Supplementary Material

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# **Supplementary** **Tables**

| **Supplementary Table 2. Genetic characterization of BL cell lines** | | | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sample** | **EBV status** | **IG-MYC translocation** | **chr1q CNA** | **TP53status** | **RNAi screen** | **POS** | **Gene** | **CDS** | **AA** |
| **BJAB** | negative | MYC gain3 | 1q21 diploid3 | mut | yes | X:41205861 | DDX3X | c.1601G>A | p.R534H |
| 17:7578271 | TP53 | c.578A>G | p.H194R |
| **BL2** | negative | t(8;22) (q24.2;q11.2)1,2 | +1q21.1q31.31,2 | wt | yes | X:41205625 | DDX3X | c.1459T>C | p.F487L |
| 13:41240288 | FOXO1 | c.62G>A | p.R21H |
| 1:23885617 | ID3 | splice site | p.? |
| 8:128748565 | MYC | . | UTR |
| 8:128748640 | MYC | . | UTR |
| 8:128748661 | MYC | . | UTR |
| 8:128748680 | MYC | . | UTR |
| 8:128748697 | MYC | . | UTR |
| 8:128748731 | MYC | . | UTR |
| 8:128750938 | MYC | c.475C>T | p.L159F |
| 8:128751032 | MYC | c.569G>A | p.S190N |
| 8;128750613 | MYC | c.180G>C | p.Q60H |
| 3:38182032 | MYD88 | c.656C>G | p.S219C |
| 19:1611800 | TCF3 | c.1862A>G | p.E621G |
| 19:1611850 | TCF3 | splice site | p.? |
| **BL60** | positive  (latency  phase III) | MYC break3 | 1q21 diploid3 | mut | yes | 13:41240349 | FOXO1 | c.1A>G | p.M1V |
| 1:23,885,667 | ID3 | c.251T>A | p.L84Q |
| 1:23,885,680 | ID3 | c.238C>G | p.L80V |
| 1:23,885,685 | ID3 | c.233T>G | p.L78R |
| 8:128748843 | MYC | c.4G>C | p.D2H |
| 8:128750681 | MYC | c.218C>T | p.T73I |
| 8:128750682 | MYC | c.140C>T | p.P47L |
| 8:128751113 | MYC | c.650G>C | p.S217T |
| 8:128751116 | MYC | c.653G>C | p.S218T |
| 19:1612356 | TCF3 | c.1663G>C | p.E555Q |
| 17:7577539 | TP53 | c.742C>T | p.R248W |
| **LY47** | positive  (latency  phase III) | t(8;22) (q24.2;q11.2)2 | +1q43q442 | wt | yes | 8:128748866 | MYC | c.27C>G | p.N9K |
| **Raji** | positive  (latency  phase III) | t(8;14) (q24;q32)1 | diploid1 | mut | yes | X:41203663 | DDX3X | splice site | p.? |
| 17:63052557 | GNA13 | c.155T>G | p.L52R |
| 8:128750639 | MYC | c.176C>T | p.A59V |
| 8:128750681 | MYC | c.218C>T | p.T73I |
| 17:7577581 | TP53 | c.700T>C | p.Y234H |
| 17:7578211 | TP53 | c.638G>A | p.R213Q |
| **Ramos** | negative | t(8;14) (q24.2;q32.3)1,2 | diploid1,2 | mut | yes | X:41206952 | DDX3X | c.1969G>A | p.V657I |
| 17:63049625 | GNA13 | c.505C>T | p.Q169\* |
| 8:128748157 | MYC | . | UTR5 |
| 8:128748735 | MYC | . | UTR5 |
| 8:128748837 | MYC | . | UTR5 |
| 19:1612336 | TCF3 | c.1683T>G | p.D561E |
| 17:7577520- 17:7577521 | TP53 | c.761-762AT>GA | p.I254D |
| **Salina** | positive  (Wp-restricted) | t(8;14) (q24.2;q32.3)2 | +1q21.2q31.32 | wt | yes | X:41203603 | DDX3X | c.976C>T | p.R326C |
| 1:23885709 | ID3 | c.209T>C | p.L70P |
| 8:128750541 | MYC | c.78C>G | p.N26K |
| **Seraphine** | positive  (latency  phase III) | t(8;14) (q24.2;q32.3)2 | +1q21.1qter2 | wt | yes | 8:128748843 | MYC | c.4G>A | p.D2N |
| 8:128748858 | MYC | c.19G>A | p.V7M |
| 8:128750542 | MYC | c.79T>C | p.Y27H |
| 8:128750683 | MYC | c.220C>G | p.P74A |
| 8:128750953 | MYC | c.490C>G | p.L164V |
| 8:128750959 | MYC | c.496T>G | p.S166A |
| **BL7** | positive  (latency  phase III) | MYC break3 | 1q21 diploid3 | wt | no |  |  |  |  |
| **BL41** | negative | t(8;14) (q24.2;q31.3)1,2 | Multiple subclonal rearrangements and gains1,2 | mut | no | 17:7577538 | TP53 | c.743G>A | p.R248Q |
| **CA46** | negative | t(8;14) (q24;q32)1 | dup(1)(q21q32)1 | mut | no | 17:7577538 | TP53 | c.743G>A | p.R248Q |
|  | MYC |  | p.P72S |
|  | MYC |  | p.P75H |
| **Cheptanges** | subclone  positive  (latency  phase III) | MYC break3 | 1q21 diploid3 | wt | no |  | MYC |  | p.P75T |
| **DG75** | negative | t(8;14) (q24;q32)1 | diploid1 | mut | no | 17:7577548 | TP53 | c.733G>A | p.G245S |
| 17:7577090 | TP53 | c.848G>A | p.R283H |
|  | MYC |  | p.C148W |
| **Namalwa** | positive  (latency  phase III) | t(8;14) (q24.2;q32.3)1,2 | +1q12q31.1;  +1q44(subclone);  dup(1)(pterp36.1); dup(1)(q11q31.1)1,2 | mut | no | 17:7577538 | TP53 | c.743G>A | p.R248Q |
| **DogKit** | negative1 | t(14;18) (q32;q21)1 | dup(1)(q21q42)1 | wt | no |  |  |  |  |
| **Gumbus** | negative1 | t(8;14) (q24;q32)1 | 1q21 diploid1 | wt | no |  |  |  |  |
| 1DSMZ (https://www.dsmz.de/home.html) | | | |  |  |  |  |  |  |
| 2Toujani et al., 2009 | |  |  |  |  |  |  |  |  |
| 3FISH analysis (MYC break probe or 1p32/1q21 probe) | | | |  |  |  |  |  |  |

