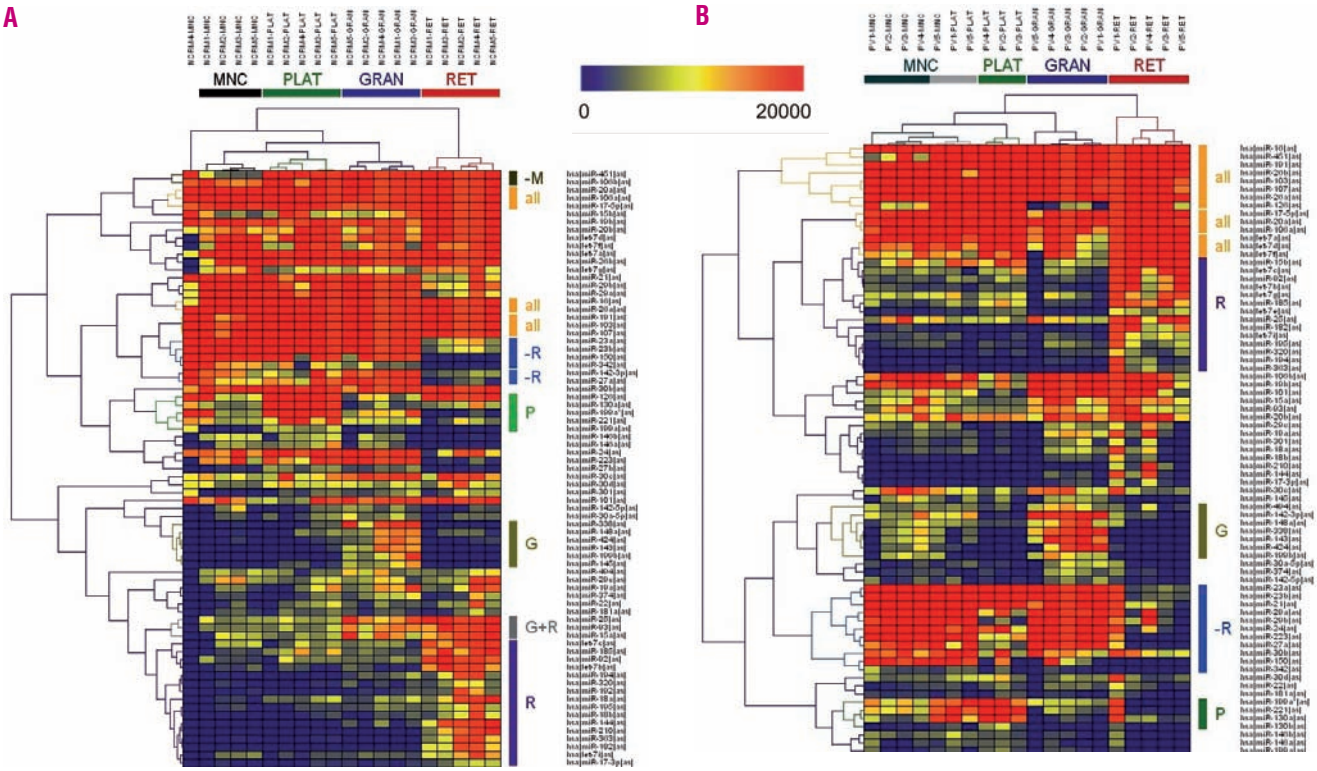
# Aberrant expression of microRNA in polycythemia vera

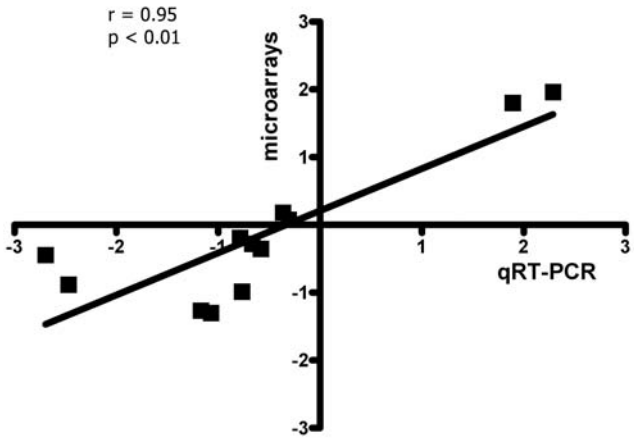
Hana Bruchova,[1,2] Michaela Merkerova,[2] and Josef T. Prchal[1,3]

[1]School of Medicine, University of Utah, Salt Lake City, UT, USA; [2]Institute of Hematology and Blood Transfusion, Prague and [3]Department of Pathophysiology, 1st School of Medicine, Charles University, Prague, Czech Republic

*Citation: Bruchova H, Merkerova M, and Prchal JT. Aberrant expression of microRNA in polycythemia vera. Haematologica 2008 doi: 10.3324/haematol.12706*




Supplementary Figure S1. MicroRNA signatures of normal and PV peripheral blood cells. Gene expression profiles of the cells were detected by CombiMatrix MicroRNA CustomArrays. The hierarchical clustering analysis determined distinctive miRNA expression clusters for particular cell lineages in controls (A) and PV patients (B). Each column represents a single sample and each row a particular miRNA. The relative gene expressions are expressed by a gradient intensity of color, as shown in the color scale at the top of the figure. The dark blue color indicates low expression and the lightest red color indicates maximal expression. The color bars on the right side of the heat map represent the cluster of miRNA specifically expressed in a particular cell lineage (all = high expression in all lineages, -M= low expression in mononuclear cells, -R = low expression in reticulocytes, R = high expression in reticulocytes, G = high expression in granulocytes, P = high expression in platelets). Seventy-five miRNA with the highest expression are shown. NORM: control, PV: polycythemia vera patient, MNC: mononuclear cells, PLAT: platelets, GRAN: granulocytes, RET: reticulocytes.




Supplementary Figure S2. Validation of microarray data by qRT-PCR. Expression of 12 miRNA was validated in specific cell lineages from five controls and five PV patients by qRT-PCR. Expression of particular miRNA detected by microarrays and qRT-PCR was averaged and relative ratios, controls versus PV patients, were calculated for both methods. The ratios obtained by microarrays and qRT-PCR were correlated to each other.