

# 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, $-\infty$ )

### 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	16.6666667
hsa-miR-19a	1.990500557	1.06695	0.53602095	2.12908	16.6666667
hsa-miR-20	1.925478851	1.304075	0.677273084	2.54907	16.6666667
hsa-miR-19b	1.887537933	1.33365	0.706555337	2.55144	16.6666667
hsa-miR-17-5p	1.729572125	1.126225	0.651158159	2.06056	16.6666667
hsa-miR-106a	1.656932745	1.2342	0.744870306	2.29774	16.6666667

**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%.