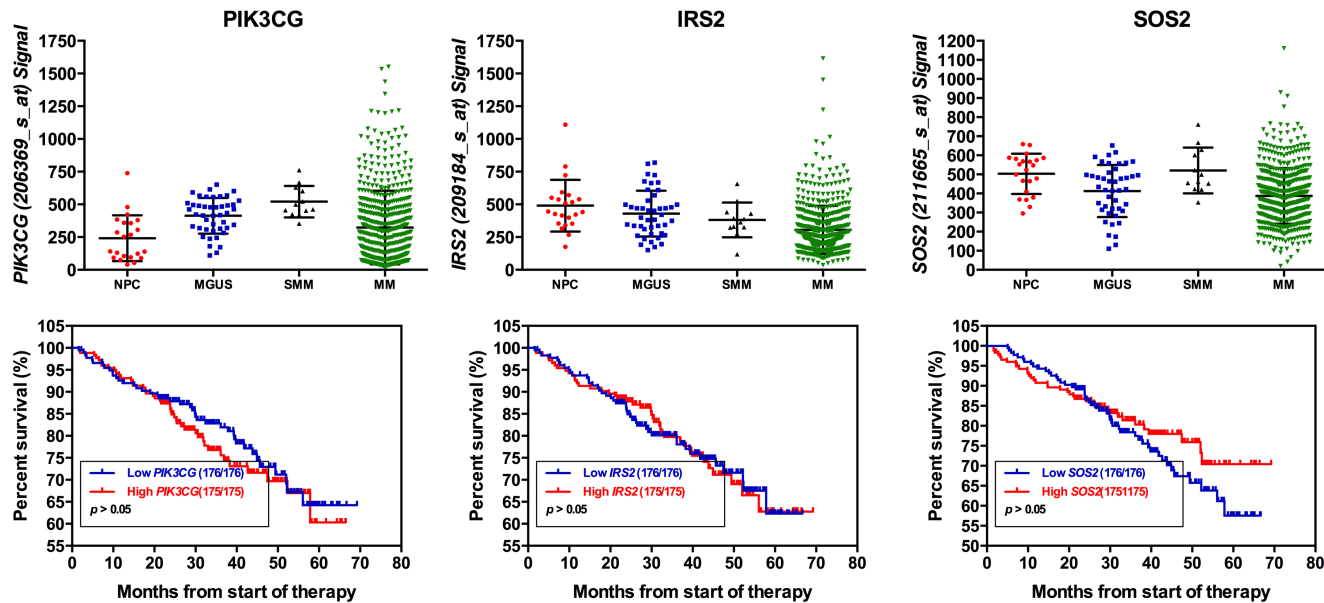
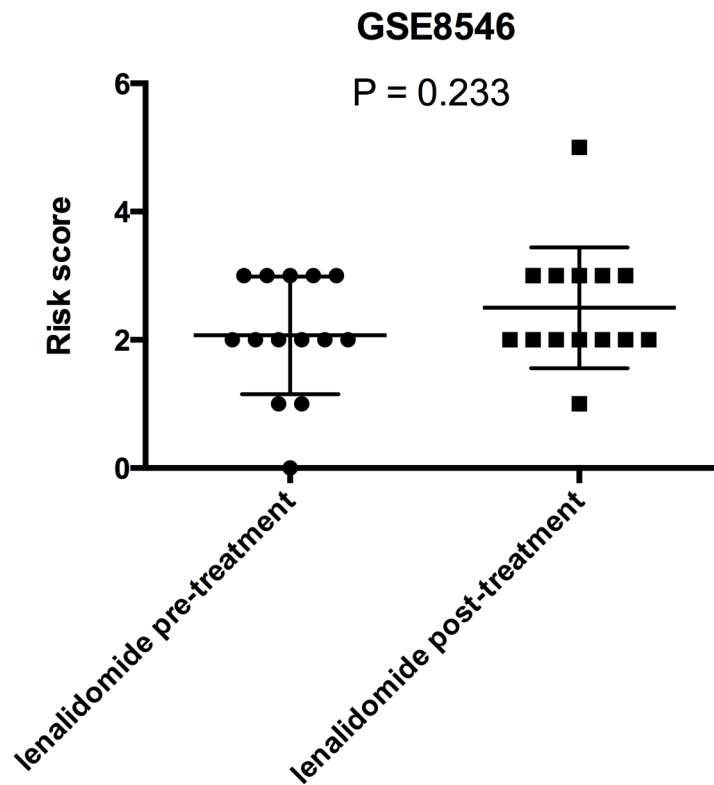


Significant Enriched Go Terms of down-regulated DEGs in SP cells based on their functions.



Gene expression of NP ( $n = 22$ ), MGUS ( $n = 44$ ), SMM ( $n = 12$ ) and MM ( $n = 559$ ) in GSE5900 and GSE2658 database (upper row). Kaplan-Meier analysis on the overall survival of MM patients in TT2 cohorts based on the gene expression (lower row).



The MMSP5 risk scores was significantly up regulated in lenalidomide-treated 15 paired patients

*GAPDH*

forward: 5-AACGTGT CAGTGGTGGACCTG-3,

reverse: 5-AGTGGGTGTCG CTGTTGAAGT-3;

*ROCK1*

forward: 5-AGGAAGGCGGACATATTAGTCCCT-3,

reverse: 5-AGACGATAGTTGGGTCCCGGC-3;

*GSK3B*

forward: 5-TGGCAGCAAGGTAACCACAG-3,

reverse: 5-CGGTTCTTAAATCGCTTGTCCTG-3;

*BRAF*

forward: 5-TCATAATGCTTGCTCTGATAGGA-3,

reverse: 5- GGCCAAAATTTAATCAGTGGA-3;

*MAPK1*

forward: 5-GTCGCCATCAAGAAAATCAGC-3,

reverse: 5-GGAAGGTTTGAGGTCACGGT-3;

*MAPK14*

forward: 5-CCCGAGCGTTACCAGAACC-3,

reverse: 5-TCGCATGAATGATGGACTGAAAT-3;