

## Erratum to: Identification of Human Erythrocyte Cytosolic Proteins Associated with Plasma Membrane During Thermal Stress

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The original version of this article unfortunately contains an error. The presentation of Figs. 4, 5 and 6 are incorrect, and erroneously altered during proof correction. The corrected figures and their captions are given below.

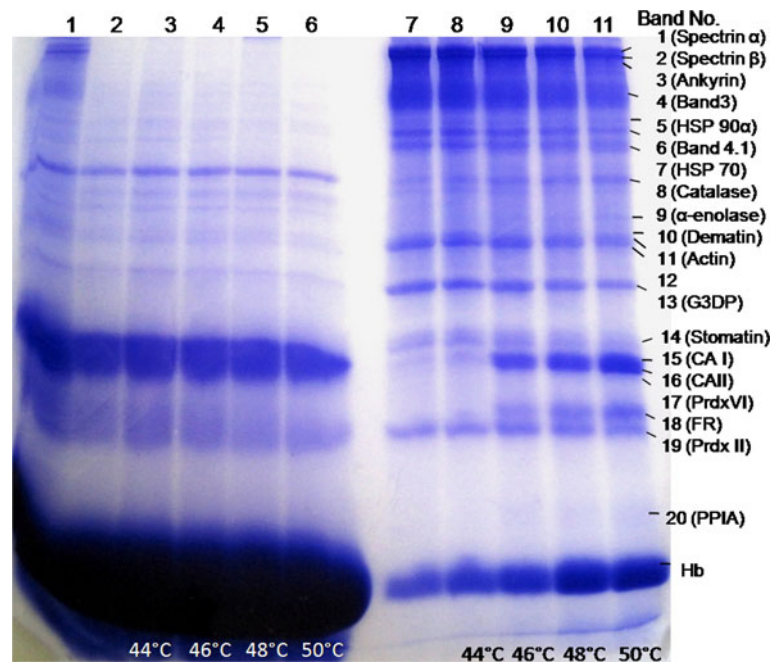
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The online version of the original article can be found under  
