**Supplementary Table 1. Clinicopathological, immunohistochemical and molecular features of the 12 rhabdoid colorectal cancers7**

**Clinicopathological features**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Case**\* | **Age**(years) | **Sex** | **Site** | **T§** | **N** | **M** | **Follow up**(months) | **Status** | **Reference** |
| RC 1 | 73 | Female | Cecum | 4 | 1 | 0 | 6  | Dead | 6 |
| RC 2 | 71 | Male | Cecum | 4 | 1 | 0 | 8  | Dead | 41 |
| RC 3 | 62 | Male | Sigma | 3 | 2 | 0 | 36  | Alive | 41 |
| RC 4 | 83 | Female | Rectum | 4 | 0 | 1 | 1  | Dead | 42 |
| RC 5 | 49 | Male | Sigma | 4 | 2 | 0 | 7  | Dead | 6 |
| RC 6 | 63 | Male | Left colon | 3 | 1 | 0 | 1  | Dead | unpublished |
| RC 7 | 71 | Female | Cecum | 4 | 1 | 0 | 8  | Dead | unpublished |
| RC 8 | 71 | Female | Rectum | 3 | 2 | 0 | 26 | Alive | unpublished |
| RC 9 | 76 | Female | Right colon | 3 | 0 | 0 | 6 | Alive | unpublished |
| RC 10 | 65 | Female | Right colon | 3 | 0 | 0 | 7 | Dead | unpublished |
| RC 11 | 81 | Male | Right colon | 3 | 1 | 0 | 33 | Alive | unpublished |
| RC 12 | 73 | Male | Right colon | 3 | 2 | 1 | 6 | Alive | unpublished |

\* cases RC1 and RC2 were subjected to exome sequencing.

**§** T, pathological stage, where T3 is infiltration of the muscular intestinal wall, and T4 is extension to perivisceral fat.

N, lymph node metastasis. M, distant metastasis.

**Immunohistochemical and microsatellite instability analysis**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Case** | **CK20** | **CDX2** | **Vimentin** | **Mhl1** | **Pms2** | **Msh2** | **Msh6** | **SmarcB1** | **MSI\*** |
| RC 1 | **-** | **-** | + | **-** | **-** | + | + | **-** | yes |
| RC 2 | **-** | **-** | + | **-** | **-** | + | + | + | yes |
| RC 3 | + | + | + | + | + | + | + | + | no |
| RC 4 | **-** | **-** | + | + | + | + | + | + | no |
| RC 5 | **-** | **-** | + | + | + | + | + | + | no |
| RC 6 | **-** | **-** | + | + | + | + | + | **-** | no |
| RC 7 | **-** | **-** | + | **-** | **-** | + | + | + | yes |
| RC 8 | **+** | **+** | + | + | + | + | + | + | no |
| RC 9 | **-** | **-** | + | **-** | **-** | + | + | + | yes |
| RC 10 | **-** | **-** | + | + | + | + | + | + | no |
| RC 11 | **-** | **-** | + | **-** | **-** | + | + | + | yes |
| RC 12 | **-** | **-** | + | + | + | + | + | + | no |

\* MSI, microsatellite instability assessed by molecular analysis of size alterations of 5 polyA

 microsatellites (BAT25, BAT26, NR21, NR22, NR24)

+, positive immunostaining; **-**, negative immunostaining.

**Supplementary Table 2. Somatic mutations of candidate genes (15 out of 20 are reported) shared by the two rhabdoid cancers at exome sequencing**

