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# Author Correction: Re-expression of *REG* family and *DUOX*s genes in CRC organoids by co-culturing with CAFs

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The original version of this Article contained errors in Table 1, where the AA change was omitted for a number of genes due to a technical error during gene mutation analysis. The correct and incorrect values appear below.

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Incorrect:

Gene Name	AA change	original tissue	organoid P21
		Variant rate (%)	Variant rate (%)
<i>PIK3CA</i>	–	41.8	46.3
<i>APC</i>	Q879*	28.5	48.6
<i>APC</i>	T1491fs	not estimated	not estimated
<i>NOTCH1</i>	–	48.1	50.7
<i>KRAS</i>	G12S	40.6	63.8
<i>TP53</i>	Y220S	72.4	99.9
<i>NTRK3</i>	T332M	80.3	99.8

Gene Name	AA change	original tissue	organoid P3	organoid P21	fold change
		Variant rate (%)	Variant rate (%)	Variant rate (%)	P3 / P21
<i>DDR2</i>	V250A	23.0	38.3	34.8	0.91
<i>APC</i>	A703fs*15	15.1	21.9	24.8	1.13
<i>APC</i>	Q1378*	57.1	71.4	70.9	0.99
<i>KRAS</i>	G12D	47.2	67.6	65.8	0.97
<i>TP53</i>	H193R	65.2	98.8	100.0	1.01
<i>NF1</i>	–	28.2	25.3	25.8	1.02

Gene Name	AA change	original tissue	organoid P22
		Variant rate (%)	Variant rate (%)
<i>NOTCH2</i>	S1636T	17.5	29.8
<i>PBRM1</i>	L893fs	not estimated	not estimated
<i>PDGFRA</i>	M133T	46.9	100.0
<i>FBXW7</i>	R505C	42.3	100.0
<i>APC</i>	E1034fs*13	29.4	45.2
<i>APC</i>	R1450*	33.2	49.3
<i>MET</i>	T495A	27.2	38.6
<i>KRAS</i>	G12D	34.9	48.5
<i>ARID2</i>	L1077R	50.6	53.8
<i>BRCA2</i>	A338fs*11	53.5	72.7
<i>ERBB2</i>	V842I	36.1	46.0
<i>SMARCA4</i>	R1325S	19.8	25.8
<i>NRG1</i>	S359R	–	28.8

Gene Name	AA change	original tissue	organoid P3	organoid P20	fold change
		Variant rate (%)	Variant rate (%)	Variant rate (%)	P3 / P20
<i>APC</i>	–	39.9	99.9	99.6	1.00
<i>ESR1</i>	R555C	11.1	31.6	31.6	1.00
<i>PIK3CA</i>	–	21.8	65.6	55.5	0.84
<i>TP53</i>	S15fs*28	15.3	93.4	91.0	0.97
<i>NOTCH2</i>	R1372Q	26.4	99.9	100.0	1.00

GENE_NAME	ffect2_AA_CHANG	original tissue	organoid P3	organoid P20	fold change
		Variant rate (%)	Variant rate (%)	Variant rate (%)	P3 / P20
<i>APC</i>	Q886*	33.0	50.5	49.5	0.98
<i>APC</i>	R1450*	25.7	42.0	46.8	1.11
<i>TP53</i>	V197M	46.4	97.2	100.0	1.03
<i>ABL1</i>	S977N	38.6	40.4	42.9	1.06
<i>MAP3K4</i>	P107L	–	–	33.7	–

Gene Name	AA change	original tissue	organoid P21
		Variant rate (%)	Variant rate (%)
<i>APC</i>	R1399fs*9	33.4	96.0
<i>ERBB3</i>	K498I	80.2	100.0
<i>PTCH1</i>	–	46.0	33.3
<i>TP53</i>	R175H	43.6	100.0
<i>ARID2</i>	R1677*	58.6	99.9
<i>ESR1</i>	–	72.5	100.0
<i>MAP2K4</i>	E333K	28.0	–

Gene Name	AA change	original tissue	organoid P23
		Variant rate (%)	Variant rate (%)
<i>APC</i>	R499*	34.6	49.2
<i>APC</i>	T1493fs*14	34.7	42.2
<i>ARID1A</i>	E1895*	29.8	47.1
<i>BRCA1</i>	K70E	11.0	12.1
<i>JAK2</i>	A920V	32.0	47.5
<i>PBRM1</i>	–	50.1	99.9
<i>PIK3CA</i>	–	33.1	52.0
<i>SETD2</i>	S295fs*5	46.4	92.8
<i>TP53</i>	R158H	44.5	99.8
<i>NOTCH1</i>	–	47.1	47.4
<i>EP300</i>	Q1867K	–	8.9

