

**Table S1: HALLMARK\_MYC\_TARGETS\_V1 with proliferation, survival, and positive/negative correlation with MYC score analysis**

| Gene   | Gene name                                                                        | Proliferation correlation |         |                   |         |                    |         | Survival          |         |                       |         | Pos/Neg target |       |
|--------|----------------------------------------------------------------------------------|---------------------------|---------|-------------------|---------|--------------------|---------|-------------------|---------|-----------------------|---------|----------------|-------|
|        |                                                                                  | Spearman TCGA             |         | Spearman METABRIC |         | Spearman GSE124647 |         | COX analysis TCGA |         | COX analysis METABRIC |         | Spearman       |       |
|        |                                                                                  | R                         | p value | R                 | p value | R                  | p value | HR                | p value | HR                    | p value | R              | p     |
| ABCE1  | ATP binding cassette subfamily E member 1                                        | 0.357                     | <0.01   | 0.551             | <0.01   | 0.504              | <0.01   | 1.61              | 0.212   | 1.27                  | 0.062   | 0.294          | <0.01 |
| ACP1   | Acid phosphatase 1                                                               | 0.496                     | <0.01   | 0.599             | <0.01   | 0.525              | <0.01   | 1.14              | 0.784   | 0.99                  | 0.906   | -0.024         | 0.56  |
| AIMP2  | aminoacyl tRNA synthetase complex interacting multifunctional protein 2          | 0.563                     | <0.01   | 0.483             | <0.01   | 0.309              | <0.01   | 2.44              | 0.034   | 1.29                  | 0.038   | 0.141          | <0.01 |
| AP3S1  | adaptor related protein complex 3 subunit sigma 1                                | 0.082                     | 0.05    | 0.36              | <0.01   | -0.163             | 0.05    | 1.73              | 0.056   | 1.05                  | 0.376   | -0.148         | <0.01 |
| APEX1  | apurinic/apyrimidinic endodeoxyribonuclease 1                                    | 0.364                     | <0.01   | 0.429             | <0.01   | 0.364              | <0.01   | 1.12              | 0.81    | 1.2                   | 0.071   | 0.095          | 0.02  |
| BUB3   | BUB3 mitotic checkpoint protein                                                  | 0.342                     | <0.01   | 0.458             | <0.01   | 0.354              | <0.01   | 1.06              | 0.858   | 1.01                  | 0.916   | -0.072         | 0.08  |
| C1QBP  | complement C1q binding protein                                                   | 0.408                     | <0.01   | 0.336             | <0.01   | 0.481              | <0.01   | 1.31              | 0.429   | 0.93                  | 0.466   | 0.082          | 0.05  |
| CAD    | carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase | -0.035                    | 0.41    | 0.003             | 0.9     | 0.309              | <0.01   | 1.15              | 0.681   | 1.35                  | 0.069   | 0.215          | <0.01 |
| CANX   | calnexin                                                                         | 0.283                     | <0.01   | 0.23              | <0.01   | 0.153              | 0.07    | 1.07              | 0.842   | 1.26                  | 0.065   | -0.034         | 0.42  |
| CBX3   | chromobox 3                                                                      | 0.542                     | <0.01   | 0.052             | 0.05    | 0.42               | <0.01   | 1.53              | 0.237   | 1.36                  | 0.002   | -0.01          | 0.81  |
| CCNA2  | cyclin A2                                                                        | 0.603                     | <0.01   | 0.647             | <0.01   | 0.542              | <0.01   | 1.3               | 0.117   | 1.94                  | <0.001  | 0.103          | 0.01  |
| CCT2   | chaperonin containing TCP1 subunit 2                                             | 0.679                     | <0.01   | 0.685             | <0.01   | 0.529              | <0.01   | 1.15              | 0.613   | 1.43                  | <0.001  | 0.11           | <0.01 |
| CCT3   | chaperonin containing TCP1 subunit 3                                             | 0.603                     | <0.01   | 0.435             | <0.01   | 0.435              | <0.01   | 2.29              | 0.028   | 1.39                  | 0.002   | 0.108          | <0.01 |
| CCT4   | chaperonin containing TCP1 subunit 4                                             | 0.505                     | <0.01   | -                 | -       | 0.495              | <0.01   | 2.1               | 0.08    | -                     | -       | 0.116          | <0.01 |
| CCT5   | chaperonin containing TCP1 subunit 5                                             | 0.726                     | <0.01   | 0.299             | <0.01   | 0.464              | <0.01   | 1.87              | 0.053   | 1.55                  | <0.001  | 0.132          | <0.01 |
| CCT7   | chaperonin containing TCP1 subunit 7                                             | 0.619                     | <0.01   | 0.583             | <0.01   | 0.636              | <0.01   | 1.98              | 0.173   | 1.04                  | 0.573   | 0.093          | 0.02  |
| CDC20  | cell division cycle 20                                                           | 0.593                     | <0.01   | 0.332             | <0.01   | 0.656              | <0.01   | 1.24              | 0.145   | 1.55                  | <0.001  | 0.031          | 0.46  |
| CDC45  | cell division cycle 45                                                           | 0.608                     | <0.01   | 0.455             | <0.01   | 0.452              | <0.01   | 1.16              | 0.314   | 1.57                  | <0.001  | 0.082          | 0.05  |
| CDK2   | cyclin dependent kinase 2                                                        | 0.368                     | <0.01   | 0.401             | <0.01   | 0.43               | <0.01   | 1.48              | 0.278   | 1.82                  | <0.001  | 0.005          | 0.9   |
| CDK4   | cyclin dependent kinase 4                                                        | 0.56                      | <0.01   | 0.491             | <0.01   | 0.403              | <0.01   | 1.55              | 0.202   | 1.54                  | <0.001  | -0.009         | 0.83  |
| CLNS1A | chloride nucleotide-sensitive channel 1A                                         | 0.349                     | <0.01   | 0.354             | <0.01   | 0.223              | <0.01   | 0.97              | 0.912   | 1.2                   | 0.003   | 0.048          | 0.25  |
| CNBP   | CCHC-type zinc finger nucleic acid binding protein                               | 0.392                     | <0.01   | 0.442             | <0.01   | 0.153              | 0.07    | 1.09              | 0.887   | 0.9                   | 0.164   | 0.075          | 0.07  |
| COPS5  | COP9 signalosome subunit 5                                                       | 0.598                     | <0.01   | 0.573             | <0.01   | 0.282              | <0.01   | 1.67              | 0.115   | 1.27                  | 0.023   | 0.015          | 0.72  |
| COX5A  | cytochrome c oxidase subunit 5A                                                  | 0.646                     | <0.01   | 0.529             | <0.01   | 0.375              | <0.01   | 1.1               | 0.804   | 1.25                  | 0.1     | -0.06          | 0.15  |
| CSTF2  | cleavage stimulation factor subunit 2                                            | 0.317                     | <0.01   | 0.247             | <0.01   | 0.262              | <0.01   | 2.08              | 0.075   | 1.48                  | 0.003   | -0.103         | 0.01  |
| CTPS1  | CTP synthase 1                                                                   | -                         | -       | -                 | -       | 0.434              | <0.01   | 1.08              | 0.891   | 0.63                  | 0.012   |                |       |
| CUL1   | cullin 1                                                                         | 0.167                     | <0.01   | 0.052             | 0.06    | 0.487              | <0.01   | 1.12              | 0.674   | 1.63                  | <0.001  | 0.041          | 0.33  |
| CYC1   | cytochrome c1                                                                    | 0.603                     | <0.01   | 0.464             | <0.01   | 0.47               | <0.01   | 1.29              | 0.591   | 1.38                  | 0.049   | 0.103          | 0.01  |
| DDX18  | DEAD-box helicase 18                                                             | 0.11                      | <0.01   | 0.08              | <0.01   | 0.578              | <0.01   | 1.25              | 0.313   | 1.05                  | 0.522   | 0.105          | 0.01  |
| DDX21  | DEXD-box helicase 21                                                             | 0.178                     | <0.01   | 0.591             | <0.01   | 0.339              | <0.01   | 1.05              | 0.875   | 1.05                  | 0.534   | 0.272          | <0.01 |
| DEK    | DEK proto-oncogene                                                               | 0.201                     | <0.01   | 0.518             | <0.01   | 0.306              | <0.01   | 2.32              | 0.032   | 1.02                  | 0.852   | 0.155          | <0.01 |

