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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☐	☒	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics 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)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☐	☒	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☐	☒	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	OptiQuant version 3.00 (SDS analysis); Image J version 1.50i (autoradiography); Caseviewer version 2.1 (IHC); raw BCL data was demultiplexed using Illumina's bcl2fastq v2.20 (https://support.illumina.com/downloads/bcl2fastq-conversion-software-v2-20.html) and adapters were clipped and reads were quality trimmed using fastq-mcf v1.05 (RNA-seq); Siemens mCT PET/CT camera software versions VG50A/VG51A/VG60A and Siemens CT camera software VA48A and Syngo.via version 10.01.03 (Imaging software); OpenClinica version 3.6 (case record form)
Data analysis	R software version 3.2.1 for Mac; Accurate tool for PET data analysis; Graphpad Prism 5.0

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/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The RNA sequencing data set presented in this manuscript is available through NCBI GEO (series accession number GSE115594). All other data supporting the findings of this study are available from the corresponding author upon request.

Field-specific reporting

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

☒ Life sciences ☐ Behavioural & social sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences

Study design

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

Sample size	Imaging feasibility trial with no pre-defined sample size, therefore no sample size calculations were performed. A total of 25 patients were enrolled. Three patients dropped out prematurely, therefore, 22 patients were evaluable for final analysis.
Data exclusions	Three patients were discontinued prematurely from the trial due to early disease progression not allowing completion of the imaging series and start of treatment.
Replication	Patients were injected with 89Zr-atezolizumab only once and underwent a PET scan on days 0, 2, 4 and 7 or 4 and 7, respectively. PET scans could not be repeated on the same time point in the same patient. All IHC was performed once per sample per staining, which was considered sufficient as IHC assays are validated assays which have been performed together with positive and negative controles. Autoradiography was performed only once per sample as patients were injected with 89Zr-atezolizumab and biopsied only once and scan procedure lasted 72 hours not allowing replication due to decay of 89Zr. SDS-PAGE was performed once per sample, as patients were injectd with 89Zr-atezolizumab only once and blood was only collected once per time point and used for several analysis. Assessment of 89Zr-atezolizumab activity in plasma/RBC and PBMCs of patients blood was performed once , as patients were injectd with 89Zr-atezolizumab only once and blood was only collected once per time point and used for several analysis. RNA sequencing was performed once per sample, which was considered sufficient as the test runs with internal controls. 89Zr-atezolizumab internalization in H292 and H358 cells was assessed once in 3 technical replicates. 89Zr-atezolizumab internalization in PBMCs and T cells of healthy volunteers was assessed once in 2 technical replicates.
Randomization	Randomization was not performed in this trial as it was a first-in-human feasibility trial and all patients received treatment with atezolizumab after molecular PET imaging.
Blinding	Blinding was not necessary in this trial, as all patients received treatment with atezolizumab after molecular PET imaging.

Materials & experimental systems

Policy information about availability of materials

n/a	Involved in the study
☒	☐ Unique materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Research animals
☐	☒ Human research participants

Antibodies

Antibodies used	- Therapeutic antibody: Atezolizumab, monoclonal antibody against PD-L1; provided by Hoffmann-La Roche/Genentech and approved for therapeutic use (detailed information can be found on the manufacturers website: https://www.roche.com/products.htm --> TECENTRIQ (atezolizumab); website accessed on August 8, 2018) - IHC, primary antibodies: Anti-PD-L1: Clone name: SP142, Supplier: Ventana Medical Systems, catalog number: 740-4859, lot-number: N/A, dilution: prediluted (dispenser); secondary antibody: OptiView DAB Detection Kit (Ventana 760-700) and OptiView Amplification Kit

(Ventana 860-099).
Anti-PD-L1: Clone name: SP263, Supplier: Ventana Medical Systems, catalog number: 790-4905, lot-number: N/A, dilution: prediluted (dispenser); secondary antibody: Optiview DAB IHC Detection (Ventana - 760-700).
Anti-CD8: Clone name: C8/144B, Supplier: Dako, catalog number: M7103, lot-number: various, dilution: lot specific; secondary antibody: UltraView Universal DAB detection kit (Ventana - 760-500)

Validation

-Therapeutic antibody:
Atezolizumab, monoclonal antibody against PD-L1; provided by Hoffmann-La Roche/Genentech and approved for therapeutic use (detailed information can be found on the manufacturers website: https://www.roche.com/products.htm --> TECENTRIQ (atezolizumab); website accessed on August 8, 2018)
- IHC, primary antibodies:
Detailed information on validation can be found on the suppliers website (all websites accessed on August 8, 2018):
SP142 --> http://www.ventana.com/product/1827?type=2357
SP263 --> http://www.ventana.com/product/1815?type=2324
C8/144B --> https://www.agilent.com/en/products/immunohistochemistry/antibodies-controls/primary-antibodies/cd8#productdetails
- IHC, secondary antibodies:
Detailed information on validation can be found on the suppliers website (all websites accessed on August 8, 2018):
OptiView DAB Detection Kit (Ventana 760-700) --> http://www.ventana.com/product/1574?type=2037
OptiView Amplification Kit (Ventana 860-099) --> http://www.ventana.com/product/1714?type=2170
UltraView Universal DAB detection kit (Ventana - 760-500) --> http://www.ventana.com/product/1414?type=1791

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

human lung mucoepidermoid pulmonary H292 (American Type Culture Collection NCIH292)
bronchioalveolar H358 tumor cell line (American Type Culture Collection NCIH358)

Authentication

The used cell lines were STR profilled before use.

Mycoplasma contamination

Cell lines were tested mycoplasma free.

Commonly misidentified lines
(See ICLAC register)

No cell lines used in this study are commonly misidentified.

Human research participants

Policy information about studies involving human research participants

Population characteristics

Patients eligible for the study had histologically or cytologically documented locally advanced or metastatic bladder cancer, NSCLC or TNBC. They were eligible for at least second-line systemic therapy, or – in case of bladder cancer and NSCLC, showed disease progression during or within 6 months of completing platinum-based adjuvant/neoadjuvant chemotherapy. Other eligibility criteria included measurability according to RECIST 1.1, presence of a tumor lesion from which a biopsy could safely be obtained, age ≥ 18 years, written informed consent, Eastern Cooperative Oncology Group performance status of 0-1 and adequate hematologic and end organ function. Exclusion criteria were central nervous system disease, leptomeningeal disease, uncontrolled tumor-related pain, effusion/ascites, hypercalcemia, hypoalbuminemia, HIV infection, active tuberculosis, hepatitis B or C infections, current or recent severe infections, other significant concomitant diseases including autoimmune diseases, recent treatment with systemic immunosuppressive or immunostimulatory medication and prior treatment with CD137 agonists or immune checkpoint inhibitors.

Method-specific reporting

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ Magnetic resonance imaging