Release Notes

- PRISSMM™: the BPC CRC dataset uses the PRISSMM™ framework developed at the Dana-Farber Cancer Institute to determine outcomes from retrospective real-world data to ascertain cancer treatment responses in the real world. Additional information can be found in the analytic data guide and information about licensing PRISSMM™ can be obtained by emailing PRISSMM@mskcc.org

- **Pathologic information**: Each pathology specimen from diagnosis through death or last follow-up is curated with specimen type, site, and histology.

- **Imaging information**: Each CT, MRI, PET-CT scan from diagnosis through death or last follow-up is curated for the presence or absence of cancer and an evaluation of whether the cancer was stable, responding, or progressing.

- **Medical oncologist’s evaluations**: Medical oncology notes (1/month) have been curated to ascertain the presence or absence of cancer and whether the cancer was stable, responding, or progressing.

- **Additional relevant biomarkers**: Information about select biomarkers not included on the NGS panels, including PDL1, MMR and MSI, are also curated.

- Colorectal cancer diagnosis is considered the index tumor for this patient cohort. There are data about other cancer diagnoses antecedent to the colorectal and subsequent to the colorectal diagnosis.
GENIE Data Model

- Demographics
- Smoking status
- Vital status
- Pancancer
  - PDL1
  - MSI
- Cancer-specific

OUTCOMES

- rxOS
- rxDFS
- rxPFS
- rxTTNT
- rxTTD
- rxTTR

Treatments

- Rx
  - INN
  - Start date
  - Stop date

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BPC CRC 2.0-public Cohort

CRC

2014 ≤ NGS ≤2018

BPC Phase 1 Institutions

Eligible & randomly selected

1,485 final cohort

Cancer Types

 Colon Adenocarcinoma 71%
 Rectal Adenocarcinoma 19%
 Colorectal Adenocarcinoma 7%
 Other 3%

Cancer Types

 Colon Adenocarcinoma 71%
 Rectal Adenocarcinoma 19%
 Colorectal Adenocarcinoma 7%
 Other 3%

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BPC CRC 2.0-public Demographics

Age at Diagnosis

Sex

Primary Race

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BPC CRC 2.0-public: Sites of Metastases at Diagnosis

Patients with Distant Metastases at Diagnosis
- Yes: 704 (47%)
- No: 784 (53%)

Location of Metastasis
- Liver: 54%
- Other: 17%
- Lung: 14%
- Lymph Nodes: 8%
- Bone: 3%
- Subcutaneous Tissue: 2%
- Adrenal: 1%
- Brain: 1%
- Pleura: <1%
- Subcutaneous Tissue: 2%

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www.aacr.org/bpc_crc  #aacrgenie GENIE BPC CRC 2.0-public
# BPC CRC 2.0-public: Detailed Clinical Genomics

## Mutated Genes (1551 profiled samples)

<table>
<thead>
<tr>
<th>Gene</th>
<th># Mut</th>
<th>#</th>
<th>Freq</th>
</tr>
</thead>
<tbody>
<tr>
<td>APC</td>
<td>1.810</td>
<td>1,114</td>
<td>74.9%</td>
</tr>
<tr>
<td>TP53</td>
<td>1.187</td>
<td>1,107</td>
<td>71.4%</td>
</tr>
<tr>
<td>KRAS</td>
<td>678</td>
<td>669</td>
<td>43.1%</td>
</tr>
<tr>
<td>PIK3CA</td>
<td>367</td>
<td>327</td>
<td>21.1%</td>
</tr>
<tr>
<td>SMAD4</td>
<td>247</td>
<td>224</td>
<td>15.1%</td>
</tr>
<tr>
<td>LRP1B</td>
<td>52</td>
<td>27</td>
<td>14.8%</td>
</tr>
<tr>
<td>KMT2D</td>
<td>336</td>
<td>208</td>
<td>14.0%</td>
</tr>
<tr>
<td>FBXW7</td>
<td>226</td>
<td>203</td>
<td>13.7%</td>
</tr>
<tr>
<td>COL7A1</td>
<td>40</td>
<td>35</td>
<td>12.5%</td>
</tr>
<tr>
<td>BRAF</td>
<td>200</td>
<td>190</td>
<td>12.3%</td>
</tr>
<tr>
<td>SOX9</td>
<td>200</td>
<td>174</td>
<td>11.7%</td>
</tr>
<tr>
<td>PTPRS</td>
<td>108</td>
<td>85</td>
<td>11.5%</td>
</tr>
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</table>

