

## POSTER SYMPOSIUM – P9

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# Towards Breast Cancer Profiling - Exploring the Potential Roles of Candidate Genes in Breast Cancer

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### OBJECTIVE

The discovery of comprehensive somatic genomic abnormalities has led to the molecular profiling of many cancer types and contributed to the development of targeted therapies. This study aims to develop the Brunei Cancer Genome Atlas, which is an atlas of genomic mutations in specific cancers of the Bruneian population, particularly in breast cancer.

### MATERIAL AND METHODS

To date, this study has evaluated the patient characteristics, performed RNA extraction from breast tumours by laser capture microdissection (LCM), as well as investigated the mRNA and protein expressions of Syk, Btk, and the hippo pathway components YAP and Mst1 in breast cancer by real-time quantitative polymerase chain reaction (qRT-PCR) and immunohistochemistry.

### RESULTS

Patients diagnosed with breast cancer were all female at a mean of 54 years old (SD: 43-65) with high expression of estrogen and progesterone receptors (ER/PR) in majority of them. Microdissected cells yielded a sufficient amount of RNA allowing for downstream experiments. The expression levels of Btk and YAP were markedly increased, whereas the Syk and Mst1 expression levels were reduced in invasive breast tumours.

### CONCLUSION

A genetic pattern in Bruneian breast cancer patients is likely to emerge which warrants further systematic genomic investigation in a larger number of breast cancer cases.

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