| **Supplementary Table 4. Genetic aberrations in aggressive B-NHL patients from the MMML consortium** | | | | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **MPINR** | **class** | ***MYC* status** | **# *MYC* mutations** | **# *MYC* box 1 mutations** | **# *MYC* box 2 mutations** | ***TP53* status** | **CNA data** |
| MPI-001 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-003 | BL | IG-MYC | 3 | 0 | 1 | 0 | yes |
| MPI-016 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-043 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-049 | BL | IG-MYC | 3 | 1 | 0 | 0 | yes |
| MPI-055 | BL | IG-MYC | 1 | 0 | 0 | 0 | yes |
| MPI-066 | BL | IG-MYC | 3 | 1 | 0 | 0 | yes |
| MPI-067 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-075 | BL | IG-MYC | 3 | 1 | 0 | 0 | yes |
| MPI-079 | BL | IG-MYC | 4 | 1 | 0 | 0 | yes |
| MPI-080 | BL | IG-MYC | 4 | 1 | 0 | 0 | yes |
| MPI-081 | BL | IG-MYC | 1 | 0 | 0 | 0 | yes |
| MPI-082 | BL | IG-MYC | 2 | 1 | 0 | 0 | yes |
| MPI-084 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-091 | BL | IG-MYC | 2 | 2 | 0 | 0 | yes |
| MPI-095 | BL | IG-MYC | 2 | 1 | 0 | 0 | yes |
| MPI-114 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-138 | BL | IG-MYC | 2 | 0 | 0 | 0 | yes |
| MPI-139 | BL | IG-MYC | 2 | 0 | 1 | 0 | yes |
| MPI-156 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-171 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-172 | BL | IG-MYC | 6 | 0 | 1 | 0 | yes |
| MPI-211 | BL | IG-MYC | 0 | NA | NA | 0 | no |
| MPI-220 | BL | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-527 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-528 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-529 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-576 | BL | IG-MYC | 1 | 0 | 0 | 0 | yes |
| MPI-586 | BL | IG-MYC | 5 | 1 | 2 | 0 | yes |
| MPI-591 | BL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-622 | BL | IG-MYC | 2 | 0 | 0 | 0 | yes |
| MPI-623 | BL | IG-MYC | 3 | 1 | 0 | 0 | yes |
| MPI-697 | BL | IG-MYC | NA | NA | NA | 0 | no |
| MPI-004 | BL | IG-MYC | 2 | 2 | 0 | 1 | yes |
| MPI-005 | BL | IG-MYC | 1 | 0 | 0 | 1 | yes |
| MPI-017 | BL | IG-MYC | 2 | 2 | 0 | 1 | yes |
| MPI-018 | BL | IG-MYC | 3 | 1 | 2 | 1 | yes |
| MPI-033 | BL | IG-MYC | 2 | 0 | 1 | 1 | yes |
| MPI-044 | BL | IG-MYC | 1 | 1 | 0 | 1 | yes |
| MPI-048 | BL | IG-MYC | 2 | 1 | 0 | 1 | yes |
| MPI-071 | BL | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-077 | BL | IG-MYC | 3 | 1 | 1 | 1 | yes |
| MPI-085 | BL | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-087 | BL | IG-MYC | 6 | 0 | 4 | 1 | yes |
| MPI-101 | BL | IG-MYC | 3 | 1 | 0 | 1 | yes |
| MPI-123 | BL | IG-MYC | NA | NA | NA | 1 | no |
| MPI-144 | BL | IG-MYC | 1 | 1 | 0 | 1 | yes |
| MPI-323 | BL | IG-MYC | 7 | 0 | 4 | 1 | yes |
| MPI-417 | BL | IG-MYC | 1 | 0 | 0 | 1 | yes |
| MPI-532 | BL | IG-MYC | 1 | 0 | 0 | 1 | yes |
| MPI-568 | BL | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-579 | BL | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-580 | BL | IG-MYC | 1 | 0 | 0 | 1 | yes |
| MPI-588 | BL | IG-MYC | 2 | 0 | 2 | 1 | yes |
| MPI-589 | BL | IG-MYC | 4 | 2 | 0 | 1 | yes |
| MPI-590 | BL | IG-MYC | 1 | 0 | 0 | 1 | yes |
| MPI-618 | BL | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-621 | BL | IG-MYC | 3 | 1 | 1 | 1 | yes |
| MPI-625 | BL | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-680 | BL | IG-MYC | NA | NA | NA | 1 | no |
| MPI-747 | BL | IG-MYC | NA | NA | NA | 1 | no |
| MPI-008 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-009 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-010 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-012 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-014 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-015 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-030 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-036 | DLBCL | IG-MYC | 8 | 1 | 2 | 0 | yes |
| MPI-040 | DLBCL | neg | 0 | NA | NA | 0 | no |
| MPI-046 | DLBCL | non-IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-047 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-053 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-073 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-074 | DLBCL | non-IG-MYC | 11 | 0 | 0 | 0 | yes |
| MPI-076 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-083 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-096 | DLBCL | neg | 0 | NA | NA | 0 | no |
| MPI-105 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-109 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-110 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-111 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-113 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-115 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-118 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-127 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-128 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-130 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-133 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-136 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-141 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-145 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-146 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-149 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-151 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-154 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-159 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-163 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-164 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-165 | DLBCL | non-IG-MYC | 38 | 13 | 0 | 0 | no |
| MPI-168 | DLBCL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-173 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-176 | DLBCL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-180 | DLBCL | NA | 0 | NA | NA | 0 | yes |
| MPI-183 | DLBCL | neg | 0 | NA | NA | 0 | no |
| MPI-184 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-188 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-189 | DLBCL | IG-MYC | 4 | 1 | 0 | 0 | yes |
| MPI-191 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-193 | DLBCL | neg | 0 | NA | NA | 0 | no |
| MPI-194 | DLBCL | neg | 1 | 0 | 1 | 0 | yes |
| MPI-195 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-199 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-201 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-203 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-205 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-206 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-207 | DLBCL | neg | 0 | NA | NA | 0 | no |
| MPI-209 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-210 | DLBCL | IG-MYC | 3 | 0 | 0 | 0 | no |
| MPI-223 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-232 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-236 | DLBCL | NA | 0 | NA | NA | 0 | no |
| MPI-237 | DLBCL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-241 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-244 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-247 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-248 | DLBCL | non-IG-MYC | 0 | NA | NA | 0 | no |
| MPI-261 | DLBCL | NA | NA | NA | NA | 0 | yes |
| MPI-269 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-270 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-271 | DLBCL | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-272 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-273 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-274 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-277 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-278 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-279 | DLBCL | NA | NA | NA | NA | 0 | yes |
| MPI-281 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-282 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-285 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-286 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-287 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-288 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-289 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-290 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-291 | DLBCL | non-IG-MYC | NA | NA | NA | 0 | yes |
| MPI-293 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-299 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-302 | DLBCL | non-IG-MYC | NA | NA | NA | 0 | yes |
| MPI-304 | DLBCL | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-306 | DLBCL | neg | 1 | 0 | 0 | 0 | yes |
| MPI-308 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-309 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-312 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-318 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-319 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-321 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-324 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-326 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-327 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-330 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-331 | DLBCL | non-IG-MYC | NA | NA | NA | 0 | yes |
| MPI-334 | DLBCL | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-335 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-337 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-338 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-342 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-343 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-344 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-345 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-346 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-347 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-348 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-349 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-350 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-351 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-352 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-353 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-355 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-356 | DLBCL | non-IG-MYC | NA | NA | NA | 0 | yes |
| MPI-357 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-358 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-359 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-360 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-363 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-364 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-365 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-366 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-367 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-369 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-370 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-371 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-374 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-377 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-378 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-379 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-386 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-387 | DLBCL | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-388 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-389 | DLBCL | IG-MYC | 2 | 0 | 0 | 0 | yes |
| MPI-391 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-393 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-394 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-395 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-396 | DLBCL | IG-MYC | 1 | 0 | 0 | 0 | yes |
| MPI-397 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-398 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-399 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-401 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-402 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-403 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-406 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-407 | DLBCL | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-411 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-412 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-413 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-414 | DLBCL | non-IG-MYC | NA | NA | NA | 0 | yes |
| MPI-415 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-416 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-419 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-423 | DLBCL | non-IG-MYC | NA | NA | NA | 0 | yes |
| MPI-435 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-436 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-438 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-443 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-475 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-531 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-539 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-541 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-543 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-546 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-547 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-548 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-552 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-555 | DLBCL | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-565 | DLBCL | IG-MYC | NA | NA | NA | 0 | no |
| MPI-566 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-567 | DLBCL | neg | 1 | 0 | 0 | 0 | yes |
| MPI-578 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-585 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-594 | DLBCL | neg | 1 | 0 | 0 | 0 | yes |
| MPI-596 | DLBCL | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-597 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-598 | DLBCL | neg | NA | NA | NA | 0 | yes |
| MPI-624 | DLBCL | neg | 0 | NA | NA | 0 | yes |
| MPI-627 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-628 | DLBCL | IG-MYC | 2 | 2 | 0 | 0 | yes |
| MPI-634 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-635 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-637 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-638 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-644 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-648 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-650 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-652 | DLBCL | non-IG-MYC | NA | NA | NA | 0 | no |
| MPI-679 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-686 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-689 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-690 | DLBCL | IG-MYC | NA | NA | NA | 0 | no |
| MPI-694 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-698 | DLBCL | IG-MYC | NA | NA | NA | 0 | no |
| MPI-700 | DLBCL | IG-MYC | NA | NA | NA | 0 | no |
| MPI-701 | DLBCL | IG-MYC | NA | NA | NA | 0 | no |
| MPI-703 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-704 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-706 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-713 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-723 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-724 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-730 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-731 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-735 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-745 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-746 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-748 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-749 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-769 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-795 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-796 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-798 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-799 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-800 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-801 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-807 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-810 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-811 | DLBCL | NA | NA | NA | NA | 0 | no |
| MPI-813 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-814 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-815 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-818 | DLBCL | NA | NA | NA | NA | 0 | no |
| MPI-821 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-822 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-826 | DLBCL | NA | NA | NA | NA | 0 | no |
| MPI-830 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-839 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-840 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-841 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-842 | DLBCL | neg | NA | NA | NA | 0 | no |
| MPI-031 | DLBCL | non-IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-045 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-062 | DLBCL | neg | 1 | 0 | 0 | 1 | no |
| MPI-063 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-098 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-108 | DLBCL | neg | 1 | 0 | 0 | 1 | yes |
| MPI-119 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-120 | DLBCL | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-121 | DLBCL | non-IG-MYC | 0 | NA | NA | 1 | no |
| MPI-132 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-135 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-142 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-162 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-178 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-182 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-185 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-186 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-187 | DLBCL | IG-MYC | 1 | 0 | 0 | 1 | yes |
| MPI-190 | DLBCL | non-IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-192 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-202 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-204 | DLBCL | neg | 0 | NA | NA | 1 | no |
| MPI-208 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-224 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-235 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-239 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-243 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-246 | DLBCL | neg | 0 | NA | NA | 1 | yes |
| MPI-295 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-314 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-316 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-320 | DLBCL | non-IG-MYC | NA | NA | NA | 1 | yes |
| MPI-329 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-339 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-340 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-341 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-373 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-400 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-404 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-410 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-418 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-424 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-440 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-441 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-550 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-554 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-556 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-557 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-558 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-559 | DLBCL | neg | NA | NA | NA | 1 | yes |
| MPI-646 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-651 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-655 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-702 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-708 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-714 | DLBCL | IG-MYC | NA | NA | NA | 1 | no |
| MPI-737 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-812 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-820 | DLBCL | neg | NA | NA | NA | 1 | no |
| MPI-006 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-024 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-026 | intermediate | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-050 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-054 | intermediate | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-094 | intermediate | non-IG-MYC | 1 | 0 | 0 | 0 | yes |
| MPI-099 | intermediate | non-IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-107 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-117 | intermediate | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-126 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-131 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-216 | intermediate | neg | NA | NA | NA | 0 | no |
| MPI-225 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-245 | intermediate | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-250 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-275 | intermediate | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-284 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-292 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-310 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-317 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-322 | intermediate | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-325 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-333 | intermediate | IG-MYC | NA | NA | NA | 0 | yes |
| MPI-336 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-362 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-372 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-439 | intermediate | neg | NA | NA | NA | 0 | yes |
| MPI-530 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-569 | intermediate | IG-MYC | 0 | NA | NA | 0 | yes |
| MPI-574 | intermediate | IG-MYC | 3 | 0 | 0 | 0 | yes |
| MPI-582 | intermediate | neg | 0 | NA | NA | 0 | yes |
| MPI-583 | intermediate | IG-MYC | 2 | 1 | 0 | 0 | yes |
| MPI-592 | intermediate | neg | 1 | 0 | 0 | 0 | yes |
| MPI-593 | intermediate | IG-MYC | 6 | 2 | 1 | 0 | yes |
| MPI-691 | intermediate | neg | NA | NA | NA | 0 | no |
| MPI-808 | intermediate | neg | NA | NA | NA | 0 | no |
| MPI-843 | intermediate | neg | NA | NA | NA | 0 | no |
| MPI-007 | intermediate | neg | 0 | NA | NA | 1 | yes |
| MPI-037 | intermediate | non-IG-MYC | 0 | NA | NA | 1 | no |
| MPI-038 | intermediate | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-060 | intermediate | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-061 | intermediate | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-072 | intermediate | IG-MYC | 3 | 1 | 1 | 1 | yes |
| MPI-116 | intermediate | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-143 | intermediate | neg | 0 | NA | NA | 1 | no |
| MPI-161 | intermediate | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-175 | intermediate | neg | NA | NA | NA | 1 | yes |
| MPI-294 | intermediate | neg | NA | NA | NA | 1 | yes |
| MPI-311 | intermediate | neg | NA | NA | NA | 1 | yes |
| MPI-368 | intermediate | neg | NA | NA | NA | 1 | yes |
| MPI-587 | intermediate | IG-MYC | 0 | NA | NA | 1 | yes |
| MPI-619 | intermediate | IG-MYC | 4 | 0 | 1 | 1 | yes |
| MPI-654 | intermediate | neg | NA | NA | NA | 1 | no |
| MPI-661 | intermediate | neg | NA | NA | NA | 1 | no |

