# HICF1 - Final Report v1

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## Univariate Analysis

Table 1: Univariate Analysis against MRD outcome

|  | p.value | uncorrected | corrected.p.value | corrected | MRDneg0 | MRDpos1 | MRDneg1 | sum | testused |
|---|---|---|---|---|---|---|---|---|---|
| TP53_ALL | 0.00004 | *** | 0.002 | ** | 105 | 19 | 2 | 209 | Fisher's Exact Test |
| TP53_del | 0.012 | * | 0.513 | n.s. | 107 | 6 | 0 | 209 | Fisher's Exact Test |
| TP53_cnLOH | 0.055 | trend | 1 | n.s. | 107 | 4 | 0 | 209 | Fisher's Exact Test |
| TP53_mut | 0.00001 | *** | 0.001 | *** | 107 | 15 | 0 | 209 | Fisher's Exact Test |
| TP53_bi | 0.009 | ** | 0.360 | n.s. | 106 | 9 | 1 | 209 | Fisher's Exact Test |
| ATM_ALL | 0.002 | ** | 0.085 | trend | 83 | 44 | 24 | 209 | Fisher's Exact Test |
| ATM_mut | 0.036 | * | 1 | n.s. | 88 | 31 | 19 | 209 | Fisher's Exact Test |
| ATM_del | 0.0005 | *** | 0.022 | * | 98 | 28 | 9 | 209 | Fisher's Exact Test |
| ATM_cnLOH | 0.203 | n.s. | 1 | n.s. | 106 | 4 | 1 | 209 | Fisher's Exact Test |
| ATM_mt1 | 1 | n.s. | 1 | n.s. | 101 | 5 | 6 | 209 | Fisher's Exact Test |
| BIRC3_ALL | 0.094 | trend | 1 | n.s. | 94 | 22 | 13 | 209 | Fisher's Exact Test |
| BIRC3_mut | 0.375 | n.s. | 1 | n.s. | 99 | 4 | 8 | 209 | Fisher's Exact Test |
| BIRC3_del | 0.002 | ** | 0.076 | trend | 101 | 21 | 6 | 209 | Fisher's Exact Test |
| ATM_bi | 0.002 | ** | 0.088 | trend | 102 | 19 | 5 | 209 | Fisher's Exact Test |
| BIRC3_bi | 0.360 | n.s. | 1 | n.s. | 106 | 3 | 1 | 209 | Fisher's Exact Test |
| X11q_mono | 0.046 | * | 1 | n.s. | 104 | 10 | 3 | 209 | Fisher's Exact Test |
| ATM_mono | 0.836 | n.s. | 1 | n.s. | 93 | 12 | 14 | 209 | Fisher's Exact Test |
| BIRC3_mono | 0.066 | trend | 1 | n.s. | 100 | 1 | 7 | 209 | Fisher's Exact Test |
| NOTCH1_mut | 0.069 | trend | 1 | n.s. | 88 | 9 | 19 | 209 | Fisher's Exact Test |
| SF3B1_mut | 0.415 | n.s. | 1 | n.s. | 85 | 26 | 22 | 209 | Fisher's Exact Test |
| X6q._del_ALL | 0.595 | n.s. | 1 | n.s. | 98 | 6 | 9 | 209 | Fisher's Exact Test |
| X13q_ALL | 0.267 | n.s. | 1 | n.s. | 54 | 59 | 53 | 209 | Fisher's Exact Test |
| X13del_homo | 0.832 | n.s. | 1 | n.s. | 95 | 13 | 12 | 209 | Fisher's Exact Test |