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Chr** | **Exon** | **Mutations**a | **Base change** | **Aminoacid change** | **SIFT**b | **Polyphen2\_HDIV**c | **Polyphen2\_HVAR**d | **MutationTaster**e | **Mutation Assessor**f | **Case** | **Previously reported in cancer** |
| **CROCC** | 1 | 4 | NS | 481G>T | Ala161Ser | T | D | D | D | N | RC 1 | NO |
| 25 | SPL | 3705A>G  | ac lost | . | . | . | . | . | RC 1 | NO |
| 35 | NS | 5654T>C | Val1885Ala | T | D | P | D | L | RC 2 | NO |
| **DNAH7** | 2 | 27 | NS | 4264C>A | Pro1422Thr  | D | D | D | D | M | RC 1 | NO |
|  |  | 25 | NS | 4017G>T | Lys1339Asn | D | D | D | D | H | RC 2 | NO |
| **ENAH** | 1 | 3 | SG  | 241C>T | Arg81\* | T | . | . | A | . | RC 1 | Endometrial carcinoma |
| 12 | NS | 1626G>C | Gln542His | T | D | D | D | N | RC 2 | NO |
| **EPPK1** | 8 | 1 | NS  | 3134C>T | Ala1045Val  | T | D | D | D | L | RC 1 | NO |
| 1 | NS | 5131G>A | Asp1711Asn | T | P | B | N | L | RC 2 | NO |
| **DMD** | X | 6 | NS  | 235A>G | Ile79Val | D | D | D | D | M | RC 1 | NO |
| 21 | NS | 2725C>T | His909Tyr | D |  D  |  D  |  D | L  | RC 2 | NO |
| **NEXN** | 1 | 12 | NS  | 1562 C>T | Ala521Val | T | D | D | P | M | RC 1 | NO |
| 11 | NS | 1370 C>T | Ala457Val |  T |  P | P | D  |  L | RC 2 | NO |
| **SPIRE2** | 16 | 3 | NS  | 349G>A | Glu117Lys | D | D | D | D | M | RC 1 | NO |
| 15 | NS | G2093A | Arg698His | D | B | B | D | M | RC 2 | NO |
| **SPTBN4** | 19 | 19 | NS  |  3991G>A | Gly1331Ser | D | P | B | P | N | RC 1 | Colorectal, pancreatic cancer |
| 25 | NS | 5120G>A | Arg1707His | D | D | D | D | L | RC 2 | Endometrial carcinoma |
| **TTN** | 2 | 115 | NS  | 28364C>T | Thr9455Ile | D | D | D | D | L | RC 1 | NO |
| 144 | NS  | 39448A>G | Thr13150Ala  |  D | P  | P |  D | M  | RC 2 | NO |
| 154 | NS | 59291A>C | Asn19764Thr  | D  | P  | P  | D  | M  | RC 2 | NO |
| **MUS81** | 11 | 5 | NS  | 539G>C | Arg180Pro | P | P | B | N | L | RC 1 | NO |
| 1 | NS | 110G>A | Arg37His | D | D | P | P | L | RC 2 | NO |
| **ERCC6** | 10 | 5 | NS | 1330G>A | Gly444Arg | T | B | B | N | M | RC 1 | SkIn cutaneous melanoma |
| 10 | NS | 1996C>T | Arg666Cys | D | D | D | D | M | RC 2 | NO |
| **PSMD3** | 17 | 3 | NS | 526A>G | Met176Val | T | B | B | D | N | RC 1 | NO |
| 5 | NS | 793G>A | Asp265Asn | D | P | B | D | M | RC 2 | NO |
| **CDC27** | 17 | 11 | NS  | 1199A>G | Lys400Arg | T | P | P | D | M | RC 2 | NO |
| 14 | NS | 1922A>G | Tyr641Cys | D | D | P | P | H | RC 1 | Kidney chromophobe |
| **CTDP1** | 18 | 8 | NS  | 1523C>T | Pro508Leu | T | B | B | N | L | RC 2 | NO |
| 12 | NS | 2614A>G | Ser872Gly | T | D | P | D | . | RC 1 | NO |
| **KIAA1543** | 19 | 15 | NS  | 3053T>C | Met1018Thr | D | D | D | D | M | RC 2 | Colorectal adenocarcinoma |
| 18 | NS | 3433G>A | Ala1145Thr | D | D | P | D | L | RC 1 | NO |

aNS, non synonimous; SG, stop gain; SPL, splicing. bD, deleterious; T, tolerated. cD, probably damaging; P, possibly damaging; B, benign. dD, probably damaging; P, possibly damaging; B, benign.

eA, disease causing automatic; D, disease causing; N, polymorphism; P, polymorphism automatic.

fH: high (functional); M: medium (functional); L: low (non-functional); N: neutral (non-functional).

