

# Robust Sampling of Defective Pathways in Multiple Myeloma

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**Table S1.** GSE85837. List of most discriminatory genes in Multiple Myeloma. HC stands for healthy controls and MM for Multiple Myeloma patients. In bold face the LOCXX genes are highlighted.

| Gene         | Mean-HC | Std-HC | Mean-MM | Std-HC | FR   | Accuracy |
|--------------|---------|--------|---------|--------|------|----------|
| EFNA3        | 7.23    | 0.13   | 7.43    | 0.12   | 2.27 | 71.4     |
| LOC654078    | 7.26    | 0.15   | 7.5     | 0.12   | 2.06 | 82.1     |
| LOC732313    | 7.38    | 0.11   | 7.17    | 0.14   | 1.96 | 85.7     |
| LOC154822    | 7.35    | 0.13   | 7.09    | 0.12   | 1.94 | 92.9     |
| LOC340096    | 7.29    | 0.1    | 7.45    | 0.12   | 1.9  | 92.9     |
| LOC100101266 | 7.37    | 0.12   | 7.57    | 0.09   | 1.86 | 100      |
| PCDH9        | 7.48    | 0.07   | 7.34    | 0.12   | 1.77 | 100      |
| REPS2        | 6.93    | 0.11   | 6.81    | 0.09   | 1.67 | 100      |
| LOC651896    | 7.16    | 0.1    | 7.33    | 0.14   | 1.64 | 100      |
| RCVRN        | 7.32    | 0.16   | 7.46    | 0.09   | 1.6  | 100      |
| LOC100130549 | 7.31    | 0.13   | 7.46    | 0.08   | 1.59 | 100      |
| LOC100134744 | 7.1     | 0.13   | 6.92    | 0.15   | 1.56 | 100      |
| LOC645405    | 7.41    | 0.14   | 7.19    | 0.18   | 1.53 | 100      |
| B4GALNT2     | 6.62    | 0.12   | 6.78    | 0.15   | 1.53 | 100      |
| FLJ37453     | 7.23    | 0.16   | 7.4     | 0.14   | 1.52 | 100      |
| ZC3H14       | 6.52    | 0.1    | 6.71    | 0.16   | 1.48 | 100      |
| DPRX         | 6.91    | 0.08   | 6.79    | 0.07   | 1.47 | 100      |
| EXOG         | 7.44    | 0.08   | 7.28    | 0.13   | 1.47 | 100      |
| LOC728846    | 7.23    | 0.11   | 7.08    | 0.16   | 1.47 | 100      |
| LOC100129054 | 7.34    | 0.1    | 7.2     | 0.1    | 1.45 | 100      |
| LOC643713    | 7.58    | 0.1    | 7.66    | 0.07   | 1.37 | 100      |
| EIF4EBP3     | 6.83    | 0.11   | 6.98    | 0.15   | 1.35 | 100      |
| RSAD2        | 7.38    | 0.1    | 7.55    | 0.1    | 1.34 | 100      |
| LOC100129781 | 8.27    | 0.1    | 8.05    | 0.14   | 1.32 | 100      |
| SEC15L2      | 7.5     | 0.15   | 7.32    | 0.1    | 1.32 | 100      |
| RFX3         | 7.09    | 0.21   | 7.29    | 0.12   | 1.31 | 100      |
| LOC653227    | 7.21    | 0.16   | 7.4     | 0.12   | 1.3  | 100      |
| LOC650599    | 7.44    | 0.16   | 7.27    | 0.17   | 1.28 | 100      |
| LOC100130451 | 7.47    | 0.13   | 7.32    | 0.11   | 1.27 | 100      |
| LOC728393    | 7.34    | 0.1    | 7.43    | 0.14   | 1.26 | 100      |
| MIR891A      | 6.96    | 0.14   | 6.78    | 0.15   | 1.26 | 100      |
| OR52A1       | 6.49    | 0.08   | 6.62    | 0.12   | 1.25 | 100      |
| ORM1         | 7.35    | 0.16   | 7.17    | 0.1    | 1.25 | 100      |
| CST4         | 7.26    | 0.14   | 7.39    | 0.08   | 1.24 | 100      |
| LOC100133840 | 8.52    | 0.37   | 8.25    | 0.23   | 1.24 | 100      |
| LOC645139    | 7.28    | 0.14   | 7.4     | 0.15   | 1.24 | 100      |
| LOC284232    | 7.41    | 0.16   | 7.28    | 0.15   | 1.23 | 100      |
| PTH          | 7.37    | 0.12   | 7.21    | 0.19   | 1.23 | 100      |
| GPR4         | 6.59    | 0.09   | 6.74    | 0.13   | 1.21 | 100      |