| X13q_het | 0.330 | n.s. | 1 | n.s. | 66 | 46 | 41 | 209 | Fisher's Exact Test |
| X13qdelRB1 | 0.743 | n.s. | 1 | n.s. | 84 | 24 | 23 | 209 | Fisher's Exact Test |
| X13q_Ox | 0.248 | n.s. | 1 | n.s. | 88 | 12 | 19 | 209 | Fisher's Exact Test |
| X13q_Rossi | 1 | n.s. | 1 | n.s. | 73 | 32 | 34 | 209 | Fisher's Exact Test |
| Trisomy_12 | 0.002 | ** | 0.100 | trend | 82 | 8 | 25 | 209 | Fisher's Exact Test |
| Trisomy_18 | 0.060 | trend | 1 | n.s. | 102 | 0 | 5 | 209 | Fisher's Exact Test |
| Trisomy_19 | 0.029 | * | 1 | n.s. | 101 | 0 | 6 | 209 | Fisher's Exact Test |
| XPO1_ALL | 0.160 | n.s. | 1 | n.s. | 100 | 13 | 7 | 209 | Fisher's Exact Test |
| XPO1_gain | 0.054 | trend | 1 | n.s. | 105 | 8 | 2 | 209 | Fisher's Exact Test |
| XPO1_mutation | 0.764 | n.s. | 1 | n.s. | 102 | 6 | 5 | 209 | Fisher's Exact Test |
| SAMHD1_ALL | 0.054 | trend | 1 | n.s. | 105 | 8 | 2 | 209 | Fisher's Exact Test |
| SAMHD1_mut | 0.006 | ** | 0.254 | n.s. | 107 | 7 | 0 | 209 | Fisher's Exact Test |
| SAMHD1_cnLOH_Del | 0.437 | n.s. | 1 | n.s. | 105 | 4 | 2 | 209 | Fisher's Exact Test |
| MYD88_mut | 1 | n.s. | 1 | n.s. | 105 | 1 | 2 | 209 | Fisher's Exact Test |
| MED12mutation | 0.360 | n.s. | 1 | n.s. | 106 | 3 | 1 | 209 | Fisher's Exact Test |
| X8q_ALL | 0.323 | n.s. | 1 | n.s. | 104 | 6 | 3 | 209 | Fisher's Exact Test |
| X8q24_gain | 0.203 | n.s. | 1 | n.s. | 106 | 4 | 1 | 209 | Fisher's Exact Test |
| ZFPM2_mut | 1 | n.s. | 1 | n.s. | 105 | 2 | 2 | 209 | Fisher's Exact Test |
| Subclones | 0.050 | trend | 1 | n.s. |  |  |  |  | Wilcoxon Test |
| Total_num_CNAs | 0.483 | n.s. | 1 | n.s. |  |  |  |  | Wilcoxon Test |
| No_alteration | 0.622 | n.s. | 1 | n.s. | 104 | 1 | 3 | 209 | Fisher's Exact Test |
| Binet | 0.770 | n.s. | 1 | n.s. | 72 | 36 | 35 | 209 | Fisher's Exact Test |
| page_at_randomisation | 0.100 | trend | 1 | n.s. |  |  |  |  | Wilcoxon Test |
| patient_gender | 0.443 | n.s. | 1 | n.s. | 33 | 76 | 74 | 209 | Fisher's Exact Test |
| vh_mutation_status | 0.0003 | *** | 0.015 | * | 55 | 60 | 40 | 181 | Fisher's Exact Test |
| ALC | 0.017 | * | 0.671 | n.s. |  |  |  |  | Wilcoxon Test |
| WBC | 0.013 | * | 0.513 | n.s. |  |  |  |  | Wilcoxon Test |
| cd38 | 0.707 | n.s. | 1 | n.s. | 45 | 40 | 59 | 147 | Fisher's Exact Test |

