**Supplementary Methods**

Microsatellite instability (MSI) Status

Tumor MSI status was analyzed using polymerase chain reaction (PCR) assays by all studies with the exception of NSHDS and EPIC\_Sweden. Study-specific marker panels for PCR-based MSI assays are provided in **Supplementary Table S2**. CCFR, CPS-II, HPFS, MCCS, NFCCR, and NHS used the Bethesda Consensus Panel (1) with minor variability (2-6). In DACHS (7), a mononucleotide marker panel, which has high concordance with the Bethesda Consensus Panel for the detection of MSI-high status, was used. In DALS (8), a panel of two mononucleotide and ten tetranucleotide repeats was used, and that panel has shown high concordance with the Bethesda Panel for MSI-high detection (9). For these PCR-based methods, high-level MSI (MSI-high) was defined as presence of instability in ≥30% of markers. EPIC\_Sweden and NSHDS (10) used immunohistochemical detection of deficiency for mismatch repair (MMR) proteins MLH1, MSH2, MSH6, and PMS2 (following protein nomenclature recommendations by an expert panel) (11). In EDRN, both immunohistochemistry (MLH1, MSH2, MSH6, and PMS2) and PCR (seven-marker panel) were performed to determine MMR status (12). Because studies have shown high concordance of the PCR-based test (for the detection of high-level MSI) and immunohistochemistry-based test (for the detection of MMR protein loss) (13), tumors with MMR protein loss were included as MSI-high tumors. In TCGA, we utilized MSI status designations based on calls using mSINGS (14) on sequencing data and previously published TCGA calls (15, 16). Tumors with valid data by MSI (or MMR) testing that did not show MSI-high status (or MMR protein loss) were categorized as “non-MSI-high”, which included both MSI-low and microsatellite stable tumors.

CpG island methylator phenotype (CIMP) Status

CIMP status was determined by methylation assay using different panels across studies (**Supplementary Table S3**). In CCFR, CPS-II, EPIC\_Sweden, HPFS, MCCS, NHS, and NSHDS, MethyLight assay (17) was used to determine CIMP status. CPS-II, HPFS, and NHS used an eight-gene panel; CCFR and MCCS used a five-gene panel. DALS and DACHS used methylation-specific PCR assays and different panels of five CpG islands. For TCGA data, we utilized CIMP status as determined using an array-based method. We created two CIMP categories for this analysis: CIMP-high and CIMP-low/negative. The CIMP-positive status in a certain study (18) was shown to be nearly equivalent to the CIMP-high status in other studies (17, 19).

*BRAF* and *KRAS* Mutation Status

For *BRAF*, the CCFR, CPS-II, MCCS, and NFCCR evaluated *BRAF* (c.1799T>A, p.V600E) mutations using a fluorescent allele-specific PCR assay (20, 21). DACHS used both Sanger sequencing and immunohistochemical analysis of p.V600E expression to determine *BRAF* mutation status (22). DALS evaluated *BRAF* mutations using Sanger sequencing (23). EDRN tested *BRAF* c.1799T>A mutations status using primarily real-time PCR. HPFS and NHS performed PCR and pyrosequencing to identify *BRAF* codon 600 mutation (24). NSHDS and EPIC\_Sweden used real-time PCR using an allelic discrimination assay (10) to detect *BRAF* c.1799T>A mutations. In TCGA, we utilized *BRAF* codon 600 mutation data, as previously described (16).

For *KRAS*, the CCFR, CPS-II, DALS, NSHDS, and EPIC\_Sweden used Sanger sequencing to assess mutations in *KRAS* codons 12 and 13 (10, 25-27). DACHS determined *KRAS* mutation status by a single stranded conformational polymorphism technique or by Sanger sequencing (28). EDRN tested for *KRAS* codons 12, 13, and 61 primarily using Sanger sequencing. MCCS used real-time PCR with high resolution melting analysis, followed by Sanger sequencing for positive tumors to identify *KRAS* codons 12 and 13 mutations (29). HPFS and NHS performed PCR and pyrosequencing to identify *KRAS* mutations in codons 12, 13, 61, and 146 (30). In TCGA, we utilized *KRAS* mutation data for codons 12, 13, 59, 61, 117, 146, as previously described (16). In this study, for data harmonization, *KRAS* mutation positivity was defined as the presence of any mutation in *KRAS* codon 12 or 13.

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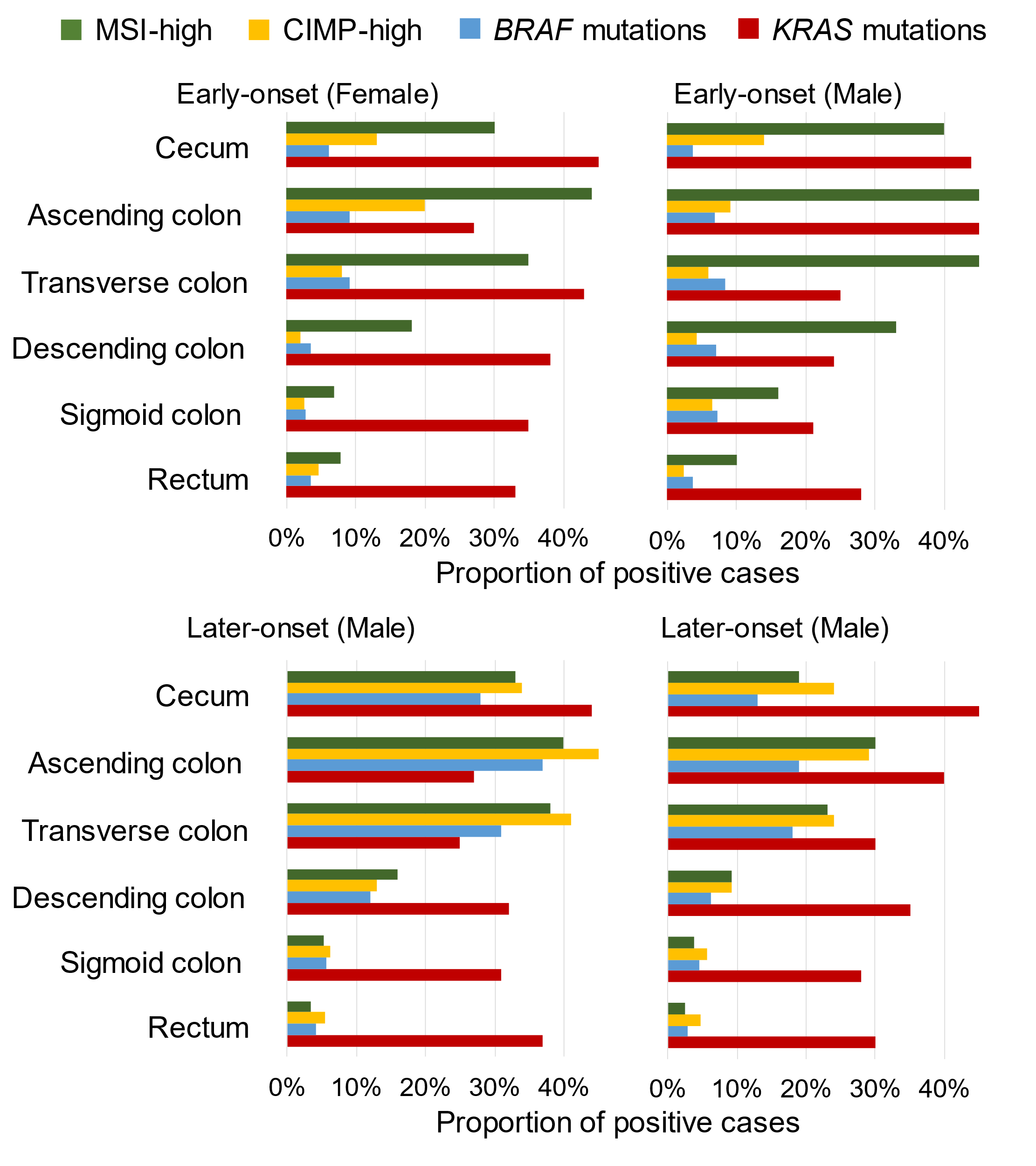
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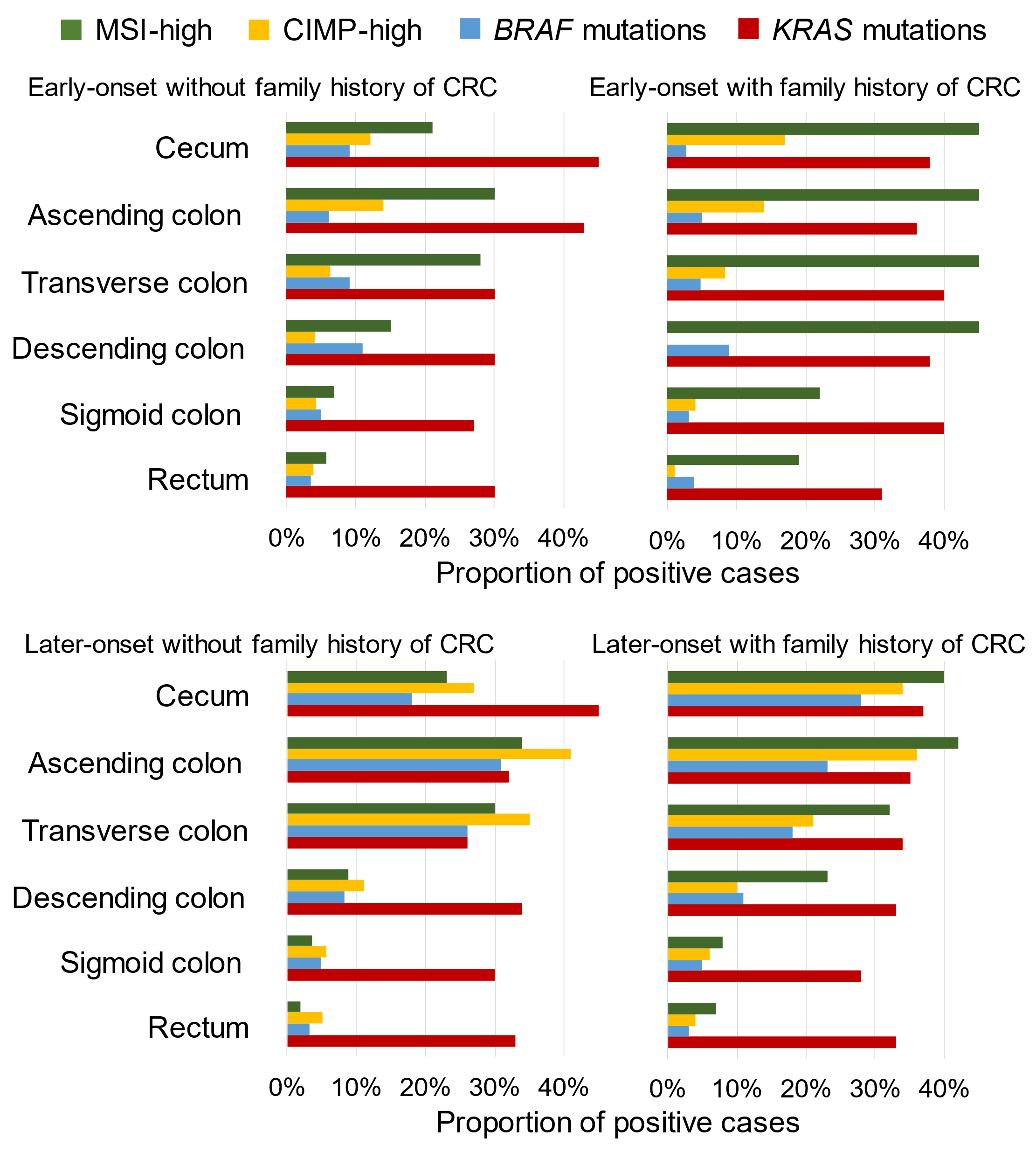
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Supplementary Figure 1. Prevalence of MSI-High Status, CIMP-High Status, *BRAF* Mutations, and *KRAS* Mutations along Sublocations by Sexes.

