# Literature Presentation - Colorectal Cancer

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# Multi-omics Approach Reveals Distinct Differences in Left- and Right-Sided Colon Cancer

(genomics, transcriptomics, epigenomics)

# Hypothesis

There is a difference in the underlying molecular features present in left-sided and right-sided colon cancer

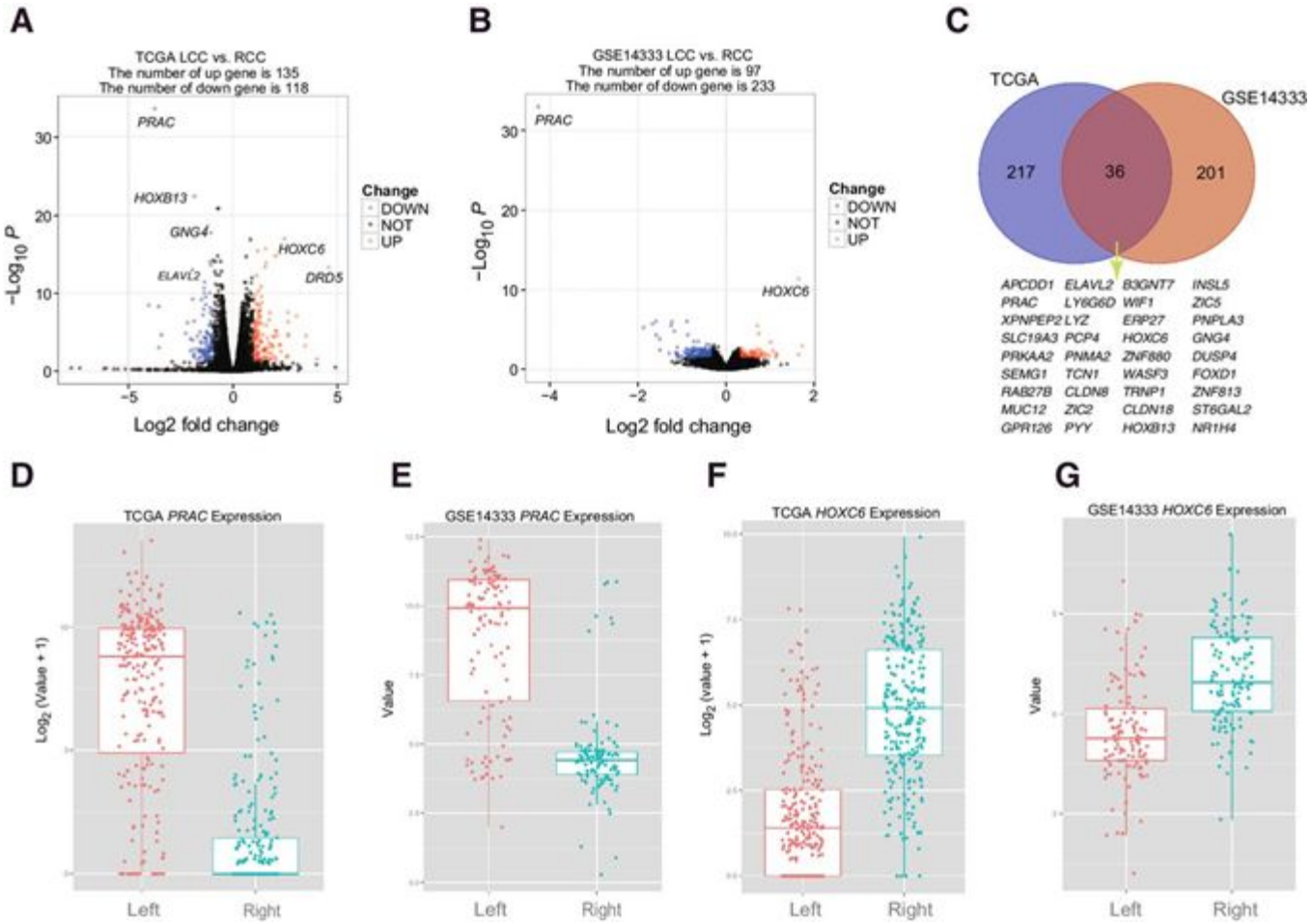
- embryologic origins
- microenvironments
- distinct blood supplies
- patient demographic

# Methodology

- TCGA data portal
- colon adenocarcinoma (COAD) somatic mutation data retrieval and processing
- COAD level three DNA methylation data (HM450k) retrieval and processing
- Gene expression data processing and normalization
- Integrated analysis of miRNAs and mRNAs
- Network construction
- Immunohistochemistry staining