**Supplementary Table 3.** Rhabdoid colorectal cancers (RC): molecular alterations, centrosome aberrations and ploidy

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Case | MSI1 | *BRAF*2 | *KRAS*2 |  *CROCC* Gene Mutation LOH |  Centrosome Aberrations3 Numerical Structural |  Ploidy | *SMARCB1*mutation |
| RC 1 | yes | V600E | WT | c.481G>Tp.Ala161Serc.3705-2A>Gsplicing  | no | reduced<1 per cell | round or fragmented, incorrectly positioned | abnormal | WT |
| RC 2 | yes | V600E | WT | c.5654T>Cp.Val1885Ala | no | reduced<1 per cell | round or fragmented, incorrectly positioned | abnormal | WT |
| RC 3 | no | WT | WT | WT | yes | reduced<1 per cell | round, close to the nucleus or incorrectly positioned | abnormal | WT |
| RC 4 | no | V600E | WT | WT | yes | reduced<1 per cell | round, incorrectly positioned | abnormal | WT |
| RC 5 | no | V600E | WT | WT | yes | reduced<1 per cell | round or fragmented, incorrectly positioned | abnormal | WT |
| RC 6 | no | V600E | G12V | WT | yes | reduced<1 per cell | round or fragmented, incorrectly positioned | abnormal | WT |
| RC 7 | yes | V600E | WT | WT | yes | reduced<1 per cell | round or fragmented, incorrectly positioned | abnormal | WT |
| RC 8 | no | WT | WT | WT | yes | reduced<1 per cell | round or fragmented, incorrectly positioned | n.d. | WT |
| RC 9 | yes | V600E | WT | c.3959G>Tp.Ser1320Ilec.4976G>Ap.Arg1659His | no | reduced<1 per cell | round or fragmented, incorrectly positioned | n.d. | WT |
| RC 10 | no | WT | WT |  WT | yes | reduced<1 per cell |  round, incorrectly positioned | n.d. | WT |
| RC 11 | yes | WT | WT | c.4528G>Ap.Ala1510Thr | no | reduced<1 per cell | round or fragmented, incorrectly positioned | n.d. | WT |
| RC 12 | no | WT | WT | WT | yes | reduced<1 per cell | round or fragmented, incorrectly positioned | n.d. | WT |

**1**MSI, microsatellite instability indicative of deficiency or proficiency in DNA mismatch repair; tested by presence/absence of immunostaining for the 4 proteins involved (Mlh1, Pms2, Msh2, Msh6) and confirmed by molecular testing alterations in size of 5 polyA microsatellites (BAT25, BAT 26, NR21, NR22, NR24) (<http://oncologypro.esmo.org/Science-Education/Factsheets-on-Biomarkers/Microsatellite-Instability-Defective-DNA-Mismatch-Repair> ).

**2**WT, wild type; mutations are indicated as nucleotide and aminoacid changes.

**3**Assessed using immunostaining with anti-CROCC and anti-gamma tubulin antibodies.

**Supplementary Table 4. Rhabdoid tumours of infants (RI): molecular alterations, centrosome aberrations, and ploidy.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Case | Age (years) | Sex | SMARCB1 Alterations Mutation ICH | Centrosome Aberrations1Numerical Structural | Ploidy | CROCCMutation | Follow up(months) | Status |
| RI 1 | 2 | F | Yes | - | normal~1 per cell | Single, large centriol | diploid | WT | n.a. | n.a. |
| RI 2 | 2 months | M | Yes | - | normal~ 1 per cell | Single, large centriol | diploid | WT | 3 | Dead |
| RI 3 | 4 | M | WT | + | normal1-2 per cell | Single, large centriol | diploid | WT | 33 | Alive |
| RI 4 | 5 | M | Yes | - | normal~ 1 per cell | Single, large centriol | diploid | WT | 21 | Dead |
| RI 5 | 10 | F | WT | + | normal1-2 per cell | Single, large centriol | diploid | WT | 92 | Alive |
| RI 6 | 6 | M | Yes | - | normal~1 per cell | Single, large centriol | diploid | WT | n.a. | n.a. |
| RI 7 | 19 | F | Yes | - | normal~1 per cell | Single, large centriol | diploid | WT | 46 | Alive |
|  |  |  |  |  |  |  |  |  |  |  |

