**SUPPLEMENTARY TABLES**

**Supplementary Table S1. Overview of the molecular assays performed in this study**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Patient ID** | **Tumor purity** |  | **MMR status** | **MSI status** | **WES** | **IDH1 status** | **IDH2 status** | **MGMT status** |  | **EGFR status at diagnosis** |  | **EGFR status at relapse** | **TERTp status** | **TS** |
|  | **D** | **R** |  | **D** | **R** | **D** | **R** |  | **EGFRvIII** | **FISH** |  | **EGFRvIII** | **FISH** |
| **MMR deficient samples** | #2 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #3 | 75 | 80 |  | y | y | y | y | y | y | y | y |  | y | y |  | y | y | y | y |
| #6 | 80 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #12 | 75 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #17 | 70 | 75 |  | y | y | y | y | y | y | y | y |  | y | y |  | y | n | y | y |
| #18 | 70 | 75 |  | y | y | y | y | y | y | y | y |  | y | n |  | y | y | y | y |
| #20 | 75 | 75 |  | y | y | y | y | y | y | y | y |  | y | n |  | y | n | y | y |
| #31 | 85 | 80 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #35 | 75 | 75 |  | n.e. | y | n | n | y | y | y | y |  | y | y |  | y | y | y | n.e. |
| #41 | 85 | 85 |  | y | y | y | y | y | y | y | y |  | y | y |  | y | y | y | y |
| #45 | 80 | 85 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #46 | 75 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #50 | 70 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #53 | 70 | 70 |  | y | y | y | y | y | y | y | y |  | y | y |  | y | y | y | y |
| **MMR proficient samples** | #1 | 75 | 70 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #4 | 90 | 85 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #5 | 85 | 80 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | n.e. |
| #7 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #8 | 75 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #9 | 90 | 85 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #10 | 80 | 85 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #11 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #13 | 75 | 75 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #14 | 80 | 85 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #15 | 80 | 80 |  | y | n.e. | y | n | y | y | y | y |  | y | n |  | y | y | y | y |
| #16 | 75 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #19 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | n.e. |  | y | n | y | y |
| #21 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #22 | 85 | 85 |  | y | n.e. | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #23 | 85 | 90 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | n | y | y |
| #24 | 90 | 90 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #25 | 90 | 85 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #26 | 70 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #27 | 80 | 75 |  | y | y | y | y | y | y | y | y |  | y | y |  | y | y | y | y |
| #28 | 75 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #29 | 75 | 80 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #30 | 80 | 85 |  | y | y | y | n | y | y | y | n.e. |  | y | y |  | y | y | y | y |
| #32 | 85 | 85 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #33 | 90 | 85 |  | y | y | y | n | y | y | y | y |  | n.e. | y |  | n.e. | y | y | y |
| #34 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | n |  | y | n | y | y |
| #36 | 70 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #37 | 80 | 85 |  | y | n.e. | n | n | y | y | y | y |  | y | y |  | n.e. | y | n.e. | n.e. |
| #38 | 85 | 85 |  | y | y | y | y | y | y | y | y |  | y | y |  | y | y | y | y |
| #39 | 80 | 85 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #40 | 90 | 90 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | n.e. |
| #42 | 70 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #43 | 75 | 75 |  | y | y | n | n | y | y | y | y |  | y | y |  | n.e. | y | y | y |
| #44 | 75 | 75 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #47 | 75 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #48 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #49 | 75 | 75 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #51 | 70 | 70 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | n.e. |
| #52 | 80 | 80 |  | y | y | y | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #54 | 70 | 75 |  | y | y | y | y | y | y | y | y |  | y | y |  | y | y | y | y |
| #55 | 75 | 75 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #56 | 80 | 80 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |
| #57 | 80 | 75 |  | y | y | n | n | y | y | y | y |  | y | y |  | y | y | y | y |

The table lists analyses performed with each sample. Samples selected for WES analysis are highlighted. When not indicated (D=at diagnosis; R= at relapse), both primary tumor and recurrent specimens underwent the same tests. MMR, mismatch repair; MSI, microsatellite instability; WES, whole exome sequencing; TERTp, TERT promoter TS, telomere length; y analyzed; n, not analyzed; n.e., not evaluable.