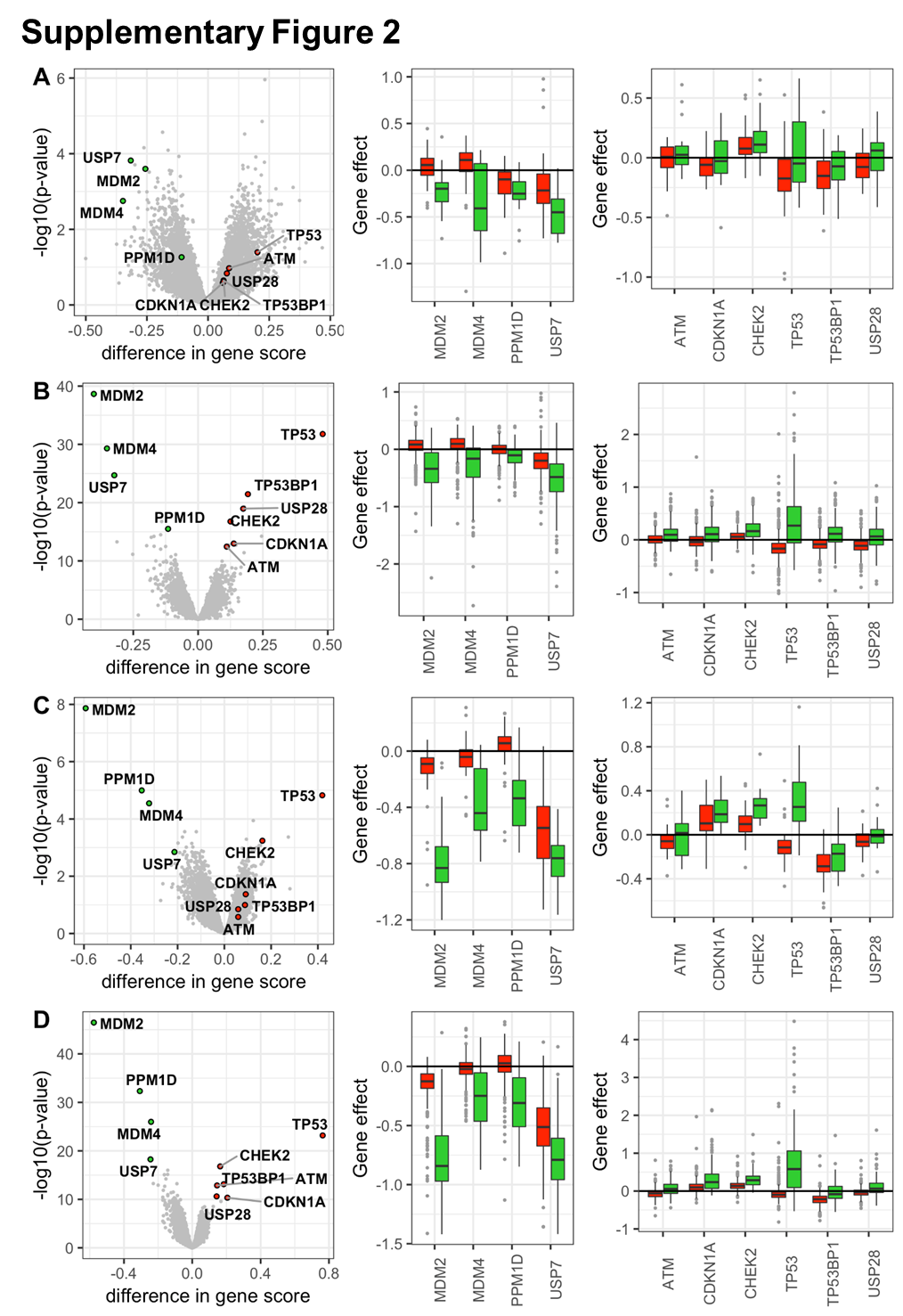
| **Supplementary Table 5. Annotation of TP53 mutation and MDM4 gain in cell lines from the Achilles project.** | | | | |
| --- | --- | --- | --- | --- |
| **Name** | **tumor type** | **subtype** | ***TP53* status** | ***MDM4* gain (CCLE)** |
| **CADOES1** | bone | Ewings | wt | gain |
| **EW8** | bone | Ewings | NA | NA |
| **EWS502** | bone | Ewings | NA | NA |
| **A673** | bone | Ewings | mut | normal |
| **TC71** | bone | Ewings | mut | normal |
| **SJSA1** | bone | Osteosarcoma | wt | normal |
| **CAL51** | breast | 0 | wt | normal |
| **CAL120** | breast | 0 | mut | normal |
| **MDAMB453** | breast | Adenocarcinoma | wt | gain |
| **MCF7** | breast | Carcinoma | wt | gain |
| **ZR7530** | breast | ductal Carcinoma | wt | gain |
| **HCC1187** | breast | ductal Carcinoma | mut | gain |
| **HCC2218** | breast | ductal Carcinoma | mut | gain |
| **HCC70** | breast | ductal Carcinoma | mut | normal |
| **BT20** | breast | ductal Carcinoma | mut | normal |
| **BT474** | breast | ductal Carcinoma | mut | normal |
| **EFM19** | breast | ductal Carcinoma | mut | normal |
| **HCC1395** | breast | ductal Carcinoma | mut | normal |
| **HCC1954** | breast | ductal Carcinoma | mut | normal |
| **SF767** | central\_nervous\_system | 0 | wt | NA |
| **LN319** | central\_nervous\_system | 0 | mut | NA |
| **LN428** | central\_nervous\_system | 0 | mut | NA |
| **CH157MN** | central\_nervous\_system | 0 | NA | NA |
| **IOMMLEE** | central\_nervous\_system | 0 | NA | NA |
| **LN215** | central\_nervous\_system | 0 | NA | NA |
| **LN464** | central\_nervous\_system | 0 | NA | NA |
| **A1207** | central\_nervous\_system | 0 | NA | NA |
| **LN235** | central\_nervous\_system | 0 | NA | NA |
| **LN340** | central\_nervous\_system | 0 | NA | NA |
| **LN382** | central\_nervous\_system | 0 | NA | NA |
| **LN443** | central\_nervous\_system | 0 | NA | NA |
| **LNZ308** | central\_nervous\_system | 0 | NA | NA |
| **SF172** | central\_nervous\_system | 0 | NA | NA |
| **U178** | central\_nervous\_system | 0 | NA | NA |
| **U343** | central\_nervous\_system | 0 | NA | NA |
| **A172** | central\_nervous\_system | 0 | wt | normal |
| **AM38** | central\_nervous\_system | 0 | wt | normal |
| **DBTRG05MG** | central\_nervous\_system | 0 | wt | normal |
| **DKMG** | central\_nervous\_system | 0 | wt | normal |
| **KNS81** | central\_nervous\_system | 0 | wt | normal |
| **U87MG** | central\_nervous\_system | 0 | wt | normal |
| **LN229** | central\_nervous\_system | 0 | mut | normal |
| **U251MG** | central\_nervous\_system | 0 | mut | normal |
| **CAS1** | central\_nervous\_system | 0 | mut | normal |
| **GB1** | central\_nervous\_system | 0 | mut | normal |
| **HS683** | central\_nervous\_system | 0 | mut | normal |
| **KALS1** | central\_nervous\_system | 0 | mut | normal |
| **KNS60** | central\_nervous\_system | 0 | mut | normal |
| **SF126** | central\_nervous\_system | 0 | mut | normal |
| **SF295** | central\_nervous\_system | 0 | mut | normal |
| **SNU1105** | central\_nervous\_system | 0 | mut | normal |
| **SW1783** | central\_nervous\_system | 0 | mut | normal |
| **T98G** | central\_nervous\_system | 0 | mut | normal |
| **YKG1** | central\_nervous\_system | 0 | mut | normal |
| **HEC1A** | endometrium | Adenocarcinoma; uterus | mut | normal |
| **EFE184** | endometrium | Carcinoma | mut | normal |
| **MM1S** | haematopoietic\_and\_lymphoid\_tissue | 0 | wt | gain |
| **L363** | haematopoietic\_and\_lymphoid\_tissue | plasma cell leukemia | mut | gain |
| **OPM2** | haematopoietic\_and\_lymphoid\_tissue | Multiple myeloma | mut | gain |
| **JJN3** | haematopoietic\_and\_lymphoid\_tissue | plasma cell leukemia | wt | NA |
| **KMS12BM** | haematopoietic\_and\_lymphoid\_tissue | Multiple myeloma | mut | normal |
| **SKMM2** | haematopoietic\_and\_lymphoid\_tissue | plasma cell leukemia | mut | normal |
| **MONOMAC6** | haematopoietic\_and\_lymphoid\_tissue | AML | mut | normal |
| **SKNO1** | haematopoietic\_and\_lymphoid\_tissue | AML M2 | mut | NA |
| **KASUMI1** | haematopoietic\_and\_lymphoid\_tissue | AML M2 | mut | normal |
| **HL60** | haematopoietic\_and\_lymphoid\_tissue | AML M3 | mut | normal |
| **NB4** | haematopoietic\_and\_lymphoid\_tissue | AML M3 | mut | normal |
| **OCIAML2** | haematopoietic\_and\_lymphoid\_tissue | AML M4 | wt | gain |
| **OCIAML3** | haematopoietic\_and\_lymphoid\_tissue | AML M4 | wt | gain |
| **OCIAML5** | haematopoietic\_and\_lymphoid\_tissue | AML M4 | wt | gain |
| **HNT34** | haematopoietic\_and\_lymphoid\_tissue | AML M4 | wt | NA |
| **PLB985** | haematopoietic\_and\_lymphoid\_tissue | AML M4 | NA | NA |
| **MV411** | haematopoietic\_and\_lymphoid\_tissue | AML M5 | wt | normal |
| **AML193** | haematopoietic\_and\_lymphoid\_tissue | AML M5 | mut | normal |
| **MONOMAC1** | haematopoietic\_and\_lymphoid\_tissue | AML M5 | mut | normal |
| **THP1** | haematopoietic\_and\_lymphoid\_tissue | AML M5 (Monocytic) | mut | gain |
| **MOLM13** | haematopoietic\_and\_lymphoid\_tissue | AML M5a | wt | normal |
| **NOMO1** | haematopoietic\_and\_lymphoid\_tissue | AML M5a | mut | normal |
| **F36P** | haematopoietic\_and\_lymphoid\_tissue | AML M6 | mut | normal |
| **X697** | haematopoietic\_and\_lymphoid\_tissue | B-ALL | wt | gain |
| **NALM6** | haematopoietic\_and\_lymphoid\_tissue | B-ALL | wt | normal |
| **RS411** | haematopoietic\_and\_lymphoid\_tissue | B-ALL | wt | normal |
| **SEM** | haematopoietic\_and\_lymphoid\_tissue | B-ALL | mut | normal |
| **REH** | haematopoietic\_and\_lymphoid\_tissue | B-ALL | NA | normal |
| **LAMA84** | haematopoietic\_and\_  lymphoid\_tissue | CML-BC (megakaryocytic) | mut | normal |
| **K562** | haematopoietic\_and\_  lymphoid\_tissue | CML-BC myeloid | mut | normal |
| **SLR21** | kidney | 0 | NA | NA |
| **SKRC20** | kidney | 0 | NA | NA |
| **SLR20** | kidney | 0 | NA | NA |
| **SLR23** | kidney | 0 | NA | NA |
| **SLR24** | kidney | 0 | NA | NA |
| **SLR25** | kidney | 0 | NA | NA |
| **SLR26** | kidney | 0 | NA | NA |
| **UOK101** | kidney | 0 | NA | NA |
| **ACHN** | kidney | 0 | wt | normal |
| **X786O** | kidney | Adenocarcinoma | mut | normal |
| **HCT116** | large\_intestine | 0 | wt | normal |