|           |                                                          |        |       |        |       |       |       |      |       |      |        |        |       |
|-----------|----------------------------------------------------------|--------|-------|--------|-------|-------|-------|------|-------|------|--------|--------|-------|
| DHX15     | DEAH-box helicase 15                                     | 0.122  | <0.01 | 0.523  | <0.01 | 0.277 | <0.01 | 1.4  | 0.247 | 1.28 | 0.023  | 0      | 0.99  |
| DUT       | deoxyuridine triphosphatase                              | 0.38   | <0.01 | 0.348  | <0.01 | 0.257 | <0.01 | 0.66 | 0.247 | 0.88 | 0.034  | 0.167  | <0.01 |
| EEF1B2    | eukaryotic translation elongation factor 1 beta 2        | 0.117  | <0.01 | 0.333  | <0.01 | 0.172 | 0.04  | 1.06 | 0.89  | 0.95 | 0.477  | 0.347  | <0.01 |
| EIF1AX    | eukaryotic translation initiation factor 1A X-linked     | 0.203  | <0.01 | 0.447  | <0.01 | 0.213 | 0.01  | 1.66 | 0.288 | -    | -      | 0.068  | 0.1   |
| EIF2S1    | eukaryotic translation initiation factor 2 subunit alpha | 0.406  | <0.01 | -      | -     | 0.309 | <0.01 | 1.76 | 0.18  | 1.89 | <0.001 | 0.033  | 0.43  |
| EIF2S2    | eukaryotic translation initiation factor 2 subunit beta  | 0.604  | <0.01 | 0.303  | <0.01 | 0.443 | <0.01 | 1.83 | 0.118 | 1.34 | 0.008  | 0.106  | 0.01  |
| EIF3B     | eukaryotic translation initiation factor 3 subunit B     | 0.523  | <0.01 | -0.052 | 0.06  | 0.491 | <0.01 | 0.69 | 0.358 | 0.9  | 0.38   | 0.307  | <0.01 |
| EIF3D     | eukaryotic translation initiation factor 3 subunit D     | 0.162  | <0.01 | -0.034 | 0.21  | 0.276 | <0.01 | 1.59 | 0.368 | 0.88 | 0.33   | 0.306  | <0.01 |
| EIF3J     | eukaryotic translation initiation factor 3 subunit J     | 0.453  | <0.01 | 0.483  | <0.01 | 0.305 | <0.01 | 1.59 | 0.313 | 0.97 | 0.655  | 0.056  | 0.18  |
| EIF4A1    | eukaryotic translation initiation factor 4A1             | 0.471  | <0.01 | 0.52   | <0.01 | -     | -     | 1.68 | 0.194 | 0.96 | 0.525  | 0.261  | <0.01 |
| EIF4E     | eukaryotic translation initiation factor 4E              | 0.36   | <0.01 | 0.587  | <0.01 | 0.294 | <0.01 | 2.32 | 0.075 | 1.13 | 0.086  | 0.078  | 0.06  |
| EIF4G2    | eukaryotic translation initiation factor 4 gamma 2       | 0.12   | <0.01 | 0.427  | <0.01 | 0.061 | 0.47  | 2.19 | 0.196 | 0.93 | 0.252  | -0.089 | 0.03  |
| EIF4H     | eukaryotic translation initiation factor 4H              | 0.14   | <0.01 | 0.378  | <0.01 | 0.328 | <0.01 | 2.02 | 0.023 | 1.31 | 0.02   | 0.047  | 0.26  |
| EPRS      | glutamyl-prolyl-tRNA synthetase                          | 0.254  | <0.01 | 0.269  | <0.01 | 0.289 | <0.01 | 0.95 | 0.89  | 0.98 | 0.838  | -0.018 | 0.67  |
| ERH       | ERH mRNA splicing and mitosis factor                     | 0.489  | <0.01 | 0.434  | <0.01 | 0.326 | <0.01 | 1.32 | 0.578 | 0.86 | 0.265  | -0.146 | <0.01 |
| ETF1      | eukaryotic translation termination factor 1              | 0.238  | <0.01 | 0.5    | <0.01 | 0.085 | 0.32  | 1.37 | 0.428 | 1.07 | 0.682  | -0.039 | 0.35  |
| EXOSC7    | exosome component 7                                      | 0.321  | <0.01 | 0.044  | 0.1   | 0.32  | <0.01 | 0.59 | 0.294 | 0.76 | 0.053  | 0.048  | 0.25  |
| FAM120A   | family with sequence similarity 120A                     | -0.059 | 0.15  | -0.026 | 0.34  | -0.21 | 0.01  | 0.84 | 0.595 | 1.03 | 0.815  | -0.083 | 0.05  |
| FBL       | fibrillarin                                              | 0.303  | <0.01 | 0.191  | <0.01 | 0.461 | <0.01 | 1.23 | 0.596 | 0.95 | 0.556  | 0.321  | <0.01 |
| G3BP1     | G3BP stress granule assembly factor 1                    | 0.261  | <0.01 | 0.386  | <0.01 | 0.206 | 0.01  | 0.73 | 0.369 | 1.17 | 0.074  | 0.009  | 0.83  |
| GLO1      | glyoxalase I                                             | 0.51   | <0.01 | 0.474  | <0.01 | 0.287 | <0.01 | 1.74 | 0.165 | 0.95 | 0.626  | 0.009  | 0.83  |
| GNL3      | G protein nucleolar 3                                    | 0.359  | <0.01 | 0.498  | <0.01 | -     | -     | 1.66 | 0.079 | 1.14 | 0.117  | 0.286  | <0.01 |
| GOT2      | glutamic-oxaloacetic transaminase 2                      | 0.407  | <0.01 | 0.021  | 0.45  | 0.165 | 0.05  | 0.98 | 0.954 | 1.34 | 0.027  | 0      | 1     |
| GSPT1     | G1 to S phase transition 1                               | 0.285  | <0.01 | 0.249  | <0.01 | 0.009 | 0.91  | 1.54 | 0.166 | 1.53 | <0.001 | -0.09  | 0.03  |
| H2AFZ     | H2A histone family, member Z                             | 0.684  | <0.01 | 0.706  | <0.01 | 0.557 | <0.01 | 2.69 | 0.072 | 1.89 | <0.001 | -0.005 | 0.91  |
| HDAC2     | histone deacetylase 2                                    | 0.358  | <0.01 | 0.458  | <0.01 | 0.383 | <0.01 | 1.57 | 0.083 | 1.22 | 0.032  | 0.012  | 0.77  |
| HDDC2     | HD domain containing 2                                   | 0.25   | <0.01 | 0.117  | <0.01 | 0.122 | 0.15  | 1.2  | 0.581 | 1.01 | 0.944  | -0.037 | 0.37  |
| HDGF      | heparin binding growth factor                            | 0.446  | <0.01 | 0.381  | <0.01 | 0.222 | <0.01 | 1.01 | 0.975 | 1.41 | 0.007  | 0.084  | 0.04  |
| HNRNPA1   | heterogeneous nuclear ribonucleoprotein A1               | 0.275  | <0.01 | 0.471  | <0.01 | 0.188 | 0.03  | 0.7  | 0.406 | 0.93 | 0.233  | 0.135  | <0.01 |
| HNRNPA2B1 | Heterogeneous Nuclear Ribonucleoprotein A2/B1            | 0.476  | <0.01 | -0.183 | <0.01 | 0.528 | <0.01 | 2.43 | 0.109 | 1    | 0.98   | -0.085 | 0.04  |
| HNRNPA3   | heterogeneous nuclear ribonucleoprotein A3               | 0.268  | <0.01 | 0.239  | <0.01 | 0.164 | 0.05  | 0.49 | 0.247 | 0.72 | 0.006  | 0.023  | 0.58  |
| HNRNPC    | heterogeneous nuclear ribonucleoprotein C                | 0.516  | <0.01 | -      | -     | 0.431 | <0.01 | 1.54 | 0.487 | -    | -      | -0.09  | 0.03  |
| HNRNPCL1  |                                                          | -      | -     | 0.041  | 0.13  | -     | -     | -    | -     | 0.78 | 0.508  | -0.048 | 0.08  |
| HNRNPD    | heterogeneous nuclear ribonucleoprotein D                | 0.327  | <0.01 | 0.351  | <0.01 | 0.262 | <0.01 | 0.76 | 0.576 | 1.45 | 0.01   | 0.106  | 0.01  |
| HNRNPR    | heterogeneous nuclear ribonucleoprotein R                | 0.271  | <0.01 | 0.269  | <0.01 | 0.351 | <0.01 | 0.85 | 0.785 | 1.12 | 0.424  | 0.116  | <0.01 |
| HNRNPU    | heterogeneous nuclear ribonucleoprotein U                | 0.27   | <0.01 | -0.094 | <0.01 | 0.227 | <0.01 | 0.83 | 0.776 | 0.92 | 0.424  | -0.162 | <0.01 |