Abbreviations: CIMP, CpG island methylator phenotype; MSI, microsatellite instability.



Supplementary Figure 2. Prevalence of MSI-High Status, CIMP-High Status, *BRAF* Mutations, and *KRAS* Mutations along Sublocations by Family History of Colorectal Cancer.

Abbreviations: CIMP, CpG island methylator phenotype; MSI, microsatellite instability.

Supplementary Table 1. Patients and Molecular Characteristics of Colorectal Cancer According to Participating Studies

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Patients characteristics\* | N | CCFR | CPS II | DACHS | DALS | EDRN | EPIC\_  Sweden | HPFS | MCCS | NFCCR | NHS | NSHDS | TCGA |
| All cases | 14004 | 6491 | 856 | 2007 | 1071 | 218 | 137 | 607 | 482 | 547 | 784 | 311 | 493 |
| Sex |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Female | 6712 (48%) | 3166 (49%) | 421 (49%) | 842 (42%) | 483 (45%) | 85 (39%) | 58 (42%) | 0 (0%) | 224 (46%) | 216 (39%) | 784 (100%) | 196 (63%) | 237 (48%) |
| Male | 7292 (52%) | 3325 (51%) | 435 (51%) | 1165 (58%) | 588 (55%) | 133 (61%) | 79 (58%) | 607 (100%) | 258 (54%) | 331 (61%) | 0 (0%) | 115 (37%) | 256 (52%) |
| Mean age ± SD | 62·7±12·5 | 54.2±12.3 | 74·1±6·5 | 68·8±10·8 | 65·4±9·5 | 62·6±12·5 | 64·0±7·7 | 70·5±8·8 | 67·8±8·4 | 60·0±9·3 | 67·0±8·5 | 64·6±8·2 | 65·8±12·7 |
| Family history of CRC |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Absent | 9421 (81%) | 4192 (66%) | 658 (85%) | 1700 (86%) | 898 (84%) | 189 (87%) | N/A | 481 (79%) | 400 (83%) | 454 (90%) | 646 (84%) | 297 (96%) | 358 (86%) |
| Present | 2,167 (19%) | 2190 (34%) | 114 (15%) | 269 (14%) | 173 (16%) | 28 (13%) | N/A | 126 (21%) | 82 (17%) | 51 (10%) | 119 (16%) | 11 (4%) | 59 (14%) |
| Primary tumor location |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Cecum | 2142 (15%) | 922 (14%) | 174 (20%) | 228 (11%) | 257 (24%) | 32 (15%) | 20 (15%) | 123 (20%) | 58 (12%) | 90 (16%) | 114 (15%) | 43 (14%) | 81 (16%) |
| Ascending  colon | 1962 (14%) | 790 (12%) | 137 (16%) | 287 (14%) | 154 (14%) | 30 (14%) | 15 (11%) | 82 (14%) | 57 (12%) | 50 (9%) | 226 (29%) | 37 (12%) | 97 (20%) |
| Transverse colon | 1390 (10%) | 611 (9%) | 127 (15%) | 199 (10%) | 148 (14%) | 12 (6%) | 12 (9%) | 57 (9%) | 50 (10%) | 56 (10%) | 60 (8%) | 28 (9%) | 30 (6%) |
| Descending colon | 1039 (7.4%) | 481 (7%) | 62 (7%) | 138 (7%) | 121 (11%) | 20 (9%) | 6 (4%) | 36 (6%) | 24 (5%) | 44 (8%) | 65 (8%) | 22 (7%) | 20 (4%) |
| Sigmoid  colon | 3310 (24%) | 1494 (23%) | 179 (21%) | 415 (21%) | 391 (37%) | 43 (20%) | 35 (26%) | 156 (26%) | 113 (23%) | 129 (24%) | 159 (20%) | 87 (28%) | 109 (22%) |
| Rectum | 4161 (30%) | 2193 (34%) | 177 (21%) | 740 (37%) | 0 (0%) | 81 (37%) | 49 (36%) | 153 (25%) | 180 (37%) | 178 (33%) | 160 (20%) | 94 (30%) | 156 (32%) |
| AJCC disease stage |  |  |  |  |  |  |  |  |  |  |  |  |  |
| I | 3279 (25%) | 1465 (24%) | 372 (43%) | 369 (18%) | 359 (35%) | 88 (44%) | N/A | 153 (29%) | 57 (21%) | 93 (18%) | 177 (24%) | 62 (21%) | 84 (18%) |
| II and III | 8228 (63%) | 3971 (66%) | 440 (51%) | 1352 (67%) | 578 (57%) | 88 (44%) | N/A | 302 (58%) | 164 (61%) | 368 (72%) | 459 (62%) | 190 (63%) | 316 (67%) |
| IV | 1457 (11%) | 622 (10%) | 44 (5%) | 285 (14%) | 86 (8%) | 23 (12%) | N/A | 70 (13%) | 48 (18%) | 51 (10%) | 105 (14%) | 49 (16%) | 74 (16%) |
| MSI status |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Non-MSI-high | 10903 (83%) | 4895 (80%) | 544 (82%) | 1625 (90%) | 884 (84%) | 169 (83%) | 107 (84%) | 515 (88%) | 419 (87%) | 480 (89%) | 600 (80%) | 244 (85%) | 421 (87%) |
| MSI-high | 2193 (17%) | 1212 (20%) | 120 (18%) | 187 (10%) | 171 (16%) | 35 (17%) | 20 (16%) | 67 (12%) | 62 (13%) | 60 (11%) | 153 (20%) | 43 (15%) | 63 (13%) |
| CIMP status |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Low/negative | 7926 (84%) | 2842 (87%) | 583 (75%) | 1679 (85%) | 697 (83%) | N/A | 99 (80%) | 450 (83%) | 401 (89%) | N/A | 562 (74%) | 227 (80%) | 386 (80%) |
| High | 1561 (16%) | 417 (13%) | 193 (25%) | 305 (15%) | 139 (17%) | N/A | 24 (20%) | 90 (17%) | 48 (11%) | N/A | 193 (26%) | 56 (20%) | 96 (20%) |
| *BRAF* |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Wild-type | 10957 (89%) | 5087 (90%) | 583 (85%) | 1697 (93%) | 792 (90%) | 71 (81%) | 92 (75%) | 543 (92%) | 385 (86%) | 437 (90%) | 603 (79%) | 222 (78%) | 445 (91%) |
| Mutant | 1396 (11%) | 592 (10%) | 104 (15%) | 135 (7%) | 90 (10%) | 17 (19%) | 31 (25%) | 48 (8%) | 61 (14%) | 50 (10%) | 159 (21%) | 64 (22%) | 45 (9%) |
| *KRAS* |  |  |  |  |  |  |  |  |  |  |  |  |  |
| Wild-type | 6710 (67%) | 2627 (67%) | 385 (68%) | 1247 (68%) | 675 (69%) | 56 (63%) | 96 (77%) | 333 (57%) | 316 (71%) | N/A | 489 (64%) | 214 (74%) | 272 (55%) |
| Mutant | 3369 (33%) | 1270 (33%) | 178 (32%) | 590 (32%) | 310 (31%) | 33 (37%) | 29 (23%) | 256 (43%) | 132 (29%) | N/A | 276 (36%) | 76 (26%) | 219 (45%) |

\* Percentage indicates the proportion of patients with a specific patient and molecular characteristic among all patients or in strata of the studies.

