Supplemental Table 1. Patient and tumor characteristics.

Characteristic	miRNA sequencing cohort, n=90 No	%	RT-qPCR cohort 1, n=29[*] No	%	RT-qPCR cohort 1 extended, n=45[†] No	%	RT-qPCR cohort 2, n=20[‡] No	%
Age (years)								
Median	52.9		58.2		58.1		56	
Range	22-84		22-78		22-81		30-81	
Tumour histology								
Squamous	90	100	29	100	45	100	20	100
Tumor stage (FIGO)								
1b -2b	70	78	19	65	33	73	13	65
3b-4a	20	22	10	35	12	27	7	35
Tumor volume (cm^3)[§]								
Median	26		41		31		60	
Range	3-267		3-218		3-218		3-321	
Lymph node status[ǁ]								
Positive	44	49	15	51	19	42	11	55
Negative	46	51	14	49	26	58	9	45
HPV type[¶]								
HPV16	50	56	10	34	23	51	13	60
HPV18	14	16	11	38	14	31	2	10
HPV other	16	18	6	21	6	13	2	
HPV negative	8	9	2	7	2	4	0	
HPV16+HPV18	1	1					3	15
Hypoxia status[**]								
More hypoxic	26	29	10	34	18	40	10	50
Less hypoxic	64	71	19	66	27	60	10	50
Observation time (months)[††]								
Median	39		27.3		36		36	
Range	5-60		4.6-60		4.6-60		2-60	
Recurrence[‡‡]	19	21	10	34	11	24	10	50
Disease specific death[‡‡]	16	18	9	31	10	22	9	45

FIGO, Federation International de Gynecologie et d'Obstetrique.

[*] Subgroup of patients in sequencing cohort.

[†] Subgroup of patients in sequencing cohort, includes patients in RT-qPCR cohort 1.

[‡] Patients not in sequencing cohort.

[§] Determined from MR-images before treatment. Calculated based on 3 orthogonal diameters (a,b,c) as (π/6)abc. Undetermined for 6 tumors in sequencing cohort, two in RT-qPCR cohort 1, four in RT-qPCR cohort 1 extended, and one in RT-qPCR cohort 2.

[ǁ] Detected by MRI or CT at diagnosis, according to the response evaluation criteria in solid tumors version 1.1.

[¶] Collected from (Lando, M. *et al*, 2013).

[**] Output from 6-gene hypoxia classifier collected from (Fjeldbo, C.S. *et al*, 2016b).

[††] Based on patients without recurrence.

[‡‡] Follow-up data up to 60 months.

Supplemental Table 2. Exiqon microRNA LNA™ PCR primer sets

Candidate reference RNA	Product no.
miR-151a-5p	204007
miR-152-3p	204294
miR-505-3p	204214
miR-532-5p	204221
miR-652-3p	204387
miR-671-3p	204024
miR-28-5p	204322
miR-423-5p	204488
RNU6	203907
MiRNA of investigation	
miR-210-3p	204333
miR-9-5p	204513

Supplemental Table 4. Ranking of 20 candidate reference miRNAs in RefFinder

MiRNA	Overall ranking		Comparative ΔCt		BestKeeper		NormFinder		GeNorm	
	Rank	Stability	Rank	Stability	Rank	Stability	Rank	Stability	Rank	Stability
miR-28-5p	1	1.78	1	0.79	2	1.27	1	0.39	5	0.48
miR-423-3p	2	2.45	3	0.80	1	1.24	3	0.44	4	0.42
miR-505-3p	3	3.46	2	0.79	7	1.31	2	0.40	6	0.52
miR-151a-5p	4	3.98	4	0.82	5	1.31	9	0.50	1	0.00
miR-151b	5	4.47	5	0.82	6	1.31	10	0.50		
miR-532-5p	6	4.74	6	0.82	3	1.28	4	0.48	7	0.56
miR-671-3p	7	5.21	7	0.82	8	1.31	7	0.49	3	0.34
miR-152-3p	8	6.16	8	0.84	4	1.30	5	0.48	9	0.61
miR-652-3p	9	8.49	9	0.84	9	1.32	8	0.50	8	0.58
miR-140-5p	10	8.80	10	0.84	10	1.34	6	0.49	10	0.63
miR-664a-3p	11	11.00	11	0.91	11	1.37	11	0.62	11	0.65
miR-96-5p	12	12.47	12	0.94	14	1.45	12	0.66	12	0.67
miR-425-3p	13	13.00	13	0.94	13	1.44	13	0.66	13	0.69
miR-181c-3p	14	13.47	14	0.97	12	1.39	14	0.69	14	0.72
miR-126-3p	15	15.00	15	0.99	15	1.46	15	0.72	15	0.75
miR-598-3p	16	16.00	16	1.03	16	1.54	16	0.79	16	0.77
miR-708-3p	17	17.73	17	1.06	19	1.66	17	0.83	18	0.83
miR-708-5p	18	18.24	18	1.08	18	1.65	18	0.86	19	0.85
miR-301b-3p	19	18.72	19	1.09	20	1.70	19	0.87	17	0.80
miR-214-5p	20	19.20	20	1.10	17	1.60	20	0.88	20	0.87

