

---

# Supplement: A tail-based test to detect differential expression in RNA-sequencing data

Journal Title  
XX(X):1-25  
©The Author(s) 2018  
Reprints and permission:  
sagepub.co.uk/journalsPermissions.nav  
DOI: 10.1177/ToBeAssigned  
www.sagepub.com/

SAGE

Jiong Chen<sup>1\*</sup>, Xinlei Mi<sup>2\*</sup>, Jing Ning<sup>3</sup>, Xuming He<sup>4</sup>, and Jianhua Hu<sup>2</sup>

## Section A

In the third set of simulation studies, we generated raw counts of gene-level expression data. We fitted edgeR, DESeq2, and Limma+voom using raw count data and converted the gene-level measurements to exon-level Log2-RPKM measurement to fit our methods.

For a gene  $g$ , its mean expression level  $\gamma_g$  was generated from an exponential distribution with mean 100. We generated covariate  $C_i$  from a normal distribution  $N(2.5, 0.5^2)$ . Then we let the regulating factor  $\delta_g = 1$  for the normal group. We generated the count data for  $N_{gj}$  of gene  $g$  for subject  $i$  from a negative binomial distribution.

We investigated the following two scenarios.

Scenario *DE-3* (null scenario):  $\delta_g = 1$  for all genes in the cancer group.

Scenario *DE-4* (alternative scenario): For the cancer group,  $\delta_g = 1 + X_g$  for 5% of the

---

<sup>1</sup>Data Science, LinkedIn, 700 East Middlefield, Mountain View, CA 94043, USA

<sup>2</sup>Department of Biostatistics, Columbia University, New York, NY 10032, USA

<sup>3</sup>Department of Biostatistics, The University of Texas MD Anderson Cancer Center, Houston, TX 77030, USA

<sup>4</sup>Department of Statistics, University of Michigan at Ann Arbor, Ann Arbor, MI 48109, USA

\* Co-first authors

### Corresponding author:

Jianhua Hu, Department of Biostatistics, Columbia University, New York, NY 10032, USA

Email: jh3992@cumc.columbia.edu

**Table 1.** FPRs at the nominal level of 5% for scenario *DE-3*. The values in the table are percentages.

Scenario <i>DE-3</i>	Nominal	5%			
	Level				
Gene Length	Sample Size	<i>TTS</i>	<i>edgeR</i>	<i>DESeq2</i>	<i>Limma</i>
5	40	5.60	4.34	5.04	4.94
	60	5.38	4.30	5.00	5.06
	80	5.64	4.62	5.08	5.10
	100	5.34	4.50	5.40	4.88
10	40	5.48	4.50	5.08	4.96
	60	5.38	4.76	5.46	4.96
	80	5.16	4.52	5.02	5.00
	100	5.36	4.50	4.92	4.88
30	40	5.26	3.98	4.74	4.54
	60	5.60	4.22	5.04	4.94
	80	5.02	4.20	4.82	4.80
	100	4.50	3.96	4.34	4.52

expression data to simulate up-regulated DE genes and  $\delta_g = (1 + X_g)^{-1}$  for 5% of the expression data to simulate down-regulated DE genes, where  $X_g$  follows an exponential distribution with rate=2. Let  $\delta_g = 1$  for the remaining 90% of the expression data to simulate non-DE genes.

In each scenario, we ran 5,000 Monte Carlo samples. For the quantile related test, we used  $\tau = 0.5$  for testing both scenarios at a nominal level of 5%.

To convert the gene-level count data to exon-level count data, we allocated the count of gene  $g$  from subject  $i$  to  $m_i$  exon regions with probabilities  $p_1^g, \dots, p_j^g$  and  $\sum_{j=1}^{m_i} p_j^g = 1$ . Following the allocation method of Lin and Sun<sup>56</sup>, we generated  $p_j^g$  by  $p_j^g = P_j^g / \sum_{j=1}^{m_i} P_j^g$ , where  $P_j^g$  follows the standard exponential distribution. The majority of the reads were mapped to 1 or 2 exon regions when  $k \leq 5$ .

The results for scenario *DE-3* are shown in Table 1. The FPRs of the four tests considered here are all around the nominal level.

The results for scenario *DE-4* are shown in Table 2. All methods have correct FPRs at the appropriate level and achieve similar TPRs for various exon lengths and sample sizes. Such results demonstrate that the proposed test is robust and comparable with *edgeR*, *DESeq2*, and *Limma* even when the data do not follow our assumed model.

**Table 2.** FPRs and TPRs at the nominal level of 5% for scenarios *DE-4*. The values in the table are percentages.

Scenario		FPR				TPR			
<i>DE-4</i>									
Gene Length	Sample Size	<i>TTS</i>	<i>edgeR</i>	<i>DESeq2</i>	<i>Limma</i>	<i>TTS</i>	<i>edgeR</i>	<i>DESeq</i>	<i>Limma</i>
5	40	5.60	4.29	5.53	5.60	60.80	60.20	61.80	60.40
	60	5.47	4.69	5.36	5.84	72.60	71.80	73.60	71.00
	80	5.49	4.73	5.33	5.00	75.80	76.60	76.80	75.40
	100	5.33	4.58	5.29	5.51	79.60	78.80	80.20	77.80
10	40	5.69	4.36	5.22	5.18	62.00	61.40	63.60	59.60
	60	4.93	4.09	4.71	5.02	71.60	72.00	72.00	70.60
	80	5.40	4.40	5.07	5.69	78.80	77.80	79.00	76.80
	100	5.53	4.87	5.38	5.73	80.20	80.20	80.40	79.80
30	40	5.47	4.33	5.18	5.07	65.40	63.00	65.00	61.60
	60	4.98	4.47	4.87	5.56	71.80	70.80	72.00	69.60
	80	5.00	4.51	4.87	5.18	77.00	75.40	76.80	76.40
	100	5.44	4.80	5.38	5.04	77.80	78.00	78.00	77.00

## Section B

We list Lemma 1, proof of Lemma 1, and proof of Theorem 1 in this section.

**Lemma 1.** *If  $\lim_{n_1, n_0 \rightarrow \infty} (n_1 + n_0)^{-1} U_f$  exists,  $E\|C_i\|_1^3 < \infty$ , the number of exon region  $m_i$  is some fixed number, and  $f_{ij}$  are uniformly bounded away from 0 and infinity, then we have the Bahadur representation on  $\hat{\gamma}(\tau)$ ,*

$$\hat{\gamma}(\tau) - \gamma(\tau) = U_f^{-1} \sum_i m_i^{-1} \sum_{j=1}^{m_i} C_i^* \psi_\tau(e_{ij}(\tau)) + o_p((n_0 + n_1)^{-\frac{1}{2}}),$$

and the representation of  $\bar{e}_\tau(d)$ ,

$$\bar{e}_\tau(d) = (\sum_{D_i=d} \sum_j^{m_i} e_{ij}^+(\tau))^{-1} \sum_{D_i=d} \sum_j^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) + o_p((N_0 + N_1)^{-\frac{1}{2}}).$$

**Proof of Lemma 1** The Bahadur representation of the  $(K + 2) \times 1$  parameter estimator  $\hat{\beta}(\tau)$ , according to Koenker<sup>42</sup> equation 4.4, can be written as

$$\hat{\beta}(\tau) - \beta(\tau) = D_\beta^{-1} (n_0 + n_1)^{-1} \sum_i m_i^{-1} \sum_{j=1}^{m_i} \mathbf{x}_i^* \psi_\tau(e_{ij}(\tau)) + (n_0 + n_1)^{-1/2} R_n,$$

where diagonal matrix  $D_\beta = \lim_{(n_0+n_1) \rightarrow \infty} (n_0 + n_1)^{-1} \sum_i \hat{f}_{n(0)} \mathbf{x}_i^* \mathbf{x}_i^{*T}$ ,  $\hat{f}_{n(0)}$  is the estimated conditional density function of  $e_{ij}$  given  $(D_i, C_i)$  evaluated at 0,  $\mathbf{x}_i^* = (1, D_i^*, C_i^*)$ ,  $R_n = o_p(1)$ , and  $\psi_\tau(e_{ij}(\tau)) = \tau - e_{ij}^-$ .

Then, as  $n_0, n_1 \rightarrow \infty$ ,  $\sum_i \hat{f}_{n(0)} \mathbf{x}_i^* \mathbf{x}_i^{*T} = \begin{pmatrix} \sum_i \hat{f}_{n(0)} & 0 & 0 \\ 0 & \sum_i \hat{f}_{n(0)} D_i^{*2} & 0 \\ 0 & 0 & \sum_i \hat{f}_{n(0)} C_i^* C_i^{*T} \end{pmatrix}$ ,

so the diagonal matrix  $D_\beta = \begin{pmatrix} \frac{\sum_i \hat{f}_{n(0)}}{(n_0+n_1)} & 0 & 0 \\ 0 & \frac{\sum_i \hat{f}_{n(0)} D_i^{*2}}{(n_0+n_1)} & 0 \\ 0 & 0 & \frac{\sum_i \hat{f}_{n(0)} C_i^* C_i^{*T}}{(n_0+n_1)} \end{pmatrix} + o_p(1)$ .

