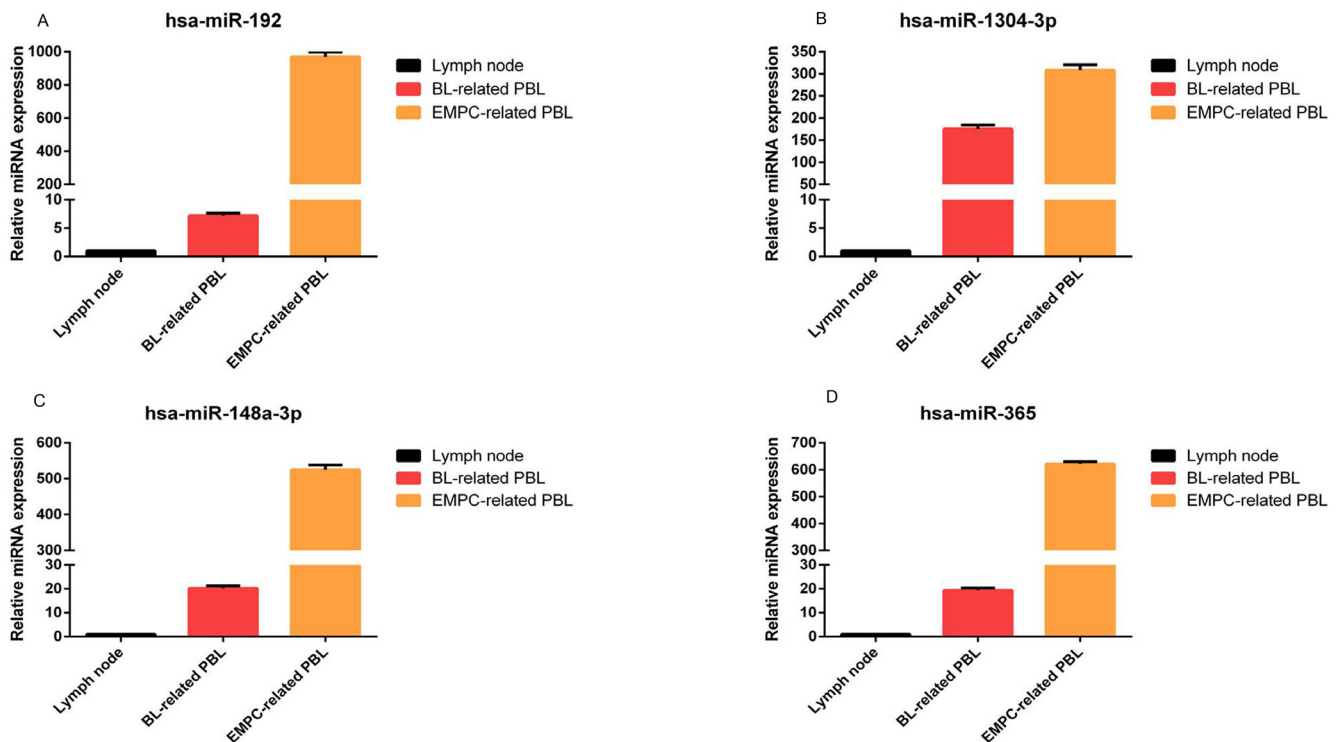


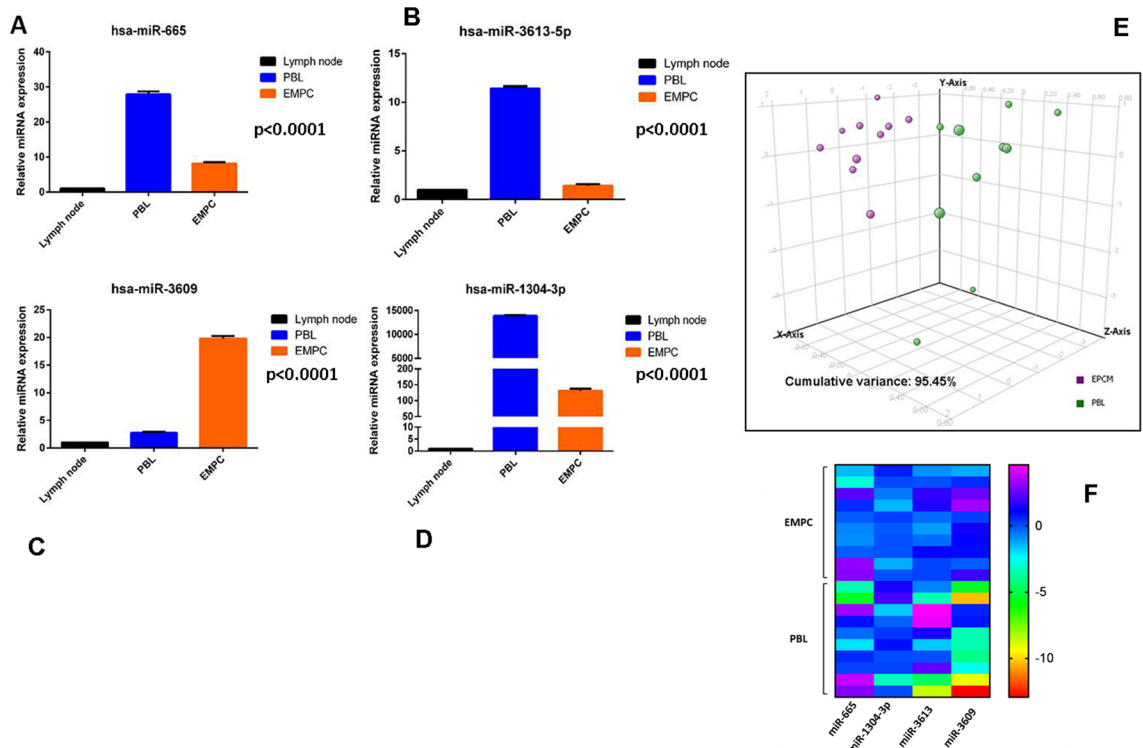
MicroRNAs sequencing unveils distinct molecular subgroups of plasmablastic lymphoma