Supplemental Table 5. MiRNA family affiliation of candidate reference miRNAs.

MiRNA	Family ID	Family Accession	Chromosome
miR-28-5p			chr3
miR-151a-5p	mir-28	MIPF0000057	chr8
miR-151b			chr14
miR-152-3p	mir-148	MIPF0000056	chr17
miR-423-3p	mir-423	MIPF0000329	chr17
miR-505-3p	mir-505	MIPF0000217	chrX
miR-532-5p	mir-188	MIPF0000113	chrX
miR-652-3p	mir-652	MIPF0000333	chrX
miR-671-3p	mir-671	MIPF0000358	chr7

Supplemental Table 6. PCR efficiency.

Candidate reference RNA	PCR efficiency	Comment
miR-151a-5p	99%	
miR-152-3p	101%	
miR-505-3p	99%	
miR-532-5p	70 %	Low efficiency *
miR-652-3p	93%	
miR-671-3p	NA	High Cq values (>33 at 80x) *
miR-28-5p	111%	Suboptimal efficiency compared to miR-151a-5p *
miR-423-5p	102 %	
RNU6	108%	
MiRNA of investigation		
miR-210-3p	95%	
miR-9-5p	101%	

* indicate exclusion from further analysis

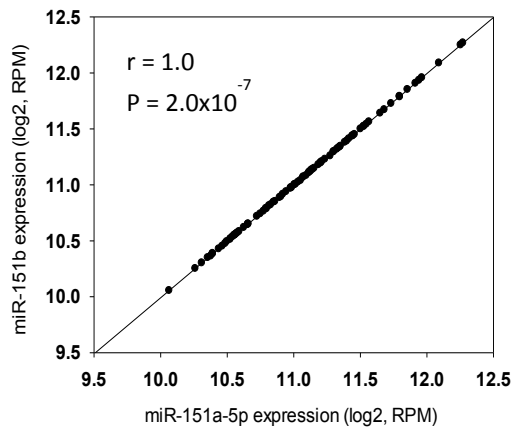**Supplemental Table 7. RT-qPCR Cq values for candidate reference RNAs**

Reference RNA	Cq Range	Cq Max	Cq Min	Mean	Std Dev
miR-151a-5p	2.13	29.14	27.00	28.09	0.52
miR-152-3p	2.10	29.86	27.76	28.81	0.51
miR-505-3p	3.65	33.28	29.63	31.93	0.70
miR-652-3p	2.32	31.14	28.81	29.86	0.53
miR-423-3p	2.10	30.01	27.91	28.73	0.56
RNU6	6.32	27.50	21.19	23.50	1.60

