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Using tissue removed during routine surgery, together with donors' genetic information, to understand how genetic differences affect the way human tissues respond to disease and treatment

Submission date 20/11/2026	**Recruitment status** Not yet recruiting	[X] Prospectively registered [_] Protocol [_] Statistical analysis plan [_] Results [_] Individual participant data [X] Record updated in last year
Registration date 20/11/2026	**Overall study status** Ongoing	
Last Edited 20/11/2026	**Condition category** Surgery	

Plain English summary of protocol

Background and study aims

Many diseases are influenced by small differences in our DNA. Large genetic studies have identified thousands of genetic variants linked to disease, but researchers often do not know exactly which genes and cell types are affected. This makes it harder to develop new treatments. The Multiscale Analysis of Surgical Tissue (MAST) study aims to improve understanding of how genetic differences affect human tissues at the molecular and cellular level. By studying tissue samples collected during surgery and comparing them with genetic information, researchers hope to identify genes, biological pathways and potential drug targets that may help improve the diagnosis and treatment of a wide range of diseases.

Who can participate?

Adults aged 18 years and over who are scheduled to undergo surgery at a participating study site and are able to provide written informed consent may be eligible to take part.

What does the study involve?

Participants will be asked to provide written informed consent before taking part. The study mainly uses tissue that would otherwise be discarded after surgery. Depending on the type of operation and the participant’s consent, researchers may also collect up to two small additional tissue samples during the operation and/or a small blood sample of up to 4 mL.

The collected samples will be analysed in laboratories using a range of molecular and genetic techniques. Researchers will study gene activity, proteins, metabolites and other cellular features, and compare these findings with participants’ genetic information. No experimental treatment, drug or medical device is being tested, and taking part will not change a participant’s usual clinical care.

What are the possible benefits and risks of participating?
Participants are unlikely to receive any direct medical benefit from taking part. However, the information collected may help researchers better understand how diseases develop and may support the development of new medicines, diagnostic tests and treatments in the future. Risks are expected to be low. The study mainly uses tissue that would otherwise be discarded. Participants who choose to provide additional tissue samples or a blood sample may experience minor discomfort, bruising, bleeding or a small risk of infection associated with sample collection.

Where is the study run from?
The study is run from Multiscale Laboratories Limited, London, United Kingdom. The first participating centre is Royal Surrey County Hospital in Guildford, England.

When is the study starting and how long is it expected to run for?
December 2026 to December 2036.

Who is funding the study?
Multiscale Laboratories Limited (UK).

Who is the main contact?
Dr Jonathan Millar, Multiscale Laboratories Limited
jm@multiscalelabs.com

Contact information

Type(s)
Public, Principal investigator, Scientific

Contact name
Dr Jonathan Millar

ORCID ID
https://orcid.org/0000-0002-4853-9377

Contact details
Multiscale Laboratories Limited
167-169 Great Portland Street
London
United Kingdom
W1W 5PF
+44 7469046408
jm@multiscalelabs.com

Additional identifiers

Integrated Research Application System (IRAS)
375362

Central Portfolio Management System (CPMS)
75620

Study information

Scientific Title
Multiscale Analysis of Surgical Tissue

Acronym
MAST

Study objectives
Primary objective:
To identify molQTL in surgical tissue specimens (discarded tissue and, where justified, tissue obtained by additional sampling) in a broad variety of cell types and states.

Secondary objectives:
1. To contribute summary-level (not individual) data to reference atlases of cell-type-specific gene expression across human tissues to support future research, including therapeutic target validation, diagnostic development, and disease mechanism studies
2. To share pseudonymised molecular, cellular and genetic data with approved external researchers (including academic, international, and commercial partners) for the purpose of openness and advancing medicine

Analytic objectives:
1. To generate molecular and cellular data from collected tissue
2. To generate genotype or genome sequence data from collected tissue or blood
3. To combine genetic and molecular/cellular data, in the context of clinical metadata, to identify the read-outs under direct or indirect genetic control
4. To identify candidate therapeutic targets and biomarkers of disease state or treatment response by linking molQTL programmes to disease-associated genetic variants

Ethics approval required
Ethics approval required

Ethics approval(s)
Approved 17/11/2026, London - South East Research Ethics Committee (Health Research Authority 2 Redman Place, London, E20 1JQ, United Kingdom; +44 207 104 8000; londonsoutheast.rec@hra.nhs.uk), ref: 26/LO/0829

Primary study design
Observational

Secondary study design
Cross sectional study

Study type(s)

Health condition(s) or problem(s) studied
Patients undergoing elective surgery.

