

- 1 **Supplementray Table 1 Sample information.**
- 2 **Supplementray Table 2 Different gene expression (DGE) of each two samples.**
- 3 **Supplementray Figure 1 Barley leaves at six growth stages after infection (0 h, 24 h, 48 h, 72 h, 96**
4 **h, and 120 h).**
- 5 **Supplementray Figure 2 Mean Quality Distribution of A (C0, TR130348).** The base position in reads
6 is as the X-axis, and the mean Qphred is as the Y-axis.
- 7 **Supplementray Figure 3 Base Distribution of A (C0, TR130348).** The base position in reads is as the
8 X-axis, and the percentage of ATGC base is as the Y-axis.
- 9 **Supplementray Figure 4 Gene depth distribution of A (C0, TR130348).** The relative position in gene
10 is as X-axis, the number of reads is Y-axis.
- 11 **Supplementray Figure 5 Gene Saturation of A (C0, TR130348).**
- 12 **Supplementray Figure 6 Total DGEs from each sample was clustered.**
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14 **Supplementary Table 1** Sample information.

Accession no.	Sampling hour	Sample code	Group name
TR130348	0	C0	A
TR130349	24	C24	B
TR130350	48	C48	C
TR130351	72	C72	D
TR130352	96	C96	E
TR130353	120	C120	F

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Supplementary Table 2 Summary of differently expressed genes (DEG).

Accession	A	B	C	D	E
B	103				
C	93	39			
D	44	42	49		
E	49	102	108	27	16
F	73	29	36	21	

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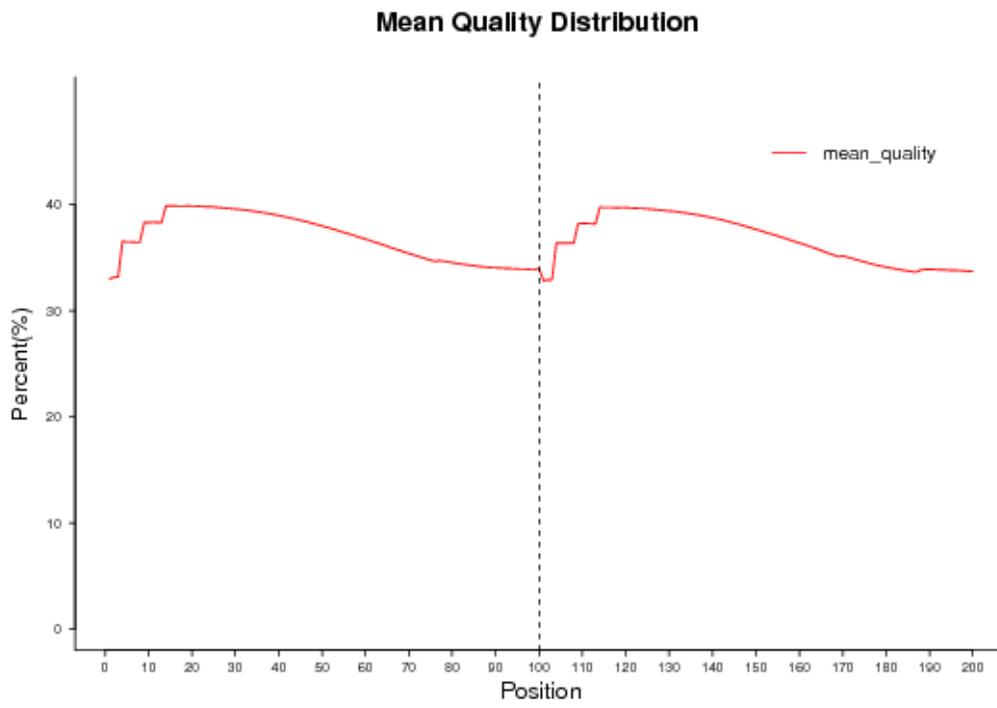
0 h 24 h 48 h 72 h 96 h 120 h

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18 **Supplementary Figure 1**

