

Supplementary Table S1. RNA yield obtained from various types of tissue when using TissueLyser rather than pestle grinding. Tissue was disrupted using TissueLyser II apparatus (QIAGEN), either in RLT buffer (*Protocol_O*) or in QIAzol (*Protocol_PC_O*).

Type of starting material	Method of tissue disruption	Protocol used	RNA concentration measured by NanoDrop (ng/ μ L)
Mouse skin biopsy, sample no.1	TissueLyser	<i>Protocol_O</i>	1.37
Mouse skin biopsy, sample no.2	TissueLyser	<i>Protocol_O</i>	5.65
Pig skin biopsy, sample no.1	TissueLyser	<i>Protocol_O</i>	2.53
Pig skin biopsy, sample no.2	TissueLyser	<i>Protocol_O</i>	1.98
Mouse skin biopsy, sample no.1	TissueLyser	<i>Protocol_PC+O</i>	84.25
Mouse skin biopsy, sample no.2	TissueLyser	<i>Protocol_PC+O</i>	392.46
Pig skin biopsy, sample no.1	TissueLyser	<i>Protocol_PC+O</i>	102.84
Pig skin biopsy, sample no.2	TissueLyser	<i>Protocol_PC+O</i>	237.74
Human breast cancer tissue	TissueLyser	<i>Protocol_O</i>	14.09
Human breast cancer tissue	TissueLyser	<i>Protocol_PC+O</i>	106.57

Supplementary Table S2. List of TaqMan gene expression assays, used in the analysis of low abundant transcripts

Gene of interest	Assay ID
<i>CDKN1A</i>	Hs00355782_m1
<i>Gli1</i>	Hs01110766_m1
<i>IL-8</i>	Hs00174103_m1
<i>Hes5</i>	Hs01387463_g1
<i>Rad51</i>	Hs00947967_m1
<i>MYC</i>	Hs00153408_m1
<i>TP53</i>	Hs01034249_m1
<i>USP2</i>	Hs00275859_m1

Supplementary Table S3. Analysis of low-abundant transcripts in samples extracted with *Protocol_O* and *Protocol_P*. Color-coded fields inform about the expression levels and thus feasibility of the assay (green – both samples from the sample pair *Protocol_O-Protocol_P* with Ct values not higher than Ct = 35; orange – at least one sample in the pair resulted in Ct >35; red – at least one sample in the pair resulted with no signal).

Gene name	Sample name							No. of sample pair analyzed	Mean difference (Ct)	p-value (paired t-test)
	98_ rectum	105_ testis	42_ breast	47_ breast	93_ colon	5_ testis	102_ uterus			
<i>CDKN1</i>		>35	>35	No Ct		>35		n = 6	0.80	0.06
<i>Gli1</i>	No Ct	No Ct	No Ct	No Ct	>35	>35	>35	n = 3	0.38	0.46
<i>IL-8</i>		No Ct	>35	No Ct		>35	>35	n = 5	0.91	0.11
<i>Hes5</i>	>35	No Ct	No Ct	No Ct	>35	>35	>35	n = 3	0.62	0.13
	97_ rectum	106_ testis	41_ breast	48_ breast	94_ colon	6_ testis	101_ uterus			
<i>Rad51</i>			No Ct	No Ct			>35	n = 5	0.77	0.12
<i>MYC</i>		>35	>35	No Ct		>35	>35	n = 6	0.57	0.27
<i>TP53</i>			>35	No Ct				n = 6	0.87	0.10
<i>USP2</i>		No Ct	No Ct	No Ct			>35	n = 4	-0.08 *	0.95

* minus sign means that samples extracted with Protocol_P had on average lower Ct values