Supplemental figure 1

A)

```
miR-151a-5p    UCGAGGAGCUCACAGUCUAGU.....
miR-151b       UCGAGGAGCUCACAGUCU........
miR-28-5p      ..AAGGAGCUCACAGUCUAUUGAG..
```
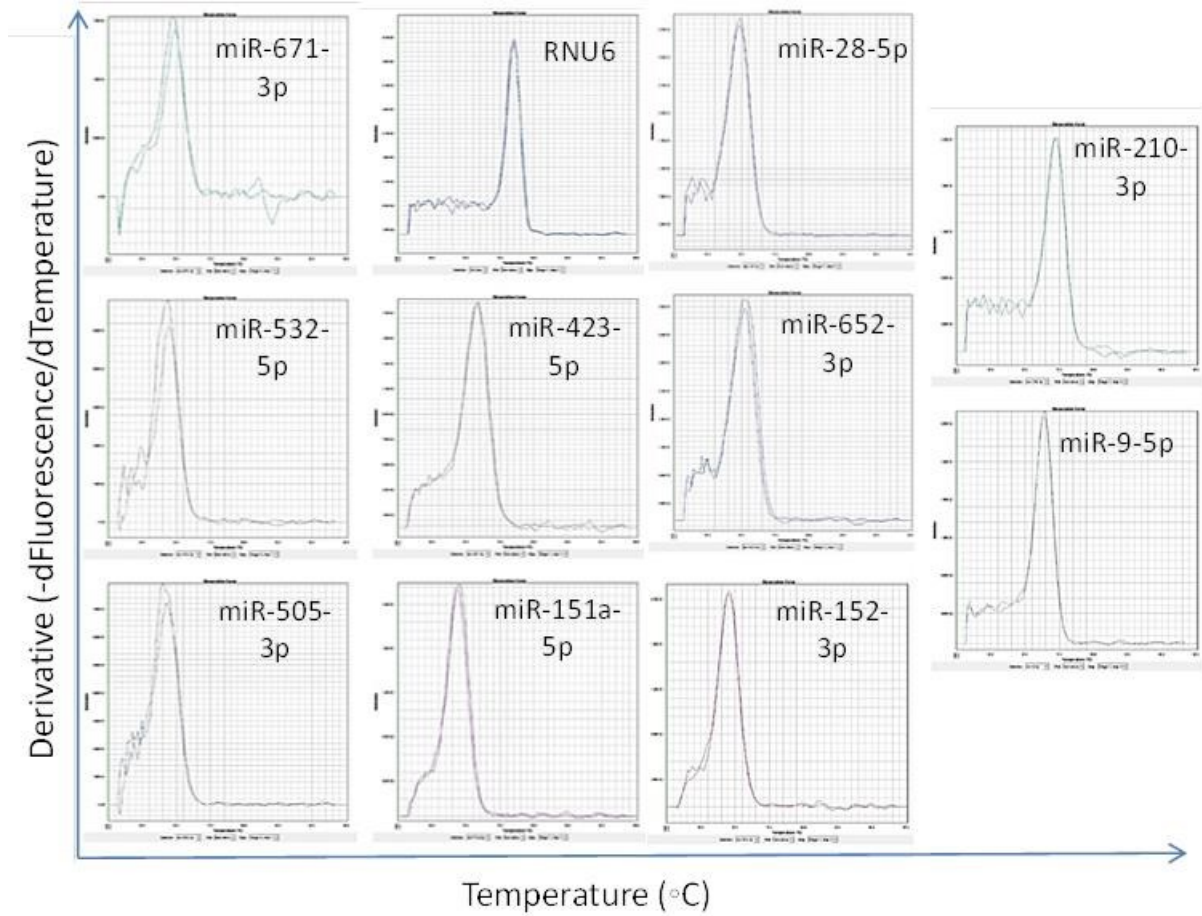
B)

r = 1.0

P = 2.0×10^{-7}

miR-151b expression (log2, RPM)

miR-151a-5p expression (log2, RPM)

C)

r = 0.4

P = 1.6×10^{-4}

miR-28-5p expression (log2, RPM)

miR-151a-5p expression (log2, RPM)

