Expression of Interest - Insights Q4

Please complete and email a copy of this form to: **enquiries@genomiQa.com**
Enquiries please email above or call +61 426 181 538

Whole genome analysis for research purposes

CRO/Pharma Company

*Contact Name:*_____

Organisation:_____

email:_____

Address:_____

_____

_____ Postcode: _____

Phone/Mobile:_____

Study Details (Proposed)

*Study Name:*_____

Number of participants:_____

Project Code #:_____

Return samples to: (if applicable)

*Name:*_____

Address:_____

_____ Postcode: _____

email:_____

genomiQa insightsQ4 options

Authorisation

Please mark with a cross **(X)**

GERMLINE (30X) - Whole genome analysis from **blood sample** to patient reported classifers versus clinincal outcomes (Upto 3 classifiers included)		I confirm the patients will be/or have been consented to conduct genomic analysis and that de-identified clinical and genomic data may be used for research purposes and for quality assurance by the provider. We have read the terms and conditions outlined on page 2 of this form.
CANCER (60X) + GERMLINE(30X) - Whole genome analysis from **blood and tissue sample** to patient reported classifiers versus clinical outcomes (Upto 3 Classifiers Included)		**Signature:** **Date:**

Classifiers - to be discussed and agreed

Group A vs Group B - examples of possible classifiers below

Tx Response, Toxicity, Survival O/S, Survival PFS

Other classifiers to be assessed (Please list)

_____

_____

Objective of Study:

_____

_____

Other information to support planning for the the experiment:

_____

_____

Are you interested in in depth analysis using AI platofrms? Y/N

Specimen Type	SPECIMEN REQUIREMENTS	
Fixed Tissue	One (1) tumour-containing FFPE block for investigation	Could result in poor quality sequencing
Unstained Slides	FFPE or frozen tissue sections	Could result in poor quality sequencing
Core Needle Bopsy	Tissue piece snap frozen plus or minus RNAlater	Preferred tumour sample
Blood Sample	5-10 ml blood collected in EDTA tubes	

Terms and Conditions

WHOLE GENOME ANALYSIS: Based on available data, genomiQa's germline and somatic analysis has >99% and >95% accuracy of specific variants for germline and tumour testing respectively. Depending on the analysis selected, genomiQa will identify tumour specific mutations which may suggest treatment options or look for inherited genetic variants that may indicate an increased risk of hereditary cancer as well as other conditions.

Whole genome analysis may uncover sensitive information about a study participants health or disease risks, including risk for diseases other than the one being studied or for diseases that currently have no treatment. We do not currently have all of the scientific knowledge to know the best ways to treat every cancer, and all of the genetic causes of diseases are not know, which means currently no test can detect every mutation associated with treatment prognosis or an increased risk for cancer or other diseases.

New information may replace or add to the information that was used to analyse the study results. Based on this new information, you understand and agree that genomiQa may, at its sole discretion, amend or modify a research report, which may result in a change in the classifiers value. You hereby irrevocably waive any and all claims against genomiQa for any amendment or modification of the test report and result.

genomiQa has measures in place to ensure quality of the test and to minimise technical error, however as with all medical tests, there is a chance of a false positive or a false negative result.

In some instances the tissue sample we receive for cancer analysis may not have enough tumour or the DNA is of poor quality to be able to perfom the test, in this instance we will ask for more tissue to be obtained.

We do not know the impact of all variants in a person's genome. Therefore the test may identify the presence of Variants of Uncertain Significance (VUS), which are genetic variants that require further research to determine if they are associated with treatment prognosis or an increased risk for disease.

Testing positive for a mutation means a genetic variant that increases risk for a certain type of cancer or other condition was identified. A positive result does not nescessarilly mean that a study participant may have or will develop the disease in their lifetime. A test which is inclusive means that no mutations were identified which are associated with an increased risk for the disease that was being investigated. However, this does not eliminate the participants risk of developing a disease.

The analysis being conducted is for research purposes only and will not be used to diagnose a patient.

genomiQa does not provide medical services, diagnosis, treatment, or advice.

Please refer to genomiqa.com for more information.