

Supplementary Table 3: Contribution of the 13 validated miRNAs in the most representative networks (KEGG, GO, GSEA). In green the up-regulated pathways, in orange those that resulted down-regulated (section of this Table is represented in **Figure 4B**). Of interest, miR-221-3p, miR-320a, miR-652-3p and miR-942-5p seem to down-regulate the same networks.

	hsa-let-7a-5p	hsa-let-7b-5p	hsa-miR-125a-5p	hsa-miR-148b-3p	hsa-miR-181a-5p	hsa-miR-182-5p	hsa-miR-185-5p	hsa-miR-221-3p	hsa-miR-25-3p	hsa-miR-320a	hsa-miR-652-3p	hsa-miR-942-5p	hsa-miR-99b-5p
Frequencies of canonical pathways (KEGG dataset)													
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	0	0,007	0	0	0,005	0	0	0,007	0	0,004	0	0	0,01
KEGG_LYSOSOME	0	0	0,008	0	0,005	0	0,004	0,01	0	0,002	0	0	0
PID_P38_MK2_PATHWAY	0	0	0	0	0	0	0	0,004	0	0,004	0,004	0,005	0
REACTOME_KERATAN_SULFATE_DEGRADATION	0	0,007	0	0	0,005	0	0	0,007	0	0,004	0	0	0,01
REACTOME_LYSOSOME_VESICLE_BIOGENESIS	0	0,007	0	0	0,005	0	0	0,007	0	0	0	0	0,01
REACTOME_SPHINGOLIPID_METABOLISM	0,001	0,009	0,001	0	0	0	0	0,003	0	0	0	0,005	0
Frequencies of biological processes (GO dataset)													
GO_MEMBRANE_LIPID_METABOLIC_PROCESS	0,001	0	0,007	0	0	0	0	0,002	0	0	0	0	0
GO_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	0,009	0,01	0	0	0	0,004	0	0,006	0,005	0	0	0,001	0
GO_SOMATIC_CELL_DNA_RECOMBINATION	0	0	0	0	0	0	0	0,004	0	0,004	0,004	0,005	0
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS	0	0	0	0	0	0	0	0,004	0	0,004	0,004	0,005	0
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_GERMLINE_RECOMBINATION_WITHIN_A_SINGLE_LOCUS	0	0	0	0	0	0	0	0,004	0	0,004	0,004	0,005	0
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNOGLOBULINS	0	0	0	0	0	0	0	0,004	0	0,004	0,004	0,005	0
GO_SOMATIC_RECOMBINATION_OF_IMMUNOGLOBULIN_GENE_SEGMENTS	0	0	0	0	0	0	0	0,004	0	0,004	0,004	0,005	0
GO_SPHINGOLIPID_METABOLIC_PROCESS	0,001	0	0,001	0	0	0	0	0,003	0	0	0	0	0
Frequencies of cellular components (GO dataset)													
GO_LYSOSOMAL_LUMEN	0	0,004	0	0,008	0	0	0	0,006	0,008	0	0	0,003	0
GO_LYTIC_VACUOLE	0	0,006	0,001	0	0	0	0	0	0	0	0	0	0,006
GO_PRESYNAPTIC_MEMBRANE	0	0,001	0	0	0	0	0	0,002	0	0	0	0,002	0
GO_VACUOLAR_LUMEN	0	0,004	0	0,008	0	0	0	0,006	0,008	0	0	0,003	0
GO_VACUOLE	0,006	0	0	0	0,006	0	0	0	0	0	0	0	0
Frequencies of molecular functions (GO dataset)													
GO_ATPASE_ACTIVATOR_ACTIVITY	0,008	0,009	0,008	0,009	0	0,01	0,007	0	0,008	0,006	0,009	0	0
GO_ATPASE_BINDING	0,008	0,009	0	0	0	0,01	0,007	0	0	0,006	0	0	0
GO_ATPASE_REGULATOR_ACTIVITY	0	0	0,008	0	0	0	0	0	0	0,006	0,009	0	0
GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	0	0	0	0	0	0	0	0,002	0	0	0,003	0,001	0
GO_MITOGEN_ACTIVATED_PROTEIN_KINASE_KINASE_BINDING	0	0	0	0	0	0	0	0,002	0	0	0,003	0,001	0
GO_SULFURIC_ESTER_HYDROLASE_ACTIVITY	0	0	0	0	0,008	0	0	0	0	0,006	0	0	0
Immunological signatures (GSEA)													
GSE10325_LUPUS_BCELL_VS_LUPUS_MYELOID_DN	0	0,002	0	0	0,006	0,001	0,003	0	0	0	0	0,006	0,006
GSE10325_LUPUS_CD4_TCELL_VS_LUPUS_MYELOID_DN	0	0,005	0	0,004	0	0	0,003	0	0	0	0	0	0,007
GSE15330_HSC_VS_GRANULOCYTE_MONOCYTE_PROGENITOR_IKAROS_KO_UP	0,003	0,002	0,006	0	0	0,007	0	0	0	0	0,004	0	0
GSE22886_NAIVE_CD8_TCELL_VS_DC_DN	0,007	0,002	0,007	0	0	0,007	0	0	0,01	0,01	0	0,002	0
GSE22886_NAIVE_TCELL_VS_MONOCYTE_DN	0,004	0	0,008	0	0	0,001	0,001	0	0	0	0	0	0
GSE29614_CTRL_VS_DAY3_TIV_FLU_VACCINE_PBMC_DN	0,008	0,009	0,008	0,009	0	0,01	0	0	0,008	0	0	0	0
GSE29614_DAY3_VS_DAY7_TIV_FLU_VACCINE_PBMC_UP	0,008	0	0,008	0,009	0	0,01	0,007	0	0,008	0,006	0	0	0
GSE29618_BCELL_VS_MDC_DN	0	0,001	0	0,002	0	0	0,006	0	0,004	0,005	0	0	0
GSE29618_BCELL_VS_MONOCYTE_DN	0	0,009	0	0	0	0,007	0	0,007	0	0	0	0	0
GSE29618_PDC_VS_MDC_DN	0,003	0,003	0	0	0	0	0	0	0,01	0,001	0,002	0	0
GSE45365_WT_VS_IFNAR_KO_CD11B_DC_DN	0	0,003	0,008	0,009	0	0	0,006	0	0	0,01	0,005	0	0
GSE9960_GRAM_NEG_VS_GRAM_POS_SEPSIS_PBMC_DN	0	0	0	0,004	0,002	0,001	0	0,009	0,01	0	0,009	0,003	0