Supplementary Tables and Figures

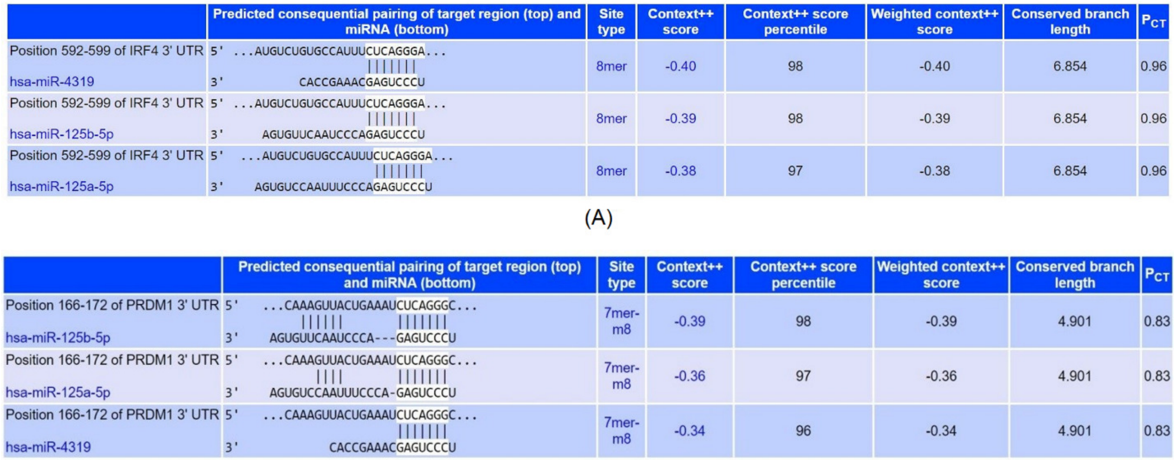
Table S1. Sequences of primers used for a reverse transcription-quantitative polymerase chain reaction

Gene symbol	Forward primer	Reverse primer
IRF4	GCTCTATGCGAAAAGACTGTG	**CCAAAGCATAGAGTCACCTGG**
BLIMP1	GGCTGAGTTTGAAGAGAAGTGT	**AACGTGTGCCCTTTGGTATG**
HPRT	CCTGGCGTCGTGATTAGTGAT	**AGACGTTCAGTCCTGTCCATAA**

Table S2: Correlation between demographics data and miR-125-5p expression

variables	miR-125b-5p expression
Age of onset, years	P: 0.153 r: 0.488
Delay of diagnosis, years	P: 0.356 r: -0.327
Course of disease, years	P: 0.156 r: -.0485
Follow-up, years	P: 0.342 r: -.0336
Age, years	P: 0.583 r: -0.198

*p-value <0.05 is statistically significant



<table>
<tr><th></th><th>Predicted consequential pairing of target region (top) and miRNA (bottom)</th><th>Site type</th><th>Context++ score</th><th>Context++ score percentile</th><th>Weighted context++ score</th><th>Conserved branch length</th><th>P_{CT}</th></tr>
<tr><td>Position 592-599 of IRF4 3' UTR
hsa-miR-4319</td><td>5' ...AUGUCUGUGCCAUUUCUCAGGGA...
|||||||
3' CACCGAAACGAGUCCCU</td><td>8mer</td><td>-0.40</td><td>98</td><td>-0.40</td><td>6.854</td><td>0.96</td></tr>
<tr><td>Position 592-599 of IRF4 3' UTR
hsa-miR-125b-5p</td><td>5' ...AUGUCUGUGCCAUUUCUCAGGGA...
|||||||
3' AGUGUUCAAUCCCAGAGUCCCU</td><td>8mer</td><td>-0.39</td><td>98</td><td>-0.39</td><td>6.854</td><td>0.96</td></tr>
<tr><td>Position 592-599 of IRF4 3' UTR
hsa-miR-125a-5p</td><td>5' ...AUGUCUGUGCCAUUUCUCAGGGA...
|||||||
3' AGUGUCCAAUUUCCCAGAGUCCCU</td><td>8mer</td><td>-0.38</td><td>97</td><td>-0.38</td><td>6.854</td><td>0.96</td></tr>
</table>

(A)