## Associations

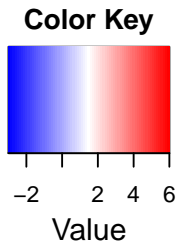Table 2: Uncorrected p-values for association between genetic lesions

| | variables | TP53_ALL | TP53_del | TP53_cnLOH | TP53_mut | TP53_bi | ATM_ALL | ATM_mut | ATM_del | ATM_cnLOH | ATM_mt1 | BIRC3_ALL | BIRC3_mut | BIRC3_del | ATM_bi | BIRC3_bi | X |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| p1 | TP53_ALL | 0 | 0 | 0.001 | 0 | 0 | 0.510 | 0.571 | 0.498 | 1 | 0.411 | 0.343 | 1 | 0.593 | 0.386 | 0.444 | |
| p2 | TP53_del | | | 1 | 0 | 0 | 0.274 | 0.530 | 0.429 | 1 | 1 | 0.422 | 1 | 0.642 | 0.634 | 1 | |
| p3 | TP53_cnLOH | | | | 0.005 | 0.002 | 1 | 0.632 | 0.505 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| p4 | TP53_mut | | | | | 0 | 0.173 | 0.186 | 0.275 | 1 | 0.631 | 0.087 | 1 | 0.189 | 0.181 | 1 | |
| p5 | TP53_bi | | | | | | 0.642 | 0.595 | 0.527 | 1 | 0.505 | 0.183 | 0.642 | 0.429 | 0.416 | 1 | |
| p6 | ATM_ALL | | | | | | | 0 | 0 | 0.031 | 0.001 | 0 | 1 | 0 | 0 | 0.031 | |
| p7 | ATM_mut | | | | | | | | 0.003 | 0.011 | 0 | 0.111 | 0.373 | 0.017 | 0 | 0.647 | |
| p8 | ATM_del | | | | | | | | | 1 | 0.283 | 0 | 0.197 | 0 | 0 | 0.002 | |
| p9 | ATM_cnLOH | | | | | | | | | | 1 | 1 | 0.018 | 1 | 0 | 1 | |
| p10 | ATM_mt1 | | | | | | | | | | | 0.277 | 1 | 0.413 | 0.650 | 1 | |
| p11 | BIRC3_ALL | | | | | | | | | | | | 1 | 0 | 0 | 0.002 | |
| p12 | BIRC3_mut | | | | | | | | | | | | | 0.042 | 1 | 0 | |
| p13 | BIRC3_del | | | | | | | | | | | | | | 0 | 0 | |
| p14 | ATM_bi | | | | | | | | | | | | | | | 1 | |
| p15 | BIRC3_bi | | | | | | | | | | | | | | | | |
| p16 | X11q_mono | | | | | | | | | | | | | | | | |
| p17 | ATM_mono | | | | | | | | | | | | | | | | |
| p18 | BIRC3_mono | | | | | | | | | | | | | | | | |
| p19 | NOTCH1_mut | | | | | | | | | | | | | | | | |