Abbreviations: AJCC, American Joint Committee on Cancer; CCFR, Colon Cancer Family Registry; CIMP, CpG island methylator phenotype; CPS-II, Cancer Prevention Study II; DACHS, Darmkrebs: Chancen der Verhütung durch Screening Study; DALS, Diet, Activity and Lifestyle Study; EDRN, Early Detection Research Network; EPIC\_Sweden, European Prospective Investigation into Cancer\_Sweden; HPFS, Health Professionals Follow-up Study; MCCS, Melbourne Collaborative Cohort Study; MSI, microsatellite instability; N/A, not available; NFCCR, Newfoundland Familial Colorectal Cancer Registries; NHS, Nurses’ Health Study; NSHDS, Northern Sweden Health and Disease Study; SD, standard deviation; TCGA, The Cancer Genome Atlas.

Supplementary Table 2. Study-Specific Markers Used to Assess Microsatellite Instability (MSI) and Definition of MSI Status

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Study**† | **Mononucleotide markers** | **Dinucleotide markers** | **Other markers** | **Threshold for interpretability** | **Definitions** |
| CCFR | BAT25, BAT26, BAT40, BAT34C4 | D5S346, D17S250, ACTC, D18S55, D10S197 | MYCL | ≥4 interpretable markers | \* MSI-high if ≥30% markers showed instability |
| CPS-II | BAT25, BAT26, BAT40, BAT34C4 | ACTC, D10S197, D17S250, D18S55, D5S346 | MYCL | ≥5 interpretable markers (unless 4 markers were unstable) | \* MSI-high if ≥30% markers showed instability |
| DACHS | BAT25, BAT26,  CAT25 | N/A | N/A | All 3 markers  interpretable | \* MSI-high if >1 marker showed instability |
| DALS | BAT26, TGFBRII | N/A | UT2127, UT2271, UT5144, UT868, UT5013, UT909, UT1205, UT5658, UT269, UT574 | ≥6/10 markers be interpretable from tetranucleotide repeat panel | \* MSI: Instability in BAT26, *TGFBRII*, or 10 tetranucleotide marker panel.   - 10 marker panel: ≥30% unstable repeats. |
| EDRN | BAT25, BAT26, CAT25 | D5S346, D17S250, D2S123 | - | - | - |
| HPFS | BAT25, BAT26, BAT40 | D18S55, D18S56, D18S67, D18S487, D2S123, D5S346, D17S250 | - | >7 interpretable markers | \* MSI-high if ≥30% markers showed instability |
| MCCS | BAT25, BAT26, BAT40, BAT34C4 | D5S346, D17S250, ACTC, D18S55, D10S197 | MYCL | ≥4 interpretable markers | \* MSI-high if ≥30% markers showed instability |
| NFCCR | BAT25, BAT26, BAT40, BAT34C4 | D5S346, D17S250, ACTC, D18S55, D10S197. | MYCL | ≥4 interpretable markers | \* MSI-high if ≥30% markers showed instability |
| NHS | BAT25, BAT26, BAT40 | D18S55, D18S56, D18S67, D18S487, D2S123, D5S346, D17S250 | - | >7 interpretable markers | \* MSI-high if ≥30% markers showed instability |

† EPIC\_Sweden and NSHDS, and an EDRN subset used immunohistochemical detection of deficiency for mismatch repair gene proteins MLH1, MSH2, MSH6, and PMS2, and not PCR based assessment of microsatellite status.

Abbreviations: CCFR, Colon Cancer Family Registry; CPS-II, Cancer Prevention Study II; DACHS, Darmkrebs: Chancen der Verhütung durch Screening Study; DALS, Diet, Activity and Lifestyle Study; EDRN, Early Detection Research Network; HPFS, Health Professionals Follow-up Study; MCCS, Melbourne Collaborative Cohort Study; MSI, microsatellite instability, NFCCR, Newfoundland Familial Colorectal Cancer Registries; NHS, Nurses’ Health Study.

Supplementary Table 3. Study-Specific Panels Used to Assess CpG Island Methylator Phenotype (CIMP) Status

|  |  |  |  |
| --- | --- | --- | --- |
| **Study**† | **Panel genes** | **Marker positive definition** | **Definition for CIMP-high (vs. CIMP-low/negative)** |
| CCFR | *CACNA1G*, *IGF2*, *NEUROG1*, *RUNX3*, *SOCS1* | PMR >10 | \* CIMP-high: ≥3/5 methylated markers |
| CPS-II | *CDKN2A*, *MLH1*, *CACNA1G*, *NEUROG1*, *RUNX3*, *SOCS1*, *IGF2*, *CRABP1* | PMR >4 (>6 for *CRABP1*, *IGF2*) | \* CIMP-high: ≥5/8 methylated markers |
| DACHS | *MGMT*, *MLH1*, MINT1, MINT2,  MINT31 |  | \* CIMP-high: ≥3/5 methylated markers |
| DALS | MINT1, MINT2, MINT31, CDKN2A9, hMLH1 |  | \* CIMP-high: ≥3/5 methylated markers |
| EPIC\_Sweden | *CDKN2A*, *MLH1*, *CACNA1G*, *NEUROG1*, *RUNX3*, *SOCS1*, *IGF2*, *CRABP1* | PMR >10 | \* CIMP-high: ≥5/8 methylated markers |
| HPFS | *CDKN2A*, *MLH1*, *CACNA1G*, *NEUROG1*, *RUNX3*, *SOCS1*, *IGF2*, *CRABP1* | PMR >4 (>6 for *CRABP1*, *IGF2*) | \* CIMP-high: ≥5/8 methylated markers |
| MCCS | *CACNA1G*, *IGF2*, *NEUROG1*, *RUNX3*, *SOCS1* | PMR >10 | \* CIMP-high: ≥3/5 methylated markers |
| NHS | *CDKN2A*, *MLH1*, *CACNA1G*, *NEUROG1*, *RUNX3*, *SOCS1*, *IGF2*, *CRABP1* | PMR >4 (>6 for *CRABP1*, *IGF2*) | \* CIMP-high: ≥5/8 methylated markers |
| NSHDS | *CDKN2A*, *MLH1*, *CACNA1G*, *NEUROG1*, *RUNX3*, *SOCS1*, *IGF2*, *CRABP1* | PMR >10 | \* CIMP-high: ≥5/8 methylated markers |

† EDRN and NFCCR did not have available CIMP data.

Abbreviations: CCFR, Colon Cancer Family Registry; CIMP, CpG island methylator phenotype; CPS-II, Cancer Prevention Study II; DACHS, Darmkrebs: Chancen der Verhütung durch Screening Study; DALS, Diet, Activity and Lifestyle Study; EPIC\_Sweden, European Prospective Investigation into Cancer\_Sweden; HPFS, Health Professionals Follow-up Study; MCCS, Melbourne Collaborative Cohort Study; NHS, Nurses’ Health Study; NSHDS, Northern Sweden Health and Disease Study; PMR, percentage of methylated reference.

Supplementary Table 4. Molecular Characteristics of Early-onset and Later-onset Colorectal Cancers According to Primary Tumor Location in Strata of Age Groups