Interventions
The study has four interrelated components:

1. Sample collection: The following specimens are collected from consenting participants:
(a) Discard tissue surplus to clinical requirements;
(b) in some cases, tissue obtained via additional sampling procedures performed at the time of surgery, and
(c) in some cases, up to 4ml of blood, obtained through venepuncture or sampling from indwelling lines.

2. In vitro stimulation: In order to broaden the range of cell states in which molecular and cellular read-outs can be observed, selected tissue samples will be exposed to a range of stimuli. These will include exposure to cytokines, chemokines, drugs, pathogens, pathogen-associated molecular patterns, damage-associated molecular patterns, hypoxia, changes in temperature, and other chemical and physical exposures. Cells and tissue are maintained in short-term culture only, for the duration of each stimulation experiment. No immortalised or permanent cell lines, induced pluripotent stem cells, or other long-term cultures will be derived, and no samples or derived cells will be used in animal research (including xenografts).

3. Molecular and cellular read-outs: A broad range of read-outs will be used to detect the consequences of genetic variation. These include bulk and single-cell/single-nuclear transcriptomics, spatial transcriptomics, proteomics, metabolomics, and cellular and tissue imaging. Single-nuclear RNA-seq is often the preferred method for solid tissue transcriptomics because it operates on isolated nuclei rather than requiring intact single-cell suspensions, making it compatible with tissues that are difficult to dissociate and preserving rare cell populations that may be lost during enzymatic dissociation.

4. Genetics: DNA extracted from tissue or blood will be genotyped using array genotyping or genome sequencing.

Intervention Type
Procedure/Surgery

Primary outcome(s)
1. Number of statistically significant molecular quantitative trait loci (molQTL; genetic variants associated with molecular or cellular read-outs such as gene expression levels) identified across surgical tissue specimens in a broad range of cell types and states measured using integrated analysis of genotype or genome sequencing data and molecular/cellular read-outs including bulk transcriptomics, single-cell RNA sequencing, single-nuclear RNA sequencing, spatial transcriptomics, proteomics, metabolomics and tissue imaging, assessed on samples collected at the time of surgery

Key secondary outcome(s)

Completion date
14/12/2036

Eligibility

Key inclusion criteria
1. Aged 18 years or older at the time of consent
2. Expected to undergo a surgical procedure at a participating site from which tissue specimens will be available
3. Capacity and willingness to provide written informed consent

Healthy volunteers allowed
No

Age group
Mixed

Lower age limit
18 Years

Upper age limit
120 Years

Sex
All

Total final enrolment
0

Key exclusion criteria
1. Current enrolment in a clinical study whose protocol prohibits co-enrolment
2. Known or suspected infection with:
2.1. Any hazard group 4 biological agent on the Advisory Committee on Dangerous Pathogens (ACDP) Approved List of biological agents
2.2. Active Mycobacterium tuberculosis complex infection
2.3. A transmissible spongiform encephalopathy (including CJD or variant CJD), or recognised increased risk of one as defined in ACDP TSE Subgroup guidance
2.4. Any other hazard group 3 agent transmissible by routes other than blood and body fluids (for example Yersinia pestis, dengue virus, West Nile virus), or any agent excluded by local health and safety guidance

Date of first enrolment
14/12/2026

Date of final enrolment
14/12/2034

Locations

Countries of recruitment
United Kingdom

England

Study participating centre
Royal Surrey County Hospital
Egerton Road

Guildford
England
GU2 7XX

Sponsor information

Organisation
Multiscale Laboratories Limited

Funder(s)

Funder type

Funder Name
Multiscale Laboratories Limited

Results and Publications

Individual participant data (IPD) sharing plan

IPD sharing plan summary
Not expected to be made available