| **SNUC1** | large\_intestine | Adenocarcinoma | mut | loss |
| **GP2D** | large\_intestine | Adenocarcinoma | wt | normal |
| **LOVO** | large\_intestine | Adenocarcinoma | wt | normal |
| **SKCO1** | large\_intestine | Adenocarcinoma | wt | normal |
| **SW48** | large\_intestine | Adenocarcinoma | wt | normal |
| **C2BBE1** | large\_intestine | Adenocarcinoma | mut | normal |
| **COLO205** | large\_intestine | Adenocarcinoma | mut | normal |
| **HT29** | large\_intestine | Adenocarcinoma | mut | normal |
| **HT55** | large\_intestine | Adenocarcinoma | mut | normal |
| **KM12** | large\_intestine | Adenocarcinoma | mut | normal |
| **RKO** | large\_intestine | Adenocarcinoma | mut | normal |
| **SW480** | large\_intestine | Adenocarcinoma | mut | normal |
| **NCIH716** | large\_intestine | Adenocarcinoma | mut | normal |
| **SW1417** | large\_intestine | Adenocarcinoma | mut | normal |
| **DLD1** | large\_intestine | Adenocarcinoma | NA | normal |
| **NCIH508** | large\_intestine | Adenocarcinoma; Cecum | mut | loss |
| **LS513** | large\_intestine | Adenocarcinoma; Cecum | wt | normal |
| **LS411N** | large\_intestine | Adenocarcinoma; Cecum | mut | normal |
| **SNUC2A** | large\_intestine | Carcinoma; Cecum | mut | normal |
| **HLF** | liver | Hepatoma | mut | normal |
| **NCIH1299** | lung | 0 | mut | loss |
| **HCC827GR5** | lung | 0 | NA | NA |
| **A549** | lung | 0 | wt | normal |
| **NCIH196** | lung | 0 | mut | normal |
| **NCIH2171** | lung | 0 | mut | normal |
| **HCC44** | lung | 0 | mut | normal |
| **HCC364** | lung | Adenocarcinoma | NA | NA |
| **HCC827** | lung | Adenocarcinoma | mut | normal |
| **NCIH1975** | lung | Adenocarcinoma | mut | normal |
| **NCIH2122** | lung | Adenocarcinoma | mut | normal |
| **NCIH1437** | lung | Adenocarcinoma | mut | normal |
| **NCIH1792** | lung | Adenocarcinoma | mut | normal |
| **NCIH23** | lung | Adenocarcinoma | mut | normal |
| **NCIH441** | lung | Adenocarcinoma | mut | normal |
| **NCIH838** | lung | Adenocarcinoma | NA | normal |
| **NCIH1650** | lung | Adenocarcinoma, BAC | mut | normal |
| **CALU1** | lung | Carcinoma, Epidermoid | NA | normal |
| **NCIH661** | lung | Large cell | mut | normal |
| **CORL23** | lung | Large cell | mut | normal |
| **HCC2814** | lung | Squamous | NA | NA |
| **LK2** | lung | Squamous | mut | normal |
| **JHESOAD1** | oesophagus | Adenocarcinoma | NA | NA |
| **OE33** | oesophagus | Adenocarcinoma | mut | normal |
| **KYSE150** | oesophagus | Squamous | mut | loss |
| **KYSE30** | oesophagus | Squamous | mut | normal |
| **KYSE450** | oesophagus | Squamous | mut | normal |
| **KYSE510** | oesophagus | Squamous | mut | normal |
| **TE15** | oesophagus | Squamous | mut | normal |
| **TE9** | oesophagus | Squamous | mut | normal |
| **TT** | oesophagus | Squamous | mut | normal |
| **TE10** | oesophagus | Squamous | mut | normal |
| **JHOC5** | ovary | 0 | wt | gain |
| **SNU840** | ovary | 0 | wt | gain |
| **OELE** | ovary | 0 | NA | NA |
| **COV434** | ovary | 0 | wt | normal |
| **COV644** | ovary | 0 | wt | normal |
| **OAW42** | ovary | 0 | wt | normal |
| **COV362** | ovary | 0 | mut | normal |
| **TYKNU** | ovary | 0 | mut | normal |
| **JHOM1** | ovary | 0 | mut | normal |
| **OV7** | ovary | 0 | mut | normal |
| **RMUGS** | ovary | 0 | mut | normal |
| **SKOV3** | ovary | 0 | mut | normal |
| **CAOV3** | ovary | Adenocarcinoma | mut | loss |
| **OVISE** | ovary | Adenocarcinoma | wt | normal |
| **CAOV4** | ovary | Adenocarcinoma | mut | normal |
| **IGROV1** | ovary | Adenocarcinoma | mut | normal |
| **COLO704** | ovary | Carcinoma | wt | gain |
| **HEYA8** | ovary | Carcinoma | wt | normal |
| **OVCAR3** | ovary | Carcinoma | mut | normal |
| **OVCAR4** | ovary | Carcinoma | mut | normal |
| **RMGI** | ovary | Clear cell carcinoma | wt | normal |
| **TOV21G** | ovary | Clear cell carcinoma | wt | normal |
| **TOV112D** | ovary | Endometrioid carcinoma | mut | normal |
| **OVCAR8** | ovary | Mixed carcinoma | mut | normal |
| **OV90** | ovary | Mixed carcinoma;  papillary serous adenocarcinoma | mut | normal |
| **EFO27** | ovary | Mucinous carcinoma | mut | normal |
| **EFO21** | ovary | Serous carcinoma | mut | loss |
| **COV504** | ovary | Serous carcinoma | mut | normal |
| **KURAMOCHI** | ovary | Undifferentiated carcinoma | mut | gain |
| **SU8686** | pancreas | 0 | mut | NA |
| **KP4** | pancreas | 0 | wt | normal |
| **L33** | pancreas | 0 | wt | normal |
| **BXPC3** | pancreas | 0 | mut | normal |
| **CFPAC1** | pancreas | 0 | mut | normal |
| **HPAC** | pancreas | 0 | mut | normal |
| **MIAPACA2** | pancreas | 0 | mut | normal |
| **PANC0327** | pancreas | 0 | mut | normal |
| **PANC0813** | pancreas | 0 | mut | normal |
| **PANC1005** | pancreas | 0 | mut | normal |
| **QGP1** | pancreas | 0 | mut | normal |
| **HPAFII** | pancreas | 0 | mut | normal |
| **PSN1** | pancreas | 0 | mut | normal |
| **HS766T** | pancreas | 0 | NA | normal |
| **KP1NL** | pancreas | Adenocarcinoma | wt | NA |
| **ASPC1** | pancreas | ascites | mut | normal |
| **KP2** | pancreas | Carcinoma | mut | normal |
| **NCIH2052** | pleura | 0 | wt | normal |
| **NCIH2452** | pleura | 0 | wt | normal |
| **VCAP** | prostate | 0 | mut | normal |
| **X22RV1** | prostate | Carcinoma | mut | gain |
| **NCIH660** | prostate | Neuroendocrine | wt | normal |
| **C32** | skin | 0 | wt | gain |
| **HS944T** | skin | 0 | wt | normal |
| **SKMEL5** | skin | 0 | wt | normal |
| **A2058** | skin | 0 | mut | normal |
| **IGR39** | skin | 0 | mut | normal |
| **COLO783** | skin | 0 | mut | normal |
| **COLO741** | skin | Carcinoma | mut | normal |
| **HUTU80** | small\_intestine | Adenocarcinoma; Duodenum | wt | normal |
| **RKN** | soft\_tissue | Leiomyosarcoma | mut | normal |
| **A204** | soft\_tissue | Rhabdomyosarcoma | wt | normal |
| **AGS** | stomach | 0 | wt | normal |
| **HUG1N** | stomach | 0 | mut | normal |
| **MKN7** | stomach | Adenocarcinoma | mut | normal |
| **NCIN87** | stomach | Carcinoma | mut | normal |
| **HT1197** | urinary\_tract | Carcinoma | wt | loss |
| **RT112** | urinary\_tract | Carcinoma; transitional cell | mut | normal |
| **TCCSUP** | urinary\_tract | Carcinoma; transitional cell | mut | normal |

