

Transcriptomic analyses reveal molecular mechanisms underlying regulation of floral attributes in *Lonicera japonica* Thunb.

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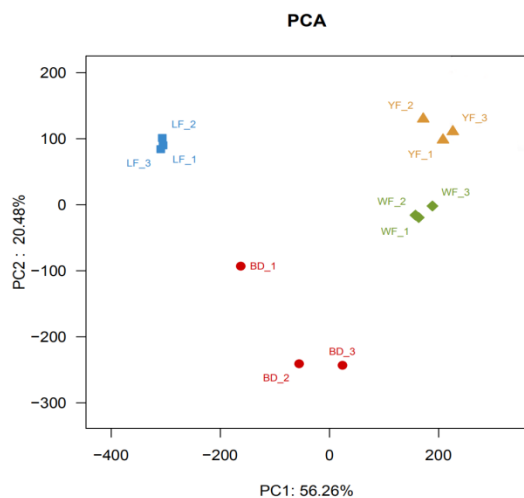
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Supplemental table 1

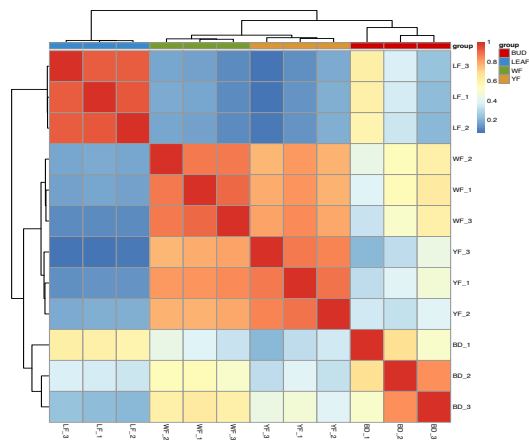
Statistical summary of in *L. japonica* sequencing data

Sample_ID	Total_Reads	Total_Bases	Error%	Q20%	Q30%	GC%
YF_1	70158528	10523779200	0.0139	96.99	92.96	44.43
YF_2	78457564	11768634600	0.0131	97.44	93.85	44.19
YF_3	79401912	11910286800	0.0131	97.42	93.82	44.04
WF_1	72636826	10895523900	0.0133	97.37	93.67	44.35
WF_2	50304546	7545681900	0.0147	96.78	92.18	44.49
WF_3	69600146	10440021900	0.0143	97.02	92.67	44.18
BD_1	55570330	8335549500	0.0142	97	92.67	44.57
BD_2	61575664	9236349600	0.0135	97.26	93.45	44.83
BD_3	58388022	8758203300	0.0133	97.37	93.64	44.87
LF_1	69873138	10480970700	0.0134	97.27	93.46	45.25
LF_2	64101688	9615253200	0.014	96.94	92.83	45.33
LF_3	65891620	9883743000	0.0137	97.11	93.17	45.31

a



b



Supplementary Fig. 1 Correlation analyses showing the relationship between samples and replicates.

(a) Principle component analysis and (b) correlation matrix showing relationship between all samples as well as replicates.



Supplementary Fig. 2 The enriched biological process GO terms of the DEGs between two samples.