

# NOVEL BIOINFORMATICS APPROACH FOR SARCOMA PROTEOGENOMICS; MUTATED NUCLEOTIDES AND AMINO-ACIDS GENERATOR (MUNAGE)

Emi Hattori, Kumiko Shiozawa, Tadashi Kondo

Division of Rare Cancer Research, National Cancer Center, Tokyo, Japan

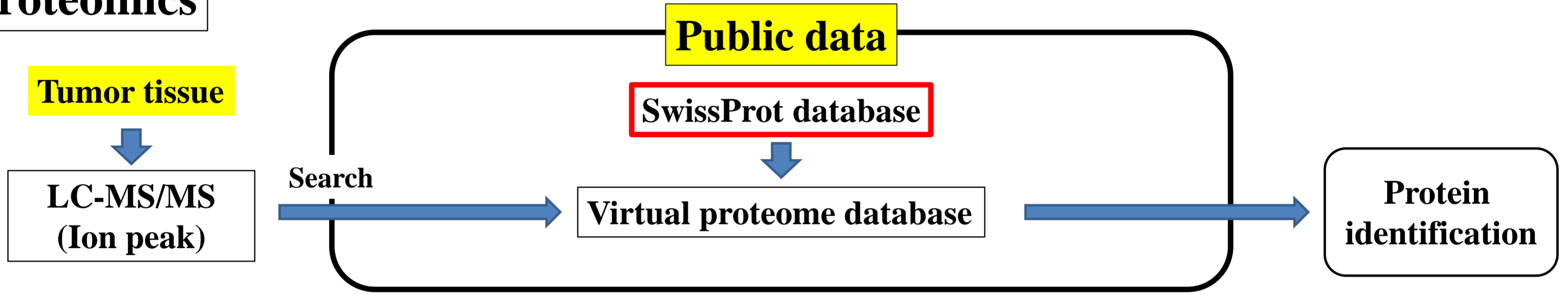
## Inconvenient truth of cancer proteomics

- Proteomics is an attractive approach in cancer research, because global protein expression patterns should reflect functional outputs of genomic aberrations. Practical biomarkers and effective targets have long been expected in cancer proteomics.
- However, despite thousand promises, and thousand papers reporting novel biomarkers or therapeutic targets in various malignancies including sarcomas, proteomics did not produce any clinically useful outcome.
- Something should be essentially wrong with previous proteomics. Without recognizing it, we cannot expect meaningful results from proteomics.

## Fundamental problem of cancer proteomics

- Proteomics is based on protein identification of mass spectrometry. Ion peaks generated by mass spectrometry are matched to theoretical ones of virtual proteome database generated by genome data. This method is quite common, and almost automated in many laboratories.
- However, this method causes bottom of trouble. This method uses public databases such as SwissProt to generate virtual proteome database. In the public databases, proteins with mutations unique to individual tumors are not recorded. Thus, the proteins generated from mutated DNAs cannot be identified by mass spectrometry.
- Indeed, all biomarker proteins reported by proteomics are those with normal sequences. They are not good biomarkers and therapeutic targets because of the lack of specificity to tumors.