# **Supplementary Figures**



**Supplementary Figure 1.** **RNAi screen identifies common and context-specific essential genes.**

**(A)** Overlap of essential genes in eight BL cell lines. Genes were ranked based on their weighted z-score and the top 250 essential genes were selected for comparison between the cell lines. The barplot shows the number of genes that scored in one or multiple cell lines as indicated at the bottom. Many top-ranking genes were cell line-specific, followed by a set of core essential genes common to all cell lines. **(B)** Integration of multiple independent RNAi screens. The RNAi screen in eight BL cell lines was combined with three RNAi screens using the same shRNA library (performed by Cellecta Inc.). Weighted z-scores were normalized using peak median absolute deviation (PMAD) to account for differences in dispersion of the data. The heatmap represents data for 5,045 genes included in the RNAi library. Core essential and non-essential genes as defined by Hart et al., 2014 are indicated. **(C)** Comparison of essential genes in eight BL and two blood cancer (1 DLBCL, 2 AML) cell lines. Genes essential in BL are shown in light blue and genes that also scored as BL-essential in the comparison of BL and solid cancer cell lines are shown in dark blue. **(D)** Genotype-specific essential genes. shRNAs were ranked by their differential effects in cell lines with and without the indicated mutation. Candidate genes essential in mutant (red) or wild-type (green) cell lines are indicated.



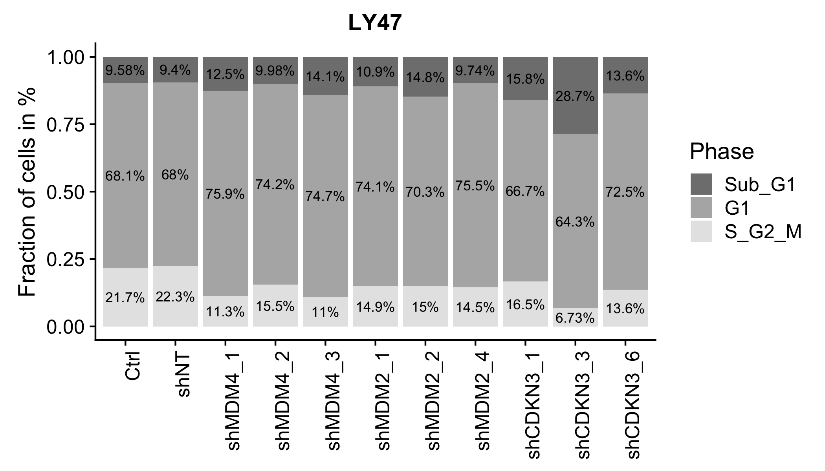
**Supplementary Figure 2.** **Genes essential in the context of *TP53* mutation.**

Volcano plots show the differences in gene dependency scores with highlighted TP53wt (green) and TP53mut (red) candidate genes. Boxplots show genes with significantly (adjusted p-value < 0.01) higher or lower gene scores in TP53wt or TP53mut cell lines, respectively. All data is from the DepMap project (https://depmap.org/portal/) showing hematopoietic/lymphoid cell lines from **(A)** combined RNAi screens (TP53wt: n=19; TP53mut: n=42) or from **(B)** CRISPR screen (TP53wt: n=55; TP53mut: n=55), and cell lines of all origins from **(C)** combined RNAi screens (TP53wt: n=245; TP53mut: n=467) or from **(D)** the CRISPR screen (TP53wt: n=164; TP53mut: n=353).

