

## Supplementary information

The effect of *Oryza sativa* L. subsp. *japonica* cultivar Yukihihikari on the immune system

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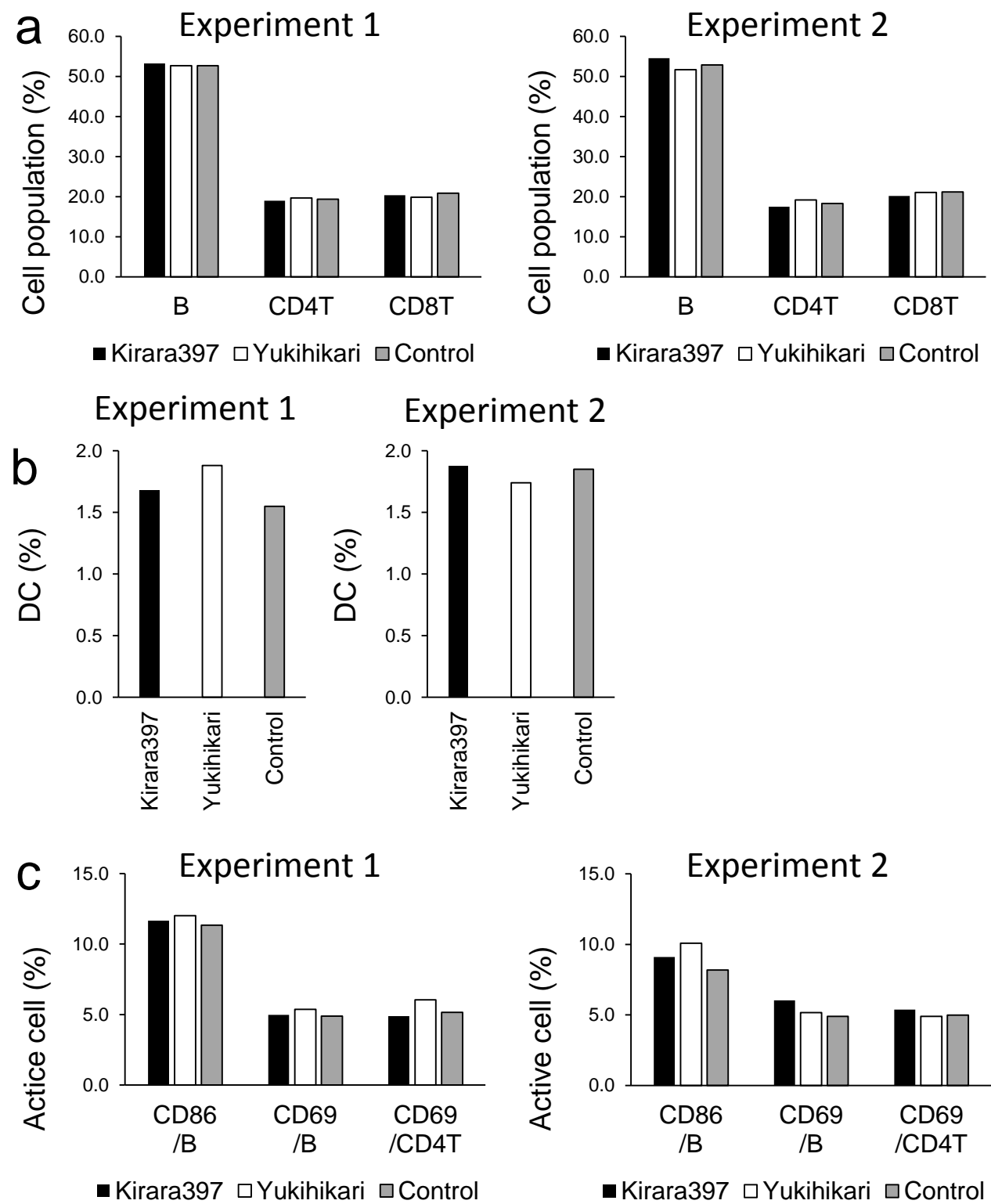
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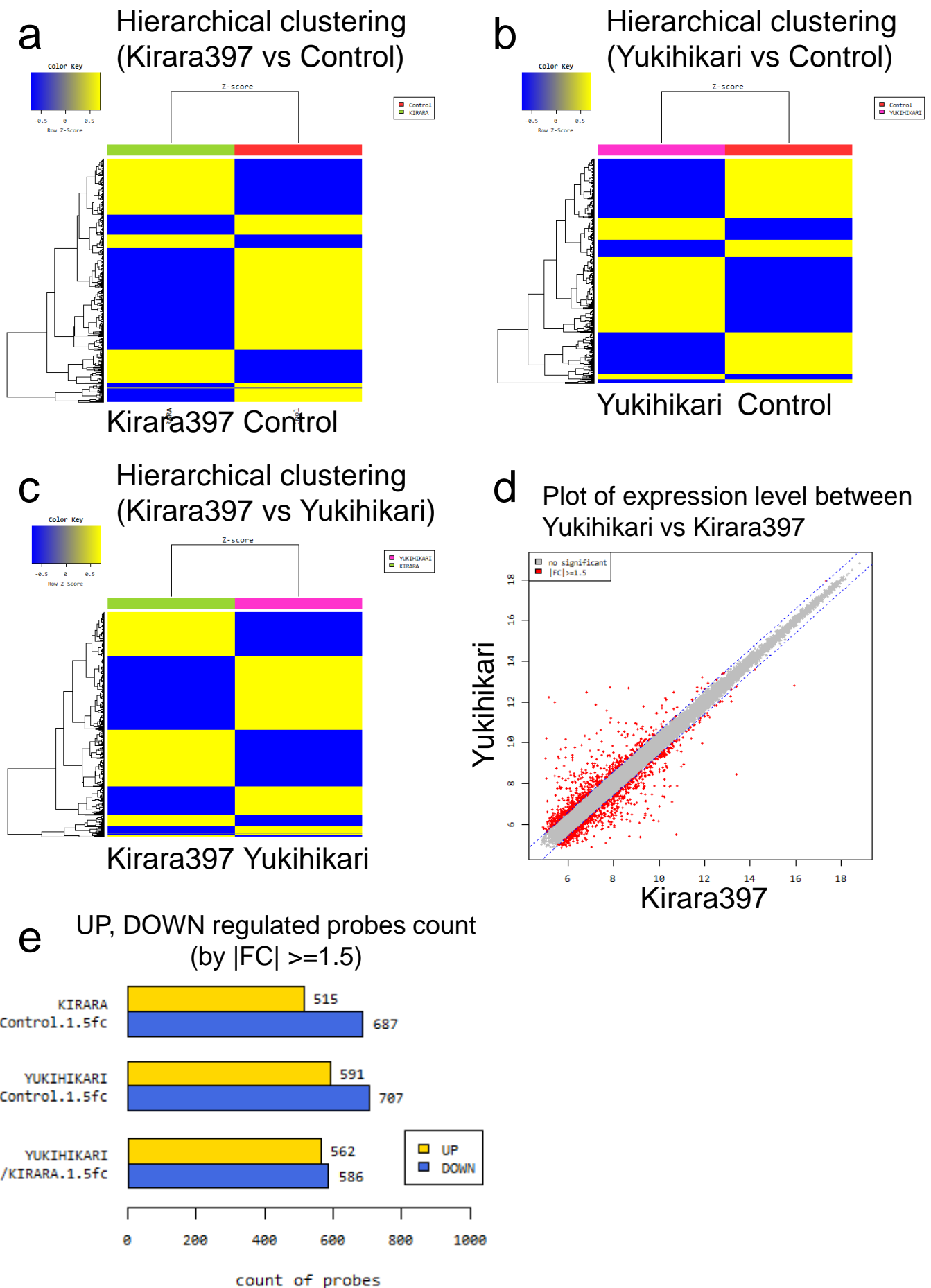
**Supplementary figure 1.** Effect of Yukihihari and Kirara397 on the proportions of B cells, CD4 T cells, CD8 T cells, DC, and activation markers on B and T cells *in vitro*. Spleen cells of C57BL/6 mice were cultured for 2 d with or without 20- $\mu$ g rice powder (Yukihihari or Kirara397). **(a)** The ratio of B cells (B220<sup>+</sup> cells) and CD4 T cells and CD8 T cells. **(b)** The ratio of DC (CD11<sup>+</sup>) cells, and **(c)** The ratio of activation marker CD86 on B cells and CD69 on B and T cells. The results of the two experiments are shown.

