Conclusions
CCND1 amplification:
- is associated with poor prognosis in ER+, Endocrine treated and Luminal A patients
- could be a potential long-term prognostic marker to stratify Luminal A patients with worse survival outcome

Luminal A vs Basal-like subtypes:
- they share common genes and pathways within CCND1 amplified tumours

Introduction
The CCND1 gene is amplified in 15% of breast cancers and associated with Estrogen receptor (ER) positive, Luminal B tumours. Patients with CCND1 amplified tumours display reduced survival times and endocrine treatment resistance. Use of the CCND1 gene as a biomarker has however been hampered by conflicting assessments of the relationship between cyclin D1 protein levels and clinicopathological characteristics, specifically, overexpression of the protein has been linked to both better and worse prognosis.

Aim
The aim is to comprehensively characterize the prognostic and predictive capacity of CCND1 amplification through focused analysis on clinically relevant and treatment specific patient subgroups.

Methods
- Gene amplification calls (GISTIC)
- Kaplan-Meier and multivariable cox regression analyses
- Differential gene expression (DGE) analysis and pathway analyses.

1) Patients included in the study

2) Clinico-pathological characteristics of patients in the study split by CCND1

3) KM estimates for IHC subgroups, Luminal-A/B, Endocrine and chemo-treated patients in Cohort 1

4) Multivariate Cox proportional hazards regression models in Cohort 1, Cohort 2 and both cohorts

5) Common genes and pathways Luminal A vs Basal-like (in CCND1 amp)

6) Expression of CCND1, CDK4/6, MKI67 in Amp vs non-Amp CCND1 tumours split by PAM50 subtypes.

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