**Table S2.** GSE24870. List of most discriminatory genes in Multiple Myeloma. HC stands for healthy controls and MM for Multiple Myeloma patients.

| Gene    | Mean-HC | Std-HC  | Mean-MM  | Std-HC | FR   | Accuracy |
|---------|---------|---------|----------|--------|------|----------|
| SIAH1   | 1492.76 | 157.47  | 732.54   | 190.41 | 9.54 | 100      |
| DUSP10  | 1551.94 | 265.98  | 550.52   | 196.17 | 9.07 | 100      |
| ZNF675  | 966.21  | 114.5   | 560.9    | 129.77 | 7.3  | 100      |
| SKIL    | 1377.16 | 492.33  | 301.08   | 374.62 | 4.9  | 100      |
| HIF1A   | 1734.75 | 342.97  | 907.48   | 188.92 | 4.88 | 100      |
| BOLA2   | 3287.72 | 456.94  | 1950.35  | 433.02 | 4.72 | 100      |
| EWSR1   | 340.9   | 70.27   | 541.11   | 98.19  | 4.24 | 100      |
| RANBP9  | 2483.48 | 411.18  | 1557.04  | 322.21 | 4.2  | 100      |
| SRSF10  | 2442.5  | 294.75  | 1564.54  | 254.76 | 4.17 | 100      |
| PNRC2   | 4828.98 | 545.62  | 3282.73  | 546.81 | 4.12 | 100      |
| SAP18   | 5575.27 | 693.24  | 3892.6   | 619.04 | 3.98 | 100      |
| SP3     | 3654.02 | 358.57  | 2628.63  | 423.08 | 3.96 | 100      |
| RLF     | 555.03  | 93.06   | 293.84   | 101.66 | 3.86 | 100      |
| DAZAP2  | 7054.34 | 944.96  | 4838.82  | 976.8  | 3.8  | 100      |
| EMP1    | 2161.81 | 653.22  | 870.19   | 440.99 | 3.72 | 100      |
| YTHDF3  | 1020.97 | 168.51  | 661.45   | 141.92 | 3.7  | 100      |
| KRR1    | 1720.96 | 206.06  | 1096.02  | 215.62 | 3.68 | 100      |
| VCPKMT  | 640.05  | 142.3   | 328.6    | 111.56 | 3.64 | 100      |
| BCLAF1  | 1706.19 | 280.71  | 997.64   | 199.14 | 3.62 | 100      |
| CSRP1   | 557.23  | 167.37  | 1014.72  | 197.07 | 3.6  | 100      |
| FKBP2   | 848.76  | 169.22  | 1572.74  | 405.16 | 3.55 | 100      |
| ACAP2   | 1742.66 | 265.43  | 1032.09  | 233.19 | 3.5  | 100      |
| RPL8    | 6703.09 | 974.89  | 10375.96 | 1736.2 | 3.48 | 100      |
| BTG3    | 945.9   | 164.61  | 515.79   | 186.12 | 3.47 | 100      |
| RNF138  | 3598.19 | 307.16  | 2375.59  | 585.09 | 3.47 | 100      |
| NECAP1  | 289.12  | 49.65   | 164.72   | 38.53  | 3.46 | 100      |
| ZNHIT1  | 357.15  | 115.73  | 734.59   | 154.49 | 3.44 | 100      |
| RGS1    | 2616.15 | 657.61  | 1012.82  | 910.61 | 3.37 | 100      |
| ALDOA   | 1471.41 | 393.3   | 2609     | 570.92 | 3.36 | 100      |
| CD69    | 6679.83 | 1473.33 | 3158.37  | 1163.1 | 3.36 | 100      |
| RGS1    | 1656.65 | 543.27  | 527.12   | 430.49 | 3.35 | 100      |
| PSPH    | 1131.34 | 509.58  | 259.17   | 95.61  | 3.28 | 100      |
| ARL4A   | 3766.28 | 698.13  | 2220.35  | 698.69 | 3.28 | 100      |
| MARCH7  | 3771.23 | 568.36  | 2373.61  | 583.58 | 3.27 | 100      |
| BCAP31  | 588.68  | 175.22  | 1210     | 365.28 | 3.25 | 100      |
| ALDOA   | 1653.02 | 397.55  | 2900.39  | 653.88 | 3.25 | 100      |
| SNRNP70 | 2140.91 | 225.99  | 3368.45  | 655.35 | 3.24 | 100      |
| DUSP6   | 3173.01 | 929.38  | 1396.33  | 426.89 | 3.23 | 100      |
| MED13L  | 2187.96 | 322.75  | 1378.38  | 235.8  | 3.21 | 100      |

