

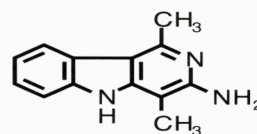
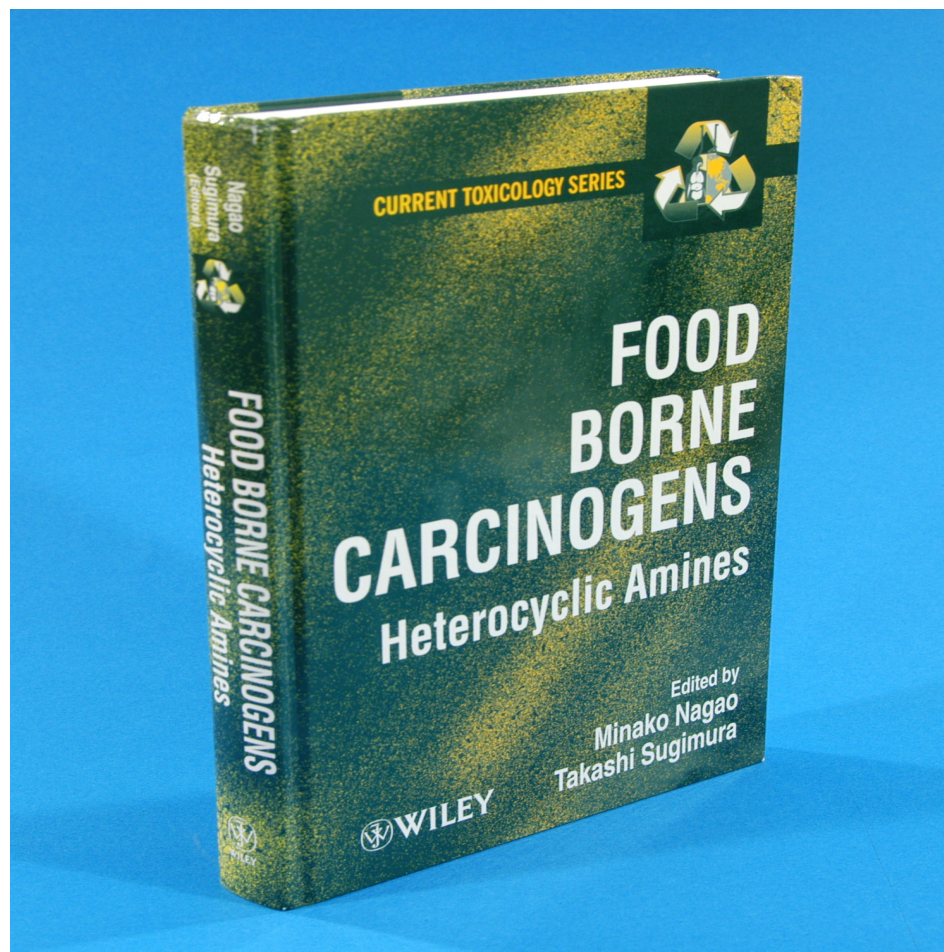
**IARC 50<sup>th</sup> Anniversary Conference**  
**Global Cancer Occurrence, Causes and Avenues to Prevention**

***Mechanisms: DNA damage, Repair and Mutagenesis***

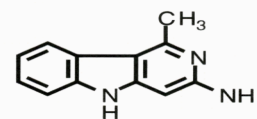
**Exploration of Cancer Etiology using  
Whole Genome/Exome Analysis  
and Comprehensive DNA Adduct Analysis**

**Hitoshi Nakagama**  
**National Cancer Center, Japan**

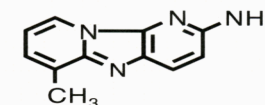
## Heterocyclic Amine (HCA); Food-borne Carcinogens Produced in Cooked Meats



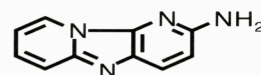
**Trp-P-1**



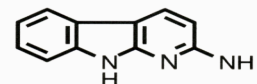
**Trp-P-2**



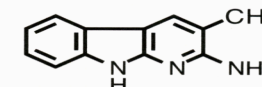
**Glu-P-1**



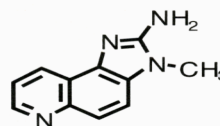
**Glu-P-2**



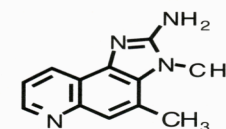
**AαC**



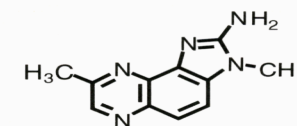
**MeAαC**



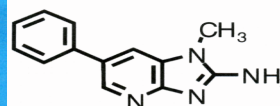
**IQ**



**MeIQ**

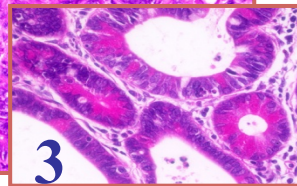
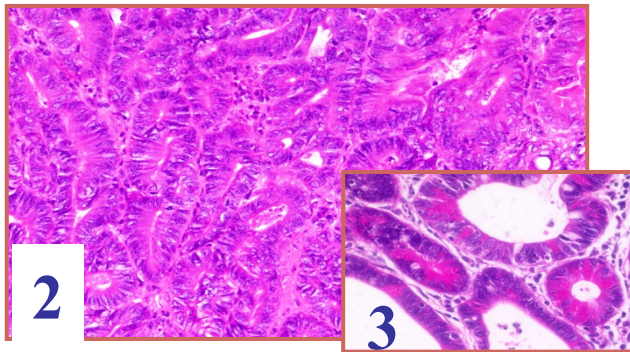
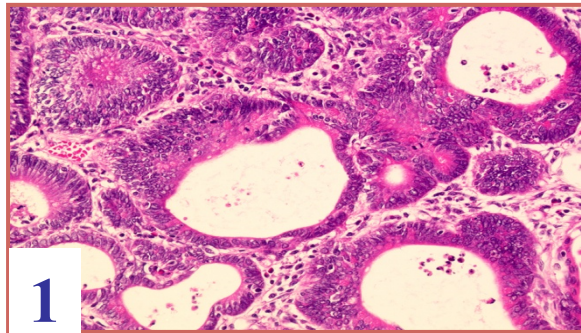


**MeIQx**



**PhIP**

## Representative Histological Features and Genetic Alterations observed in PhIP-induced Rat Colon Cancers



Tubular growth pattern (No. 1, 2), and differentiation into Paneth cells (No. 3)

### 1. *Apc* (approx. 10 ~ 15 %)

Exon 14 or 15 (codons 635, 869, 1413)

5'-GTGGGAT-3' to 5'-GTGGAT-3'

(G deletion)

Intron 10 & exon 11 junction

5'-tagGGGGG-3' to 5'-tatGGGGG-3'

(G to T)

5'-tagGGGGG-3' to 5'-tagGGGG-3'

(G deletion)

### 2. $\beta$ -catenin (25 ~ 50 %)

Codons 32, 34, 36, 37, 38 (mainly G to T/A)

