Integrative Network Analysis Identifies Novel Drivers of Pathogenesis and Progression in Newly Diagnosed Multiple Myeloma

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SUPPLEMENTARY FIGURES

Fig. S1 – Contribution of each of the experimental covariates.
Fig. S2 – Scale-free topology model fit for various soft threshold values ($\beta$). We chose $\beta = 4$, being the minimum value allowing to reach a scale-free topology fit index of at least 0.9.
Fig. S3 – Correlation between network modules’ eigengenes.
Fig. S4 - Association of coexpression modules with rISS disease stage and genomic alterations. Red indicates positive correlation of the module with respect to the corresponding trait (i.e. overall up-regulation of module activity in the presence of the alteration), blue indicates negative correlation. Grey indicates no significant associations. For somatic mutations, only genes from the top 50 significant associations are shown. Complete data is given as supplementary material.
Fig. S5 – Distribution of the number of mutations in the cohort.
Fig. S6 – Distribution of mutations in the cohort for top 100 mutated genes.

Fig. S7 – (A) Distribution of number of clones in the patient cohort. Clonality was estimated based on somatic mutations and copy number alterations. (B) High clonality (>4 clones) is associated with higher mutational burden. Significance was assessed by Wilcoxon Rank Sum test.
Fig. S8 – Clustering of cell lines based on the genes in module M16. The two cell lines chosen for validation of M16 hub genes, NCI-H929 and KMS-26, are in the module activation area.
Fig. S9 – Enrichment score of cell lines for genes in module M16 as calculated by GSVA (Gene Set Variation Analysis). Positive values indicate activation of the module, i.e. concordance with module eigengene. Red arrows indicate cell lines chosen for validation of M16 hub genes, NCI-H929 and KMS-26.
**Fig. S10** – Apoptosis assay (72h): (a) KMS-26 cells. (b) NCI-H929 cells.