|          |                                                                    |       |       |       |       |       |       |      |       |      |        |        |       |
|----------|--------------------------------------------------------------------|-------|-------|-------|-------|-------|-------|------|-------|------|--------|--------|-------|
| HPRT1    | hypoxanthine phosphoribosyltransferase 1                           | 0.6   | <0.01 | 0.599 | <0.01 | 0.402 | <0.01 | 1.27 | 0.461 | 1.29 | 0.005  | 0.042  | 0.31  |
| HSP90AB1 | heat shock protein 90 alpha family class B member 1                | 0.642 | <0.01 | 0.371 | <0.01 | 0.513 | <0.01 | 1.91 | 0.059 | 1.67 | <0.001 | 0.164  | <0.01 |
| HSPD1    | heat shock protein family D (Hsp60) member 1                       | 0.744 | <0.01 | 0.728 | <0.01 | 0.676 | <0.01 | 1.76 | 0.041 | 1.3  | 0.002  | 0.198  | <0.01 |
| HSPE1    | heat shock protein family E (Hsp10) member 1                       | 0.643 | <0.01 | -     | -     | 0.541 | <0.01 | 1.59 | 0.09  | -    | -      | -0.136 | <0.01 |
| IARS     | Isoleucyl-TRNA Synthetase 1                                        | 0.275 | <0.01 | 0.519 | <0.01 | 0.333 | <0.01 | 1.66 | 0.117 | 1.22 | 0.056  | 0.108  | <0.01 |
| IFRD1    | interferon related developmental regulator 1                       | -0.07 | 0.09  | 0.063 | 0.02  | 0.113 | 0.18  | 1.36 | 0.18  | 0.9  | 0.416  | 0.204  | <0.01 |
| ILF2     | interleukin enhancer binding factor 2                              | 0.454 | <0.01 | 0.488 | <0.01 | 0.518 | <0.01 | 1.65 | 0.171 | 1.19 | 0.099  | -0.066 | 0.11  |
| IMPDH2   | inosine monophosphate dehydrogenase 2                              | 0.242 | <0.01 | 0.126 | <0.01 | 0.467 | <0.01 | 0.86 | 0.61  | 0.76 | 0.002  | 0.316  | <0.01 |
| KARS     | Lysyl-TRNA Synthetase 1                                            | 0.456 | <0.01 | 0.331 | <0.01 | 0.179 | 0.03  | 1.87 | 0.111 | 1.46 | 0.004  | 0.14   | <0.01 |
| KPNA2    | karyopherin subunit alpha 2                                        | 0.661 | <0.01 | 0.751 | <0.01 | 0.505 | <0.01 | 1.28 | 0.215 | 1.22 | 0.001  | 0.003  | 0.94  |
| KPNB1    | karyopherin subunit beta 1                                         | 0.317 | <0.01 | 0.424 | <0.01 | 0.07  | 0.41  | 0.77 | 0.54  | 0.86 | 0.263  | 0.076  | 0.07  |
| LDHA     | lactate dehydrogenase A                                            | 0.465 | <0.01 | 0.418 | <0.01 | 0.007 | 0.93  | 1.18 | 0.61  | 1.24 | 0.03   | -0.031 | 0.46  |
| LSM2.00  | LSM2 homolog, U6 small nuclear RNA and mRNA degradation associated | 0.522 | <0.01 | 0.173 | <0.01 | 0.501 | <0.01 | 0.85 | 0.656 | 1.44 | 0.02   | 0.042  | 0.31  |
| LSM7.00  | LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated | 0.162 | <0.01 | 0.446 | <0.01 | 0.408 | <0.01 | 1.16 | 0.545 | 1.1  | 0.501  | 0.063  | 0.13  |
| MAD2L1   | mitotic arrest deficient 2 like 1                                  | 0.647 | <0.01 | 0.804 | <0.01 | 0.598 | <0.01 | 1.19 | 0.364 | 1.39 | <0.001 | 0.14   | <0.01 |
| MCM2     | minichromosome maintenance complex component 2                     | 0.528 | <0.01 | 0.362 | <0.01 | 0.558 | <0.01 | 1.07 | 0.776 | 1.74 | <0.001 | 0.109  | <0.01 |
| MCM4     | minichromosome maintenance complex component 4                     | 0.483 | <0.01 | 0.418 | <0.01 | 0.631 | <0.01 | 1.43 | 0.081 | 1.46 | <0.001 | 0.092  | 0.03  |
| MCM5     | minichromosome maintenance complex component 5                     | 0.254 | <0.01 | 0.082 | <0.01 | 0.402 | <0.01 | 0.73 | 0.287 | 1.49 | <0.001 | 0.133  | <0.01 |
| MCM6     | minichromosome maintenance complex component 6                     | 0.457 | <0.01 | 0.384 | <0.01 | 0.624 | <0.01 | 1.31 | 0.34  | 1.79 | <0.001 | 0.022  | 0.6   |
| MCM7     | minichromosome maintenance complex component 7                     | 0.429 | <0.01 | 0.296 | <0.01 | 0.599 | <0.01 | 1.1  | 0.723 | 1.45 | <0.001 | 0.213  | <0.01 |
| MRPL23   | mitochondrial ribosomal protein L23                                | 0.282 | <0.01 | 0.119 | <0.01 | 0.356 | <0.01 | 0.9  | 0.668 | 1.29 | 0.047  | 0.015  | 0.71  |
| MRPL9    | mitochondrial ribosomal protein L9                                 | 0.211 | <0.01 | 0.349 | <0.01 | 0.211 | 0.01  | 1.12 | 0.783 | 1.27 | 0.087  | -0.008 | 0.84  |
| MRPS18B  | mitochondrial ribosomal protein S18B                               | 0.469 | <0.01 | 0.317 | <0.01 | 0.319 | <0.01 | 0.87 | 0.744 | 0.77 | 0.076  | 0.049  | 0.24  |
| MYC      | MYC proto-oncogene, bHLH transcription factor                      | 0.126 | <0.01 | 0.429 | <0.01 | 0.471 | <0.01 | 0.82 | 0.246 | 1.02 | 0.634  | 1      | <0.01 |
| NAP1L1   | nucleosome assembly protein 1 like 1                               | 0.366 | <0.01 | 0.387 | <0.01 | 0.185 | 0.03  | 0.54 | 0.174 | 1.03 | 0.78   | 0.279  | <0.01 |
| NCBP1    | nuclear cap binding protein subunit 1                              | 0.186 | <0.01 | 0.131 | <0.01 | 0.204 | 0.02  | 1.98 | 0.095 | 1.57 | 0.001  | -0.054 | 0.19  |
| NCBP2    | nuclear cap binding protein subunit 2                              | 0.44  | <0.01 | 0.373 | <0.01 | 0.383 | <0.01 | 0.94 | 0.911 | 1.71 | <0.001 | 0.068  | 0.1   |
| NDUFAB1  | NADH:ubiquinone oxidoreductase subunit AB1                         | 0.589 | <0.01 | 0.522 | <0.01 | 0.194 | 0.02  | 1.29 | 0.502 | 0.99 | 0.953  | -0.131 | <0.01 |
| NHP2     | NHP2 ribonucleoprotein                                             | 0.508 | <0.01 | 0.548 | <0.01 | 0.48  | <0.01 | 1.26 | 0.491 | 1.27 | 0.027  | 0.145  | <0.01 |
| NME1     | NME/NM23 nucleoside diphosphate kinase 1                           | 0.673 | <0.01 | 0.594 | <0.01 | 0.486 | <0.01 | 0.87 | 0.559 | 1.32 | <0.001 | 0.109  | <0.01 |
| NOLC1    | nucleolar and coiled-body phosphoprotein 1                         | 0.466 | <0.01 | 0.531 | <0.01 | 0.535 | <0.01 | 1.72 | 0.183 | 1.38 | 0.008  | 0.302  | <0.01 |
| NOP16    | NOP16 nucleolar protein                                            | 0.559 | <0.01 | 0.362 | <0.01 | 0.422 | <0.01 | 1.52 | 0.166 | 1.73 | <0.001 | 0.259  | <0.01 |
| NOP56    | NOP56 ribonucleoprotein                                            | 0.546 | <0.01 | 0.293 | <0.01 | -     | -     | 1.56 | 0.188 | 1.61 | <0.001 | 0.311  | <0.01 |
| NPM1     | nucleophosmin 1                                                    | 0.581 | <0.01 | -     | -     | 0.473 | <0.01 | 1.17 | 0.718 | -    | -      | 0.151  | <0.01 |
| ODC1     | ornithine decarboxylase 1                                          | 0.127 | <0.01 | 0.174 | <0.01 | 0.156 | 0.07  | 0.98 | 0.929 | 1.11 | 0.161  | 0.297  | <0.01 |