**1**Assessed using immunostaining with anti-CROCC and anti-gamma tubulin antibodies.

|  |  |  |  |
| --- | --- | --- | --- |
| **Characteristics** |  | Dataset AN (%) | Dataset BN (%) |
|  |  |  |  |
| **N of patients**  |  | 141 (100) | 102 (100) |
|  |  |  |  |
| **Age median** |  | 60 | 64 |
| **Sex** | female | 78 (55.3) | 53 (52) |
|  | male | 63 (44.7) | 49 (48) |
|  |  |  |  |
| **Localization** | right | 41(29) | 28 (27,5) |
|  | left | 100 (71) | 74 (72,5) |
|  |  |  |  |
| **Site of distant metastases** | liver | 45 (95.7) | 83 (81) |
|  | lung | 2 (4.3) | 35 (34.3) |
|  | peritoneum | 0 | 22 (21.5) |
|  | Bone | 0 | 6 (5.8) |
|  | CNS | 0 | 2 (2) |
|  |  |  |  |
| **Number of metastatic sites** | 1 | 20 (42.6) |  49 (48) |
|  | 2 | 0 | 44 (43) |
|  | >2 | 0 | 9 (9) |
|  | not available | 27 (57.4) | 0 |
|  |  |  |  |
| **Stage** | I | 12 (8.5) | 0 |
|  | II | 60 (42.6) |  21 (20.5) |
|  | III | 22 (15.6) | 29 (28.5) |
|  | IV | 47 (33.3) | 52 (51.0) |
|  |  |  |  |
| **Microsatellite instability** | absent | 118 (83) | 83 (81) |
|  | present | 23 (17) | 14 (14) |
|  | not available | 0 | 5 (5) |
|  |  |  |  |
| ***KRAS*** | wild type | 91 (65) | 41 (40.2) |
|  | mutant | 50 (35) | 50 (49) |
|  | not available | 0 | 11 (10.8) |
|  |  |  |  |
| **BRAFV600E** | wild type | 131 (93) | 90 (88) |
|  | mutantnot available | 10 (7)0 | 7 (7)5(5) |

**Supplementary Table 5**: Clinicopathologic and molecular features of classical colorectal cancers analyzed.

**Abbreviations:** Right includes: Proximal caecum, ascending and transverse colon. Left includes: Distal descending, sigmoid colon, rectum. Microsatellite instability was assessed with molecular testing polyA mononucleotides and immunohistochemistry for mismatch repair proteins Mlh1, Msh2, Msh6 and Pms2.

|  |
| --- |
|  Sanger *CROCC* sequencing primers |
| Gene | Sense | Antisense |  |
|  CROCC  | 5’AAATTGGAGGAGACGGCTTT3’  | 5’CAGCTTCTGCTCCTTGTCCT3’ |  |
|  RT-PCR primers |
| CROCC-152bp | 5’ACATGACCGCCAAGTACTCC3’ | 5’CCTCCCGTAGCTGTTGTAGC3’ |  |
| CROCC-173bp | 5’CTGAGGGACACAGAGCACAG3’ | 5’TCCTCACTCAGAGCCTGGTT3’ |  |
| RAC1 | 5′-GCCAATGTTATGGTAGAT-3′ | 5′-GACTCACAAGGGAAAAGC-3′ |  |
| CDX2  | 5’ AAAGTGAGCTGGCTGCCACACTTG 3’ | 5’ TCCATCAGTAGATGCTGTTCGTGG 3’ |  |
| KRT20 | 5’CTGAATAAGGTCTTTGATGACC 3’ | 5’ATGCTTGTGTAGGCCATCGA 3’ |  |
| CDH1 | 5’GAACGCATTGCCACATACAC 3’ | 5’ATTCGGGCTTGTTGTCATTC 3’ |  |
| LAMA5 | 5’AAGATGGCGAAGCGGCTCT 3’ | 5’ TTGAAGTAGGGCGGGTGCAG 3’ |  |
| KRT18 |

