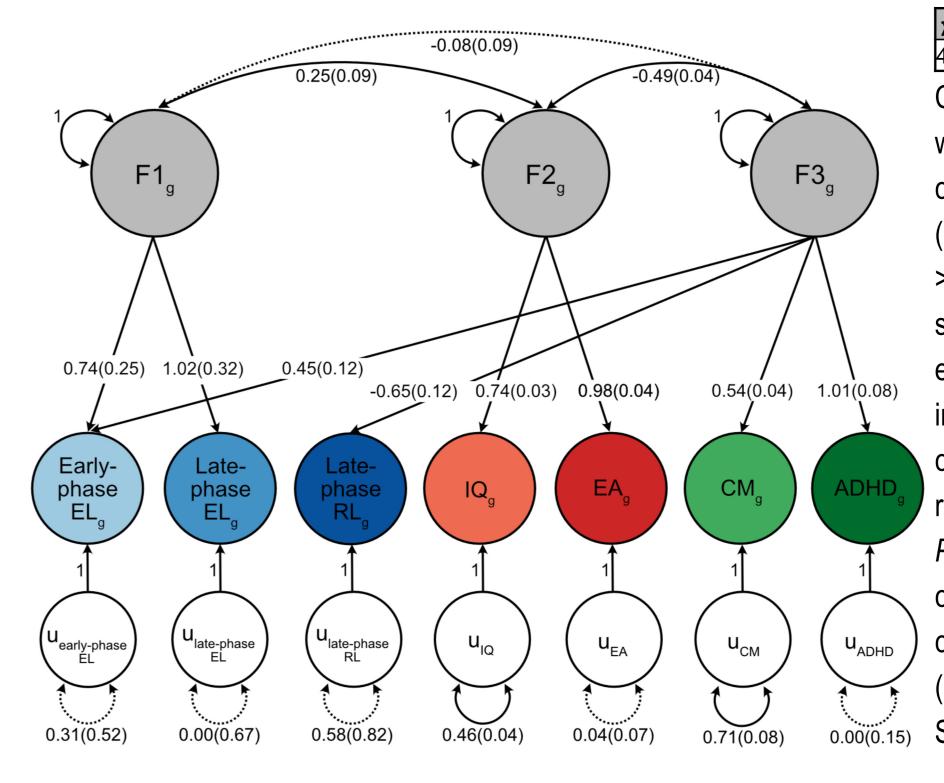
#### Gene-, gene-set and gene-property analyses

All analyses were carried out within FUMA software. No results passed multiple-testing-adjusted thresholds.

# Genetic links with later-life cognitive, behavioral and health outcomes



Genetic correlations of vocabulary traits with later-life cognitive, behavioral and health outcomes estimated using HDL software. Bars represent standard errors. \* *P*<0.05; \*\* *P*<1.1x10<sup>-6</sup>. Abbreviations: ADHD, Attention-Deficit/ Hyperactivity Disorder; AGG, aggresision, ASD, Autism Spectrum Disorder; EA, educational attainment; EL, expressive language; HC, head circumference; INT, internalising symptoms; IQ, general intelligence; MALT, maltreatment; RL, receptive language



40.81 11 2.6x10<sup>-5</sup> 74.81 0.99 0.11 Confirmatory factor analysis (CFA) with GenomicSEM for genetically correlated traits with early vocabulary (see above). Factors that explained >0.2 variance and paths with a standardised factor loading >0.35 in exploratory factor analysis were included. CFA standardised path coefficients are shown. Dashed lines coefficients with *P*>0.05. Model fit was assessed with information Akaike chi-square, criterion (AIC), Comparative Fit Index (CFI) and Standardised Root Mean Squared Residual (SRMR).

AIC CFI SRMR

#### In a nutshell - we found that ...

early vocabulary traits show low to moderate SNP-h<sup>2</sup>. Their genetic architectures may change during early development: genetic links with cognition trace back to toddlerhood and not infancy, and childhood maltreatment has an opposite association with early-phase expressive compared to late-phase receptive vocabulary.

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