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <40** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.76 (1.54-2.02) | <0.001 |
| Non-MSI-high | 482 (66%) | 44 (52%) | 36 (37%) | 33 (42%) | 43 (67%) | 112 (77%) | 214 (83%) |  |  |
| MSI-high | 243 (34%) | 40 (48%) | 61 (63%) | 45 (58%) | 21 (33%) | 33 (23%) | 43 (17%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.07 (0.68-1.69) | 0.77 |
| Low/negative | 245 (94%) | 27 (87%) | 22 (96%) | 28 (93%) | 19 (100%) | 58 (92%) | 91 (97%) |  |  |
| High | 15 (5.8%) | 4 (13%) | 1 (4.3%) | 2 (7%) | 0 (0%) | 5 (7.9%) | 3 (3.2%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 0.80 (0.60-1.08) | 0.15 |
| Wild-type | 629 (95%) | 74 (95%) | 82 (99%) | 64 (94%) | 55 (96%) | 134 (94%) | 220 (95%) |  |  |
| Mutant | 31 (4.7%) | 4 (5.1%) | 1 (1.2%) | 4 (5.9%) | 2 (3.5%) | 8 (5.6%) | 12 (5.2%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.19 (0.99-1.42) | 0.065 |
| Wild-type | 228 (69%) | 33 (79%) | 20 (59%) | 22 (67%) | 16 (53%) | 49 (69%) | 88 (73%) |  |  |
| Mutant | 103 (31%) | 9 (21%) | 14 (41%) | 11 (33%) | 14 (47%) | 22 (31%) | 33 (27%) |  |  |
| **Age 40-49** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.96 (1.77-2.15) | <0.001 |
| Non-MSI-high | 1809 (83%) | 178 (68%) | 132 (61%) | 104 (63%) | 144 (78%) | 457 (93%) | 794 (94%) |  |  |
| MSI-high | 358 (17%) | 83 (32%) | 85 (39%) | 61 (37%) | 41 (22%) | 34 (6.9%) | 54 (6.4%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.74 (1.38-2.18) | <0.001 |
| Low/negative | 813 (94%) | 106 (86%) | 71 (83%) | 68 (93%) | 77 (96%) | 180 (97%) | 311 (97%) |  |  |
| High | 56 (6.4%) | 17 (14%) | 15 (17%) | 5 (6.8%) | 3 (3.8%) | 5 (2.7%) | 11 (3.4%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.46 (1.17-1.68) | <0.001 |
| Wild-type | 1900 (95%) | 236 (96%) | 179 (89%) | 148 (90%) | 158 (94%) | 446 (96%) | 733 (97%) |  |  |
| Mutant | 102 (5.1%) | 11 (4%) | 22 (11%) | 16 (10%) | 10 (6.0%) | 20 (4.3%) | 23 (3.0%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.08 (0.98-1.20) | 0.11 |
| Wild-type | 807 (65%) | 74 (44%) | 61 (59%) | 61 (66%) | 79 (72%) | 211 (70%) | 321 (69%) |  |  |
| Mutant | 429 (35%) | 93 (56%) | 43 (41%) | 32 (34%) | 30 (28%) | 89 (30%) | 142 (31%) |  |  |
| **Age 50-59** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.08 (1.88-2.30) | <0.001 |
| Non-MSI-high | 2140 (86%) | 253 (73%) | 182 (64%) | 145 (71%) | 170 (86%) | 584 (95%) | 806 (96%) |  |  |
| MSI-high | 344 (14%) | 93 (27%) | 101 (36%) | 60 (29%) | 27 (14%) | 33 (5.3%) | 30 (3.6%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.94 (1.69-2.23) | <0.001 |
| Low/negative | 1678 (91%) | 194 (80%) | 157 (77%) | 122 (84%) | 138 (95%) | 452 (98%) | 615 (97%) |  |  |
| High | 159 (9%) | 48 (20%) | 48 (23%) | 23 (16%) | 8 (5.5%) | 11 (2.4%) | 21 (3.3%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.53 (1.36-1.72) | <0.001 |
| Wild-type | 2166 (92%) | 289 (89%) | 225 (85%) | 165 (85%) | 165 (91%) | 552 (96%) | 770 (96%) |  |  |
| Mutant | 176 (8%) | 36 (11%) | 39 (15%) | 30 (15%) | 16 (8.8%) | 23 (4.0%) | 32 (4.0%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.11 (1.03-1.20) | 0.008 |
| Wild-type | 1233 (67%) | 139 (56%) | 123 (64%) | 86 (61%) | 97 (66%) | 347 (71%) | 441 (72%) |  |  |
| Mutant | 597 (33%) | 111 (44%) | 70 (36%) | 54 (39%) | 50 (34%) | 140 (29%) | 172 (28%) |  |  |
| **Age 60-69** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.10 (1.93-2.28) | <0.001 |
| Non-MSI-high | 3244 (86%) | 429 (72%) | 340 (68%) | 265 (70%) | 243 (90%) | 946 (96%) | 1021 (97%) |  |  |
| MSI-high | 541 (14%) | 165 (28%) | 162 (32%) | 113 (30%) | 27 (10%) | 39 (4.0%) | 35 (3.3%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 2.04 (1.87-2.22) | <0.001 |
| Low/negative | 2497 (83%) | 334 (69%) | 250 (62%) | 196 (65%) | 186 (91%) | 712 (94%) | 819 (96%) |  |  |
| High | 515 (17%) | 150 (31%) | 156 (38%) | 105 (35%) | 19 (9.3%) | 49 (6.4%) | 36 (4.2%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.95 (1.79-2.12) | <0.001 |
| Wild-type | 3108 (86%) | 427 (76%) | 329 (69%) | 259 (73%) | 230 (91%) | 859 (94%) | 1004 (96%) |  |  |
| Mutant | 496 (14%) | 133 (24%) | 151 (31%) | 97 (27%) | 22 (8.7%) | 56 (6.1%) | 37 (3.6%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.01 (0.96-1.07) | 0.67 |
| Wild-type | 2141 (67%) | 283 (56%) | 295 (68%) | 224 (70%) | 154 (67%) | 574 (70%) | 611 (68%) |  |  |
| Mutant | 1061 (33%) | 218 (44%) | 141 (32%) | 98 (30%) | 75 (33%) | 242 (30%) | 287 (32%) |  |  |
|  |  |  |  |  |  |  |  |  |  |
| **Age ≥70** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.27 (2.08-2.47) | <0.001 |
| Non-MSI-high | 3228 (82%) | 536 (74%) | 466 (62%) | 301 (68%) | 229 (86%) | 843 (95%) | 853 (98%) |  |  |
| MSI-high | 707 (18%) | 189 (26%) | 286 (38%) | 139 (32%) | 38 (14%) | 40 (4.5%) | 15 (1.7%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.95 (1.82-2.09) | <0.001 |
| Low/negative | 2693 (77%) | 442 (69%) | 356 (53%) | 266 (64%) | 190 (84%) | 718 (93%) | 721 (93%) |  |  |
| High | 816 (23%) | 203 (31%) | 312 (47%) | 151 (36%) | 36 (16%) | 58 (7.5%) | 56 (7.2%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 2.15 (1.97-2.34) | <0.001 |
| Wild-type | 3154 (84%) | 523 (76%) | 482 (67%) | 310 (74%) | 220 (91%) | 800 (95%) | 819 (98%) |  |  |
| Mutant | 591 (16%) | 162 (24%) | 241 (33%) | 107 (26%) | 23 (9.5%) | 38 (4.5%) | 20 (2.4%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.93 (0.88-0.98) | 0.008 |
| Wild-type | 2301 (66%) | 345 (55%) | 458 (68%) | 306 (78%) | 152 (66%) | 546 (70%) | 494 (63%) |  |  |
| Mutant | 1179 (34%) | 279 (45%) | 211 (32%) | 87 (22%) | 79 (34%) | 233 (30%) | 290 (37%) |  |  |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity (i.e., MSI-high, CIMP-high, *BRAF* mutation, or *KRAS* mutation) and Ptrend were calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male), family history of colorectal cancer (present vs. absent), and study (i.e., cohort).

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; MSI, microsatellite instability; OR, odds ratio.

Supplementary Table 5. Molecular Characteristics of Early-onset and Later-onset According to Primary Tumor Location in Strata of Family History of Colorectal Cancer