<table>
<tr><th></th><th>Predicted consequential pairing of target region (top) and miRNA (bottom)</th><th>Site type</th><th>Context++ score</th><th>Context++ score percentile</th><th>Weighted context++ score</th><th>Conserved branch length</th><th>P_{CT}</th></tr>
<tr><td>Position 166-172 of PRDM1 3' UTR
hsa-miR-125b-5p</td><td>5' ...CAAAGUUACUGAAAUCUCAGGGC...
|||||| |||||||
3' AGUGUUCAAUCCCA---GAGUCCCU</td><td>7mer-m8</td><td>-0.39</td><td>98</td><td>-0.39</td><td>4.901</td><td>0.83</td></tr>
<tr><td>Position 166-172 of PRDM1 3' UTR
hsa-miR-125a-5p</td><td>5' ...CAAAGUUACUGAAAUCUCAGGGC...
|||| |||||||
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</table>

(B)

Figure S1. pairing seed sequence of miR-125b-5p with 3′ UTRs *IRF-4 (A)* and *BLIMP-1(B)* genes is shown by Targetscan database respectively.

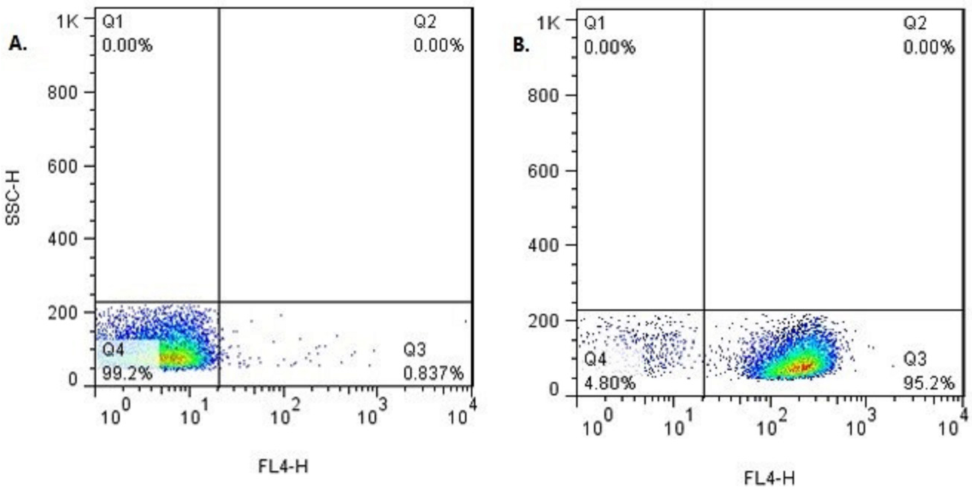

Figure S2: Flow cytometry results in detecting the purity of isolated B (A) lymphocytes Isotype B Cells (B).

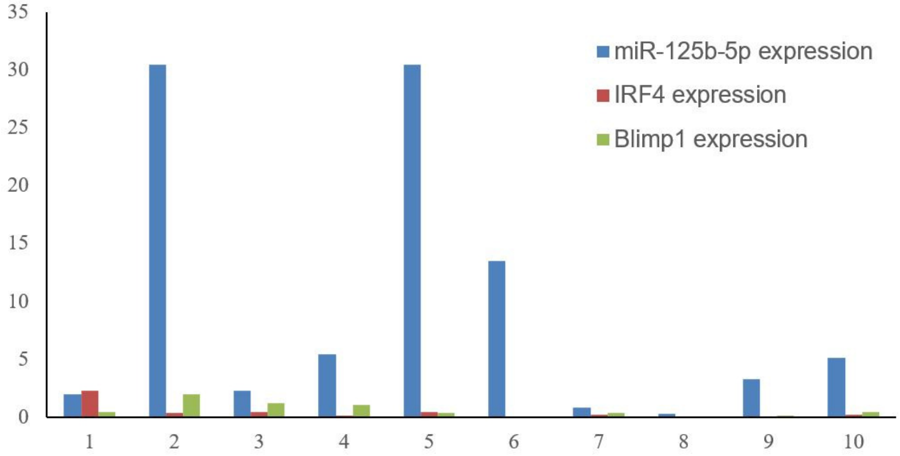

Figure S3: **Relative expressions of miR-125b, *IRF-4* and *BLIMP-1* in each CVID patient.**