

Supplementary data

**Comparison of acute myeloid leukemia and myelodysplastic syndromes with *TP53* aberrations**

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**Supplementary Table 2. Antibodies used for immunophenotyping of blast cells of AML and MDS patients with *TP53* aberrations.** Abbreviations: BD, Becton Dickinson; BC, Beckman Coulter.

| Antibody     | Fluorochrome | Clone       | Company |
|--------------|--------------|-------------|---------|
| IgG1 (mouse) | FITC         | X40         | BD      |
| IgG1 (mouse) | PE           | X40         | BD      |
| IgG1 (mouse) | ECD          | 679.1Mc7    | BC      |
| IgG1 (mouse) | PC5.5        | 679.1Mc7    | BC      |
| IgG1 (mouse) | PC7          | 679.1Mc7    | BC      |
| IgG1 (mouse) | APC          | 679.1Mc7    | BC      |
| IgG1 (mouse) | APC-AF 700   | 679.1Mc7    | BC      |
| IgG1 (mouse) | APC-AF 750   | 679.1Mc7    | BC      |
| IgG1 (mouse) | PB           | 679.1Mc7    | BC      |
| IgG1 (mouse) | V500-C       | X40         | BD      |
| HLA-DR       | FITC         | L243        | BD      |
| CD10         | FITC         | ALB1        | BC      |
| CD4          | PE           | 13B8.2      | BC      |
| CD117        | PE           | 104D2D1     | BC      |
| CD15         | PE           | HI98        | BD      |
| CD34         | ECD          | 581         | BC      |
| CD123        | PC5.5        | SSDCLY107D2 | BC      |
| CD33         | PC5.5        | D3HL60.251  | BC      |
| CD19         | PC7          | J3-119      | BC      |
| CD13         | PC7          | Immu103.44  | BC      |
| CD11b        | PC7          | Bear1       | BC      |
| CD56         | APC          | N901        | BC      |
| CD2          | APC          | S5.2        | BD      |
| CD7          | APC-AF 700   | 8H8.1       | BC      |
| CD5          | APC-AF 750   | BL1a        | BC      |
| CD14         | APC-AF 750   | RM052       | BC      |
| CD45         | V500-C       | 2D1         | BD      |

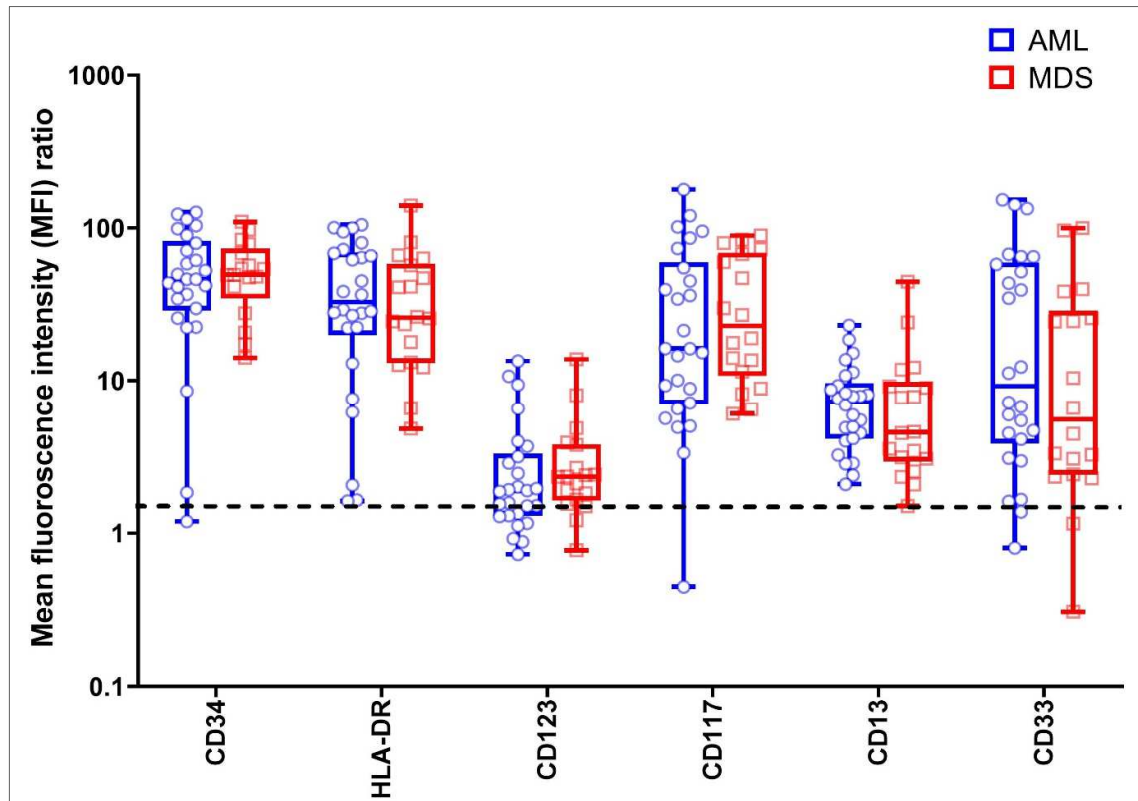
**Supplementary Table 2. *TP53* mutations of patients with AML and MDS, analyzed in the study.**  
Abbreviations: VAF, variant allele frequency; UPN, unique patient number; NA, not available.  
Disruptive, EAp53 and RFS refer to the *TP53*-specific scores as outlined in “Methods” of the main text.