Using the right bottom corner of  $D_\beta^{-1}$ , we can obtain the following,

$$\begin{aligned} & \hat{\gamma}(\tau) - \gamma(\tau) \\ &= \left[ \left\{ \frac{\sum_i \hat{f}_{n(0)} C_i^* C_i^{*T}}{(n_0+n_1)} \right\}^{-1} + o_p(1) \right] (n_0 + n_1)^{-1} \sum_i m_i^{-1} \sum_{j=1}^{m_i} C_i^* \psi_\tau(e_{ij}(\tau)) + \\ & o_p((n_0 + n_1)^{-\frac{1}{2}}). \\ &= \left( \sum_i \hat{f}_{n(0)} C_i^* C_i^{*T} \right)^{-1} \sum_i m_i^{-1} \sum_{j=1}^{m_i} C_i^* \psi_\tau(e_{ij}(\tau)) + o_p((n_0 + n_1)^{-\frac{1}{2}}). \end{aligned}$$

The last equality follows from the central Limit Theorem for  $\sum_i m_i^{-1} \sum_{j=1}^{m_i} C_i^* \psi_\tau(e_{ij}(\tau))$

. The proof of the second part of Lemma 2.1 is equivalent to proving

$$\begin{aligned}
& \left\{ \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} \hat{e}_{ij}^+(\tau) \right\}^{-1} \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} e_{ij}(\tau) \hat{e}_{ij}^+(\tau) \\
& - \{n_d(1-\tau)\}^{-1} \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) \\
& = o_p((n_0 + n_1)^{-\frac{1}{2}})
\end{aligned}$$

Then, we need to verify the first and second equations below:

$$n_d^{-1} \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} \hat{e}_{ij}^+(\tau) = 1 - \tau + o_p((n_0 + n_1)^{-\frac{1}{2}})$$

$$n_d^{-1} \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} e_{ij}(\tau) \{ \hat{e}_{ij}^+(\tau) - e_{ij}^+(\tau) \} = o_p((n_0 + n_1)^{-\frac{1}{2}}).$$

We can demonstrate the first equation by the second inequality in corollary 2.1 of Koenker<sup>42</sup>,

$$n_d^{-1} \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} \hat{e}_{ij}^+(\tau) \leq 1 - \tau \leq n_d^{-1} \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} \hat{e}_{ij}^+(\tau) + n_d^{-1} p;$$

hence,  $n_d^{-1} \sum_{D_i=d} m_i^{-1} \sum_j^{m_i} \hat{e}_{ij}^+(\tau) = (1 - \tau) + o_p(n_d^{-1}) = (1 - \tau) + o_p((n_1 + n_0)^{-1/2})$ .

To prove the second equation, we can use lemma 4.6 of He and Shao<sup>33</sup> and lemma 11.2 of Owen<sup>71</sup>. For more details, refer to Koenker<sup>42</sup> and He and Shao<sup>33</sup>.

**Proof of Theorem 1** According to Lemma 1, and  $\delta(\tau) = 0$ , under the null hypothesis, we can write

$$\begin{aligned}
T_\tau^{TTS}(n_1, n_0) &= \left\{ \sum_{D_i=1} \sum_{j=1}^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) / N_1 - \sum_{D_i=0} \sum_{j=1}^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) / N_0 \right\} (1 - \tau)^{-1} \\
&- \{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \} U_f^{-1} \sum_{i=1}^n m_i^{-1} \sum_{j=1}^{m_i} \mathbf{C}_i^* \psi_\tau(e_{ij}(\tau)) \\
&+ o_p((n_0 + n_1)^{-1/2}) \\
&= T_\tau^*(n_1, n_0) + o_p((n_0 + n_1)^{-1/2}).
\end{aligned}$$

where

$$T_{\tau}^*(n_1, n_0) = \left\{ \sum_{D_i=1} \sum_{j=1}^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) / N_1 - \sum_{D_i=0} \sum_{j=1}^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) / N_0 \right\} (1 - \tau)^{-1} \\ - \{ \bar{C}_{\tau}^T(1) - \bar{C}_{\tau}^T(0) \} U_f^{-1} \sum_{i=1}^n m_i^{-1} \sum_{j=1}^{m_i} C_i^* \psi_{\tau}(e_{ij}(\tau)).$$

Under the null hypothesis, the mean and variance of the test statistics are

$$E(T_{\tau}^*(n_1, n_0)) = \left\{ \sum_{D_i=1} \sum_{j=1}^{m_i} E(e_{ij}(\tau) e_{ij}^+(\tau)) / N_1 - \sum_{D_i=0} \sum_{j=1}^{m_i} E(e_{ij}(\tau) e_{ij}^+(\tau)) / N_0 \right\} (1 - \tau)^{-1} \\ = (1 - \tau)^{-1} E(e_{ij}(\tau) e_{ij}^+(\tau)) (1 - 1) = 0.$$

$$\begin{aligned}
& \text{Var}(T_\tau^*(n_1, n_0)) = \\
& (1 - \tau)^{-2}(V_1/N_1^2 + V_0/N_0^2) \\
& + \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} \left\{ \sum_i m_i^{-2} \sum_{j=1}^{m_i} C_i^* C_i^{*T} \tau(1 - \tau) \right\} U_f^{-1} \left\{ \bar{C}_\tau(1) - \bar{C}_\tau(0) \right\} \\
& + \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} \left\{ \sum_i m_i^{-2} \sum_{j \neq j'} C_i^* C_i^{*T} (\zeta - \tau^2) \right\} U_f^{-1} \left\{ \bar{C}_\tau(1) - \bar{C}_\tau(0) \right\} \\
& + (1 - \tau)^{-1} \left\{ \sum_{D_i=1} \sum_{j=1}^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) / N_1 \right\} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} \times \\
& U_f^{-1} \sum_{D_i=1}^n m_i^{-1} \sum_{j=1}^{m_i} C_i^* \psi_\tau(e_{ij}(\tau)) \\
& - (1 - \tau)^{-1} \left\{ \sum_{D_i=0} \sum_{j=1}^{m_i} e_{ij}(\tau) e_{ij}^+(\tau) / N_0 \right\} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} \times \\
& U_f^{-1} \sum_{D_i=0}^n m_i^{-1} \sum_{j=1}^{m_i} C_i^* \psi_\tau(e_{ij}(\tau)) \\
& - (1 - \tau)^{-1} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} / N_1 \sum_{D_i=1}^n \sum_{j=1}^{m_i} C_i^* m_i^{-1} e_{ij} e_{ij}^+ \psi_\tau(e_{ij}(\tau)) \\
& + (1 - \tau)^{-1} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} / N_0 \sum_{D_i=0}^n \sum_{j=1}^{m_i} C_i^* m_i^{-1} e_{ij} e_{ij}^+ \psi_\tau(e_{ij}(\tau)) \\
& = (1 - \tau)^{-2}(V_1/N_1^2 + V_0/N_0^2) \\
& + \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} \left[ \sum_i m_i^{-2} \left\{ \sum_{k=1}^{m_j} C_i^* C_i^{*T} \tau(1 - \tau) + \sum_{j \neq j'} C_i^* C_i^{*T} (\zeta - \tau^2) \right\} \right] \times \\
& U_f^{-1} \left\{ \bar{C}_\tau(1) - \bar{C}_\tau(0) \right\} \\
& - (1 - \tau)^{-1} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} / N_1 \times \\
& \left\{ \sum_{D_i=1}^n \sum_{j_1=1}^{m_i} \sum_{j_2=1}^{m_i} C_i^* m_i^{-1} e_{ij_1} e_{ij_2}^+ \psi_\tau(e_{ij_2}(\tau)) - \sum_{D_i=1}^n \sum_{j_1=1}^{m_i} e_{ij_1} e_{ij_1}^+ \sum_{j_2=1}^{m_i} m_i^{-1} C_i^* \psi_\tau(e_{ij_2}(\tau)) \right\} \\
& + (1 - \tau)^{-1} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} / N_0 \times \\
& \left\{ \sum_{D_i=0}^n \sum_{j_1=1}^{m_i} \sum_{j_2=1}^{m_i} C_i^* m_i^{-1} e_{ij_1} e_{ij_2}^+ \psi_\tau(e_{ij_2}(\tau)) - \sum_{D_i=0}^n \sum_{j_1=1}^{m_i} e_{ij_1} e_{ij_1}^+ \sum_{j_2=1}^{m_i} m_i^{-1} C_i^* \psi_\tau(e_{ij_2}(\tau)) \right\}
\end{aligned}$$

where

$$V_d = \sum_{D_i=d} \sum_{j=1}^{m_i} \text{var}(e_{ij}e_{ij}^+) + \sum_{D_i=d} \sum_{j \neq j'} \text{cov}(e_{ij}e_{ij}^+, e_{ij'}e_{ij'}^+),$$

which can be estimated by  $s_{n_0, n_1}^2$ .