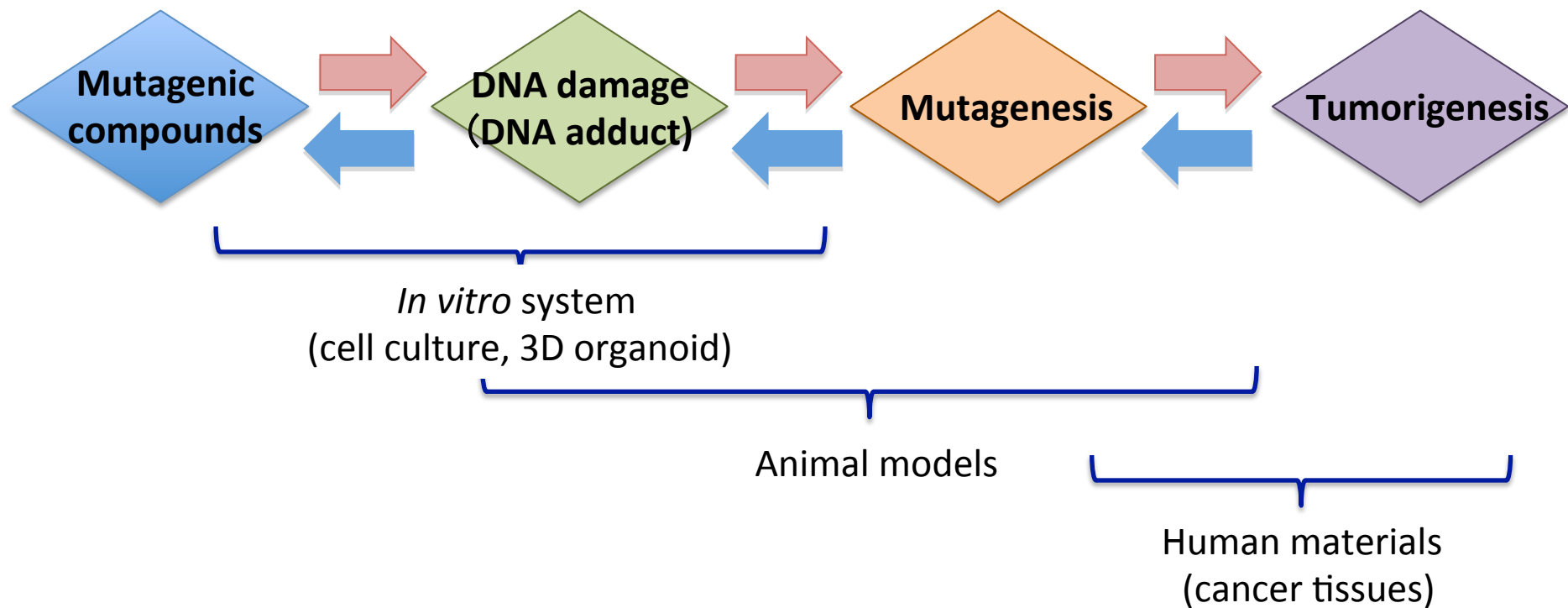
& G:C to C:G

### 3. *K-ras* and *p53* mutations are rarely observed. *Genomic instability* (MSI) is not evident.

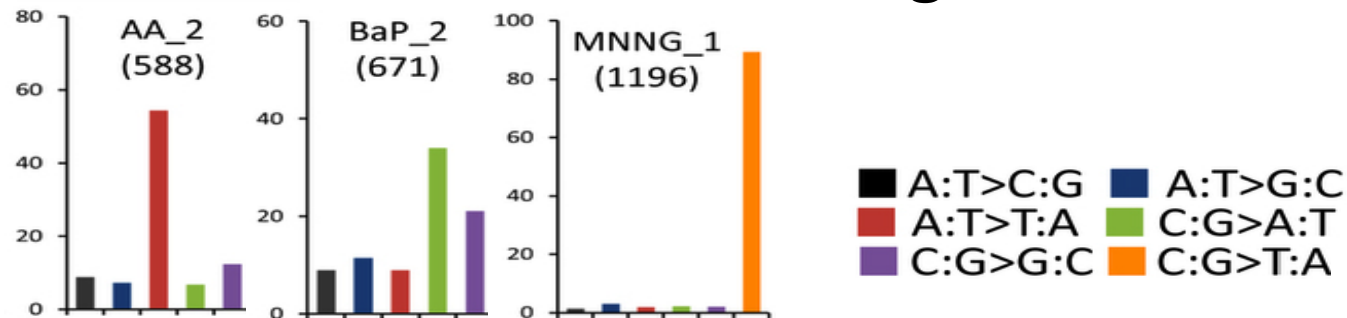
\* IQ-induced colon cancers

→ Codons 523 or 921 in *Apc* (C to T / T to C)

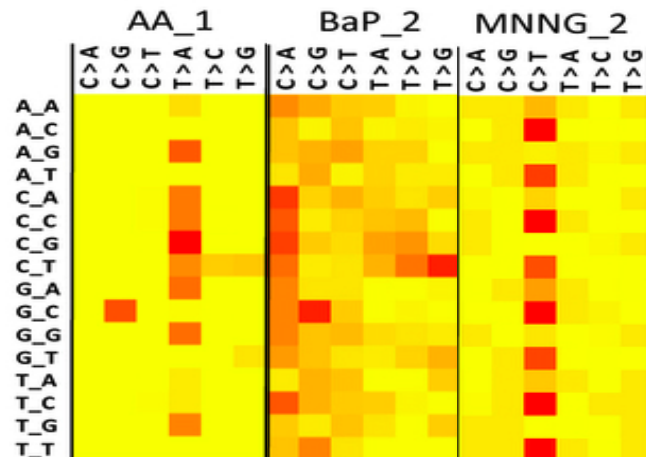
# Bottom-up and Top-down Approaches for Exploration of Cancer Etiology



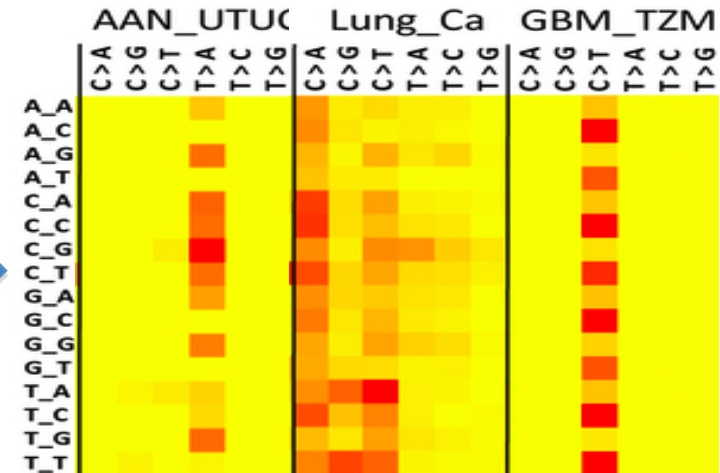
# Mutagens/Carcinogens Induce Specific Mutation Patterns and Mutational Signature