| Patient | <i>TP53</i> mutation             | VAF                  | Disruptive       | EAp53                           | RFS                         |
|---------|----------------------------------|----------------------|------------------|---------------------------------|-----------------------------|
| UPN1    | splice site mutation             | 85,3                 | NA               | no score                        | no score                    |
| UPN2    | p.R248Q;<br>p.V216M              | 3,7;<br>17,4         | yes<br>no        | 78,95<br>73,3                   | -0,04<br>0,10               |
| UPN3    | p.C275Y                          | 35,1                 | no               | 93,47                           | 0,41                        |
| UPN4    | p.L145P                          | 11,2                 | no               | 72,75                           | 0,23                        |
| UPN5    | R248Q                            | 48,8                 | yes              | 78,95                           | -0,04                       |
| UPN6    | p.R156P                          | 92                   | no               | 42,93                           | -0,62                       |
| UPN7    | p.D281Y                          | 79,5                 | no               | 96,23                           | 0,36                        |
| UPN8    | p.G245S                          | 91                   | no               | 86,45                           | 0,02                        |
| UPN9    | p.N131I                          | 62,6                 | no               | 81,75                           | 0,30                        |
| UPN10   | p.G262fs                         | 51                   | yes              | no score                        | no score                    |
| UPN11   | p.V216M                          | 66                   | no               | 73,3                            | 0,10                        |
| UPN12   | p.R273H                          | 50                   | no               | 66,12                           | 0,25                        |
| UPN13   | p.R249T;<br>p.NK131K             | 36,8;<br>33,5        | yes;<br>yes      | 95,93;<br>no score              | 0,51;<br>-0,01              |
| UPN14   | p.D281N                          | 27,4                 | no               | 69,88                           | -0,002                      |
| UPN15   | p.Q136E                          | 60                   | no               | 50,94                           | -0,09                       |
| UPN16   | p.D259fs;<br>p.V143M             | 30;<br>6             | yes;<br>no       | no score;<br>51,72              | no score;<br>-1,33          |
| UPN17   | p.Y220C                          | 77                   | no               | 72,52                           | 0,09                        |
| UPN18   | p.V216M;<br>p.C176R              | 25,7<br>7            | no;<br>yes       | 73,3;<br>97,94                  | 0,097;<br>0,39              |
| UPN19   | p.Q104X;<br>p.R273H;<br>p.Q65X   | 4,6;<br>24,3;<br>6,3 | no;<br>no;<br>no | no score;<br>no score;<br>66,12 | -0,29;<br>0,54;<br>no score |
| UPN20   | p.K132R                          | 77,5                 | no               | 69                              | 0,46                        |
| UPN21   | p.V216M                          | 77,5                 | no               | 73,3                            | 0,10                        |
| UPN22   | p.E286*                          | 37,5                 | yes              | no score                        | 0,85                        |
| UPN23   | p.R156P                          | 48,8                 | no               | 42,93                           | -0,62                       |
| UPN24   | p.R248Q                          | 72,5                 | yes              | 78,95                           | -0,04                       |
| UPN25   | p.R175H;<br>splice site mutation | 39;27;<br>40         | no;<br>NA        | 78,51;<br>no score              | -0,14;<br>no score          |
| UPN26   | p.R273H                          | 68,2                 | no               | 66,12                           | 0,25                        |
| UPN27   | splice site mutation             | 77,0                 | NA               | no score                        | no score                    |
| UPN28   | p.H179L                          | 37,3                 | yes              | 97,12                           | 0,68                        |
| UPN29   | p.E298*                          | 61,8                 | yes              | no score                        | no score                    |
| UPN30   | p.C277G                          | 49,4                 | no               | 93,39                           | -0,57                       |