$$\begin{aligned} s_{n_0, n_1}^2 &= (1 - \tau)^{-2} \left\{ V_1 / \left( \sum_{D_i=1} m_i \right)^2 + V_0 / \left( \sum_{D_i=0} m_i \right)^2 \right\} \\ &+ \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} \left[ \sum_i m_i^{-2} \left\{ \sum_{k=1}^{m_j} C_i^* C_i^{*T} \tau (1 - \tau) + \sum_{j \neq j'} C_i^* C_i^{*T} (\zeta - \tau^2) \right\} \right] \\ &\times U_f^{-1} \left\{ \bar{C}_\tau(1) - \bar{C}_\tau(0) \right\} \\ &- (1 - \tau)^{-1} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} / N_1 \\ &\times \left\{ \sum_{D_i=1}^n \sum_{j_1=1}^{m_i} \sum_{j_2=1}^{m_i} C_i^* m_i^{-1} \hat{e}_{ij_1} \hat{e}_{ij_1}^+ \tau - \sum_{D_i=1}^n \sum_{j_1=1}^{m_i} \hat{e}_{ij_1} \hat{e}_{ij_1}^+ \sum_{j_2=1}^{m_i} m_i^{-1} C_i^* \psi_\tau(\hat{e}_{ij_2}(\tau)) \right\} \\ &+ (1 - \tau)^{-1} \left\{ \bar{C}_\tau^T(1) - \bar{C}_\tau^T(0) \right\} U_f^{-1} / N_0 \\ &\times \left\{ \sum_{D_i=0}^n \sum_{j_1=1}^{m_i} \sum_{j_2=1}^{m_i} C_i^* m_i^{-1} \hat{e}_{ij_1} \hat{e}_{ij_1}^+ \tau - \sum_{D_i=0}^n \sum_{j_1=1}^{m_i} \hat{e}_{ij_1} \hat{e}_{ij_1}^+ \sum_{j_2=1}^{m_i} m_i^{-1} C_i^* \psi_\tau(\hat{e}_{ij_2}(\tau)) \right\} \end{aligned}$$

By the central limit theorem,  $T_\tau^*(n_1, n_0)$  is asymptotically normal with mean 0 and variance. Thus, by Lemma 1 and  $T_\tau(n_1, n_0) - T_\tau^*(n_1, n_0) = o_p((n_0 + n_1)^{-1/2})$ , we prove the asymptotic normality of the test statistic  $T_\tau(n_1, n_0)$ .



## Section C

Tables 3, 4, 5, 6, 7, 8 list genes that are detected by *TTS* but not by the other methods, with the supporting medical literature.

**Table 3.** List of genes detected by *TTS* but missed by *QRS<sub>c</sub>*

Test method	Gene list
<i>QRS<sub>c</sub></i>	<i>ADAMTS9, C3ORF21, MBD4, ZMAT3, FOXP1, GSK3B PLD1, SIAH2, C3orf33, EHHADH, IQCB1, RPL14 BTLA, CCR5, DOCK3, CTNNB1, IGF2BP2, MYD88 PFKFB4, PIK3CB, VPRBP, TLR9, VHL, LRRN1 PAK2, EAF2, TF, VGLL4, RASSF1, FHIT, FLNB</i>
Reference	27,44,89,112,129,131 16,19,21,35,63,90 3,17,20,88,99,134 4,24,60,106,109,132 1,40,74,79,118,126,135

**Table 4.** List of genes detected by *TTS* but missed by *LME*

Test method	Gene list
<i>LME</i>	<i>ADAMTS9, C3orf33, CCR5, CTNNA1, EHHADH, FHIT, FLNB, GSK3B, IGF2BP2, IQCB1, PAK2, RPL14, SENP2, SIAH2, UBA3, VPRBP, VGLL4</i>
Reference	17,19,35,44,88,135 1,3,21,40,90,131 50,63,106,108,126

**Table 5.** List of genes detected by *TTS* but missed by *Limma* and *edgeR*

Test method	Gene list
<i>Limma</i>	<i>ADAMTS9, C3orf33, CCR5, FHIT, GSK3B, IGF2BP2</i> <i>PAK2, RABL3, RBM5, SETD2, TF</i>
Reference	3,17,35,44,131,135 40,79,93,105,127
<i>edgeR</i>	<i>CACNA2D3, CAMK1, CCR5, FBXL2, GSK3B, SETD2</i> <i>SLC6A20</i>
Reference	15,17,52,54,105,131 101

**Table 6.** List of genes detected by *TTS* but missed by *DESeq2*, part 1

Gene list	<i>ABCC5, ABHD5, ACTL6A, AGTR1</i> <i>ALDH1L1, ATP11B, ATP1B3, ATR</i> <i>B3GALNT1, BAP1, BCHE, BTLA</i> <i>C3orf1, C3orf21, C3orf33, CACNA2D2</i> <i>CACNA2D3, CAMK1, CBLB, CCDC37</i> <i>CCR5, CD86, CDC25A, CDCP1</i> <i>CHL1, CLDN18, COPB2, CSTA</i> <i>CTDSPL, CTNNB1, CX3CR1, DCBLD2</i> <i>DCUN1D1, DLEC1, DOCK3, DTX3L,</i> <i>DVL3, EAF2, EHHADH, EIF2A</i> <i>EIF4A2, EIF4G1, EIF5A2, EPHB3</i> <i>ETV5, FAM107A, FBXL2, FGD5</i>
Reference	19,34,110,118 29,66,70,92 5,58,68,77 7,19,99,103 12,35,116,129 51,52,54,96 17,18,31,114 9,25,59,84 9,81,83,88 47,98,122,134 11,37,85,120 15,24,73,130

**Table 7.** List of genes detected by *TTS* but missed by *DESeq2*, part 2

Gene list	<i>FHIT, FLNB, FNDC3B, FOXP1 FXR1, GATA2, GORASP1, GSK3B HDAC11, HES1, HYAL1, HYAL2 IGF2BP2, IL17RD, IL17RE, IQCB1 IQSEC1, KIAA1524, LEPREL1, LIMD1 LMCD1, LPP, LRIG1 LRRN1, LTF, LZTFL1, MAGI1, MASP1, MBD4, MCM2, METTL6 MINA, MME, MYD88, MYLK, NEK10 NEK4, NISCH, NPRL2 OPA1, P2RY14, PAK2, PDCD6IP PFKFB4, PIK3CB, PLD1, PLS1</i>
Reference	1,10,27,135 19,24,43,131 2,41,107 3,21,115 22,24,86,87 14,45,46 13,24,36,111 39,78,89,94 20,49,95,97 61,64,69,102 40,53,60,80,117 16,25,109 62,72,113

**Table 8.** List of genes detected by *TTS* but missed by *DESeq2*, part 3

Gene list	<i>POLQ, PTH1R, PTPRG</i> <i>RABL3, RAP2B, RASSF1, RFC4</i> <i>RNF7, RPL14, RPL22L1, RUVBL1</i> <i>RYBP, SATB1, SEMA3B, SENP2</i> <i>SETD2, SIAH2, SLC4A7, SLC6A20</i> <i>SLCO2A1, SMARCC1, SPCS1, TBL1XR1, TF</i> <i>TFRC, TGFBR2, THPO, THRB, TIGIT</i> <i>TKT, TLR9, TNFSF10</i> <i>TRAIP, TRIM59, UBA3, UBE2E2</i> <i>VGLL4, VHL, VPRBP, WWTR1</i> <i>XPC, ZMAT3, ZMYND10</i>
Reference	25,74,75,127 48,67,90,123 57,82,104,108 28,63,101,105 23,55,79,100,133 8,38,48,121,125 4,32,119 24,50,91,124 65,106,126,132 29,112,128

