Supplementary Information

Protocol for Microarray analysis and Quantitative RT-PCR (qPCR)

MM.1S, U266, and 8266R5 cells were treated with 20, 40, and 40 μM PRIMA-1^{Met}, respectively for 8 hrs and total RNA was isolated. Gene expression was analyzed with Illumina RNA analysis Beadchips (Illumina Inc. San Diego, CA) representing ~48,000 human genes (Human HT12) as described by us earlier.[28.29] Array data analysis was carried out with Bead Studio software as reported previously.[28,29] Genes showing at least a 2.0-fold difference in expression levels between control and PRIMA-1^{Met}-treated cells were considered to be modulated by PRIMA-1^{Met}. To quantify and validate the expression of p53 target genes of interest at their mRNA level, qRT-PCR assays using glyceraldehyde-3-phosphate dehydrogenase (GAPDH) as a reference gene were performed as described previously.[28,29]