

# Sex-specific miRNA differences in liquid biopsies from subjects with solid tumors and healthy controls

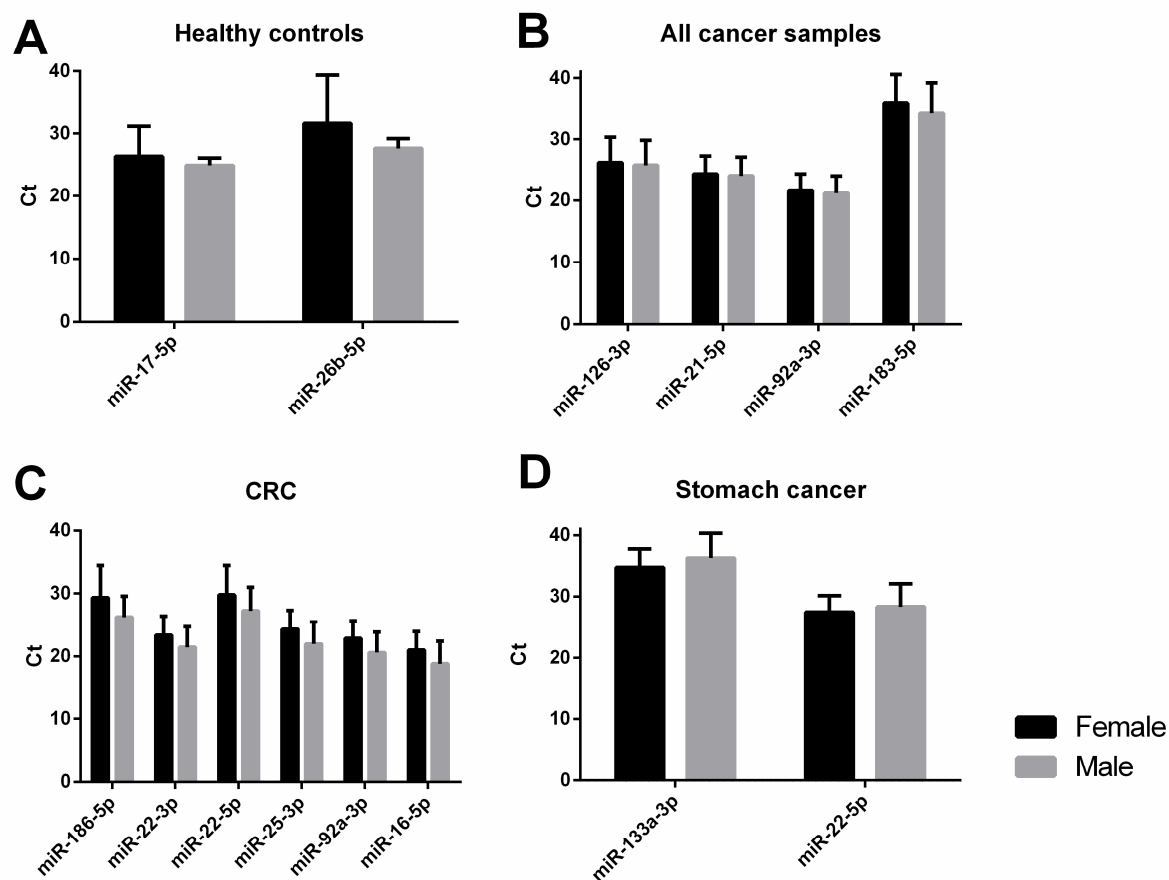
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Supplementary file 2: Table S1. Genes and regions analyzed for methylation status.