| p20 | SF3B1_mut | | | | | | | | | | | | | | | | |
| p21 | X6q_del_ALL | | | | | | | | | | | | | | | | |
| p22 | X13q_ALL | | | | | | | | | | | | | | | | |
| p23 | X13del_homo | | | | | | | | | | | | | | | | |
| p24 | X13q_het | | | | | | | | | | | | | | | | |
| p25 | X13qdelIRB1 | | | | | | | | | | | | | | | | |
| p26 | X13q_Ox | | | | | | | | | | | | | | | | |
| p27 | X13q_Rossi | | | | | | | | | | | | | | | | |
| p28 | Trisomy_12 | | | | | | | | | | | | | | | | |
| p29 | Trisomy_18 | | | | | | | | | | | | | | | | |
| p30 | Trisomy_19 | | | | | | | | | | | | | | | | |
| p31 | XPO1_ALL | | | | | | | | | | | | | | | | |
| p32 | XPO1_gain | | | | | | | | | | | | | | | | |
| p33 | XPO1_mutation | | | | | | | | | | | | | | | | |
| p34 | SAMHD1_ALL | | | | | | | | | | | | | | | | |
| p35 | SAMHD1_mut | | | | | | | | | | | | | | | | |
| p36 | SAMHD1_cnLOH_Del | | | | | | | | | | | | | | | | |
| p37 | MYD88_mut | | | | | | | | | | | | | | | | |
| p38 | MED12mutation | | | | | | | | | | | | | | | | |
| p39 | X8q_ALL | | | | | | | | | | | | | | | | |
| p40 | X8q24_gain | | | | | | | | | | | | | | | | |
| p41 | ZFPM2_mut | | | | | | | | | | | | | | | | |
| p42 | Subclones | | | | | | | | | | | | | | | | |
| p43 | TotaLnum.CNAs | | | | | | | | | | | | | | | | |
| p44 | No_alteration | | | | | | | | | | | | | | | | |
| p45 | Binet | | | | | | | | | | | | | | | | |
| p46 | age_at_randomisation | | | | | | | | | | | | | | | | |
| p47 | patient_gender | | | | | | | | | | | | | | | | |
| p48 | vh.mutation_status | | | | | | | | | | | | | | | | |
| p49 | MRD | | | | | | | | | | | | | | | | |
| p50 | ALC | | | | | | | | | | | | | | | | |
| p51 | WBC | | | | | | | | | | | | | | | | |
| p52 | cd38 | | | | | | | | | | | | | | | | |

