

# Abstract 3113: Characterization of *NRG1* gene fusion events in solid tumors

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## Background:

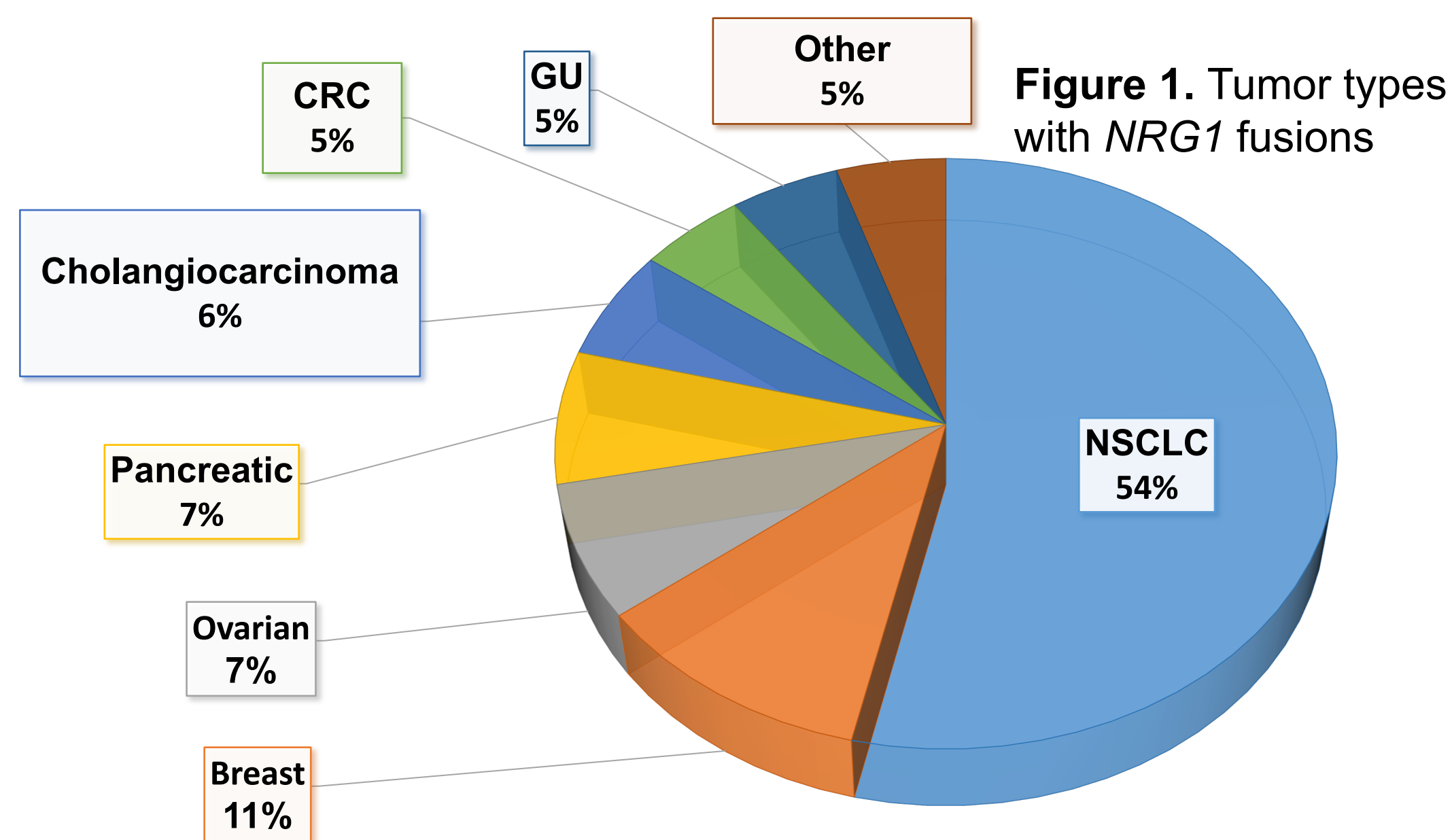
- NRG1* fusions are actionable genomic drivers present in various tumor types. Published reported incidence was 0.2% in an analysis of 16,019 tumor specimens.
- NRG1* gene encodes for neuregulin 1, which serves as a ligand for ErbB3 and ErbB4 receptors, induces dimerization and activates downstream signaling through the MAPK and PI3K-AKT pathways.
- Cancers harboring *NRG1* fusions have responded to ErbB-targeted treatments.

