

Linking brain phenotypes
with cardiovascular risk
factors through GWAS



Brain image- derived phenotypes (IDPs)

White Matter Hyperintensity (WMH):

- total volume (T2 FLAIR)
- lesion count

QSM and T2* applied on WMH

QSM for (left and right):

- Caudate
- Putamen
- Pallidum
- Substantia Nigra
- Amygdala

*Iron
quantification
in different
areas*

Cardiovascular risk factors and diseases

- **Hypertension**
- **Diastolic blood pressure**
- **Systolic blood pressure**
- **Glucose**
- **Diabetes**
- **HDL**
- **LDL**
- **Triglycerides**
- **Body mass index (BMI)**
- *Coffee intake*
- *Current tobacco smoking*
- *Sleep duration*
- *Alcohol intake frequency*
- *Time spent doing moderate physical activity*
- **Stroke**

More environmental variables

Data used

2017 UKBioBank GWAS round 2 by Neale lab

- ❑ https://github.com/Nealelab/UK_Biobank_GWAS
- ❑ [UKBB GWAS Imputed v3 - File Manifest Release 20180731 - Google Sheets](#)

Brain phenotypes:

- BIG40 (2020) for all except WMH lesion count
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- ❑ https://www.fmrib.ox.ac.uk/ukbiobank/gwas_resources/index.html
 - ❑ <https://open.win.ox.ac.uk/ukbiobank/big40/>

But why these phenotypes?

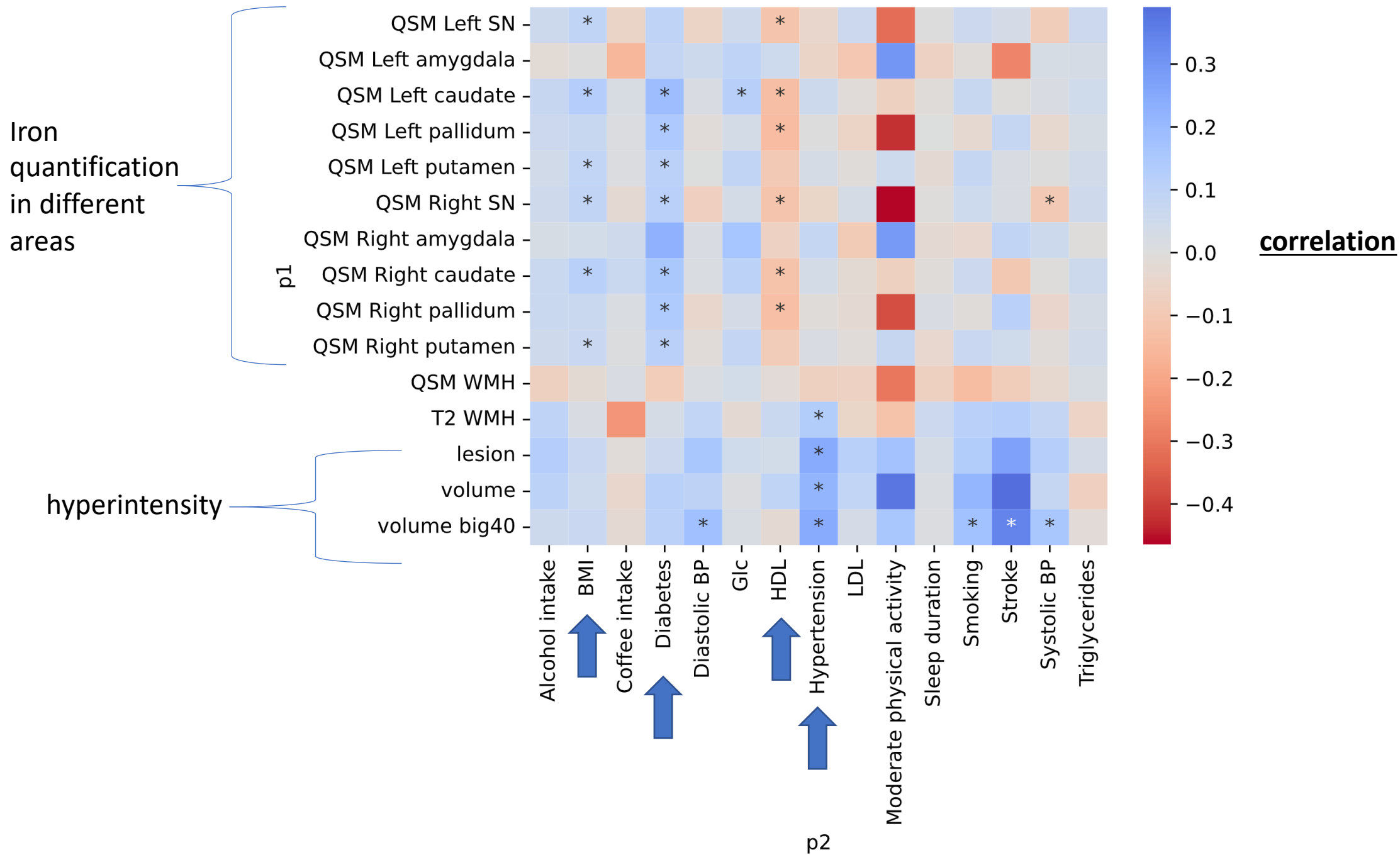
- Chosen based on significant **phenotypic correlations** found in other studies
 - Mainly based on results by:
 - Wang, C., Martins-Bach, A.B., Alfaro-Almagro, F. *et al.* Phenotypic and genetic associations of quantitative magnetic susceptibility in UK Biobank brain imaging. *Nat Neurosci* **25**, 818–831 (2022).

Question: are these correlations only due to environmental **confounders** or can we find **genetic** correlations as well?

1. Estimating genetic correlation

with linkage disequilibrium score regression

ldsc



2. Cross-GWAS coherence test

PascalX

(results are pending...)

See more
about
methods and
results

<https://github.com/peruginiandrea/scripts>

