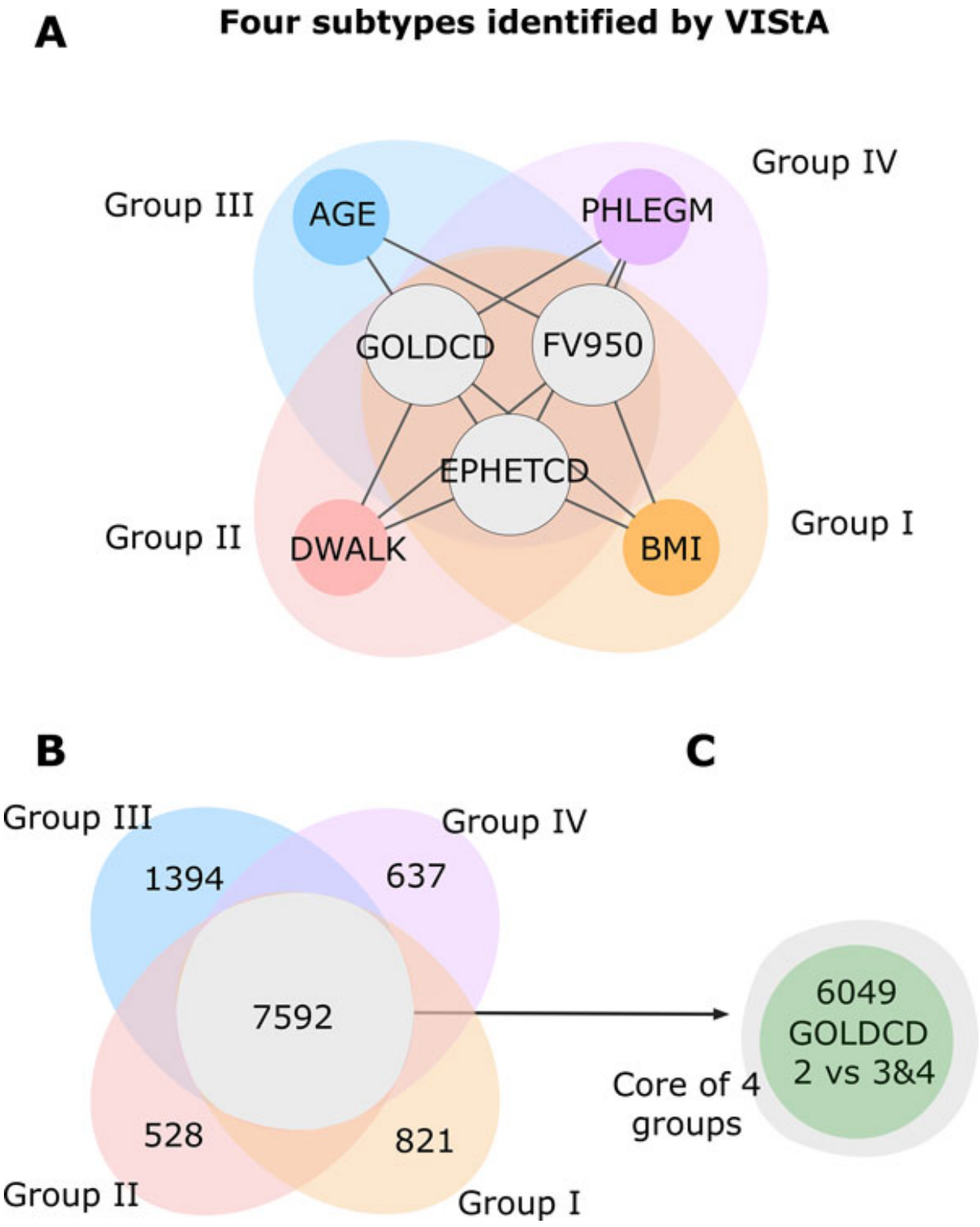
Figure 3.

Resolution: **standard** / high



Four subtypes and differentially expressed genes. **A** The combinations of phenotypic measures that define the subtypes predicted by the VIStA method: all four subtypes share a common core of high values of GOLDCD, FV950 and EMPHETCD, reflecting disease severity. Each of the individual subtypes I-IV presents one additional clinical characteristic: BMI (subtype I), DWALK (II), AGE (III) or PHLEGM (IV). **B** Venn diagram showing the number of differentially expressed genes unique to each subtype, as well as common to all four subtypes. The common genes show a large overlap with the genes differentially expressed between subjects with GOLDCD 2 and subjects with GOLDCD 3&4, indicating that these genes reflect mostly disease severity.

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