cancers

Supplementary materials

Genetic Analysis of Multiple Myeloma Identifies Cytogenetic Alterations Implicated in Disease Complexity and Progression

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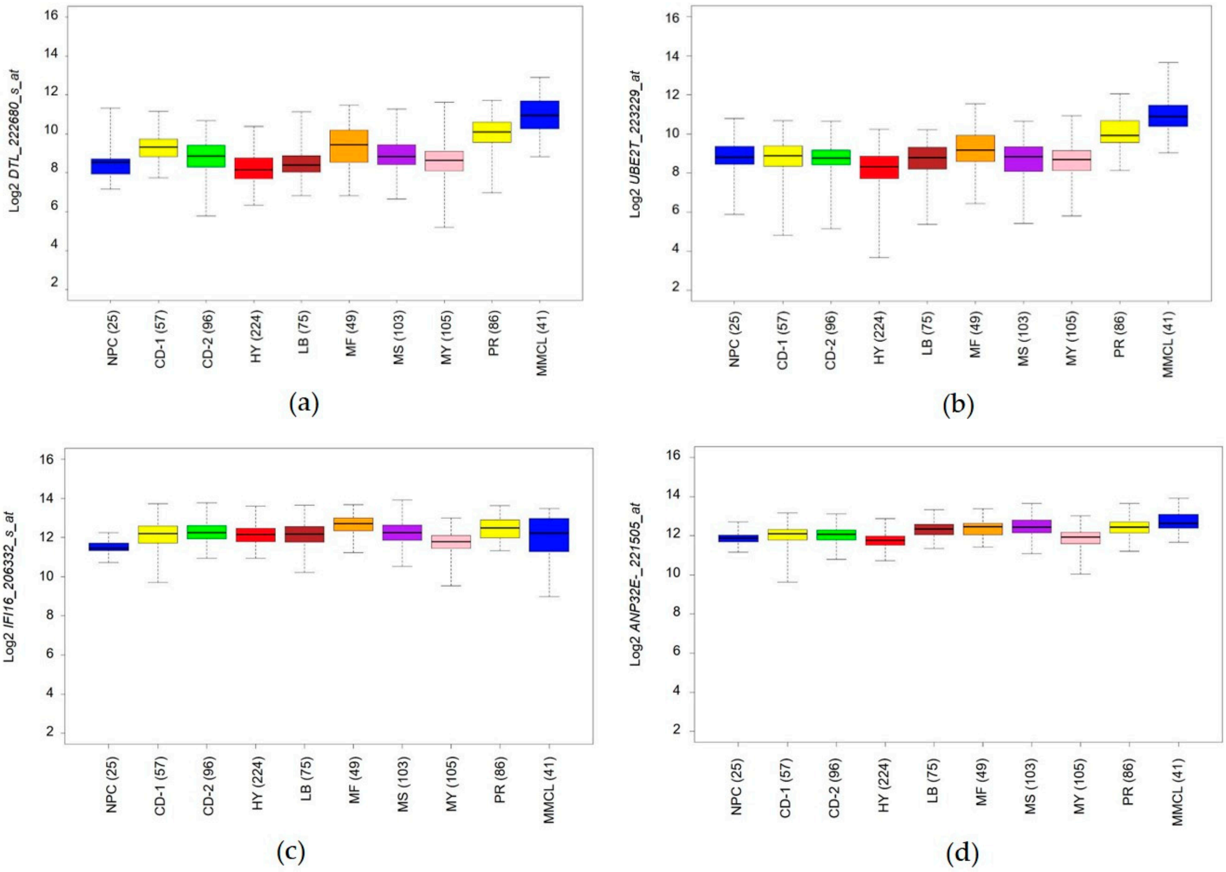
Table S1. Correlation between the TT2 and TT3 cohorts.

Subgroup	r^2	Slope
CD1	0.0035	y = 0.0956x + 1.1095
CD2	0.0394	y = 0.2896x + 0.9152
HY	0.0296	y = 0.3348x + 0.9085
LB	0.0713	y = 0.3553x + 0.915
MF	0.2041	y = 0.6034x + 0.354
MS	0.0373	y = 0.3265x + 0.7612
MY	0.1232	y = 0.5178x + 0.4635
PR	0.0819	y = 0.4078x + 0.6326

Correlation of gene expression intensity between the TT2 and TT3 cohorts in 8 subgroups from Figure 5b.



(a) (b)

(c) (d)

Figure S1. Gene expression of the four identified driver genes in molecular subgroups.Boxplots of the MAS5.0 transformed Affymetrix Signal for the four identified driver genes (a) DTL (b) UBE2T (c) IFI16 and (d) ANP32E in CD138-selected plasma cells isolated from bone marrow aspirates from healthy donors (NPC) and newly diagnosed MM (CD-1, CD-2, HY, LB, MF, MS, MY and PR). Also included are expression values from multiple myeloma cell lines (MMCL). The number of cases represented in each box plot is indicated by the number in parentheses above the sample identifier.