**Table S3.** GSE6477. List of most discriminatory genes in the Hyper-diploid differentiation. HD stands for Hyperdiploid and NHD for Non-Hyperdiploid.

| Gene        | Mean-HD        | Std-HD        | Mean-NHD       | Std-NHD        | FR          | Accuracy     |
|-------------|----------------|---------------|----------------|----------------|-------------|--------------|
| NCAM1       | 1751.61        | 1169.25       | 890.58         | 876.06         | 0.64        | 67.74        |
| MIR5193     | 809.44         | 378.63        | 503.5          | 367.85         | 0.63        | 70.32        |
| DYNLT3      | 648.12         | 170.14        | 816.8          | 195.85         | 0.6         | 74.84        |
| ANXA7       | 838.13         | 280.48        | 1091.48        | 279.86         | 0.55        | 82.58        |
| RPN2        | 12529.96       | 4573.32       | 17045.27       | 5056.27        | 0.53        | 82.58        |
| RBMS1       | 682.86         | 374.45        | 930.39         | 406.3          | 0.5         | 86.45        |
| GTF2H1      | 675.62         | 190.22        | 536.04         | 132.33         | 0.49        | 85.81        |
| TMED2       | 6556.89        | 1938.02       | 8494.5         | 2313.89        | 0.49        | 87.1         |
| ANP32A      | 598.76         | 207.93        | 402.75         | 150.5          | 0.49        | 85.81        |
| RBMS1       | 881.11         | 501.31        | 1455.24        | 716.63         | 0.49        | 88.39        |
| PIK3R3      | 386.39         | 212.85        | 199.4          | 124.38         | 0.48        | 88.39        |
| SLTM        | 995.04         | 310.36        | 728.98         | 243.03         | 0.48        | 90.32        |
| TMX4        | 417.56         | 223.14        | 721.24         | 386.87         | 0.47        | 89.68        |
| IVD         | 396.18         | 161.79        | 275.07         | 128.13         | 0.47        | 90.32        |
| CHMP6       | 149.99         | 89.22         | 217.53         | 103.36         | 0.46        | 90.32        |
| RBMS1       | 1075.15        | 464.03        | 1567.75        | 642.59         | 0.46        | 90.97        |
| KCNN3       | 670.95         | 809.75        | 1265.95        | 898.83         | 0.46        | 90.97        |
| CLTA        | 2241.79        | 727.21        | 1612.5         | 610.42         | 0.45        | 90.97        |
| GYG1        | 2273.96        | 900.78        | 1579.71        | 676.35         | 0.45        | 89.68        |
| IDH2        | 4933.21        | 2652.22       | 2801.42        | 1685.73        | 0.45        | 87.74        |
