

Analysis of Co-occurring Patterns Among 14 Common Oncogenes in Non-small Cell Lung Cancer

Emily Yajun Zhu MS¹, Yimei Han MS¹, Ricardo Martinez PhD¹, Lisa M. Hess PhD¹
¹Eli Lilly and Company, Indianapolis, USA

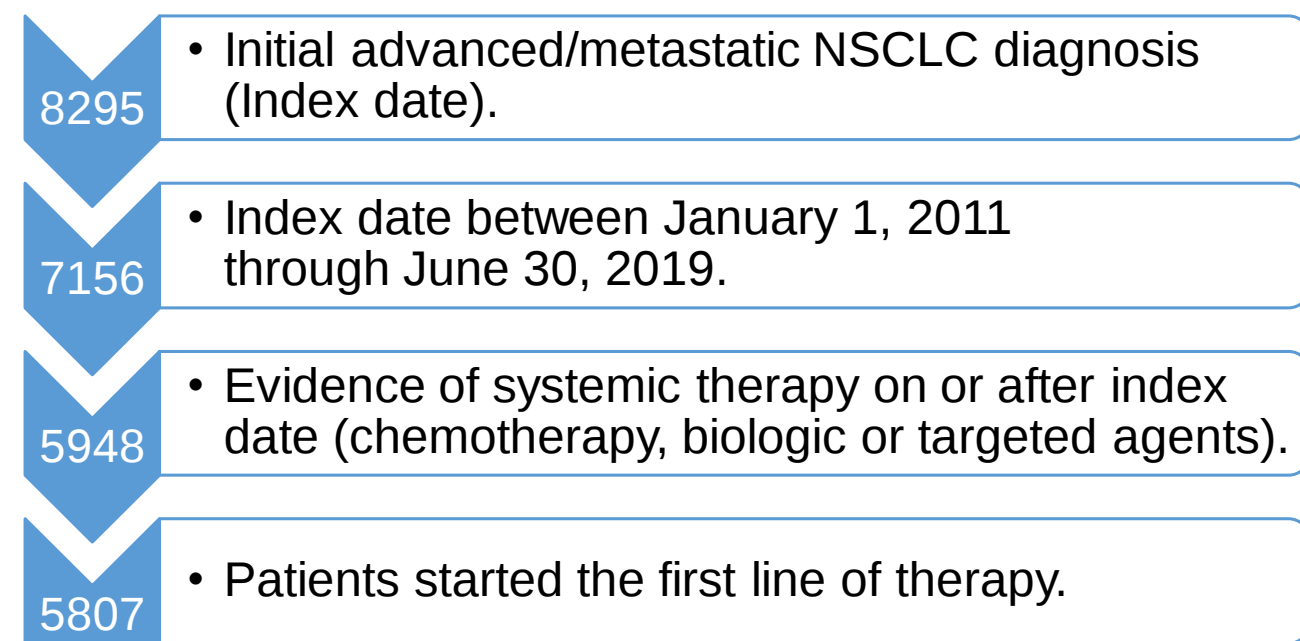
OBJECTIVES

- The study was designed to evaluate co-occurrence patterns of genes known to play a role in the development of non-small cell lung cancer (NSCLC).

