

Correction to: Prognostic Features of Signal Transducer and Activator of Transcription 3 in an ER(+) Breast Cancer Model System

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CITATION: Li-Yu D. Liu, Li-Yun Chang, Wen-Hung Kuo et al. Correction to: Prognostic Features of Signal Transducer and Activator of Transcription 3 in an ER(+) Breast Cancer Model System. *Cancer Informatics* 2014;13:125–129 doi: 10.4137/CIN.S20237.

RECEIVED: August 15, 2014. **ACCEPTED FOR PUBLICATION:** September 15, 2014.

ACADEMIC EDITOR: JT Efrid, Editor in Chief

TYPE: Corrigendum

FUNDING: The original article was funded by grants (NSC95-2314-B-002-255-MY3 and NSC982314-B-002-093-MY2) to Fon-Jou Hsieh.

COMPETING INTERESTS: Authors disclose no potential conflicts of interest.

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The authors of Li-Yu D. Liu, Li-Yun Chang, Wen-Hung Kuo et al. Prognostic features of signal transducer and activator of transcription 3 in an ER(+) breast cancer model system. *Cancer Informatics*. 2014;13:21–45. doi: 10.4137/CIN.S12493. recently brought to the attention of the Editor in Chief, Dr. J. T. Efrid, corrections they wished to make to the paper. The Editor in Chief reviewed these with reference to applicable Committee on Publication Ethics guidelines and determined that publication of a separate corrigendum was an appropriate response to the authors' request. The authors' full statement is given hereafter.

We, as the authors of the paper “Prognostic features of signal transducer and activator of transcription 3 in an ER (+) breast cancer model system”, published in *Cancer Informatics* 2014;13 21–45, wish to correct Figures 3F, 7A, 7B, S6.2–6.3, S7.1–7.5 and Tables 2, 3.

We made unexpected mistakes during generating genome-wide data of 90th percentile Kaplan-Meier survival analysis on the gene of interest using R package. We have generated multiple sets of survival curves beginning with the earlier publications. To the best of our knowledge, all of them are correct except for 72 A cohort and a few data in 90 A cohort in this paper. The new Figure 3F, Tables 2–3 and Figures S6.2–6.3 have the corrected data, marked in red in Tables 2–3.

Additionally, we have made new Figures 7A and B to replace the old ones to be consistent with the original text.

In some instances, the text of the article also reflects errors in the data, and is hereby corrected as follows:

Page 23, right column.

This sentence from the original article:

Kaplan-Meier survival analyses²¹ were done using the “survival” package in R (version 2.15.1) for the gene profiles of 90 A cohort, 91 A cohort, 181 A cohort or the extracted gene pools of interest in the assigned cohorts.

is corrected to read as follows:

Kaplan-Meier survival analyses²¹ were done using the “survival” package in R (version 2.15.1) for the gene profiles of 90 A cohort, 72 A cohort, 181 A cohort or the extracted gene pools of interest in the assigned cohorts.

Page 30, legends of tables 2 and 3

To be consistent with new Figure 3F, the legend of Table 2 from the original article:

Table 2. The prognostic values for inferred target genes of *STAT3* and *MYC* in the 90 A cohort.