|  |
| --- |
| 5’ TTTCCCAGATCATGGAGGAG 3’ |

 |

|  |
| --- |
| 5’AGCCCATGAGGTTTTTCTGA3’ |

 |  |
| VIM  | 5’TGACAATGCGTCTCTGGCAC 3’ | 5’CCTGGATTTCCTCTTCGTGG 3’ |  |
| 18S  | 5’GGGAGCCTGAGAAACGGC 3’ | 5’GGGTCGGGAGTGGGTAATTT 3’ |  |
| ACTB | GCTCACCATGGATGATGATATCGC | ATAGGAATCCTTCTGACCCATGCC |  |
| ACTG2 | 5’-CCGCCCTAGACATCAGGGT-3’ | 5’-TCTTCTGGTGCTACTCGAAGC-3’ |  |
| SMARCB1 | 5’TCCGTATGTTCCGAGGTTC3’ | 5’CTTCCACTTCCGAGGCTTT3’ |  |
| CEP152 | 5'-CCATGTCAGCTTGTTCTTCC-3' | 5'-CACCTTTCTCTTCTCCTGCT-3' |  |
| CEP192 | 5’CCCAACGACCTAATGATGTTCA3’ | 5’GCTCCCAAGTCGCTTGTAGATT3’ |  |
| CDKN2B | 5’TACAGGAGTCTCCGTTGGC3’ | 5’GTGAGAGTGGCAGGGTCTG3’ |  |
| CDKN2A | 5’CCACCCTGGCTCTGACCAT3’ | 5’GCCACTCGGGCGCTG3’ |  |
| CDH2 | 5'-GGCATAGTCTATGGAGAAGT-3' | 5'-GCTGTTGTCAGAAGTCTCTC-3' |  |

**Supplementary Table 6. Sequencing and Reverse transcription PCR primers**

**Supplementary Table 7A. *CROCC* regions covered by the custom panel used for next-generation targeted sequencing.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene** | **Chr** | **Start** | **End** |  | **Gene** | **Chr** | **Start** | **End** |  | **Gene** | **Chr** | **Start** | **End** |
| CROCC | chr1 | 17248461 | 17248565 |  | CROCC | chr1 | 17271988 | 17272118 |  | CROCC | chr1 | 17287230 | 17287347 |
| CROCC | chr1 | 17248554 | 17248670 |  | CROCC | chr1 | 17272134 | 17272224 |  | CROCC | chr1 | 17287637 | 17287723 |
| CROCC | chr1 | 17249085 | 17249217 |  | CROCC | chr1 | 17272675 | 17272775 |  | CROCC | chr1 | 17292117 | 17292245 |
| CROCC | chr1 | 17249160 | 17249244 |  | CROCC | chr1 | 17272738 | 17272848 |  | CROCC | chr1 | 17292222 | 17292343 |
| CROCC | chr1 | 17250720 | 17250829 |  | CROCC | chr1 | 17273186 | 17273323 |  | CROCC | chr1 | 17292322 | 17292437 |
| CROCC | chr1 | 17250799 | 17250931 |  | CROCC | chr1 | 17274660 | 17274791 |  | CROCC | chr1 | 17292383 | 17292508 |
| CROCC | chr1 | 17250873 | 17250992 |  | CROCC | chr1 | 17274780 | 17274917 |  | CROCC | chr1 | 17292504 | 17292599 |
| CROCC | chr1 | 17250976 | 17251089 |  | CROCC | chr1 | 17274933 | 17275069 |  | CROCC | chr1 | 17292628 | 17292729 |
| CROCC | chr1 | 17256284 | 17256403 |  | CROCC | chr1 | 17275203 | 17275319 |  | CROCC | chr1 | 17292742 | 17292867 |
| CROCC | chr1 | 17256414 | 17256546 |  | CROCC | chr1 | 17275297 | 17275411 |  | CROCC | chr1 | 17292883 | 17293016 |
| CROCC | chr1 | 17256533 | 17256633 |  | CROCC | chr1 | 17275424 | 17275510 |  | CROCC | chr1 | 17293026 | 17293116 |
| CROCC | chr1 | 17256637 | 17256752 |  | CROCC | chr1 | 17277375 | 17277491 |  | CROCC | chr1 | 17294680 | 17294776 |
| CROCC | chr1 | 17256905 | 17257024 |  | CROCC | chr1 | 17277480 | 17277608 |  | CROCC | chr1 | 17294770 | 17294880 |
| CROCC | chr1 | 17257013 | 17257116 |  | CROCC | chr1 | 17277597 | 17277687 |  | CROCC | chr1 | 17294899 | 17294999 |
| CROCC | chr1 | 17257674 | 17257770 |  | CROCC | chr1 | 17279663 | 17279769 |  | CROCC | chr1 | 17295543 | 17295679 |
| CROCC | chr1 | 17257742 | 17257870 |  | CROCC | chr1 | 17279774 | 17279898 |  | CROCC | chr1 | 17295668 | 17295803 |
| CROCC | chr1 | 17257818 | 17257943 |  | CROCC | chr1 | 17279902 | 17280005 |  | CROCC | chr1 | 17295792 | 17295910 |
| CROCC | chr1 | 17263077 | 17263164 |  | CROCC | chr1 | 17279976 | 17280095 |  | CROCC | chr1 | 17296213 | 17296351 |
| CROCC | chr1 | 17263141 | 17263233 |  | CROCC | chr1 | 17280645 | 17280757 |  | CROCC | chr1 | 17296329 | 17296458 |
| CROCC | chr1 | 17263263 | 17263365 |  | CROCC | chr1 | 17280746 | 17280866 |  | CROCC | chr1 | 17296433 | 17296527 |
| CROCC | chr1 | 17263352 | 17263433 |  | CROCC | chr1 | 17280826 | 17280935 |  | CROCC | chr1 | 17296665 | 17296798 |
| CROCC | chr1 | 17264084 | 17264185 |  | CROCC | chr1 | 17281146 | 17281235 |  | CROCC | chr1 | 17296794 | 17296903 |
| CROCC | chr1 | 17264174 | 17264285 |  | CROCC | chr1 | 17281217 | 17281347 |  | CROCC | chr1 | 17296879 | 17296990 |
| CROCC | chr1 | 17264739 | 17264868 |  | CROCC | chr1 | 17281374 | 17281456 |  | CROCC | chr1 | 17296947 | 17297081 |
| CROCC | chr1 | 17264859 | 17264949 |  | CROCC | chr1 | 17281702 | 17281837 |  | CROCC | chr1 | 17297117 | 17297245 |
| CROCC | chr1 | 17264963 | 17265050 |  | CROCC | chr1 | 17281854 | 17281992 |  | CROCC | chr1 | 17297164 | 17297289 |
| CROCC | chr1 | 17265348 | 17265463 |  | CROCC | chr1 | 17282004 | 17282124 |  | CROCC | chr1 | 17297842 | 17297965 |
| CROCC | chr1 | 17265665 | 17265771 |  | CROCC | chr1 | 17282412 | 17282530 |  | CROCC | chr1 | 17297937 | 17298073 |
| CROCC | chr1 | 17266338 | 17266447 |  | CROCC | chr1 | 17282518 | 17282647 |  | CROCC | chr1 | 17298176 | 17298280 |
| CROCC | chr1 | 17266441 | 17266572 |  | CROCC | chr1 | 17282591 | 17282712 |  | CROCC | chr1 | 17298746 | 17298876 |
| CROCC | chr1 | 17266584 | 17266695 |  | CROCC | chr1 | 17284990 | 17285092 |  | CROCC | chr1 | 17298849 | 17298930 |
| CROCC | chr1 | 17270505 | 17270588 |  | CROCC | chr1 | 17285081 | 17285215 |  | CROCC | chr1 | 17298955 | 17299075 |
| CROCC | chr1 | 17270780 | 17270893 |  | CROCC | chr1 | 17285248 | 17285359 |  |  |  |  |  |
| CROCC | chr1 | 17271855 | 17271963 |  | CROCC | chr1 | 17287132 | 17287241 |  |  |  |  |  |

