

Characterization of Sideness-related Differentiated Genetic Alterations in Stage I-IV Colorectal Cancer Patients by using Whole Exome Sequencing

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BACKGROUND

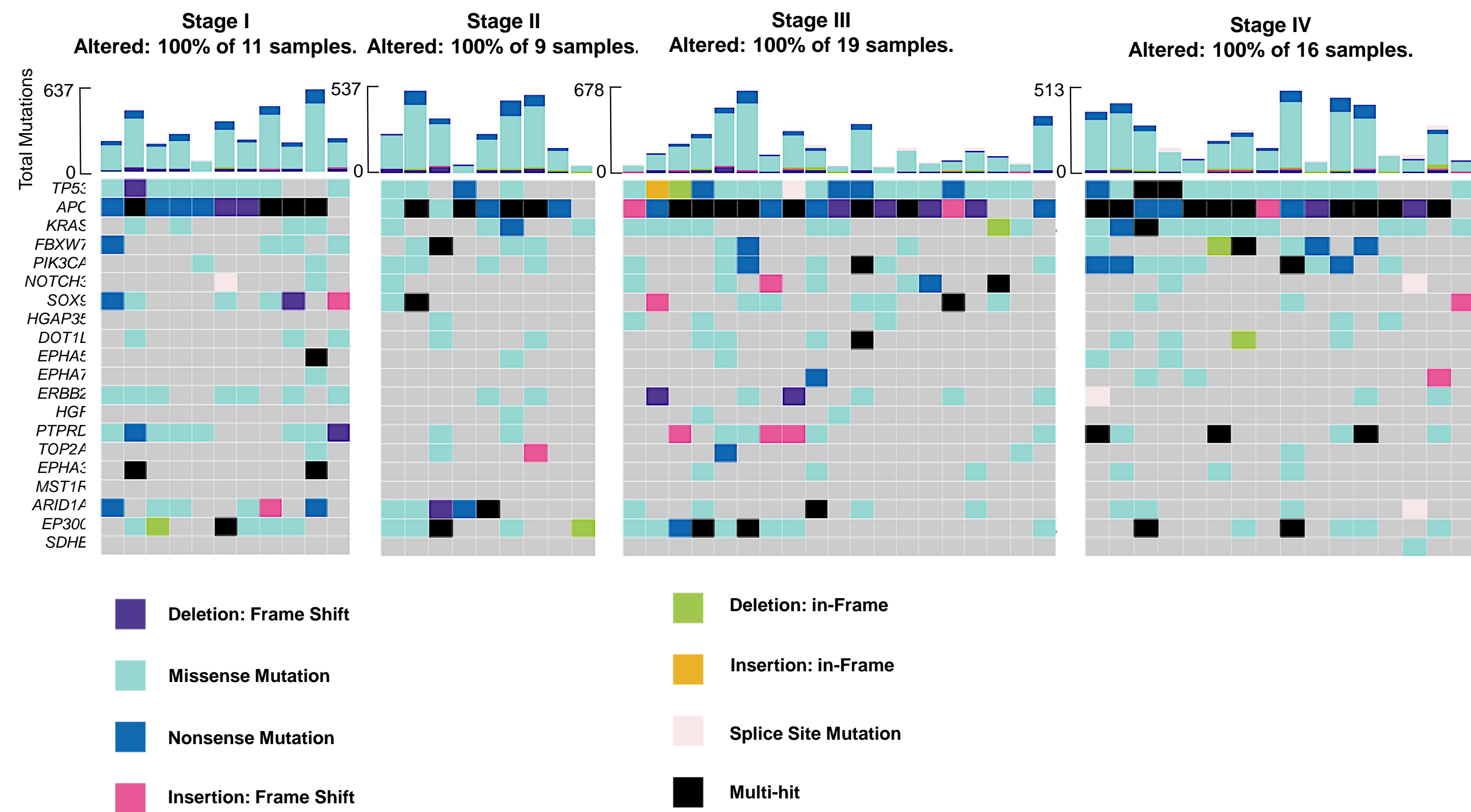
Although constituting a single organ, the right colon and left colon arise from midgut and hindgut embryonic precursors respectively. In the context of these embryonic origins, tumor laterality has been associated with differential microsatellite instability (MSI), aneuploidic karyotype, and loss of heterozygosity between the left and right colon. Differential genetic mutation profiles are not fully characterized in the context of left vs right laterality colorectal cancer (CRC). Therefore, we investigated associations between CRC anatomical site and somatic gene mutation patterns using whole exome sequencing.