Mutation Signature induced in Culture Cells by Chemicals



Mutation Signature observed in Human Cancers

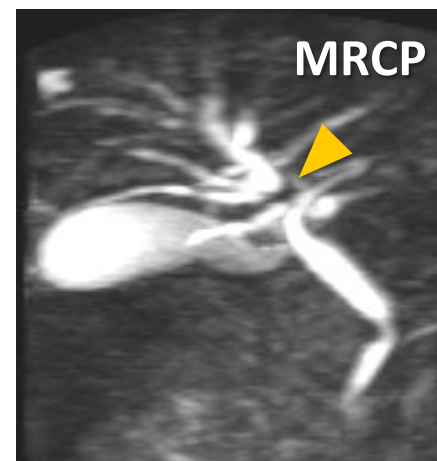


Olivier et al., Scientific Reports, 2014

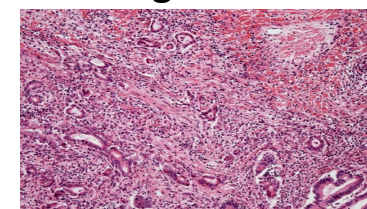


## Analysis of Somatic Mutations observed in Occupational Cholangiocarcinoma

	Case 1	Case 2	Case 3	Case 4
Age	40	39	31	34
Sex	M	M	M	M
Duration of Exposure	DCM; 1y5m	DCM; None	DCM; None	DCM; None
	DCP; 11y11m	DCP; 7y4m	DCP; 6y6m	DCP; 6y1m
Smoking Habit (/Day)	20 cigarette	20 cigarette	None	None



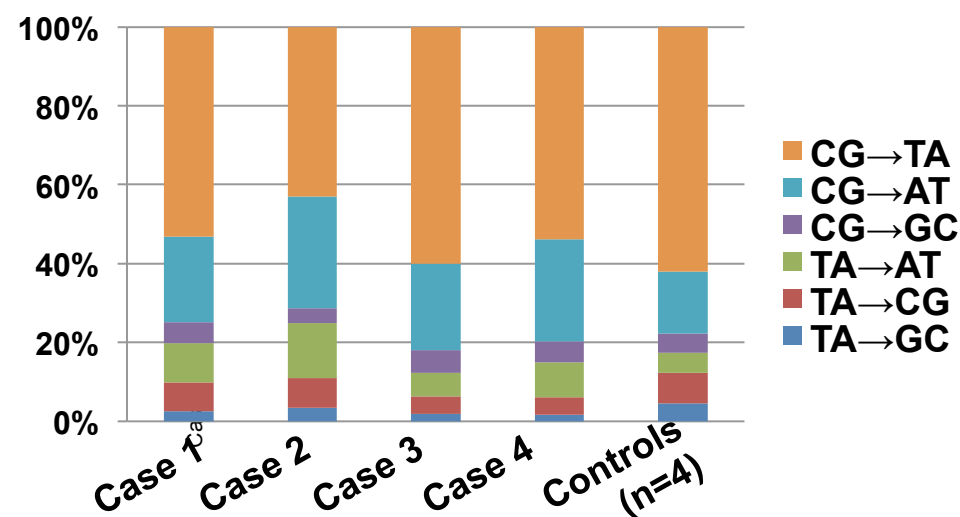
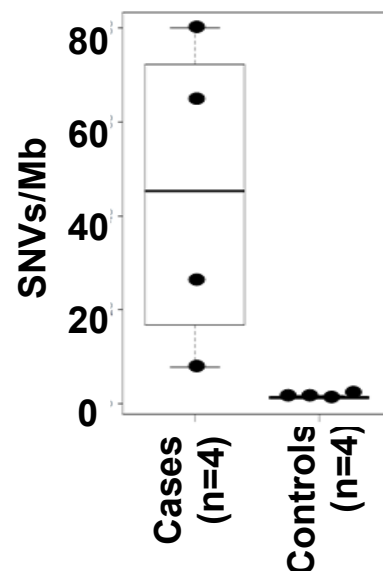
Histology of Cholangiocarcinoma



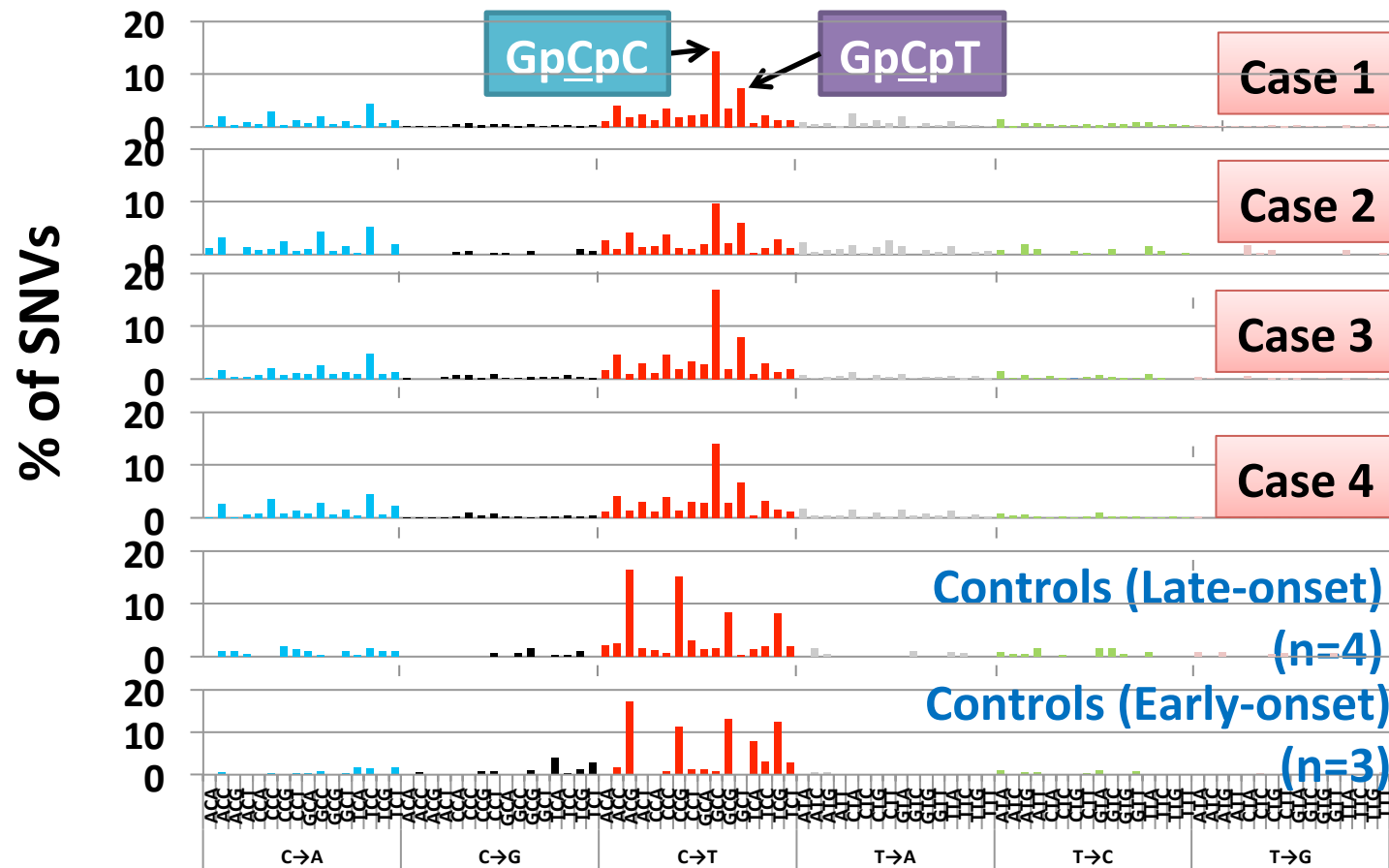
- Massive fibrosis
- Infiltration of inflammatory cells

