



Supplemental Figure 1: Quantitative, reverse transcription (RT) polymerase chain reaction (qRT-PCR) analysis of *FOXM1* gene expression in 8 myeloma patients for which 3 sequential CD138⁺ fractionated bone marrow tumor samples at baseline (white columns, newly diagnosed disease), initiation of HDT (high-dose therapy) and autologous hematopoietic stem cell transplantation (ASCT) therapy (grey columns) and consolidation / maintenance therapy (black columns) were available. In the course of the latter, three patients (1, 2 and 8) and one patient (7) experienced a clinically significant and incipient FOXM1^{High} relapse, respectively. Total RNA was extracted using Quick-RNA MiniPrep (Zymo Research) and reverse transcribed using oligo dT primers and SuperScript III RT (Invitrogen). Data analysis relied on the $\Delta\Delta C_t$ method. Primers were purchased from Integrated DNA Technologies (Coralville, Iowa). Sequences are available upon request. All increases in *FOXM1* gene expression are relative to the patient-specific baseline value, which was set at 1. All patients were consented in accordance with rules and regulations of the US Food and Drug Administration and the Declaration of Helsinki. Tumor samples were collected with institutional approval supplied with IRB 201503809 entitled “FOXM1 role in myeloma.”