## References

1. Bandaru, S., Zhou, AX., Rouhi, P., Zhang, Y., Bergo, MO., Cao, Y., Akyürek, LM. . Targeting filamin B induces tumor growth and metastasis via enhanced activity of matrix metalloproteinase-9 and secretion of VEGF-A. *Oncogenesis* 2014; **3**: e119.
2. Baumgart, A., Mazur, PK., Anton, M., Rudelius, M., Schwamborn, K., Feuchtinger, A., Behnke, K., Walch, A., Braren, R., Peschel, C., Duyster, J., Siveke, JT., Dechow, T. Opposing role of Notch1 and Notch2 in a Kras(G12D)-driven murine non-small cell lung cancer model. *Oncogene* 2015; **34**:(5) 578-588.
3. Bell, J. L., Wächter, K., Mühleck, B., Pazaitis, N., Köhn, M., Lederer, M., Hüttelmaier, S. Insulin-like growth factor 2 mRNA-binding proteins (IGF2BPs): post-transcriptional drivers of cancer progression? *Cellular and Molecular Life Sciences* 2013; **70**:(15), 2657-2675.
4. Belmont, L., Rabbe, N., Antoine, M., Cathelin, D., Guignabert, C., Kurie, J., Cadranel, J., Wislez, M. Expression of TLR9 in tumor-infiltrating mononuclear cells enhances angiogenesis and is associated with a worse survival in lung cancer. *International Journal of Cancer* 2014; **134**: 765-777.
5. Beumer, JH., Fu, KY., Anyang, BN., Siegfried, JM., Bakkenist, CJ. Functional analyses of ATM, ATR and Fanconi anemia proteins in lung carcinoma : ATM, ATR and FA in lung carcinoma. *BMC Cancer* 2015; **15**: 649.
6. Braga, EA., Loginov, VI., Pronina, IV., Khodyrev, DS., Rykov, SV., Burdenny, AM., Friedman, MV., Kazubskaya, TP., Kubatiev, AA., Kushlinskii, NE. Upregulation of RHOA and NKIRAS1 genes in lung tumors is associated with loss of their methylation as well as with methylation of regulatory miRNA genes. *Biochemistry* 2015; **80**:(4), 483-494.
7. Brass, N., Rác, A., Heckel, D., Remberger, K., Sybrecht, GW., Meese, EU. Amplification of the genes BCHE and SLC2A2 in 40% of squamous cell carcinoma of the lung. *Cancer Research* 1997; **57**:(11), 2290-2294.
8. Buchhagen, DL. Frequent involvement of chromosome 3p alterations in lung carcinogenesis: allelotypes of 215 established cell lines at six chromosome 3p loci. *J Cell Biochem* 1996; **24**:198-209.
9. Butler MW, Fukui T, Salit J, Shaykhiev R, Mezey JG, Hackett NR, Crystal RG. Modulation of cystatin A expression in human airway epithelium related to genotype, smoking, COPD, and lung cancer. *Cancer Research* 2001; **71**:(7), 2572-2581.
10. Cai, C., Rajaram, M., Zhou, X., Liu, Q., Marchica, J., Li, J., Powers, R. S. Activation of multiple cancer pathways and tumor maintenance function of the 3q amplified oncogene FND3B. *Cell Cycle* 2012; **11**:(9), 1773-1781.
11. Cao, Y., Wei, M., Li, B., Liu, Y., Lu, Y., Tang, Z., Lu, T., Yin, Y., Qin, Z., Xu, Z. Functional role of eukaryotic translation initiation factor 4 gamma 1 (EIF4G1) in NSCLC. *Oncotarget* 2016; **7**:(17), 24242-24251.
12. Carboni GL, Gao B, Nishizaki M, Xu K, Minna JD, Roth JA, Ji L. CACNA2D2-mediated apoptosis in NSCLC cells is associated with alterations of the intracellular calcium signaling and disruption of mitochondria membrane integrity. *Oncogene* 2003; **22**:(4), 615-626.
13. Dorr, C., Janik, C., Weg, M., Been, R. A., Bader, J., Kang, R., Ng, B., Foran, L., Landman, SR., O'Sullivan, M.G., Steinbach, M., Sarver, A.L., Silverstein, K., Largaespada, DA., Starr, T. K. Transposon Mutagenesis Screen Identifies Potential Lung Cancer Drivers and CUL3 as

- a Tumor Suppressor. *Molecular Cancer Research: MCR* 2015; **13**:(8), 1238-1247.
14. Chang, CY., Lin, SC., Su, WH., Ho, CM., Jou, YS. Somatic LMCD1 mutations promoted cell migration and tumor metastasis in hepatocellular carcinoma. *Oncogene* 2012; **31**:(21), 2640-2652.
  15. Chen, BB., Glasser, JR., Coon, TA., Mallampalli, RK. F-box protein FBXL2 exerts human lung tumor suppressor-like activity by ubiquitin-mediated degradation of cyclin D3 resulting in cell cycle arrest. *Oncogene* 2012; **31**:(20), 2566-2579.
  16. Chen, Q., Hongu, T., Sato, T., Zhang, Y., Ali, W., Cavallo, J. A., van der Velden, A., Tian, H., Di Paolo, G., Nieswandt, B., Kanaho, Y., Frohman, M. A. Key roles for the lipid signaling enzyme phospholipase d1 in the tumor microenvironment during tumor angiogenesis and metastasis. *Science Signaling* 2012; **5**: ra79.
  17. Cheng, Z., Shi, Y., Yuan, M., Xiong, D., Zheng, J., Zhang, Z. Chemokines and their receptors in lung cancer progression and metastasis. *Journal of Zhejiang University. Science. B* 2016; **17**:(5), 342-351.
  18. Chiu, KL., Kuo, TT., Kuok, QY., Lin, YS., Hua, CH., Lin, CY., Su, PY., Lai, LC., Sher, YP. ADAM9 enhances CDCP1 protein expression by suppressing miR-218 for lung tumor metastasis. *Scientific Reports* 2015; **5**: 16426.
  19. Comtesse, N., Keller, A., Diesinger, I., Bauer, C., Kayser, K., Huwer, H., Lenhof, H. P., Meese, E. Frequent overexpression of the genes FXR1, CLAPM1 and EIF4G located on amplicon 3q26-27 in squamous cell carcinoma of the lung. *International Journal of Cancer* 2007; **120**: 2538-2544.
  20. Coste, I., Le Corf, K., Kfoury, A., Hmitou, I., Druillennec, S., Hainaut, P., Eychene, A., Lebecque, S., Renno, T. Dual function of MyD88 in RAS signaling and inflammation, leading to mouse and human cell transformation. *Journal of Clinical Investigation* 2010; **120**: 3663-3667.
  21. de Miguel, F. J., Sharma, R. D., Pajares, M. J., Montuenga, L. M., Rubio, A., Pio, R. Identification of alternative splicing events regulated by the oncogenic factor SRSF1 in lung cancer. *Cancer Research* 2014; **74**: 1105-1115.
  22. De, P., Carlson, J., Leyland-Jones, B., Dey, N. Oncogenic nexus of cancerous inhibitor of protein phosphatase 2A (CIP2A): An oncoprotein with many hands. *Oncotarget* 2014; **5**:(13), 4581-4602.
  23. DelBove, J., Rosson, G., Strobeck, M., Chen, J., Archer, T. K., Wang, W., Knudsen, E. S., Weissman, B. E. Identification of a core member of the SWI/SNF complex, BAF155/SMARCC1, as a human tumor suppressor gene. *Epigenetics* 2011; **6**:(12), 1444-1453.
  24. Dmitriev, A. A., Kashuba, V. I., Haraldson, K., Senchenko, V. N., Pavlova, T. V., Kudryavtseva, A. V., Anedchenko, E. A., Krasnov, G. S., Pronina, I. V., Loginov, V. I., Kondratieva, T. T., Kazubskaya, T. P., Braga, E. A., Yenamandra, S. P., Ignatjev, I., Ernberg, I., Klein, G., Lerman, M. I., Zabarovsky, E. R. Genetic and epigenetic analysis of non-small cell lung cancer with NotI-microarrays. *Epigenetics* 2012; **7**: 502-513.
  25. Erdogan, E., Klee, EW., Thompson, EA., Fields, AP. Meta-analysis of oncogenic protein kinase Ciota signaling in lung adenocarcinoma. *Clinical Cancer Research* 2009; **15**:(5), 1527-1533.



