\*\*\*A Comprehensive Genome-wide Analysis of Long Non-coding RNA and mRNA Expression Profiles of JAK2V617F-positive Classical Myeloproliferative Neoplasms\*\*\*

Authors: Jie Zhou

Tongji University School of Medicine, Shanghai 200092, China; Department of Gastroenterology, Tongji Hospital of Tongji University, Shanghai 200065, China

Corresponding author: Jian-fei Fu

Contact Information:

Jie Zhou

Shanghai Tongji Hospital, Shanghai 200065, China

Tongji University School of Medicine, Shanghai 200092, China

Mobile: +86 18817871147

Email: [wuyizhoujie@163.com](mailto:wuyizhoujie@163.com)

\*\*\*General Introduction\*\*\*

This dataset contains data underlying the research of: A Comprehensive Genome-wide Analysis of Long Non-coding RNA and mRNA Expression Profiles of JAK2V617F-positive Classical Myeloproliferative Neoplasms.

The data in this data set was collected in Laboratory of the Tongji University School of Medicine, between October 2019 and October 2020.

\*\*\*Purpose of the test campaign\*\*\*

The purpose of these experiments was to investigate clarify the expression and regulation patterns of lncRNAs in JAK2V617F-positive classical myeloproliferative neoplasms (cMPNs), and to explore new potential carcinogenic factor of cMPNs. A total of 12 samples (six JAK2V617F-positive cMPNs patients [+] and six normal controls [-]) were included in the microarray analysis.

\*\*\*Test equipment\*\*\*

The Agilent Array platform was employed for microarray analysis. The sample preparation and microarray hybridization were performed based on the manufacturer’s standard protocols with minor modifications. Briefly, mRNA was purified from total RNA after removal of rRNA (mRNA-ONLY™ Eukaryotic mRNA Isolation Kit, Epicentre). Then, each sample was amplified and transcribed into fluorescent cRNA along the entire length of the transcripts without 3’ bias utilizing a random priming method. The labeled cRNAs were hybridized onto the Human LncRNA Array v3.0 (8 x 60K, Arraystar). After washing the slides, the arrays were scanned by the Agilent Scanner G2505C. Agilent Feature Extraction software (version 11.0.1.1) was used to analyze acquired array images. Quantile normalization and subsequent data processing were performed using the GeneSpring GX v11.5.1 software package (Agilent Technologies).

\*\*\*Description of the data in this data set\*\*\*

Full names and definitions of column headings: CLD(+), GAM(-), JM(-), JQG(-), LCE(+), SP(+), WQQ(-), XGQ(+), XJ(+), ZAM(-), ZHL(-), and ZYM(+) represent the number of different samples, and “(+)” represents MPN patients who are JAK2V617F positive while “(-)” represents JAK2V617F-negative controls. primaryID represents the lncRNAs and mRNAs detected in this data set.