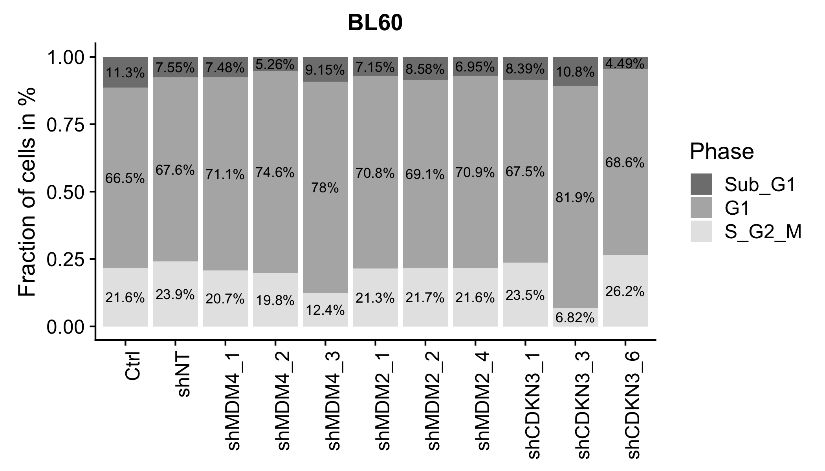
**Supplementary Figure 3**

**A**

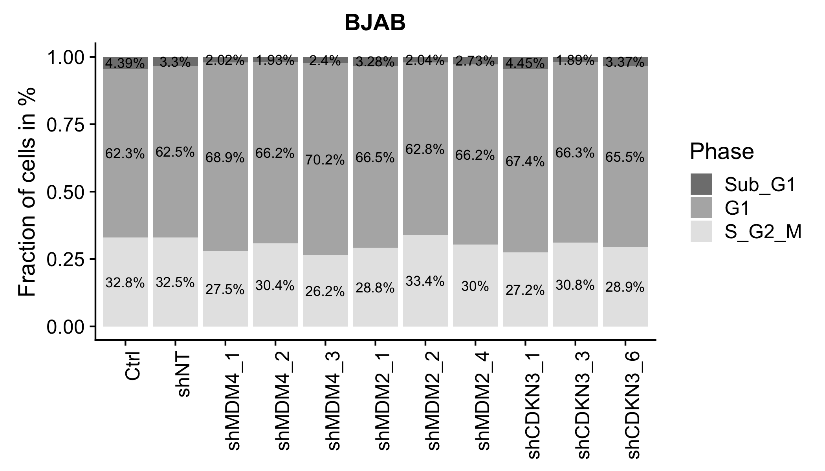
**D**



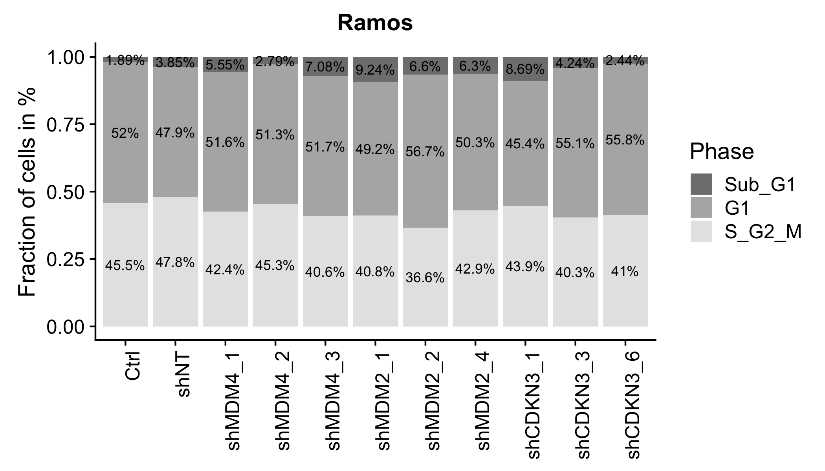
**LY47**



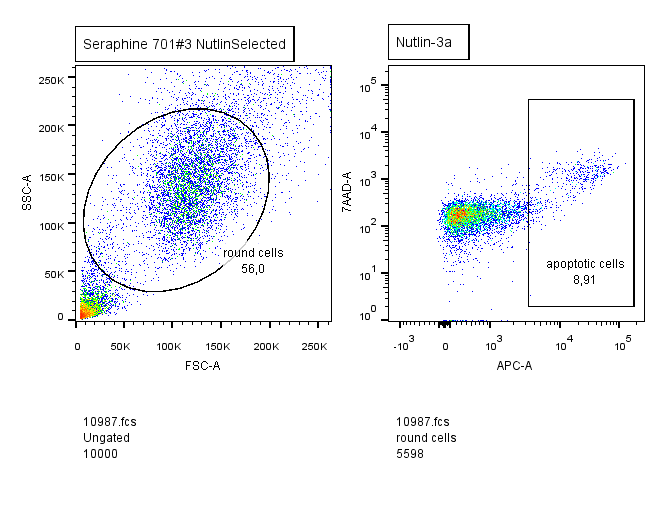
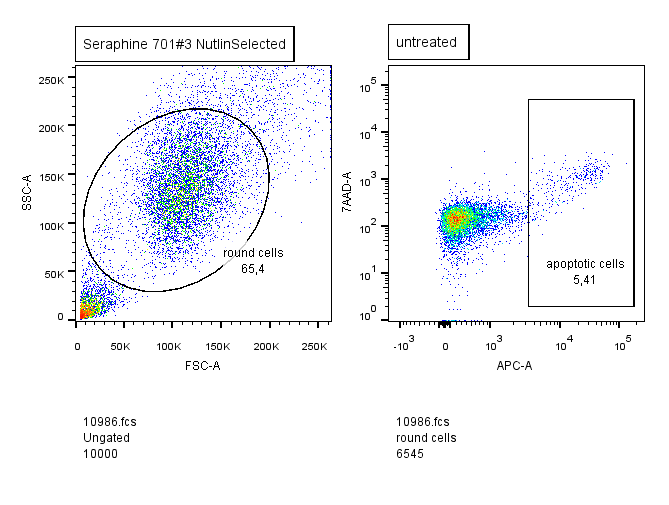
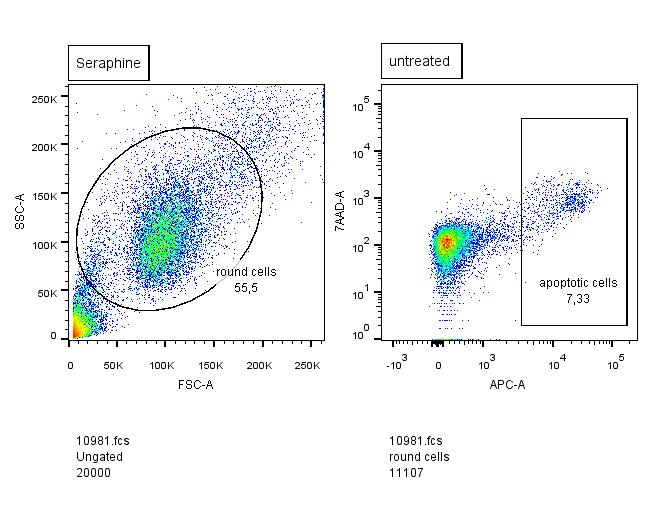
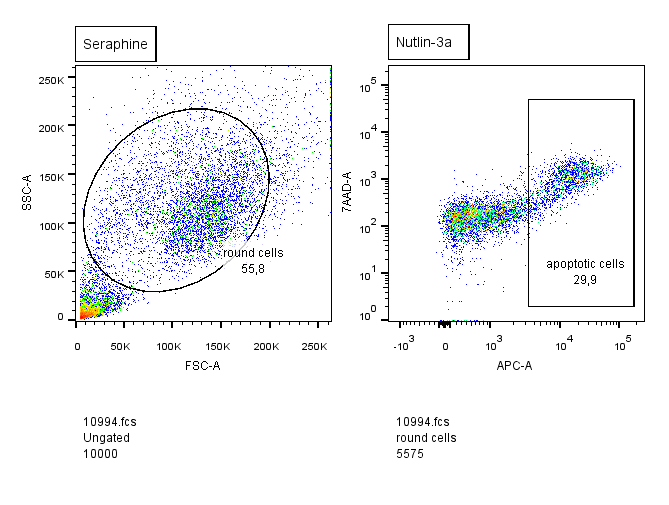
**BL60**



**BJAB**



**Ramos**



**Annexin-V-APC**

**30%**

**Nutlin-3**

**Nutlin-3**

**Seraphine-TP53ko**

**Seraphine-TP53wt**

**9%**

**7%**

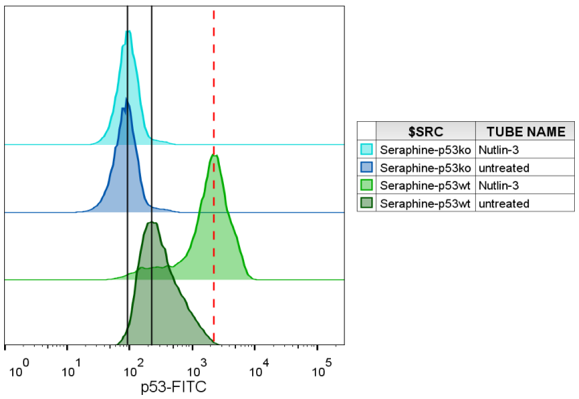
**5%**

**DMSO**

**DMSO**

**7-AAD**

**C**



**p53wt**

**DMSO**

**p53wt**

**Nutlin-3**

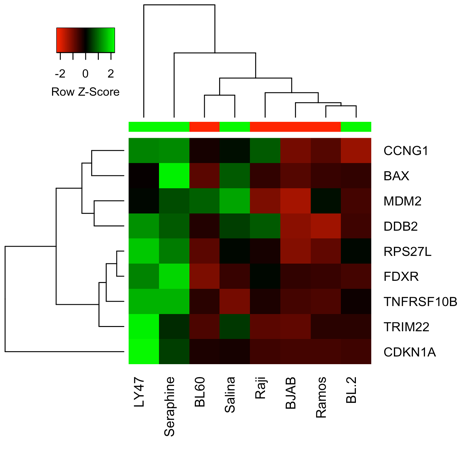
**p53ko**

**DMSO**

**p53ko**

**Nutlin-3**

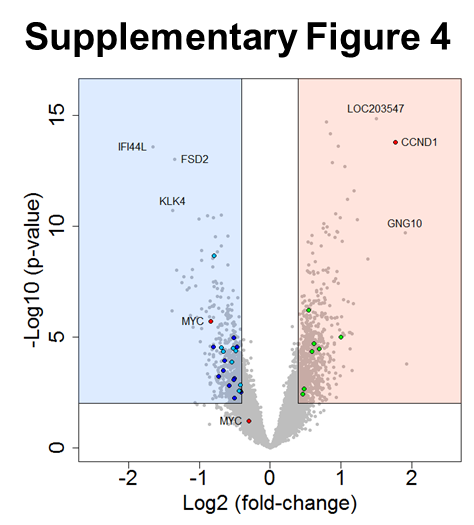
**p53-FITC**



**B**

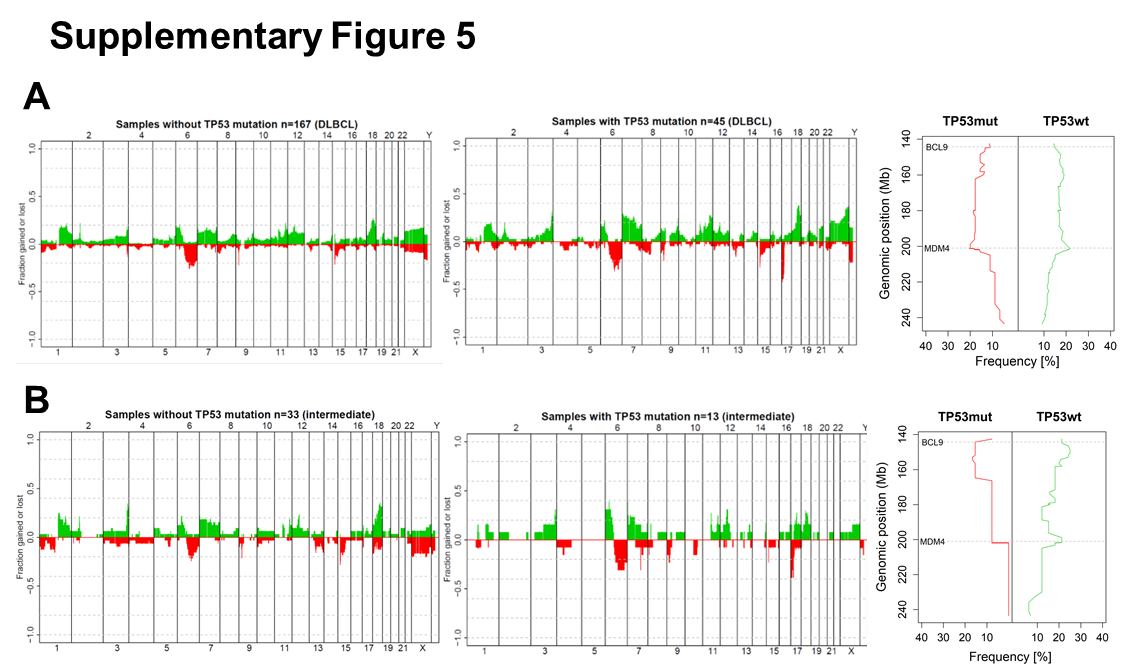
**Supplementary Figure 3.** **p53 reactivation causes cytotoxic effects.**