26. Feng, H., Lopez, GY., Kim, CK., Alvarez, A., Duncan, CG., Nishikawa, R., Nagane, M., Su, AJ., Auron, PE., Hedberg, ML., Wang, L., Raizer, JJ., Kessler, JA., Parsa, AT., Gao, WQ., Kim, SH., Minata, M., Nakano, I., Grandis, JR., McLendon, RE., Bigner, DD., Lin, HK., Furnari, FB., Cavenee, WK., Hu, B., Yan, H., Cheng, SY. EGFR phosphorylation of DCBLD2 recruits TRAF6 and stimulates AKT-promoted tumorigenesis. *Journal of Clinical Investigation* 2012; **124**:(9), 3741-3756.
27. Feng, J., Zhang, X., Zhu, H., Wang, X., Ni, S., Huang, J. High expression of FoxP1 is associated with improved survival in patients with non-small cell lung cancer. *American Journal of Clinical Pathology* 2012; **138**: 230-235.
28. Gorbatenko, A., Olesen, C. W., Boedtkjer, E., Pedersen, S. F. (2014). Regulation and roles of bicarbonate transporters in cancer. *Frontiers in Physiology* **5**: 130.
29. Guo, S., Yan, F., Xu, J., Bao, Y., Zhu, J., Wang, X., Wu, J., Li, Y., Pu, W., Liu, Y., Jiang, Z., Ma, Y., Chen, X., Xiong, M., Jin, L., Wang, J. Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). *Clinical Epigenetics* 2015; **7**:(1) 3.
30. Hardcastle, T. J., Kelly, K. A. BaySeq: Empirical Bayesian Methods For Identifying Differential Expression In Sequence Count Data. *BMC Bioinformatics* 2010; **11**: 422-436.
31. He, N., Li, C., Zhang, X., Sheng, T., Chi, S., Chen, K., Wang, Q., Vertrees, R., Logrono, R., Xie, J. Regulation of lung cancer cell growth and invasiveness by beta-TRCP. *Molecular Carcinogenesis* 2005; **42**:(1), 18-28.
32. He, W., Wang, Q., Xu, J., Xu, X., Padilla, M. T., Ren, G., Gou, X., Lin, Y. Attenuation of TNFSF10/TRAIL-induced apoptosis by an autophagic survival pathway involving TRAF2- and RIPK1/RIP1-mediated MAPK8/JNK activation. *Autophagy* 2012; **8**:(12), 1811-1821.
33. He, X. M., Shao, Q. M. A general Bahadur representation of M-estimators and its application to linear regression with nonstochastic designs. *Annals of Statistics* 1996; **24**: 2608-2630.
34. He, Y., Correa, AM., Raso, MG., Hofstetter, WL., Fang, B., Behrens, C., Roth, JA., Zhou, Y., Yu, L., Wistuba, II., Swisher, SG., Pataer, A. The role of PKR/eIF2 signaling pathway in prognosis of non-small cell lung cancer. *PLoS One* 2011; **6**:(11), e24855.
35. Hu, F., Yang, S., Lv, S., Peng, Y., Meng, L., Gou, L., Zhang, X. Analysis of AC3-33 gene expression in multiple organ cancer and adjacent normal tissue by RNA in situ hybridization. *Oncology Letter* 2015; **9**: 2795-2798.
36. Iijima, H., Tomizawa, Y., Iwasaki, Y., Sato, K., Sunaga, N., Dobashi, K., Saito, R., Nakajima, T., Minna, JD., Mori, M. Genetic and epigenetic inactivation of LTF gene at 3p21.3 in lung cancers. *International Journal of Cancer* 2006; **118**:(4), 797-801.
37. Ji, XD., Li, G., Feng, YX., Zhao, JS., Li, JJ., Sun, ZJ., Shi, S., Deng, YZ., Xu, JF., Zhu, YQ., Koeffler, HP., Tong, XJ., Xie, D. EphB3 is overexpressed in non-small-cell lung cancer and promotes tumor metastasis by enhancing cell survival and migration. *Cancer Research* 2011; **71**:(3) 1156-1166.
38. Jiang, XP., Elliott, RL., Head, JF. Manipulation of iron transporter genes results in the suppression of human and mouse mammary adenocarcinomas. *AntiCancer Research* 2010; **30**:(3) 759-765.
39. Kang, J. U., Koo, S. H., Kwon, K. C., Park, J. W., Kim, J. M. Identification of novel candidate target genes, including EPHB3, MASP1 and SST at 3q26.2-q29 in squamous cell carcinoma of the lung. *BMC Cancer* 2009; **9**: 237.

40. Kikuchi, T., Hassanein, M., Amann, J. M., Liu, Q. F., Slebos, R. J., Rahman, J., Kaufman, J. M., Zhang, X. Q., Hoeksema, M. D., Harris, B. K., Li, M., Shyr, Y., Gonzalez, A. L., Zimmerman, L. J., Liebler, D. C., Massion, P. P., Carbone, D. P. In-depth Proteomic Analysis of Nonsmall Cell Lung Cancer to Discover Molecular Targets and Candidate Biomarkers. *Molecular & Cellular Proteomics* 2012; **11**: 916-932.
41. Koenke, E., Witt, O., Oehme, I. HDAC Family Members Intertwined in the Regulation of Autophagy: A Druggable Vulnerability in Aggressive Tumor Entities. *Cells* 2015; **4**(2), 135—168.
42. Koenker, R. *Quantile Regression*. 2005; Cambridge University Press.
43. Kumar, MS., Hancock, DC., Molina-Arcas, M., Steckel, M., East, P., Diefenbacher, M., Armenteros-Monterroso, E., Lassailly, F., Matthews, N., Nye, E., Stamp, G., Behrens, A., Downward, J. The GATA2 transcriptional network is requisite for RAS oncogene-driven non-small cell lung cancer. *Cell* 2012; **149**(3), 642-655.
44. Kumar, S., Rao, N., Ge, R. Emerging Roles of ADAMTSs in Angiogenesis and Cancer. *Cancers* 2012; **4**(4), 1252-1299.
45. Kuriyama, S., Yoshida, M., Yano, S., Aiba, N., Kohno, T., Minamiya, Y., Goto, A., Tanaka, M. LPP inhibits collective cell migration during lung cancer dissemination. *Oncogene* 2016; **35**(8), 952-964.
46. Kvarnbrink, S., Karlsson, T., Edlund, K., Botling, J., Lindquist, D., Jirstrom, K., Micke, P., Henriksson, R., Johansson, M., Hedman, H. LRIG1 is a prognostic biomarker in non-small cell lung cancer. *Acta Oncologica* 2015; **54**(8), 1113-1119.
47. Kwong, J., Lee, JY., Wong, KK., Zhou, X., Wong, DT., Lo, KW., Welch, WR., Berkowitz, RS., Mok, SC. Candidate tumor-suppressor gene DLEC1 is frequently downregulated by promoter hypermethylation and histone hypoacetylation in human epithelial ovarian cancer. *Neoplasia* 2006; **8**(4), 268-278.
48. Lazar, V., Suo, C., Orear, C., van den Oord, J., Balogh, Z., Guegan, J., Job, B., Meurice, G., Ripoché, H., Calza, S., Hasmats, J., Lundeberg, J., Lacroix, L., Vielh, P., Dufour, F., Lehtiö, J., Napieralski, R., Eggermont, A., Schmitt, M., Cadranel, J., Besse, B., Girard, P., Blackhall, F., Validire, P., Soria, JC., Dessen, P., Hansson, J., Pawitan, Y. Integrated molecular portrait of non-small cell lung cancers. *BMC Med Genomics* 2013; **6**: 53.
49. Leithner, K., Wohlkoenig, C., Stacher, E., Lindenmann, J., Hofmann, NA., Gallé, B., Guelly, C., Quehenberger, F., Stiegler, P., Smolle-Jüttner, FM., Philipsen, S., Popper, HH., Hrszenjak, A., Olschewski, A., Olschewski, H. Hypoxia increases membrane metallo-endopeptidase expression in a novel lung cancer ex vivo model - role of tumor stroma cells. *BMC Cancer* 2014; **14**: 40.
50. Li, L.H., Wang, M.S., Yu, G. Y., Chen, P., Li, H., Wei, D.P., Zhu, J., Xie, L., Jia, H. X., Shi, J. Y., Li, C. J., Yao, W. T., Wang, Y. C., Gao, Q., Jeong, L. S., Lee, H. W., Yu, J. H., Hu, F. Q., Mei, J., Wang, P., Chu, Y. W., Qi, H., Yang, M., Dong, Z. M., Sun, Y., Hoffman, R. M., Jia, L. J. Overactivated Neddylaton Pathway as a Therapeutic Target in Lung Cancer. *Journal of the National Cancer Institute* 2014; **106**: dju083.
51. Li, P., Wang, X., Liu, Z., Liu, H., Xu, T., Wang, H., Gomez, DR., Nguyen, QN., Wang, LE., Teng, Y., Song, Y., Komaki, R., Welsh, JW., Wei, Q., Liao, Z. Single Nucleotide Polymorphisms in CBLB, a Regulator of T-Cell Response, Predict Radiation Pneumonitis and Outcomes After Definitive Radiotherapy for Non-Small-Cell Lung Cancer. *Clinical Lung*