Number of SNVs Analyzed by whole exon analysis

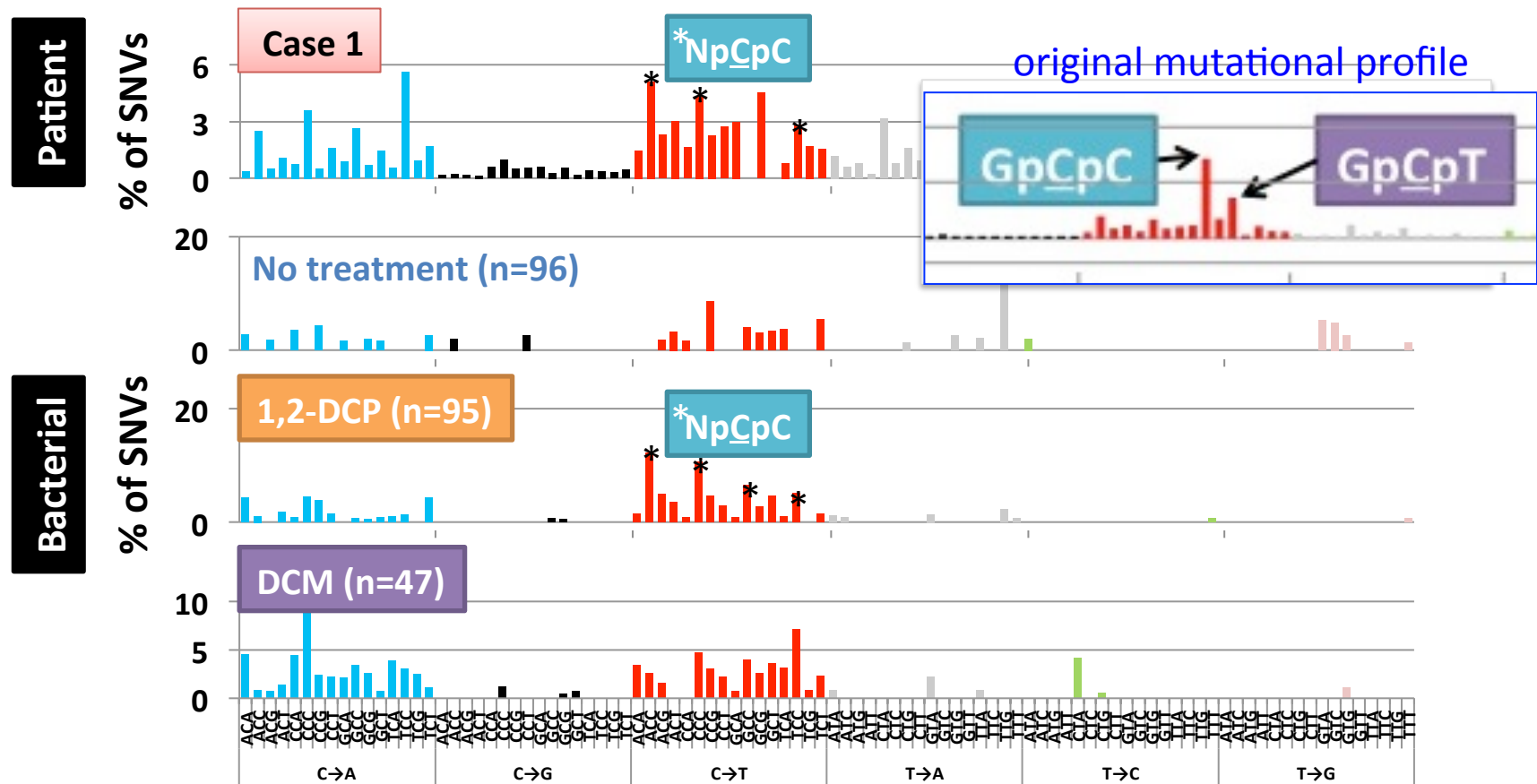
Total number of SNVs in Cases; 1,451±1,089



