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## Author Correction: Global network analysis in *Schizosaccharomyces pombe* reveals three distinct consequences of the common 1-kb deletion causing juvenile CLN3 disease

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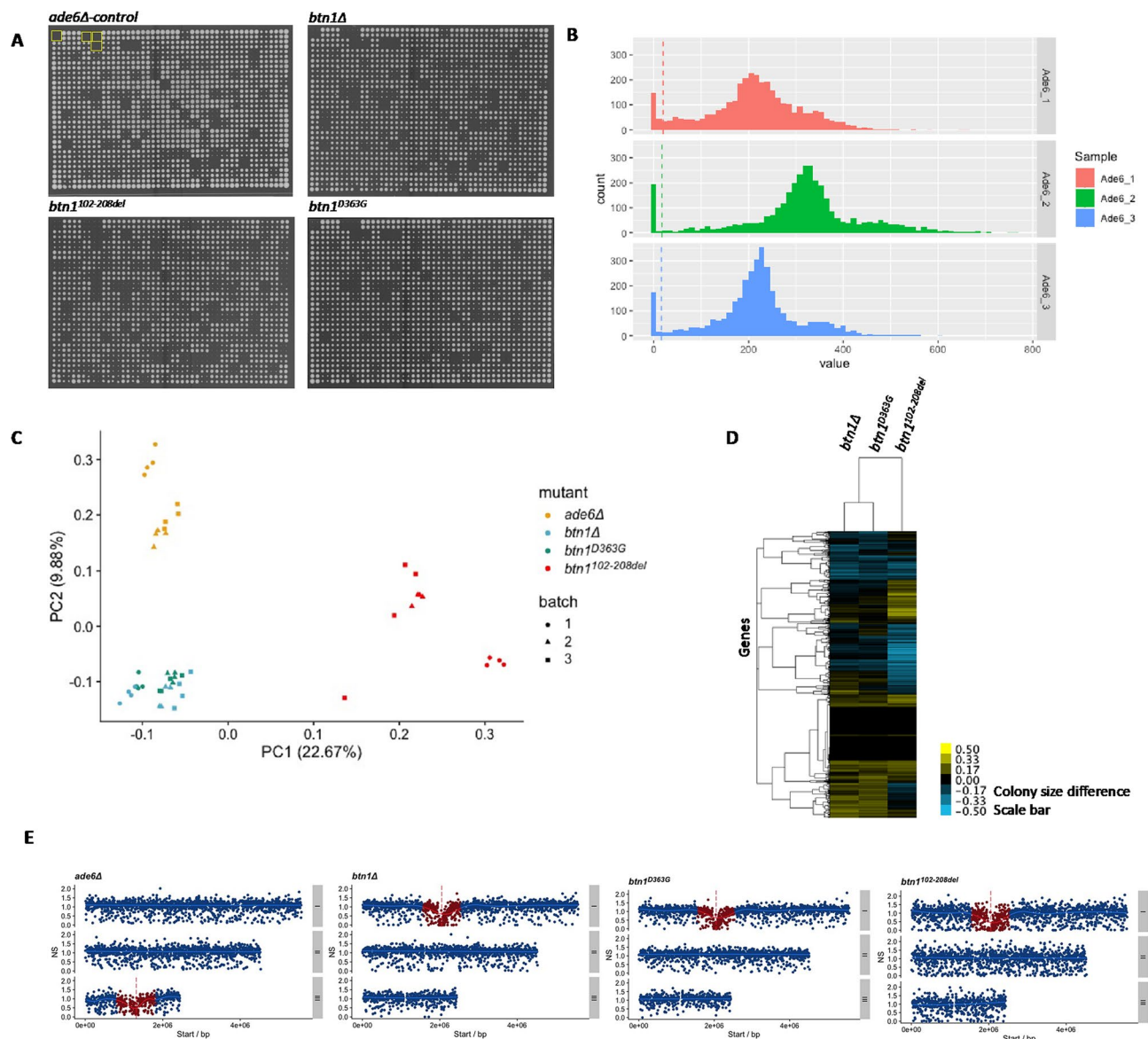
The original version of this Article contained errors in Figure 1c, where data points in the bar graph plot appeared incorrectly in green colour. As a results, the Figure legend,

“General overview of SGA analysis of *btn1* mutants versus *ade6* control. (A) Representative images of the SGA plates for control (*ade6*) and query mutants (*btn1Δ*, *btn1<sup>D363G</sup>*, *btn1<sup>102-208del</sup>*), with empty control quadrants shown for *ade6* (yellow boxes). (B) Exclusion of small colonies for *ade6* control across batches as they represent high variability therefore reducing noise. (C) Principle component biplot of the variance within the SGA data for *ade6* control (yellow) and query-mutants *btn1Δ* (blue), *btn1<sup>D363G</sup>* (green), *btn1<sup>102-208del</sup>* (red), with experimental batch indicated. (D) Cluster analysis for each strain and all the genes with their normalised colony size difference against *ade6* control with batch effects removed. Interactions are coloured in blue for negative interactions ( $< -0.5$ ) and yellow for positive interactions ( $> 0.5$ ). (E) Gene linkage of normalised fitness score for *ade6* control and query mutants *btn1Δ*, *btn1<sup>D363G</sup>*, *btn1<sup>102-208del</sup>* from one experiment. Vertical dashed line represents *ade6* or *btn1* gene location, red points represent interaction scores excluded from data since less than 500 kb/500,000 bps from query gene location.”