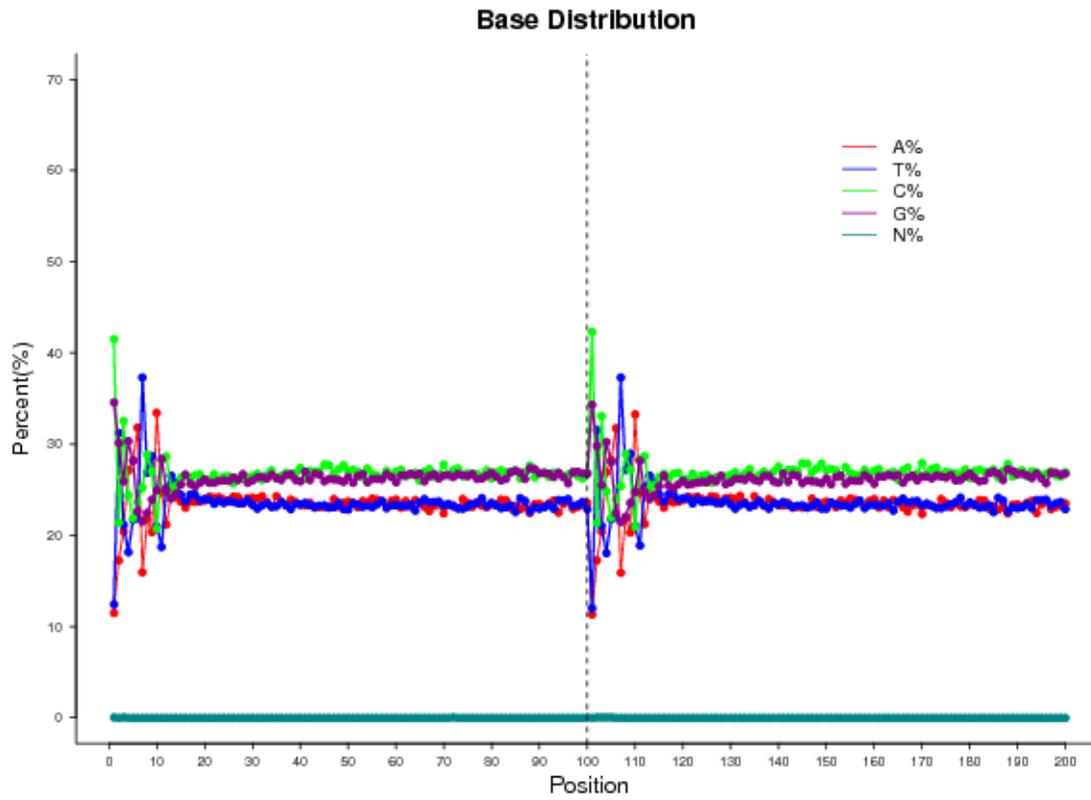
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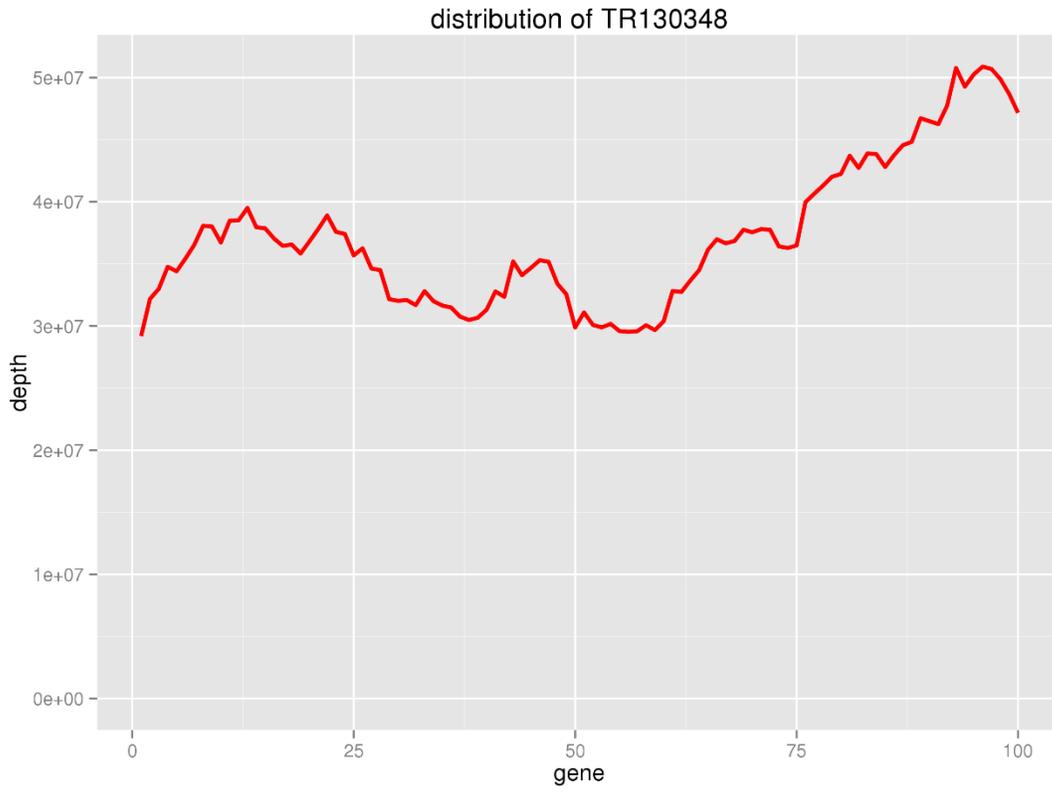
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23 **Supplementary Figure 2**