## Methods:

- Retrospective evaluation of tumor specimens tested at a CLIA-certified lab (Caris Life Sciences)
- RNA-sequencing by ArcherDx fusion assay or Caris MI transcriptome sequencing
- NRG1* fusions with  $\geq 3$  junction reads were identified for review and characterization of fusion class, intact functional domains, domain prediction, breakpoints, and frame retention

## Results:

- An updated analysis included 44,570 tumor specimens
- The incidence of *NRG1* fusions remained at 0.2% (n=82)



***NRG1* fusions are detected at a low incidence (0.2%) across tumor types with a diversity of fusion partners.**

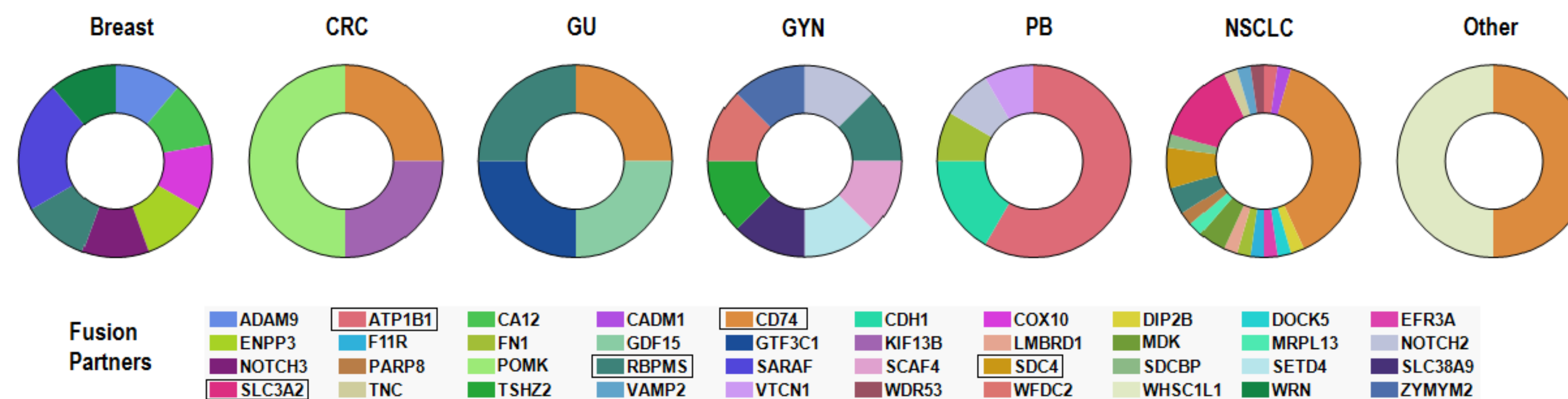


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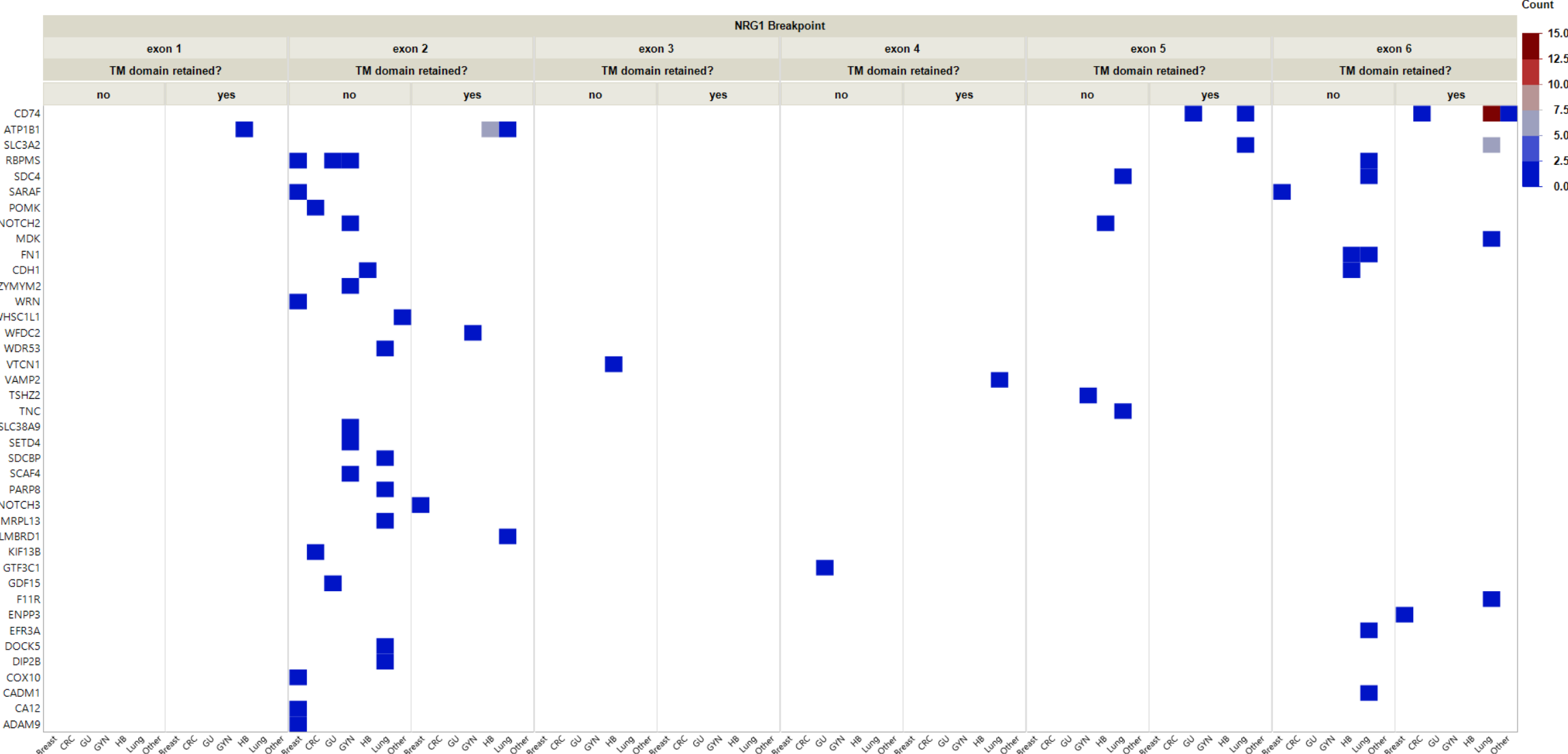
## Figure 2: *NRG1* fusion partners across tumor types