|         |                                                     |        |       |       |       |        |       |      |        |      |        |        |       |
|---------|-----------------------------------------------------|--------|-------|-------|-------|--------|-------|------|--------|------|--------|--------|-------|
| ORC2    | origin recognition complex subunit 2                | -      | -     | 0.068 | 0.01  | 0.348  | <0.01 | -    | -      | 0.96 | 0.85   | -0.125 | <0.01 |
| ORC2L   | Origin Recognition Complex Subunit 2                | -0.064 | 0.13  | -     | -     | -      | -     | 0.88 | 0.78   | -    | -      | 0.035  | 0.39  |
| PA2G4   | proliferation-associated 2G4                        | 0.733  | <0.01 | 0.143 | <0.01 | 0.543  | <0.01 | 1.7  | 0.223  | 1.89 | <0.001 | 0.06   | 0.15  |
| PABPC1  | poly(A) binding protein cytoplasmic 1               | 0.441  | <0.01 | 0.413 | <0.01 | 0.3    | <0.01 | 1.32 | 0.287  | 0.95 | 0.393  | 0.342  | <0.01 |
| PABPC4  | poly(A) binding protein cytoplasmic 4               | 0.119  | <0.01 | 0.069 | 0.01  | -      | -     | 1.68 | 0.152  | 1.16 | 0.165  | 0.318  | <0.01 |
| PCBP1   | poly(rC) binding protein 1                          | 0.242  | <0.01 | 0.18  | <0.01 | -0.001 | 0.99  | 1.3  | 0.669  | 1    | 0.978  | 0.016  | 0.69  |
| PCNA    | proliferating cell nuclear antigen                  | 0.617  | <0.01 | 0.654 | <0.01 | 0.382  | <0.01 | 1.36 | 0.247  | 1.16 | 0.026  | -0.039 | 0.35  |
| PGK1.00 | phosphoglycerate kinase 1                           | 0.487  | <0.01 | 0.573 | <0.01 | 0.295  | <0.01 | 2.99 | <0.001 | 1.11 | 0.081  | -0.002 | 0.96  |
| PHB     | prohibitin                                          | 0.489  | <0.01 | 0.243 | <0.01 | 0.364  | <0.01 | 0.79 | 0.524  | 1.3  | 0.009  | 0.17   | <0.01 |
| PHB2    | prohibitin 2                                        | 0.339  | <0.01 | 0.341 | <0.01 | 0.372  | <0.01 | 1.08 | 0.856  | 0.84 | 0.224  | 0.173  | <0.01 |
| POLD2   | DNA polymerase delta 2, accessory subunit           | 0.571  | <0.01 | 0.175 | <0.01 | 0.555  | <0.01 | 1.57 | 0.162  | 1.44 | 0.001  | 0.19   | <0.01 |
| POLE3   | DNA polymerase epsilon 3, accessory subunit         | 0.381  | <0.01 | 0.38  | <0.01 | 0.418  | <0.01 | 0.98 | 0.973  | 1.35 | 0.038  | -0.029 | 0.49  |
| PPIA    | peptidylprolyl isomerase A                          | 0.692  | <0.01 | 0.625 | <0.01 | 0.223  | <0.01 | 1.65 | 0.153  | 0.96 | 0.433  | 0.072  | 0.09  |
| PPM1G   | protein phosphatase, Mg2+/Mn2+ dependent 1G         | 0.543  | <0.01 | 0.081 | <0.01 | 0.397  | <0.01 | 1.26 | 0.591  | 1.98 | <0.001 | 0.015  | 0.71  |
| PRDX3   | peroxiredoxin 3                                     | 0.25   | <0.01 | 0.414 | <0.01 | 0.049  | 0.56  | 2.15 | 0.064  | 0.93 | 0.114  | -0.038 | 0.36  |
| PRDX4   | peroxiredoxin 4                                     | 0.575  | <0.01 | 0.485 | <0.01 | 0.225  | <0.01 | 2.26 | 0.008  | 1.09 | 0.364  | 0.14   | <0.01 |
| PRPF31  | pre-mRNA processing factor 31                       | 0.152  | <0.01 | 0.134 | <0.01 | 0.156  | 0.07  | 1.39 | 0.288  | 1.36 | 0.017  | 0.081  | 0.05  |
| PRPS2   | phosphoribosyl pyrophosphate synthetase 2           | 0.243  | <0.01 | 0.322 | <0.01 | 0.272  | <0.01 | 1.15 | 0.628  | 0.91 | 0.385  | 0.042  | 0.31  |
| PSMA1   | proteasome 20S subunit alpha 1                      | 0.565  | <0.01 | 0.563 | <0.01 | 0.07   | 0.41  | 1.31 | 0.53   | 1.1  | 0.294  | -0.068 | 0.1   |
| PSMA2   | proteasome 20S subunit alpha 2                      | 0.561  | <0.01 | 0.371 | <0.01 | 0.28   | <0.01 | 2.72 | 0.022  | 0.9  | 0.422  | -0.137 | <0.01 |
| PSMA4   | proteasome 20S subunit alpha 4                      | 0.534  | <0.01 | 0.496 | <0.01 | 0.224  | <0.01 | 1.27 | 0.499  | 1.07 | 0.535  | -0.151 | <0.01 |
| PSMA6   | proteasome 20S subunit alpha 6                      | 0.624  | <0.01 | 0.674 | <0.01 | -      | -     | 1.26 | 0.518  | 1.16 | 0.051  | -0.17  | <0.01 |
| PSMA7   | proteasome 20S subunit alpha 7                      | 0.525  | <0.01 | 0.161 | <0.01 | 0.464  | <0.01 | 1.37 | 0.244  | 2.02 | 0.008  | -0.005 | 0.9   |
| PSMB2   | proteasome 20S subunit beta 2                       | 0.426  | <0.01 | 0.369 | <0.01 | -0.138 | 0.1   | 1.61 | 0.259  | 1.49 | 0.001  | -0.1   | 0.02  |
| PSMB3   | proteasome 20S subunit beta 3                       | 0.416  | <0.01 | 0.218 | <0.01 | 0.11   | 0.19  | 0.75 | 0.394  | 1.38 | 0.01   | -0.085 | 0.04  |
| PSMC4   | proteasome 26S subunit, ATPase 4                    | 0.508  | <0.01 | 0.449 | <0.01 | 0.337  | <0.01 | 0.88 | 0.733  | 1.1  | 0.19   | -0.173 | <0.01 |
| PSMC6   | proteasome 26S subunit, ATPase 6                    | 0.472  | <0.01 | 0.53  | <0.01 | 0.253  | <0.01 | 1.76 | 0.183  | 1.12 | 0.22   | -0.168 | <0.01 |
| PSMD1   | proteasome 26S subunit, non-ATPase 1                | 0.348  | <0.01 | 0.293 | <0.01 | 0.152  | 0.07  | 1.81 | 0.186  | 1.38 | 0.019  | -0.081 | 0.05  |
| PSMD14  | proteasome 26S subunit, non-ATPase 14               | 0.595  | <0.01 | 0.659 | <0.01 | 0.399  | <0.01 | 2.75 | 0.007  | 1.14 | 0.177  | -0.153 | <0.01 |
| PSMD3   | proteasome 26S subunit, non-ATPase 3                | 0.415  | <0.01 | 0.164 | <0.01 | 0.272  | <0.01 | 1.29 | 0.451  | 1.27 | 0.092  | 0.061  | 0.14  |
| PSMD7   | proteasome 26S subunit, non-ATPase 7                | 0.413  | <0.01 | 0.499 | <0.01 | 0.067  | 0.43  | 2.51 | 0.004  | 1.14 | 0.104  | 0.062  | 0.14  |
| PSMD8   | proteasome 26S subunit, non-ATPase 8                | 0.545  | <0.01 | 0.014 | 0.62  | 0.348  | <0.01 | 1.43 | 0.429  | 1.01 | 0.949  | -0.053 | 0.2   |
| PTGES3  | prostaglandin E synthase 3                          | 0.659  | <0.01 | 0.573 | <0.01 | 0.406  | <0.01 | 2.53 | 0.037  | 1.03 | 0.585  | -0.056 | 0.18  |
| PWP1    | PWP1 homolog, endonuclein                           | 0.475  | <0.01 | 0.479 | <0.01 | 0.257  | <0.01 | 1.41 | 0.509  | 1.6  | 0.005  | 0.075  | 0.07  |
| RAD23B  | RAD23 homolog B, nucleotide excision repair protein | 0.307  | <0.01 | 0.244 | <0.01 | 0.028  | 0.74  | 2.27 | 0.089  | 1.12 | 0.371  | -0.121 | <0.01 |
| RAN     | RAN, member RAS oncogene family                     | 0.754  | <0.01 | 0.63  | <0.01 | 0.603  | <0.01 | 1.3  | 0.479  | 1.14 | 0.173  | 0.151  | <0.01 |
| RANBP1  | RAN binding protein 1                               | 0.609  | <0.01 | 0.613 | <0.01 | 0.388  | <0.01 | 0.8  | 0.579  | 1.14 | 0.145  | 0.185  | <0.01 |
| RFC4    | replication factor C subunit 4                      | 0.554  | <0.01 | 0.68  | <0.01 | 0.347  | <0.01 | 1.05 | 0.88   | 1.55 | <0.001 | -0.007 | 0.86  |