**Supplementary Table 6B. *SMARCB1* regions covered by the custom panel used for next-generation target sequencing.**

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Chr** | **Start** | **End** |
| SMARCB1 | chr22 | 24129273 | 24129399 |
| SMARCB1 | chr22 | 24129388 | 24129525 |
| SMARCB1 | chr22 | 24133860 | 24133955 |
| SMARCB1 | chr22 | 24133944 | 24134059 |
| SMARCB1 | chr22 | 24134048 | 24134131 |
| SMARCB1 | chr22 | 24135623 | 24135745 |
| SMARCB1 | chr22 | 24135734 | 24135825 |
| SMARCB1 | chr22 | 24135814 | 24135938 |
| SMARCB1 | chr22 | 24143076 | 24143205 |
| SMARCB1 | chr22 | 24143197 | 24143323 |
| SMARCB1 | chr22 | 24145425 | 24145504 |
| SMARCB1 | chr22 | 24145493 | 24145590 |
| SMARCB1 | chr22 | 24145621 | 24145731 |
| SMARCB1 | chr22 | 24158877 | 24158996 |
| SMARCB1 | chr22 | 24158985 | 24159111 |
| SMARCB1 | chr22 | 24159071 | 24159175 |
| SMARCB1 | chr22 | 24167296 | 24167399 |
| SMARCB1 | chr22 | 24167388 | 24167477 |
| SMARCB1 | chr22 | 24167466 | 24167579 |
| SMARCB1 | chr22 | 24167556 | 24167657 |
| SMARCB1 | chr22 | 24175705 | 24175834 |
| SMARCB1 | chr22 | 24175729 | 24175856 |
| SMARCB1 | chr22 | 24176270 | 24176395 |
| SMARCB1 | chr22 | 24176384 | 24176517 |

