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SciScore Report

Below you will find your SciScore report containing three tables. Your score is calculated based on adherence to scientific rigor criteria (Table 1) and identification of key biological resources (Table 2). Table 3 contains statistical tests and oligonucleotides but is not scored. If SciScore makes any mistakes, please [contact us](#) to help us learn and improve.

Table 1: Rigor Adherence Table

<u>Ethics</u>
IRB: Ethical approval was obtained from National Research Ethics Service Committee South Central Oxford B (16/SC/0012) .
Consent: All patients provided written informed consent .
<u>Inclusion and Exclusion Criteria</u>
Eligible patients were {greater than or equal to}18 years , had a pathological or radiological diagnosis of NSCLC , were scheduled for surgical resection , had disease >2 cm in diameter and were Eastern Cooperative Oncology Group (ECOG) performance status 0-2 .
<u>Attrition</u>
Inter-cohort comparison of immunohistochemistry for the exogenous hypoxia marker pimonidazole was a co-primary trial endpoint and performed using , whenever possible , three entire tumor cross sections .
<u>Sex as a biological variable</u>
not detected.
<u>Subject Demographics</u>
Age: not detected.
Weight: not detected.
<u>Randomization</u>
not detected.
<u>Blinding</u>
not detected.
<u>Power Analysis</u>
not detected.
<u>Replication</u>

not detected.	
<u>Protocol Information</u>	
Identifiers: METHODS Study design , patients and treatment This was an open-label , non-randomized , 2-cohort , window of opportunity study (NCT02628080) conducted at the Oxford Cancer and Haematology Centre (Oxford , UK) .	NCT02628080

Table 2: Key Resources Table

Your Sentences	REAGENT or RESOURCE	SOURCE	IDENTIFIER
<u>Recombinant DNA</u>			
Secondary imaging endpoints were change in tumor perfusion using dynamic hypoxia PET , perfusion CT (pCT) and dynamic contrast-enhanced (DCE) MRI .	pCT		Suggestion: RRID:Addgene_60620(link)
<u>Software and Algorithms</u>			
FastQC was used to evaluate quality of sequencing reads at both base and read levels (24) .	FastQC		Suggestion: (FastQC, RRID:SCR_014583)(link)
Filtered reads were aligned to the human reference genome (hg19) using STAR (25) .	STAR		Suggestion: (STAR, RRID:SCR_015899)(link)
Statistical analyses used Stata v15.0 (StataCorp , USA) and R v3.6.3 (Comprehensive R Archive Network ,	StataCorp		Suggestion: (Stata, RRID:SCR_012763)(link)
Gene Set Variation Analysis (GSVA) was carried out using the GSVA Bioconductor package (34). sigQC protocol was used to evaluate signature applicability and compute signature summary scores (35).	GSVA		
	Bioconductor		Suggestion: (Bioconductor, RRID:SCR_006442)(link)
Heatmaps were created using the Pheatmap R package (https://CRAN.R-project.org/package=pheatmap).	Pheatmap		Suggestion: (pheatmap, RRID:SCR_016418)(link)

Other Entities Detected

Your Sentences	Recognized Entity
Statistical Tests	
Spearman 's coefficients were reported for correlation analysis .	Spearman 's coefficients
Inter-cohort differences in expression were compared using independent samples t-test for hypoxia signature analysis and Wilcoxon rank-sum test for all other expression analysis (equal variances).	t-test
	Wilcoxon rank-sum test

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For a full description of scored criteria and tips for improving your score, please see <https://www.scicrunch.com/sciscorereport-faq>