# Main Findings

- Multiple FMGSs were identified in both LCC & RCC, and somatic mutation patterns were identified that co-occurred with certain genes linked to cancer
  - LCC & RCC had distinct driver patterns that should be considered in future targeted cancer therapy.
- Hypermethylation occurred in RCC
  - Changes in DNA methylation status already thought to be involved in colorectal cancer initiation/development
- Oncogenes were overexpressed & tumor-suppressor genes were repressed in RCC
- Difference in non-coding RNAs between LCC & RCC
  - 15 cancer-related miRNA differentially expressed LCC vs RCC
- Pathway alteration differences observed between LCC & RCC linked to growth/migration of cancer cells
- RCCs tend to be more aggressive through orchestrating invasive gene modules

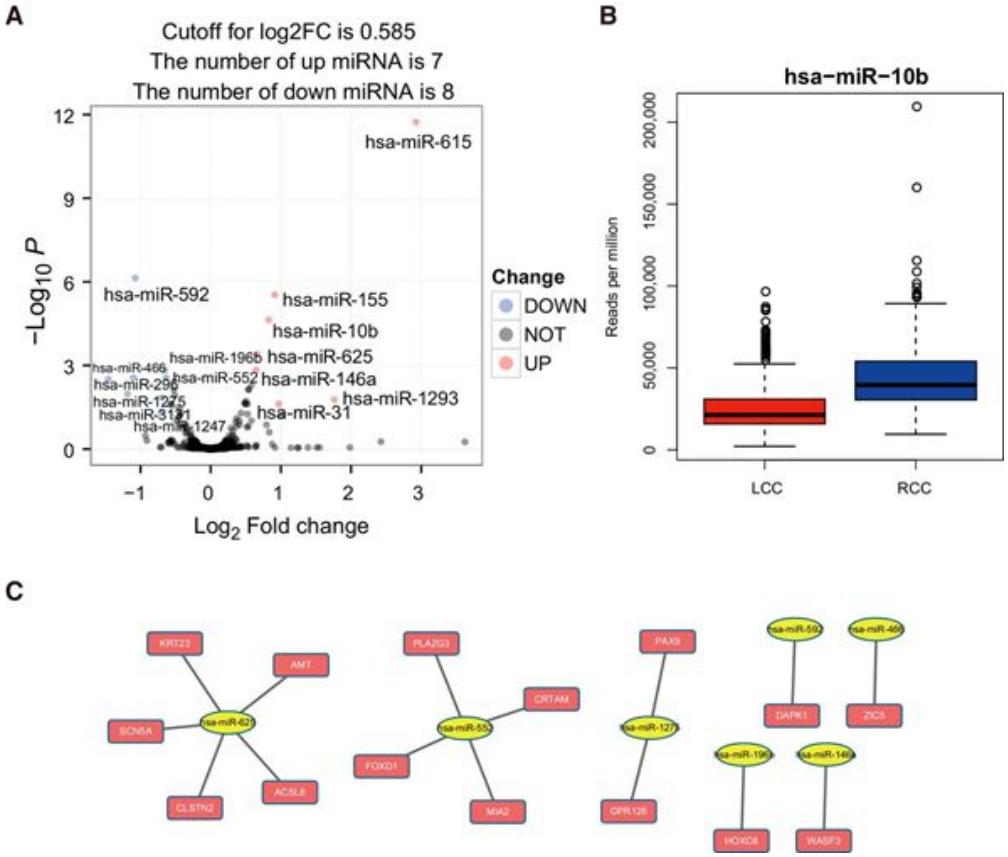



**A/B** - Volcano plots showing overexpressed & underexpressed genes in RCC from 2 different data sets

**C** - Venn diagram for DEGs between the 2 data sets

**D-G** - boxplot distributions of PRAC & HOXC6 expression level

# Figure 2




**A** - Volcano plot showing 11 miRNAs overexpressed, 5 miRNAs underexpressed (TCGA data)

**B** - Box plot showing miR-10b expression level is higher in RCC than LCC

**C** - Integrated analysis using nodes showing some DEGs regulated by miRNA

# Diagnosis and Treatment of Metastatic Colorectal Cancer

(genomic, proteinomic)

# Goals

Find new treatment strategies that use pathologic and molecular tumor testing to select therapy have the potential to improve prognosis of metastatic CRC

- 20% patients have metastatic CRC; 25% patients develop metastases
- 5 year survival rate less than 20%

# Methods

- PubMed and Cochrane databases: randomized clinical trials (RCTs), meta-analyses, and systematic reviews
- US Food and Drug Administration (FDA) documents in the public domain: drugs in treatments
- Evaluated 222 phase 3 RCTs, 111 meta-analyses, 97 systematic reviews, and 4 practice guidelines
- Compared the treatments and their respective results

# Conclusion

- Necessary improvements on molecular/genomic profiling
- Used for more targeted therapies
- Treat specific biological features of tumors
- Greater benefit and less toxicity of treatment

# Questions

- Some median survival rates are only improved by 2 to 4 months while others are extended by over 30 months. Is this a result of certain types of tumors being more aggressive, or are some target treatments simply less effective?
- Combining the findings of the research and review paper, should patients with RCC receive different treatments than those with LCC? Should the RCC treatments be more aggressive?
- What can future researchers do to address the limitations the authors addressed in the review paper?