|         |                                                                                                 |        |       |        |       |       |       |      |       |      |        |        |       |
|---------|-------------------------------------------------------------------------------------------------|--------|-------|--------|-------|-------|-------|------|-------|------|--------|--------|-------|
| RNPS1   | RNA binding protein with serine rich domain 1                                                   | 0.321  | <0.01 | 0.254  | <0.01 | 0.369 | <0.01 | 1.18 | 0.68  | 1.1  | 0.26   | 0.023  | 0.58  |
| RPL14   | ribosomal protein L14                                                                           | 0.243  | <0.01 | 0.182  | <0.01 | 0.329 | <0.01 | 0.72 | 0.265 | 1.01 | 0.896  | 0.2    | <0.01 |
| RPL18   | ribosomal protein L18                                                                           | 0.165  | <0.01 | 0.328  | <0.01 | 0.041 | 0.63  | 0.92 | 0.735 | 0.93 | 0.382  | 0.187  | <0.01 |
| RPL22   | ribosomal protein L22                                                                           | 0.169  | <0.01 | 0.258  | <0.01 | 0.208 | 0.01  | 0.58 | 0.171 | 0.83 | 0.006  | 0.24   | <0.01 |
| RPL34   | ribosomal protein L34                                                                           | 0.025  | 0.55  | 0.623  | <0.01 | 0.103 | 0.22  | 0.73 | 0.233 | 1.23 | 0.014  | 0.162  | <0.01 |
| RPLP0   | ribosomal protein lateral stalk subunit P0                                                      | 0.339  | <0.01 | 0.587  | <0.01 | 0.344 | <0.01 | 1.2  | 0.575 | 0.98 | 0.735  | 0.303  | <0.01 |
| RPS10   | ribosomal protein S10                                                                           | 0.265  | <0.01 | 0.23   | <0.01 | 0.103 | 0.23  | 0.81 | 0.501 | 1.08 | 0.575  | 0.243  | <0.01 |
| RPS2    | ribosomal protein S2                                                                            | 0.322  | <0.01 | 0.328  | <0.01 | -     | -     | 1.1  | 0.723 | 0.95 | 0.513  | 0.189  | <0.01 |
| RPS3    | ribosomal protein S3                                                                            | 0.087  | 0.04  | 0.318  | <0.01 | 0.121 | 0.16  | 0.75 | 0.292 | 1.01 | 0.893  | 0.236  | <0.01 |
| RPS5    | ribosomal protein S5                                                                            | 0.232  | <0.01 | 0.552  | <0.01 | 0.423 | <0.01 | 1.06 | 0.853 | 0.93 | 0.332  | 0.495  | <0.01 |
| RPS6    | ribosomal protein S6                                                                            | 0.066  | 0.11  | 0.315  | <0.01 | 0.106 | 0.21  | 0.83 | 0.498 | 0.77 | 0.002  | 0.262  | <0.01 |
| RRM1    | ribonucleotide reductase catalytic subunit M1                                                   | 0.423  | <0.01 | 0.228  | <0.01 | 0.314 | <0.01 | 1.08 | 0.821 | 1.55 | <0.001 | -0.018 | 0.67  |
| RRP9    | ribosomal RNA processing 9, U3 small nucleolar RNA binding protein                              | 0.328  | <0.01 | 0.207  | <0.01 | 0.456 | <0.01 | 1.09 | 0.8   | 1.2  | 0.393  | 0.231  | <0.01 |
| RSL1D1  | ribosomal L1 domain containing 1                                                                | 0.367  | <0.01 | 0.193  | <0.01 | 0.272 | <0.01 | 0.91 | 0.844 | 0.83 | 0.052  | 0.247  | <0.01 |
| RUVBL2  | RuvB like AAA ATPase 2                                                                          | 0.482  | <0.01 | 0.373  | <0.01 | 0.515 | <0.01 | 1.22 | 0.499 | 1.71 | <0.001 | 0.063  | 0.13  |
| SERBP1  | SERPINE1 mRNA binding protein 1                                                                 | 0.239  | <0.01 | -0.075 | <0.01 | 0.462 | <0.01 | 0.87 | 0.757 | 1.05 | 0.717  | 0.263  | <0.01 |
| SET     | SET nuclear proto-oncogene                                                                      | 0.49   | <0.01 | 0.373  | <0.01 | 0.309 | <0.01 | 1.38 | 0.542 | 1.3  | 0.012  | 0.089  | 0.03  |
| SF3A1   | splicing factor 3a subunit 1                                                                    | -0.133 | <0.01 | 0.162  | <0.01 | 0.1   | 0.24  | 0.32 | 0.009 | 0.88 | 0.384  | 0.189  | <0.01 |
| SF3B3   | splicing factor 3b subunit 3                                                                    | 0.282  | <0.01 | -0.006 | 0.82  | 0.203 | 0.02  | 1.96 | 0.038 | 1.59 | <0.001 | 0.205  | <0.01 |
| SLC25A3 | solute carrier family 25 member 3                                                               | 0.484  | <0.01 | 0.392  | <0.01 | 0.344 | <0.01 | 1.48 | 0.4   | 1.17 | 0.283  | 0.11   | <0.01 |
| SMARCC1 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin subfamily c member 1 | 0.193  | <0.01 | 0.355  | <0.01 | 0.368 | <0.01 | 1.06 | 0.876 | 0.95 | 0.663  | 0.169  | <0.01 |
| SNRPA   | small nuclear ribonucleoprotein polypeptide A                                                   | 0.419  | <0.01 | 0.027  | 0.32  | 0.423 | <0.01 | 0.85 | 0.665 | 1.57 | 0.001  | 0.145  | <0.01 |
| SNRPA1  | small nuclear ribonucleoprotein polypeptide A'                                                  | 0.607  | <0.01 | 0.457  | <0.01 | 0.537 | <0.01 | 1.29 | 0.318 | 1.51 | <0.001 | -0.018 | 0.67  |
| SNRPB2  | small nuclear ribonucleoprotein polypeptide B2                                                  | 0.486  | <0.01 | 0.391  | <0.01 | 0.136 | 0.11  | 1.62 | 0.083 | 1.77 | <0.001 | -0.104 | 0.01  |
| SNRPD1  | small nuclear ribonucleoprotein D1 polypeptide                                                  | 0.702  | <0.01 | 0.624  | <0.01 | 0.644 | <0.01 | 1.56 | 0.218 | 1.33 | 0.034  | 0.118  | <0.01 |
| SNRPD2  | small nuclear ribonucleoprotein D2 polypeptide                                                  | 0.504  | <0.01 | 0.433  | <0.01 | 0.527 | <0.01 | 0.97 | 0.923 | 1.46 | 0.009  | 0.02   | 0.63  |
| SNRPD3  | small nuclear ribonucleoprotein D3 polypeptide                                                  | 0.484  | <0.01 | -      | -     | 0.391 | <0.01 | 1.07 | 0.863 | -    | -      | 0.004  | 0.92  |
| SNRPG   | small nuclear ribonucleoprotein polypeptide G                                                   | 0.569  | <0.01 | 0.412  | <0.01 | 0.509 | <0.01 | 1.53 | 0.218 | 1.27 | 0.056  | -0.212 | <0.01 |
| SRM     | spermidine synthase                                                                             | 0.304  | <0.01 | 0.044  | 0.1   | 0.407 | <0.01 | 1.49 | 0.128 | 1.16 | 0.124  | 0.201  | <0.01 |
| SRPK1   | SRSF protein kinase 1                                                                           | 0.388  | <0.01 | 0.453  | <0.01 | 0.122 | 0.15  | 1.35 | 0.323 | 1.73 | <0.001 | 0.183  | <0.01 |
| SRSF1   | serine and arginine rich splicing factor 1                                                      | -      | -     | 0.262  | <0.01 | 0.437 | <0.01 | -    | -     | 1.28 | 0.074  | -0.21  | <0.01 |
| SRSF2   | serine and arginine rich splicing factor 2                                                      | -      | -     | 0.455  | <0.01 | -     | -     | -    | -     | 1.57 | 0.002  | 0.223  | <0.01 |
| SRSF3   | serine and arginine rich splicing factor 3                                                      | -      | -     | 0.481  | <0.01 | 0.594 | <0.01 | -    | -     | 0.86 | 0.246  | 0.221  | <0.01 |

|         |                                                                                |       |       |        |       |       |       |      |       |      |        |        |       |
|---------|--------------------------------------------------------------------------------|-------|-------|--------|-------|-------|-------|------|-------|------|--------|--------|-------|
| SRSF7   | serine and arginine rich splicing factor 7                                     | -     | -     | 0.237  | <0.01 | 0.221 | <0.01 | -    | -     | 0.9  | 0.437  | 0.137  | <0.01 |
| SSB     | small RNA binding exonuclease protection factor La                             | 0.516 | <0.01 | 0.524  | <0.01 | 0.419 | <0.01 | 2.02 | 0.184 | 1.01 | 0.912  | 0.05   | 0.23  |
| SSBP1   | single stranded DNA binding protein 1                                          | 0.489 | <0.01 | 0.558  | <0.01 | 0.086 | 0.31  | 1.26 | 0.567 | 0.82 | 0.074  | -0.16  | <0.01 |
| STARD7  | StAR related lipid transfer domain containing 7                                | 0.361 | <0.01 | 0.484  | <0.01 | 0.159 | 0.06  | 0.72 | 0.505 | 0.97 | 0.765  | 0.072  | 0.08  |
| SYNCRIP | synaptotagmin binding cytoplasmic RNA interacting protein                      | 0.176 | <0.01 | 0.475  | <0.01 | 0.433 | <0.01 | 1.9  | 0.084 | 1.21 | 0.056  | 0.041  | 0.32  |
| TARDBP  | TAR DNA binding protein                                                        | 0.463 | <0.01 | -0.128 | <0.01 | 0.288 | <0.01 | 2.07 | 0.481 | 0.96 | 0.802  | -0.012 | 0.77  |
| TCP1    | t-complex 1                                                                    | 0.506 | <0.01 | 0.592  | <0.01 | -     | -     | 2.41 | 0.001 | 1.08 | 0.313  | 0.01   | 0.81  |
| TFDP1   | transcription factor Dp-1                                                      | 0.14  | <0.01 | 0.358  | <0.01 | 0.269 | <0.01 | 0.94 | 0.868 | 1.09 | 0.394  | 0.43   | 0.104 |
| TOMM70A | translocase of outer mitochondrial membrane 70                                 | 0.434 | <0.01 | 0.326  | <0.01 | 0.198 | 0.02  | 1.51 | 0.324 | 1.34 | 0.056  | 0.07   | 0.09  |
| TRA2B   | transformer 2 beta homolog                                                     | 0.415 | <0.01 | 0.259  | <0.01 | 0.571 | <0.01 | 1.28 | 0.731 | 1.07 | 0.604  | 0.084  | 0.04  |
| TRIM28  | tripartite motif containing 28                                                 | 0.323 | <0.01 | 0.048  | 0.08  | 0.486 | <0.01 | 1.14 | 0.732 | 1.37 | 0.003  | 0.096  | 0.02  |
| TUFM    | Tu translation elongation factor, mitochondrial                                | 0.331 | <0.01 | 0.044  | 0.1   | 0.26  | <0.01 | 1.04 | 0.922 | 1.28 | 0.056  | -0.039 | 0.35  |
| TXNL4A  | thioredoxin like 4A                                                            | 0.589 | <0.01 | -      | -     | 0.318 | <0.01 | 1.93 | 0.032 | -    | -      | 0.111  | <0.01 |
| TYMS    | thymidylate synthetase                                                         | 0.557 | <0.01 | 0.631  | <0.01 | 0.387 | <0.01 | 1.31 | 0.174 | 1.47 | <0.001 | 0.103  | 0.01  |
| U2AF1   | U2 small nuclear RNA auxiliary factor 1                                        | 0.228 | <0.01 | 0.102  | <0.01 | 0.381 | <0.01 | 1.11 | 0.784 | 1.36 | 0.015  | -0.05  | 0.23  |
| UBA2    | ubiquitin like modifier activating enzyme 2                                    | 0.428 | <0.01 | 0.331  | <0.01 | 0.388 | <0.01 | 1.18 | 0.682 | 0.9  | 0.667  | 0.198  | <0.01 |
| UBE2E1  | ubiquitin conjugating enzyme E2 E1                                             | 0.324 | <0.01 | 0.409  | <0.01 | 0.232 | <0.01 | 2.48 | 0.058 | 0.96 | 0.606  | 0.02   | 0.63  |
| UBE2L3  | ubiquitin conjugating enzyme E2 L3                                             | 0.393 | <0.01 | -0.125 | <0.01 | 0.232 | <0.01 | 0.56 | 0.253 | 1.25 | 0.019  | -0.011 | 0.8   |
| USP1    | ubiquitin specific peptidase 1                                                 | 0.232 | <0.01 | 0.504  | <0.01 | 0.462 | <0.01 | 0.76 | 0.378 | 1.06 | 0.578  | 0.084  | 0.04  |
| VBP1    | VHL binding protein 1                                                          | 0.464 | <0.01 | 0.611  | <0.01 | 0.221 | <0.01 | 2.19 | 0.04  | 1.02 | 0.827  | -0.062 | 0.14  |
| VDAC1   | voltage dependent anion channel 1                                              | 0.533 | <0.01 | 0.496  | <0.01 | 0.196 | 0.02  | 2.66 | 0.009 | 1.14 | 0.213  | -0.063 | 0.13  |
| VDAC3   | voltage dependent anion channel 3                                              | 0.523 | <0.01 | 0.421  | <0.01 | 0.148 | 0.08  | 0.73 | 0.295 | 1.28 | 0.012  | 0.001  | 0.99  |
| XPO1    | exportin 1                                                                     | 0.211 | <0.01 | 0.323  | <0.01 | 0.368 | <0.01 | 1.62 | 0.265 | 1.5  | 0.013  | 0.014  | 0.74  |
| XPOT    | exportin for tRNA                                                              | 0.457 | <0.01 | 0.566  | <0.01 | 0.415 | <0.01 | 1.49 | 0.105 | 1.7  | <0.001 | 0.081  | 0.05  |
| XRCC6   | X-ray repair cross complementing 6                                             | 0.424 | <0.01 | 0.41   | <0.01 | 0.197 | 0.02  | 0.53 | 0.173 | 0.98 | 0.812  | 0.146  | <0.01 |
| YWHAE   | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon | 0.264 | <0.01 | -0.048 | 0.08  | 0.346 | <0.01 | 1.34 | 0.512 | 1.01 | 0.948  | -0.11  | <0.01 |
| YWHAQ   | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein theta   | 0.338 | <0.01 | 0.431  | <0.01 | 0.281 | <0.01 | 1.2  | 0.609 | 1.21 | 0.088  | 0.105  | 0.01  |