# Predominant GpCpY Trinucleotide Mutational Signatures in C:G to T:A Transitions

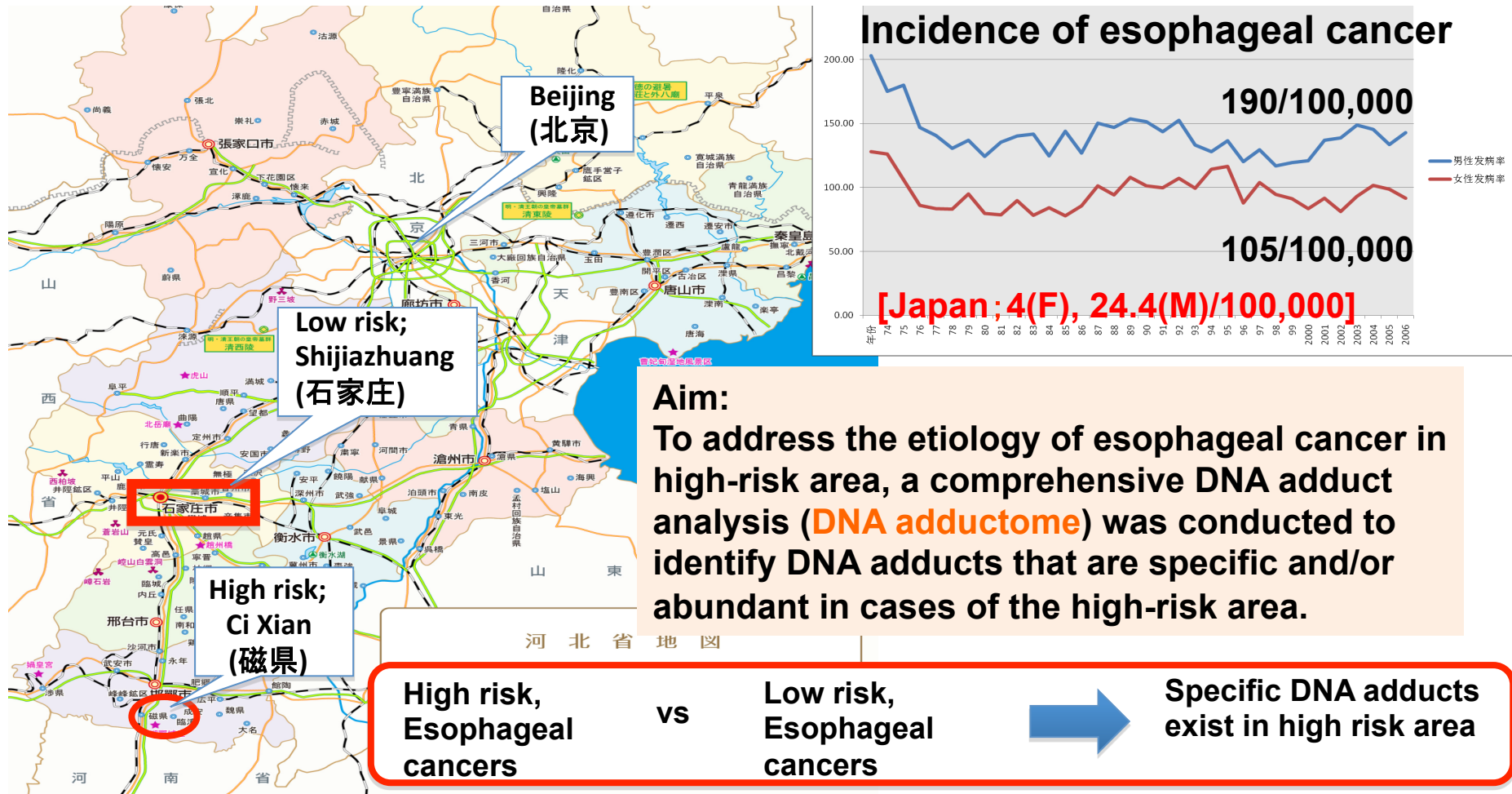


# Overlapped Mutational Signatures among 1,2-DCP Exposed Bacteria and Occupational Cholangiocarcinoma Genomes





# Esophageal Cancer (EC) ---Several high risk areas exist in China---



# DNA Adductome Analysis of Esophagus Cancers in China: Surgical Specimens Collected from Cases in High- and Low-risk Areas

High-risk

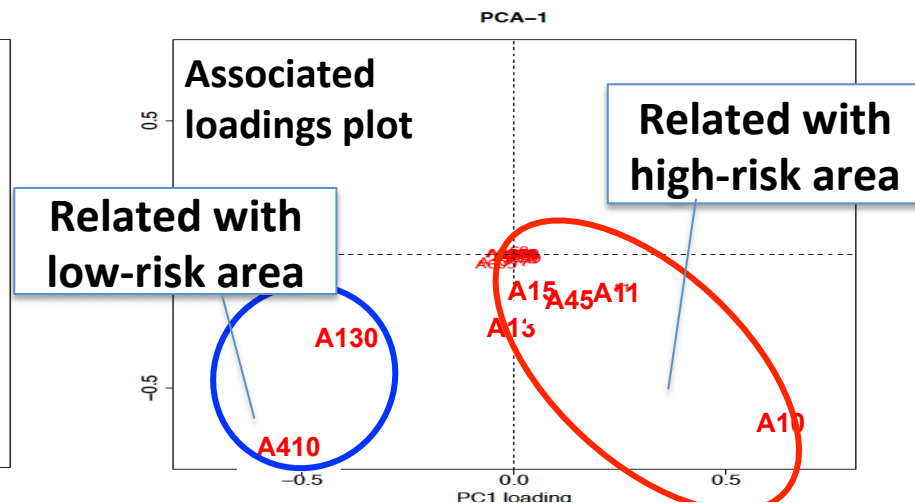
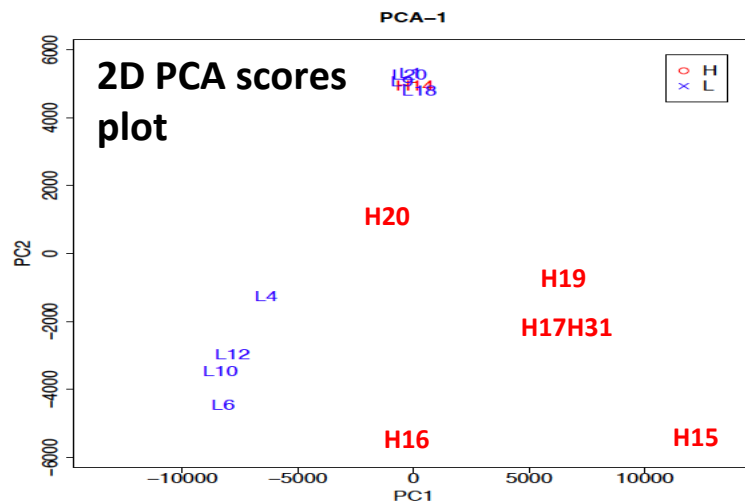
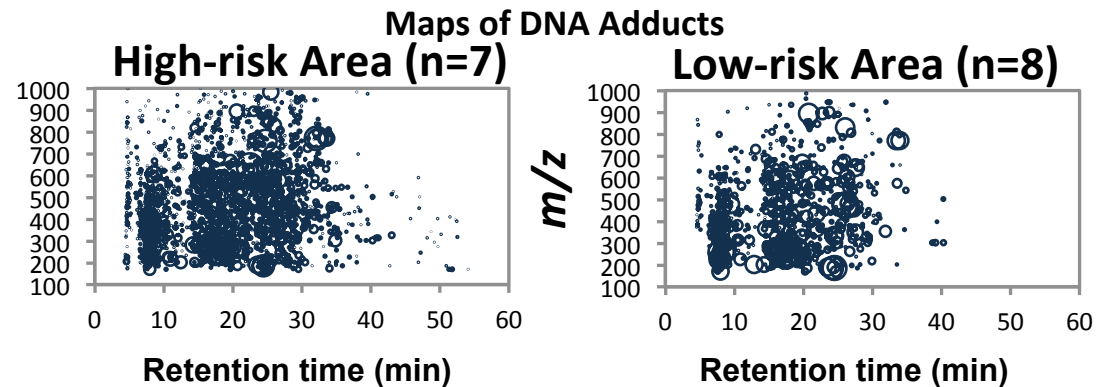


