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Supplementary Information for

Unraveling The Effects of *DICER1* Overexpression on Immune-Related Genes Expression in Mesenchymal Stromal/Stem Cells: Insights for Therapeutic Applications

Hamid Reza Bidkhori, M.D., Ph.D.[1], Moein Farshchian, Ph.D.[2, 3], Halimeh Hassanzadeh, M.Sc.[2], Reza Jafarzadeh Esfehani, M.D., Ph.D.[4], Reihaneh Alsadat Mahmoudian, Ph.D.[5, 6], Mahdi Moradi Marjaneh, M.D., Ph.D.[7], Houshang Rafatpanah, Ph.D.[1*]

1. Immunology Research Centre, Division of Inflammation and Inflammatory Diseases, Mashhad University of Medical Sciences, Mashhad, Iran
2. Stem Cells and Regenerative Medicine Department, Academic Center for Education, Culture, and Research (ACECR)-Khorasan Razavi, Iran
3. Division of Oncology, Laboratory of Cellular Therapy, Department of Medical and Surgical Sciences for Children and Adults, University Hospital of Modena and Reggio Emilia, Modena, Italy
4. Blood Borne Infections Research Center, Academic Center for Education, Culture, and Research (ACECR) - Khorasan Razavi, Iran
5. Basic Sciences Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
6. Cancer Research Center, Mashhad University of Medical Sciences, Iran
7. Department of Infectious Disease, Faculty of Medicine, Imperial College London, London, United Kingdom

Table S1: Primer sequences used in real-time polymerase chain reaction

Gene	Primer sequence (5´-3´)	Amplicon size (bp)
COX2	F: CCAGAGCAGGCAGATGAAATACC R: ACCAGAAGGGCAGGATACAGC	168
DDX58	F: TGTGCTCCTACAGGTTGTGGA R: CACTGGGATCTGATTCGCAAAA	120
IFIH1	F: TCGAATGGGTATTCCACAGACG R: GTGGCGACTGTCCTCTGAA	152
INF-γ	F: CTTTAAAGATGACCAGAGCATCCA R: GGCGACAGTTCAGCCATCAC	189
MYD88	F: ACTGCTCGAGCTGCTTACCAA R: CTCCTGCTGCTGCTTCAAGAT	106
RNaseL	F: GGCCTTCTGAACATTCCAAAAG R: TCCGGATGAACTTTAGCAGATC	141
TLR3	F: CAAACACAAGCATTCGGAATCTG R: AAGGAATCGTTACCAACCACATT	*145*
TLR4	F: AGTTGATCTACCAAGCCTTGAGT R: GCTGGTTGTCCCAAAATCACTTT	*94*
TDO2	F: ACCTCCGTGCTTCTCAGACAG R: GACCTCCTTTGCTGGCTCTATTC	*151*
TSG6	F: GCTGCTGGATGGATGGCTAAG R: CTCCTTTGCGTGTGGGTTGTAG	*156*
RPLP0	F: TGGTCATCCAGCAGGTGTTCGA R: ACAGACACTGGCAACATTGCGG	*119*

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*Corresponding Address: P.O.Box: 9177899191, Immunology Research Centre, Division of Inflammation and Inflammatory Diseases, Mashhad University of Medical Sciences, Mashhad, Iran
Email: RafatPanahH@mums.ac.ir