METHODS

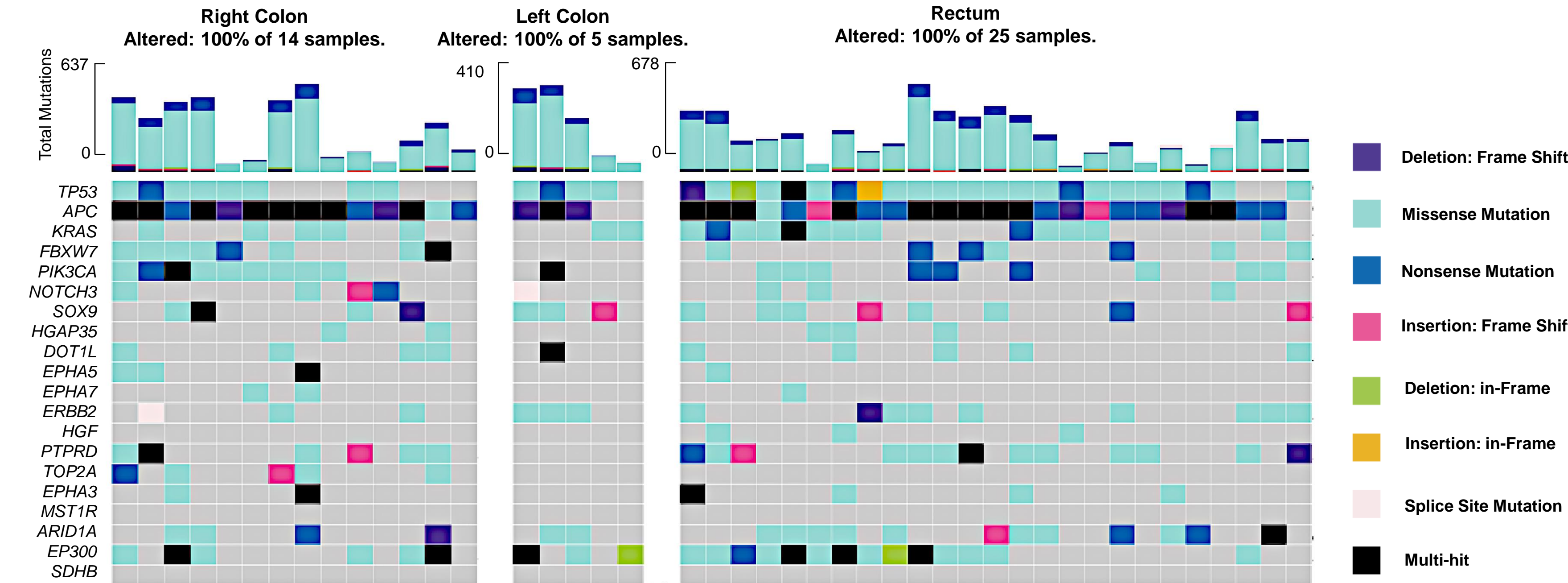
- Whole exome sequencing data were collected from 55 FFPE samples from different stages (stage I: 11, II: 9; III: 19, IV: 16), treatment-naïve CRC patients using the Personalis® tumor-only ImmunoID NeXT Platform^{®1,2}, which captures somatic mutations (SNVs), copy number variants (CNVs), percent MSI in the exome, oncovirus detection, etc.
- The R package maftools was used to identify differential rates of mutation between samples resected from the rectum, left, and right colon respectively. Maftools-derived mutated gene lists, filtered to $p < 0.5$ and odds-ratio > 1 , were assessed for pathway enrichment with Enrichr.