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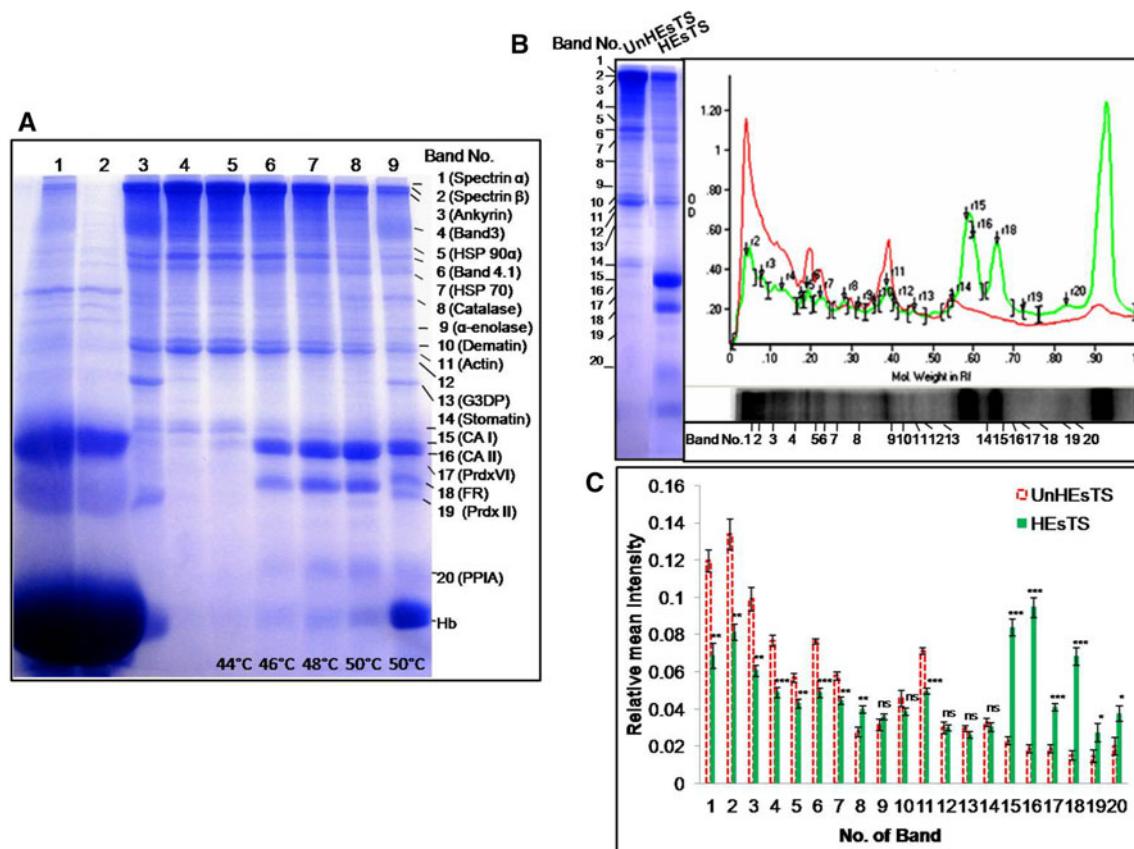
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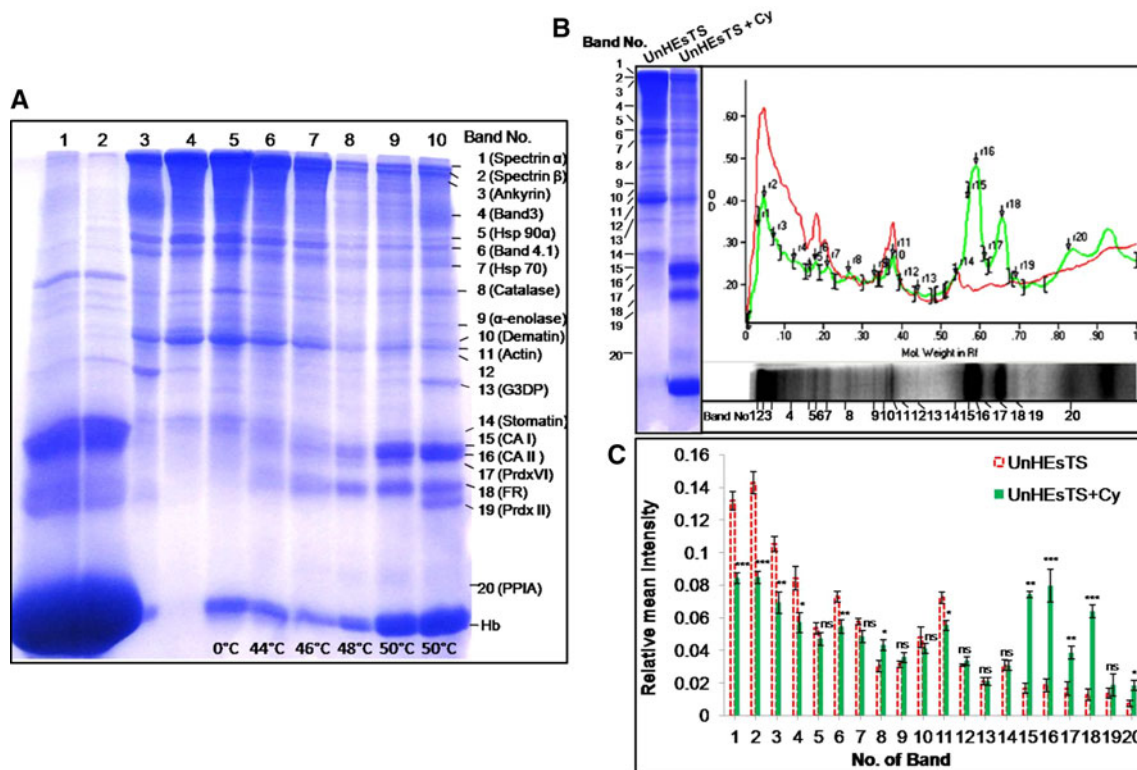
**Fig. 4** Analysis of erythrocyte lysate (cytosol) and membrane proteins obtained from erythrocyte cell suspension exposed to various temperatures by SDS-PAGE (12 % gel) and stained with CBB. Lane 1 unheated erythrocytes (whole cells, *UnHEs*); lane 2 unheated erythrocyte lysate (*UnHEsCy*); lanes 3–6 lysates (*HEsCy*) obtained from heat-stressed erythrocytes exposed to 44, 46, 48 and 50 °C for