Table 3: Corrected p-values for association between genetic lesions

| | variables | TP53_ALL | TP53_del | TP53_cnLOH | TP53_mut | TP53_bi | ATM_ALL | ATM_mut | ATM_del | ATM_cnLOH | ATM_mt1 | BIRC3_ALL | BIRC3_mut | BIRC3_del | ATM_bi | BIRC3_bi | X |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| p 1 | TP53_ALL | | 0.001 | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| p 2 | TP53_del | | | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| p 3 | TP53_cnLOH | | | | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| p 4 | TP53_mut | | | | | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| p 5 | TP53_bi | | | | | | 1 | 1 | 0 | 1 | 1 | 0.014 | 1 | 1 | 1 | 1 | |
| p 6 | ATM_ALL | | | | | | | 0 | 0 | 1 | 0.127 | 1 | 1 | 0 | 0.001 | 1 | |
| p 7 | ATM_mut | | | | | | | | 1 | 1 | 1 | 0 | 1 | 1 | 0 | 1 | |
| p 8 | ATM_del | | | | | | | | | 1 | 1 | 1 | 1 | 0 | 0 | 1 | |
| p 9 | ATM_cnLOH | | | | | | | | | | 1 | 1 | 1 | 1 | 0.368 | 1 | |
| p 10 | ATM_mt1 | | | | | | | | | | | 1 | 1 | 1 | 1 | 1 | |
| p 11 | BIRC3_ALL | | | | | | | | | | | | 0 | 0 | 0.021 | 0.024 | |
| p 12 | BIRC3_mut | | | | | | | | | | | | | 1 | 1 | 0.590 | |
| p 13 | BIRC3_del | | | | | | | | | | | | | | 0.003 | 1 | |
| p 14 | ATM_bi | | | | | | | | | | | | | | | 1 | |
| p 15 | BIRC3_bi | | | | | | | | | | | | | | | | |
| p 16 | X11q_mono | | | | | | | | | | | | | | | | |
| p 17 | ATM_mono | | | | | | | | | | | | | | | | |
| p 18 | BIRC3_mono | | | | | | | | | | | | | | | | |
| p 19 | NOTCH1_mut | | | | | | | | | | | | | | | | |
| p 20 | SF3B1_mut | | | | | | | | | | | | | | | | |
| p 21 | X6q_del_ALL | | | | | | | | | | | | | | | | |
| p 22 | X13q_ALL | | | | | | | | | | | | | | | | |
| p 23 | X13del_homo | | | | | | | | | | | | | | | | |
| p 24 | X13q_het | | | | | | | | | | | | | | | | |
| p 25 | X13qdelIRB1 | | | | | | | | | | | | | | | | |
| p 26 | X13q_Ox | | | | | | | | | | | | | | | | |
| p 27 | X13q_Rossi | | | | | | | | | | | | | | | | |
| p 28 | Trisomy_12 | | | | | | | | | | | | | | | | |
| p 29 | Trisomy_18 | | | | | | | | | | | | | | | | |
| p 30 | Trisomy_19 | | | | | | | | | | | | | | | | |
| p 31 | XPO1_ALL | | | | | | | | | | | | | | | | |
| p 32 | XPO1_gain | | | | | | | | | | | | | | | | |
| p 33 | XPO1_mutation | | | | | | | | | | | | | | | | |
| p 34 | SAMHD1_ALL | | | | | | | | | | | | | | | | |
| p 35 | SAMHD1_mut | | | | | | | | | | | | | | | | |
| p 36 | SAMHD1_cnLOH_Del | | | | | | | | | | | | | | | | |
| p 37 | MYD88_mut | | | | | | | | | | | | | | | | |
| p 38 | MED12mutation | | | | | | | | | | | | | | | | |
| p 39 | X8q_ALL | | | | | | | | | | | | | | | | |
| p 40 | X8q24_gain | | | | | | | | | | | | | | | | |
| p 41 | ZFPM2_mut | | | | | | | | | | | | | | | | |
| p 42 | Subclones | | | | | | | | | | | | | | | | |
| p 43 | TotaLnum_CNAs | | | | | | | | | | | | | | | | |
| p 44 | No_alteration | | | | | | | | | | | | | | | | |
| p 45 | Binet | | | | | | | | | | | | | | | | |
| p 46 | age_at_randomisation | | | | | | | | | | | | | | | | |
| p 47 | patient_gender | | | | | | | | | | | | | | | | |
| p 48 | vh_mutation_status | | | | | | | | | | | | | | | | |
| p 49 | MRD | | | | | | | | | | | | | | | | |
| p 50 | ALC | | | | | | | | | | | | | | | | |
| p 51 | WBC | | | | | | | | | | | | | | | | |
| p 52 | cd38 | | | | | | | | | | | | | | | | |