| TBCE        | 457.33         | 122.66        | 570.83         | 141.69         | 0.44        | 89.03        |
| SNORA11E    | 160.87         | 177.77        | 313.1          | 267.12         | 0.44        | 89.68        |
| TMBIM6      | 4390.19        | 1397.85       | 6202.94        | 2070.17        | 0.44        | 92.26        |
| NPM1        | 12693.69       | 5693.08       | 8904.49        | 3273.24        | 0.43        | 90.32        |
| ACTR1A      | 529.6          | 189.74        | 681.85         | 167.87         | 0.43        | 90.32        |
| MXI1        | 1715.98        | 573.71        | 2280.57        | 815.38         | 0.43        | 89.68        |
| RAB5B       | 692.88         | 156.29        | 892.08         | 195.69         | 0.42        | 90.32        |
| GCOM1       | 610.35         | 212.59        | 465.32         | 117.51         | 0.42        | 89.68        |
| ASXL1       | 786.84         | 187.64        | 960.9          | 221.83         | 0.42        | 88.39        |
| <b>CD63</b> | <b>8510.71</b> | <b>3333.8</b> | <b>12647.6</b> | <b>4976.83</b> | <b>0.42</b> | <b>90.97</b> |
| CSNK1A1     | 1294.35        | 399.71        | 1041.05        | 345.01         | 0.42        | 89.03        |
| FXR1        | 1243.72        | 508.89        | 915.4          | 441.91         | 0.41        | 87.74        |
| IDH2        | 855.2          | 272.45        | 600            | 208.22         | 0.41        | 87.1         |
| LDLRAP1     | 555.8          | 291.32        | 849.05         | 376.97         | 0.41        | 89.03        |
| COG2        | 864.35         | 208.97        | 1043.07        | 245.19         | 0.4         | 89.03        |
| PAK1        | 147.96         | 87.25         | 96.02          | 78.15          | 0.4         | 89.03        |
| NSL1        | 585.37         | 201.89        | 763.87         | 252.35         | 0.4         | 89.68        |
| SEC31A      | 2726.55        | 1104.94       | 3360.84        | 1004.18        | 0.4         | 90.32        |
| GTF3C1      | 260            | 174.76        | 394.1          | 208.92         | 0.4         | 90.97        |
| YWHAZ       | 4381.4         | 1183.21       | 5665.59        | 1821.07        | 0.4         | 90.97        |
| RPL13A      | 24183.75       | 13371.77      | 14671.14       | 7879.12        | 0.4         | 89.68        |
| PPP6C       | 1692.43        | 474.29        | 1314.39        | 468.99         | 0.4         | 89.03        |
| RPN2        | 14438.29       | 6054.34       | 19511.13       | 6307.89        | 0.39        | 89.68        |

**Table S4.** GSE6477. List of most discriminatory genes to predict the Chromosome-13 deletion. N stands for normal and DEL for Ch-13 deleted.

