

**Table S2. Upregulated miRNAs and CpG islands**

**57 different miRNAs upregulated  $\geq$  two-fold with minimal basal expression in untreated cells**

hsa-miR-100	hsa-miR-155	hsa-miR-218-2	hsa-miR-373
hsa-miR-101-1	hsa-miR-15b	hsa-miR-219-1	hsa-miR-373*
hsa-miR-101-2	hsa-miR-17	hsa-miR-219-2	hsa-miR-425
hsa-miR-106a	hsa-miR-181a	hsa-miR-220	hsa-miR-429
hsa-miR-126	hsa-miR-192	hsa-miR-221	hsa-miR-494
hsa-miR-126*	hsa-miR-193a	hsa-miR-222	hsa-miR-516
hsa-miR-132	hsa-miR-193b	hsa-miR-27b	hsa-miR-7-2
hsa-miR-135-1	hsa-miR-196-1	hsa-miR-29b-2	hsa-miR-9-1
hsa-miR-145	hsa-miR-19a	hsa-miR-301	hsa-miR-92
hsa-miR-147	hsa-miR-205	hsa-miR-30a	hsa-miR-9-2
hsa-miR-148a	hsa-miR-21	hsa-miR-32	hsa-miR-9-3
hsa-miR-148b	hsa-miR-210	hsa-miR-324	hsa-miR-96
hsa-miR-150	hsa-miR-212	hsa-miR-34b	
hsa-miR-151	hsa-miR-213	hsa-miR-34c	
hsa-miR-152	hsa-miR-215	hsa-miR-361	

**27 different miRNAs upregulated  $\geq$  two-fold with minimal basal expression in untreated cells and located within a CpG island**

hsa-miR-126	hsa-miR-193b	hsa-miR-27b	hsa-miR-7-2
hsa-miR-126*	hsa-miR-210	hsa-miR-34b	hsa-miR-9-1
hsa-miR-132	hsa-miR-212	hsa-miR-34c	hsa-miR-92
hsa-miR-148a	hsa-miR-218-2	hsa-miR-373	hsa-miR-9-2
hsa-miR-152	hsa-miR-219-1	hsa-miR-373*	hsa-miR-9-3
hsa-miR-192	hsa-miR-219-2	hsa-miR-425	hsa-miR-96
hsa-miR-193a	hsa-miR-220	hsa-miR-494	

**7 DNA unmethylated CpG islands  
in the metastatic cell lines  
(corresponding to 8 miRNAs)**

hsa-miR-132/212  
hsa-miR-152  
hsa-miR-210  
hsa-miR-219-1  
hsa-miR-425  
hsa-miR-92  
hsa-miR-494

**11 DNA methylated CpG islands  
both in normal and cancer cells  
(corresponding to 13 miRNAs)**

hsa-miR-126/126\*  
hsa-miR-192  
hsa-miR-193a  
hsa-miR-193b  
hsa-miR-218-2  
hsa-miR-219-2  
hsa-miR-220  
hsa-miR-27b  
hsa-miR-373/373\*  
hsa-miR-7-2  
hsa-miR-96

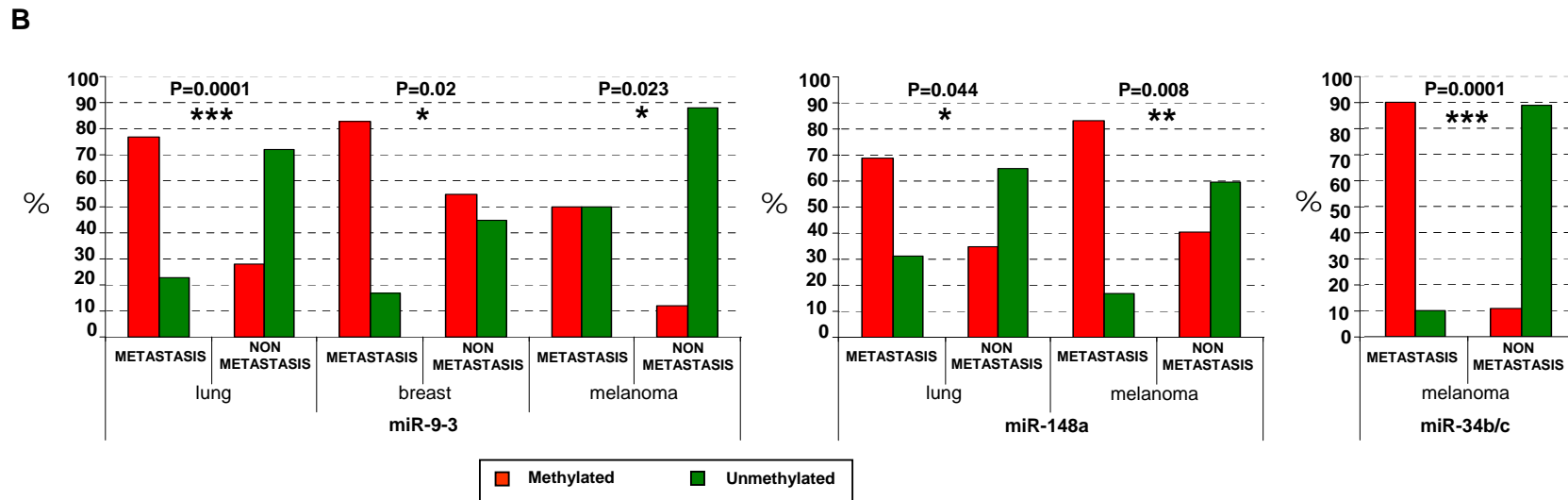
**5 DNA methylated CpG islands  
only in cancer cells  
(corresponding to 6 miRNAs)**

hsa-miR-9-1  
hsa-miR-9-2  
hsa-miR-9-3  
hsa-miR-148a  
hsa-miR-34b/34c

**Table S4. Distribution of cases relating methylation, according to the presence or not of metastasis in the metastasis associated miRNAs (A) and frequency of CpG island hypermethylation of the metastasis-associated miRNAs according to the presence or absence of lymph node metastasis in different tumor types (B)**

**A**

	miR-9-3		miR-148a		miR-34b/c	
	metastasis	no metastasis	metastasis	no metastasis	metastasis	no metastasis
<b>METHYLATED</b>	57 (77%)	35 (28.9%)	42 (65.7%)	48 (47.1%)	46 (59%)	48 (37.2%)
<b>UNMETHYLATED</b>	17 (23%)	86 (71.1%)	22 (34.3%)	54 (52.9%)	32 (41%)	81 (62.8%)
<b>n</b>	74	121	64	102	78	129



P values were calculated by using Pearson's  $\chi^2$  test is represented.