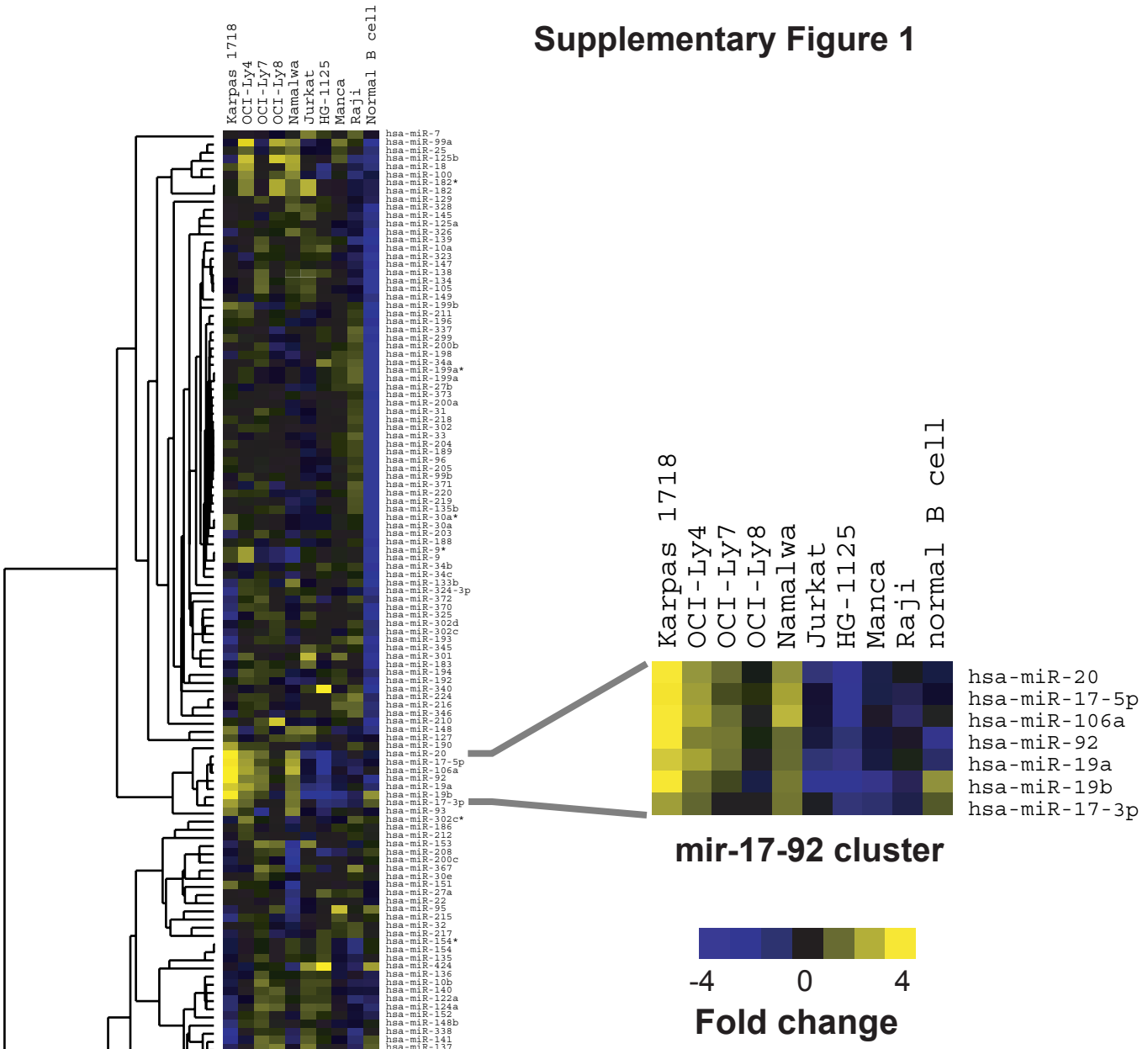
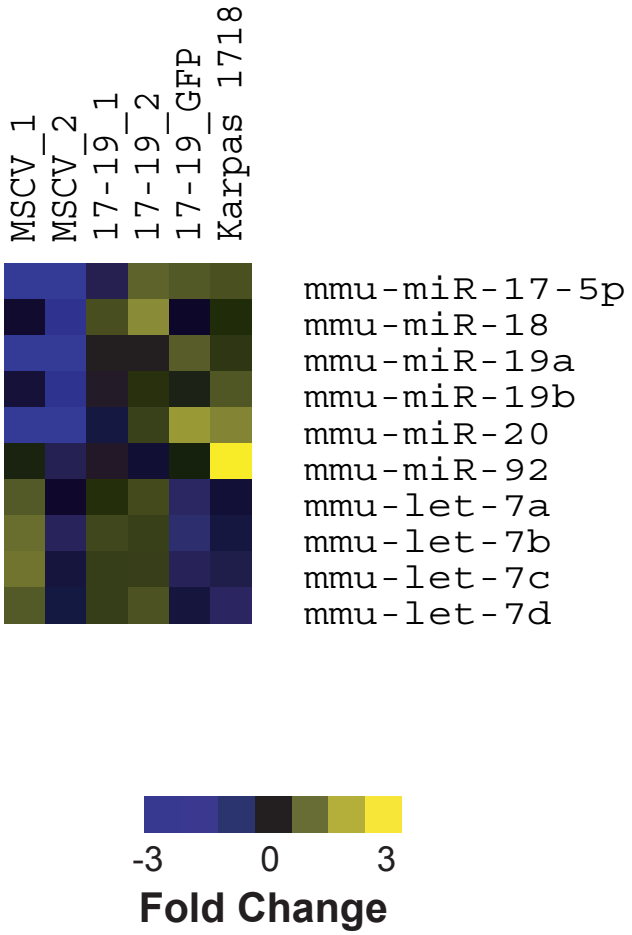
Supplementary Figure 1



