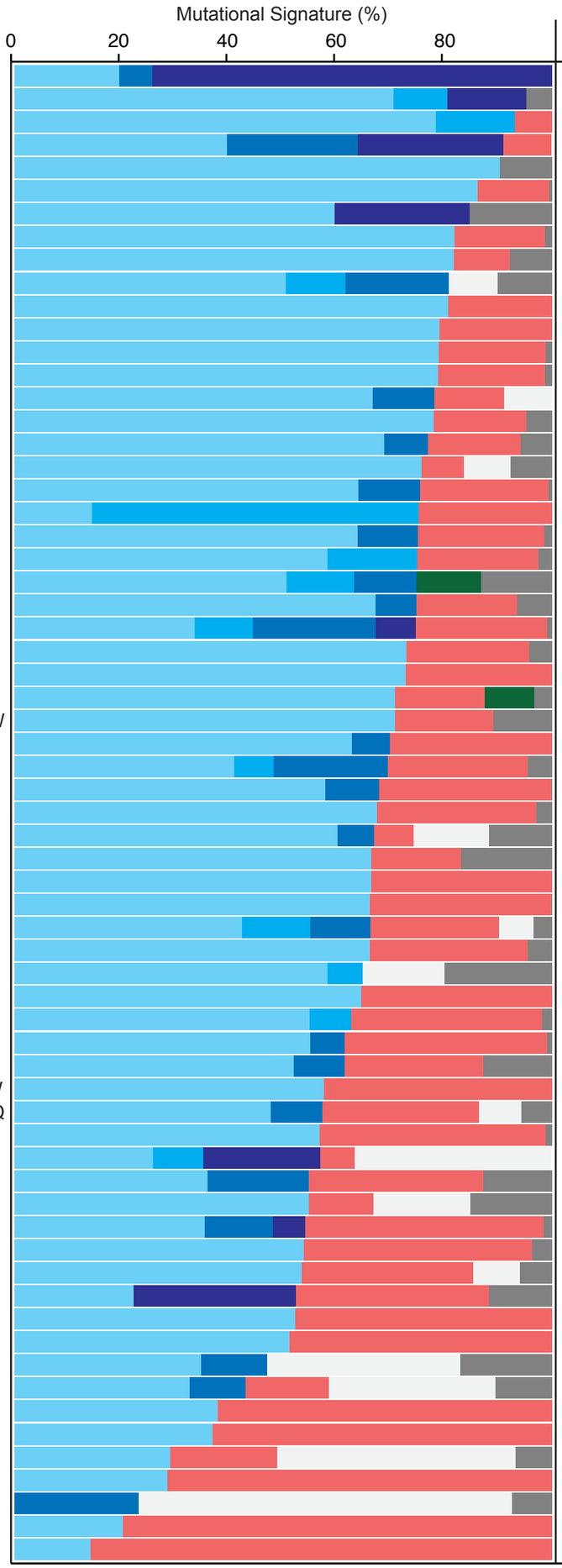
## Supplementary Figure S2

### MSI (hypermutated)




| TCGA ID | Primary Signature | Secondary Signature | MSI Signature (%) | Mutations (n) | SNVs (n) | Indels (%) | MSIsensor Score | *MLH1* Methylation Score |
|---|---|---|---|---|---|---|---|---|
| TCGA-AP-A054 | 26 | 6 | 100 | 1730 | 1503 | 13.1 | 31.98 | 0.87 |
| TCGA-BS-A0TA | 6 | 26 | 95 | 685 | 581 | 15.2 | 19.35 | 0.39 |
| TCGA-D1-A177 | 6 | 15 | 93 | 1199 | 894 | 25.4 | 31.48 | 0.75 |
| TCGA-BG-A0M4 | 6 | 26 | 91 | 877 | 763 | 13.0 | 29.16 | 0.68 |
| TCGA-A5-A0GB | 6 | 1 | 90 | 1061 | 851 | 19.8 | 36.50 | 0.83 |
| TCGA-BS-A0U8 | 6 | 1 | 86 | 671 | 512 | 23.7 | 24.27 | 0.83 |
| TCGA-DI-A0WH | 6 | 26 | 85 | 920 | 782 | 15.0 | 25.06 | 0.71 |
| TCGA-D1-A101 | 6 | 1 | 82 | 684 | 597 | 12.7 | 16.28 | 0.40 |
| TCGA-AP-A0LG | 6 | 1 | 82 | 639 | 521 | 18.5 | 24.16 | 0.85 |
| TCGA-D1-A160 | 6 | 20 | 81 | 750 | 613 | 18.3 | 21.45 | 0.63 |
| TCGA-BS-A0TJ | 6 | 1 | 81 | 1077 | 849 | 21.1 | 32.67 | 0.75 |
| TCGA-A5-A0VQ | 6 | 1 | 79 | 557 | 453 | 18.7 | 15.57 | 0.81 |
| TCGA-AP-A0LT | 6 | 1 | 79 | 1004 | 782 | 22.1 | 37.41 | 0.82 |
| TCGA-D1-A0ZO | 6 | 1 | 79 | 908 | 713 | 21.5 | 28.32 | 0.60 |
| TCGA-AP-A0LE | 6 | 1 | 78 | 801 | 624 | 22.1 | 33.29 | 0.85 |
| TCGA-D1-A17R | 6 | 1 | 78 | 374 | 334 | 10.7 | 9.94 | 0.58 |
| TCGA-D1-A17H | 6 | 1 | 77 | 1019 | 805 | 21.0 | 30.83 | 0.54 |
| TCGA-B5-A0K2 | 6 | 8 | 76 | 453 | 371 | 18.1 | 10.65 | 0.57 |
| TCGA-BG-A18B | 6 | 1 | 76 | 553 | 421 | 23.9 | 23.12 | 0.75 |
