CORRIGENDUM

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lncRNA HAR1B has potential to be a predictive marker for pazopanib therapy in patients with sarcoma

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Subsequently to the publication of the above paper, the authors realized that the layouts of Tables I and III had been presented incorrectly, and that they had overlooking acknowledging researchers who had provided them with the cell lines in the Acknowledgements section of the paper.

Consequently, the correctly organized versions of Tables I and 3 are shown on the subsequent pages. Concerning the oversight with the Acknowledgements section, this section of the declarations should be changed to the following (added text is highlighted in bold):

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Note that the above errors did not affect the results or conclusions reported in this paper, and all the authors agree with this corrigendum. The authors thank the editor of Oncology Letters for presenting them with the opportunity of publishing this Corrigendum and apologize to the readership of the journal for any inconvenience caused.

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Table I. Summary of patient/tumor characteristics and treatment outcomes for 23 patients/tumors analyzed via microarray analyses.

| Factors                  | Total, n (%) (n=23) | Responder, n (%) (n=13) | Non-Responder, n (%) (n=10) |
|--------------------------|---------------------|------------------------|---------------------------|
| Sex                      |                     |                        |                           |
| Male                     | 14 (61)             | 7 (54)                 | 7 (70)                    |
| Female                   | 9 (39)              | 6 (46)                 | 3 (30)                    |
| Age (years)              |                     |                        |                           |
| Median                   | 65                  | 65                     | 62                        |
| Range                    | 20-76               | 20-76                  | 31-76                     |
| ECOG Performance Status  |                     |                        |                           |
| 0                        | 9 (39)              | 7 (54)                 | 2 (20)                    |
| 1                        | 13 (57)             | 5 (38)                 | 8 (80)                    |
| 2                        | 1 (4)               | 1 (8)                  | 0 (0)                     |
| >2                       | 0 (0)               | 0 (0)                  | 0 (0)                     |
| Treatment line           |                     |                        |                           |
| 1st line                 | 1 (4)               | 1 (8)                  | 0 (0)                     |
| 2nd line                 | 12 (52)             | 7 (54)                 | 5 (50)                    |
| 3rd line                 | 7 (30)              | 3 (23)                 | 4 (40)                    |
| 4th line                 | 3 (13)              | 2 (15)                 | 1 (10)                    |
| Pathology                |                     |                        |                           |
| Myxoid LPS               | 5 (22)              | 2 (15)                 | 3 (30)                    |
| LMS                      | 3 (13)              | 2 (15)                 | 1 (10)                    |
| UPS                      | 3 (13)              | 2 (15)                 | 1 (10)                    |
| SFT                      | 2 (9)               | 1 (8)                  | 1 (10)                    |
| OS                       | 2 (9)               | 1 (8)                  | 1 (10)                    |
| ASPS                     | 2 (9)               | 2 (15)                 | 0 (0)                     |
| US                       | 1 (4)               | 1 (8)                  | 0 (0)                     |
| AS                       | 1 (4)               | 1 (8)                  | 0 (0)                     |
| ES                       | 1 (4)               | 1 (8)                  | 0 (0)                     |
| ESFT                     | 2 (9)               | 0 (0)                  | 2 (20)                    |
| CCS                      | 1 (4)               | 0 (0)                  | 1 (10)                    |
| Primary site             |                     |                        |                           |
| Extremity                | 12 (52)             | 8 (62)                 | 4 (40)                    |
| Trunk                    | 2 (9)               | 1 (8)                  | 1 (10)                    |
| Retroperitoneum          | 1 (4)               | 1 (8)                  | 0 (0)                     |
| Thoracic cavity          | 1 (4)               | 1 (8)                  | 0 (0)                     |
| Liver                    | 1 (4)               | 1 (8)                  | 0 (0)                     |
| Pancreas                 | 1 (4)               | 1 (8)                  | 0 (0)                     |
| Abdominal cavity         | 1 (4)               | 0 (0)                  | 1 (10)                    |
| Oral                     | 1 (4)               | 0 (0)                  | 1 (10)                    |
| Pelvis                   | 1 (4)               | 0 (0)                  | 1 (10)                    |
| Sternum                  | 1 (4)               | 0 (0)                  | 1 (10)                    |
| Eye                      | 1 (4)               | 0 (0)                  | 1 (10)                    |

ECOG, Eastern Cooperative Oncology Group; LPS, liposarcoma; LMS, leiomyosarcoma; UPS, undifferentiated pleomorphic sarcoma; SFT, solitary fibrous tumor; OS, osteosarcoma; ASPS, alveolar soft part sarcoma; US, undifferentiated sarcoma; AS, Angiosarcoma; ES, epithelioid sarcoma; ESFT, Ewing sarcoma family tumor; CCS, clear cell sarcoma.
Table III. Functional clusters identified by functional annotation clustering.