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <50 (early-onset)** |  |  |  |  |  |  |  |  |  |
| **Family history of CRC absent** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.71 (1.54-1.89) | <0.001 |
| Non-MSI-high | 1786 (88%) | 172 (79%) | 135 (70%) | 108 (72%) | 153 (85%) | 440 (93%) | 172 (79%) |  |  |
| MSI-high | 255 (12%) | 47 (21%) | 59 (30%) | 41 (28%) | 28 (15%) | 32 (6.8%) | 48 (5.8%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.46 (1.16-1.83) | 0.001 |
| Low/negative | 761 (94%) | 87 (88%) | 62 (86%) | 61 (94%) | 70 (96%) | 184 (96%) | 87 (88%) |  |  |
| High | 49 (6.0%) | 12 (12%) | 10 (14%) | 4 (6.2%) | 3 (4.1%) | 8 (4.2%) | 12 (3.9%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.35 (1.17-1.56) | <0.001 |
| Wild-type | 1805 (95%) | 197 (94%) | 162 (91%) | 127 (89%) | 156 (96%) | 442 (95%) | 197 (94%) |  |  |
| Mutant | 101 (5.3%) | 17 (9%) | 12 (6%) | 17 (9%) | 16 (11%) | 7 (4.9%) | 23 (3.5%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.10 (0.99-1.22) | 0.062 |
| Wild-type | 805 (67%) | 73 (47%) | 55 (57%) | 58 (70%) | 79 (70%) | 219 (73%) | 73 (47%) |  |  |
| Mutant | 400 (33%) | 82 (53%) | 42 (43%) | 25 (30%) | 34 (30%) | 82 (27%) | 135 (30%) |  |  |
| **Family history of CRC present** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.11 (1.84-2.41) | <0.001 |
| Non-MSI-high | 463 (59%) | 46 (38%) | 32 (29%) | 27 (31%) | 31 (50%) | 117 (78%) | 210 (81%) |  |  |
| MSI-high | 324 (41%) | 74 (62%) | 78 (71%) | 60 (69%) | 31 (50%) | 33 (22%) | 48 (19%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.96 (1.25-3.09) | 0.004 |
| Low/negative | 273 (93%) | 44 (83%) | 30 (86%) | 33 (92%) | 23 (100%) | 47 (96%) | 96 (99%) |  |  |
| High | 20 (6.8%) | 9 (17%) | 5 (14%) | 3 (8.3%) | 0 (0%) | 2 (4.1%) | 1 (1.0%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.12 (0.87-1.44) | 0.37 |
| Wild-type | 679 (96%) | 107 (97%) | 95 (95%) | 80 (95%) | 51 (91%) | 127 (97%) | 219 (96%) |  |  |
| Mutant | 30 (4.2%) | 3 (2.7%) | 5 (5.0%) | 4 (4.8%) | 5 (8.9%) | 4 (3.1%) | 9 (3.9%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.11 (0.93-1.31) | 0.24 |
| Wild-type | 218 (64%) | 32 (62%) | 25 (64%) | 25 (60%) | 15 (63%) | 39 (60%) | 82 (69%) |  |  |
| Mutant | 123 (36%) | 20 (38%) | 14 (36%) | 17 (40%) | 9 (38%) | 26 (40%) | 37 (31%) |  |  |
| **Age ≥50 (later-onset)** |  |  |  |  |  |  |  |  |  |
| **Family history of CRC absent** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.27 (2.12-2.42) | <0.001 |
| Non-MSI-high | 6566 (87%) | 964 (77%) | 726 (66%) | 519 (70%) | 467 (91%) | 1821 (96%) | 2069 (98%) |  |  |
| MSI-high | 1019 (13%) | 281 (23%) | 366 (34%) | 218 (30%) | 45 (8.8%) | 68 (3.6%) | 41 (1.9%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.99 (1.88-2.11) | <0.001 |
| Low/negative | 5292 (82%) | 760 (73%) | 562 (59%) | 420 (65%) | 365 (89%) | 1486 (94%) | 1699 (95%) |  |  |
| High | 1133 (18%) | 284 (27%) | 395 (41%) | 226 (35%) | 47 (11%) | 90 (5.7%) | 91 (5.1%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.98 (1.87-2.11) | <0.001 |
| Wild-type | 6341 (87%) | 966 (82%) | 722 (69%) | 520 (74%) | 441 (92%) | 1700 (95%) | 1992 (97%) |  |  |
| Mutant | 919 (13%) | 215 (18%) | 329 (31%) | 181 (26%) | 40 (8.3%) | 88 (4.9%) | 66 (3.2%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.97 (0.94-1.01) | 0.20 |
| Wild-type | 4396 (66%) | 581 (54%) | 664 (68%) | 488 (74%) | 293 (66%) | 1152 (70%) | 1218 (67%) |  |  |
| Mutant | 2220 (34%) | 491 (46%) | 316 (32%) | 170 (26%) | 149 (34%) | 495 (30%) | 599 (33%) |  |  |
| **Family history of CRC present** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.89 (1.73-2.06) | <0.001 |
| Non-MSI-high | 1714 (77%) | 215 (60%) | 221 (58%) | 170 (68%) | 151 (77%) | 457 (92%) | 500 (93%) |  |  |
| MSI-high | 502 (23%) | 141 (40%) | 158 (42%) | 81 (32%) | 44 (23%) | 42 (8%) | 36 (7%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.89 (1.68-2.14) | <0.001 |
| Low/negative | 1331 (83%) | 180 (66%) | 172 (64%) | 149 (79%) | 129 (90%) | 330 (94%) | 371 (96%) |  |  |
| High | 280 (17%) | 91 (34%) | 95 (36%) | 40 (21%) | 15 (10%) | 22 (6%) | 17 (4%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.71 (1.53-1.92) | <0.001 |
| Wild-type | 1791 (87%) | 240 (72%) | 270 (77%) | 194 (82%) | 156 (89%) | 433 (95%) | 498 (97%) |  |  |
| Mutant | 278 (13%) | 95 (28%) | 82 (23%) | 42 (18%) | 19 (11%) | 24 (5%) | 16 (3%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.04 (0.96-1.13) | 0.28 |
| Wild-type | 1064 (67%) | 162 (63%) | 174 (65%) | 113 (66%) | 97 (67%) | 262 (72%) | 256 (67%) |  |  |
| Mutant | 526 (33%) | 96 (37%) | 92 (35%) | 59 (34%) | 48 (33%) | 103 (28%) | 128 (33%) |  |  |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity (i.e., MSI-high, CIMP-high, *BRAF* mutation, or *KRAS* mutation) and Ptrend were calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male) and study (i.e., cohort).

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; MSI, microsatellite instability; OR, odds ratio.

Supplementary Table 6. Jass Classification of Early-onset and Later-onset Colorectal Cancers According to Primary Tumor Location

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <50 (early-onset)** |  |  |  |  |  |  |  |  |  |
| Tumor subtype§ |  |  |  |  |  |  |  |  |  |
| Type 1 | 1 (0.2%) | 0 (0%) | 0 (0%) | 0 (0%) | 1 (1.7%) | 0 (0%) | 0 (0%) | 1.43 (0.51-3.97) | 0.49 |
| Type 2 | 17 (2.6%) | 5 (5.4%) | 4 (7.5%) | 0 (0%) | 1 (1.7%) | 5 (3.2%) | 2 (0.8%) | 1.47 (1.14-1.91) | 0.003 |
| Type 3 | 201 (31%) | 42 (46%) | 18 (34%) | 9 (20%) | 15 (25%) | 45 (29%) | 72 (29%) | 1.14 (1.03-1.25) | <0.001 |
| Type 4 | 376 (57%) | 28 (30%) | 15 (28%) | 26 (59%) | 39 (65%) | 104 (66%) | 164 (65%) | 0.72 (0.65-0.79) | <0.001 |
| Type 5 | 62 (9.4%) | 17 (18%) | 16 (30%) | 9 (20%) | 4 (6.7%) | 3 (1.9%) | 13 (5.2%) | 1.55 (1.34-1.78) | <0.001 |
| **Age ≥50 (later-onset)** |  |  |  |  |  |  |  |  |  |
| Tumor subtype§ |  |  |  |  |  |  |  |  |  |
| Type 1 | 511 (8.3%) | 157 (16%) | 222 (25%) | 91 (17%) | 16 (3.6%) | 23 (1.4%) | 2 (0.1%) | 1.89 (1.77-2.02) | <0.001 |
| Type 2 | 202 (3.2%) | 45 (4.7%) | 70 (8.0%) | 40 (7.3%) | 13 (3.0%) | 24 (1.5%) | 10 (0.6%) | 1.46 (1.35-1.59) | <0.001 |
| Type 3 | 1992 (32%) | 396 (41%) | 268 (31%) | 149 (27%) | 154 (35%) | 463 (29%) | 562 (32%) | 1.06 (1.03-1.09) | <0.001 |
| Type 4 | 3287 (53%) | 302 (31%) | 253 (29%) | 242 (44%) | 242 (55%) | 1079 (67%) | 1169 (66%) | 0.71 (0.69-0.73) | <0.001 |
| Type 5 | 195 (3.2%) | 60 (6.3%) | 62 (7.1%) | 25 (4.6%) | 15 (3.4%) | 18 (1.1%) | 15 (0.9%) | 1.58 (1.46-1.72) | <0.001 |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity and Ptrend were calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male), family history of colorectal cancer (present vs. absent), and study (i.e., cohort).

§ Tumor subtypes described by Jass38 as follows: Type 1 = MSI-high, CIMP-high, *BRAF* mutant, *KRAS* wild-type; Type 2 = non-MSI-high, CIMP-high, *BRAF* mutant, *KRAS* wild-type; Type 3 = non-MSI-high, CIMP-low/negative, *BRAF* wild-type, *KRAS* mutant; Type 4 = non-MSI-high, CIMP-low/negative, *BRAF* wild-type, *KRAS* wild-type; Type 5 = MSI-high, CIMP-low/negative, *BRAF* wild-type, *KRAS* wild-type.

Abbreviations: AJCC, American Joint Committee on Cancer; CIMP, CpG island methylator phenotype; MSI, microsatellite instability.

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; MSI, microsatellite instability; OR, odds ratio.

Supplementary Table 7. Molecular Characteristics of Early-onset and Later-onset According to Primary Tumor Location in Strata of CIMP Status