**Supplementary Table S2. List of GBM-associated genes used to focus WES data analysis on somatic variants of interest**

|  |
| --- |
| **GBM associated genes**  |
| *ACVR1* | *CDKN2B* | *FUBP1* | *MDM4* | *PDGFRA* | *TACC3* |
| *AKT1* | *CIC* | *H3F3A* | *MET* | *PIK3CA* | *TERT* |
| *ASCL1* | *DAXX* | *IDH1* | *MYCN* | *PIK3R1* | *TP53* |
| *ATRX* | *EGFR* | *IDH2* | *NDRG1* | *PTEN* |  |
| *BRAF* | *EPCAM* | *KIAA1549* | *NF1* | *RB1* |  |
| *CDK4* | *FGFR1* | *LTBP4* | *NF2* | *SMARCA4* |  |
| *CDK6* | *FGFR2* | *LZTR1* | *NFKBIA* | *SMARCB1* |  |
| *CDKN2A* | *FGFR3* | *MDM2* | *NOTCH1* | *SPRED1* |  |
| **MMR genes** |
| *MLH1* | *MLH3* | *MSH2* | *MSH4* | *MSH5* | *MSH6* |
| *PMS1* | *PMS2* | *POLD1* | *POLE* |  |  |

**Supplementary Table S3. Evaluation MMR protein expression and MSI status in paired GBM samples**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **Patient ID** | **MMR status at diagnosis** |  | **MMR status at relapse** | **MSI status** |
|  | **MLH1** | **PMS2** | **MSH2** | **MSH6** |  | **MLH1** | **PMS2** | **MSH2** | **MSH6** |
| **MMR deficient samples** | #2 | ++ | ++ | ++ | ++ |  | ++ | ++ | ± | ± | MSS |
| #3 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ± | MSS |
| #6 | ++ | ++ | ± | ± |  | ++ | ++ | -- | -- | MSS |
| #12 | ++ | ++ | ++ | ++ |  | ++ | ++ | ± | ± | MSS |
| #17 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | -- | MSS |
| #18 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | -- | MSS |
| #20 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ± | MSS |
| #31 | ++ | ++ | ++ | ++ |  | ++ | -- | ++ | ++ | n.a. |
| #35 | n.e. | n.e. | n.e. | n.e. |  | ++ | ++ | ++ | ± | n.a. |
| #41 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ± | MSS |
| #45 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ± | MSS |
| #46 | ± | ± | ++ | ++ |  | ± | ± | ++ | ++ | MSS |
| #50 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ± | MSS |
| #53 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | -- | MSS |
| **MMR proficient samples** | #1 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #4 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #5 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #7 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #8 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #9 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #10 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #11 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #13 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #14 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #15 | ++ | ++ | ++ | ++ |  | n.e. | n.e. | n.e. | n.e. | MSS |
| #16 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #19 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #21 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #22 | ++ | ++ | ++ | ++ |  | n.e. | n.e. | n.e. | n.e. | n.a. |
| #23 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #24 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #25 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #26 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #27 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #28 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #29 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #30 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #32 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #33 | ++ | ++ | ++ | ++ |  | ++ | n.e. | ++ | ++ | MSS |
| #34 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #36 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #37 | ++ | ++ | ++ | ++ |  | n.e. | n.e. | n.e. | n.e. | n.a. |
| #38 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #39 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #40 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #42 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #43 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #44 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #47 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #48 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #49 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #51 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #52 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #54 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | MSS |
| #55 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #56 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |
| #57 | ++ | ++ | ++ | ++ |  | ++ | ++ | ++ | ++ | n.a. |

MSI, microsatellite instability; MSS, microsatellite stability; n.a., not analyzed; n.e., not evaluable; ++, marker expressed in the totality of tumor cells; ±, marker partially expressed in tumor cells; --, marker not expressed in tumor cells. Samples showing partial or complete loss of specific MMR proteins are shown in red.