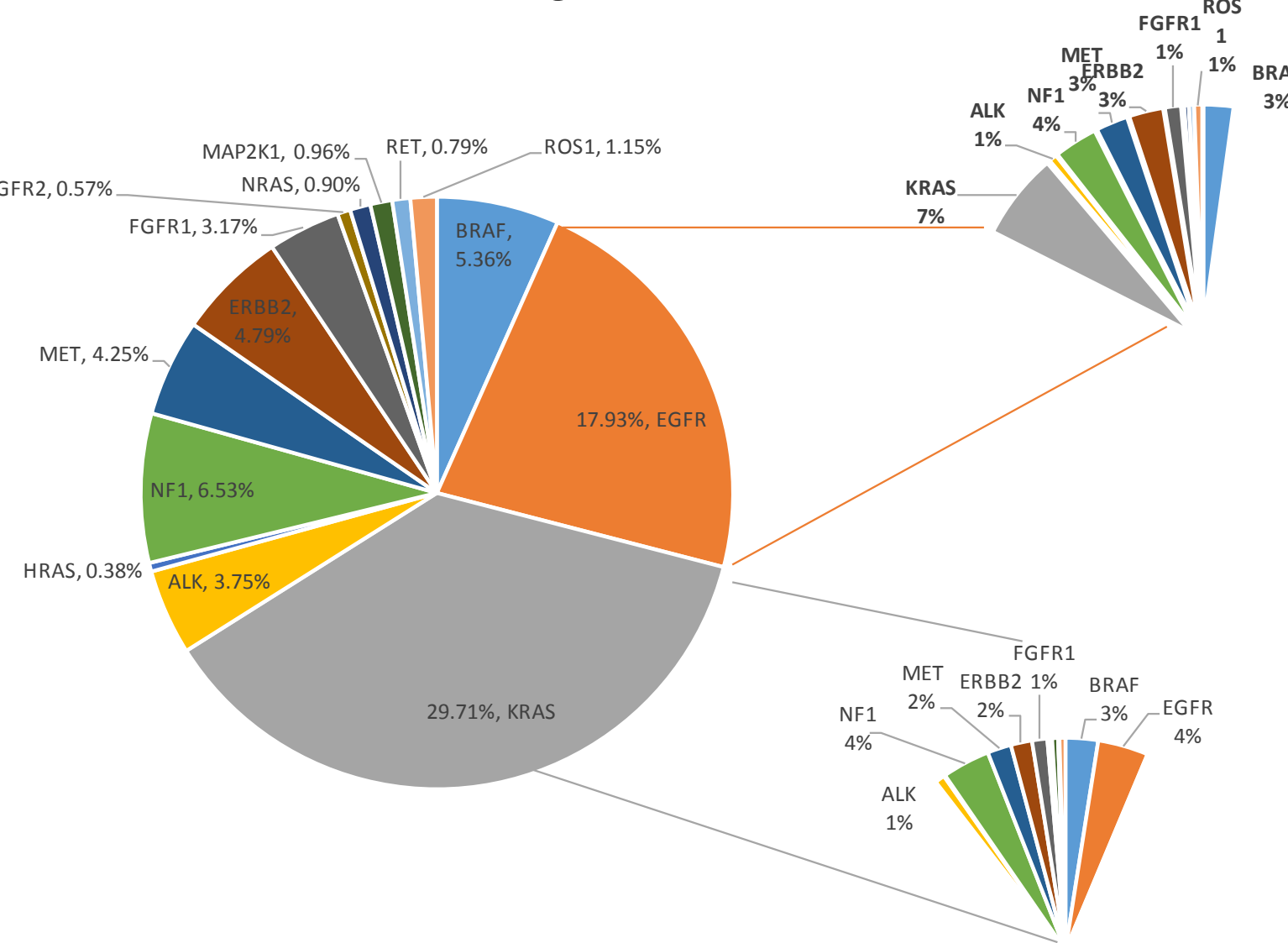
METHODS

- The Flatiron Clinico-Genomic Database (CGDB) is a linked data source including electronic medical record and genomics data from Foundation Medicine, Inc.
- Patients with advanced or metastatic NSCLC were eligible for this study if they received anti-cancer therapy within 180 days after diagnosis.
- 14 common genes known to have activating alterations in NSCLC.
- Pie chart and Spearman Rank correlation matrix were used.