15 min, respectively (60  $\mu$ l protein in each lane); lane 7 unheated erythrocyte membrane (*UnHEMs*); lanes 8–11 erythrocyte membranes (*HEMs*) obtained from heat-stressed erythrocytes exposed to 44, 46, 48 and 50 °C for 15 min, respectively (60  $\mu$ g protein in each lane). This is a representative pattern obtained for four different samples



**Fig. 5** Analysis of Triton shells obtained from erythrocyte membranes exposed to various temperatures. **a** Separation of proteins of Triton shells obtained from unheated (*UnHEMs*) and heat-stressed (*HEMs*) erythrocyte membranes by SDS-PAGE (12 % gel) and stained with CBB followed by mass spectrometric identification (Table 2). Lane 1 unheated erythrocytes (whole cells, *UnHEs*, 60  $\mu$ l); lane 2 unheated erythrocyte lysate (*UnHEsCy*, 60  $\mu$ l); lane 3 unheated erythrocyte membrane (*UnHEMs*, 60  $\mu$ g); lanes 4–8 Triton shells obtained from unheated (*UnHEsTS*) and heat-stressed (*HEsTS*)

erythrocytes exposed to 44, 46, 48 and 50  $^{\circ}$ C for 15 min, respectively (50  $\mu$ g protein in each lane); lane 9 membranes (*HEMs*) from heat-stressed erythrocytes exposed to 50  $^{\circ}$ C for 15 min (60  $\mu$ g). **b** Densitometric spectra of *UnHEsTS* (red peaks) and *HEsTS* (green peaks). **c** Bar diagram shows changes in protein intensity ( $n = 4$ ). The data are mean  $\pm$  SE ( $n = 4$ ). Upper symbol indicates the differences versus control (*UnHEsTS*). \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ; *ns* nonsignificant (Color figure online)



**Fig. 6** Analysis of interactions of Triton shells and cytosolic proteins obtained from unheated erythrocytes (*UnHEs*) under heat stress. **a** Separation of proteins of Triton shells interacted with cytosolic proteins under heat stress by SDS-PAGE (12 % gel) and stained with CBB followed by mass spectrometric identification (Table 3). *Lane 1* unheated erythrocytes (whole cells, 60  $\mu$ l); *lane 2* unheated erythrocyte lysate (60  $\mu$ l); *lane 3* unheated erythrocyte membrane (60  $\mu$ g); *lane 4* Triton shells obtained from unheated erythrocyte membrane (50  $\mu$ g); *lanes 5–9* Triton shells (derived from unheated erythrocyte

membranes) were incubated with the unheated lysate at 0, 44, 46, 48 and 50  $^{\circ}$ C for 15 min, respectively (50  $\mu$ g protein in each lane); *Lane 10* Membranes from heat-stressed erythrocytes exposed to 50  $^{\circ}$ C for 15 min. (60  $\mu$ g). **b** Densitometric spectra of UnHEsTS (red peaks) and UnHEsTS + Cy (green peaks). **c** Bar diagram shows changes in protein intensity ( $n = 4$ ). The data are mean  $\pm$  SE ( $n = 4$ ). Upper symbol indicates the differences versus control (UnHEsTS). \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ ; ns nonsignificant (Color figure online)