

**Supplementary Table VI. Expression change, *in silico* predicted effects, and genes predicted to be targeted by the commonly selected downregulated miRNA in the Relapse and Refractory DLBCL cohort of miRNA transcriptome analysis. The downregulated miRNA predicts to upregulate the genes responsible for cell cycle and replication. Fold change values are from the miRNA transcriptome analysis**

microRNA	Target gene predicted (increased expression)	Predicted effects on cell	Predicted function of micro-RNA	Fold change in relapse	Fold change in refractory
miR-193b-5p	Polymerase eta activation induced cytidinedeaminase DEAD/DEAH box RNA helicases	Error prone replication cell cycle	Tumour suppressor	- 4.6	-5
miR-326	BUB1 RELT CD10	NFKB Cell cycle error Cancer stem cell features	Tumour suppressor	-5	-6
miR-1307-5p	JAK1 TGFA PAIN	Increased tumour fitness Affects major BCR pathway genes	Tumour suppressor	-3	-3
miR-671-5p	CD4 IL-2R MAPKK	IL-2R, MAPK as poor prognostic marker in DLBCL	Tumour suppressor	-4.3	-5.8