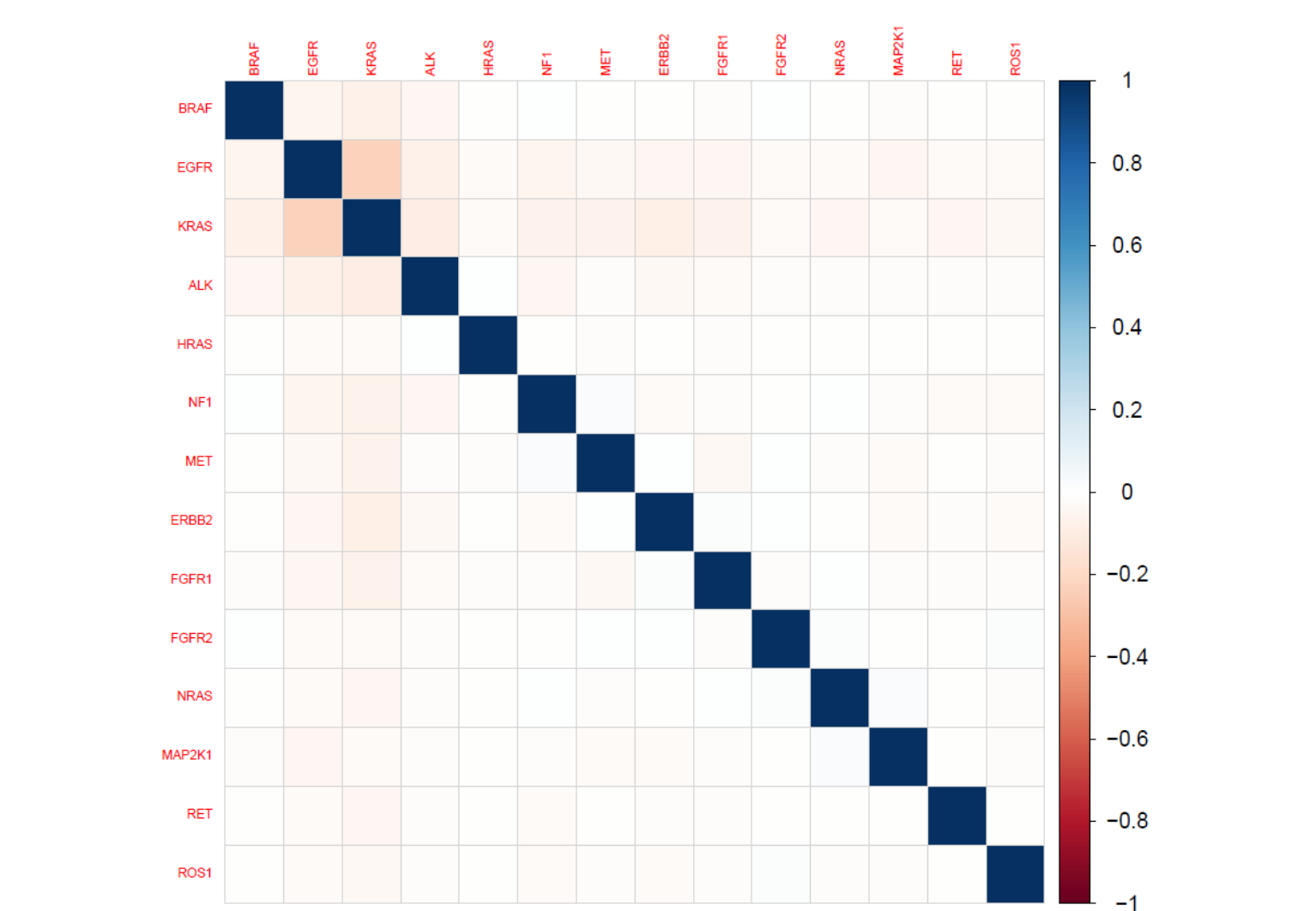
Patient Attrition



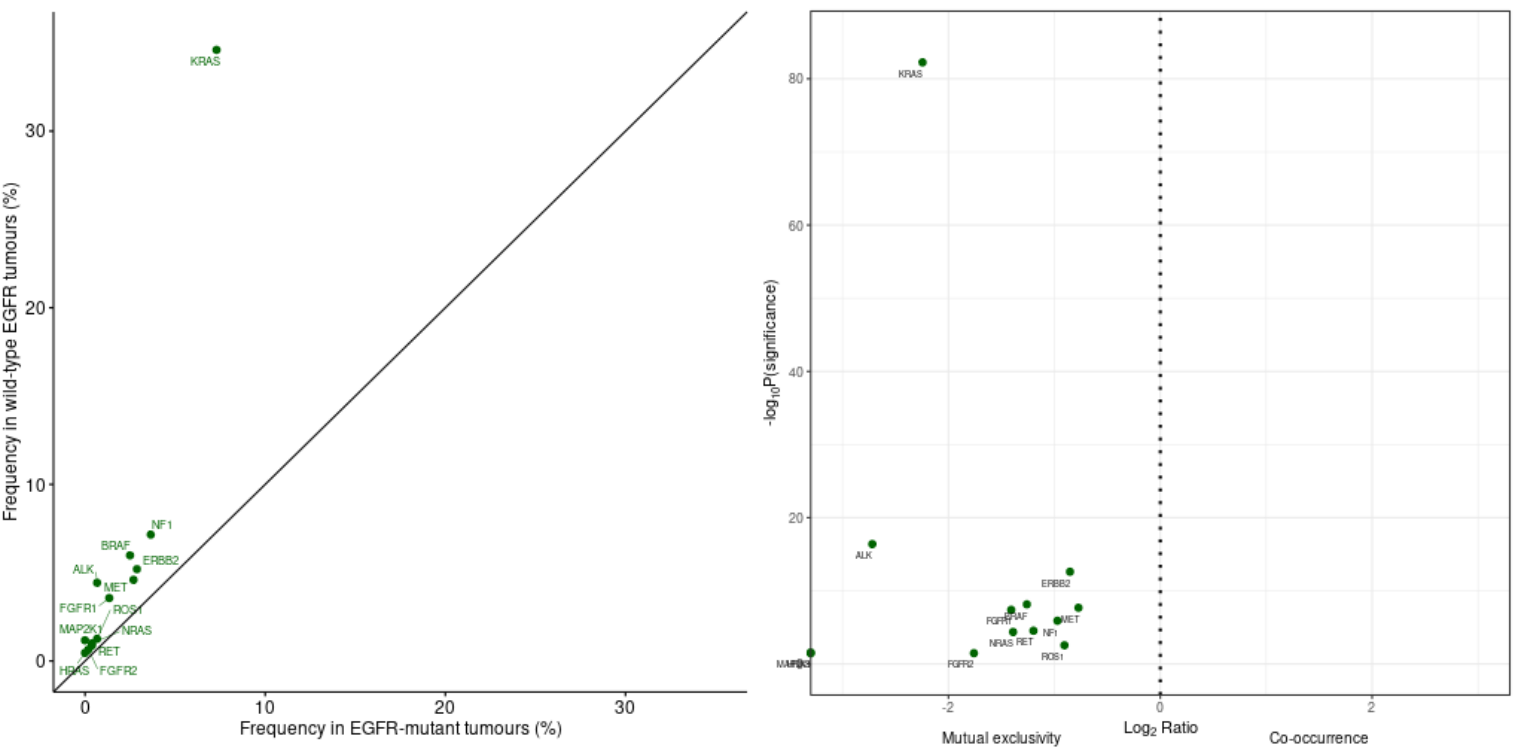
Distribution of 14 Oncogenes



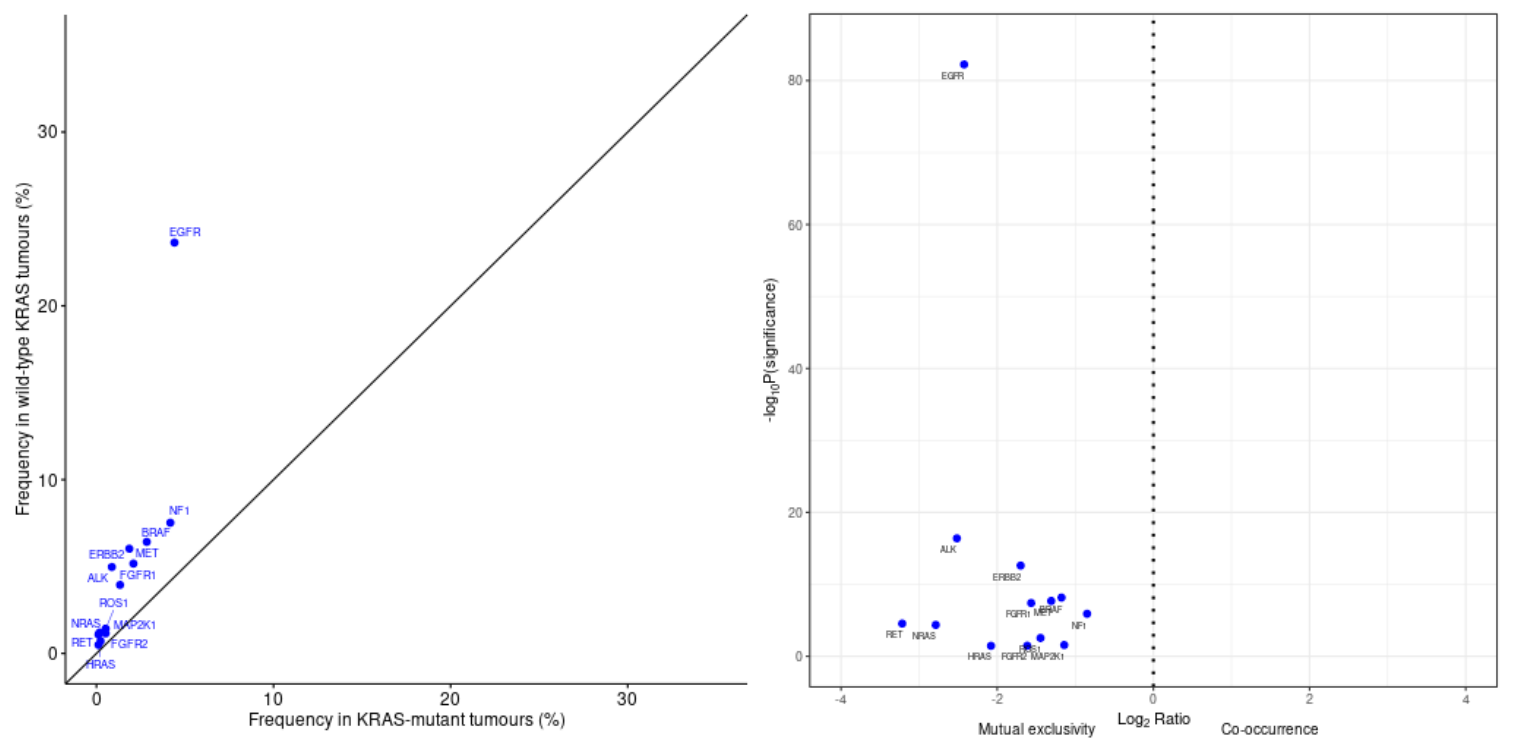
Spearman Rank Correlation Matrix



Spectrum of Co-occurrence in EGFR-Mutant Patients