Low-risk

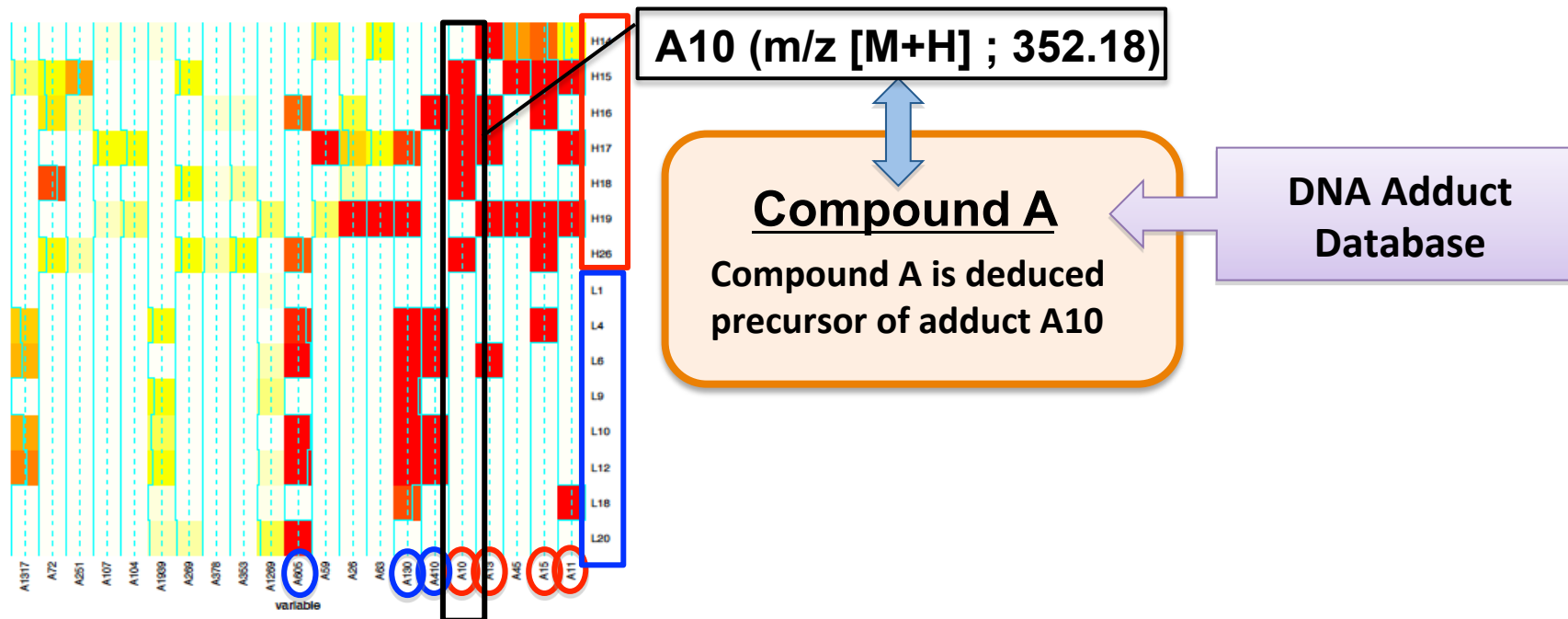


Surgical Specimens

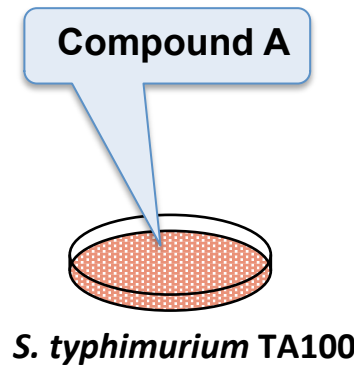
$m/z$



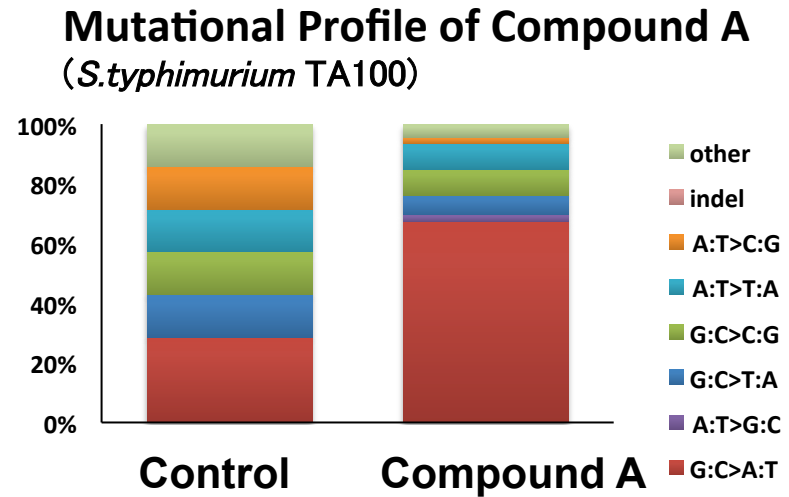
**DNA Adductome Analysis Revealed Adduct A10 Is Specific and/or Abundant in Cases from High-risk Area**



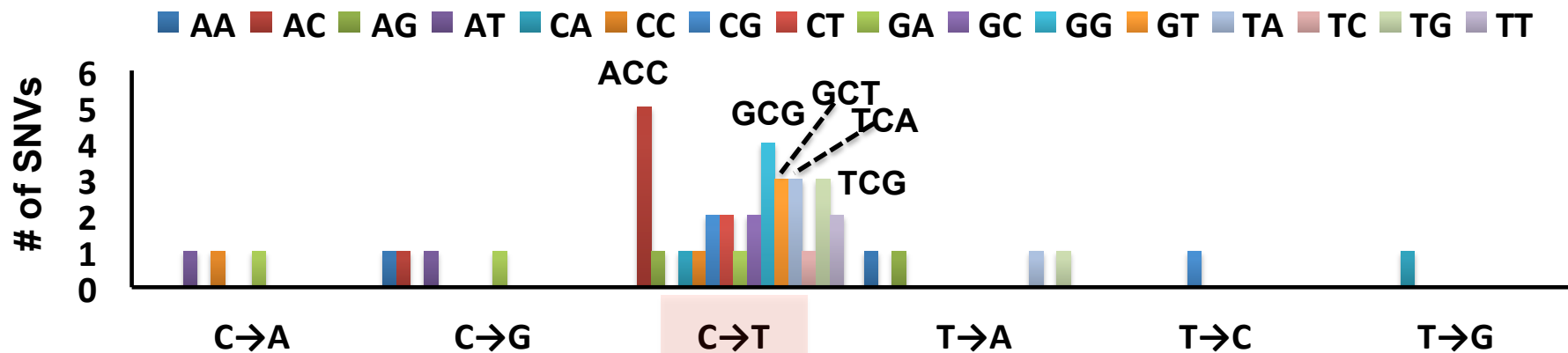
## Global Mutations Analyzed by Next-Generation Sequencing