**Note:** For each gene correlation was performed with proliferation score in all cohorts and R value as well as *p* value are shown. COX analysis was performed to examine survival difference in TCGA and METABRIC cohorts and hazard ratio (HR) and *p* value are shown for each gene. Correlation analysis was performed for each gene using TCGA cohort in order to quantify the positive or negative impact of each target gene on the overall MYC score. Spearman R value and *p* value for each gene is shown. Of note, gene information was not available in TCGA for the following genes and METABRIC data was used instead: HNRNPCL1, ORC2, RPS5, SRSF1, SRSF2, SRSF3, SRSF7.

**Table S2: HALLMARK\_MYC\_TARGETS\_V2 with proliferation, survival, and positive/negative correlation with MYC score analysis**

| Gene     | Gene name                                                               | Proliferation correlation |         |          |         |          |         | Survival analysis |         |      |         | Pos/neg targets |         |
|----------|-------------------------------------------------------------------------|---------------------------|---------|----------|---------|----------|---------|-------------------|---------|------|---------|-----------------|---------|
|          |                                                                         | Spearman                  |         | Spearman |         | Spearman |         | COX               |         | COX  |         | Spearman        |         |
|          |                                                                         | R                         | P value | R        | P value | R        | P value | HR                | P value | HR   | P value | R               | P value |
| AIMP2    | aminoacyl tRNA synthetase complex interacting multifunctional protein 2 | 0.467                     | <0.01   | 0.624    | <0.01   | 0.48     | <0.01   | 2.44              | 0.034   | 1.29 | 0.038   | 0.141           | <0.01   |
| BYSL     | bystin like                                                             | 0.459                     | <0.01   | 0.732    | <0.01   | 0.724    | <0.01   | 1.49              | 0.208   | 1.69 | <0.001  | 0.392           | <0.01   |
| CBX3     | chromobox 3                                                             | 0.194                     | 0.02    | 0.385    | <0.01   | 0.353    | <0.01   | 1.53              | 0.237   | 1.36 | 0.002   | -0.01           | 0.81    |
| CDK4     | cyclin dependent kinase 4                                               | 0.322                     | <0.01   | 0.548    | <0.01   | 0.358    | <0.01   | 1.55              | 0.202   | 1.54 | <0.001  | -0.009          | 0.83    |
| DCTPP1   | Deoxycytidine-Triphosphatase 1                                          | 0.379                     | <0.01   | 0.453    | <0.01   | 0.187    | <0.01   | 1.64              | 0.098   | 0.98 | 0.792   | -0.02           | 0.63    |
| DDX18    | DEAD-box helicase 18                                                    | 0.586                     | <0.01   | -0.035   | 0.4     | 0.219    | <0.01   | 1.29              | 0.591   | 1.38 | 0.049   | 0.105           | 0.01    |
| DUSP2    | dual specificity phosphatase 2                                          | 0.29                      | <0.01   | 0.109    | <0.01   | 0.151    | <0.01   | 0.83              | 0.245   | 1.3  | 0.089   | 0.363           | <0.01   |
| EXOSC5   | Exosome Component 5                                                     | 0.518                     | <0.01   | 0.572    | <0.01   | 0.559    | <0.01   | 0.83              | 0.536   | 1.39 | 0.011   | 0.256           | <0.01   |
| FARSA    | phenylalanyl-tRNA synthetase subunit alpha                              | 0.489                     | <0.01   | 0.553    | <0.01   | 0.562    | <0.01   | 2.46              | 0.016   | 1.43 | 0.004   | 0.14            | <0.01   |
| GNL3     | G protein nucleolar 3                                                   | -                         | -       | 0.387    | <0.01   | 0.25     | <0.01   | 1.74              | 0.165   | 0.95 | 0.626   | 0.286           | <0.01   |
| GRWD1    | glutamate rich WD repeat containing 1                                   | 0.224                     | <0.01   | 0.503    | <0.01   | 0.404    | <0.01   | 1.22              | 0.641   | 1.32 | 0.101   | 0.184           | <0.01   |
| HK2      | hexokinase 2                                                            | 0.214                     | 0.01    | 0.092    | 0.03    | 0.055    | 0.04    | 1.13              | 0.559   | 1.03 | 0.674   | 0.008           | 0.85    |
| HSPD1    | heat shock protein family D (Hsp60) member 1                            | 0.713                     | <0.01   | 0.633    | <0.01   | 0.451    | <0.01   | 1.76              | 0.041   | 1.3  | 0.002   | 0.198           | <0.01   |
| HSPE1    | heat shock protein family E (Hsp10) member 1                            | 0.52                      | <0.01   | 0.556    | <0.01   | -        | -       | 1.59              | 0.09    | -    | -       | -0.136          | <0.01   |
| IMP4     | IMP U3 small nucleolar ribonucleoprotein 4                              | 0.495                     | <0.01   | 0.495    | <0.01   | 0.275    | <0.01   | 1.71              | 0.205   | 1.14 | 0.338   | 0.036           | 0.39    |
| IPO4     | importin 4                                                              | 0.631                     | <0.01   | 0.584    | <0.01   | 0.596    | <0.01   | 1.73              | 0.112   | 1.68 | <0.001  | 0.283           | <0.01   |
| LAS1L    | LAS1 like ribosome biogenesis factor                                    | 0.559                     | <0.01   | 0.535    | <0.01   | 0.487    | <0.01   | 1.31              | 0.557   | 1.51 | 0.002   | -0.015          | 0.72    |
| MAP3K6   | mitogen-activated protein kinase kinase kinase 6                        | 0.274                     | <0.01   | -0.189   | <0.01   | -0.197   | <0.01   | 0.95              | 0.81    | 0.71 | <0.001  | 0.027           | 0.52    |
| MCM4     | minichromosome maintenance complex component 4                          | 0.65                      | <0.01   | 0.428    | <0.01   | 0.633    | <0.01   | 1.43              | 0.081   | 1.46 | <0.001  | 0.092           | 0.03    |
| MCM5     | minichromosome maintenance complex component 5                          | 0.436                     | <0.01   | 0.354    | <0.01   | 0.365    | <0.01   | 0.73              | 0.287   | 1.49 | <0.001  | 0.133           | <0.01   |
| TPHOSPH1 | M-phase phosphoprotein 10                                               | 0.397                     | <0.01   | 0.182    | <0.01   | 0.218    | <0.01   | 2.06              | 0.086   | 1.24 | 0.163   | -0.06           | 0.15    |
| MRT04    | MRT4 homolog, ribosome maturation factor                                | 0.634                     | <0.01   | 0.61     | <0.01   | 0.542    | <0.01   | 1.1               | 0.806   | 1.29 | 0.067   | 0.271           | <0.01   |
| MYBBP1A  | MYB binding protein 1a                                                  | 0.42                      | <0.01   | 0.359    | <0.01   | 0.301    | <0.01   | 0.97              | 0.929   | 0.98 | 0.932   | 0.292           | <0.01   |
| MYC      | MYC proto-oncogene, bHLH transcription factor                           | 0.501                     | <0.01   | 0.291    | <0.01   | 0.319    | <0.01   | 0.82              | 0.246   | 1.02 | 0.634   | 1               | <0.01   |