- Cancer* 2016; **17**:(4), 253-262
52. Li, Y., Zhu, CL., Nie, CJ., Li, JC., Zeng, T., Zhou, J., Chen, J., Chen, K., Li, F., Liu, HB., Qin, YR., Guan, XY. Investigation of Tumor Suppressing Function of CACNA2D3 in Esophageal Squamous Cell Carcinoma. *PLoS ONE* 2013; **8**:(4), e60027.
  53. Liu, SG., Yuan, SH., Wu, HY., Huang, CS., Liu, J. The programmed cell death 6 interacting protein insertion/deletion polymorphism is associated with non-small cell lung cancer risk in a Chinese Han population. *Tumour Biology* 2014; **35**:(9), 8679-8683.
  54. Liu, X., Yu, X., Xie, J., Zhan, M., Yu, Z., Xie, L., Zeng, H., Zhang, F., Chen, G., Yi, X., Zheng, J. ANGPTL2/LILRB2 signaling promotes the propagation of lung cancer cells. *Oncotarget* 2015; **6**:(25), 21004-21015.
  55. Liu, Y., Sun, W., Zhang, K., Zheng, H., Ma, Y., Lin, D., Zhang, X., Feng, L., Lei, W., Zhang, Z., Guo, S., Han, N., Tong, W., Feng, X., Gao, Y., Cheng, S. Identification of genes differentially expressed in human primary lung squamous cell carcinoma. *Lung Cancer* 2007; **56**:(3), 307-317.
  56. Lin, W., Sun, F. CEDER: Accurate detection of differentially expressed genes by combining significance of exons using RNA-Seq *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 2012; **9**: 1281-1292.
  57. Loginov, VI., Dmitriev, AA., Senchenko, VN., Pronina, IV., Khodyrev, DS., Kudryavtseva, AV., Krasnov, GS., Gerashchenko, GV., Chashchina, LI., Kazubskaya, TP., Kondratieva, TT., Lerman, MI., Angeloni, D., Braga, EA., Kashuba, VI. Tumor Suppressor Function of the SEMA3B Gene in Human Lung and Renal Cancers. *PLoS One* 2015; **10**:(5), e0123369.
  58. Mesri, M., Birse, C., Heidbrink, J., McKinnon, K., Brand, E., Bermingham, CL., Feild, B., Fitzhugh, W., He, T., Ruben, S., Moore, PA. Identification and characterization of angiogenesis targets through proteomic profiling of endothelial cells in human cancer tissues. *PLoS One* 2013; **8**:(11), e78885.
  59. Micke, P., Mattsson, JS., Edlund, K., Lohr, M., Jirstrom, K., Berglund, A., Botling, J., Rahnenfuhrer, J., Marincevic, M., Pontén, F., Ekman, S., Hengstler, J., Wöll, S., Sahin, U., Türeci, O. Aberrantly activated claudin 6 and 18.2 as potential therapy targets in non-small-cell lung cancer. *International Journal of Cancer* 2014; **135**:(9), 2206-2214.
  60. Minchenko, O. H., Tsuchihara, K., Minchenko, D. O., Bikfalvi, A., Esumi, H. Mechanisms of regulation of PFKFB expression in pancreatic and gastric cancer cells. *World Journal of Gastroenterology* 2014; **14**: 13705-12717.
  61. Moniz, L. S., Stambolic, V. Nek10 Mediates G2/M Cell Cycle Arrest and MEK Autoactivation in Response to UV Irradiation . *Molecular and Cellular Biology* 2011; **31**:(1), 30-42.
  62. Montgrain, PR., Phun, J., Vander Werff, R., Quintana, RA., Davani, AJ., Hastings, RH. Parathyroid-hormone-related protein signaling mechanisms in lung carcinoma growth inhibition. *Springerplus* 2015; **4**: 268.
  63. Müller, S., Chen, Y., Ginter, T., Schäfer, C., Buchwald, M., Schmitz, L. M., Klitzsch, J., Schütz, A., Haitel, A., Schmid, K., Moriggl, R., Kenner, L., Friedrich, K., Haan, C., Petersen, I., Heinzel, T., Krämer, O. H. SIAH2 antagonizes TYK2-STAT3 signaling in lung carcinoma cells. *Oncotarget* 2014; **30**: 3184-3196.
  64. Nguyen, C. L., Possemato, R., Bauerlein, E. L., Xie, A., Scully, R., Hahn, W. C. Nek4 Regulates Entry into Replicative Senescence and the Response to DNA Damage in Human Fibroblasts. *Molecular and Cellular Biology* 2012; **32**:(19), 3963—3977.

65. Noguchi, S., Saito, A., Horie, M., Mikami, Y., Suzuki, HI., Morishita, Y., Ohshima, M., Abiko, Y., Mattsson, JS., König, H., Lohr, M., Edlund, K., Botling, J., Micke, P., Nagase, T. An integrative analysis of the tumorigenic role of TAZ in human non-small cell lung cancer. *Clinical Cancer Research* 2014; **20**:(17), 4660-4672.
66. Oguri T, Achiwa H, Sato S, Bessho Y, Takano Y, Miyazaki M, Muramatsu H, Maeda H, Niimi T, Ueda R. The determinants of sensitivity and acquired resistance to gemcitabine differ in non-small cell lung cancer: a role of ABCC5 in gemcitabine sensitivity. *Molecular Cancer Therapeutics* 2006; **5**:(7), 1800-1806.
67. O'Leary, MN., Schreiber, KH., Zhang, Y., Duc, A-CE., Rao, S., Hale, JS., Academia, EC., Shah, SR., Morton, JF., Holstein, CA., Martin, DB., Kaeberlein, M., Ladiges, WC., Fink, PJ., Mackay, VL., Wiest, DL., Kennedy, BK. The Ribosomal Protein Rpl22 Controls Ribosome Composition by Directly Repressing Expression of Its Own Paralog, Rpl2211. *PLoS Genetics* 2013; **9**:(8), e1003708.
68. Oleinik, NV., Krupenko, NI., Krupenko, SA. Epigenetic Silencing of ALDH1L1, a Metabolic Regulator of Cellular Proliferation, in Cancers. *Genes Cancer* 2011; **2**:(2), 130-139.
69. Ostrow, KL., Michailidi, C., Guerrero-Preston, R., Hoque, MO., Greenberg, A., Rom, W., Sidransky, D. Cigarette smoke induces methylation of the tumor suppressor gene NISCH. *Epigenetics* 2011; **8**:(4), 383-388.
70. Ou, J., Miao, H., Ma, Y., Guo, F., Deng, J., Wei, X., Zhou, J., Xie, GF., Shi, H., Xue, B., Liang, H., Yu, L. Loss of Abhd5 Promotes Colorectal Tumor Development and Progression by Inducing Aerobic Glycolysis and Epithelial-Mesenchymal Transition. *Cell Reports* 2014; **9**:(5), 1798-1811.
71. Owen, A. B. *Empirical Likelihood* 2001; Chapman & Hall/CRC.
72. Pitterle DM, Jolicoeur EM, Bepler G. Hot spots for molecular genetic alterations in lung cancer. *In Vivo* 1998; **12**:(6), 643-658.
73. Pastuszak-Lewandoska D, Czarnecka KH, Migdalska-Sek M, Nawrot E, Domańska D, Kiszalkiewicz J, Kordiak J, Antczak A, Górski P, Brzezińska-Lasota E. Decreased FAM107A Expression in Patients with Non-small Cell Lung Cancer. *Adv Exp Med Biol* 2015; **852**: 39-48.
74. Pelosi, G., Fumagalli, C., Trubia, M., Sonzogni, A., Rekhman, N., Maisonneuve, P., Galetta, D., Spaggiari, L., Veronesi, G., Scarpa, A., Malpeli, G., Viale, G. Dual role of RASSF1 as a tumor suppressor and an oncogene in neuroendocrine tumors of the lung. *AntiCancer Research* 2010; **30**: 4269-4281.
75. Peng, YG., Zhang, ZQ., Chen, YB., Huang, JA. Rap2b promotes proliferation, migration, and invasion of lung cancer cells. *Journal of Receptor and Signal Transduction Research* 2016; **36**:(5), 459-464.
76. Qian J, Hassanein M, Hoeksema MD, Harris BK, Zou Y, Chen H, Lu P, Eisenberg R, Wang J, Espinosa A, Ji X, Harris FT, Rahman SM, Massion PP. The RNA binding protein FXR1 is a new driver in the 3q26-29 amplicon and predicts poor prognosis in human cancers. *Proceedings of the National Academy of Sciences of the United States of America* 2015; **112**:(11), 3469-3474
77. Qian, J., Zou, Y., Wang, J., Zhang, B., Massion, P. P. Global gene expression profiling reveals a suppressed immune response pathway associated with 3q amplification in squamous carcinoma of the lung. *Genomics Data* 2015; **5**, 272-274.