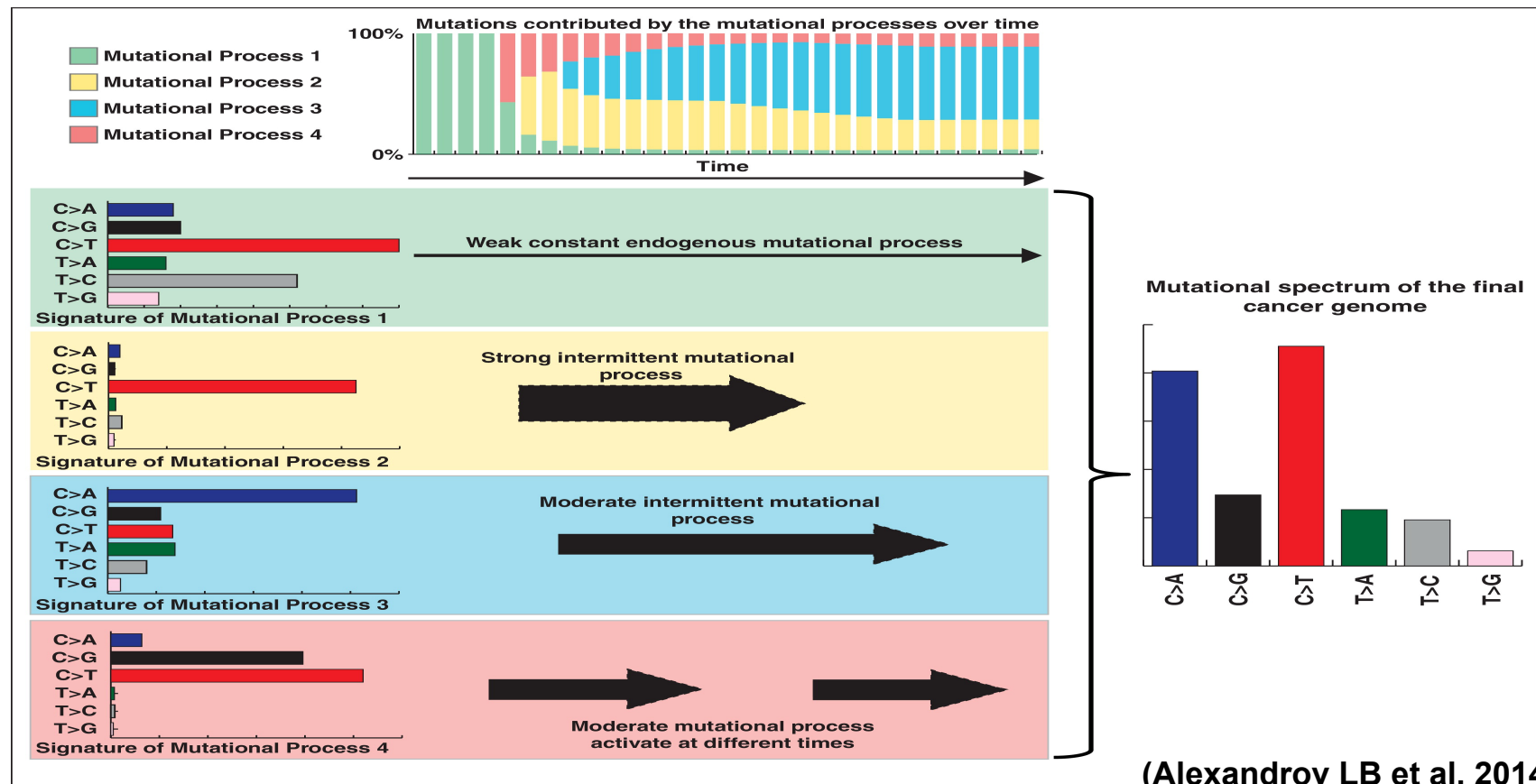
## Whole Genome Sequencing



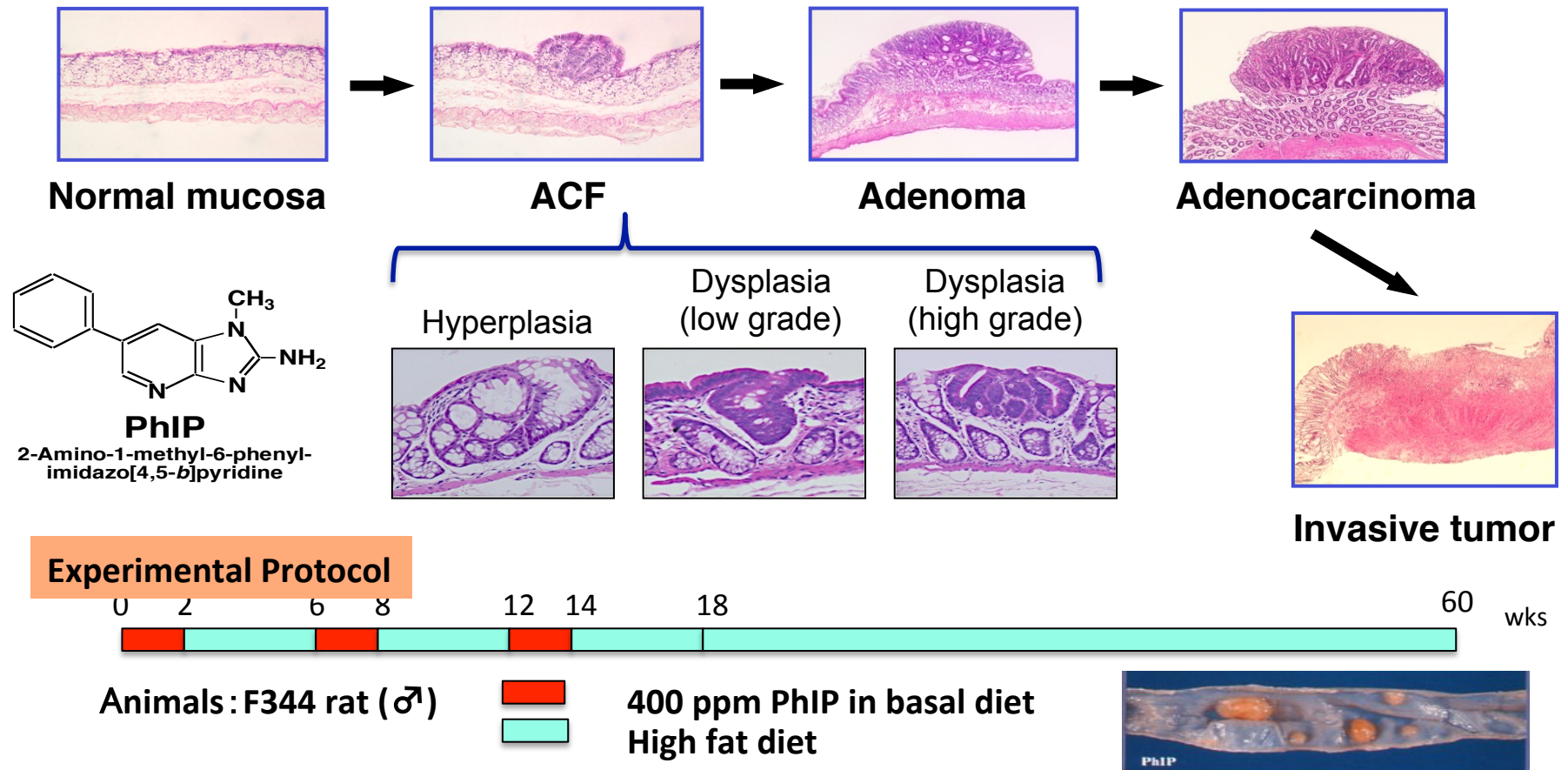
## Trinucleotides Base Substitution Pattern