Supplementary Figure 1. MicroRNA expression map of leukemia and lymphoma cell lines. MicroRNA expression levels in cell lines previously described to carry the 13q31-q32 amplicon, including Karpas 1718, OCI-Ly4, OCI-Ly7 and OCI-Ly8, were compared to those in leukemia and lymphoma cell lines lacking this genetic lesion and to normal B-cells isolated from cortical blood. Total RNA was labeled with Cy3 and hybridized to microarrays that contain probes to 191 human mature microRNAs. Background subtracted one-channel measurements were log transformed (base 2) and median center normalized. Four independent data sets for each cell line were collapsed by median, and hierarchically clustered by gene only. Yellow indicates high expression relative to the median and blue indicates low expression. The node that corresponds to the mir-17-92 locus is expanded on the right.

Supplementary Figure 2.



Supplementary Figure 2. Ectopic expression of mir17-92 in *E*μ-*myc/mir17-19b* B-cell lymphomas. MicroRNA expression from two control *E*μ-*myc/MSCV* lymphomas (MSCV_1, MSCV_2) and two *E*μ-*myc/mir17-19b* lymphomas (17-19_1, 17-19_2) was quantitated by microarray analysis. Also measured was microRNA expression levels for *E*μ-*myc/mir17-19b* lymphoma cells that were purified by FACS sorting for linked GFP expression (17-19_GFP). Total RNA was labeled with Cy3 and hybridized to microarrays that contain probes to 198 mouse mature microRNAs. Background subtracted one-channel measurements were log transformed (base 2) and median center normalized. Four independent data sets for each cell line were collapsed by median, except for 17-19_2 lymphoma, which had two data sets only. Karpas 1718, the cell line with the highest 13q31 amplification, is shown for comparison. The heat map indicates expression of each conserved (mouse/human) microRNA in the *mir17-92* locus, with four *let-7* microRNAs shown for comparison. Yellow indicates high expression relative to the median and blue indicates low expression.

Supplementary Table 1

Significant Genes List

Input Parameters

Imputation Engine	10-Nearest Neighbor Imputer
Data Type	Two Class, unpaired data
Data in log scale?	TRUE
Number of Permutations	100
Blocked Permutation?	FALSE
RNG Seed	1234567
(Delta, Fold Change)	(0.20243, 2.00000)
(Upper Cutoff, Lower Cutoff)	(1.65693, -∞)

Computed Quantities

Computed Exchangeability Factor S0	0.085654726
S0 percentile	0
False Significant Number (Median, 90 percentile)	(1.00000, 4.20000)
False Discovery Rate (Median, 90 percentile)	(16.66667, 70.00000)
Pi0Hat	1