**Supplementary Table 8.** Antibodies employed and working conditions for immunohistochemistry, immunofluorescence or western blot analysis of tissues and cell lines.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Antibody** | **Company** | **Clone** | **Source** | **dilution** |
| α tubulin | ABCAM | 18251 | rabbit polyclonal | 1:100 |
| β tubulin | COVANCE | TUJ1 | mouse monoclonal | 1:500 |
| γ tubulin | ABCAM | TU-30 | mouse monoclonal | 1:100 |
| CROCC | ABCAM | NBP1-80820 | rabbit polyclonal | 1:200 |
| CENTRIN 1 | ABCAM | AB101332  | rabbit polyclonal |  1:50 |
| SMARCB1 | BD | BAF47 | mouse monoclonal |  1:50 |
| γH2AX | ABCAM | p S139 | rabbit polyclonal | 1:500 |
| β actin | SANTA CRUZ | C4 | mouse monoclonal |  1: 5000 |

**Supplementary Table 9. Rhabdoid colorectal cancer reported in literature between 1993-2015**

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Number** | **Case** | **Age** | **Sex** | **location** | **metastasis** | **type** | **survival (m)** | **(BRAF, KRAS and MMR)** | **SMARCB1 (IHC)** |
| 1 | Baba | 45 | F | ? | ? | ? | 1.5 | ND | ND |
| 2 | Romera | 77 | M | DC | no | pure | 2 | ND | ND |
| 3 | chetty | 72 | F | cecum | yes | composite | ? | ND | ND |
| 4 | Yang | 75 | M | colon | no | pure | 0.5 | ND | ND |
| 5 | markus | 84 | F | colon | No | composite | ? alive | ND | ND |
| 6 | Nakamura | 76 | M | cecum | yes | pure | 2 | ND | ND |
| 7 | Kono | 66 | M | cecum | no | composite | 1.5 | ND | ND |
| 8 | Mastoraki | 62 | F | colon | yes | pure | 4 | ND | ND |
| 9 | Seok | 63 | M | cecum | yes | pure | ? | ND | ND |
| 10 | Hoon-kuy | 69 | F | sigmoid | no | composite | 6 | ND | ND |
| 11 | Lee | 62 | M | sigmoid | no | composite | 36 alive | ND | ND |
| 12 | Lee | 83 | M | rectum | yes | composite | 1 | ND | ND |
| 13 | Agaimy | 79 | M | cecum | no | composite | 6 | Yes (BRAF/D) | Neg |
| 14 | kalyan | 31 | F | cecum | yes | composite | 4 | Yes (KRAS/P) | ++ |
| 15 | Remo | 73 | F | cecum | no | composite | 6 | Yes (BRAF/D) | Neg |
| 16 | Pancione | 71 | F | cecum | yes | pure | 8 | Yes (BRAF/D) | ++ |
| 17 | Stulpinas | 49 | M | rectum | yes | composite | 7 | Yes (BRAF/P) | ++ |
| 18 | Moussaly | 87 | F | Transverse | no | composite | 2 | ND | ND |
| 19 | Cho | 73 | M | cecum | no | composite | 1 alive | ND | ND |
| 20 | Sanchez | 77 | M | Transverse | no | pure | 2 | Yes (WT/P) | ND |
| 21 | Sanchez | 65 | M | Descending | no | pure | 12 alive | Yes (WT/P) | ND |
| 22 | Sanchez | 63 | M | Descending | no | pure | 1 | Yes (KRAS/P) | ++ |
| 23 | Sanchez | 71 | F | Cecum | no | composite | 8 | Yes (BRAF/D) | ++ |

All RC reported are characterized by loss of CK20 and positivity for Vimentin (IHC).

Molecular test BRAF (V600E), KRAS, MMR: ND: Not Done (14/23=60%);

Location: cecum: (10/23=43%)

Type: composite; (13/23= 56%)

MMR= D, Defective; P, Proficient