Odds ratios and p-values for association between genes are represented in this heat map. Note that blue is mutually exclusive, red is associated. Also, the colour key is not symmetrical, colours used:

- -3 -> oddsratio<0.1

- -2 -> oddsratio>=0.1  oddsratio < 0.2

- -1 -> oddsratio>=0.2  oddsratio < 0.4

- 0 -> oddsratio>=0.4  oddsratio < 0.6

- 1 -> oddsratio>=0.6  oddsratio < 0.8

- 2 -> oddsratio>=1  oddsratio < 3

- 3 -> oddsratio>=3  oddsratio < 10

- 4 -> oddsratio>=10  oddsratio < 15

- 5 -> oddsratio>=15  oddsratio < 20

- 6 -> oddsratio>20
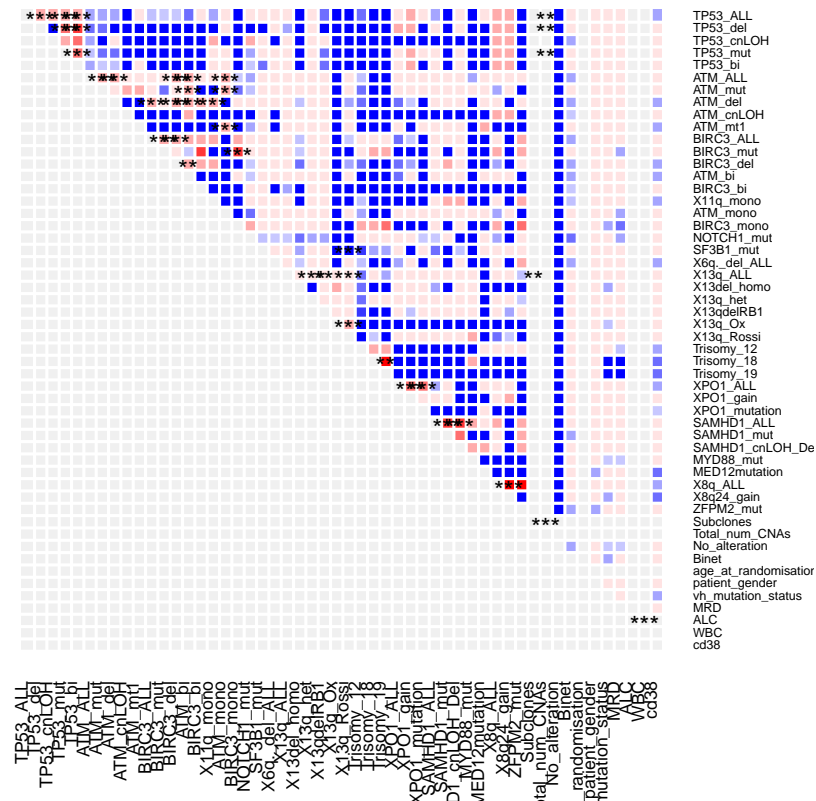


## Model building - from here, only 209 data points will be used

## Association on model data

This was calculated to see if there are Colinearities that have to be taken into account for the modelling. There are fewer associations than in the 239 data set.

Table 4: Corrected p-values for association between genetic lesions, n=209

| β | variables | TP53_ALL | TP53_del | TP53_cnLOH | TP53_mut | TP53_bi | ATM_ALL | ATM_mut | ATM_del | ATM_cnLOH | ATM_mt1 | BIRC3_ALL | BIRC3_mut | BIRC3_del | ATM_bi | BIRC3_bi | X11q_mono |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| p1 | TP53_ALL | | | | | | | | | | | | | | | | |
| p2 | TP53_del | 0.001 | | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| p3 | TP53_cnLOH | | | 1 | 0 | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| p4 | TP53_mut | | | | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| p5 | TP53_bi | | | | | 0 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| p6 | ATM_ALL | | | | | | 0 | 0 | 1 | 0.127 | 0.014 | 1 | 0 | 0.001 | 1 | 0.57 | |
| p7 | ATM_mut | | | | | | | 1 | 1 | 1 | 1 | 1 | 0 | 0 | 1 | 0 | |
| p8 | ATM_del | | | | | | | | 1 | 1 | 0 | 1 | 0 | 0.368 | 1 | 0 | |
| p9 | ATM_cnLOH | | | | | | | | | 1 | 1 | 1 | 1 | 1 | 1 | 1 | |
| p10 | ATM_mt1 | | | | | | | | | | 1 | 1 | 0 | 1 | 1 | 1 | |
| p11 | BIRC3_ALL | | | | | | | | | | | 0 | 1 | 0.021 | 1 | 0.18 | |
| p12 | BIRC3_mut | | | | | | | | | | | | 1 | 1 | 0.024 | 1 | |
| p13 | BIRC3_del | | | | | | | | | | | | | 0.003 | 0.590 | 0.01 | |