**(A)** Seraphine-TP53wt (green) and Seraphine-TP53ko (blue) were exposed to 10µM Nutlin-3 or DMSO for 12h and p53 levels were assayed in flow cytometry using intracellular staining. **(B)** Expression of p53 target genes in Burkitt lymphoma cell lines. The heatmap is showing row-normalized RPKM values from RNA sequencing. The genes were previously reported to be direct targets of p53 and were differentially expressed in aggressive B-cell lymphomas with p53 mutation (as shown in figure 6). *TP53* status of the cell lines is indicated (green = TP53wt, red = TP53mut). **(C)** Cell lines LY47 (TP53wt), BJAB, BL60 and Ramos (TP53mut) were transduced with shRNAs targeting MDM4 or a non-targeting control (shNT) at >80% rate and the proportion of cycling cells was measured in flow cytometry using 7-AAD after 5 days. **(D)** Cells were treated with 10µM Nutlin-3 or DMSO for 48h and apoptotic cells were measured in flow cytometry using Annexin-V-APC and 7-AAD staining.



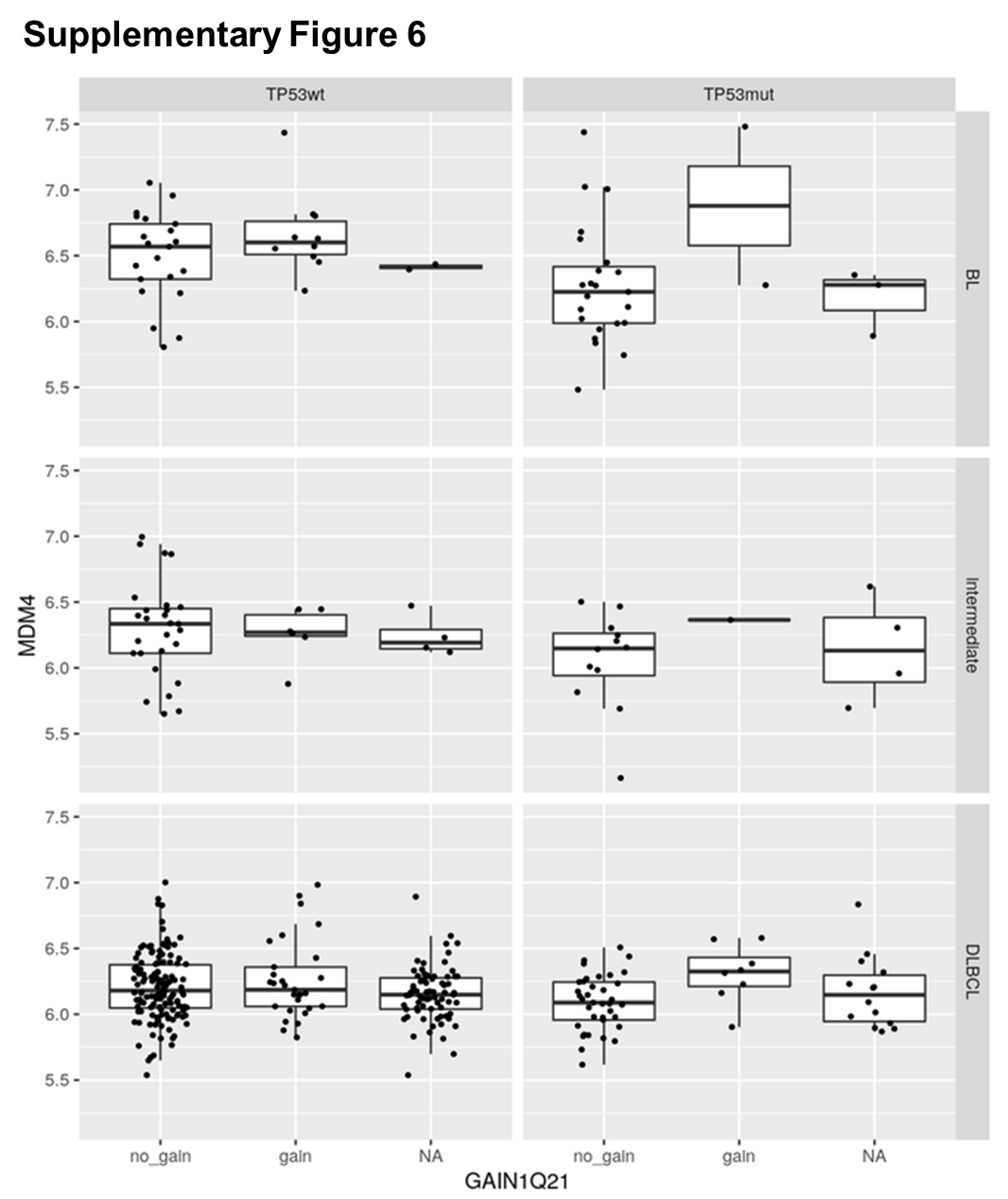
**Supplementary Figure 4. Molecular impact of MDM2 or MDM4 knock-down.**

Differential gene expression changes after MDM4 and MDM2 knock-down in the BL cell line Seraphine-TP53wt. Related to Figure 3C.



**Supplementary Figure 5. Genetic profile in TP53wt and TP53mut aggressive B-NHL patients.**

Chromosomal gains (green) and losses (red) in **(A)** DLBCL and **(B)** intermediate phenotype patients from the MMML consortium. The copy number profiles for TP53wt patients are shown on the left and for TP53mut patients in the middle. The mirror plot on the right shows the frequency of a gain on 1q.



**Supplementary Figure 6. Basal MDM4 mRNA in aggressive lymphomas stratified by *TP53* mutation and 1q status.**

Gene expression for 61 BL, 54 intermediate and 297 DLBCL patients from the MMML cohort were available from Gene Expression Omnibus (GSE43677).

# **Supplementary Methods**

**Genetic annotation of cell lines**

Mutations in BL cell lines were identified from genomic DNA using a self-designed amplicon panel (1) or from RNA sequencing on the Illumina HiSeq2000. Sequences were mapped against the human reference genome hg19 using the STAR alignment tool. Mutations were called as described previously (2). Genetic information for non-BL cell lines was extracted from CCLE (https://portals.broadinstitute.org/ccle/home) and COSMIC (GDSC, http://www.cancerrxgene.org/).

**RT-qPCR**

Total RNA was isolated with RNeasy Mini Kit (Qiagen) and on-column DNase I (Qiagen) digestion. RNA was reverse-transcribed by Super-Script III First-Strand Synthesis Supermix (Invitrogen) and quantified using QuantiFast SYBR Green RT-PCR (Qiagen) or Power SYBR Green Master Mix (Applied Biosystems) on a LightCycler 480 Real-Time PCR System, software v1.5 (Roche Applied Sciences).

**CRISPR/Cas9 gene knock-out**

sgRNAs were co-expressed with Cas9 from lentiCRISPRv2 (Addgene, Cambridge, MA, USA, plasmid #52961). Seraphine cells with effective p53 knock-out were selected using puromycin and Nutlin-3.

**RNAi screen.** The DECIPHERTM Human Module 1 shRNA library (#DHPAC-M1-P) consisting of 27,500 targeting 5,045 genes in key signaling pathways was obtained from Cellecta Inc. (Mountain View, CA, USA). shRNAs were co-expressed with puromycin resistance gene and red fluorescence protein (RFP) from a barcoded pRSI12-U6-(sh)-UbiC-TagRFP-2A-Puro vector backbone. shRNA were infected 80 times (5.4x106 cells) in three replicates aiming at 50% transduction efficiency. One replicate was harvested on day 2 post-transduction while remaining cells were treated with puromycin at the minimal lethal dose for 48h and harvested in two replicates on day 14 post-transduction. During sampling >1,000-fold representation of shRNAs was maintained. DNA extraction and shRNA barcode amplification were performed according to the Cellecta Manual for pooled barcoded lentiviral shRNA libraries “HT RNAi Genetic Screens with DECIPHER™ or Custom Pooled shRNA Libraries” (version v5e from 2013-09-06). Barcode sequences are listed in the Supplementary Methods section under Primers and Sequences. shRNA barcodes were sequenced at the DKFZ Genomics and Proteomics Core Facility (GPCF) using 50bp single-end sequencing on one lane of the Illumina HiSeq2000. 40% “random” PhiX sequences were added to avoid that the sequencer loses focus while reading the common identifier.