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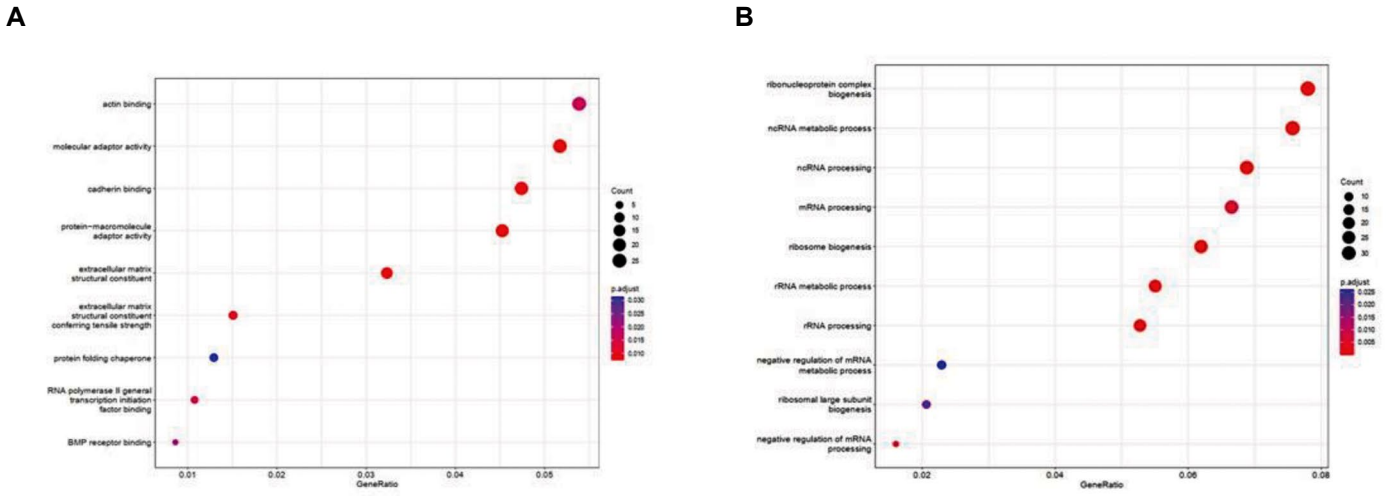

Fig.S1: Functional enrichment and pathway analysis of differential expression genes (DEGs). **A.** Gene Ontology (GO) annotations consist of molecular function (MF) enrichment analysis results of all module genes and **B.** Biological process (BP) enrichment analysis results of all module genes.

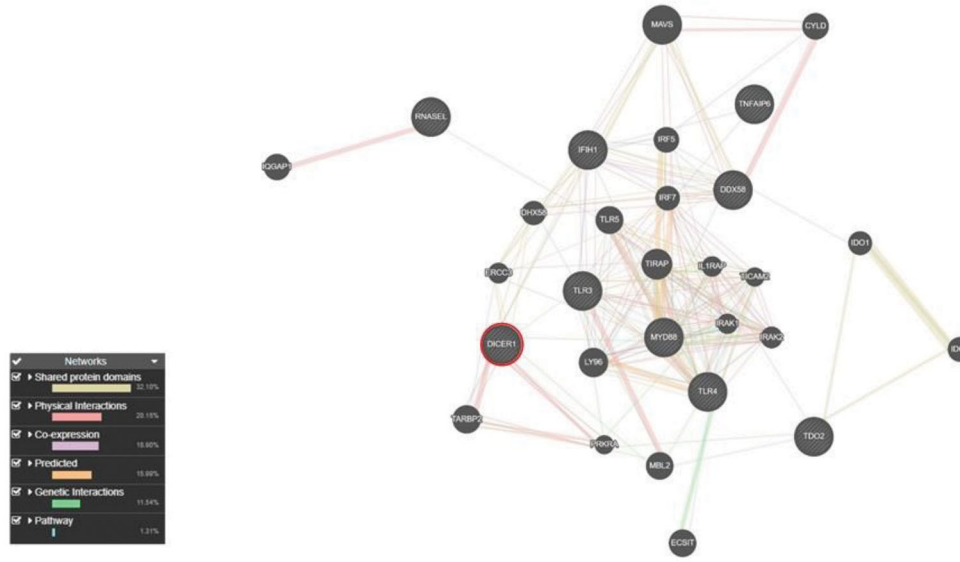

Fig.S2: The GeneMANIA network illustrates the closest interactions between DICER1 and other human genes. The line colors signify different types of connections, including shared protein domains, co-expression, co-localization, predictive and physical interactions with DICER1.