| p14 | ATM_bi | | | | | | | | | | | | | | 1 | 1 | |
| p15 | BIRC3_bi | | | | | | | | | | | | | | | 1 | |
| p16 | X11q_mono | | | | | | | | | | | | | | | | |
| p17 | ATM_mono | | | | | | | | | | | | | | | | |
| p18 | BIRC3_mono | | | | | | | | | | | | | | | | |
| p19 | NOTCH1_mut | | | | | | | | | | | | | | | | |
| p20 | SF3B1_mut | | | | | | | | | | | | | | | | |
| p21 | X6q_delALL | | | | | | | | | | | | | | | | |
| p22 | X13q_ALL | | | | | | | | | | | | | | | | |
| p23 | X13del_homo | | | | | | | | | | | | | | | | |
| p24 | X13q_het | | | | | | | | | | | | | | | | |
| p25 | X13qdelRB1 | | | | | | | | | | | | | | | | |
| p26 | X13q_Ox | | | | | | | | | | | | | | | | |
| p27 | X13q_Rossi | | | | | | | | | | | | | | | | |
| p28 | Trisomy_12 | | | | | | | | | | | | | | | | |
| p29 | Trisomy_18 | | | | | | | | | | | | | | | | |
| p30 | Trisomy_19 | | | | | | | | | | | | | | | | |
| p31 | XPO1ALL | | | | | | | | | | | | | | | | |
| p32 | XPO1_gain | | | | | | | | | | | | | | | | |
| p33 | XPO1_mutation | | | | | | | | | | | | | | | | |
| p34 | SAMHD1ALL | | | | | | | | | | | | | | | | |
| p35 | SAMHD1_mut | | | | | | | | | | | | | | | | |
| p36 | SAMHD1cnLOH_Del | | | | | | | | | | | | | | | | |
| p37 | MYD88_mut | | | | | | | | | | | | | | | | |
| p38 | MED12mutation | | | | | | | | | | | | | | | | |
| p39 | X8q_ALL | | | | | | | | | | | | | | | | |
| p40 | X8q24_gain | | | | | | | | | | | | | | | | |
| p41 | ZFPM2_mut | | | | | | | | | | | | | | | | |
| p42 | Subclones | | | | | | | | | | | | | | | | |
| p43 | Total_num_CNAs | | | | | | | | | | | | | | | | |
| p44 | No_alteration | | | | | | | | | | | | | | | | |
| p45 | Binet | | | | | | | | | | | | | | | | |
| p46 | age_at_randomisation | | | | | | | | | | | | | | | | |
| p47 | patient_gender | | | | | | | | | | | | | | | | |
| p48 | vh_mutation_status | | | | | | | | | | | | | | | | |
| p49 | MRD | | | | | | | | | | | | | | | | |
| p50 | ALC | | | | | | | | | | | | | | | | |
| p51 | WBC | | | | | | | | | | | | | | | | |
| p52 | cd38 | | | | | | | | | | | | | | | | |
| p | | | | | | | | | | | | | | | | | |