Correct:

		original tissue	organoid P21	
Gene Name	AA change	Variant rate (%)	Variant rate (%)	
#11	<i>PIK3CA</i>	C420R	41.8	46.3
	<i>APC</i>	Q879*	28.5	48.6
	<i>APC</i>	T1491fs	not estimated	not estimated
	<i>NOTCH1</i>	G890S	48.1	50.7
	<i>KRAS</i>	G12S	40.6	63.8
	<i>TP53</i>	Y220S	72.4	99.9
	<i>NTRK3</i>	T332M	80.3	99.8

  

		original tissue	organoid P3	organoid P21	fold change	
Gene Name	AA change	Variant rate (%)	Variant rate (%)	Variant rate (%)	P3 / P21	
#21	<i>DDR2</i>	V250A	23.0	38.3	34.8	0.91
	<i>APC</i>	A703fs*15	15.1	21.9	24.8	1.13
	<i>APC</i>	Q1378*	57.1	71.4	70.9	0.99
	<i>KRAS</i>	G12D	47.2	67.6	65.8	0.97
	<i>TP53</i>	H193R	65.2	98.8	100.0	1.01
	<i>NF1</i>	-	28.2	25.3	25.8	1.02

  

		original tissue	organoid P22	
Gene Name	AA change	Variant rate (%)	Variant rate (%)	
#25	<i>NOTCH2</i>	S1636T	17.5	29.8
	<i>PBRM1</i>	L893fs	not estimated	not estimated
	<i>PDGFRA</i>	M133T	46.9	100.0
	<i>FBXW7</i>	R505C	42.3	100.0
	<i>APC</i>	E1034fs*13	29.4	45.2
	<i>APC</i>	R1450*	33.2	49.3
	<i>MET</i>	T495A	27.2	38.6
	<i>KRAS</i>	G12D	34.9	48.5
	<i>ARID2</i>	L1077R	50.6	53.8
	<i>BRCA2</i>	A338fs*11	53.5	72.7
	<i>ERBB2</i>	V842I	36.1	46.0
	<i>SMARCA4</i>	R1325S	19.8	25.8
	<i>NRG1</i>	S359R		28.8

  

		original tissue	organoid P3	organoid P20	fold change	
Gene Name	AA change	Variant rate (%)	Variant rate (%)	Variant rate (%)	P3 / P20	
#28	<i>APC</i>	-	39.9	99.9	99.6	1.00
	<i>ESR1</i>	R555C	11.1	31.6	31.6	1.00
	<i>PIK3CA</i>	E545K	21.8	65.6	55.5	0.84
	<i>TP53</i>	S15fs*28	15.3	93.4	91.0	0.97
	<i>NOTCH2</i>	R1372Q	26.4	99.9	100.0	1.00

  

		original tissue	organoid P3	organoid P20	fold change	
Gene Name	AA change	Variant rate (%)	Variant rate (%)	Variant rate (%)	P3 / P20	
#32	<i>APC</i>	Q886*	33.0	50.5	49.5	0.98
	<i>APC</i>	R1450*	25.7	42.0	46.8	1.11
	<i>TP53</i>	V197M	46.4	97.2	100.0	1.03
	<i>ABL1</i>	S977N	38.6	40.4	42.9	1.06
	<i>MAP3K4</i>	P107L			33.7	-

  

		original tissue	organoid P21	
Gene Name	AA change	Variant rate (%)	Variant rate (%)	
#33	<i>APC</i>	R1399fs*9	33.4	96.0
	<i>ERBB3</i>	K498I	80.2	100.0
	<i>PTCH1</i>	-	46.0	33.3
	<i>TP53</i>	R175H	43.6	100.0
	<i>ARID2</i>	R1677*	58.6	99.9
	<i>ESR1</i>	-	72.5	100.0
	<i>MAP2K4</i>	E333K	28.0	

  

		original tissue	organoid P23	
Gene Name	AA change	Variant rate (%)	Variant rate (%)	
#44	<i>APC</i>	R499*	34.6	49.2
	<i>APC</i>	T1493fs*14	34.7	42.2
	<i>ARID1A</i>	E1895*	29.8	47.1
	<i>BRCA1</i>	K70E	11.0	12.1
	<i>JAK2</i>	A920V	32.0	47.5
	<i>PBRM1</i>	-	50.1	99.9
	<i>PIK3CA</i>	E545K	33.1	52.0
	<i>SETD2</i>	S295fs*5	46.4	92.8
	<i>TP53</i>	R158H	44.5	99.8
	<i>NOTCH1</i>	N2117K	47.1	47.4
	<i>EP300</i>	Q1867K		8.9

**Table 1.** Comparison of variant rates of cancer-associated genes between original tumor tissues and organoids of principal 7 cases.

The original article has been corrected.



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