6 Positive Significant Genes

Gene Name	Score(d)	Numerator(r)	Denominator(s+s0)	Fold Change	q-value (%)
hsa-miR-92	2.181254144	1.124125	0.515357187	2.34459	16.66666667
hsa-miR-19a	1.990500557	1.06695	0.53602095	2.12908	16.66666667
hsa-miR-20	1.925478851	1.304075	0.677273084	2.54907	16.66666667
hsa-miR-19b	1.887537933	1.33365	0.706555337	2.55144	16.66666667
hsa-miR-17-5p	1.729572125	1.126225	0.651158159	2.06056	16.66666667
hsa-miR-106a	1.656932745	1.2342	0.744870306	2.29774	16.66666667

Supplementary Table 1 Legend. Significance Analysis of Microarray (SAM) analysis of 13q31 amplicon cell lines. The normalized, collapsed data set from Supplementary Figure 1 was used for SAM analysis using 2-fold minimum change restriction. Data was divided into two classes based on published presence of the amplicon as follows: Karpas 1618, OCI-Ly4, OCI-Ly7, OCI-Ly8 positive; Namalwa, HG1125, Jurkat, Manca, Raji, Negative. Six positive significant genes and zero negative significant genes were identified using a delta value of 0.202. The false discovery rate was 17%.

Supplementary Table 2 : single miRNAs overexpressed in *Eμ-myc*/+ HSCs

Pool #	miRNA subset[a]	# of recepient animals	# of animals developed lyphoma by 6 months	# of GFP positive tumors[b]
1	mmu-mir-206 mmu-mir-30a mmu-mir-30c-2 mmu-mir-26b mmu-mir-135b mmu-mir-213 mmu-mir-199a-2 mmu-mir-350	3	3	0
2	mmu-mir-205 mmu-mir-129-2 mmu-mir-350 mmu-mir-126 mmu-mir-219-2 mmu-mir-130a mmu-mir-129-2 mmu-mir-103-2	3	1	0
3	mmu-mir-296 mmu-mir-124a-2 mmu-mir-15b mmu-mir-16-2 mmu-mir-302 mmu-mir-186 mmu-mir-32 mmu-mir-31	3	2	0
4	mmu-mir-101 mmu-mir-30c-1 mmu-mir-30e mmu-mir-200a mmu-mir-200b mmu-mir-25 mmu-mir-93 mmu-mir-106b	3	3	0
5	mmu-mir-339 mmu-mir-129-1 mmu-mir-96 mmu-mir-183 mmu-mir-29a mmu-mir-141 mmu-mir-200c mmu-mir-290	3	1	0
6	mmu-mir-291 mmu-mir-292	3	1	0

	mmu-mir-293 mmu-mir-295 mmu-mir-330 mmu-mir-150 mmu-mir-344 mmu-mir-211			
7	mmu-mir-7-2 mmu-mir-9-3 mmu-mir-326 mmu-mir-181c mmu-mir-23a mmu-mir-27a mmu-mir-24-2 mmu-mir-328	3	2	0
8	mmu-mir-140 mmu-mir-10a-2 mmu-mir-100 mmu-let-7a-2 mmu-mir-125b-1 mmu-mir-34c mmu-mir-34b mmu-mir-190	3	2	0
9	mmu-mir-184 mmu-let-7g mmu-mir-191 mmu-mir-26a-1 mmu-mir-331 mmu-let-7i mmu-mir-26a-2 mmu-mir-216	3	2	0
10	mmu-mir-217 mmu-mir-103-1 mmu-mir-340 mmu-mir-324 mmu-mir-195 mmu-mir-132 mmu-mir-22 mmu-mir-144	3	1	0
11	mmu-mir-193 mmu-mir-301 mmu-mir-142 mmu-mir-10a-2 mmu-mir-338 mmu-mir-342 mmu-mir-345 mmu-mir-337	3	1	0
12	mmu-mir-136	3	0	0

mmu-mir-329
hsa-mir-200b
hsa-mir-200a
hsa-mir-30c-1
hsa-mir-197
hsa-mir-214
hsa-mir-199a-2

[a] 8 individual MSCV constructs, each overexpressing a specific miRNA, were pooled at equal DNA concentration. The pooled DNA was used to produce vius to infect *Eμ-myc*/+ fetal liver cells for adoptive transfer.

[b] Recipient animals were monitored for at least 6 months for tumor growth. For those that developed lymphomas, tumor cells were prepared from the enlarged lymph nodes, and then subjected to FACS analysis for GFP expression. The GFP expression is an indication that the tumors are derived from transduced Em-myc/+ fetal liver cells.