| Cluster Number | Annotation Terms | P-value | Source Database | Accession No. |
|----------------|------------------|---------|-----------------|---------------|
| A, Cluster 1   | VWC_out          | <0.01   | SMART           | SM00215       |
|                | VWFC domain      | <0.01   | InterPro        | IPR001007     |
|                | domain:VWFC 1    | <0.01   | UniProt         | None          |
|                | domain:VWFC 2    | <0.01   | UniProt         | None          |
|                | VWC              | <0.01   | SMART           | SM00214       |
| B, Cluster 2   | Cell membrane    | <0.01   | UniProt         | KW-1003       |
|                | Signal peptide   | <0.01   | UniProt         | None          |
|                | Signal           | <0.01   | UniProt         | KW-0732       |
|                | Glycoprotein     | <0.01   | UniProt         | KW-0325       |
|                | Disulfide bond   | <0.01   | UniProt         | None          |
| C, Cluster 3   | EGF-like, conserved site | <0.01 | InterPro | IPR013032 |
|                | EGF-like calcium-binding domain | <0.01 | InterPro | IPR001881 |
|                | EGF-like domain  | <0.01   | InterPro        | IPR000742     |
|                | EGF_CA           | <0.01   | SMART           | SM00179       |
|                | domain:EGF-like 4 | <0.01 | UniProt | None |
| D, Cluster 4   | VWC_out          | <0.01   | SMART           | SM00215       |
|                | VWFC domain      | <0.01   | InterPro        | IPR001007     |
|                | domain:TIL       | <0.01   | UniProt         | None          |
|                | domain:VWFD 3    | <0.01   | UniProt         | None          |
|                | domain:VWFD 2    | <0.01   | UniProt         | None          |
| E, Cluster 5   | Signaling receptor activity | <0.01 | Gene Ontology | GO:0038023 |
|                | Molecular transducer activity | <0.01 | Gene Ontology | GO:0060089 |
|                | Glycoprotein     | <0.01   | UniProt         | KW-0325       |
|                | topological domain: Extracellular | <0.01 | UniProt | None |
|                | Intrinsic component of plasma membrane | <0.01 | Gene Ontology | GO:0031226 |
| F, Cluster 6   | Neurogenesis     | <0.01   | Gene Ontology   | GO:0022008    |
|                | Neuron differentiation | <0.01 | Gene Ontology | GO:0030182    |
Table III. Continued.

F, Cluster number 6, 23 annotation terms included, enrichment score of 1.40

| Top 5 categorized annotation term of each cluster<sup>a</sup> | P-value<sup>b</sup> | Source database<sup>c</sup> | Accession no. |
|------------------------------------------------------------|-------------------|---------------------------|---------------|
| Generation of neurons                                     | <0.01             | Gene Ontology             | GO:0048699    |
| Cell projection organization                               | <0.01             | Gene Ontology             | GO:0030030    |
| Axon development                                           | 0.02              | Gene Ontology             | GO:0061564    |

G, Cluster number 7, 12 annotation terms included, enrichment score of 1.33

| Top 5 categorized annotation term of each cluster<sup>a</sup> | P-value<sup>b</sup> | Source database<sup>c</sup> | Accession no. |
|--------------------------------------------------------------|-------------------|---------------------------|---------------|
| Inositol phosphate metabolic process                         | <0.01             | Gene Ontology             | GO:0043647    |
| Polyol metabolic process                                     | <0.01             | Gene Ontology             | GO:0019751    |
| Alcohol metabolic process                                    | <0.01             | Gene Ontology             | GO:0006066    |
| Organic hydroxy compound metabolic process                   | 0.01              | Gene Ontology             | GO:1901615    |
| Carbohydrate metabolic process                               | 0.04              | Gene Ontology             | GO:0005975    |

Seven functional annotation clusters with an enrichment score >1.3 are listed. <sup>a</sup>Among each cluster, 5 annotation terms are listed from lower enrichment P-values with its accession no. and source database referred from DAVID (https://david.ncicrf.gov). <sup>b</sup>A modified Fisher Exact P-value was generated from gene enrichment analysis. <sup>c</sup>Each database is available at the following URLs: SMART, http://smart.embl-heidelberg.de; InterPro, https://www.ebi.ac.uk/interpro; UniProt, https://www.uniprot.org; Gene Ontology, http://geneontology.org. vWF, von Willebrand factor; VWC, von Willebrand factor type C domain; VWFC, von Willebrand factor type C; EGF, epidermal growth factor; EGF_CA, Calcium-binding EGF-like domain; VWFD, von Willebrand factor type D.