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <50 (early-onset)** |  |  |  |  |  |  |  |  |  |
| **CIMP-low/negative** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.04 (1.75-2.37) | <0.001 |
| Non-MSI-high | 863 (84%) | 93 (70%) | 56 (62%) | 56 (61%) | 74 (79%) | 215 (95%) | 369 (93%) |  |  |
| MSI-high | 167 (16%) | 39 (30%) | 35 (38%) | 36 (39%) | 20 (21%) | 11 (4.9%) | 26 (6.6%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.30 (1.03-1.64) | 0.029 |
| Wild-type | 1004 (97%) | 129 (98%) | 86 (93%) | 86 (95%) | 89 (95%) | 230 (97%) | 384 (97%) |  |  |
| Mutant | 35 (3.4%) | 2 (1.5%) | 6 (6.5%) | 5 (5.5%) | 5 (5.3%) | 7 (3.0%) | 10 (2.5%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.07 (0.94-1.21) | 0.30 |
| Wild-type | 477 (65%) | 46 (48%) | 38 (58%) | 43 (69%) | 49 (71%) | 115 (69%) | 186 (69%) |  |  |
| Mutant | 252 (35%) | 50 (52%) | 27 (42%) | 19 (31%) | 20 (29%) | 51 (31%) | 85 (31%) |  |  |
| **CIMP-high** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.48 (0.81-2.70) | 0.20 |
| Non-MSI-high | 48 (70%) | 11 (55%) | 11 (69%) | 2 (33%) | 2 (67%) | 9 (90%) | 13 (93%) |  |  |
| MSI-high | 21 (30%) | 9 (45%) | 5 (31%) | 4 (67%) | 1 (33%) | 1 (10%) | 1 (7.1%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 0.73 (0.44-1.21) | 0.23 |
| Wild-type | 41 (60%) | 12 (63%) | 11 (69%) | 5 (71%) | 1 (33%) | 3 (30%) | 9 (69%) |  |  |
| Mutant | 27 (40%) | 7 (37%) | 5 (31%) | 2 (29%) | 2 (67%) | 7 (70%) | 4 (31%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.42 (0.83-2.43) | 0.20 |
| Wild-type | 39 (66%) | 11 (58%) | 8 (67%) | 3 (60%) | 2 (67%) | 6 (75%) | 9 (75%) |  |  |
| Mutant | 20 (34%) | 8 (42%) | 4 (33%) | 2 (40%) | 1 (33%) | 2 (25%) | 3 (25%) |  |  |
| **Age ≥50 (later-onset)** |  |  |  |  |  |  |  |  |  |
| **CIMP-low/negative** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.95 (1.80-2.13) | <0.001 |
| Non-MSI-high | 6121 (94%) | 802 (88%) | 614 (84%) | 468 (87%) | 460 (94%) | 1765 (98%) | 2012 (98%) |  |  |
| MSI-high | 399 (6.1%) | 108 (12%) | 113 (16%) | 70 (13%) | 30 (6.1%) | 43 (2.4%) | 35 (1.7%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.41 (1.29-1.55) | <0.001 |
| Wild-type | 6241 (96%) | 866 (96%) | 674 (92%) | 494 (93%) | 464 (97%) | 1750 (98%) | 1993 (97%) |  |  |
| Mutant | 249 (3.8%) | 38 (4.2%) | 56 (7.7%) | 39 (7.3%) | 16 (3.3%) | 39 (2.2%) | 61 (3.0%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.13 (1.09-1.18) | <0.001 |
| Wild-type | 3934 (64%) | 411 (48%) | 382 (55%) | 327 (64%) | 291 (63%) | 1203 (70%) | 1320 (68%) |  |  |
| Mutant | 2251 (36%) | 444 (52%) | 314 (45%) | 182 (36%) | 170 (37%) | 522 (30%) | 619 (32%) |  |  |
| **CIMP-high** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.75 (1.57-1.96) | <0.001 |
| Non-MSI-high | 632 (45%) | 157 (42%) | 173 (35%) | 90 (35%) | 35 (56%) | 80 (70%) | 97 (95%) |  |  |
| MSI-high | 768 (55%) | 217 (58%) | 319 (65%) | 165 (65%) | 28 (44%) | 34 (30%) | 5 (5%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.44 (1.30-1.60) | <0.001 |
| Wild-type | 604 (44%) | 148 (39%) | 176 (36%) | 101 (41%) | 31 (52%) | 61 (54%) | 87 (84%) |  |  |
| Mutant | 782 (56%) | 227 (61%) | 310 (64%) | 148 (59%) | 29 (48%) | 52 (46%) | 16 (16%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.72 (0.64-0.80) | <0.001 |
| Wild-type | 1082 (79%) | 269 (75%) | 408 (85%) | 220 (88%) | 53 (88%) | 77 (71%) | 55 (52%) |  |  |
| Mutant | 282 (21%) | 91 (25%) | 72 (15%) | 29 (12%) | 7 (12%) | 32 (29%) | 51 (48%) |  |  |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity (i.e., MSI-high, *BRAF* mutation, or *KRAS* mutation) and Ptrend were calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male), family history of colorectal cancer (present vs. absent), and study (i.e., cohort).

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; MSI, microsatellite instability; OR, odds ratio

Supplementary Table 8. Molecular Characteristics of Early-onset and Later-onset According to Primary Tumor Location in Strata of *BRAF* Status

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <50 (early-onset)** |  |  |  |  |  |  |  |  |  |
| ***BRAF*-wild-type** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.92 (1.75-2.09) | <0.001 |
| Non-MSI-high | 1875 (80%) | 189 (65%) | 135 (54%) | 105 (56%) | 146 (74%) | 478 (90%) | 822 (92%) |  |  |
| MSI-high | 478 (20%) | 102 (35%) | 115 (46%) | 83 (44%) | 52 (26%) | 53 (10%) | 73 (8.2%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.71 (1.32-2.21) | <0.001 |
| Low/negative | 1004 (96%) | 129 (91%) | 86 (89%) | 86 (95%) | 89 (99%) | 230 (99%) | 384 (98%) |  |  |
| High | 41 (4%) | 12 (9%) | 11 (11%) | 5 (5.5%) | 1 (1.1%) | 3 (1.3%) | 9 (2.3%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.16 (1.06-1.26) | <0.001 |
| Wild-type | 949 (65%) | 92 (48%) | 69 (55%) | 69 (62%) | 84 (66%) | 247 (70%) | 388 (70%) |  |  |
| Mutant | 519 (35%) | 99 (52%) | 57 (45%) | 43 (38%) | 43 (34%) | 108 (30%) | 169 (30%) |  |  |
| ***BRAF*-mutant** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.47 (0.94-2.29) | 0.093 |
| Non-MSI-high | 104 (87%) | 11 (85%) | 18 (86%) | 13 (76%) | 9 (75%) | 27 (100%) | 26 (90%) |  |  |
| MSI-high | 15 (13%) | 2 (15%) | 3 (14%) | 4 (24%) | 3 (25%) | 0 (0%) | 3 (10%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.28 (0.79-2.07) | 0.32 |
| Low/negative | 35 (56%) | 2 (22%) | 6 (55%) | 5 (71%) | 5 (71%) | 7 (50%) | 10 (71%) |  |  |
| High | 27 (44%) | 7 (78%) | 5 (45%) | 2 (29%) | 2 (29%) | 7 (50%) | 4 (29%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.41 (0.05-2.92) | 0.38 |
| Wild-type | 67 (97%) | 10 (100%) | 11 (100%) | 9 (100%) | 9 (100%) | 12 (92%) | 16 (94%) |  |  |
| Mutant | 2 (2.9%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 1 (7.7%) | 1 (5.9%) |  |  |
| **Age ≥50 (later-onset)** |  |  |  |  |  |  |  |  |  |
| ***BRAF*-wild-type** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.95 (1.83-2.08) | <0.001 |
| Non-MSI-high | 7253 (91%) | 1011 (85%) | 763 (78%) | 551 (80%) | 537 (91%) | 2038 (97%) | 2353 (98%) |  |  |
| MSI-high | 709 (9%) | 179 (15%) | 212 (22%) | 138 (20%) | 52 (8.8%) | 69 (3.3%) | 59 (2.4%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.66 (1.55-1.77) | <0.001 |
| Low/negative | 6241 (91%) | 866 (85%) | 674 (79%) | 494 (83%) | 464 (94%) | 1750 (97%) | 1993 (96%) |  |  |
| High | 604 (9%) | 148 (15%) | 176 (21%) | 101 (17%) | 31 (6.3%) | 61 (3.4%) | 87 (4.2%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.13 (1.08-1.17) | <0.001 |
| Wild-type | 4383 (62%) | 480 (46%) | 472 (54%) | 387 (64%) | 322 (62%) | 1298 (69%) | 1424 (67%) |  |  |
| Mutant | 2685 (38%) | 574 (54%) | 402 (46%) | 217 (36%) | 198 (38%) | 580 (31%) | 714 (33%) |  |  |
| ***BRAF*-mutant** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.88 (1.65-2.14) | <0.001 |
| Non-MSI-high | 498 (41%) | 91 (28%) | 129 (31%) | 84 (38%) | 33 (56%) | 83 (73%) | 78 (94%) |  |  |
| MSI-high | 716 (59%) | 230 (72%) | 288 (69%) | 137 (62%) | 26 (44%) | 30 (27%) | 5 (6.0%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.80 (1.58-2.06) | <0.001 |
| Low/negative | 249 (24%) | 38 (14%) | 56 (15%) | 39 (21%) | 16 (36%) | 39 (43%) | 61 (79%) |  |  |
| High | 782 (76%) | 227 (86%) | 310 (85%) | 148 (79%) | 29 (64%) | 52 (57%) | 16 (21%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.67 (0.53-0.85) | 0.001 |
| Wild-type | 1024 (95%) | 256 (95%) | 374 (98%) | 181 (95%) | 54 (98%) | 96 (94%) | 63 (85%) |  |  |
| Mutant | 49 (4.6%) | 13 (4.8%) | 8 (2.1%) | 10 (5.2%) | 1 (1.8%) | 6 (5.9%) | 11 (15%) |  |  |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity (i.e., MSI-high, CIMP-high, *KRAS* mutation)and Ptrend were calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male), family history of colorectal cancer (present vs. absent), and study (i.e., cohort).