78. Ramnath, N., Hernandez, FJ., Tan, DF., Huberman, JA., Natarajan, N., Beck, AF., Hyland, A., Todorov, IT., Brooks, JS., Bepler, G. MCM2 is an independent predictor of survival in patients with non-small-cell lung cancer. *Journal of Clinical Oncology* 2001; **19**:(22), 4259-4266.
79. Regina, S., Rollin, J., Bléchet, C., Iochmann, S., Reverdiau, P., Gruel, Y. Tissue factor expression in non-small cell lung cancer: relationship with vascular endothelial growth factor expression, microvascular density, and K-ras mutation. *Journal of Thoracic Oncology* 2008; **3**: 689-697.
80. Roberts, E. R., Thomas, K. J. The role of mitochondria in the development and progression of lung cancer. *Computational and Structural Biotechnology Journal* 2013; **6**: e201303019.
81. Schmall, A., Al-Tamari, HM., Herold, S., Kampschulte, M., Weigert, A., Wietelmann, A., Vipotnik, N., Grimminger, F., Seeger, W., Pullamsetti, SS., Savai, R. Macrophage and cancer cell cross-talk via CCR2 and CX3CR1 is a fundamental mechanism driving lung cancer. *American Journal of Respiratory and Critical Care Medicine* 2015; **191**:(4), 437-447.
82. Selinger, CI., Cooper, WA., Al-Sohaily, S., Mladenova, DN., Pangon, L., Kennedy, CW., McCaughan, BC., Storzaker, C., Kohonen-Corish, MR. Loss of special AT-rich binding protein 1 expression is a marker of poor survival in lung cancer. *Journal of Thoracic Oncology* 2011; **6**:(7), 1179-1189.
83. Senchenko, V., Anedchenko, E., Kondratieva, T., Krasnov, G., Dmitriev, A., Zabarovska, V., Pavlova, T., Kashuba, V., Lerman, M., Zabarovsky, E. Simultaneous down-regulation of tumor suppressor genes RBSP3/CTDSPL, NPRL2/G21 and RASSF1A in primary non-small cell lung cancer. *BMC Cancer* 2010; **10**: 75.
84. Senchenko, V., Krasnov, G., Dmitriev, A., Kudryavtseva, A., Anedchenko, E., Braga, E., Pronina, I., Kondratieva, T., Ivanov, S., Zabarovsky, E., Lerman, M. Loss of special AT-rich binding protein 1 expression is a marker of poor survival in lung cancer. *PLoS ONE* 2011; **6**:(3), e15612.
85. Shaoyan, X., Juanjuan, Y., Yalan, T., Ping, H., Jianzhong, L., Qinian, W. Downregulation of EIF4A2 in non-small-cell lung cancer associates with poor prognosis. *Clinical Lung Cancer* 2013; **14**:(6), 658-665.
86. Sharp, TV., Al-Attar, A., Foxler, DE., Ding, L., de A Vallim, TQ., Zhang, Y., Nijmeh, HS., Webb, TM., Nicholson, AG., Zhang, Q., Kraja, A., Spendlove, I., Osborne, J., Mardis, E., Longmore, GD. The chromosome 3p21.3-encoded gene, LIMD1, is a critical tumor suppressor involved in human lung cancer development. *Proceedings of the National Academy of Sciences of the United States of America* 2008; **105**:(50), 19932-19937.
87. Sheng, X., Wang, Z. Protein arginine methyltransferase 5 regulates multiple signaling pathways to promote lung cancer cell proliferation. *BMC Cancer* 2016; **16**: 567.
88. Shigemitsu, K., Sekido, Y., Usami, N., Mori, S., Sato, M., Horio, Y., Hasegawa, Y., Bader, S. A., Gazdar, A. F., Minna, J. D., Hida, T., Yoshioka, H., Imaizumi, M., Ueda, Y., Takahashi, M., Shimokata, K. Genetic alteration of the beta-catenin gene (CTNNB1) in human lung cancer and malignant mesothelioma and identification of a new 3p21.3 homozygous deletion. *Oncogene* 2001; **12**: 4249-4257.
89. Shin, M. C., Lee, S. J., Choi, J. E., Cha, S. I., Kim, C. H., Lee, W. K., Kam, S., Kang, Y. M., Jung, T. H., Park, J. Y. Glu346Lys Polymorphism in the Methyl-CpG Binding Domain 4 Gene and the Risk of Primary Lung Cancer. *Japanese Journal of Clinical Oncology* 2006; **36**: 483-488.

90. Shriver, S. P., Shriver, M. D., Tirpak, D. L., Bloch, L. M., Hunt, J. D., Ferrell, R. E., Siegfried, J. M. Trinucleotide repeat length variation in the human ribosomal protein L14 gene (RPL14): localization to 3p21.3 and loss of heterozygosity in lung and oral cancers. *Mutation Research* 1998; **406**: 9-23.
91. Soo Lee, N., Jin Chung, H., Kim, H.-J., Yun Lee, S., Ji, J.-H., Seo, Y., Han, S.-H., Choi, M., Yun, M., Lee, S.-G., Myung, K., Kim, Y., Kang, H., Kim, H. TRAIIP/RNF206 is required for recruitment of RAP80 to sites of DNA damage. *Nature Communications* 2016; **7**: 10463.
92. Sun, W., Wang, W., Lei, J., Li, H., Wu, Y. Actin-like protein 6A is a novel prognostic indicator promoting invasion and metastasis in osteosarcoma. *Oncology Reports* 2017; **37**:(4), 2405-2417.
93. Sutherland, LC., Wang, K., Robinson, AG. RBM5 as a putative tumor suppressor gene for lung cancer. *Journal of Thoracic Oncology* 2010; **5**:(3), 294-298.
94. Tan, XL., Moyer, AM., Fridley, BL., Schaid, DJ., Niu, N., Batzler, AJ., Jenkins, GD., Abo, RP., Li, L., Cunningham, JM., Sun, Z., Yang, P., Wang, L. Genetic variation predicting cisplatin cytotoxicity associated with overall survival in lung cancer patients receiving platinum-based chemotherapy. *Clinical Cancer Research* 2011; **17**:(17), 5801-5811.
95. Tan, X., Chen, M. MYLK and MYL9 expression in non-small cell lung cancer identified by bioinformatics analysis of public expression data. *Tumour Biology* 2014; **35**:(12), 12189-12200.
96. Tessema, M., Yingling, CM., Picchi, MA., Wu, G., Liu, Y., Weissfeld, JL., Siegfried, JM., Tesfaigzi, Y., Belinsky, SA. Epigenetic Repression of CCDC37 and MAP1B Links Chronic Obstructive Pulmonary Disease to Lung Cancer. *Journal of Thoracic Oncology* 2015; **10**:(8), 1181-1188.
97. Thakur, C., Chen, F. Current understanding of mdg/MINA in human cancers. *Genes & Cancer* 2015; **6**:(7-8), 288-302.
98. Thang, ND., Yajima, I., Kumasaka, M. Y., Iida, M., Suzuki, T., Kato, M. Deltex-3-like (DTX3L) stimulates metastasis of melanoma through FAK/PI3K/AKT but not MEK/ERK pathway. *Oncotarget* 2015; **6**:(16), 14290-14299.
99. Thommen, D., Schreiner, J., Muller, P., Herzig, P., Roller, A., Belousov, A., Umana, P., Pisa, P., Klein, C., Bacac, M., Fischer, O., Moersig, W., Prince, S., Levitsky, V., Karanikas, V., Lardinois, D., Zippelius, A. Progression of Lung Cancer Is Associated with Increased Dysfunction of T Cells Defined by Coexpression of Multiple Inhibitory Receptors. *Cancer Immunology Research* 2015; **3**:(12), 1344-1355.
100. Too, I. H. K., Ling, M. H. T. Signal Peptidase Complex Subunit 1 and Hydroxyacyl-CoA Dehydrogenase Beta Subunit Are Suitable Reference Genes in Human Lungs. *ISRN Bioinformatics* 2012; **20120**: 790452.
101. Tsou, J. A., Galler, J. S., Wali, A., Ye, W., Siegmund, K. D., Groshen, S., Laird, P., Turla, S., Koss, MN., Pass, HI., Laird-Offringa, I. A. DNA methylation profile of 28 potential marker loci in malignant mesothelioma. *Lung Cancer* 2007; **58**:(2), 220-230.
102. Ueda, K., Kawashima, H., Ohtani, S., Deng, WG., Ravoori, M., Bankson, J., Gao, B., Girard, L., Minna, JD., Roth, JA., Kundra, V., Ji, L. The 3p21.3 tumor suppressor NPRL2 plays an important role in cisplatin-induced resistance in human non-small-cell lung cancer cells. *Cancer Research* 2006; **66**:(19), 9682-9690.