- Notable heterogeneity in fusion partners
- Boxed genes denote the most common fusion partners

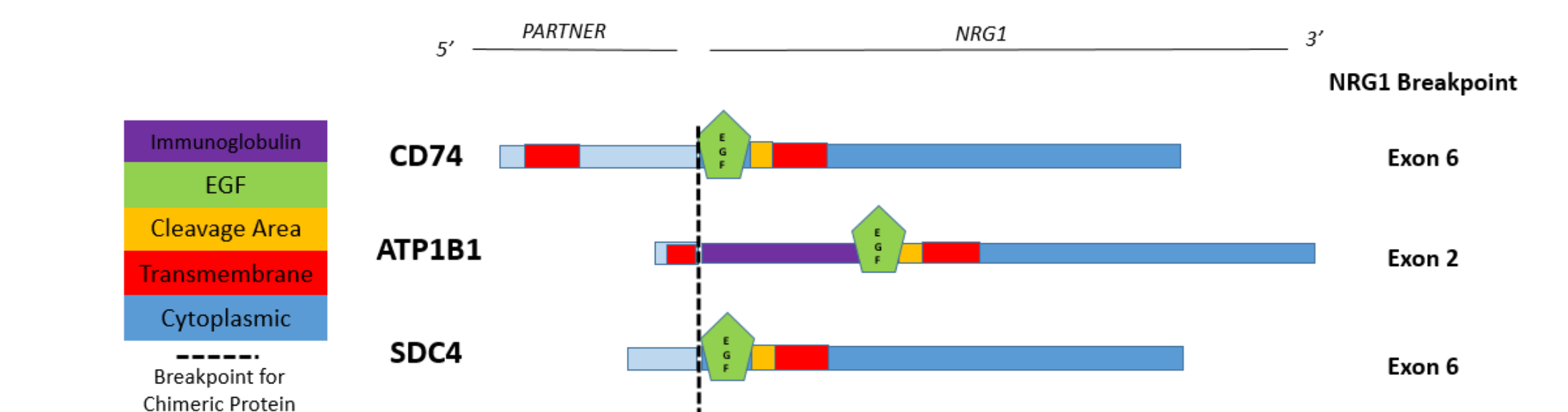


Abbreviations: CRC, colorectal; GU, gynecological; PB, pancreatobiliary; NSCLC, non-small cell lung cancer; Other, sarcoma, unknown primary

## Figure 3: Fusion event characteristics



## Figure 4: Schematic representation of common *NRG1* fusions



## Conclusions:

- In a much larger sample, the incidence of *NRG1* fusions across tumor types remained 0.2% (82/44,570).
- There is notable variation within *NRG1* fusions across tumors. The biologic and clinical significance of this heterogeneity is unclear.
- Therapeutic studies should incorporate *NRG1* fusion variants in any efficacy results.

Reference: Jonna et al, Clin Cancer Res 2019