**Supplementary figure 2.** DNA microarray analysis of spleen cells treated with Yukihihari and Kirara397. Cells were prepared as shown in Suppl Fig.1 and total RNA was prepared and subjected to DNA microarray analysis. **(a)** Heat maps of expression levels between Yukihihari *versus* control. **(b)** Kirara397 *versus* control. **(c)** Yukihihari *versus* Kirara397. **(d)** The plot of expression levels between Yukihihari *versus* Kirara397, and **(e)** gene numbers significantly up- and down-regulated.

**Supplementary figure 3.** RNA sequencing analysis of spleen cells treated with Kirara397 and Yukihihari. Total RNA was prepared as shown in Supplementary Fig. 2 and subjected to RNA sequencing analysis. Differential expression volcano plots (Kirara397 *versus* control, Yukihihari *versus* control, and Yukihihari *versus* Kirara397) are shown. Red dots represent genes that are significantly upregulated and blue dots represent those that are significantly down-regulated. X-axis: log<sub>2</sub> fold change of gene expression. Y-axis: statistically significant difference of the differential expression in log<sub>10</sub> (p-value).

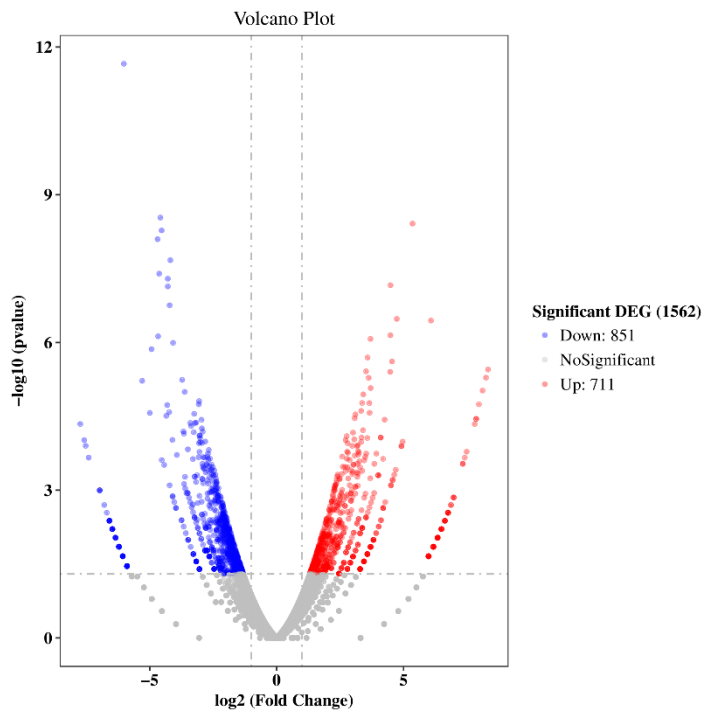


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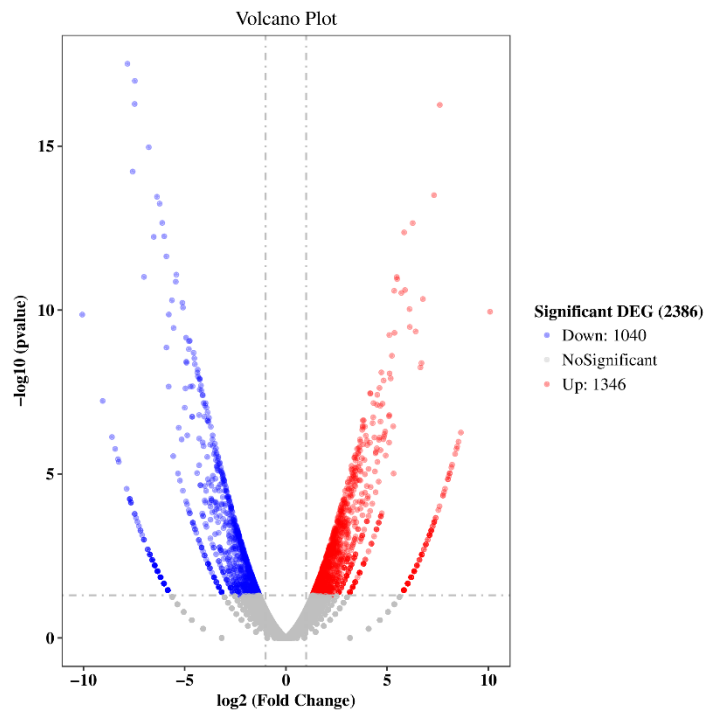