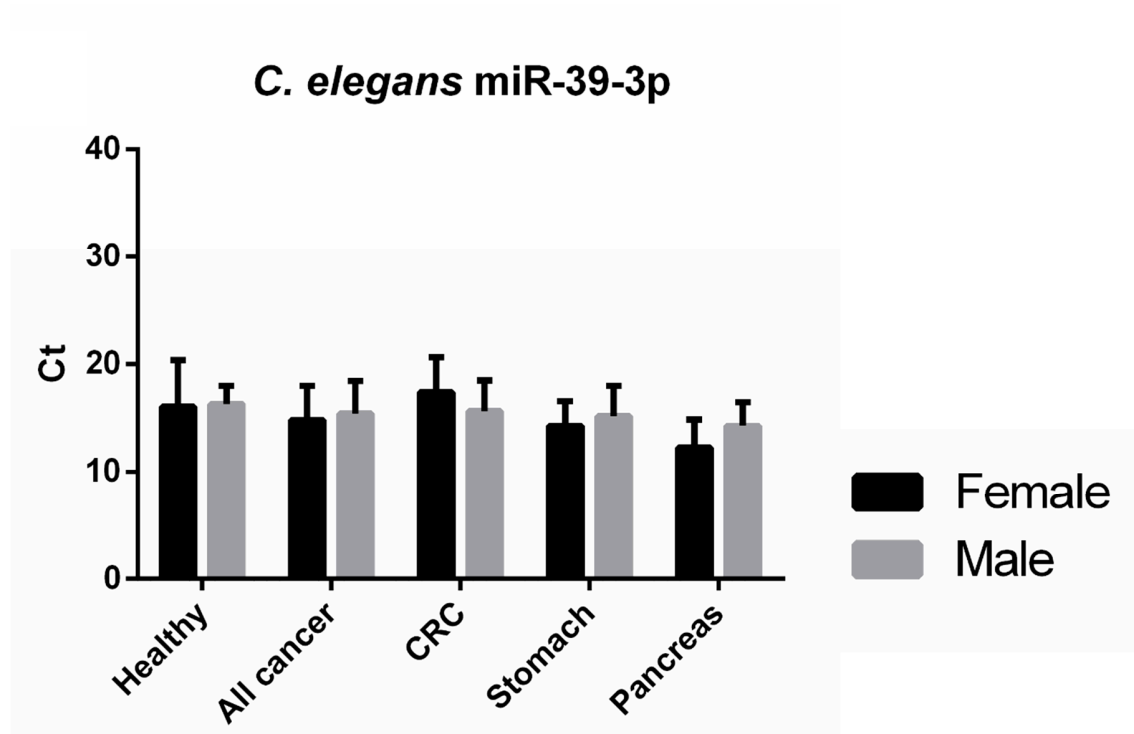
Gene	NCBI Reference Sequence	Region	Sequence
<i>ALKBH3</i>	NC_000011.10	43880721-43880820	ctaccggac tgaggactgc gcaccggaag tagtggcggc gctgcgtaac gtcgagagga agtgctgat gccgcggcct gtgattggga gttgctggag
<i>APC</i>	NC_000005.10	112737681-112737780	ctagggctag gcaggctgtg cggttgggcg gggccctgtg ccccactcg gagtgcgggt cggaagcgg agagagaagc agctgtgtaa tccgctggat
<i>GATA5</i>	NC_000020.11	62475990-62476090	aagactggaa gcccgggccc ctgaggctcc gcagccccct ccgcgccgcc ccggcccgcc ccgcgcgc cgccttcc ctccccgcgc ccgcccttc t
<i>GSTP1</i>	NC_000011.10	67583636-67583735	ctccggggac tccaggggcg ccctctcgg ccgacccccg gggtgcagcg gccgccgggg ctggggccgg cgggagtcg cgggaccctc cagaagagcg
<i>MDR1</i>	NC_000007.14	87600483-87600384	ggcagagttg ggggtctggc agcgcgttct ggactttgcc cgccgccagt gcgattctcc ctccgggtc cagtgcgcgc ggacgatgct tctcccacc
<i>MGMT</i>	NC_000010.11	129467232-129467305	cgcccctaga acgctttgcg tcccagccc cgcaggtcct cgcggtgcgc accgtttgcg acttggtgag tgtc
<i>MLH1</i>	NC_000003.12	36992887-36993005	tattcgtgct cagcctcgtg gtggcgctg acgtcgcgtt cgcgggtagc tacgatgagg cggcgacaga ccaggcacag ggcccatcg cctccggag gctccaccac caaataacg
<i>RASSF1A</i>	NC_000003.12	50340772 - 50340673	gccgtgtggg gttgcacgcg gtgccccgcg cgatgcgcag cgcgttgga cgtccagcc ggggtcggcc cttccagcg cgccagcgg gtgcccagtc
<i>SEPTIN9</i>	NC_000017.11	77373482-77373543	ctgccacca gccatcatgt cggacccgc ggtcaacgcg cagctggatg ggtcatttc gg
<i>SFN</i>	NC_000001.11	26863259-26863372	ccgaacgcta ttaggacatg gcagccttca tgaaaggcg cgtggagaag ggagaggagc tctctgcga agagcgaac ctgctctcag tagcctataa gaacgtggtg ggcg
<i>SHOX2</i>	NC_000003.12	158103869-158103755	cgaccctaaa cgcttaacc acagagatca acaggttcaa gcggaatatt cgcgatctc ggttctatt ggtgtctcaa agcctttca tgcaaccagc agctcgatg tttaa
<i>VIM</i>	NC_000010.11	17229166-17229265	gcttctcgt aggtccctat tggctggcg gctccggcg tgggatggca gtggagggg accctcttc ctaacgggt tataaaaaca ggcctcgg

