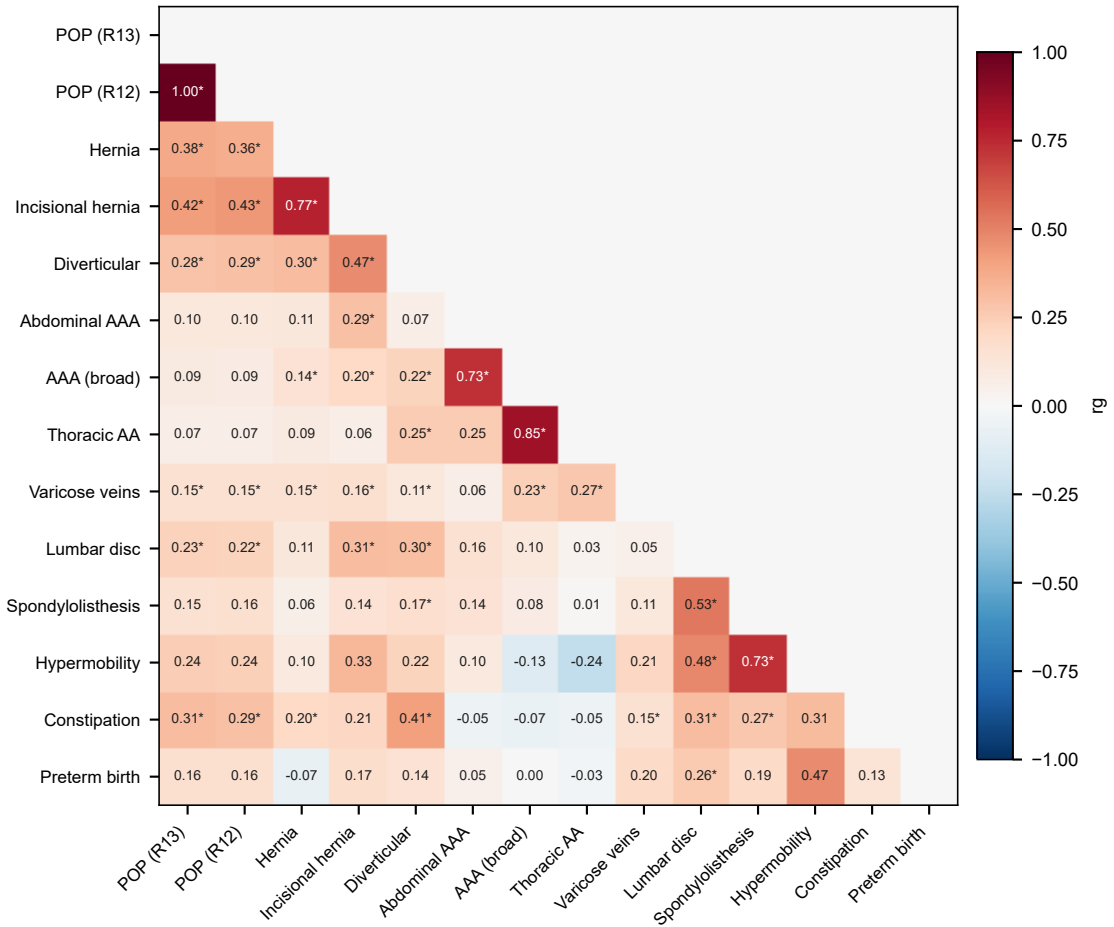


Locus-level (colocalisation) evidence at PCOLCE2 exists only for POP (PP4 = 0.954 with the fibroblast cis-eQTL). All other endpoints here have genome-wide rg only — no PCOLCE2-locus colocalisation was attempted or claimed for them. The "assembly-biased matrix-decay" framework is a working hypothesis resting on rg and patient-tissue transcriptomics, not a validated disease classification.