

Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

- | n/a | Confirmed |
|-------------------------------------|---|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The statistical test(s) used AND whether they are one- or two-sided
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of all covariates tested |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals) |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
<i>Give P values as exact values whenever suitable.</i> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated |

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

- | | |
|-----------------|--|
| Data collection | <p>For the DFCI trial analysis, extraction of genes and cancer types was performed by recursively traversing trial CTMLs with custom scripts and summarized with R ggplot2 and gtsummary.</p> <p>For the impact analysis, consent dates were extracted from DFCI's OnCore trial registration database. For our analytic cohort, time from MatchMiner ingestion date to consent date was calculated on a DFCI HIPAA compliant server.</p> |
| Data analysis | <p>For the DFCI trial analysis, all cancer types from trials were annotated with their corresponding OncoTree metatype (OncoTree version: oncotree_legacy_1.1). Trial phases and disease center were extracted from the summary field of trial json files with Python (v. 2.7) pandas json_normalize function.</p> <p>For the impact analysis, filtering was performed with Python (v. 2.7) pandas commands and the MatchMiner ingestion date to consent date time period was analyzed for MMC and non-MMC using a two-tailed Wilcoxon rank sum test with R gtsummary.</p> |

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

The time intervals between MatchMiner ingestion date and consent date for each patient (which are presented in the Results section “Impact of MatchMiner on PM trial consent” and in Figure 4) are available in Supplementary Tables 3 and 4. Detailed trial eligibility data (which are discussed in results section “Features of PM trials in MatchMiner” and in Figure 3) are unavailable due to contractual restrictions with clinical trial sponsors regarding the sharing of potentially proprietary eligibility criteria.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

We report the gender of MatchMiner consents in the impact analysis result. We obtained consent for their use in our manuscript. We had 106 female participants and 53 male participants. Reporting gender was used to provide context for our patient population.

Population characteristics

From our impact analysis, the average age of MMC patients is 60 years old (min=8, max=86) with most patients between 50-64 years old (n=70, 44%) (Supplementary Table 2). 67% of patients are female (n=106) and 33% are male (n=53). Most patients are white (n=137, 86%), followed by African American (n=7, 4%), Asian (n=6, 4%), and other/unknown (n=6, 4%).

Recruitment

This was a retrospective study. No subjects were recruited.

Ethics oversight

This study was approved by the institutional investigational review board at Dana-Farber Cancer Institute, which determined that neither the physicians nor the patients needed to be consented for this retrospective study.

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

Life sciences Behavioural & social sciences Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size

For the impact analysis, sample size for the analytic cohort was determined based on the number of MatchMiner consents and the number of consents on those same PM trials.

Data exclusions

No data was excluded from the impact trial analysis.

Replication

Because our impact analysis was a retrospective study over an approximately 4 year period with many institution specific variables, we do not think our study is repeatable.

Randomization

Because we conducted a retrospective study for the impact analysis, no randomization occurred.

Blinding

Blinding was not relevant for our impact analysis, because it was a retrospective measure.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

n/a	Included in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging