## Table S1. 25 miRNAs that are up- or downregulated in MALT lymphoma compared to gastritis tissue

| upregulated miRNAs | P-value | Fold change | downregulated miRNAs | P-value | Fold change |
|---|---|---|---|---|---|
| miR-1224-5p | 0.025 | 2.318 | let-7a | 0.032 | 1.866 |
| miR-135a* | 0.028 | 1.774 | let-7f | 0.034 | 1.825 |
| miR-150 | 0.006 | 2.758 | miR-103 | 0.048 | 1.516 |
| miR-150* | 0.015 | 1.701 | miR-107 | 0.01 | 1.562 |
| miR-188-5p | 0.049 | 2.668 | miR-141 | 0.016 | 1.726 |
| miR-345 | 0.039 | 1.757 | miR-146a | 0.021 | 2.408 |
| miR-371-5p | 0.044 | 1.65 | miR-200a | 0.026 | 1.604 |
| miR-513b | 0.035 | 1.594 | miR-200b | 0.044 | 4.403 |
| miR-513c | 0.005 | 1.637 | miR-200c | 0.028 | 1.823 |
|  |  |  | miR-21 | 0.021 | 1.912 |
|  |  |  | miR-223 | 0.02 | 2.369 |
|  |  |  | miR-31 | 0.044 | 1.55 |
|  |  |  | miR-34a | 0.041 | 1.627 |
|  |  |  | miR-375 | 0.04 | 2.927 |
|  |  |  | miR-429 | 0.006 | 1.554 |
|  |  |  | miR-7 | 0.012 | 1.905 |

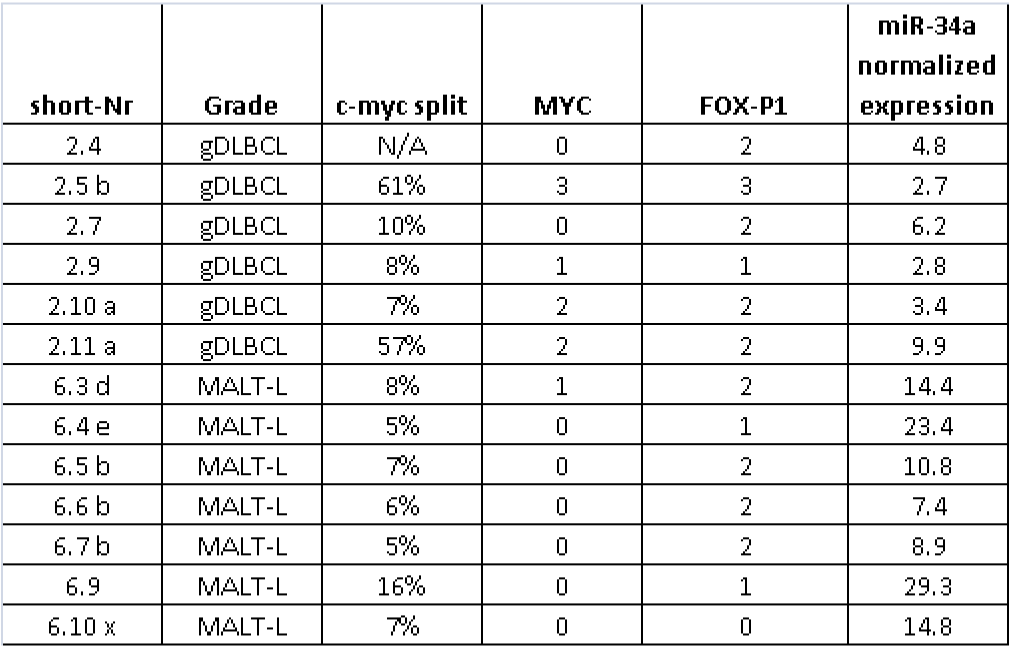
## Table S2. 88 miRNAs that are up- or downregulated in gastric DLBCL compared to MALT lymphoma

| upregulated miRNA | P-value | Fold change | downregulated miRNA | P-value | Fold change |
|---|---|---|---|---|---|
| miR-1224-5p | 0.024 | 1.988 | let-7a | <0.001 | 7.097 |
| miR-1225-3p | 0 | 1.615 | let-7b | 0.003 | 4.259 |
| miR-1225-5p | 0.002 | 3.55 | let-7c | 0.001 | 2.677 |
| miR-1226* | 0 | 1.88 | let-7d | 0.005 | 2.139 |
| miR-1228 | 0 | 2.461 | let-7e | 0.003 | 2.317 |
| miR-125a-3p | 0.001 | 2.405 | let-7f | <0.001 | 5.447 |
| miR-125b-1* | 0.021 | 1.933 | let-7g | <0.001 | 5.426 |
| miR-134 | 0.001 | 3.124 | let-7i | 0.002 | 2.344 |
| miR-135a* | 0.026 | 1.598 | miR-100 | 0.024 | 1.681 |
| miR-149* | 0.001 | 1.699 | miR-103 | 0.001 | 2.018 |
| miR-150* | 0 | 2.895 | miR-107 | <0.001 | 2.161 |
| miR-187* | 0.004 | 1.502 | miR-10a | 0.024 | 1.593 |
| miR-188-5p | 0.013 | 3.319 | miR-125b | 0.031 | 2.424 |
| miR-296-5p | 0 | 2.246 | miR-126 | 0.008 | 1.905 |
| miR-320a | 0.001 | 1.452 | miR-130a | <0.001 | 1.827 |
| miR-371-5p | 0 | 3.386 | miR-140-3p | 0.001 | 1.719 |
| miR-373* | 0 | 2.167 | miR-142-3p | 0.006 | 4.168 |
| miR-483-5p | 0.009 | 1.909 | miR-143 | 0.047 | 1.78 |
| miR-516a-5p | 0.013 | 1.52 | miR-145 | 0.029 | 2.916 |
| miR-557 | 0 | 2.328 | miR-146a | 0.027 | 1.829 |
| miR-572 | 0.017 | 3.188 | miR-150 | <0.001 | 8.726 |
| miR-575 | 0.005 | 1.838 | miR-151-5p | 0.001 | 1.924 |
| miR-601 | 0.002 | 1.782 | miR-15a | <0.001 | 2.431 |
| miR-623 | 0.003 | 1.624 | miR-15b | 0.013 | 1.947 |
| miR-630 | 0.01 | 3.211 | miR-16 | <0.001 | 4.679 |
| miR-638 | 0.027 | 4.148 | miR-192 | 0.019 | 3.761 |
| miR-659 | 0.003 | 1.752 | miR-194 | 0.044 | 2.361 |
| miR-663 | 0 | 2.321 | miR-195 | <0.001 | 2.815 |
| miR-671-5p | 0.02 | 2.9 | miR-199a-3p | <0.001 | 2.327 |
| miR-939 | 0.01 | 2.616 | miR-199a-5p | 0.002 | 1.669 |
| miR-99b* | 0.001 | 1.536 | miR-200a | 0.033 | 2.088 |
|  |  |  | miR-200b | 0.04 | 4.228 |
|  |  |  | miR-200c | 0.048 | 4.137 |
|  |  |  | miR-21 | 0.027 | 3.241 |
|  |  |  | miR-214 | 0.002 | 1.496 |
|  |  |  | miR-22 | 0.036 | 2.4 |
|  |  |  | miR-223 | <0.001 | 2.095 |
|  |  |  | miR-23a | <0.001 | 3.88 |
|  |  |  | miR-23b | <0.001 | 4.277 |
|  |  |  | miR-24 | <0.001 | 3.758 |
|  |  |  | miR-26a | <0.001 | 3.317 |
|  |  |  | miR-26b | <0.001 | 2.908 |
|  |  |  | miR-27a | 0.002 | 3.259 |
|  |  |  | miR-27b | 0.001 | 3.026 |
|  |  |  | miR-28-5p | 0.003 | 1.556 |
|  |  |  | miR-29a | <0.001 | 6.41 |
|  |  |  | miR-29b | <0.001 | 4.766 |
|  |  |  | miR-29c | <0.001 | 4.425 |
|  |  |  | miR-30a | 0.009 | 1.767 |
|  |  |  | miR-30b | 0.001 | 3.081 |
|  |  |  | miR-30c | 0.001 | 2.127 |
|  |  |  | miR-30e | 0.002 | 1.597 |
|  |  |  | miR-338-3p | 0.008 | 1.536 |
|  |  |  | miR-342-3p | 0.001 | 2.269 |
|  |  |  | miR-34a | 0.002 | 2.298 |
|  |  |  | miR-497 | <0.001 | 2.002 |
|  |  |  | miR-768-3p | <0.001 | 5.4 |

## Table S3. Expression and/or genetic changes of Bcl6, Myc, FoxP1 and p53 of all DLBCL and MALTL cases of a gastric lymphoma tissue microarray

| Diagnosis | BCL6 | MYC expression | FOXP1 expression | MYC FISH | FOXP1 breaks | FOXP1 gains | p53 expression/status |
|---|---|---|---|---|---|---|---|
| **DLBCL** | 3 | 3 | 0 | no break, disome | normal | normal | negative |
| **DLBCL** | 3 | 3 | 3 | no break, di- to tetraso | normal | normal | negative |
| **DLBCL** | 3 | 3 | 3 | no break, disome | normal | normal | negative |
| **DLBCL** | 3 | 3 | 3 | failed | failed | failed | negative |
| **DLBCL** | 3 | 3 | 3 | no break, disome | normal | normal | p53 5%+, p21- negative, mutation possible |
| **DLBCL** | 3 | 3 | 3 | N/A | N/A | N/A | p53 5%+, p21 not evaluable, mutation not excluded |
| **DLBCL** | 3 | 3 | 3 | failed | normal | normal | p53 5%+, p21- negative, mutation possible |
| **DLBCL** | 3 | 3 | 3 | no break, disome | normal | normal | negative |
| **DLBCL** | 3 | 3 | 3 | 1% breaks, below cut- | normal | normal | negative |
| **DLBCL** | 3 | N/A | N/A | no break, disome | normal | gained | negative |
| **DLBCL** | 3 | 3 | 0 | no break, disome | normal | normal | negative |
| **DLBCL** | 3 | 3 | 3 | no break, di- to trisome | normal | normal | negative |
| **DLBCL** | 3 | 3 | 0 | no break, disome | normal | normal | negative |
| **DLBCL** | 3 | 3 | 3 | 2% break, below cut-of | normal | normal | p53 20%+, p21 20%+, p53 upregulated |
| **DLBCL** | 3 | 3 | 2 | failed | normal | normal | p53 50%+, p21 1%+, p53 mutated |
| **DLBCL** | 2 | 3 | 2 | failed | failed | failed | negative |
| **DLBCL** | 2 | 3 | 3 | no break, disome | normal | normal | negative |
| **DLBCL** | 2 | 3 | 3 | N/A | N/A | N/A | negative |
| **DLBCL** | 2 | 2 | 3 | no break, disome | normal | gained | p53 5%+, p21 5%+, p53 upregulated |
| **DLBCL** | 0 | 2 | 3 | failed | normal | normal | negative |
| **DLBCL** | 0 | 2 | 3 | failed | failed | failed | negative |
| **DLBCL** | 0 | 3 | 3 | no tumor | no tumor | no tumor | negative |
| **DLBCL** | 0 | 3 | 0 | failed | normal | normal | negative |
| **DLBCL** | 0 | 0 | 3 | failed | normal | normal | negative |
| **DLBCL** | 0 | 3 | 0 | no break, disome | normal | normal | negative |
| **DLBCL** | 0 | 0 | 0 | failed | N/A | N/A | negative |
| **DLBCL** | 0 | N/A | 3 | no break, disome | normal | normal | p53 5%+, p21- negative, mutation possible |
| **DLBCL** | 0 | 3 | 3 | failed | failed | failed | p53 70%+, p21- negative, p53 mutated |
| **DLBCL** | 0 | 0 | 0 | no break, disome | normal | normal | negative |
| **DLBCL** | 0 | 0 | 0 | no break, disome | normal | normal | negative |
| **DLBCL** | 0 | 3 | 3 | failed | failed | failed | negative |
| **DLBCL** | 0 | 2 | 3 | failed | normal | normal | p53 70%+, p21 5%+, p53 mutation |
| **DLBCL** | 0 | N/A | N/A | failed | normal | normal | p53 5%+, p21- negative, mutation possible |
| **DLBCL** | 0 | N/A | 3 | failed | failed | failed | negative |
| **DLBCL** | 0 | 3 | 0 | no breaks, disome | normal | normal | p53 50%+, p21 15%+, p53 mutation not excluded |
| **DLBCL** | N/A | 3 | N/A | failed | failed | failed | negative |
| **DLBCL** | N/A | 2 | 3 | failed | failed | failed | negative |
| **DLBCL** | N/A | 3 | 3 | no break, disome | normal | gained | negative |
| **DLBCL** | N/A | 3 | N/A | failed | normal | gained | negative |
| **MALTL** | 2 | 2 | 2 | failed | failed | failed | negative |
| **MALTL** | 2 | 2 | 3 | no break, disome | normal | normal | p53 30%+, p21- negative, p53 mutated |
| **MALTL** | 2 | 2 | 0 | no break, disome | normal | normal | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 3 | failed | failed | failed | negative |
| **MALTL** | 0 | 2 | 2 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | N/A | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 2 | 0 | no break, disome | normal | normal | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 2 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 2 | 3 | failed | failed | failed | negative |
| **MALTL** | 0 | N/A | N/A | N/A | N/A | N/A | p53 30%+, p21- negative, p53 mutated |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | no break, disome | normal | normal | p53 50%+, p21 negative, p53 mutated |
| **MALTL** | 0 | 0 | 0 | no break | normal | normal | negative |
| **MALTL** | 0 | N/A | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | N/A | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | N/A | no break, trisome | normal | normal | negative |
| **MALTL** | 0 | 0 | 0 | no break, disome | normal | normal | p53 70%+, p21- negative, p53 mutated |
| **MALTL** | 0 | 2 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 3 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | no break, di- to trisome | normal | normal | p53 30%+, p21- negative, p53 mutated |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | N/A | N/A | N/A | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | no break, di- to trisome | normal | normal | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | p53 70%+, p21- negative, p53 mutated |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | p53 50%+, p21 negative, p53 mutated |
| **MALTL** | 0 | N/A | N/A | no break, disome | normal | normal | p53 30%+, p21 10%+, p53 upregulated, probably not mutated |
| MALTL | 0 |  | N/A | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | N/A | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 2 | no break, disome | no break, di | no break, | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | N/A | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 3 | 0 | no break, disome | normal | normal | negative |
| **MALTL** | 0 | 2 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 3 | N/A | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 0 | failed | failed | failed | negative |
| **MALTL** | 0 | 0 | 2 | failed | failed | failed | negative |
| **MALTL** | 0 | 3 | 0 | failed | failed | failed | p53 10%+, p21 5%+, no mutation |
| **MALTL** |  | 0 | 0 | no break, di- to tetraso | normal | normal | negative |

**Table S4. Expression and/or genetic status of Myc, FoxP1 and miR-34a of MALT lymphoma and gastric DLBCL cases used for microRNA expression profiling**



| short-Nr | Grade | c-myc split | MYC | FOX-P1 | miR-34a normalized expression |
|---|---|---|---|---|---|
| 2.4 | gDLBCL | N/A | 0 | 2 | 4.8 |
| 2.5 b | gDLBCL | 61% | 3 | 3 | 2.7 |
| 2.7 | gDLBCL | 10% | 0 | 2 | 6.2 |
| 2.9 | gDLBCL | 8% | 1 | 1 | 2.8 |
| 2.10 a | gDLBCL | 7% | 2 | 2 | 3.4 |
| 2.11 a | gDLBCL | 57% | 2 | 2 | 9.9 |
| 6.3 d | MALT-L | 8% | 1 | 2 | 14.4 |
| 6.4 e | MALT-L | 5% | 0 | 1 | 23.4 |
| 6.5 b | MALT-L | 7% | 0 | 2 | 10.8 |
| 6.6 b | MALT-L | 6% | 0 | 2 | 7.4 |
| 6.7 b | MALT-L | 5% | 0 | 2 | 8.9 |
| 6.9 | MALT-L | 16% | 0 | 1 | 29.3 |
| 6.10 x | MALT-L | 7% | 0 | 0 | 14.8 |

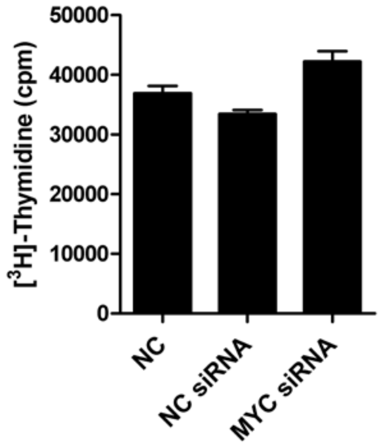


**Figure S1. siRNA-mediated knockdown of Myc in the marginal zone lymphoma cell line SSK41 does not reduce proliferation.** SSK41 cells were electroporated with a Myc-specific siRNA or a negative control (NC) siRNA 72 h prior to the quantification of proliferation by [$^3$H] thymidine incorporation.

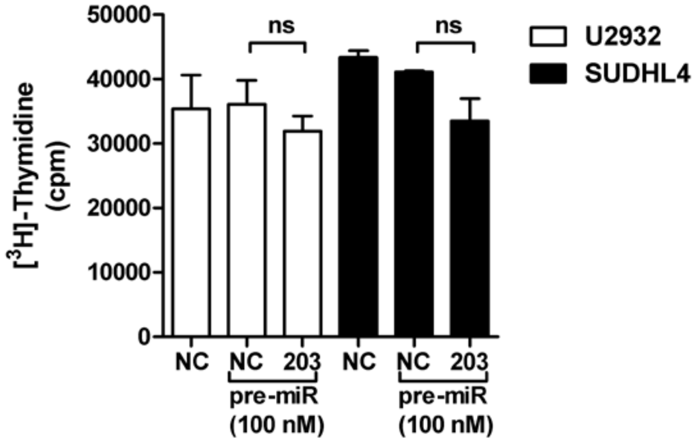


**Figure S2. Ectopic expression of miR-203 does not impair proliferation of DLBCL cell lines.** U2932 (white) and SUDHL-4 (black) cells were electroporated with pre-miR-203 or a scrambled negative control pre-miR (NC) 72 h prior to the quantification of proliferation by [$^3$H] thymidine incorporation.

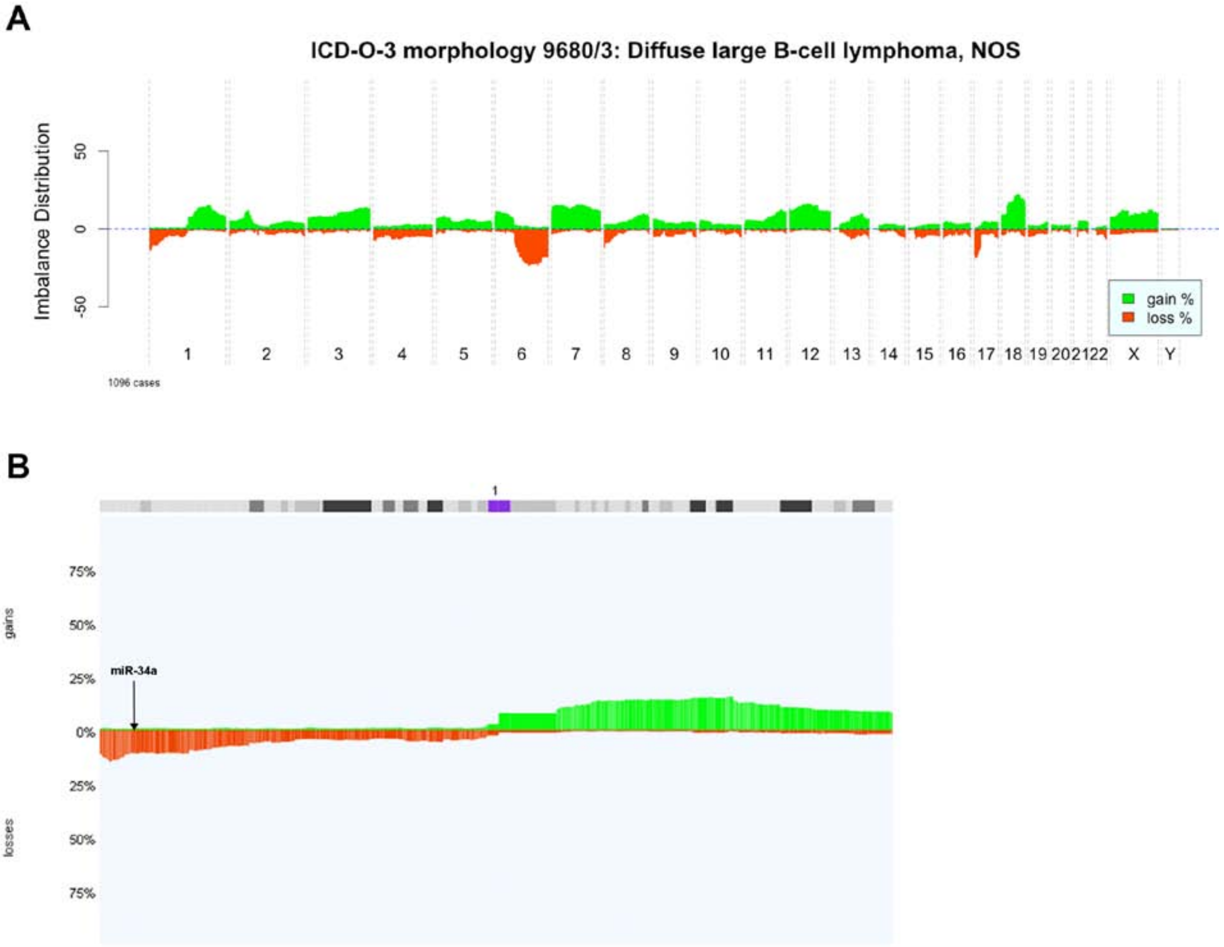


**Figure S3. The miR-34a locus resides in a commonly deleted region in DLBCL as reported from the CGH results of 1096 cases accessed through the Progenetix database.** (A) A summary of CGH profiling of 1096 cases of DLBCL from the Progenetix data collection. The histoplot reveals the most common sites of DNA copy number changes for each chromosome. The percentage of cases with gains (green) and losses (red) is indicated. (B) Histoplot depicting the CGH data for chromosome 1 in detail. The miR-34a locus is located on 1p36 and appears to be deleted in roughly 10% of all 1096 DLBCL cases analyzed.

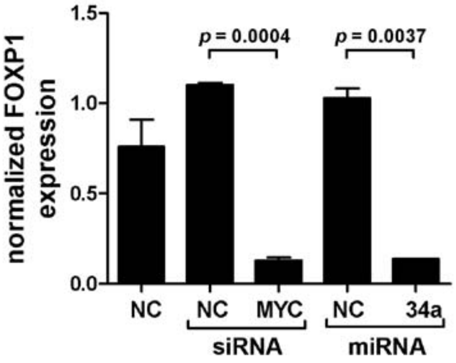


**Figure S4. siRNA-mediated knock-down of Myc reduces FoxP1 expression as efficiently as miR-34a re-introduction in DLBCL cells.** U2932 cells were electroporated with either a Myc-specific siRNA, pre-miR34a or the appropriate negative control (NC) oligonucleotides and analyzed with respect to FoxP1 expression 48 h later. FoxP1 transcript levels were normalized to GAPDH expression.