Supplemental Fig. 1. **MiR-28 family members of candidate reference miRNAs**. A) Sequence alignment of miR-151a-5p, miR-151b and miR-28-5p. Regression plots of miR-151a-5p vs miR-151b (B) and miR-28-5p (C) expression levels (log2, RPM) and corresponding correlation coefficient (r) and p-value from Pearson's correlation analysis.
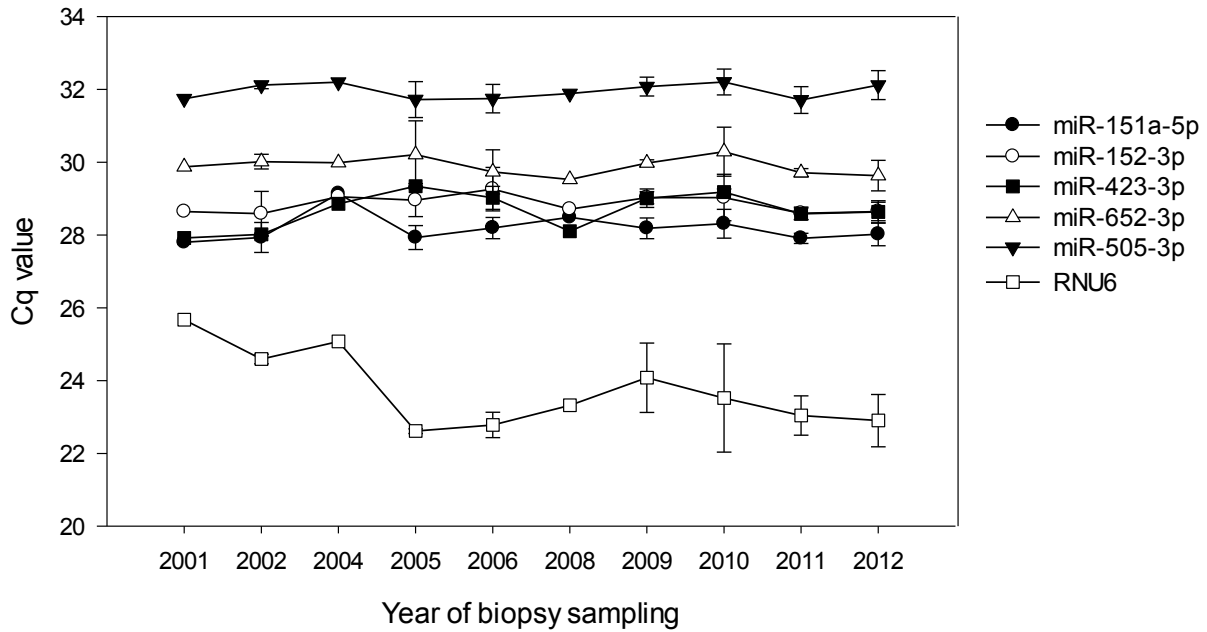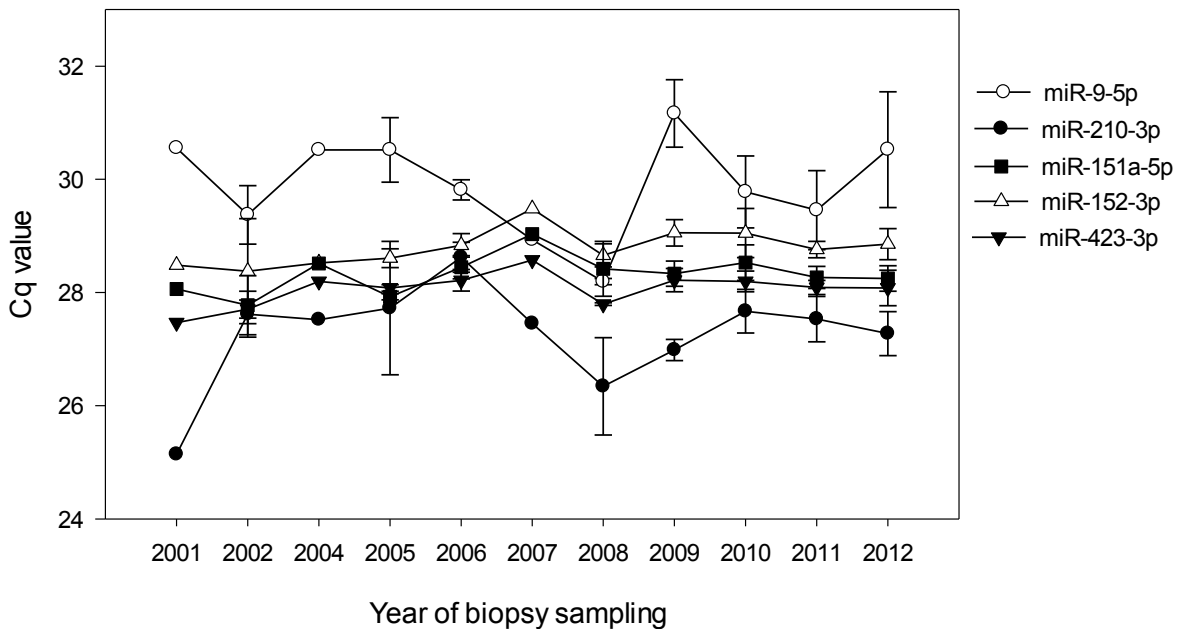
Supplemental figure 2