**Supplementary Table S4. Summary of alignment and coverage metrics for each sequenced sample**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Sample** | **Nr. reads** | **Reads aligned in pairs (%)** | **Aligned bases** | **HQ aligned bases (%)** | **HQ aligned bases (Q20 %)** | **Duplication rate (%)** | **Usable bases on bait (%)** | **Mean bait coverage** | **Fold enrichment** | **Target bases 10X** | **Target bases 20X** | **Target bases 30X** |
| MSH6 - | #17/I° | 116233010 | 0,99709 | 14238369329 | 97,06 | 94,61 | 23,06 | 63,91 | 75,1 | 22,14 | 97,19 | 92,49 | 84,24 |
| #18/I° | 95081570 | 0,99845 | 11717548591 | 97,42 | 95,09 | 5,00 | 67,16 | 80,3 | 23,21 | 95,10 | 86,77 | 75,74 |
| #33/I° | 147001984 | 0,99721 | 18076668128 | 97,30 | 94,92 | 17,45 | 66,71 | 106,9 | 23,06 | 97,30 | 94,31 | 89,36 |
| #17/II° | 148685652 | 0,99721 | 18252427195 | 97,05 | 94,80 | 25,92 | 57,98 | 84,0 | 20,06 | 97,50 | 94,11 | 87,99 |
| #18/II° | 98269098 | 0,99611 | 12059186659 | 97,40 | 94,98 | 20,41 | 65,07 | 67,1 | 22,50 | 95,79 | 87,98 | 76,48 |
| #53/II° | 192923246 | 0,99839 | 23747091650 | 97,13 | 94,82 | 10,76 | 67,06 | 152,3 | 23,19 | 97,85 | 96,33 | 93,74 |
| MSH6 + | #27/I° | 122643676 | 0,99831 | 15105342453 | 95,68 | 92,82 | 9,82 | 56,52 | 121,9 | 29,30 | 97,15 | 95,90 | 93,41 |
| #38/I° | 130274418 | 0,99846 | 16056622807 | 95,83 | 93,07 | 11,95 | 57,07 | 128,0 | 29,58 | 96,78 | 94,67 | 91,07 |
| #54/I° | 122937420 | 0,99861 | 15157245545 | 95,90 | 95,90 | 10,88 | 57,76 | 123,8 | 29,93 | 96,87 | 95,73 | 94,01 |
| #27/II° | 110927294 | 0,99854 | 13656991195 | 95,86 | 93,01 | 11,71 | 58,75 | 112,3 | 30,43 | 97,39 | 96,33 | 94,56 |
| #38/II° | 98668772 | 0,99649 | 12158686235 | 95,73 | 93,80 | 7,64 | 51,23 | 91,2 | 26,56 | 97,01 | 95,07 | 91,89 |
| #54/II° | 114209836 | 0,99832 | 14051331984 | 95,86 | 93,08 | 9,24 | 54,80 | 110,7 | 28,37 | 97,18 | 95,81 | 93,71 |
| MSH6 +/- | #3/I° | 65002960 | 0,99865 | 7933278257 | 96,00 | 94,32 | 6,44 | 75,24 | 108,3 | 47,64 | 95,48 | 92,51 | 88,10 |
| #20/I° | 76641530 | 0,99882 | 9314399917 | 95,79 | 94,09 | 14,59 | 74,51 | 114,8 | 47,24 | 95,86 | 93,63 | 90,27 |
| #41/I° | 70511106 | 0,99838 | 8552828929 | 95,34 | 93,56 | 5,83 | 72,45 | 113,5 | 46,31 | 96,10 | 93,51 | 89,49 |
| #3/II° | 112052516 | 0,99853 | 13703732096 | 95,82 | 93,98 | 12,02 | 71,49 | 166,8 | 45,26 | 96,48 | 95,34 | 93,78 |
| #20/II° | 75746370 | 0,99860 | 9222259173 | 95,59 | 93,65 | 10,52 | 71,54 | 114,1 | 45,34 | 96,13 | 94,35 | 91,59 |
| #41/II° | 71705800 | 0,99878 | 8743751793 | 95,79 | 93,85 | 7,07 | 73,52 | 115,6 | 46,56 | 95,99 | 93,72 | 90,27 |
|  | MEAN | 109417570 | 0,99800 | 13430431219 | 96,25 | 94,13 | 12,24 | 64,60 | 110,4 | 32,59 | 96,62 | 93,81 | 89,43 |