# Somatic Mutations in Cancer Genomes are the Cumulative Result of the Mutational Processes Over Time

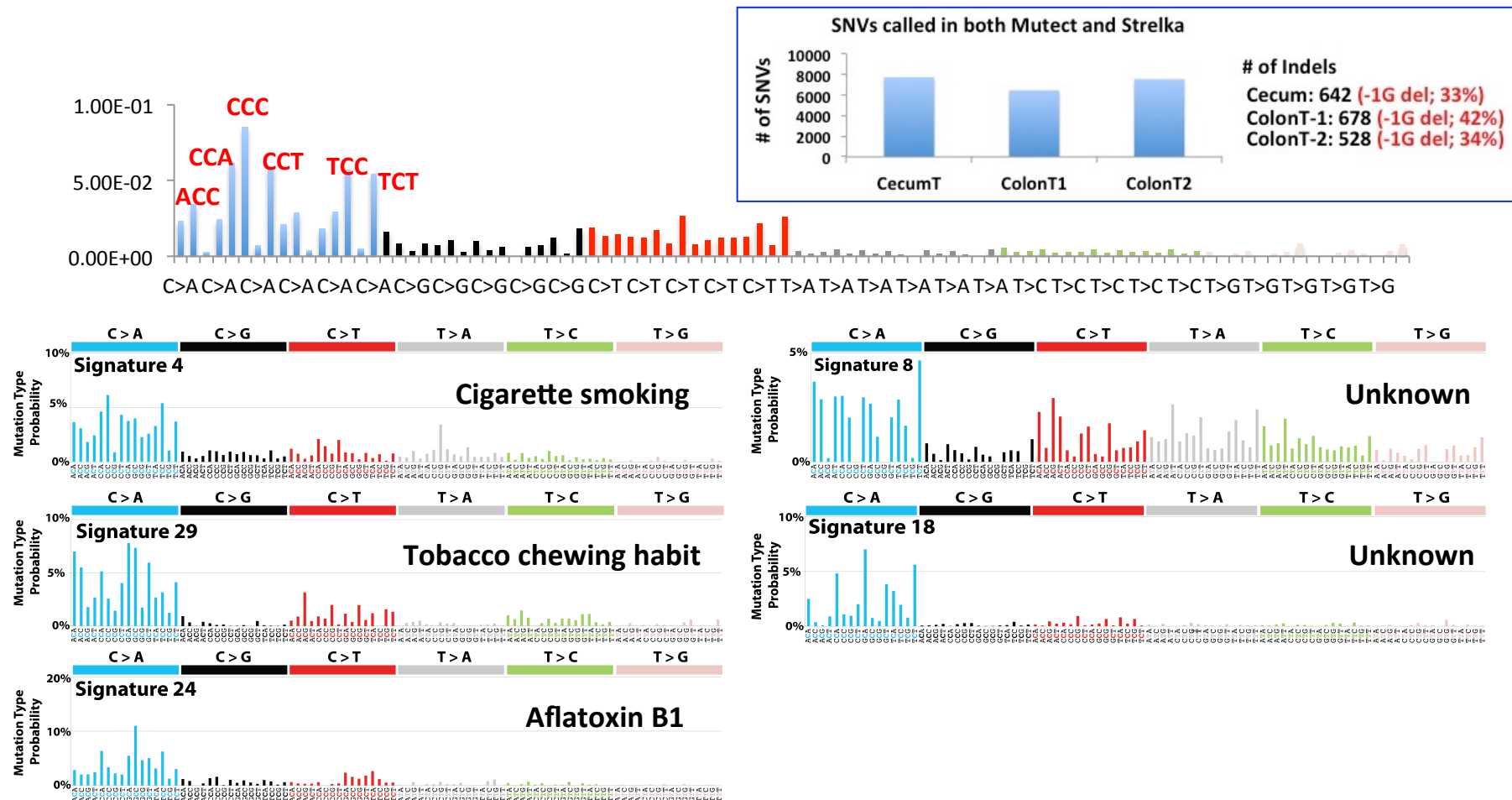


# Chronological Profiles of Mutational Signatures during Sequential Progression of Colonic Lesions in Animal Models





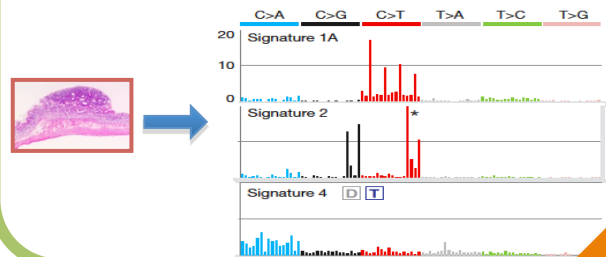
# Trinucleotide Mutational Signature of PhIP-induced Colon Tumor



# A Comprehensive Approach for Exploration of Cancer Etiology

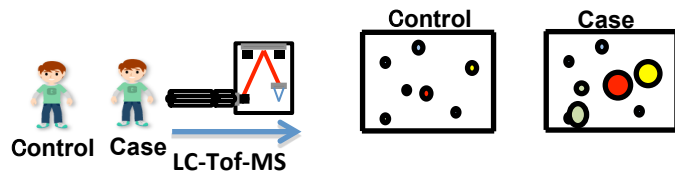
## Genome analysis

Analysis of characteristic mutational signature observed in human cancers



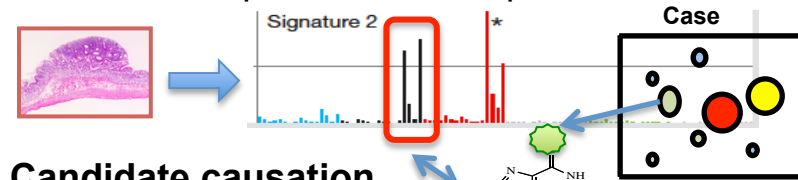
## Adductome analysis

Comprehensive DNA adduct analysis



## Exploration of cancer etiology

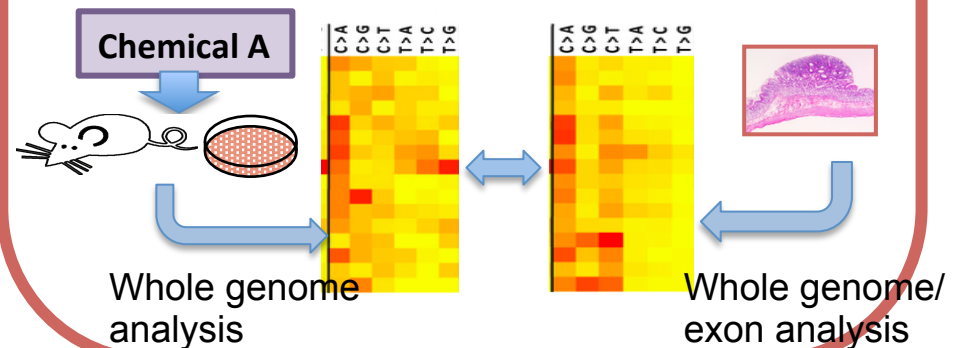
- Identification of DNA adducts, being directly responsible for mutational signatures and multistep cancer development



Candidate causation

Chemical A

- Verification for candidate etiology using genome analysis



# Acknowledgement

## National Cancer Center

### *Cancer Development Systems*

K. Ishino                      N. Uchiya

K. Shiizaki                  H. Sato

S. Akimoto                N. Akiba

A. Ikeda                    H. Nakagama

### *Division of Cancer Genomics*

M. Kato                    F. Hosoda

T. Shibata                Y. Totoki

### *Division of Genome Biology*

K. Shiraishi              T. Kohno

### *Division of Translational Research, Exploratory Oncology Research and Clinical Trial Center*

S. Mimaki                K. Tsuchihara

A. Ochiai                H. Esumi

## Osaka City University Graduate School of Medicine

S. Kubo

## Osaka National Hospital

S. Nakamori

## Aich Medical University School of Medicine

Y. Lin

## Tokyo Agricultural University

Y. Matsushima

## Hebei Cancer Institute

Y. He

B. Shan

## Cancer Institute/Hospital Chinese Academy of Medical Sciences

Y. Qiao

W. Wei

## Cixian Cancer Hospital

G. Song

D. Li