Table S1. Summary of RNA-seq data for all samples (NS: normal seedlings; AS: albino seedlings)

Sample name	AS1	AS2	AS3	NS1	NS2	NS3
Raw reads	45814168	42688558	49928860	44625318	40903168	47002140
Raw bases	6.87G	6.4G	7.49G	6.69G	6.14G	7.05G
Clean reads	43502554	41516750	47879454	44577456	39749774	45336072
Clean bases	6.53G	6.23G	7.18G	6.69G	5.96G	6.8G
Error rate(%)	0.03	0.03	0.03	0.03	0.03	0.03
Q20(%)	97.13	97.33	96.99	97.46	97.33	97.27
Q30(%)	92.3	92.67	91.75	93.1	92.72	92.62
GC content(%)	45.76	45.6	45.66	48.21	45.55	45.4