|         |                                                                    |        |       |       |       |       |       |      |       |      |        |        |       |
|---------|--------------------------------------------------------------------|--------|-------|-------|-------|-------|-------|------|-------|------|--------|--------|-------|
| NDUFAF4 | NADH:ubiquinone oxidoreductase complex assembly factor 4           | 0.306  | <0.01 | 0.341 | <0.01 | 0.115 | <0.01 | 1.24 | 0.468 | 1.29 | 0.028  | 0.189  | <0.01 |
| NIP7    | nucleolar pre-rRNA processing protein NIP7                         | 0.324  | <0.01 | 0.344 | <0.01 | 0.299 | <0.01 | 1.41 | 0.356 | 1.22 | 0.092  | 0.233  | <0.01 |
| NOC4L   | nucleolar complex associated 4 homolog                             | 0.442  | <0.01 | 0.452 | <0.01 | 0.364 | <0.01 | 1.01 | 0.98  | 1.5  | 0.01   | 0.059  | 0.15  |
| NOLC1   | nucleolar and coiled-body phosphoprotein 1                         | 0.619  | <0.01 | 0.479 | <0.01 | 0.532 | <0.01 | 1.72 | 0.183 | 1.38 | 0.008  | 0.302  | <0.01 |
| NOP16   | NOP16 nucleolar protein                                            | 0.56   | <0.01 | 0.713 | <0.01 | 0.694 | <0.01 | 1.52 | 0.166 | 1.73 | <0.001 | 0.259  | <0.01 |
| NOP2    | NOP2 nucleolar protein                                             | 0.373  | <0.01 | 0.641 | <0.01 | 0.582 | <0.01 | 1.1  | 0.775 | 1.66 | <0.001 | 0.202  | <0.01 |
| NOP56   | NOP56 ribonucleoprotein                                            | -      | -     | 0.68  | <0.01 | 0.553 | <0.01 | 1.56 | 0.188 | 1.61 | <0.001 | 0.311  | <0.01 |
| NPM1    | nucleophosmin 1                                                    | 0.416  | <0.01 | 0.409 | <0.01 | -     | -     | 1.17 | 0.718 | -    | -      | 0.015  | <0.01 |
| PA2G4   | proliferation-associated 2G4                                       | 0.462  | <0.01 | 0.664 | <0.01 | 0.596 | <0.01 | 1.7  | 0.223 | 1.89 | <0.001 | 0.06   | 0.15  |
| PES1.00 | pescadillo ribosomal biogenesis factor 1                           | 0.671  | <0.01 | 0.541 | <0.01 | 0.331 | <0.01 | 0.75 | 0.416 | 1.27 | 0.239  | 0.286  | <0.01 |
| PHB     | prohibitin                                                         | 0.419  | <0.01 | 0.591 | <0.01 | 0.388 | <0.01 | 0.79 | 0.524 | 1.3  | 0.009  | 0.17   | <0.01 |
| PLK1    | polo like kinase 1                                                 | 0.405  | <0.01 | 0.586 | <0.01 | 0.579 | <0.01 | 1.36 | 0.048 | 3.33 | <0.001 | 0.065  | 0.12  |
| PLK4    | polo like kinase 4                                                 | 0.411  | <0.01 | 0.357 | <0.01 | 0.53  | <0.01 | 1.24 | 0.277 | 1.98 | <0.001 | 0.05   | 0.23  |
| PPAN    | peter pan homolog                                                  | 0.369  | <0.01 | 0.433 | <0.01 | -     | -     | 1.09 | 0.666 | -    | -      | 0.313  | <0.01 |
| PPRC1   | PPARG related coactivator 1                                        | 0.49   | <0.01 | 0.257 | <0.01 | 0.482 | <0.01 | 1.78 | 0.231 | 1.38 | 0.018  | 0.341  | <0.01 |
| PRMT3   | protein arginine methyltransferase 3                               | 0.108  | 0.2   | 0.235 | <0.01 | 0.339 | <0.01 | 0.89 | 0.728 | 1.06 | 0.658  | 0.192  | <0.01 |
| PUS1    | pseudouridine synthase 1                                           | 0.469  | <0.01 | 0.513 | <0.01 | 0.54  | <0.01 | 1.07 | 0.819 | 1.38 | 0.003  | 0.146  | <0.01 |
| RABEPK  | Rab9 effector protein with kelch motifs                            | 0.129  | 0.13  | 0.241 | <0.01 | 0.071 | <0.01 | 0.71 | 0.383 | 0.76 | 0.085  | -0.062 | 0.14  |
| RCL1    | RNA terminal phosphate cyclase like 1                              | 0.099  | 0.25  | 0.171 | <0.01 | 0.107 | <0.01 | 1.43 | 0.368 | 0.85 | 0.259  | 0.302  | <0.01 |
| RRP12   | ribosomal RNA processing 12 homolog                                | 0.288  | <0.01 | 0.591 | <0.01 | 0.576 | <0.01 | 1.76 | 0.152 | 1.28 | 0.056  | 0.173  | <0.01 |
| RRP9    | ribosomal RNA processing 9, U3 small nucleolar RNA binding protein | 0.496  | <0.01 | 0.565 | <0.01 | 0.453 | <0.01 | 1.09 | 0.8   | 1.2  | 0.393  | 0.231  | <0.01 |
| SLC19A1 | solute carrier family 19 member 1                                  | 0.21   | 0.01  | 0.58  | <0.01 | 0.631 | <0.01 | 1.37 | 0.19  | 1.55 | <0.001 | 0.193  | <0.01 |
| SLC29A2 | solute carrier family 29 member 2                                  | 0.294  | <0.01 | 0.401 | <0.01 | -     | -     | 0.91 | 0.597 | -    | -      | 0.267  | <0.01 |
| SORD    | sorbitol dehydrogenase                                             | 0.096  | 0.26  | 0.25  | <0.01 | 0.32  | <0.01 | 1.05 | 0.797 | 1.09 | 0.139  | -0.069 | 0.1   |
| SRM     | spermidine synthase                                                | 0.508  | <0.01 | 0.477 | <0.01 | 0.379 | <0.01 | 1.49 | 0.128 | 1.16 | 0.124  | 0.201  | <0.01 |
| SUPV3L1 | Suv3 like RNA helicase                                             | 0.514  | <0.01 | 0.428 | <0.01 | 0.426 | <0.01 | 1.47 | 0.07  | 1.64 | 0.002  | 0.173  | <0.01 |
| TBRG4   | transforming growth factor beta regulator 4                        | -0.228 | <0.01 | 0.66  | <0.01 | 0.517 | <0.01 | 2.01 | 0.03  | 1.46 | <0.001 | 0.22   | <0.01 |
| TCOF1   | treacle ribosome biogenesis factor 1                               | 0.216  | 0.01  | 0.46  | <0.01 | 0.173 | <0.01 | 1.32 | 0.479 | 1.3  | 0.412  | 0.155  | <0.01 |
| TFB2M   | transcription factor B2, mitochondrial                             | 0.291  | <0.01 | 0.227 | <0.01 | 0.161 | <0.01 | 1.61 | 0.149 | 0.95 | 0.554  | -0.029 | 0.49  |



|               |                                                     |       |       |       |       |       |       |      |       |      |        |       |       |
|---------------|-----------------------------------------------------|-------|-------|-------|-------|-------|-------|------|-------|------|--------|-------|-------|
| <b>TMEM97</b> | <b>transmembrane protein 97</b>                     | 0.382 | <0.01 | 0.499 | <0.01 | 0.562 | <0.01 | 0.76 | 0.19  | 1.37 | <0.001 | 0.16  | <0.01 |
| <b>UNG</b>    | <b>uracil DNA glycosylase</b>                       | 0.479 | <0.01 | 0.472 | <0.01 | 0.464 | <0.01 | 1.02 | 0.963 | 1.3  | 0.004  | 0.106 | 0.01  |
| <b>UTP20</b>  | <b>UTP20 small subunit<br/>processome component</b> | 0.044 | 0.61  | -0.01 | 0.81  | 0.136 | <0.01 | 1.06 | 0.822 | 1.12 | 0.763  | 0.095 | 0.02  |
| <b>WDR43</b>  | <b>WD repeat domain 43</b>                          | 0.453 | <0.01 | 0.191 | <0.01 | 0.402 | <0.01 | 1.37 | 0.42  | 1.44 | 0.025  | 0.31  | <0.01 |
| <b>WDR74</b>  | <b>WD repeat domain 74</b>                          | 0.583 | <0.01 | 0.548 | <0.01 | 0.457 | <0.01 | 1.01 | 0.967 | 1.35 | 0.003  | 0.219 | <0.01 |

**Note:** For each gene, correlation was performed with proliferation score in all cohorts and R value as well as *p* value are shown. COX analysis was performed to examine survival difference in TCGA and METABRIC cohorts and hazard ratio (HR) and *p* value are shown for each gene. Correlation analysis was performed for each gene using TCGA cohort in order to quantify the positive or negative impact of each target gene on the overall MYC score. Spearman R value and *p* value for each gene is shown.