The following information is listed: the number of passing Illumina's quality filters (Nr.reads); the percentage of reads correctly aligned in pairs and aligned to the reference (Reads aligned in pairs); the total number of bases that are aligned to the reference sequence, those mapped at high quality and with base call quality of Q20 or higher (columns 4, 5 and 6); the fraction of aligned bases that were filtered out because they were in reads marked as duplicates (Duplication rate); the percentage of aligned, de-duped, on-bait bases out of the passing-filter bases available (Usable bases on bait); the number of aligned reads mapping to bait regions (Mean bait coverage); the fold by which the baited region has been amplified above genomic background (Fold enrichment); the fraction of all target bases achieving 10X, 20X and 30X or greater coverage (in the last three columns).

**Supplementary Table S5. Raw mutational burden for matched primary-recurrence GBM samples**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Sample ID** | **Mutect2 pairs** | **Functional SNVs** | **Splicing functional SNV** |
| **First surgery vs second surgery** | #17/I° | #17/I° vs #17/II° | 14 | 0 |
| #18/I° | #18/I° vs #18/II° | 18 | 1 |
| #53/I° | #53/I° vs #53/II° | 115 | 0 |
| Mean | MSH6 - | 49 | 0 |
| #27/I° | #27/I° vs #27/II° | 9 | 0 |
| #38/I° | #38/I° vs #38/II° | 16 | 0 |
| #54/I° | #54/I° vs #54/II° | 45 | 1 |
| Mean | MSH6 + | 23 | 0 |
| #3/I° | #3/I° vs #3/II° | 21 | 0 |
| #20/I° | #20/I° vs #20/II° | 49 | 0 |
| #41/I° | #41/I° vs #41/II° | 14 | 0 |
| Mean | MSH6 ± | 28 | 0 |
| **Second surgery vs first surgery** | #17/II° | #17/II° vs #17/I° | 296 | 1 |
| #18/II° | #18/II° vs #18/I° | 4465 | 166 |
| #53/II° | #53/II° vs #53/I° | 15018 | 614 |
| Mean | MSH6 - | 6593 | 260 |
| #27/II° | #27/II° vs #27/I° | 50 | 0 |
| #38/II° | #38/II° vs #38/I° | 116 | 0 |
| #54/II° | #54/II° vs #54/I° | 64 | 0 |
| Mean | MSH6 + | 77 | 0 |
| #3/II° | #3/II° vs #3/I° | 6 | 0 |
| #20/II° | #20/II° vs #20/I° | 4 | 0 |
| #41/II° | #41/II° vs #41/I° | 2 | 0 |
| Mean | MSH6 ± | 4 | 0 |

For each sample, the variant calling was performed using the matched tumors indicated in the second column (Mutect2 pairs), where the latter specimen in the pair chosen as normal samples for the analysis.

**Supplementary Table S6. List of sample-specific mutations identified in the genes encoding DNA mismatch-repair proteins (MMR)**



Only mutations with a variant allele frequency (VAF) of 10% or greater and with a variant sequencing depth of at least 10 reads were included. Regions of interest were covered by a mean value of 100 high-quality reads (data not shown).