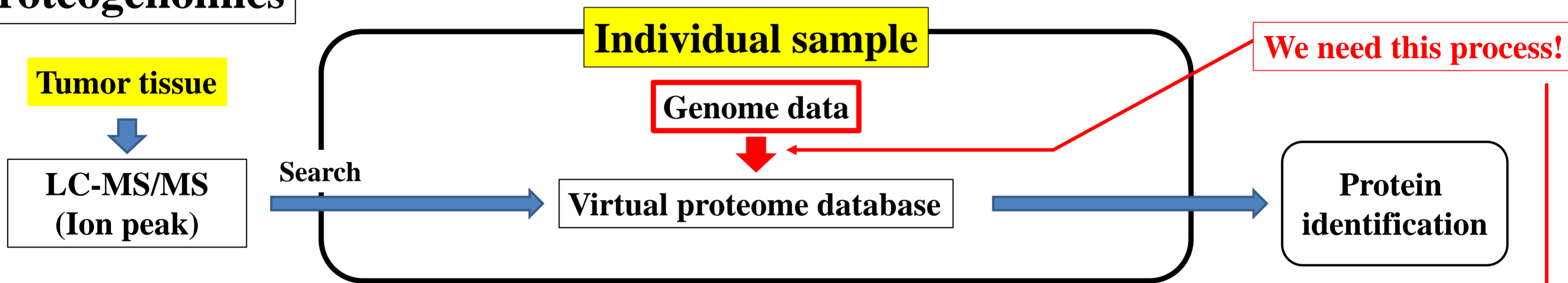
### Proteomics



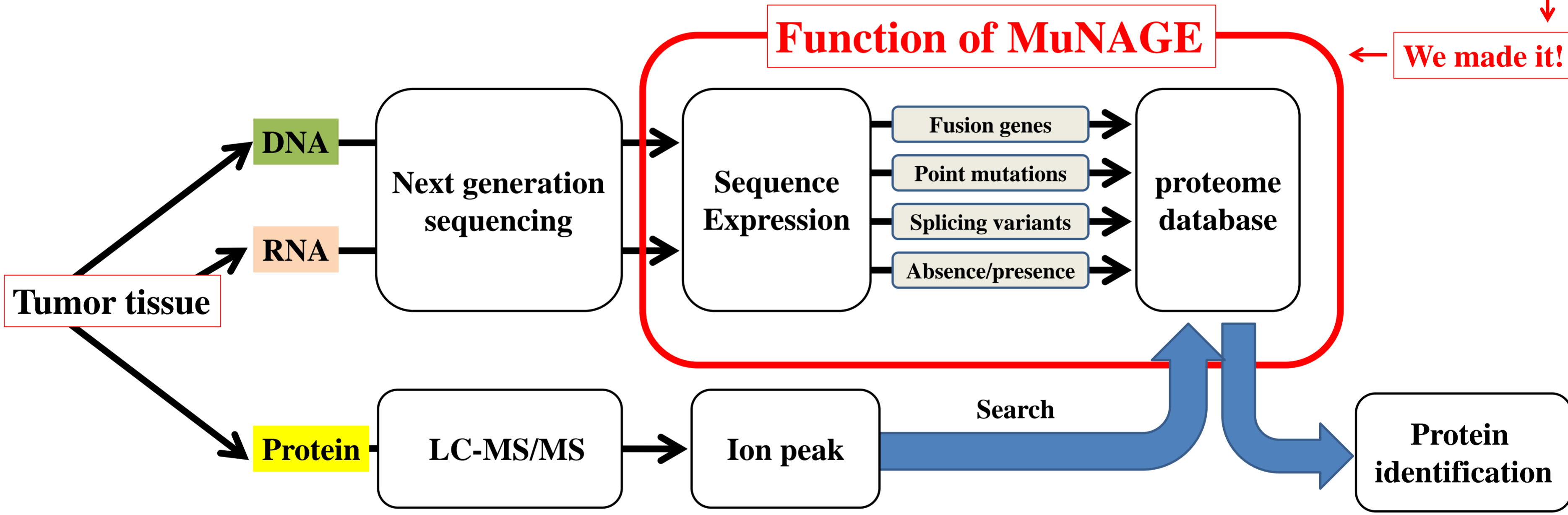
## Proteogenomics: Breakthrough for cancer proteomics

- In proteogenomics, proteome database for protein identification is created using genome data of individual tumor tissues. Using such database unique to individual tumors, we can identify proteins with mutations.