SUPPLEMENTARY MATERIALS

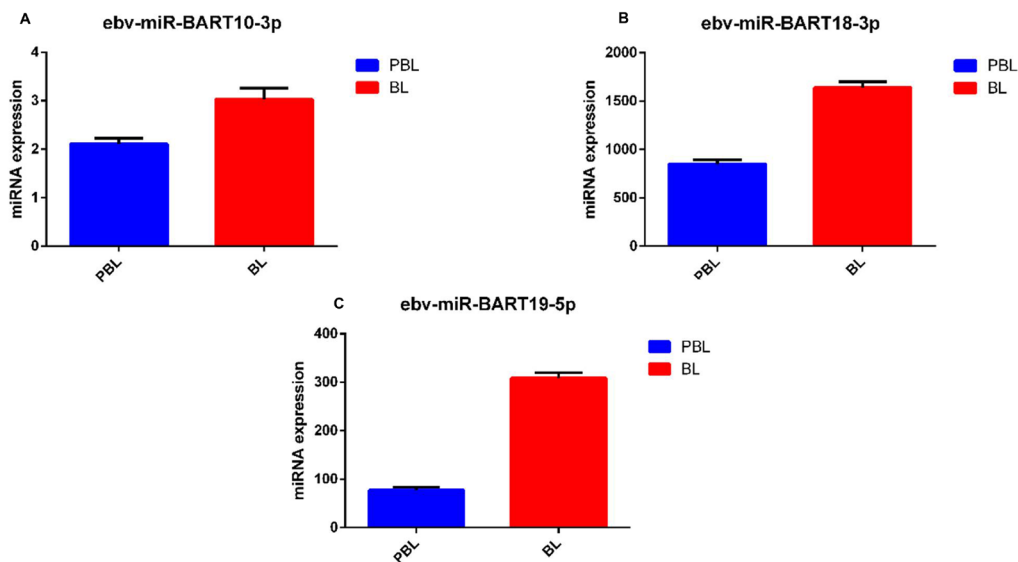
For Supplementary Tables see in Supplementary Files



Supplementary Figure 1: Differential expression of hsa-miR-192-5p (A), hsa-miR-1304-3p (B), hsa-miR-148a-3p (C) and hsa-miR-365-3p (D) expression in BL-related versus EMPC-related PBLs validation group. Values are expressed as mean \pm standard deviation (ST). Statistical significance was determined with Student's unpaired t-test ($p < 0.005$).



Supplementary Figure 2: hsa-miR-3613-5p, hsa-miR-1304-3p and hsa-miR-3609 expression in PBL versus EMPC validation cohort by using RT-qPCR (A). Values are expressed as mean \pm standard deviation (ST). Statistical significance was determined with Student's unpaired t-test ($p < 0.005$). Principal component analysis indicated that based on the expression of as few as 4 miRNAs (A-D), an independent set of cases was correctly classified as PBL or EPCM, the two entities being clearly distinct (E). Based on the expression of such miRNA, cases were then clustered (F)



Supplementary Figure 3: EBV-viral miRNAs (EBV-miR-Bart10-3p (A), EBV-miR-18-3p (B), EBV-miR-19-5p (C)) expression in PBL versus BL validation sets by using RT-qPCR. Values are expressed as mean \pm standard deviation (ST). Statistical significance was determined with Student's unpaired t-test ($p < 0.005$).