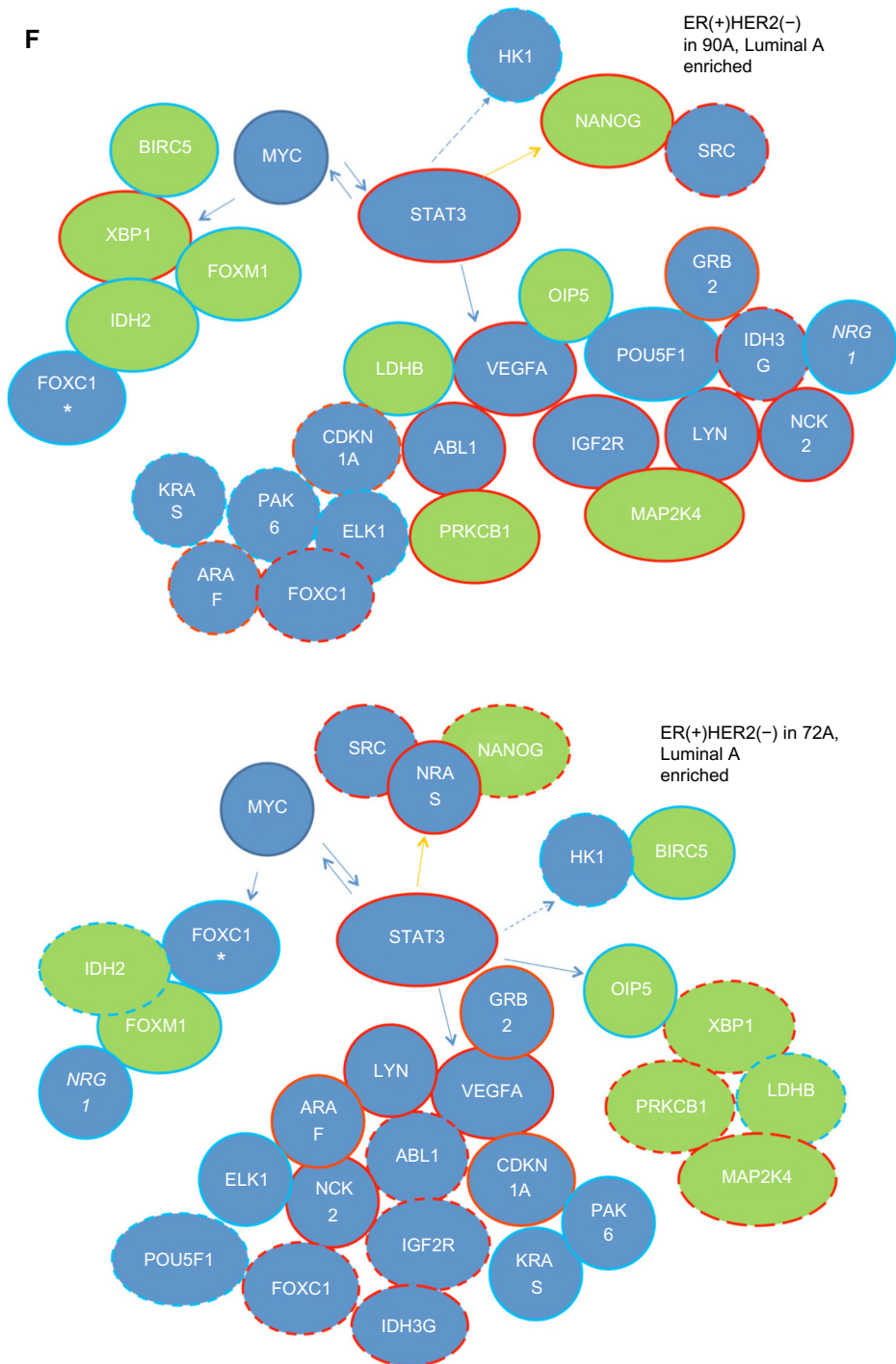


Figure 3F.

is corrected to read as follows:

Table 2. The prognostic values for inferred target genes of *STAT3* and *MYC* or of **STAT3* in the 90 A cohort (Fig. 3F).

To be consistent with new Figure 3F, the legend of Table 3 from the original article:

Table 3. The prognostic values for inferred target genes of *STAT3* and *MYC* in the 72 A cohort.

is corrected to read as follows:

Table 3. The prognostic values for inferred target genes of *STAT3* and *MYC* or of **STAT3* in the 72 A cohort (Fig. 3F).

