Supplementary file:

Bayesian Multilevel Regression Model Specifications for Subject-level Data at Baseline/Disease Progression

A Bayesian multilevel regression model was applied for the subject-level data separately at the time of baseline and disease progression. Let binary outcome Y_{ijk} denote the mutation status of gene *k* for the i^{th} patient in the j^{th} study, and X_j the moderators from j^{th} study, including the type of technology used to gather molecular information, and type of study which is either an observational or experimental study. Denote p_{ijk} the corresponding mutation probability of gene *k* for the i^{th} patient in the j^{th} study.

$$Y_{ijk} \sim Bernoulli(p_{\mathrm{ijk}})$$

$$logit(p_{ijk}) = log\left(\frac{p_{ijk}}{1-p_{ijk}}\right) = \mu + \alpha_i + \beta_j + \eta_k$$

where α_i is subject effect, β_j is study effect, and η_k is gene effect.

We assumed normal distributions on the regression coefficients,

$$\alpha_i \sim N(0, \sigma_\alpha^2),\ \beta_j \sim N\left(\beta_j^{tech} + \beta_j^{type}, \sigma_\beta^2\right),\ \ \eta_k \sim N\left(0, \sigma_\eta^2\right),$$

with X_j effects estimated by β_j^{tech} and β_j^{type} and a random error term. Weakly-informative *Cauchy* prior distributions [1] were applied on μ, β_j^{tech} and β_j^{type} and half-*Cauchy* prior distributions [2] on the standard deviations $\sigma_\alpha, \sigma_\beta, \sigma_\eta$.

$$\mu, \beta_j^{type}, \beta_j^{tech} \sim C(0, A = 2.5),$$

$$\sigma_\alpha, \sigma_\beta, \sigma_\eta \sim C^+(0, A = 2.5).$$

[1] Gelman, A., Jakulin, A., Pittau, M. G., & Su, Y. S. (2008). A weakly informative default prior distribution for logistic and other regression models. *The annals of applied statistics*, *2*(4), 1360-1383.
[2] Gelman, A. (2006). Prior distributions for variance parameters in hierarchical models. *Bayesian analysis*, *1*(3), 515-533.

33 Genes Identified in MCL Literature
Tumor Suppressor
TP53 (Tumor Protein P53)
RB1 (RB Transcriptional Corepressor 1)
DNA Damage Response
ATM (Ataxia Telangiectasia Mutated)
NOTCH Signaling Pathway
NOTCH1 (Notch homolog 1)
NOTCH2 (Notch homolog 2)
SPEN (Spen Family Transcriptional Repressor)
CDK Kinase Regulators
CCND1 (Cyclin D1)
CCND3 (Cyclin D3)
CDKN2A (Cyclin Dependent Kinase Inhibitor 2A)
Histone Modification/Epigenetic
KMT2D (Lysine Methyltransferase 2D)
KMT2C (Lysine Methyltransferase 2C)
KMT2A (Lysine Methyltransferase 2A)
NSD2 (Nuclear Receptor Binding SET Domain Protein 2)
BCOR (BCL6 Corepressor)
Apoptosis Regulators
BIRC3 (Baculoviral IAP Repeat Containing 3)
MYC (MYC Proto-Oncogene)
B-cell Receptor Signaling
CARD11 (Caspase Recruitment Domain Family Member 11) [NF-KB]
TRAF2 (TNF Receptor Associated Factor 2) [NF-KB; JNK]
MAP3K14 (Mitogen-Activated Protein KK Kinase 14)
BTK (Bruton Tyrosine Kinase)
Protein Ligase
UBR5 (Ubiquitin Protein Ligase E3 Component N-Recognin 5)
Myelopoiesis
TET2 (Tet Methylcytosine Dioxygenase 2)
Immune Response
IGH (immunoglobulin Heavy Locus)
MEF2B (Myocyte Enhancer Factor 2B)
SP140 (SP140 Nuclear Body Protein)
TLR2 (Toll Like Receptor 2)
S1PR1 (Sphingosine-1-Phosphate Receptor 1)
Chromatin Modification
SMARCA4 (SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 4)
ARID2 (AT-Rich Interaction Domain 2)
ARID1B (AT-Rich Interaction Domain 1B)
CHD2 (Chromodomain Helicase DNA Binding Protein 2)
Other
RIMS2 (Regulating Synaptic Membrane Exocytosis 2)
FAT4 (FAT Atypical Cadherin 4)