## Structural Variant Genes (253 profiled samples)

<table>
<thead>
<tr>
<th>Gene</th>
<th># SV</th>
<th>#</th>
<th>Freq</th>
</tr>
</thead>
<tbody>
<tr>
<td>APC</td>
<td>19</td>
<td>19</td>
<td>7.5%</td>
</tr>
<tr>
<td>TP53</td>
<td>14</td>
<td>14</td>
<td>5.5%</td>
</tr>
<tr>
<td>CTNNB1</td>
<td>13</td>
<td>13</td>
<td>5.1%</td>
</tr>
<tr>
<td>BRAF</td>
<td>8</td>
<td>7</td>
<td>2.8%</td>
</tr>
<tr>
<td>PRKN</td>
<td>6</td>
<td>6</td>
<td>2.4%</td>
</tr>
<tr>
<td>SMAD4</td>
<td>4</td>
<td>4</td>
<td>1.6%</td>
</tr>
<tr>
<td>TCF7L2</td>
<td>4</td>
<td>4</td>
<td>1.6%</td>
</tr>
<tr>
<td>PBRM1</td>
<td>4</td>
<td>4</td>
<td>1.6%</td>
</tr>
<tr>
<td>NTRK1</td>
<td>4</td>
<td>4</td>
<td>1.6%</td>
</tr>
<tr>
<td>ATM</td>
<td>3</td>
<td>3</td>
<td>1.2%</td>
</tr>
<tr>
<td>PTEN</td>
<td>3</td>
<td>3</td>
<td>1.2%</td>
</tr>
<tr>
<td>NF1</td>
<td>3</td>
<td>3</td>
<td>1.2%</td>
</tr>
</tbody>
</table>

## CNA Genes (1487 profiled samples)

<table>
<thead>
<tr>
<th>Gene</th>
<th>Cytoband</th>
<th>CNA</th>
<th>#</th>
<th>Freq</th>
</tr>
</thead>
<tbody>
<tr>
<td>ARFRP1</td>
<td>20q13.33</td>
<td>AMP</td>
<td>19</td>
<td>10.4%</td>
</tr>
<tr>
<td>FGF14</td>
<td>13q33.1</td>
<td>AMP</td>
<td>16</td>
<td>8.8%</td>
</tr>
<tr>
<td>RTEL1</td>
<td>20q13.33</td>
<td>AMP</td>
<td>20</td>
<td>5.3%</td>
</tr>
<tr>
<td>FLT3</td>
<td>13q12.2</td>
<td>AMP</td>
<td>73</td>
<td>4.9%</td>
</tr>
<tr>
<td>BCL2L1</td>
<td>20q11.21</td>
<td>AMP</td>
<td>67</td>
<td>4.5%</td>
</tr>
<tr>
<td>MYC</td>
<td>8q24.21</td>
<td>AMP</td>
<td>67</td>
<td>4.5%</td>
</tr>
<tr>
<td>SRC</td>
<td>20q11.23</td>
<td>AMP</td>
<td>52</td>
<td>4.3%</td>
</tr>
<tr>
<td>FLT1</td>
<td>13q12.3</td>
<td>AMP</td>
<td>61</td>
<td>4.1%</td>
</tr>
<tr>
<td>CDK8</td>
<td>13q12.13</td>
<td>AMP</td>
<td>49</td>
<td>4.1%</td>
</tr>
<tr>
<td>TOP1</td>
<td>20q12</td>
<td>AMP</td>
<td>37</td>
<td>4.0%</td>
</tr>
<tr>
<td>AGO2</td>
<td>8q24.3</td>
<td>AMP</td>
<td>15</td>
<td>4.0%</td>
</tr>
<tr>
<td>DNMT3B</td>
<td>20q11.21</td>
<td>AMP</td>
<td>28</td>
<td>3.8%</td>
</tr>
</tbody>
</table>