Supplemental Fig. 2. **Specificity of the PCR products**. Melting curve analysis generated for the amplified product of candidate reference RNAs and miRNAs of investigation. Change in fluorescence is plotted versus temperature.
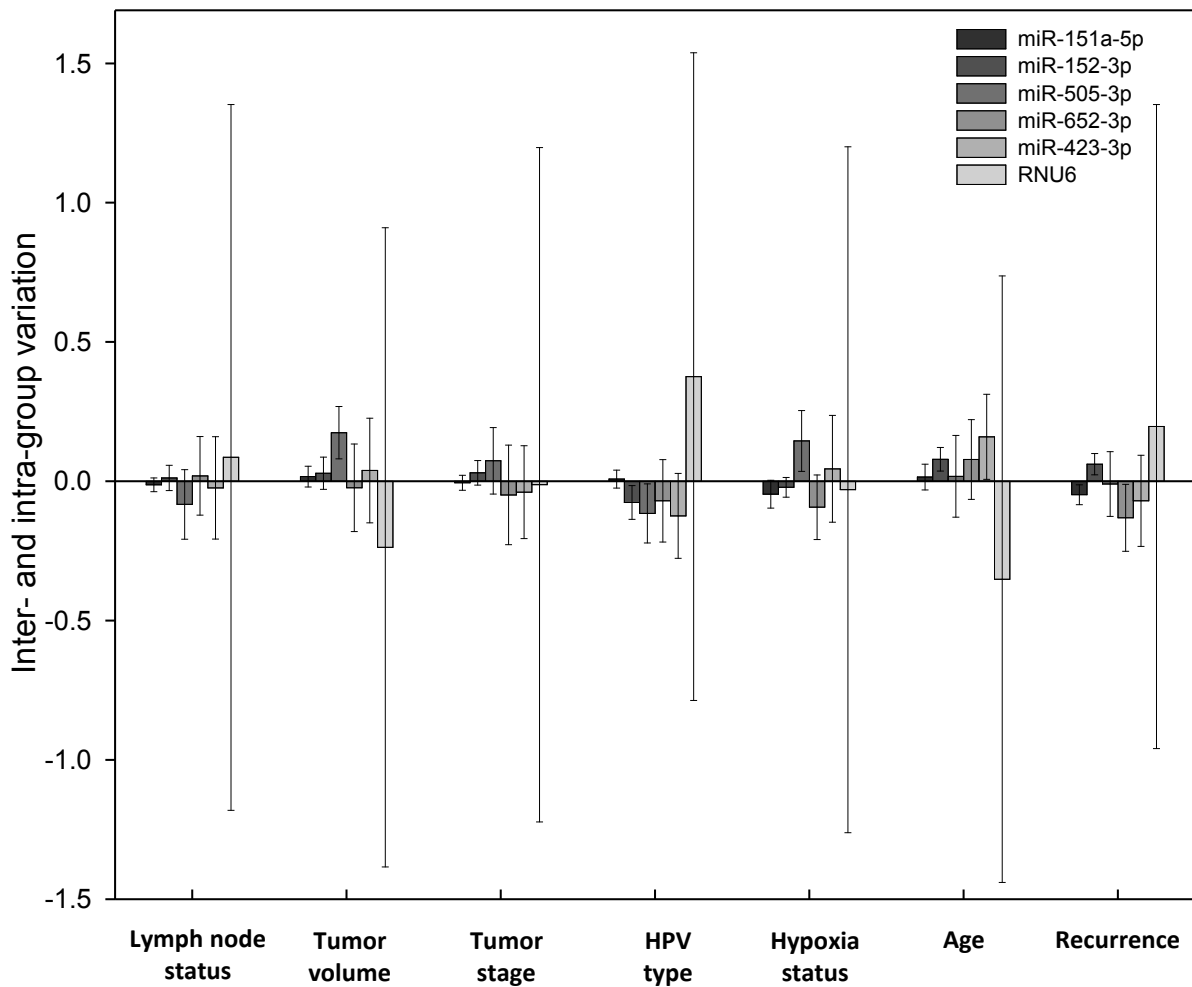
Supplemental figure 3

A)

B)

Supplemental Fig. 3. **Cq values versus year of biopsy sampling**. Raw Cq values from RT-qPCR analyses of A) candidate reference miRNAs and RNU6 versus year of biopsy sampling in RT-qPCR cohort 1 (29 samples) and B) the selected reference miRNAs and miRNAs of investigation versus year of biopsy sampling in RT-qPCR cohort 1 extended. Points and error bars indicate mean Cq value and standard deviation. Spearman rank order correlation analysis showed no significance between the miRNAs or RNU6 and the year of biopsy sampling.

Supplemental figure 4

Supplemental Fig. 4. **Inter–and Intra–group variation calculated by NormFinder**. The columns represent the inter–group variation and the error bars the average of the intra–group variances. The top–ranked gene has an inter–group variation as close to zero as possible and as small error bars as possible.