Model data, n=209

# Logistic regression model

## Simple logistic regression models

For these models, I used the variables that turned out significant in the univariate analysis (model 1-4 in table 5). This is a commonly used procedure, but it can mean that I selected variables that are highly colinear (or co-occuring), TP53 variables for example.

## Summarized Model

For these models, I summarized the data even more:

- all trisomies are grouped together

- for each lesion, I used the broadest variable

## Discussion of different models

You can see that the model gets better, the simpler it is. It basically makes no sense at all to put everything we have into a regression model, it is better to use the broadest defined variables (Have to discuss this with Chris though). One good thing with the model that uses only genetic data is that it is as good as the model that includes vh mutation status. It is not really better, but apparently, vh mutation status is a measure that is hard to obtain, and not very reliable. We could argue that genetic testing can almost replace vh mutation status as a predictor for MRD. To harden this argument, I calculated the missclassification error for both models and they are almost identical, yet we have more unclassified when using the vh mutation status.

Table 5: Multiple log regression, n=209

| | uncorrected all | uncorrected genetic | corrected all | corrected genetic | summarized genetic | summarized vhmut |
|---|---|---|---|---|---|---|
| | | | *Dependent variable:* | | | |
| | | | MRD | | | |
| Tri_ALL1 | | | | | −0.83* (0.47) | −1.06** (0.54) |
| TP53_ALL1 | 1.11 (1.31) | 1.49 (1.19) | 1.49 (1.25) | 1.04 (0.93) | 2.71*** (0.77) | 2.88*** (1.07) |
| TP53_del1 | 17.95 (9,579.62) | 18.88 (5,618.88) | | | | |
| TP53_cnLOH1 | 18.26 (6,522.64) | 18.92 (5,344.79) | | | | |
| TP53_mut1 | 17.39 (2,867.15) | 17.51 (2,649.92) | 16.16 (1,138.99) | 16.93 (1,012.72) | | |
| TP53_bi1 | −18.12 (9,659.72) | −19.23 (4,622.34) | | | | |
| ATM_ALL1 | 17.36 (3,180.05) | 1.43 (1.65) | 0.43 (0.47) | 0.35 (0.43) | 0.98*** (0.33) | 0.83** (0.37) |
| ATM_mut1 | −17.34 (3,180.05) | −1.38 (1.70) | | | | |
| ATM_del1 | −17.48 (3,180.05) | 0.09 (1.47) | −0.29 (0.95) | 0.52 (0.85) | | |
| BIRC3_ALL1 | −0.92 (1.44) | −1.50 (1.35) | | | | |
| BIRC3_del1 | 1.09 (1.53) | 1.37 (1.38) | 0.57 (0.94) | 0.52 (0.87) | | |
| ATM_bi1 | 19.00 (3,180.05) | 1.81 (1.21) | 1.37* (0.72) | 0.78 (0.64) | | |
| X11q_mono1 | 1.56 (1.62) | 0.15 (1.26) | | | | |
| BIRC3_mono1 | | | | | | |
| NOTCH1_mut1 | −0.91 (0.60) | −0.85 (0.58) | | | −0.58 (0.50) | −0.71 (0.55) |
| Trisomy_121 | −0.60 (0.57) | −0.31 (0.50) | −1.04** (0.52) | −0.79* (0.45) | | |
| Trisomy_181 | −15.94 (2,665.11) | −16.06 (2,322.88) | | | | |
| Trisomy_191 | −15.53 (2,495.26) | −15.78 (2,197.33) | | | | |
| XPO1_gain1 | 1.14 (1.00) | 1.23 (0.98) | | | | |
| SAMHD1_ALL1 | −0.26 (1.65) | 0.21 (1.33) | | | 1.59* (0.83) | 1.37 (0.85) |
| SAMHD1_mut1 | 18.72 (2,362.11) | 18.51 (2,202.25) | | | | |
| Subclones | −0.11 (0.29) | −0.07 (0.25) | | | | |
| vh_mutation_statusunmutated | 0.72* (0.40) | | 0.75** (0.35) | | | 0.89** (0.36) |
| ALC | 0.004 (0.01) | | | | | |
| WBC | −0.002 (0.01) | | | | | |
| SF3B1_mut1 | | | | | −0.05 (0.37) | |
| Constant | −0.85** (0.39) | −0.44 (0.27) | −0.87*** (0.28) | −0.48** (0.21) | −0.44* (0.24) | −0.87*** (0.29) |
| Observations | 178 | 209 | 181 | 209 | 209 | 181 |
| Log Likelihood | −88.53 | −108.17 | −100.29 | −120.56 | −123.10 | −101.52 |
| Akaike Inf. Crit. | 225.05 | 258.33 | 218.58 | 257.12 | 260.21 | 217.05 |

*Note:* $^{*}$p<0.1; $^{**}$p<0.05; $^{***}$p<0.01

## Missclassification Error

Table 6: Missclassification for summarized models

| | model | true_MRD_neg | correct_MRD_neg | false_MRD_neg | true_MRD_pos | correct_MRD_pos | false_MRD_pos | missclasserror | unclassified |
|---|---|---|---|---|---|---|---|---|---|
| p1 | sum_genetic | 107 | 84 | 39 | 102 | 63 | 23 | 0.297 | 0 |
| p2 | sum_vhmut | 95 | 68 | 30 | 86 | 56 | 27 | 0.315 | 29 |