| TCGA-AX-A0J1 | 15 | 1 | 75 | 8041 | 7699 | 4.3 | 29.85 | 0.69 |
| TCGA-D1-A163 | 6 | 1 | 75 | 886 | 665 | 24.9 | 29.96 | 0.61 |
| TCGA-D1-A17A | 6 | 1 | 75 | 374 | 302 | 19.3 | 12.22 | 0.53 |
| TCGA-AP-A05N | 6 | 15 | 75 | 384 | 303 | 21.1 | 12.59 | 0.83 |
| TCGA-B5-A0JZ | 6 | 1 | 75 | 760 | 585 | 23.0 | 28.87 | 0.68 |
| TCGA-AX-A064 | 6 | 1 | 75 | 417 | 352 | 15.6 | 15.94 | 0.70 |
| TCGA-B5-A11J | 6 | 1 | 73 | 677 | 545 | 19.5 | 23.51 | 0.70 |
| TCGA-D1-A0ZS | 6 | 1 | 73 | 618 | 478 | 22.7 | 28.29 | 0.58 |
| TCGA-D1-A17D | 6 | 1 | 71 | 723 | 603 | 16.6 | 18.85 | 0.56 |
| TCGA-BG-A0VW | 6 | 1 | 71 | 683 | 596 | 12.7 | 18.29 | 0.60 |
| TCGA-B5-A11U | 6 | 1 | 70 | 573 | 439 | 23.4 | 27.25 | 0.65 |
| TCGA-A5-A0GA | 6 | 1 | 69 | 462 | 373 | 19.3 | 15.97 | 0.54 |
| TCGA-D1-A17U | 6 | 1 | 68 | 621 | 489 | 21.3 | 27.42 | 0.52 |
| TCGA-B5-A11H | 6 | 1 | 67 | 1569 | 1170 | 25.4 | 40.43 | 0.02 |
| TCGA-AX-A060 | 6 | 21 | 67 | 1142 | 983 | 13.9 | 36.56 | 0.83 |
| TCGA-A5-A0GI | 6 | 1 | 66 | 508 | 438 | 13.8 | 14.54 | 0.83 |
| TCGA-BS-A0UA | 6 | 1 | 66 | 500 | 403 | 19.4 | 16.89 | 0.50 |
| TCGA-A5-A0GH | 6 | 1 | 66 | 675 | 528 | 21.6 | 30.24 | 0.80 |
| TCGA-BG-A0LX | 6 | 1 | 66 | 724 | 589 | 18.6 | 26.46 | 0.78 |
| TCGA-D1-A176 | 6 | 1 | 66 | 650 | 533 | 18.0 | 19.20 | 0.67 |
| TCGA-BS-A0TE | 6 | 5 | 65 | 472 | 416 | 11.9 | 14.32 | 0.61 |
| TCGA-AX-A06H | 6 | 1 | 65 | 635 | 492 | 22.5 | 23.79 | 0.47 |
| TCGA-BG-A0VZ | 6 | 1 | 63 | 521 | 412 | 20.9 | 22.90 | 0.56 |
| TCGA-AP-A0LP | 6 | 1 | 62 | 439 | 346 | 21.2 | 17.64 | 0.74 |