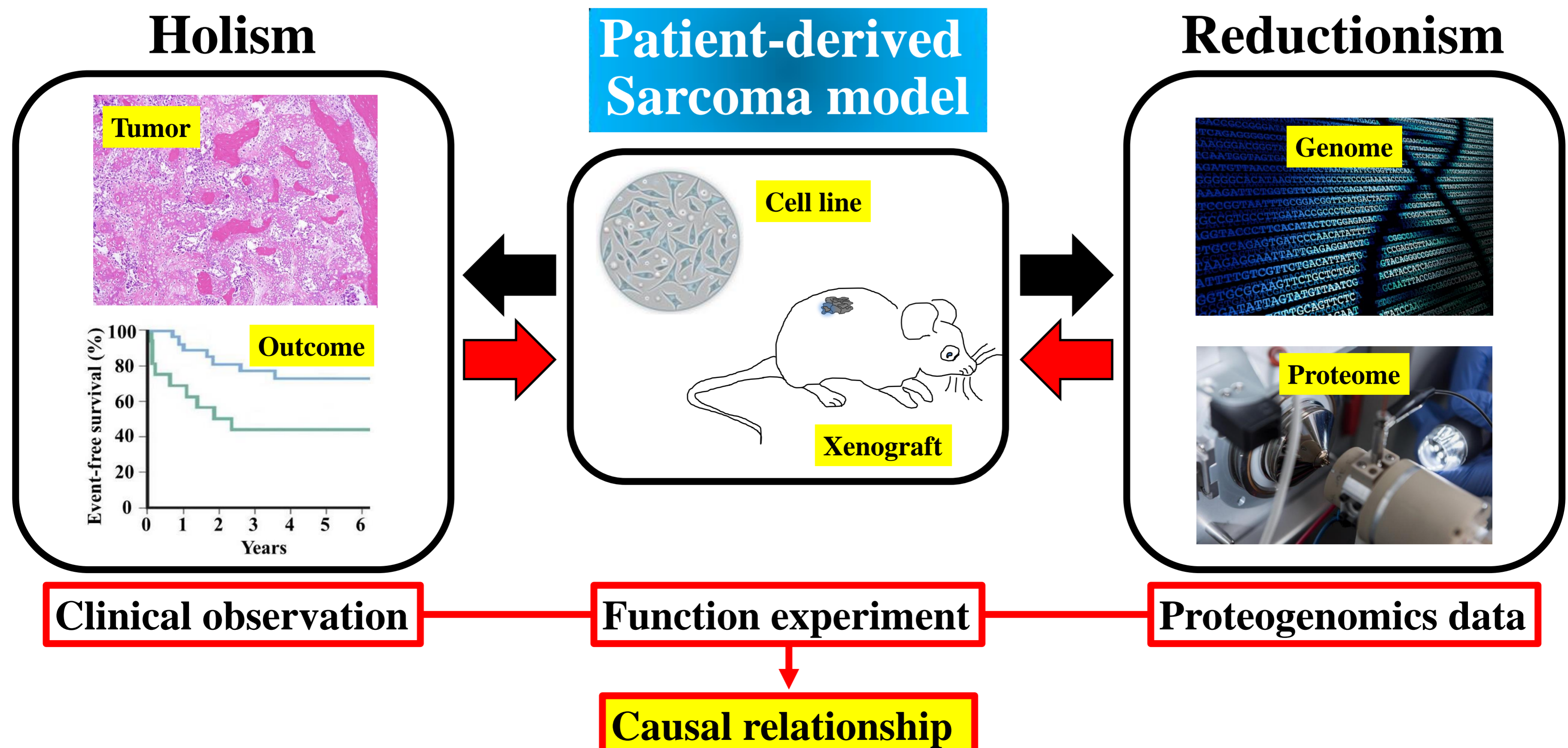
### Proteogenomics



To generate database for proteogenomics protein identification, we created software; **“Mutated Nucleotides And Amino-Acids Generator (MuNAGE)”**.



## Patient-derived sarcoma models for proteogenomics



- We established 40 PDXs and 30 cell lines from sarcoma tumor tissues.
- Please feel free to contact us if you want to use our sarcoma cell lines. We will provide them upon a request.
- Tadashi Kondo; takondo@ncc.go.jp