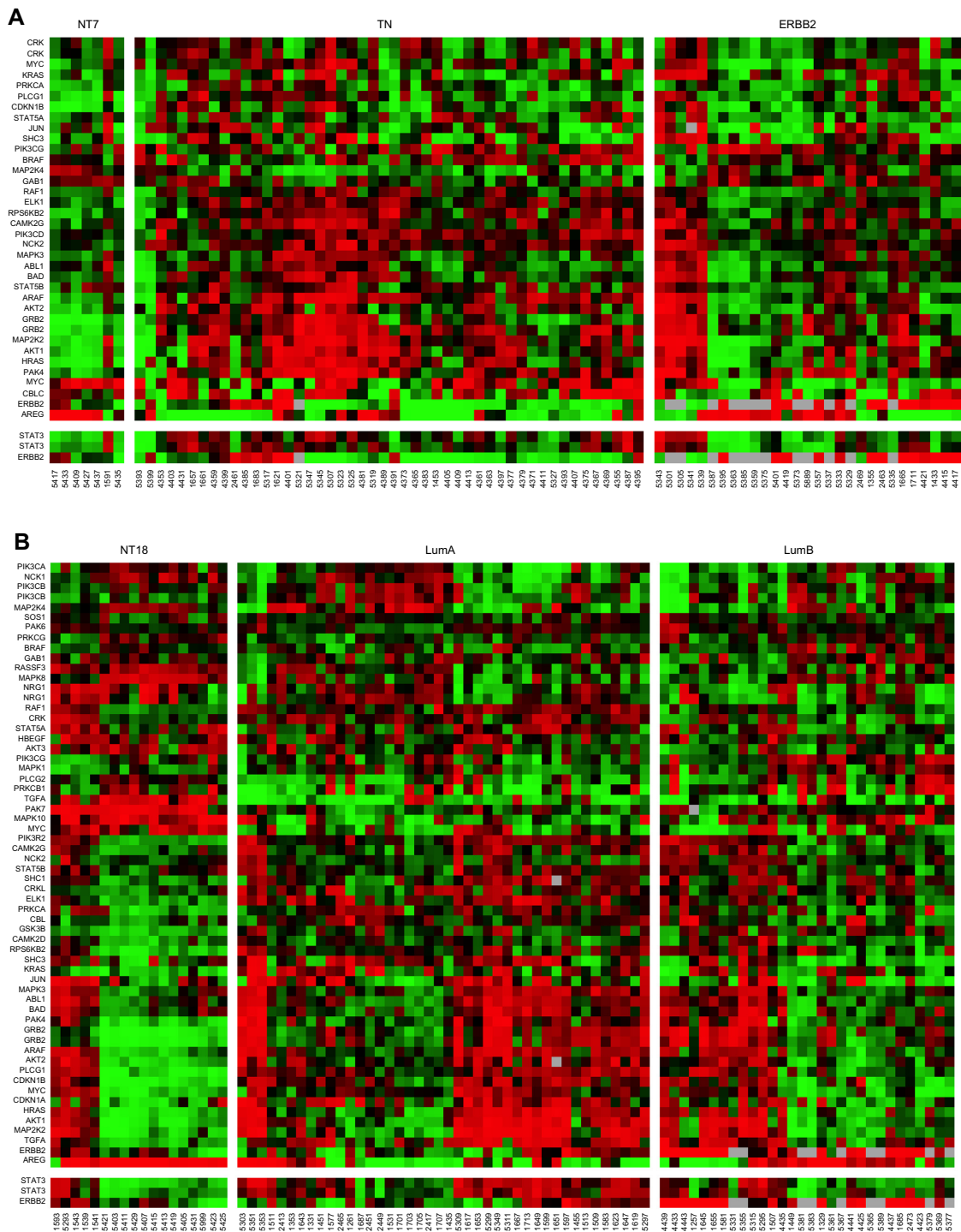


Figure 7A,B.

Page 31, right column.

This sentence from the original article:

High levels of *IDH3G* are a favorable prognosis predictor in 72 A cohort (Table 3).
should be regarded as deleted.

Page 35, left column

This sentence from the original article:

Surprisingly, *STAT3* regulates 59% (60/101) of ERBB2 signaling molecules in the 90 A cohort.

is corrected to read as follows:

Surprisingly, *STAT3* regulates 59% (60/101) of ERBB2 signaling molecules in the 90 A cohort (Table S4.12).

This sentence from the original article:



Table 2.

GENE SYMBOL (FEATURE NO.)	INCREASED EXPRESSION LEVEL	P VALUE	PATHWAYS
ABL1 (8019)	poor prognosis	0.046	ERBB2, PDGFRB, cell cycle and angiogenesis
IGF2R (1723)	poor prognosis	0.048	angiogenesis
PRKCB1 (6676)	good prognosis	0.033	ERBB2 and VEGF
MAP2 K4 (18964)	good prognosis	0.034	ERBB2
NRG1 (11559)	good prognosis	0.011	ERBB2
LYN (19236)	poor prognosis	0.001	PDGFRB and angiogenesis
STAT3 (4386)	poor prognosis	0.028	PDGFRB and angiogenesis
STAT3 (15013)	poor prognosis	0.002	PDGFRB and angiogenesis
VEGFA (1135)	poor prognosis	0.02	VEGF and angiogenesis
VEGFA (15367)	poor prognosis	0.008	VEGF and angiogenesis
OIP5 (16433)	poor prognosis	0.013	FOXC1 network
NCK2 (3851)	poor prognosis	0.029	ERBB2 and PDGFRB
LDHB (20259)	poor prognosis	0.038	Warburg effect
GRB2 (16731)	poor prognosis	0.019	ERBB2 and PDGFRB
*NANOG (C12928.2)	good prognosis	0.024	EMT
POU5F1 (6057)	good prognosis	0.02	EMT
GRB2 (1952)	poor prognosis	0.03	ERBB2 and PDGFRB