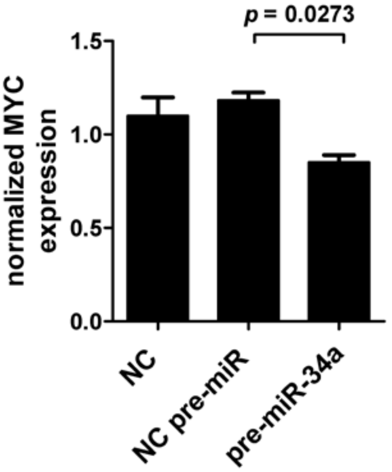


**Figure S5. miR-34a re-expression represses Myc in DLBCL cells.** U2932 cells were electroporated with pre-miR-34a or a scrambled negative control pre-miR (NC) oligonucleotide 48 h prior to the quantification of Myc expression by qPCR. Absolute expression was normalized to GAPDH.

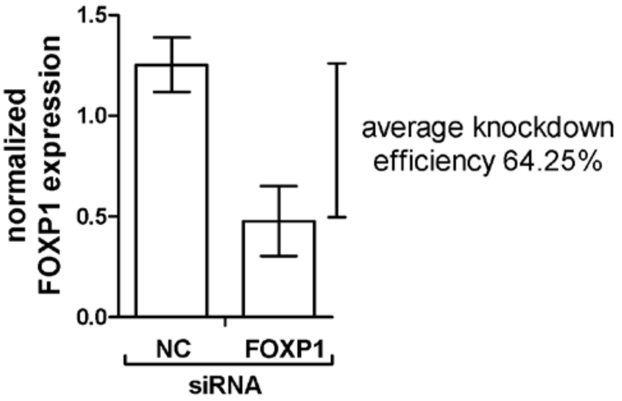


**Figure S6. Knockdown efficiency of FoxP1.** FoxP1 levels were assessed by qPCR 72 h following electroporation of U2932 cells with FoxP1-specific siRNA or negative control oligonucleotides. FoxP1 transcript levels were normalized to GAPDH expression. The error bars represent the SEM.

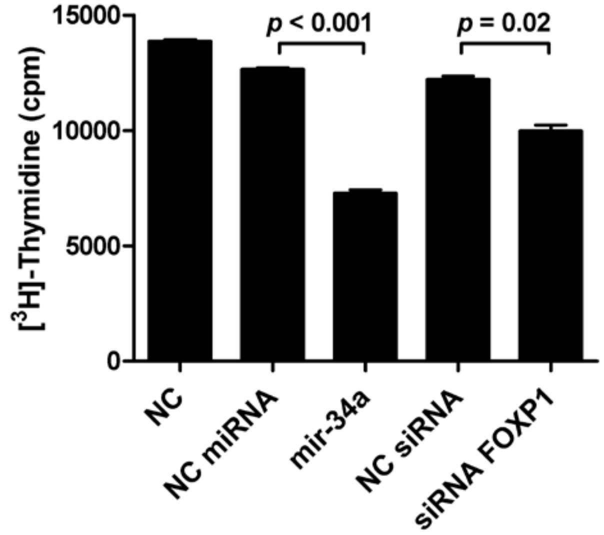


**Figure S7. Proliferation of indolent lymphoma cells was not reduced upon knock down of FoxP1 and only modestly reduced by miR-34a re-expression.** SSK41 cells were electroporated with either pre-miR-34a, FoxP1-specific siRNA or the respective negative control oligonucleotides 72 h prior to the quantification of proliferation by [$^3$H] thymidine incorporation.