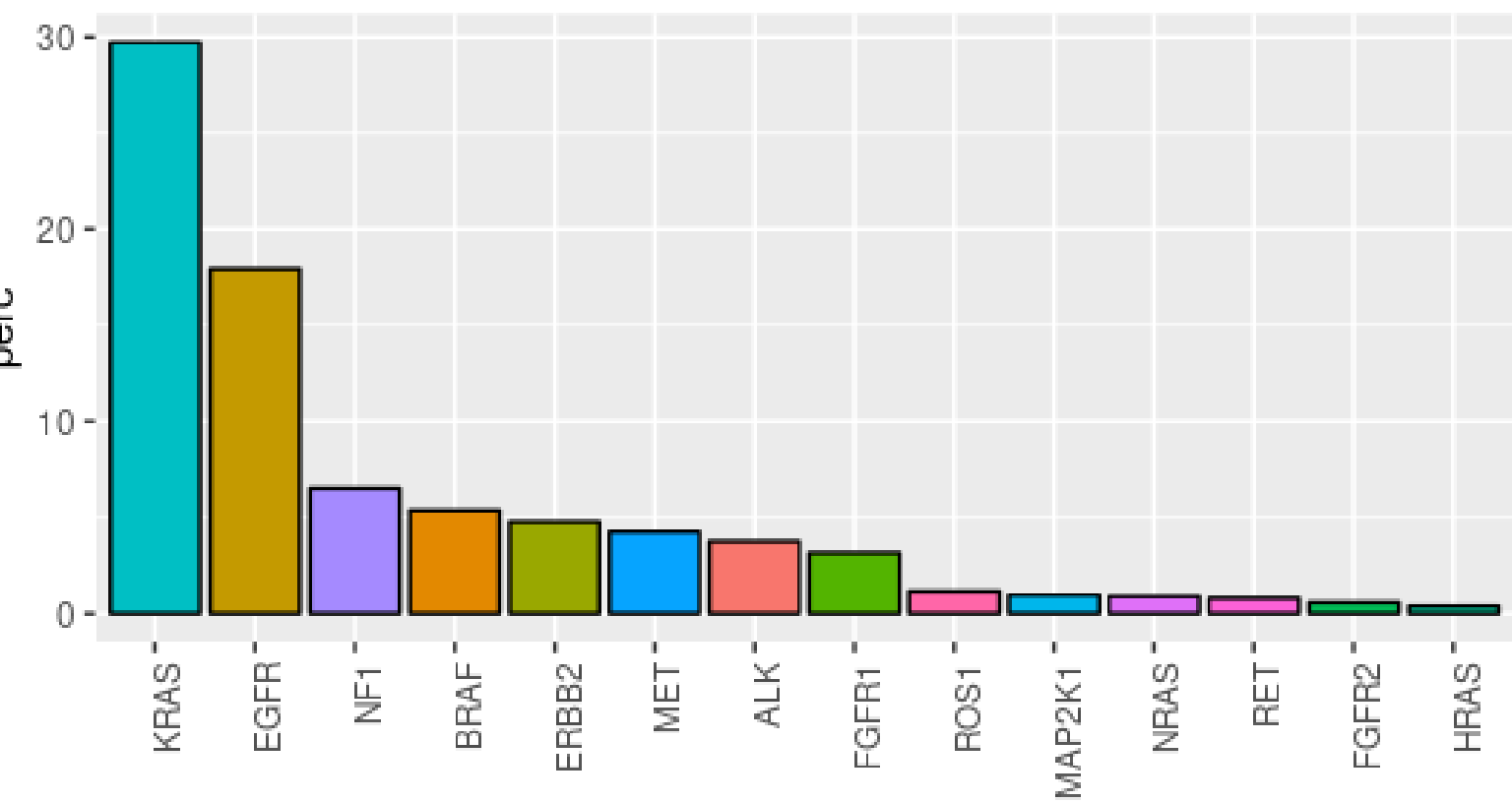


Spectrum of Co-occurrence in KRAS-Mutant Patients



RESULTS

Percentages of 14 Genes



Co-occurring Pattern

Number of Co-occurrence	Frequency	Percentage
0	1763	30.36
1	3483	59.98
2	509	8.77
3	50	0.86
4	2	0.03

CONCLUSIONS

- There are multiple ways (Pie Chart, Correlation Matrix, Volcano plot, etc.) to look at the co-occurrence pattern among gene mutation.
- Each graphic presentation has its own merit. Pie chart is helpful to have an overall view. Correlation matrix helps to observe the strength of pairwise correlation while volcano plot and scatter plot are straightforward to recognize the pattern of mutual exclusivity or co-occurrence.
- The study results show that the 14 common oncogenes share weak correlation one to each other and are mutually exclusive.