Erratum to epigenetics of colorectal cancer: emerging circulating diagnostic and prognostic biomarkers

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In the article entitled "Epigenetics of colorectal cancer: emerging circulating diagnostic and prognostic biomarkers" that appeared on page 279 of Vol 5, No 13 of *Annals of Translational Medicine (ATM)*, there are some errors. *Table 1* should be replaced by the following content.

The publisher regrets the error.

Table 1 Studies aimed to identify diagnostic miRNA for CRC through high-throughput screening and subsequent qPCR validation

Study	Country	Sample type	Discovery phase (method and sample population)	Validation phase(s) (method and sample population)	Candidate miRNAs (expression)	AUC (95% CI)	SE	SP
Ghanbari R, *et al.* 2015 (48)	Iran	Plasma	miRNA Microarray system (Agilent); 37 CRC, 8 controls	qRT-PCR; 61 CRC, 24 controls	miR-142-3p (↓)	0.71	–	–
					miR-26a-5p (↓)	0.67	–	–
Giráldez MD, *et al.* 2013 (49)	Spain	Plasma	SAM-Bead Array platform (Illumina); 21 CRC, 20 advanced adenoma, 20 controls	qRT-PCR; 42 CRC, 40 advanced adenomas, 53 controls	miR19a, miR19b (all ↑)	0.82 (0.73–0.90)	78.57%	77.36%
					miR19a, miR19b, miR15b (all ↑)	0.84 (0.76–0.92)	78.57%	79.25%
Hofsli E, *et al.* 2013 (50)	Norway	Serum	miRCURY LNA Universal RT microRNA PCR (Exiqon) (375 miRNAs); 30 CRC (stage IV), 10 controls	miRCURY LNA Universal RT microRNA PCR (34 miRNAs); 40 CRC (stage I, II), 10 controls	miR-423-5p, miR-210, miR-720, miR-320a and miR-378 (all ↑)	–	–	–
					miR-106a, miR-143, miR-103, miR-199a-3p, miR-382 and miR-151-5p (all ↓)	–	–	–
Imaoka H, *et al.* 2016 (51)	Japan	Serum	Microarray analysis; 3 CRC, 3 adenoma, 3 controls	qRT-PCR; 211 CRCs, 56 adenomas, 57 controls	miR-1290 (↑)	CRC *vs.* controls 0.83	7.01%	91.2%
						Adenoma *vs.* controls 0.72	46.4%	91.2%
Study	Country	Sample type	Discovery phase (method and sample population)	Validation phase(s) (method and sample population)	Candidate miRNAs (expression)	AUC (95% CI)	SE	SP

Table 1 *(continued)*

Table 1 *(continued)*

Study	Country	Sample type	Discovery phase (method and sample population)	Validation phase(s) (method and sample population)	Candidate miRNAs (expression)	AUC (95% CI)	SE	SP
Kanaan Z, *et al.* 2013 (52)	Kentucky (USA)	Plasma	TaqMan low-density array card (life technologies) 380 miRNAs; 20 CRC, 9 adenoma, 12 controls	qRT-PCR; 45 CRC, 16 adenoma, 26 controls	miR-139-3p, miR-431 (all ↑)	CRC *vs.* controls; 0.83 (0.73–0.93)	91%	57%
Li J, *et al.* 2015 (53)	China	Serum	TaqMan low-density array (applied biosystems) (749 miRNAs); pooled 20 CRC, 20 controls	qRT-PCR; 175 stage II/III CRC patients, 130 controls	miR-145 (↓)	0.87 (0.84–0.91)	–	–
					miR-17-3p (↑)	0.78 (0.73–0.83)	–	–
					miR-106a (↑)	0.81 (0.77–0.86)	–	–
					miR-145 (↓), miR-17-3p (↑), miR106a (↑)	0.89 (0.85–0.92)	78.5%	82.8%
Luo X, *et al.* 2013 (54)	Germany	Plasma	TaqMan microRNA array (applied biosystems) 667 miRNAs; 5 pools of CRC patients (N=50), 5 pools of controls (N=50)	qRT-PCR; 80 CRC, 50 advanced adenoma, 194 controls	miR-18a, miR-20a, miR21, miR-29a, miR-92a, miR-106b, miR-133a, miR-143, miR-145 (all ↑)	CRC *vs.* controls; 0.745 (0.708–0.846)	–	–
Ng EK, *et al.* 2009 (55)	China	Plasma	Cancer microRNA array (system biosciences) 95 miRNAs; 5 CRC, 5 controls	qRT-PCR; (I) 25 CRC,20 controls; (II) 90 CRC 50 controls	miR-17-3p (↑)	(I) 0.717 (0.633–0.800)	(I) 64%	70%
					miR-92 (↑)	(II) 0.885 (0.828–0.942)	(II) 89%	70%
Sun Y, *et al.* 2016 (56)	China	Plasma	TaqMan array (life technologies) (754 miRNAs); 40 CRC, 10 controls	qRT-PCR; 187 CRC, 47 controls	miR-96 (↑)	0.740 (0.650–0.831)	65.4%	73.3%
Vychytilova-Faltejskova P, *et al.* 2016 (57)	Czech Republic	Serum	Illumina small RNA sequencing; pooled 144 CRC, 96 controls	qRT-PCR; 203 CRC, 100 controls	miR-23a-3p (↑)	0.89	–	–
					miR-27a-3p (↑)	0.70	–	–
					miR-142 5p (↑)	0.81	–	–
					miR-376c-3p (↑)	0.65	–	–
					miR-23a-3p, miR-27a-3p, miR-142-5p, miR-376c-3p (all ↑)	0.92	89%	81%