103. Umeyama, H., Iwadate, M., Taguchi, YH. TINAGL1 and B3GALNT1 are potential therapy target genes to suppress metastasis in non-small cell lung cancer. *BMC Genomics* 2014; **15**, 1344-1355.
104. Voruganti, S., Xu, F., Qin, JJ., Guo, Y., Sarkar, S., Gao, M., Zheng, Z., Wang, MH., Zhou, J., Qian, B., Zhang, R., Wang, W. RYBP predicts survival of patients with non-small cell lung cancer and regulates tumor cell growth and the response to chemotherapy. *Cancer Letter* 2015; **369**:(2), 386-395.
105. Walter, DM., Venancio, OS., Buza, EL., Tobias, JW., Deshpande, C., Gudiel, AA., Kim-Kiselak, C., Cicchini, M., Yates, TJ., Feldser, DM. Systematic In Vivo Inactivation of Chromatin-Regulating Enzymes Identifies Setd2 as a Potent Tumor Suppressor in Lung Adenocarcinoma. *Cancer Research* 2017; **77**:(7) 1719-1729.
106. Wang, B. S., Liu, Y. Z., Yang, Y., Zhang, Y., Hao, J. J., Yang, H., Wang, X. M., Zhang, Z. Q., Zhan, Q. M., Wang, M. R. Autophagy negatively regulates cancer cell proliferation via selectively targeting VPRBP. *Clinical Science* 2013; **124**: 203-214.
107. Wang, F., Grigorieva, E. V., Li, J., Senchenko, V. N., Pavlova, T. V., Anedchenko, E. A., Kudryavtseva, A., Tsimanis, A., Angeloni, D., Lerman, M., Kashuba, Vladimir., Klein, G., Zabarovsky, E. R. HYAL1 and HYAL2 Inhibit Tumour Growth In Vivo but Not In Vitro. *PLoS ONE* 2008; **3**:(8) e3031.
108. Wang, J., Qian, J., Hoeksema, MD., Zou, Y., Espinosa, AV., Rahman, SM., Zhang, B., Massion, PP. Integrative genomics analysis identifies candidate drivers at 3q26-29 amplicon in squamous cell carcinoma of the lung. *Clinical Cancer Research* 2013; **19**: 5580-5590.
109. Wee, S., Wiederschain, D., Maira, S. M., Loo, A., Miller, A., Beaumont, R., Stegmeier, F., Yao, Y. M., Lengauer, C. PTEN-deficient cancers depend on PIK3CB. *PNAS* 2008; **105**: 13057-13062.
110. Wei, Q., Zhao, Y., Yang, ZQ., Dong, QZ., Dong, XJ., Han, Y., Zhao, C., Wang, EH. Dishevelled family proteins are expressed in non-small cell lung cancer and function differentially on tumor progression. *Lung Cancer* 2008; **62**:(2), 181-192.
111. Wei, Q., Chen, ZH., Wang, L., Zhang, T., Duan, L., Behrens, C., Wistuba, II., Minna, JD., Gao, B., Luo, JH., Liu, ZP. LZTFL1 suppresses lung tumorigenesis by maintaining differentiation of lung epithelial cells. *Oncogene* 2016; **35**:(20), 2655-2663.
112. Wen, Y., Gamazon, E. R., Bleibel, W. K., Wing, C., Mi, S., McIlwee, B. E., Delaney, S. M., Duan, S., Im, H. K., Dolan, M. E. An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. *Human Molecular Genetics* 2012; **21**: 1470-1480.
113. Wood, R. D., Doubl  , S. DNA polymerase (POLQ), double-strand break repair, and cancer. *DNA Repair* 2016; **44**, 22-32.
114. Wroblewski, JM., Bixby, DL., Borowski, C., Yannelli, JR. Characterization of human non-small cell lung cancer (NSCLC) cell lines for expression of MHC, co-stimulatory molecules and tumor-associated antigens. *Lung Cancer* 2001; **33**:(2-3), 181-194.
115. Wu, F., Xu, J., Huang, Q., Han, J., Duan, L., Fan, J., Lv, Z., Guo, M., Hu, G., Chen, L., Zhang, S., Tao, X., Ma, W., Jin, Y. The Role of Interleukin-17 in Lung Cancer. *Mediators of Inflammation* 2016; **2016**: 84940790.
116. Wu, H., Wang, W., Xu, H. Depletion of C3orf1/TIMMDC1 Inhibits Migration and Proliferation in 95D Lung Carcinoma Cells. *International Journal of Molecular Sciences* 2014; **15**:(11), 20555-20571.

117. Wu, X., Zang, W., Cui, S., Wang, M. Bioinformatics analysis of two microarray gene-expression data sets to select lung adenocarcinoma marker genes. *European Review for Medical and Pharmacological Sciences* 2012; **16**:(11), 1582-1587.
118. Xiao, w., Zhang, Q., Habermacher, G., Yang, X., Zhang, A. Y., Cai, X., Hahn, J., Liu, J., Pins, M., Doglio, L., Dhir, R., Gingrich, J., Wang, Z. U19/Eaf2 knockout causes lung adenocarcinoma, B-cell lymphoma, hepatocellular carcinoma and prostatic intraepithelial neoplasia. *Oncogene* 2008; **6**: 1536-1544.
119. Xu, IM., Lai, RK., Lin, SH., Tse, AP., Chiu, DK., Koh, HY., Law, CT., Wong, CM., Cai, Z., Wong, CC., Ng, IO. Transketolase counteracts oxidative stress to drive cancer development. *Proceedings of the National Academy of Sciences of the United States of America* 2016; **113**:(6), E725-34.
120. Xu, G., Shao, G., Pan, Q., Sun, L., Zheng, D., Li, M., Li, N., Shi, H., Ni, Y. MicroRNA-9 regulates non-small cell lung cancer cell invasion and migration by targeting eukaryotic translation initiation factor 5A2. *American Journal of Translational Research* 2017; **9**:(2), 478–488.
121. Xu, JB., Bao, Y., Liu, X., Liu, Y., Huang, S., Wang, JC. Defective expression of transforming growth factor beta type II receptor (TGFB2) in the large cell variant of non-small cell lung carcinoma. *Lung Cancer* 2007; **58**:(1), 36-43.
122. Yoo, J., Lee, SH., Lym, KI., Park, SY., Yang, SH., Yoo, CY., Jung, JH., Kang, SJ., Kang, CS. Immunohistochemical Expression of DCUN1D1 in Non-small Cell Lung Carcinoma: Its Relation to Brain Metastasis. *Cancer Research and Treatment* 2012; **44**:(1), 57-62.
123. Yuan, XS., Wang, ZT., Hu, YJ., Bao, FC., Yuan, P., Zhang, C., Cao, JL., Lv, W., Hu, J. Downregulation of RUVBL1 inhibits proliferation of lung adenocarcinoma cells by G1/S phase cell cycle arrest via multiple mechanisms. *Tumor Biology* 2016; **37**:(12), 16015-16027.
124. Zhan, W., Han, T., Zhang, C., Xie, C., Gan, M., Deng, K., Fu, M., Wang, J. TRIM59 Promotes the Proliferation and Migration of Non-Small Cell Lung Cancer Cells by Upregulating Cell Cycle Related Proteins. *PLOS ONE* 2015; **10**:(11), e0142596.
125. Zhang L, Wang J, Wei F, Wang K, Sun Q, Yang F, Jin H, Zheng Y, Zhao H, Wang L, Yu W, Zhang X, An Y, Yang L, Zhang X, Ren X. Profiling the dynamic expression of checkpoint molecules on cytokine-induced killer cells from non-small-cell lung cancer patients. *Oncotarget* 2016; **7**:(28), 43604-43615.
126. Zhang, W., Gao, Y., Li, P., Shi, Z., Guo, T., Li, F., Han, X., Feng, Y., Zheng, C., Wang, Z., Li, F., Chen, H., Zhou, Z., Zhang, L., Ji, H. VGLL4 functions as a new tumor suppressor in lung cancer by negatively regulating the YAP-TEAD transcriptional complex. *Cell Research* 2014; **24**: 331-343.
127. Zhang, W., Sun, J., Luo, J. High Expression of Rab13 is Associated with Poor Survival of Patients with Non-Small Cell Lung Cancer via Repression of MAPK8/9/10-Mediated Autophagy. *Medical Science Monitor: International Medical Journal of Experimental and Clinical Research* 2016; **22**: 1582—1588.
128. Zhang, X., He, N., Gu, D., Wickliffe, J., Salazar, J., Boldogh, I., Xie, J. Genetic Evidence for XPC-KRAS Interactions During Lung Cancer Development. *Journal of Genetics and Genomics* 2015; **42**:(10), 589-596.



129. Zhang, Y., Gu, C., Shi, H., Zhang, A., Kong, X., Bao, W., Deng, D., Ren, L., Gu, D. Association between C3orf21, TP63 polymorphisms and environment and NSCLC in never-smoking Chinese population. *Gene* 2012; **497**: 93-97.
130. Zhang, Z., Newton, K., Kummerfeld, S. K., Webster, J., Kirkpatrick, D. S., Phu, L., Eastham-Anderson, J., Liu, J., Lee, W., Wu, J., Li, H., Junttila, M., Dixit, V. M. Transcription factor Etv5 is essential for the maintenance of alveolar type II cells. *Proceedings of the National Academy of Sciences of the United States of America* 2017; **114**:(915), 3903-3908.
131. Zheng, H., Saito, H., Masuda, S., Yang, X., Takano, Y. Phosphorylated GSK3beta-ser9 and EGFR are good prognostic factors for lung carcinomas. *AntiCancer Research* 2007; **27**: 3561-3569.
132. Zhou, Q., Chen, T., Ibe, J. C., Raj, J. U., Zhou, G. Knockdown of von Hippel-Lindau protein decreases lung cancer cell proliferation and colonization. *FEBS Letter* 2012; **21**: 1510-1515.
133. Zhu, Q., Liang, X., Dai, J., Guan, X. Prostaglandin transporter, SLCO2A1, mediates the invasion and apoptosis of lung cancer cells via PI3K/AKT/mTOR pathway. *International journal of clinical and experimental pathology* 2015; **8**:(8), 9175-9181.
134. Zhu, X., Gao, G., Chu, K., Yang, X., Ren, S., Li, Y., Wu, H., Huang, Y., Zhou, C. Inhibition of RAC1-GEF DOCK3 by miR-512-3p contributes to suppression of metastasis in non-small cell lung cancer. *The International Journal of Biochemistry & Cell Biology* 2015; **61**: 103114.
135. Zöchbauer-Müller, S., Wistuba, II., Minna, JD., Gazdar, AF. Fragile histidine triad (FHIT) gene abnormalities in lung cancer. *Clinical Lung Cancer* 2000; **2**: 141-145.