<table>
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<tr>
<th>Item No</th>
<th>Recommendation</th>
<th>Reference in Manuscript</th>
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</table>
| **Title and abstract** | 1  
(a) Indicate the study’s design with a commonly used term in the title or the abstract  
(b) Provide in the abstract an informative and balanced summary of what was done and what was found | An integrated genomic analysis...  
Structured abstract |
| **Introduction** | 2  
Explain the scientific background and rationale for the investigation being reported | Introduction, paragraphs 1-3 |
| **Objectives** | 3  
State specific objectives, including any prespecified hypotheses | Introduction, paragraph 4 |
| **Methods** | 4  
Present key elements of study design early in the paper | Introduction/paragraph 4, Methods/sample collection and datasets |
| **Setting** | 5  
Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection | Methods, MDACC cohort |
| **Participants** | 6  
(a) Give the eligibility criteria, and the sources and methods of selection of participants. Describe methods of follow-up  
(b) For matched studies, give matching criteria and number of exposed and unexposed | Described in previous study where the samples were collected; reference provided on p 8  
Criteria for selecting TNBC cases from other cohorts provided (Fig. 1, p. 8-9) |
| **Variables** | 7  
Clearly define all outcomes, exposures, predictors, potential confounders, and effect modifiers. Give diagnostic criteria, if applicable | Outcomes clearly defined: pCR for neoadjuvant, Overall Survival for adjuvant |
| **Data sources/measurement** | 8*  
For each variable of interest, give sources of data and details of methods of assessment (measurement). Describe comparability of assessment methods if there is more than one group | Details for sequencing and analysis provided in methods |
| **Bias** | 9  
Describe any efforts to address potential sources of bias | Validation in independent cohorts (TCGA and METABRIC) |
| **Study size** | 10  
Explain how the study size was arrived at | Explained on p.8 under MDACC cohort |
| **Quantitative variables** | 11  
Explain how quantitative variables were handled in the analyses. If applicable, describe which groupings were chosen and why | Explained throughout (clonal mutation burden, BRCA-deficient status) |
| **Statistical methods** | 12  
(a) Describe all statistical methods, including those used to control for confounding  
(b) Describe any methods used to examine subgroups and... | Described in methods  
Described methods for... |
interactions | assessing association between BRCA-D status and OS
---|---
(c) Explain how missing data were addressed | Only cases with complete data for the given analysis were used
(d) If applicable, explain how loss to follow-up was addressed | Standard censoring in survival analysis
(e) Describe any sensitivity analyses | None done

### Results

| Participants | 13* | Report numbers of individuals at each stage of study—eg numbers potentially eligible, examined for eligibility, confirmed eligible, included in the study, completing follow-up, and analysed | P. 8 and Fig. 1
| | | | |
| | (b) Give reasons for non-participation at each stage | P. 8 and Fig. 1
| | (c) Consider use of a flow diagram | Fig 1 for TCGA cohort
| Descriptive data | 14* | Give characteristics of study participants (eg demographic, clinical, social) and information on exposures and potential confounders | S1 Table
| | Indicate number of participants with missing data for each variable of interest | S3 Table
| | Summarise follow-up time (eg, average and total amount) | For TCGA and METABRIC summarized in original publications
| Outcome data | 15* | Report numbers of outcome events or summary measures over time | Figs 3, 4
| Main results | 16 | Give unadjusted estimates and, if applicable, confounder-adjusted estimates and their precision (eg, 95% confidence interval). Make clear which confounders were adjusted for and why they were included | Unadjusted and adjusted p-values for pathway analysis in S2 Table
| | (b) Report category boundaries when continuous variables were categorized | P 19 for BRCA-D signature
| | (c) If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period
| Other analyses | 17 | Report other analyses done—eg analyses of subgroups and interactions, and sensitivity analyses | Reported in results (BRCA-D analysis)

### Discussion

| Key results | 18 | Summarise key results with reference to study objectives | Throughout discussion
| Limitations | 19 | Discuss limitations of the study, taking into account sources of potential bias or imprecision. Discuss both direction and magnitude of any potential bias | End of discussion
| Interpretation | 20 | Give a cautious overall interpretation of results considering objectives, limitations, multiplicity of analyses, results from similar studies, and other relevant evidence | Throughout discussion
| Generalisability | 21 | Discuss the generalisability (external validity) of the study | Need for additional
<table>
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<tr>
<td>Funding</td>
<td>Give the source of funding and the role of the funders for the present study and, if applicable, for the original study on which the present article is based</td>
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*Give information separately for exposed and unexposed groups.