Table 1 *(continued)*

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Study	Country	Sample type	Discovery phase (method and sample population)	Validation phase(s) (method and sample population)	Candidate miRNAs (expression)	AUC (95% CI)	SE	SP
Wang Q, *et al.* 2012 (58)	China	Plasma	miRCURY LNA™ universal RT microRNA PCR system (exiqon, demark) (742 miRNAs); 10 CRC, 10 controls	qRT-PCR; 90 CRC, 43 advanced adenoma, 58 controls	miR-601 (↓)	CRC *vs.* controls; 0.747 (0.666–0.828)	69.2%	72.4%
					miR-760 (↓)	CRC *vs.* controls; 0.788 (0.714–0.862)	80%	72.4%
Wang S, *et al.* 2015 (59)	China	Plasma	Human microRNA microarrays Agilent technologies (723 miRNAs); 47 CRC, 33 controls	qRT-PCR; (I) 55 CRC, 57 controls; (II) 22 CRC, 27 controls	miR-409-3p (↑), miR-7 (↓), miR-93 (↓)	(I) 0.866 (0.788–0.923); (II) 0.897	(I) 91%; (II) 82%	(I) 88%; (II) 89%
Xu L, *et al.* 2014 (60)	China	Plasma	TaqMan low density MiRNA arrays [applied biosystems (754 miRNAs)]; 6 CRC, 6 controls	qRT-PCR; 88 CRC, 40 controls	miR-375 (↓)	0.749 (0.654-0.844)	76.92%	64.63%
					miR-206 (↑)	0.705 (0.612-0.798	–	–
					miR-375 (↓) miR-206 (↑)	0.846 (0.775-0.917)	–	–
Zheng G, *et al.* 2014 (61)	China	Serum	Miseq sequencing; pooled serum samples (30 CRC, 25 adenoma, 30 controls)	qRT-PCR; (I) 160 CRC, 66 CA patients, 94 controls; (II) 117 CRC, 73 adenoma, 102 controls	miR-19a-3p (↑)	CRC *vs.* controls (I) 0.849	–	–
					miR-92a-3p (↑)	(I) 0.890	–	–
					miR-223-3p (↑)	(I) 0.871	–	–
					miR-422a (↓)	(I) 0.843	–	–
					miR-19a-3p, miR-223-3p, miR-92a-3p and miR-422a	(II) 0.951 (0.907–0.978	–	–
Zhu M, *et al.* 2017 (62)	China	Serum	Exiqon miRCURY-Ready-to-Use-PCR-Human-panel-I + II-V1 (168 miRNAs); 30 CRC, 30 controls	qRT-PCR; (I)136 CRC, 90 controls; (II) 30 CRC, 18 controls	miR-19a-3p, miR-21-5p, miR-425-5p (all ↑)	0.830 (0.708–0.952)	–	–

(↑), miRNAs upregulated in CRC patients compared to healthy subjects; (↓), miRNAs downregulated in CRC patients compared to healthy subjects. CRC, colorectal cancer; AUC, area under curve; SE, sensitivity; SP, specificity.

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