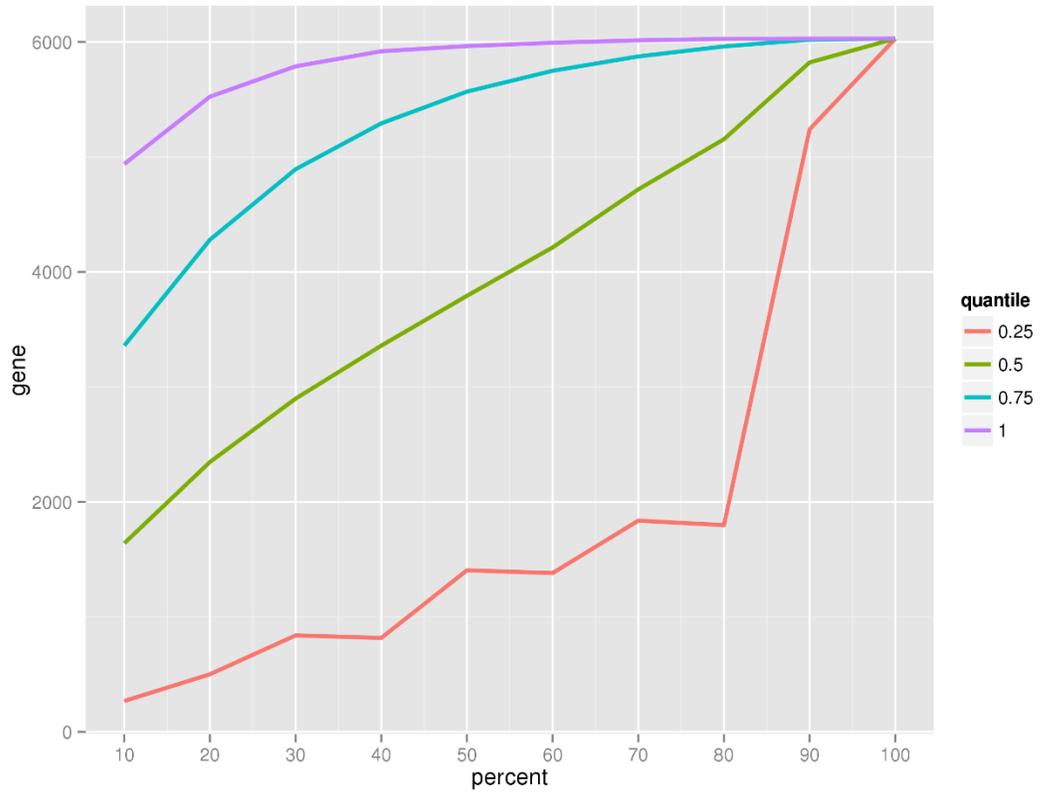
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25 **Supplementary Figure 3**



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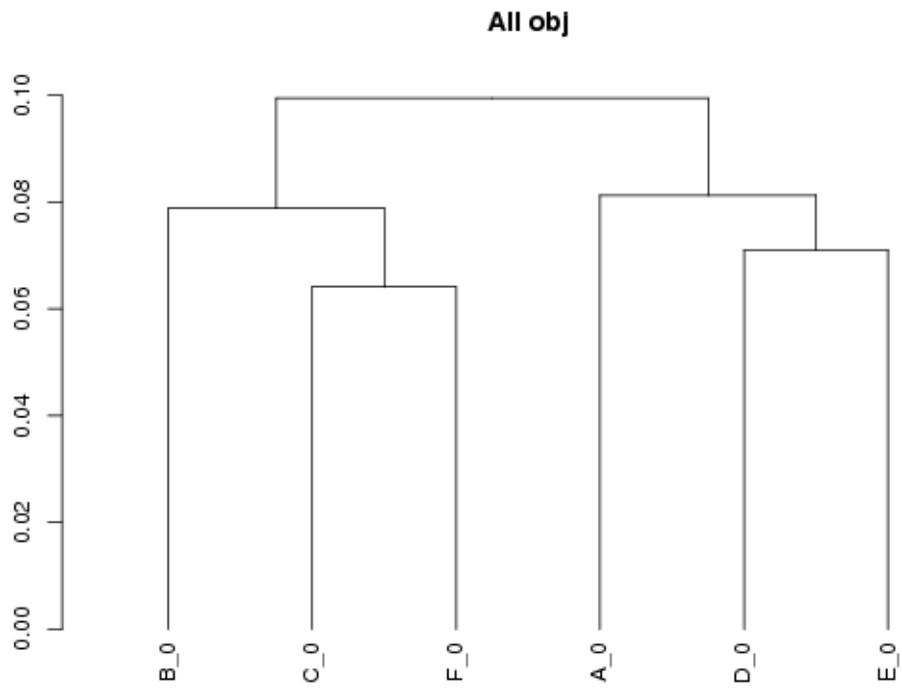
27 **Supplementary Figure 4**



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29 **Supplementary Figure 5**

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32 **Supplementary Figure 6**