**Table S3:** Baseline patient demographics and clinical characteristics of TCGA cohort

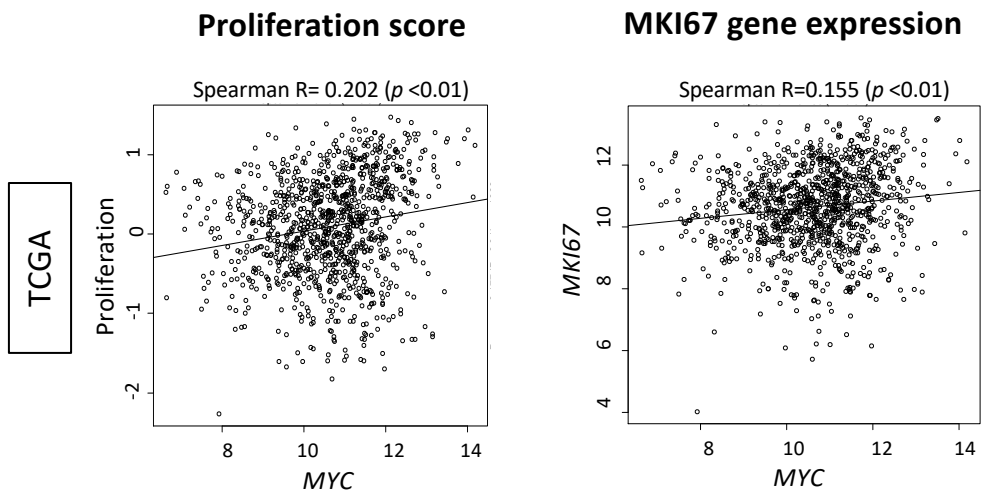
| TCGA              | MYC v1 |       |                | MYC v2 |       |                |
|-------------------|--------|-------|----------------|--------|-------|----------------|
|                   | Low    | High  | <i>p</i> value | Low    | High  | <i>p</i> value |
|                   | 713    | 352   |                | 713    | 352   |                |
| <b>Age</b>        |        |       | 0.07           |        |       | 0.056          |
| Median            | 59     | 56    |                | 59     | 56    |                |
| IQR               | 49-67  | 48-67 |                | 49-67  | 48-67 |                |
| <b>Subtype</b>    |        |       | <0.001         |        |       | <0.001         |
| ER+/HER2-         | 459    | 120   |                | 459    | 120   |                |
| TNBC              | 106    | 69    |                | 102    | 73    |                |
| HER2+             | 55     | 104   |                | 52     | 107   |                |
| Unknown           | 93     | 59    |                | 100    | 52    |                |
| <b>AJCC</b>       |        |       |                |        |       |                |
| <b>T-category</b> |        |       | <0.001         |        |       | 0.001          |
| T1                | 209    | 64    |                | 207    | 66    |                |
| T2                | 386    | 227   |                | 385    | 228   |                |
| T3                | 95     | 42    |                | 96     | 41    |                |
| T4                | 22     | 16    |                | 24     | 14    |                |
| Unknown           | 1      | 3     |                | 1      | 3     |                |
| <b>N-category</b> |        |       | 0.03           |        |       | 0.065          |
| N-                | 321    | 183   |                | 323    | 181   |                |
| N+                | 379    | 161   |                | 376    | 164   |                |
| Unknown           | 13     | 8     |                | 14     | 7     |                |
| <b>M-category</b> |        |       | 1              |        |       | 0.812          |
| M-                | 587    | 297   |                | 598    | 286   |                |
| M+                | 13     | 7     |                | 13     | 7     |                |
| Unknown           | 113    | 48    |                | 102    | 59    |                |
| <b>Stage</b>      |        |       | 0.019          |        |       | 0.053          |
| I                 | 135    | 43    |                | 132    | 46    |                |
| II                | 383    | 219   |                | 384    | 218   |                |
| III               | 166    | 76    |                | 168    | 74    |                |
| IV                | 12     | 6     |                | 12     | 6     |                |
| Unknown           | 17     | 8     |                | 17     | 8     |                |
| <b>Grade</b>      |        |       | <0.001         |        |       | <0.001         |
| G1                | 68     | 8     |                | 65     | 11    |                |
| G2                | 233    | 28    |                | 228    | 33    |                |
| G3                | 107    | 123   |                | 104    | 126   |                |
| Unknown           | 305    | 193   |                | 316    | 182   |                |

**Table S4:** Baseline patient demographics and clinical characteristics of METABRIC cohort

| METABRIC          | MYC v1 |       |                | MYC v2 |       |                |
|-------------------|--------|-------|----------------|--------|-------|----------------|
|                   | Low    | High  | <i>p</i> value | Low    | High  | <i>p</i> value |
|                   | 1276   | 628   |                | 1276   | 628   |                |
| <b>Age</b>        |        |       | <0.001         |        |       | <0.001         |
| Median            | 63     | 59    |                | 63     | 60    |                |
| IQR               | 54-72  | 48-69 |                | 53-71  | 49-70 |                |
| <b>Subtype</b>    |        |       | <0.001         |        |       | <0.001         |
| ER+/HER2-         | 1006   | 349   |                | 1039   | 316   |                |
| TNBC              | 133    | 103   |                | 122    | 114   |                |
| HER2+             | 130    | 168   |                | 108    | 190   |                |
| Unknown           | 7      | 8     |                | 7      | 8     |                |
| <b>N category</b> |        |       | <0.001         |        |       | <0.001         |
| N-                | 711    | 281   |                | 708    | 284   |                |
| N+                | 565    | 346   |                | 568    | 343   |                |
| Unknown           | 0      | 1     |                | 0      | 1     |                |
| <b>Stage</b>      |        |       | 0.009          |        |       | <0.001         |
| 0                 | 2      | 2     |                | 3      | 1     |                |
| I                 | 345    | 130   |                | 368    | 107   |                |
| II                | 522    | 278   |                | 509    | 291   |                |
| III               | 68     | 47    |                | 71     | 44    |                |
| IV                | 5      | 4     |                | 5      | 4     |                |
| Unknown           | 334    | 167   |                | 320    | 181   |                |
| <b>Grade</b>      |        |       | <0.001         |        |       | <0.001         |
| G1                | 147    | 18    |                | 154    | 11    |                |
| G2                | 588    | 152   |                | 600    | 140   |                |
| G3                | 478    | 449   |                | 467    | 461   |                |
| Unknown           | 63     | 9     |                | 55     | 16    |                |

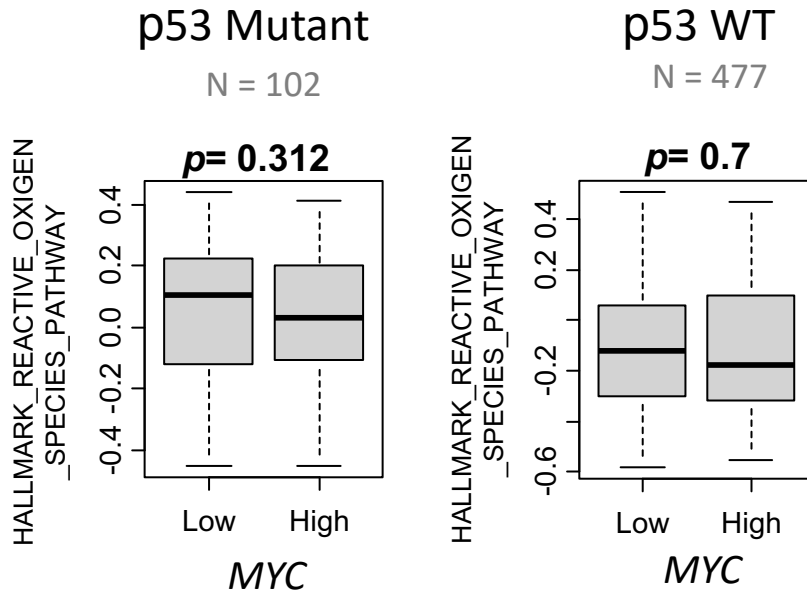
**Table S5:** Baseline patient demographics and clinical characteristics of GSE124647 cohort

| GSE124647         | MYC v1 |      |                | MYC v2 |      |                |
|-------------------|--------|------|----------------|--------|------|----------------|
|                   | Low    | High | <i>p</i> value | Low    | High | <i>p</i> value |
|                   | 94     | 46   |                | 94     | 46   |                |
| <b>Metastasis</b> |        |      | 0.237          |        |      | 0.569          |
| Local             | 9      | 10   |                | 12     | 7    |                |
| Lymph node        | 27     | 17   |                | 29     | 15   |                |
| Bone              | 10     | 1    |                | 10     | 1    |                |
| Liver             | 11     | 5    |                | 11     | 5    |                |
| Soft tissue       | 24     | 8    |                | 22     | 10   |                |
| Other             | 13     | 5    |                | 10     | 8    |                |

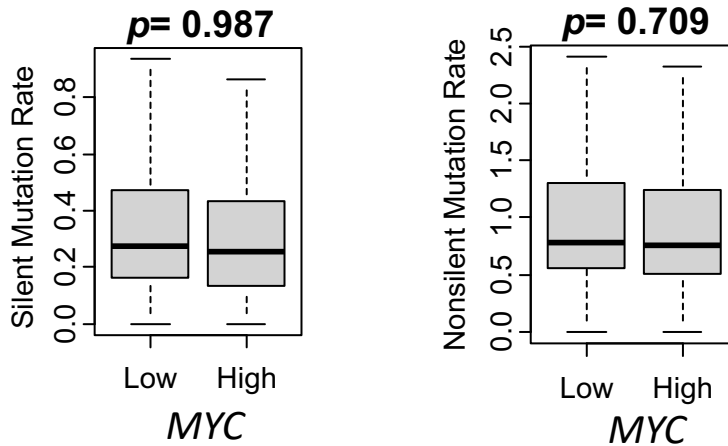


**Figure S1: MYC gene expression proliferation.** Correlation curve for TCGA cohort demonstrating significant correlation between MYC gene expression and proliferation score as well as MYC gene expression and MKI67 expression.

A



B



**Figure S2: MYC gene expression analysis (ER+/HER2-).** TCGA cohort was used to calculate high and low MYC gene expression for ER+/HER2- tumors. **(A)** High levels of gene expression was not significantly associated with increased reactive oxygen species in either p53 wildtype or mutant. **(B)** High levels of MYC expression was not significantly associated with silent or nonsilent mutation rates.