Multiplexed samples were deconvoluted by the DKFZ GPCF based on the index sequence. Raw sequencing reads were trimmed to 20bp reads using the python script “Gzim\_Trim”. Barcode sequences were identified using the DECIPHER bar code deconvoluter software (version 2010-10-05) and the library reference file (BLIB). Settings of the software were changed to “Allow 1 error” and “Correct N symbol”. The 2bp module identifier (AT for module 1) was not needed, as we did not pool different modules. The software created a tab delimited file containing the counts for all identified barcodes.

Raw shRNA counts were divided by the mean read count in the respective samples. As replicate samples were highly correlated, the mean was taken in the following analysis. shRNA fold-changes between day 2 and day 14 were calculated for each cell line. After logarithmic transformation to the basis of 2, values were normalized between cell lines by peak median absolute deviation (PMAD) using the GenePattern module “NormLines” provided by the Broad Institute (3).

Analysis of differentially expressed shRNAs was performed using GENE-E software with RIGER extension provided by the Broad Institute (https://software.broadinstitute.org/GENE-E/) as described previously (4). shRNAs were scored and ranked for their ability to distinguish between two classes using „Weight of evidence“ (WoE) statistics. WoE scores for shRNAs targeting the same gene were combined into gene scores and ranks using Kolmogorov-Smirnov (KS) statistics.

Gene depletion scores were calculated using the edgeR package and Fisher z-transformation as described previously (5,6). Control shRNAs present in triplicates and shRNAs with low read counts in the day 2 control samples (5%) were removed. The edgeR package was used to calculate the dispersion of the data and fit a negative binomial model (7). P-values for shRNA distribution were calculated by carrying out a likelihood ratio test and adjusted for multiplicity of testing by FDR method. P-values for shRNAs targeting the same gene were combined into gene depletion scores using weighted z-transformation (wZ-scores) (5,6).

To remove shRNAs with overlapping target region, shRNA sequences were mapped against the human reference genome hg19 using the Tophat2 algorithm (kindly performed byAgnes Hotz-Wagenblatt, DKFZ).

Context-specific essential genes were prioritized based on the following criteria:

(1) Genes with significantly lower shRNA counts in one group by KS score (p-value < 0.05).

(2) Genes with significantly lower shRNA counts in one group by 2nd best shRNA (p-value < 0.05)

(3) Genes that cause a viability effect in one group (median wZ-score < -0.5)

(4) Genes expressed in BL cell lines (8)

(5) Removal of shRNAs with overlapping target region

(6) Significant difference in wZ-score (p<0.05). The difference was calculated using a t-test.

**Single shRNA mediated knock-down.** shRNA sequences from the pooled shRNA library and cloned into the pRSI12-U6-(sh)-UbiC-TagRFP-2A-Puro vector backbone according to the Cellecta manual “Cloning of shRNA Templates into shRNA Expression Vectors” (version v3a, 8-29-2013). Lentiviral packaging and transduction were performed according to the Cellecta manual “Packaging and Transduction of Lentiviral Constructs” (version v.8a, 7/17/12).

**Immunoblot analysis.** Cells were lysed in RIPA buffer (150mM NaCl, 0.5% Na-Desoxycholate, 1% NP-40, 0.1% SDS, 50mM Tris pH 7.5; Merck/Millipore) and protein was quantified using the Pierce BCA Protein Assay kit (Thermo Fisher Scientific), a colorimetric assay, according to the manuals. Light absorption at 562nm was measured with the Tecan plate reader. For immunoblotting 40µg protein containing 1x Laemmli buffer (4% SDS, 20% glycerol, 10% 2-mercaptoethanol, 0.004% bromphenol blue and 0.125 M Tris HCl, pH~6.8; Sigma-Aldrich) were separated by size on pre-casted TGX gradient gels (4-15%) and transferred to a low-fluorescent PVDF membrane using the Trans-Blot Turbo Transfer system (Biorad). The membrane was incubated for at least 2h in TBS-T (137mM NaCl, 2.7mM KCl, 19mM Tris pH 7.4, 0.1% Tween 20) with 5% skim milk to reduce unspecific antibody binding. Primary antibodies were diluted in TBS-T with 5% BSA to increase specificity of binding and incubated over night at 4°C while shaking. Fluorochrome-conjugated DyLight® (CST, Danvers, MA, USA) secondary antibody targeting mouse or rabbit proteins were used at a 1:15,000 dilution. Protein bands were detected using the Odyssey fluorescent scanner (Li-cor, Lincoln, NE, USA), analyzed using the ImageStudio software provided by Li-cor and quantified using ImageJ software.

## **Primers and sequences**

|  |  |  |
| --- | --- | --- |
| **RNAi screen** | | |
| **Name** | **Sequence [5'-3']** | **Reaction** |
| FwdHTS | TTCTCTGGCAAGCAAAAGACGGCATA | 1st Round PCR |
| RevHTS1 | TAGCCAACGCATCGCACAAGCCA | 1st Round PCR |
| FwdGex | CAAGCAGAAGACGGCATACGAGA | 2nd Round PCR |
| RevGex | AATGATACGGCGACCACCGAGA | 2nd Round PCR |
| IndA | AATGATACGGCGACCACCGAGATCTACACGCAATGCGCACAACCGCAA | Multiplexing |
| IndB | AATGATACGGCGACCACCGAGATCTACACGCAGACTGCACAACCGCAA | Multiplexing |
| IndC | AATGATACGGCGACCACCGAGATCTACACGCATCAGGCACAACCGCAA | Multiplexing |
| IndD | AATGATACGGCGACCACCGAGATCTACACGCACGTAGCACAACCGCAA | Multiplexing |
| IndE | AATGATACGGCGACCACCGAGATCTACACGCAAGCGGCACAACCGCAA | Multiplexing |
| IndF | AATGATACGGCGACCACCGAGATCTACACGCAGATGGCACAACCGCAA | Multiplexing |
| IndG | AATGATACGGCGACCACCGAGATCTACACGCAGGACGCACAACCGCAA | Multiplexing |
| IndH | AATGATACGGCGACCACCGAGATCTACACGCAGCGAGCACAACCGCAA | Multiplexing |
| GexSeqS | AGAGGTTCAGAGTTCTACAGTCCGAA | Barcode sequencing |
| GexSeqIND | ACGACCACCGAGATCTACACGCA | Indexing |
| **RT-qPCR** | | |
| **Name** | **Sequence [5'-3']** | **Source** |
| qMDM4\_fwd | TGAAAGACCCAAGCCCTCT | Self-designed |
| qMDM4\_rev | CGAGAGTCTGAGCAGCATCTG | Self-designed |
| qTP53\_fwd | GGAGCACTAAGCGAGCACTG | Self-designed |
| qTP53\_rev | CACGGATCTGAAGGGTGAAA | Self-designed |
| qMDM2\_fwd | CAGTAGCAGTGAATCTACAGGGA | RT-Primer Bank |
| qMDM2\_rev | CTGATCCAACCAATCACCTGAAT | RT-Primer Bank |
| qBAX\_fwd | CCCGAGAGGTCTTTTTCCGAG | RT-Primer Bank |
| qBAX\_rev | CCAGCCCATGATGGTTCTGAT | RT-Primer Bank |
| qRRM2B\_fwd | AGAGGCTCGCTGTTTCTATGG | RT-Primer Bank |
| qRRM2B\_rev | GCAAGGCCCAATCTGCTTTTT | RT-Primer Bank |
| qCDKN1A\_fwd | GACTCTCAGGGTCGAAAACG | self-designed |
| qCDKN1A\_rev | TAGGGCTTCCTCTTGGAGAA | self-designed |
| qMCM7\_fwd | CCTACCAGCCGATCCAGTCT | RT-Primer Bank |
| qMCM7\_rev | CCTCCTGAGCGGTTGGTTT | RT-Primer Bank |
| qMCM6\_fwd | ACCTGCCTACCAGACACAAGA | RT-Primer Bank |
| qMCM6\_rev | ACAGAAAAGTTCCGCTCACAAG | RT-Primer Bank |
| qMCM10\_fwd | TGTCCCTGCGCTACCAAGA | RT-Primer Bank |
| qMCM10\_rev | GATGAGCTTTTGGGATCTGGAG | RT-Primer Bank |
| qCDKN3\_fwd | TCCGGGGCAATACAGACCAT | RT-Primer Bank |
| qCDKN3\_rev | GCAGCTAATTTGTCCCGAAACTC | RT-Primer Bank |
| qGAPDH\_fwd | GGAGCGAGATCCCTCCAAAAT | RT-Primer Bank |
| qGAPDH\_rev | GGCTGTTGTCATACTTCTCATGG | RT-Primer Bank |
| **shRNA target sequences** | | |
| **Name** | **Sequence [5'-3']** | **Cellecta ID** |
| MDM2\_1 | CTTTGGTAGTGGAATAGTGAA | CLL-H-016687 |
| MDM4\_1 | GTTCACTGTTAAAGAGGTCAT | CLL-H-016693 |
| MDM4\_2 | CACCTAGAAGTAATGGCTCAA | CLL-H-016692 |
| MDM4\_3 | ACAGTCCTTCAGCTATTTCAT | CLL-H-016695 |
| MDM4\_4 | CTCAACTGATTTACAGACAAA | CLL-H-016696 |
| MDM4\_5 | CCCTGATTGTCGAAGAACCAT | CLL-H-016694 |
| shNT | CAACAAGATGAAGAGCACCAA |  |
| **sgRNA target sequences** | | |
| **Name** | **Sequence [5'-3']** | **Source** |
| TP53\_8 | CCCCTTGCCGTCCCAAGCAA | HGLibB\_51985 |

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