| Gene             | Mean-N  | Std-N   | Mean-DEL | Std-DEL | FR   | Accuracy |
|------------------|---------|---------|----------|---------|------|----------|
| RBM26            | 1113.38 | 321.33  | 677.93   | 240.41  | 1.22 | 74.68    |
| ARGLU1           | 1178.26 | 409.25  | 722.82   | 330.49  | 1.07 | 77.85    |
| ZC3H13           | 464.93  | 128.74  | 314.06   | 93.97   | 1.07 | 79.75    |
| UFM1             | 1509.17 | 428.15  | 1007.8   | 342.35  | 0.88 | 79.75    |
| MYCBP2           | 1253.62 | 447.9   | 687.83   | 399.68  | 0.88 | 80.38    |
| STK24            | 2271.41 | 547.91  | 1613.18  | 562.56  | 0.86 | 82.28    |
| UCHL3            | 720.08  | 196.32  | 474.41   | 228.97  | 0.85 | 82.91    |
| ZMYM2            | 674.39  | 209.59  | 457.52   | 172.79  | 0.83 | 82.28    |
| CDC16            | 855.43  | 253.69  | 538.59   | 273.36  | 0.83 | 82.28    |
| MYCBP2           | 1824.1  | 545.51  | 1151.14  | 656.8   | 0.82 | 83.54    |
| GTF3A            | 3645.07 | 1016.91 | 2432.57  | 920.06  | 0.79 | 84.81    |
| PHF11            | 842.41  | 270.26  | 583.16   | 253.22  | 0.78 | 82.91    |
| ALG11 /// UTP14C | 808.96  | 189.66  | 624.59   | 150.66  | 0.71 | 84.81    |
| ANKRD10          | 747.47  | 227.57  | 478.48   | 175.61  | 0.71 | 84.81    |
| CDC16            | 1173.68 | 326.46  | 876.13   | 334.85  | 0.66 | 82.91    |
| FOXO1            | 1004.06 | 375.62  | 703.08   | 311.25  | 0.65 | 82.91    |
| MED6             | 102.42  | 59.03   | 64.01    | 52.45   | 0.59 | 85.44    |
| N4BP2L2          | 451.02  | 152.35  | 325.83   | 143.05  | 0.57 | 85.44    |
| NEK3             | 318.63  | 157.44  | 197.42   | 128.5   | 0.57 | 84.81    |
| NDUFA9           | 1170.88 | 279.47  | 1488.11  | 356.56  | 0.57 | 84.18    |
| PDS5B            | 440.62  | 134.51  | 326.27   | 112.69  | 0.55 | 83.54    |
| TGDS             | 707.29  | 198.2   | 529.65   | 184.17  | 0.55 | 84.81    |
| USP12            | 302.94  | 94.61   | 217.27   | 79.15   | 0.55 | 84.81    |
| C1orf112         | 64.93   | 59.3    | 102.57   | 76.92   | 0.52 | 84.81    |
| SUPT20H          | 554.76  | 149.03  | 422.97   | 149.25  | 0.49 | 84.81    |
| C6orf211         | 186.75  | 75.51   | 254.66   | 100.65  | 0.48 | 86.08    |
| RB1              | 710.29  | 355.66  | 434.47   | 340.02  | 0.48 | 86.08    |
| DICER1           | 539.02  | 208.06  | 412.82   | 161.52  | 0.48 | 87.34    |
| GTF3C1           | 260.01  | 170.25  | 408.11   | 210.14  | 0.47 | 86.08    |
| MPZL1            | 480.28  | 194.51  | 659.46   | 324.81  | 0.47 | 86.08    |
| RBM25            | 882.72  | 321.9   | 654.1    | 281.93  | 0.47 | 86.71    |
| NAA16            | 404.46  | 153.78  | 258.42   | 96.8    | 0.47 | 86.71    |
| OGT              | 2998.6  | 1135.25 | 2011.19  | 1029.35 | 0.47 | 86.71    |
| PCID2            | 748.44  | 153.85  | 606.26   | 172.55  | 0.47 | 86.71    |
| TPP2             | 837.33  | 256.8   | 647.28   | 248.96  | 0.47 | 87.34    |
| STK24            | 805.24  | 215.06  | 622      | 196.7   | 0.46 | 87.34    |
| CDC16            | 1182.95 | 306.31  | 864.16   | 351.92  | 0.45 | 87.34    |
| N4BP2L2          | 1054.55 | 591.22  | 517.78   | 408.26  | 0.45 | 87.34    |
| AKAP11           | 870.41  | 288.01  | 644.58   | 259.24  | 0.45 | 86.71    |
| OGT              | 3429.98 | 1228.66 | 2583.22  | 1266.24 | 0.44 | 87.34    |
| RCBTB2           | 1007.42 | 505.58  | 592.01   | 364.79  | 0.44 | 86.71    |
| CLN              | 296.03  | 90.19   | 239.54   | 103.92  | 0.44 | 87.34    |
| OGT              | 5000.14 | 1722.38 | 3800.23  | 1415.94 | 0.44 | 86.71    |