| TCGA-B5-A0K6 | 6 | 1 | 61 | 520 | 465 | 10.6 | 16.83 | 0.80 |
| TCGA-A5-A0GW | 6 | 1 | 58 | 490 | 397 | 19.0 | 24.38 | 0.59 |
| TCGA-BG-A0MQ | 6 | 1 | 57 | 926 | 722 | 21.9 | 23.55 | 0.87 |
| TCGA-D1-A17M | 6 | 1 | 57 | 640 | 535 | 16.3 | 16.57 | 0.62 |
| TCGA-B5-A11G | 12 | 6 | 57 | 871 | 688 | 21.0 | 28.95 | 0.03 |
| TCGA-BS-A0U7 | 6 | 1 | 55 | 300 | 265 | 11.7 | 3.20 | 0.57 |
| TCGA-A5-A0G9 | 6 | 8 | 55 | 609 | 538 | 11.7 | 20.59 | 0.81 |
| TCGA-AP-A0LD | 1 | 6 | 54 | 726 | 587 | 19.1 | 34.20 | 0.80 |
| TCGA-AX-A05S | 6 | 1 | 54 | 781 | 635 | 18.7 | 31.68 | 0.72 |
| TCGA-BG-A0M0 | 6 | 1 | 53 | 214 | 175 | 18.2 | 9.83 | 0.82 |
| TCGA-D1-A16N | 1 | 26 | 52 | 196 | 172 | 12.2 | 5.03 | 0.51 |
| TCGA-BS-A0UL | 6 | 1 | 52 | 572 | 497 | 13.1 | 12.99 | 0.33 |
| TCGA-D1-A174 | 6 | 1 | 51 | 1221 | 972 | 20.4 | 35.73 | 0.03 |
| TCGA-AX-A063 | 6 | 21 | 47 | 1504 | 1326 | 11.8 | 34.04 | 0.74 |
| TCGA-BK-A0C9 | 6 | 1 | 43 | 882 | 819 | 7.1 | 19.92 | 0.75 |
| TCGA-D1-A17B | 1 | 6 | 38 | 418 | 359 | 14.1 | 8.20 | 0.39 |
| TCGA-B5-A0JV | 1 | 6 | 37 | 524 | 459 | 12.4 | 22.81 | 0.81 |
| TCGA-D1-A17F | 30 | 6 | 29 | 357 | 334 | 6.4 | 4.57 | 0.32 |
| TCGA-AX-A05Y | 1 | 6 | 28 | 287 | 253 | 11.8 | 7.22 | 0.06 |
| TCGA-BS-A0UJ | 12 | 20 | 23 | 2455 | 2328 | 5.2 | 3.98 | 0.02 |
| TCGA-D1-A167 | 1 | 6 | 20 | 2450 | 2352 | 4.0 | 24.60 | 0.43 |
| TCGA-A5-A0VP | 1 | 6 | 14 | 2275 | 2230 | 2.0 | 13.09 | 0.03 |

Signatures: *POLE* 10 14 | MMR defect 6 15 20 26 | Aging 1 | HRD defect 3 | Other Other NA