now reads:

“General overview of SGA analysis of *btn1* mutants versus *ade6* control. (A) Representative images of the SGA plates for control (*ade6*) and query mutants (*btn1Δ*, *btn1<sup>D363G</sup>*, *btn1<sup>102-208del</sup>*), with empty control quadrants shown for *ade6* (yellow boxes). (B) Exclusion of small colonies for *ade6* control across batches as they represent high variability therefore reducing noise. (C) Principle component biplot of the variance within the SGA data for *ade6* control (yellow) and query-mutants *btn1Δ* (blue), *btn1<sup>D363G</sup>* (orange), *btn1<sup>102-208del</sup>* (red), with experimental batch indicated. (D) Cluster analysis for each strain and all the genes with their normalised colony size difference against *ade6* control with batch effects removed. Interactions are coloured in blue for negative interactions ( $< -0.5$ ) and yellow for positive interactions ( $> 0.5$ ). (E) Gene linkage of normalised fitness score for *ade6* control and query mutants *btn1Δ*, *btn1<sup>D363G</sup>*, *btn1<sup>102-208del</sup>* from one experiment. Vertical dashed line represents *ade6* or *btn1* gene location, red points represent interaction scores excluded from data since less than 500 kb/500,000 bps from query gene location.”

The original Figure 1 and accompanying legend appear below.



**Figure 1.** General overview of SGA analysis of *btn1* mutants versus *ade6* control. **(A)** Representative images of the SGA plates for control (*ade6*) and query mutants (*btn1Δ*, *btn1<sup>D363G</sup>*, *btn1<sup>102-208del</sup>*), with empty control quadrants shown for *ade6* (yellow boxes). **(B)** Exclusion of small colonies for *ade6* control across batches as they represent high variability therefore reducing noise. **(C)** Principle component biplot of the variance within the SGA data for *ade6* control (yellow) and query-mutants *btn1Δ* (blue), *btn1<sup>D363G</sup>* (green), *btn1<sup>102-208del</sup>* (red), with experimental batch indicated. **(D)** Cluster analysis for each strain and all the genes with their normalised colony size difference against *ade6* control with batch effects removed. Interactions are coloured in blue for negative interactions ( $< -0.5$ ) and yellow for positive interactions ( $> 0.5$ ). **(E)** Gene linkage of normalised fitness score for *ade6* control and query mutants *btn1Δ*, *btn1<sup>D363G</sup>*, *btn1<sup>102-208del</sup>* from one experiment. Vertical dashed line represents *ade6* or *btn1* gene location, red points represent interaction scores excluded from data since less than 500 kb/500,000 bps from query gene location.

Furthermore, Table 2 contained errors, where genes for the strains *btn1Δ*, *btn1<sup>D363G</sup>* and *btn1<sup>102-208del</sup>* in the column ‘Top 5 genes’ appeared incorrectly in bold font. The incorrect and correct values appear below.

Incorrect:

Strains	Interaction type	Top 5 genes
<i>btn1Δ</i>	negative	<i>pfa3, kes1, rid1, efc25, ivn1</i>
	positive	<i>apt1, blt1, cpp1, rpl2301, alg12</i>
<i>btn1<sup>D363G</sup></i>	negative	<i>pfa3, rid1, kes1, efc25, fhn1</i>
	positive	<i>grx5, cpp1, SPBC1604.03c, apt1, blt1</i>
<i>btn1<sup>102-208del</sup></i>	negative	<i>pfa3, nce103, gga22, clg1, kes1</i>
	positive	<i>SPBC29A3.21, cpp1, gfh1, tfx1, pub3</i>

Correct:

Strains	Interaction type	Top 5 genes
<i>btn1Δ</i>	negative	<i>pfa3, kes1, rid1, efc25, ivn1</i>
	positive	<i>apt1, blt1, cpp1, rpl2301, alg12</i>
<i>btn1<sup>D363G</sup></i>	negative	<i>pfa3, rid1, kes1, efc25, fhn1</i>
	positive	<i>grx5, <b>cpp1</b>, SPBC1604.03c, <b>apt1</b>, blt1</i>
<i>btn1<sup>102-208del</sup></i>	negative	<i>pfa3, nce103, gga22, clg1, <b>kes1</b></i>
	positive	<i>SPBC29A3.21, <b>cpp1</b>, gfh1, tfx1, pub3</i>

The original Article has been corrected.



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