**Supplementary figure 2.** DNA microarray analysis of spleen cells treated with Yukihikari and Kirara397. Cells were prepared as shown in Suppl Fig.1 and total RNA was prepared and subjected to DNA microarray analysis. **(a)** Heat maps of expression levels between Yukihikari *versus* control. **(b)** Kirara397 *versus* control. **(c)** Yukihikari *versus* Kirara397. **(d)** The plot of expression levels between Yukihikari *versus* Kirara397, and **(e)** gene numbers significantly up- and down-regulated.

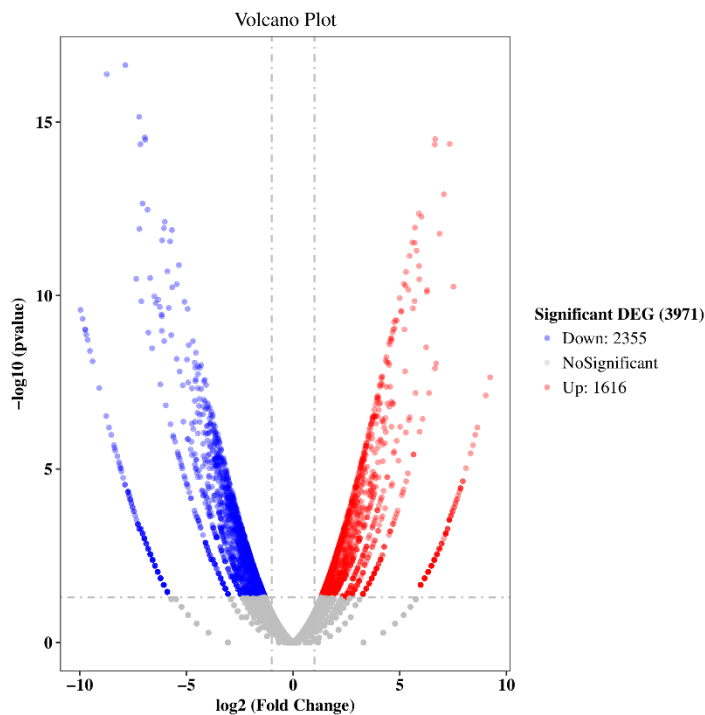
## Control vs Kirara397



## Control vs Yukihihari



## Yukihihari vs Kirara397



**Supplementary figure 3.** RNA sequencing analysis of spleen cells treated with Kirara397 and Yukihihari. Total RNA was prepared as shown in Supplementary Fig. 2 and subjected to RNA sequencing analysis. Differential expression volcano plots (Kirara397 *versus* control, Yukihihari *versus* control, and Yukihihari *versus* Kirara397) are shown. Red dots represent genes that are significantly upregulated and blue dots represent those that are significantly down-regulated. X-axis: log<sub>2</sub> fold change of gene expression. Y-axis: statistically significant difference of the differential expression in log<sub>10</sub> (p-value).