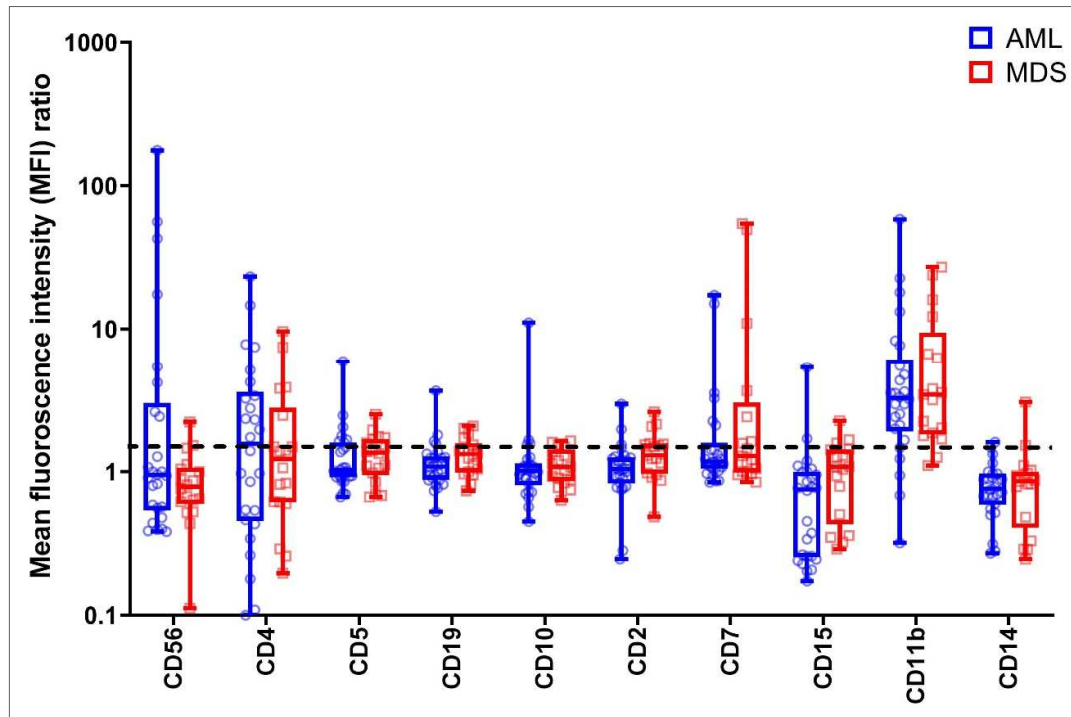
|       |                                  |               |             |                       |                    |
|-------|----------------------------------|---------------|-------------|-----------------------|--------------------|
| UPN31 | splice site mutation             | 87,1          | NA          | no score              | no score           |
| UPN32 | p.R280G                          | 65            | no          | 95,71                 | -0,52              |
| UPN33 | p.R175G                          | 55,5          | yes         | 95,2                  | 0,54               |
| UPN34 | p.I255N                          | NA            | no          | 87,39                 | -0,47              |
| UPN35 | p.R196G;<br>splice site mutation | 14,6;<br>11,1 | no          | 97,34;<br>no score    | -1,88;<br>no score |
| UPN36 | p.W146*                          | 83            | dis         | no score              | 0,79               |
| UPN37 | splice site mutation             | 73,3          | NA          | no score              | no score           |
| UPN38 | p.Y205C;<br>p. P278S             | 25,6          | no;<br>no   | 77,88;<br>84,34       | 0,23;<br>0,16      |
| UPN39 | p.V216M                          | 85,80         | no          | 73,3                  | 0,10               |
| UPN40 | P:R248Q                          | 37,50         | yes         | 78,95                 | -0,04              |
| UPN41 | p.E221fs                         | 67,60         | yes         | no score              | 0,38               |
| UPN42 | p.R175H                          | NA            | no          | 78,51                 | -0,14              |
| UPN43 | p.R175H                          | NA            | no          | 78,51                 | -0,14              |
| UPN44 | p.Y234*                          | NA            | yes         | No score              | 0,18               |
| UPN45 | p.K132*;<br>p.R196P              | NA            | yes;<br>no  | no score;<br>95,55    | no score;<br>0,40  |
| UPN46 | p.R273C                          | NA            | no          | 84,52                 | -0,13              |
| UPN47 | p.C238Y                          | NA            | no          | 92,66                 | 0,21               |
| UPN48 | p.T125P                          | NA            | no          | 88,7                  | -0,18              |
| UPN49 | p.Y234H                          | NA            | no          | 50,1                  | -0,07              |
| UPN50 | p.P278S                          | NA            | no          | 84,34                 | 0,17               |
| UPN51 | p.Asp228*                        | NA            | yes         | no score              | no score           |
| UPN52 | p.Y220C                          | NA            | no          | 72,52                 | 0,22               |
| UPN53 | p.L114Pfs*56                     | NA            | yes         | no score              | no score           |
| UPN54 | p.V173G                          | NA            | yes         | 93,47                 | 0,19               |
| UPN55 | p.R273H;<br>p.E286G              | NA            | no;<br>no   | 66,12;<br>93,06       | 0,25;<br>0,093     |
| UPN56 | p.Y220C                          | NA            | no          | 72,52                 | 0,22               |
| UPN57 | p.R273C                          | NA            | no          | 84,52                 | -0,13              |
| UPN58 | p.Q165*,<br>p.L195P,             | NA            | yes;<br>yes | no score;<br>no score | -0,35;<br>0,39     |
| UPN59 | p.M237I;<br>p.P152L              | NA            | no;<br>no   | 63,68;<br>89,03       | -1,19;<br>0,19     |
| UPN60 | p.G245S                          | Het           | no          | 86,45                 | 0,02               |
| UPN61 | p.I255T                          | 57,0          | no          | 70,87                 | -0,52              |
| UPN62 | p.R282W                          | 60,5          | no          | 73,21                 | 0,02               |
| UPN63 | p.R248Q,<br>p.P27fs*50           | 14,3;<br>17   | yes;<br>yes | 78,95;<br>no score    | -0,04;<br>no score |
| UPN64 | p.P98A                           | 21,5          | no          | 89,49                 | no score           |
| UPN65 | p.R273H                          | 81,3          | no          | 66,12                 | 0,25               |