RESULTS

Gene-level mutations stratified by stage



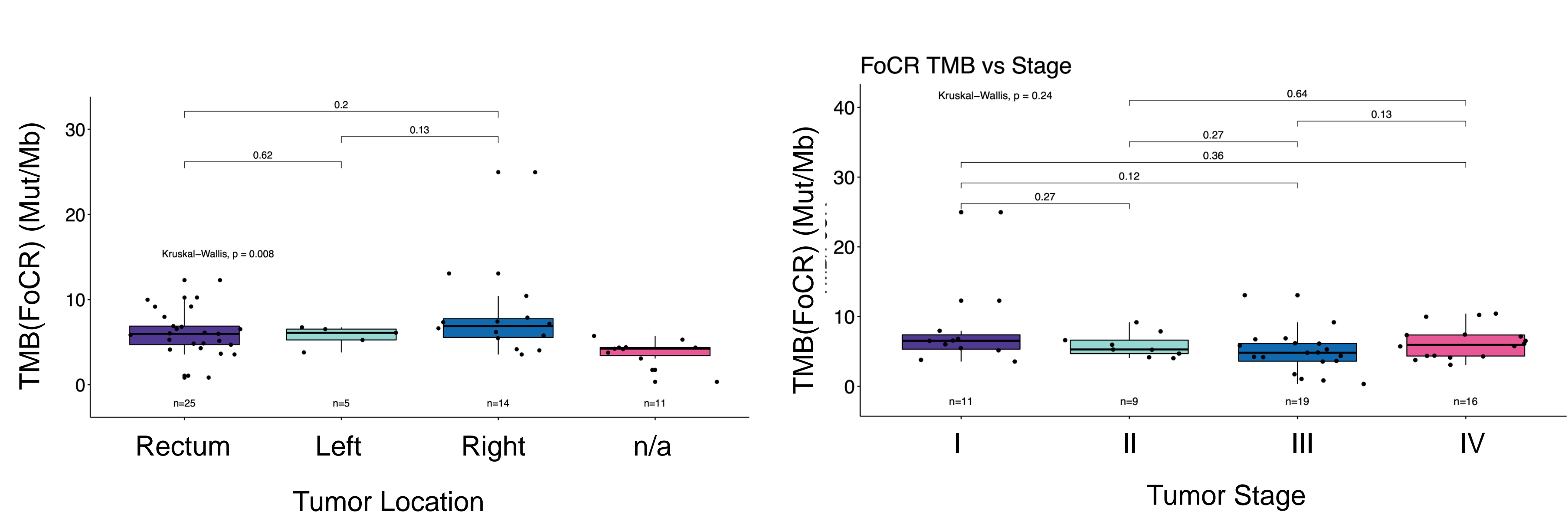
Gene-level mutations stratified by tumor laterality