**Supplementary Table S7. TERT promoter sequencing analysis in paired GBM samples**

|  |  |  |
| --- | --- | --- |
| **Patients** | **TERTp primary tumor** | **TERTp recurrence** |
| 12 | WT | WT |
| 27 | 228C>T | 228C>T |
| 10 | 250C>T | 250C>T |
| 3 | WT | 228C>T |
| 4 | 228C>T | WT |

TERTp, TERT promoter; WT, wild type.

**Supplementary Table S8. Immunologic markers expression in paired GBM samples**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Status at relapse** | **Patient ID** | **MMR status at diagnosis** | **CD8** | **HLA I** | **PD-L1** | **PD-L2** | **MMR status at relapse** | **CD8** | **HLA I** | **PD-L1** | **PD-L2** |
| **MMR deficient samples** | #2 | ++ | 2 | 50 | 0 | 0 | ± | 15 | 95 | 0 | 0 |
| #3 | ++ | 2 | 70 | 0 | 2 | ± | 8 | 90 | 0 | 1 |
| #6 | ± | 5 | 95 | 0 | 1 | -- | 21 | 95 | 0 | 2 |
| #12 | ++ | 0 | 80 | 0 | 0 | ± | 3 | 80 | 0 | 0 |
| #17 | ++ | 3 | 90 | 20 | 2 | -- | 10 | 70 | 15 | 1 |
| #18 | ++ | 3 | 85 | 0 | 2 | -- | 5 | 60 | 0 | 3 |
| #20 | ++ | 2 | 60 | 0 | 1 | ± | 3 | 50 | 0 | 1 |
| #31 | ++ | 5 | 0 | 0 | 2 | -- | 18 | 30 | 0 | 2 |
| #35 | n.e. | n.e. | n.e. | n.e. | n.e. | ± | 14 | 70 | 0 | 2 |
| #41 | ++ | 20 | 70 | 1 | 0 | ± | 27 | 70 | 1 | 0 |
| #45 | ++ | 4 | 0 | 0 | 2 | ± | 5 | 0 | 0 | 0 |
| #46 | ± | 3 | 0 | 0 | 2 | ± | 2 | 30 | 0 | 0 |
| #50 | ++ | 7 | 95 | 0 | 0 | ± | 7 | 0 | 0 | 0 |
| #53 | ++ | 1 | 0 | 0 | 0 | -- | 3 | 0 | 5 | 0 |
| **MMR proficient samples** | #1 | ++ | 4 | 90 | 0 | 3 | ++ | 17 | 80 | 0 | 1 |
| #4 | ++ | 8 | 90 | 60 | 2 | ++ | 6 | 30 | 15 | 3 |
| #5 | ++ | 5 | 90 | 80 | 2 | ++ | 6 | 95 | 0 | 1 |
| #7 | ++ | 6 | 30 | 0 | 0 | ++ | 6 | n.e. | n.e. | n.e. |
| #8 | ++ | 6 | 95 | 0 | 1 | ++ | 8 | 80 | 0 | 1 |
| #9 | ++ | 2 | 40 | 0 | 1 | ++ | 2 | 30 | 0 | 1 |
| #10 | ++ | 6 | 95 | 0 | 1 | ++ | 12 | 95 | 0 | 2 |
| #11 | ++ | 3 | 0 | 0 | 1 | ++ | 4 | 5 | 1 | 2 |
| #13 | ++ | 2 | 40 | 0 | 0 | ++ | 5 | 40 | 5 | 1 |
| #14 | ++ | 6 | 95 | 0 | 3 | ++ | 10 | 60 | 0 | 2 |