The expression patterns of these signaling molecules shown in heatmaps (Fig. 7B) indicate that *STAT3* mediated regulation of these 6 signaling molecules (*PRKCB1*, *MAP2K4*, *NRG1*, *NCK2*, *ABL1* and *GRB2*) provides a good prognostic indicator in the 90 A cohort (Table 2).

is corrected to read as follows:

The expression patterns of these signaling molecules shown in heatmaps (Fig. 7B) indicate that *STAT3* mediated regulation of these 5 signaling molecules (*MAP2K4*, *NRG1*, *NCK2*, *ABL1* and *GRB2*) provides a poor prognostic indicator in the 90 A cohort (Table 2).

Page 36, left column

This sentence from the original article: For instance, we found the expression levels of *GRB2*, *NCK2*, *STAT3*, *PRKCB1*, *MAP2K4*, *ABL1*, *IGF2R*, *LYN*, and *VEGFA* in the *STAT3* network to be predictors for poor clinical outcome in the 90 A cohort.

is corrected to read as follows:

For instance, we found the expression levels of *NANOG*, *GRB2*, *NCK2*, *STAT3*, *PRKCB1*, *MAP2K4*, *ABL1*, *IGF2R*, *LYN*, and *VEGFA* in the *STAT3* network to be predictors for poor clinical outcome in the 90 A cohort.

Table 3.

GENE SYMBOL	REGULATION STATUS	BIOCHEMICAL PATHWAY	PROGNOSIS	REGULATORS
GRB2	up	ERBB2 and PDGFRB	poor	MYC and STAT3
CDKN1A	up	p53, cell cycle and ERBB2	poor	MYC and STAT3
ARAF	up	ERBB2	poor	MYC and STAT3
NCK2	up	ERBB2 and PDGFRB	poor	MYC and STAT3
PAK6	up	ERBB2	good	MYC and STAT3
KRAS	up	ERBB2 and VEGF	good	MYC and STAT3
STAT3	up	PDGFRB and angiogenesis	poor	MYC and STAT3
ELK1	up	FOXC1 network and ERBB2	good	MYC and STAT3
OIP5	down	FOXC1 network	good	MYC and STAT3
*NRAS	up	ERBB2	poor	STAT3
LYN	up	PDGFRB and angiogenesis	poor	MYC and STAT3
VEGFA	up	angiogenesis	poor	MYC and STAT3



This sentence from the original article:

Alternately, the expression levels of *NANOG*, *OIP5*, *LDHB*, *NRG1* and *POU5F1* in the *STAT3* network are predicted to be good prognostic factors in the 90 A cohort (Fig. 3F and Table 2).

is corrected to read as follows:

Alternately, the expression levels of *OIP5*, *LDHB*, *NRG1* and *POU5F1* in the *STAT3* network are predicted to be good prognostic factors in the 90 A cohort (Fig. 3F and Table 2).

This sentence from the original article:

Moreover, there are 6 poor and 5 good prognostic factors in the *STAT3* network of 72 A cohort (Fig. 3F and Table 3).

is corrected to read as follows:

Moreover, there are 8 poor and 4 good prognostic factors in the *STAT3* network of 72 A cohort (Fig. 3F and Table 3).

Page 37, right column

This sentence from the original article:

We found 9 poor prognostic factors and 5 good prognostic factors of the *STAT3* network in the 90 A cohort (Fig. 3F and Table 2).

is corrected to read as follows:

We found 10 poor prognostic factors and 4 good prognostic factors of the *STAT3* network in the 90 A cohort (Fig. 3F and Table 2).

Page 41, right column

These sentences from the original article:

It contains relatively high levels of *GRB2*, *LYN*, *IGF2R*, *VEGFA*, *STAT3*, *NCK2*, *OIP5* and *ABL1* and low levels of *MAP2K4*, *PRKCB*, *POU5F1* and *NRG1*, indicating poor prognosis. Low levels of *LDHB* and *NANOG* predict good prognosis.

are corrected to read as follows:

It contains relatively high levels of *GRB2*, *LYN*, *IGF2R*, *VEGFA*, *STAT3*, *NCK2*, *OIP5* and *ABL1* and low levels of *MAP2K4*, *PRKCB*, *POU5F1*, *NRG1* and *NANOG*, indicating poor prognosis. Relative low levels of *LDHB* predict good prognosis.

Supplementary Files

Please also view the Supplementary Files PDF, which contains corrected versions of Supplementary Figures S6.2–S6.3 and S7.1–S7.5.