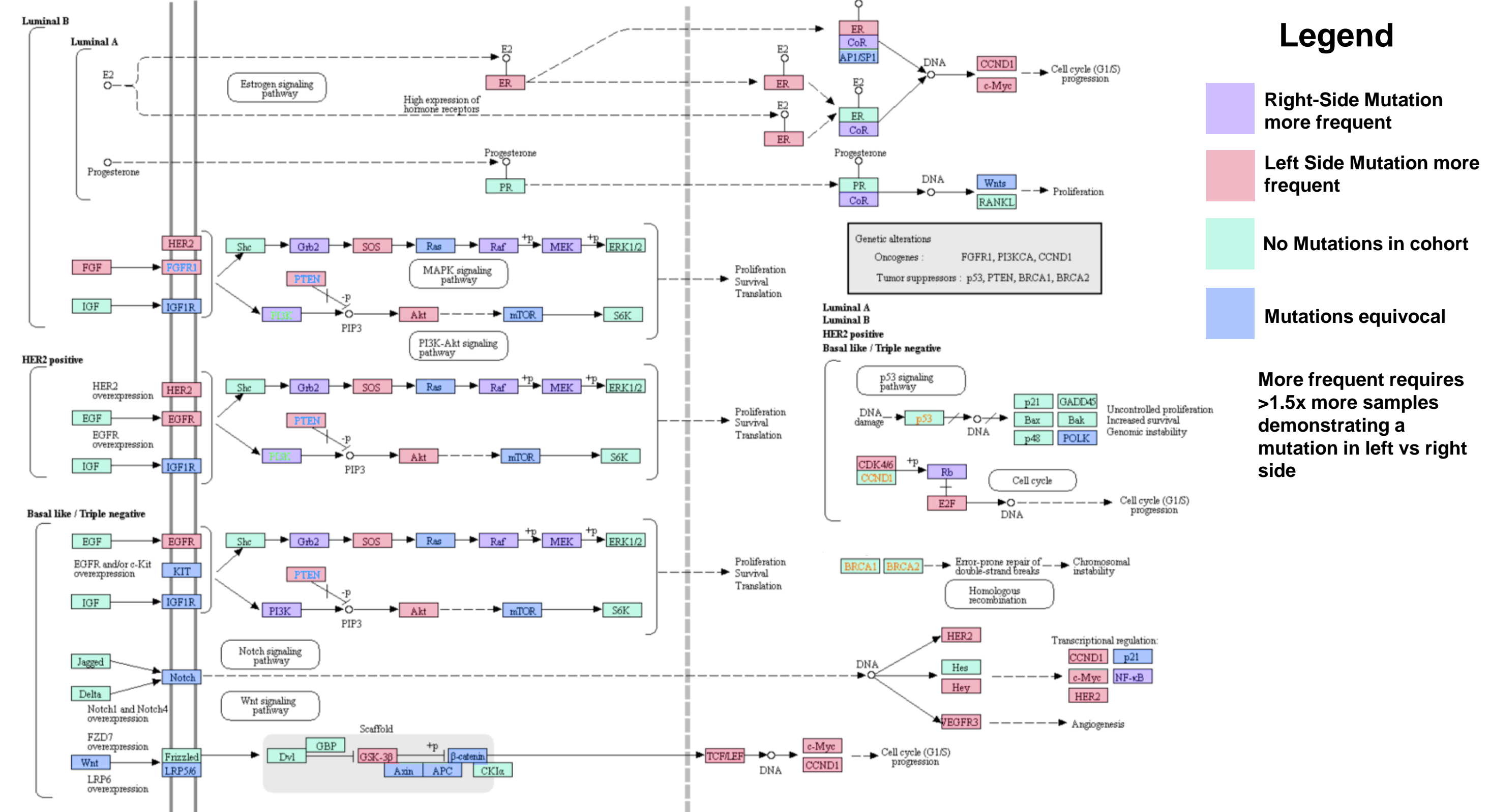
	right	left	rectum	n/a
I	2	2	7	0
II	4	1	4	0
III	3	1	5	10
IV	5	1	5	5

No bias between stage and tumor site (chi-squared, $p = 0.052$) likely driven by "na" (non-annotated tumor site status)

TMB comparable between CRC locations



Estrogen signaling in cancer (KEGG)



CONCLUSIONS

- A statistically significant increase in frequencies of estrogen pathway gene mutations on right-sided tumors, and on PI3K/AKT mutations on rectal tumors, were identified. These are consistent with prior expression-based findings indicating the association of estrogen signaling with right-sided tumors, and increased AKT expression with left-sided CRCs.
- The whole exome sequencing-based laterality associated genetic mutation results provided clinically applicable evidence that patients diagnosed with left versus right CRC tumors may benefit differential treatment therapies, and further investigation is ongoing to explore the potential correlation between tumor laterality and stage.

REFERENCES

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