Supplementary file 2: Table S2. MiRNA targets.

cel-miR-39-3p	hsa-miR-141-3p	hsa-miR-17-5p	hsa-miR-210-3p	hsa-miR-22-5p	hsa-miR-31-5p
hsa-let-7a-5p	hsa-miR-142-5p	hsa-miR-182-5p	hsa-miR-21-5p	hsa-miR-23a-3p	hsa-miR-34a-5p
hsa-miR-101-3p	hsa-miR-143-3p	hsa-miR-183-5p	hsa-miR-218-5p	hsa-miR-25-3p	hsa-miR-375-3p
hsa-miR-106a-5p	hsa-miR-145-5p	hsa-miR-186-5p	hsa-miR-221-3p	hsa-miR-26a-5p	hsa-miR-451a
hsa-miR-1225-3p	hsa-miR-148a-3p	hsa-miR-195-5p	hsa-miR-222-3p	hsa-miR-26b-5p	hsa-miR-497-5p
hsa-miR-124-3p	hsa-miR-148b-3p	hsa-miR-203a-3p	hsa-miR-223-3p	hsa-miR-27a-3p	hsa-miR-92a-3p
hsa-miR-126-3p	hsa-miR-155-5p	hsa-miR-205-5p	hsa-miR-22-3p	hsa-miR-29c-3p	hsa-miR-9-5p
hsa-miR-133a-3p	hsa-miR-16-5p	hsa-miR-20a-5p	hsa-miR-224-5p	hsa-miR-30a-5p	hsa-miR-96-5p



Supplementary file 2: Figure S1. Abundance of miRNAs in plasma samples across the different study groups. Only the mean Ct values of differentially expressed miRNAs between female and male participants (after normalization and adjustments for covariates) are depicted in this figure. Bars represent the mean value with standard deviation (SD). **A** Healthy control group  $n$  female = 8,  $n$  male = 7 **B** All cancer samples,  $n$  female = 48,  $n$  male = 80 **C** Colorectal cancer group,  $n$  female = 14,  $n$  male = 14 **D** Stomach cancer,  $n$  female = 15,  $n$  male = 8



Supplementary file 2: Figure S2. Abundance of *C. elegans* miR-39-3p spike-in control across the different study groups. 15 fmol of *C. elegans* miR-39-3p was added to each sample during RNA extraction. Bars represent the mean Ct value with SD.