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; MSI, microsatellite instability; OR, odds ratio

Supplementary Table 9. Molecular Characteristics of Early-onset and Later-onset According to Primary Tumor Location in Strata of *KRAS* Status

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <50 (early-onset)** |  |  |  |  |  |  |  |  |  |
| ***KRAS*-wild-type** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.12 (1.81-2.50) | <0.001 |
| Non-MSI-high | 813 (85%) | 68 (67%) | 42 (55%) | 48 (66%) | 78 (86%) | 224 (95%) | 353 (94%) |  |  |
| MSI-high | 139 (15%) | 33 (33%) | 34 (45%) | 25 (34%) | 13 (14%) | 13 (5%) | 21 (6%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.45 (1.11-1.90) | 0.007 |
| Low/negative | 477 (92%) | 46 (81%) | 38 (83%) | 43 (93%) | 49 (96%) | 115 (95%) | 186 (95%) |  |  |
| High | 39 (8%) | 11 (19%) | 8 (17%) | 3 (7%) | 2 (4%) | 6 (5%) | 9 (5%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.49 (1.23-1.80) | <0.001 |
| Wild-type | 949 (93%) | 92 (90%) | 69 (86%) | 69 (88%) | 84 (90%) | 247 (95%) | 388 (96%) |  |  |
| Mutant | 67 (7%) | 10 (10%) | 11 (14%) | 9 (12%) | 9 (10%) | 12 (5%) | 16 (4%) |  |  |
| ***KRAS*-mutant** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.68 (1.35-2.07) | 0.093 |
| Non-MSI-high | 408 (84%) | 82 (85%) | 37 (67%) | 21 (57%) | 30 (75%) | 90 (94%) | 148 (92%) |  |  |
| MSI-high | 78 (16%) | 15 (15%) | 18 (33%) | 16 (43%) | 10 (25%) | 6 (6.3%) | 13 (8.1%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.99 (1.20-3.31) | 0.008 |
| Low/negative | 252 (93%) | 50 (86%) | 27 (87%) | 19 (90%) | 20 (95%) | 51 (96%) | 85 (97%) |  |  |
| High | 20 (7%) | 8 (14%) | 4 (13%) | 2 (10%) | 1 (4.8%) | 2 (3.8%) | 3 (3.4%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 0.49 (0.08-3.01) | 0.44 |
| Wild-type | 519 (100%) | 99 (100%) | 57 (100%) | 43 (100%) | 43 (100%) | 108 (99%) | 169 (99%) |  |  |
| Mutant | 2 (0.4%) | 0 (0%) | 0 (0%) | 0 (0%) | 0 (0%) | 1 (0.9%) | 1 (0.6%) |  |  |
| **Age ≥50 (later-onset)** |  |  |  |  |  |  |  |  |  |
| ***KRAS*-wild-type** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.56 (1.38-1.77) | <0.001 |
| Non-MSI-high | 4378 (81%) | 455 (61%) | 438 (52%) | 381 (66%) | 336 (87%) | 1351 (96%) | 1417 (98%) |  |  |
| MSI-high | 1017 (19%) | 288 (39%) | 401 (48%) | 198 (34%) | 52 (13%) | 53 (3.8%) | 25 (1.7%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 2.31 (2.16-2.47) | <0.001 |
| Low/negative | 3934 (78%) | 411 (60%) | 382 (48%) | 327 (60%) | 291 (85%) | 1203 (94%) | 1320 (96%) |  |  |
| High | 1082 (22%) | 269 (40%) | 408 (52%) | 220 (40%) | 53 (15%) | 77 (6.0%) | 55 (4.0%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 2.09 (1.96-2.22) | <0.001 |
| Wild-type | 4383 (81%) | 480 (65%) | 472 (56%) | 387 (68%) | 322 (86%) | 1298 (93%) | 1424 (96%) |  |  |
| Mutant | 1024 (19%) | 256 (35%) | 374 (44%) | 181 (32%) | 54 (14%) | 96 (6.9%) | 63 (4.2%) |  |  |
| ***KRAS*-mutant** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.31 (2.16-2.47) | <0.001 |
| Non-MSI-high | 2553 (94%) | 542 (92%) | 365 (90%) | 199 (85%) | 186 (95%) | 567 (96%) | 694 (98%) |  |  |
| MSI-high | 167 (6.1%) | 47 (8%) | 39 (10%) | 35 (15%) | 10 (5.1%) | 22 (3.7%) | 14 (2.0%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.34 (1.22-1.48) | <0.001 |
| Low/negative | 2251 (89%) | 444 (83%) | 314 (81%) | 182 (86%) | 170 (96%) | 522 (94%) | 619 (92%) |  |  |
| High | 282 (11%) | 91 (17%) | 72 (19%) | 29 (14%) | 7 (4.0%) | 32 (5.8%) | 51 (7.6%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.24 (1.00-1.54) | 0.050 |
| Wild-type | 2685 (98%) | 574 (98%) | 402 (98%) | 217 (96%) | 198 (99%) | 580 (99%) | 714 (98%) |  |  |
| Mutant | 49 (1.8%) | 13 (2.2%) | 8 (2.0%) | 10 (4.4%) | 1 (0.5%) | 6 (1.0%) | 11 (1.5%) |  |  |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity (i.e., MSI-high, CIMP-high, or *BRAF* mutation)and Ptrend were calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male), family history of colorectal cancer (present vs. absent), and study (i.e., cohort).

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; MSI, microsatellite instability; OR, odds ratio

Supplementary Table 10. Molecular Characteristics of Early-onset and Later-onset MSI-high Colorectal Cancers According to Primary Tumor Location in Strata of Family History of Colorectal Cancer

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature of MSI-high cancer\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <50 (early-onset)** |  |  |  |  |  |  |  |  |  |
| **Family history of CRC absent** |  |  |  |  |  |  |  |  |  |
| CIMP status |  |  |  |  |  |  |  | 0.82 (0.42-1.57) | 0.54 |
| Low/negative | 77 (91%) | 18 (90%) | 15 (88%) | 16 (94%) | 9 (90%) | 6 (86%) | 13 (93%) |  |  |
| High | 8 (9.4%) | 2 (10%) | 2 (12%) | 1 (5.9%) | 1 (10%) | 1 (14%) | 1 (7.1%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.19 (0.67-2.11) | 0.56 |
| Wild-type | 209 (96%) | 42 (98%) | 49 (98%) | 31 (91%) | 24 (92%) | 28 (100%) | 35 (97%) |  |  |
| Mutant | 8 (3.7%) | 1 (2.3%) | 1 (2.0%) | 3 (8.8%) | 2 (7.7%) | 0 (0%) | 1 (2.8%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.06 (0.79-1.42) | 0.71 |
| Wild-type | 78 (66%) | 15 (63%) | 18 (67%) | 12 (67%) | 9 (56%) | 10 (77%) | 14 (70%) |  |  |
| Mutant | 40 (34%) | 9 (38%) | 9 (33%) | 6 (33%) | 7 (44%) | 3 (23%) | 6 (30%) |  |  |
| **Family history of CRC present** |  |  |  |  |  |  |  |  |  |
| CIMP status |  |  |  |  |  |  |  | 2.31 (0.72-7.41) | 0.15 |
| Low/negative | 87 (87%) | 21 (75%) | 19 (86%) | 19 (86%) | 10 (100%) | 5 (100%) | 13 (100%) |  |  |
| High | 13 (13%) | 7 (25%) | 3 (14%) | 3 (14%) | 0 (0%) | 0 (0%) | 0 (0%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 0.95 (0.55-1.65) | 0.86 |
| Wild-type | 256 (97%) | 59 (98%) | 62 (97%) | 48 (98%) | 26 (96%) | 24 (100%) | 37 (95%) |  |  |
| Mutant | 7 (2.7%) | 1 (1.7%) | 2 (3.1%) | 1 (2.0%) | 1 (3.7%) | 0 (0%) | 2 (5.1%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.02 (0.71-1.45) | 0.92 |
| Wild-type | 61 (62%) | 18 (75%) | 16 (67%) | 13 (57%) | 4 (57%) | 3 (50%) | 7 (50%) |  |  |
| Mutant | 37 (38%) | 6 (25%) | 8 (33%) | 10 (43%) | 3 (43%) | 3 (50%) | 7 (50%) |  |  |
| **Age ≥50 (later-onset)** |  |  |  |  |  |  |  |  |  |
| **Family history of CRC absent** |  |  |  |  |  |  |  |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.69 (1.43-2.01) | <0.001 |
| Low/negative | 255 (31%) | 70 (32%) | 70 (23%) | 42 (24%) | 16 (48%) | 34 (59%) | 23 (82%) |  |  |
| High | 567 (69%) | 146 (68%) | 240 (77%) | 135 (76%) | 17 (52%) | 24 (41%) | 5 (18%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.50 (1.29-1.75) | <0.001 |
| Wild-type | 435 (46%) | 115 (44%) | 132 (38%) | 88 (45%) | 28 (67%) | 43 (65%) | 29 (85%) |  |  |
| Mutant | 506 (54%) | 146 (56%) | 211 (62%) | 107 (55%) | 14 (33%) | 23 (35%) | 5 (15%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.66 (0.54-0.80) | <0.001 |
| Wild-type | 735 (86%) | 198 (85%) | 295 (91%) | 152 (86%) | 31 (86%) | 43 (74%) | 16 (59%) |  |  |
| Mutant | 117 (14%) | 34 (15%) | 28 (9%) | 24 (14%) | 5 (14%) | 15 (26%) | 11 (41%) |  |  |
| **Family history of CRC present** |  |  |  |  |  |  |  |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.49 (1.10-2.01) | 0.009 |
| Low/negative | 132 (45%) | 33 (37%) | 40 (39%) | 27 (54%) | 13 (54%) | 9 (53%) | 10 (100%) |  |  |
| High | 162 (55%) | 57 (63%) | 63 (61%) | 23 (46%) | 11 (46%) | 8 (47%) | 0 (0%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.91 (1.45-2.51) | <0.001 |
| Wild-type | 245 (58%) | 56 (44%) | 68 (51%) | 45 (65%) | 23 (68%) | 25 (81%) | 28 (100%) |  |  |
| Mutant | 176 (42%) | 70 (56%) | 65 (49%) | 24 (35%) | 11 (32%) | 6 (19%) | 0 (0%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.68 (0.50-0.93) | 0.015 |
| Wild-type | 241 (84%) | 78 (90%) | 87 (89%) | 40 (78%) | 20 (80%) | 9 (60%) | 7 (70%) |  |  |
| Mutant | 45 (16%) | 9 (10%) | 11 (11%) | 11 (22%) | 5 (20%) | 6 (40%) | 3 (30%) |  |  |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity (i.e., CIMP-high, *BRAF* mutation, or *KRAS* mutation) and Ptrend was calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male) and study (i.e., cohort).

