Supplementary Table 1 Bioinformatics researches related to t (4; 14) Multiple myeloma

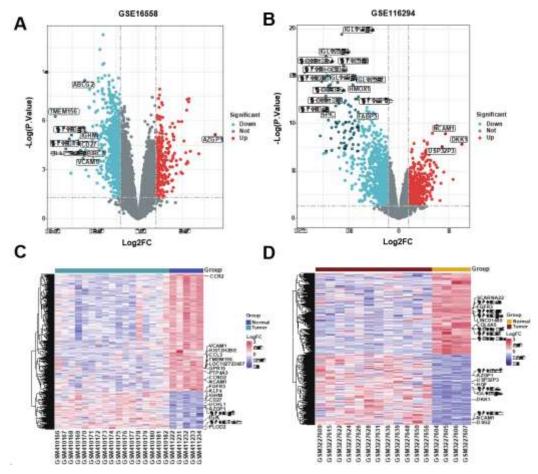
Study	Study	Study Objectives	Screening of	Molecular	In vivo	
Area			Drug	Docking	experimental	
			candidates		verification	
Enrica	t (4;14)	To explore miRNA regulatory networks in t (4;	NO	NO	NO	
et	MM	14) MM				
al.,2016						
Kai	t (4;14)	To investigate	NO	NO	Yes	
hong et	MM	the potential involvement of miRNA in t (4;14)				
al.2019		MM				
Hang et	MM	To Exploring potential drug targets and	Yes	NO	NO	
al., 2019		prognostic markers of MM				
Jin et	MM	To identify the most significantly molecular	NO	NO	NO	
al.,2019		pathways during MM progression				
Steven	MM	To explore the prognostic relevance of fusions of	NO	NO	NO	
et		MM				
al.,2020						

Cody et MM	To investigate the role of transcriptional	NO	NO	NO
al.,2022	deregulation by structural variants of MM			
Our t (4;14)	To explore small molecule drugs for the	Yes	Yes	Yes
Study MM	treatment of MM			

MM: multiple myeloma.

Supplementary Table 2 List of genome expression datasets analyzed in this study

S.no	Geo ID	Sample count (case: control)	Platform information	Tissues
			GPL6244, Affymetrix	
1.	GSE16558	17:5	Human Gene 1.0 ST	bone marrow
1.			Array	
			GPL25249, Affymetrix	
2.	GSE116294	15:4	Human Gene 2.0 ST	bone marrow
			Array	



Supplementary Figure 1 Differential gene expression in t(4;14) multiple myeloma samples versus controls. A: Volcano plot showing differentially expressed genes from GSE16558. Red indicates up-regulated genes; blue indicates genes that are down-regulated. B: Heatmap of the GSE16558 base genes comparing the control to t(4;14) multiple myeloma(MM) samples. Columns

represent samples; rows represent genes. Red denotes up-regulated differentially expressed genes(DEGs); blue denotes down-regulated DEGs. C: Volcano plot illustrating DEGs from GSE116294. Red indicates up-regulated genes; blue indicates down-regulated genes. D: Heatmap of the hub genes derived from GSE116294 comparing control to t(4;14) MM samples. Columns represent samples; rows represent genes. Red denotes up-regulated DEGs; blue denotes down-regulated DEGs.