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Top 12 Mutated Genes CRC 2.0-public

# Samples per Patient

Profiled in Copy-number alterations

- APC: 76%
- TP53: 72%
- KRAS: 44%
- PIK3CA: 22%
- SMAD4: 18%
- KMT2D: 14%
- FBXW7: 14%
- BRAF: 12%
- SOX9: 12%
- ARID1A: 11%
- ATM: 11%
- NOTCH1: 9%

Genetic Alteration:
- Inframe Mutation (putative driver)
- Inframe Mutation (unknown significance)
- Missense Mutation (putative driver)
- Missense Mutation (unknown significance)
- Truncating Mutation (putative driver)
- Truncating Mutation (unknown significance)
- Structural Variant (putative driver)
- Structural Variant (unknown significance)
- Amplification
- Deep Deletion
- No alterations
- Not profiled

# Samples per Patient

Profiled in Copy-number alterations

- Yes: 3
- No:

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Clinically Actionable Genes CRC 2.0-public

# Samples per Patient
- Profiled in Copy-number alterations
  - BRAF: 12%
  - KRAS: 44%
  - NRAS: 6%
  - NTRK1: 4%
  - NTRK3: 4%
  - NTRK2: 3%
- Profiled in Structural variants

Genetic Alteration
- Inframe Mutation (putative driver)
- Inframe Mutation (unknown significance)
- Missense Mutation (putative driver)
- Missense Mutation (unknown significance)
- Splice Mutation (unknown significance)
- Truncating Mutation (unknown significance)
- Structural Variant (putative driver)
- Structural Variant (unknown significance)
- Amplification
- Deep Deletion
- No alterations
- Not profiled

# Samples per Patient
- 0
- 3

Profiling in Copy-number alterations
- Yes
- No

Profiling in Structural variants
- Yes

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Chakravarty et al., JCO PO 2017
BPC CRC 2.0-public: Complete Treatment Histories

Number of cancer-directed drug regimens curated for each patient

Cancer-directed Drug Regimens (Includes regimens ever received for CRC irrespective of line or stage)

<table>
<thead>
<tr>
<th>Regimen</th>
<th># of patients</th>
</tr>
</thead>
<tbody>
<tr>
<td>FOLFOX</td>
<td>1172</td>
</tr>
<tr>
<td>FOLFOX + Bevacizumab</td>
<td>702</td>
</tr>
<tr>
<td>FOLFIRI</td>
<td>853</td>
</tr>
<tr>
<td>FOLFIRI + Bevacizumab</td>
<td>665</td>
</tr>
</tbody>
</table>

- Individual regimens can be calculated from the raw data found [here](#) on Synapse
- Treatment history for non-index cancers can be found [here](#) on Synapse

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www.aacr.org/bpc_crc  #aacrgenie  GENIE BPC CRC 2.0-public
BPC CRC 2.0-public: Comprehensive Patient View

Sample Patient

Pathology Reports

Disease Status by Medical Oncology Note and by Imaging

www.aacr.org/bpc_crc  #aacrgenie  GENIE BPC CRC 2.0-public

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BPC CRC 2.0-public: High Quality Clinical Data

- PFS-M = 12.9 months
- PFS-I = 10.3 months

* PFS-M and PSF-I are available by regimen for those regimens containing greater than 10 patients

* Not adjusted for delayed entry
BPC CRC 2.0-public: OS by Stage

OS from Diagnosis

- (A) Stage I
- (B) Stage II
- (C) Stage III
- (D) Stage IV

OS all stages= 62.7 months

*not adjusted for delayed entry
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Cynthia Chu
Shirin Pillai

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Jessica Lavery
Samantha Brown
Axel Martin
Michael Curry

Ken Kehl
Asha Postle
Ashley Newcomb
Kevin Haigis
John Orechia
Daniel Quinn
Simon Arango Baquero

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