| #16 | ++ | 5 | 40 | 0 | 1 | ++ | n.e. | n.e. | n.e. | n.e. |
| #19 | ++ | 0 | 0 | 0 | 0 | ++ | 1 | 5 | 0 | 2 |
| #21 | ++ | 4 | 20 | 0 | 2 | ++ | 3 | 40 | 40 | 2 |
| #23 | ++ | 7 | 50 | 0 | 1 | ++ | 6 | 50 | 0 | 0 |
| #24 | ++ | 1 | 20 | 0 | 1 | ++ | n.e. | n.e. | n.e. | n.e. |
| #25 | ++ | 1 | 30 | 0 | 3 | ++ | 6 | 70 | 5 | 3 |
| #26 | ++ | 2 | 5 | 0 | 3 | ++ | 5 | 90 | 0 | 2 |
| #27 | ++ | 8 | 5 | 0 | 1 | ++ | 14 | 95 | 0 | 0 |
| #28 | ++ | 4 | 95 | 0 | 2 | ++ | 3 | 0 | 0 | 2 |
| #29 | ++ | 2 | 0 | 0 | 1 | ++ | 5 | 0 | 0 | 1 |
| #30 | ++ | 7 | 100 | 0 | 0 | ++ | 25 | 80 | 0 | 0 |
| #32 | ++ | 3 | 80 | 0 | 0 | ++ | 26 | 5 | 10 | 0 |
| #33 | ++ | 0 | 0 | 0 | 1 | ++ | 11 | 5 | 0 | 1 |
| #34 | ++ | 3 | 0 | 0 | 0 | ++ | 3 | 0 | 0 | 0 |
| #36 | ++ | 7 | 20 | 0 | 2 | ++ | 6 | 90 | 0 | 1 |
| #38 | ++ | 1 | 0 | 0 | 1 | ++ | 2 | 0 | 0 | 0 |
| #39 | ++ | 9 | 0 | 0 | 1 | ++ | 6 | 0 | 0 | 1 |
| #40 | ++ | 4 | 80 | 0 | 1 | ++ | 5 | 80 | 0 | 2 |
| #42 | ++ | 1 | 5 | 0 | 0 | ++ | 1 | 10 | 0 | 0 |
| #43 | ++ | 1 | 30 | 0 | 0 | ++ | 3 | 5 | 0 | 1 |
| #44 | ++ | 4 | 5 | 0 | 0 | ++ | 4 | 30 | 0 | 1 |
| #47 | ++ | 0 | 0 | 0 | 1 | ++ | 5 | 0 | 0 | 0 |
| #48 | ++ | 1 | 95 | 0 | 0 | ++ | 1 | 0 | 0 | 0 |
| #49 | ++ | 3 | 30 | 0 | 1 | ++ | 2 | 50 | 0 | 1 |
| #51 | ++ | 1 | 5 | 0 | 1 | ++ | 13 | 5 | 0 | 3 |
| #52 | ++ | 2 | 0 | 0 | 0 | ++ | 3 | 5 | 0 | 0 |
| #54 | ++ | 1 | 0 | 0 | 0 | ++ | 1 | 0 | 0 | 0 |
| #55 | ++ | 2 | 70 | 0 | 1 | ++ | 2 | 90 | 0 | 1 |
| #56 | ++ | 0 | 40 | 0 | 0 | ++ | 4 | 40 | 0 | 0 |
| #57 | ++ | 4 | 0 | 0 | 3 | ++ | 3 | 0 | 0 | 0 |
| **MMR n.e.** | #15 | ++ | 2 | 30 | 0 | 1 | n.e. | n.e. | n.e. | n.e. | n.e. |
| #22 | ++ | 5 | 40 | 0 | 3 | n.e. | n.e. | n.e. | n.e. | n.e. |
| #37 | n.e. | n.e. | n.e. | n.e. | n.e. | n.e. | n.e. | n.e. | n.e. | n.e. |

CD8 values are expressed as number of marker positive cells per high magnification field; n.e., not evaluable. Samples selected for WES analysis are highlighted.