|       |                                  |               |            |                    |                    |
|-------|----------------------------------|---------------|------------|--------------------|--------------------|
| UPN66 | p.V274L;<br>p.R248W              | 50;<br>48,5   | no,<br>yes | 58,27;<br>84,11    | -0,49;<br>0,07     |
| UPN67 | p.M237I                          | 4             | no         | 63,68              | 0,19               |
| UPN68 | p.H179N                          | 98            | yes        | 85,03              | 0,36               |
| UPN69 | p.V216L,<br>p.E349X              | 27,8;<br>20   | yes;<br>no | 71,23;<br>no score | 0,097;<br>no score |
| UPN70 | p.P250L ;<br>p.R273H             | 33,5;<br>50,8 | no;<br>no  | 89;<br>66,2        | -0,25;<br>0,25     |
| UPN71 | p. M237K                         | 86,26         | yes        | 85,52              | 0,30               |
| UPN72 | p. V157F                         | 81            | no         | 55,26              | 0,50               |
| UPN73 | p.R249M                          | NA            | yes        | 95,41              | 0,17               |
| UPN74 | p.G245S                          | 69            | no         | 86,45              | 0,02               |
| UPN75 | p.K382fs*40                      | NA            | yes        | no score           | no score           |
| UPN76 | p.R283fs*22                      | NA            | yes        | no score           | no score           |
| UPN77 | p.H179R                          | 50,1          | no         | 81,91              | 0,22               |
| UPN78 | p.G245S                          | 8,9           | no         | 86,45              | 0,02               |
| UPN79 | p..R175H                         | 65            | no         | 78,51              | -0,14              |
| UPN80 | p.G199E,                         | 53,5          | no         | 69,44              | -1,97              |
| UPN81 | splice site mutation             | 69            | NA         | no score           | no score           |
| UPN82 | p.I195T                          | 77            | yes        | 72,13              | 0,41               |
| UPN83 | p.R282G;<br>p.M246V              | 42;<br>42,5   | no;<br>no  | 88,59;<br>66,21    | 0,46;<br>-0,72     |
| UPN84 | splice site mutation;<br>p.M246R | 57;<br>23,5   | NA;<br>yes | no score;<br>86,49 | no score;<br>-1,17 |