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; CRC, colorectal cancer; MSI, microsatellite instability; OR, odds ratio.

Supplementary Table 11. Molecular Characteristics of Early-onset and Later-onset According to Primary Tumor Location in Strata of Year of Diagnosis (up to 2000 vs. After 2000).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Molecular feature\* | Total N | Cecum | Ascending colon | Transverse colon | Descending colon | Sigmoid colon | Rectum | Multivariable OR (95% CI) † | Ptrend† |
| **Age <50 (early-onset)** |  |  |  |  |  |  |  |  |  |
| **Diagnosed up to 2000** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.78 (1.57-2.03) | <0.001 |
| Non-MSI-high | 895 (78%) | 105 (67%) | 70 (56%) | 60 (57%) | 71 (71%) | 229 (90%) | 360 (88%) |  |  |
| MSI-high | 255 (22%) | 51 (33%) | 56 (44%) | 46 (43%) | 29 (29%) | 26 (10%) | 47 (12%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.80 (1.39-2.33) | <0.001 |
| Low/negative | 699 (94%) | 90 (87%) | 63 (85%) | 64 (94%) | 64 (96%) | 166 (95%) | 252 (99%) |  |  |
| High | 43 (5.8%) | 14 (13%) | 11 (15%) | 4 (5.9%) | 3 (4.5%) | 8 (4.6%) | 3 (1.2%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.14 (1.00-1.30) | 0.008 |
| Wild-type | 985 (94%) | 136 (96%) | 104 (91%) | 88 (93%) | 82 (92%) | 224 (93%) | 351 (97%) |  |  |
| Mutant | 60 (5.7%) | 6 (4.2%) | 10 (8.8%) | 7 (7.4%) | 7 (7.9%) | 18 (7.4%) | 12 (3.3%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.28 (1.07-1.54) | 0.046 |
| Wild-type | 467 (67%) | 52 (50%) | 37 (55%) | 43 (69%) | 47 (72%) | 116 (75%) | 172 (71%) |  |  |
| Mutant | 229 (33%) | 52 (50%) | 30 (45%) | 19 (31%) | 18 (28%) | 39 (25%) | 71 (29%) |  |  |
| **Diagnosed after 2000** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 1.95 (1.76-2.16) | <0.001 |
| Non-MSI-high | 1396 (80%) | 117 (62%) | 98 (52%) | 77 (56%) | 116 (78%) | 340 (89%) | 648 (93%) |  |  |
| MSI-high | 346 (20%) | 72 (38%) | 90 (48%) | 60 (44%) | 33 (22%) | 41 (11%) | 50 (7.2%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.28 (0.94-1.75) | 0.12 |
| Low/negative | 359 (93%) | 43 (86%) | 30 (86%) | 32 (91%) | 32 (100%) | 72 (97%) | 150 (93%) |  |  |
| High | 28 (7.2%) | 7 (14%) | 5 (14%) | 3 (8.6%) | 0 (0%) | 2 (2.7%) | 11 (6.8%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.30 (1.10-1.53) | 0.002 |
| Wild-type | 1544 (95%) | 174 (95%) | 157 (92%) | 124 (91%) | 131 (96%) | 356 (97%) | 602 (96%) |  |  |
| Mutant | 73 (4.5%) | 9 (5%) | 13 (8%) | 13 (9.5%) | 5 (3.7%) | 10 (2.7%) | 23 (3.7%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.08 (0.96-1.21) | 0.22 |
| Wild-type | 568 (65%) | 55 (52%) | 44 (62%) | 40 (63%) | 48 (65%) | 144 (67%) | 237 (70%) |  |  |
| Mutant | 303 (35%) | 50 (48%) | 27 (38%) | 24 (38%) | 26 (35%) | 72 (33%) | 50 (48%) |  |  |
| **Age ≥50 (later-onset)** |  |  |  |  |  |  |  |  |  |
| **Diagnosed up to 2000** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.18 (2.05-2.33) | <0.001 |
| Non-MSI-high | 5345 (84%) | 818 (73%) | 559 (64%) | 461 (68%) | 415 (86%) | 1588 (95%) | 1504 (97%) |  |  |
| MSI-high | 1021 (16%) | 303 (27%) | 313 (36%) | 216 (32%) | 68 (14%) | 76 (4.6%) | 45 (2.9%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 2.20 (2.05-2.36) | <0.001 |
| Low/negative | 4487 (82%) | 698 (71%) | 450 (58%) | 403 (67%) | 363 (91%) | 1308 (95%) | 1265 (96%) |  |  |
| High | 970 (18%) | 288 (29%) | 324 (42%) | 199 (33%) | 36 (9.0%) | 74 (5.4%) | 49 (3.7%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 1.84 (1.73-1.95) | <0.001 |
| Wild-type | 5199 (86%) | 817 (78%) | 580 (69%) | 475 (74%) | 406 (90%) | 1470 (94%) | 1451 (95%) |  |  |
| Mutant | 868 (14%) | 235 (22%) | 258 (31%) | 168 (26%) | 44 (10%) | 88 (5.6%) | 75 (4.9%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 1.00 (0.95-1.04) | 0.83 |
| Wild-type | 3663 (67%) | 550 (57%) | 530 (69%) | 421 (72%) | 267 (65%) | 1019 (71%) | 876 (68%) |  |  |
| Mutant | 1776 (33%) | 421 (43%) | 237 (31%) | 161 (28%) | 144 (35%) | 408 (29%) | 405 (32%) |  |  |
| **Diagnosed after 2000** |  |  |  |  |  |  |  |  |  |
| MSI status |  |  |  |  |  |  |  | 2.10 (1.94-2.28) | <0.001 |
| Non-MSI-high | 3267 (85%) | 400 (74%) | 429 (65%) | 250 (72%) | 227 (90%) | 785 (96%) | 1176 (97%) |  |  |
| MSI-high | 571 (15%) | 144 (26%) | 236 (35%) | 96 (28%) | 24 (10%) | 36 (4.4%) | 35 (2.9%) |  |  |
| CIMP status |  |  |  |  |  |  |  | 1.71 (1.58-1.84) | <0.001 |
| Low/negative | 2381 (82%) | 272 (71%) | 313 (62%) | 181 (69%) | 151 (85%) | 574 (93%) | 890 (93%) |  |  |
| High | 520 (18%) | 113 (29%) | 192 (38%) | 80 (31%) | 27 (15%) | 44 (7.1%) | 64 (6.7%) |  |  |
| *BRAF* |  |  |  |  |  |  |  | 2.15 (1.94-2.38) | <0.001 |
| Wild-type | 3229 (89%) | 422 (81%) | 456 (72%) | 259 (80%) | 209 (92%) | 741 (96%) | 1142 (99%) |  |  |
| Mutant | 395 (11%) | 96 (19%) | 173 (28%) | 66 (20%) | 17 (7.5%) | 29 (3.8%) | 14 (1.2%) |  |  |
| *KRAS* |  |  |  |  |  |  |  | 0.99 (0.93-1.04) | 0.60 |
| Wild-type | 2012 (65%) | 217 (54%) | 346 (65%) | 195 (71%) | 136 (69%) | 448 (68%) | 670 (66%) |  |  |
| Mutant | 1061 (35%) | 187 (46%) | 185 (35%) | 78 (29%) | 60 (31%) | 207 (32%) | 344 (34%) |  |  |

\* Percentage indicates the proportion of patients with a specific patient molecular characteristic among all patients or in strata of tumor location (cecum, ascending colon, transverse colon, descending colon, sigmoid colon, and rectum).

† Multivariable odds ratio (OR) (with 95% confidence interval) for molecular marker positivity (i.e., MSI-high, CIMP-high, *BRAF* mutation, or *KRAS* mutation) and Ptrend were calculated by the linear trend test across the ordinal categories of subsite location variable [from rectum (1) to ascending colon (5)] in the multivariable logistic regression model adjusted for sex (female vs. male) and study (i.e., cohort).

Abbreviations: CI, confidence interval; CIMP, CpG island methylator phenotype; MSI, microsatellite instability; OR, odds ratio.