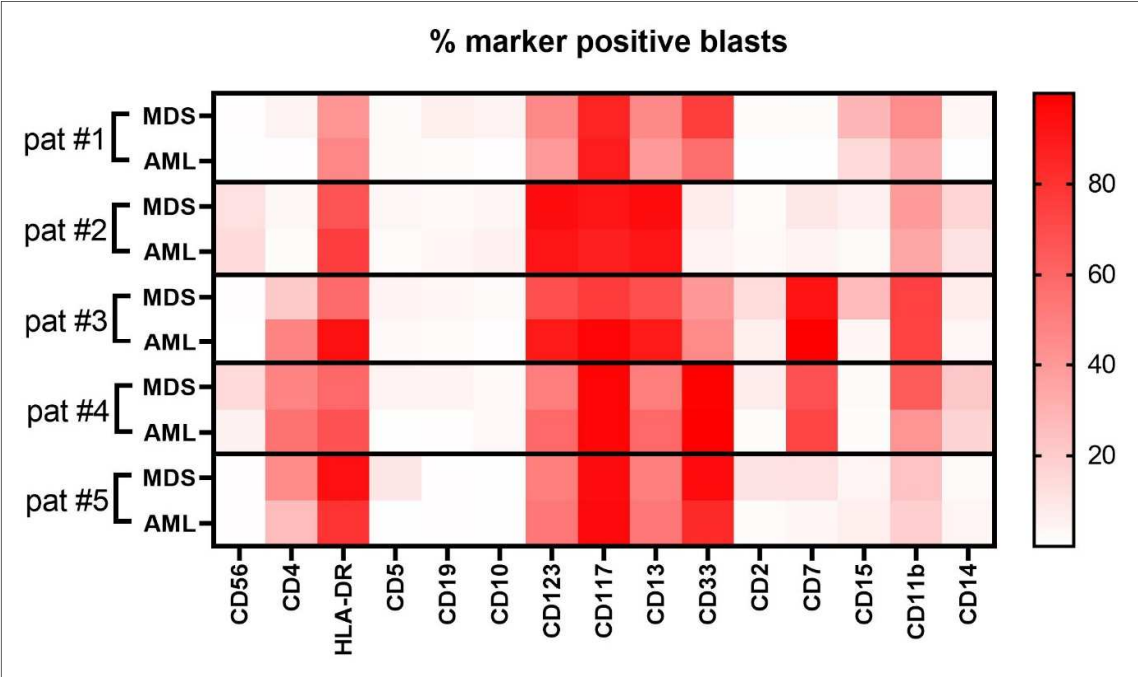
**Supplementary Figure 1. Geometric mean fluorescence intensity (MFI) of myeloid progenitor markers.** No statistically significant difference in MFI values were noted between AML (n=26) and MDS (n=18) patients with *TP53* aberrations.



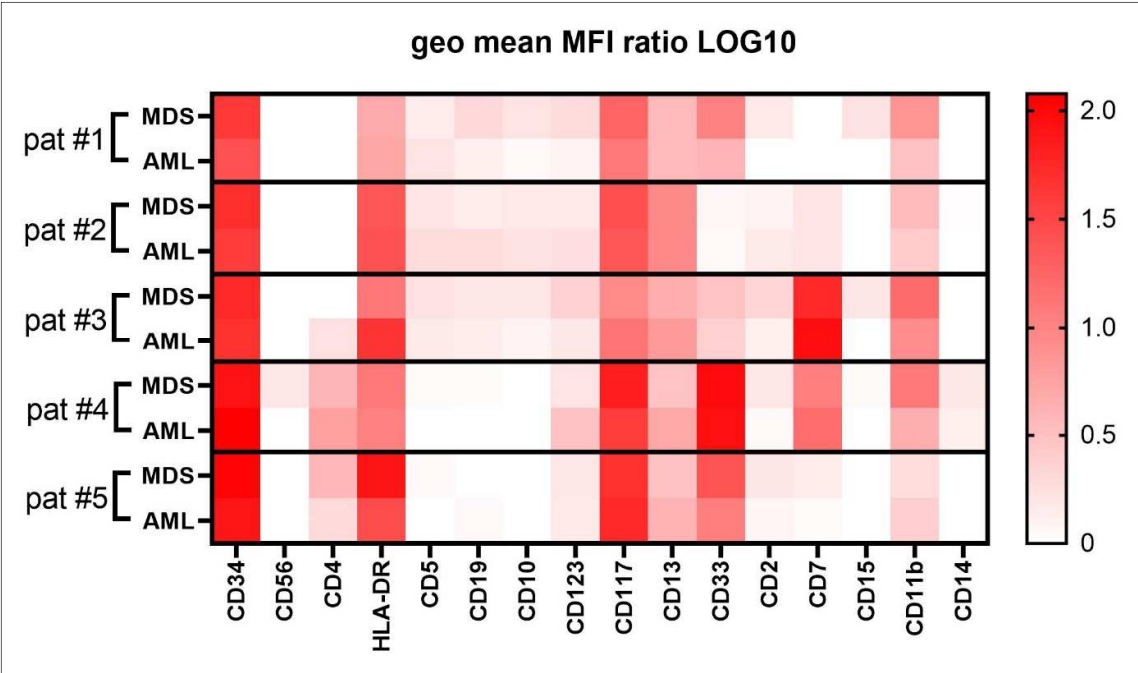
**Supplementary Figure 2. Geometric mean fluorescence intensity (MFI) of aberrant markers.** No statistically significant difference in MFI values were noted between AML (n=26) and MDS (n=18) patients with *TP53* aberrations.



**Supplementary Figure 3. Heatmap displaying percent (%) positive immature blast cells for surface markers of 5 MDS patients with *TP53* aberrations transformed to AML. Abbreviation: pat, patient.**



**Supplementary Figure 4. Heatmap displaying the mean fluorescence intensity (MFI) for surface markers of 5 MDS patients with *TP53* aberrations transformed to AML. The MFI values are log10 transformed. Abbreviation: pat, patient.**



**Supplementary Figure 5. Survival of patients with AML and MDS with *TP53* aberrations.** Overall survival probability of AML and transformed MDS patients, calculated from the time of transformation.

