

Full title:

Genome of Paulownia (*Paulownia fortunei*) illuminates the related transcripts,
miRNA and proteins for salt resistance

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Supplementary Figures and Tables

Figure S1 Sequencing data assessment. Base composition of clean data in PF2(a1), PF2S(b1), PF4(c1) and PF4S(d1); base quality of clean data in PF2(a2), PF2S(b2), PF4(c2) and PF4S(d2); reads distribution on PF2(a3), PF2S(b3), PF4(c3) and PF4S(d3) genes.

Figure S2 Cluster analysis of DEGs in four comparisons: PF2S vs PF2, PF4S vs PF4, PF4 vs PF2 and PF4S vs PF2S.

Figure S3 Gene ontology analysis of DEGs in PF2S vs PF2(a) and PF4S vs PF4 (b).

Figure S4 The detailed information of four samples' proteins. a: Distribution of protein's sequences coverage; b: peptide length distribution; c: protein mass distribution.

Figure S5 COG and Gene ontology analysis (a:COG analysis, b:biological process; c: cellular component; d: molecular function) of all proteins.

Figure S6 Gene ontology function classification in all up-regulation(a), all down-regulation(b) and Autotetraploid predominant salt response key proteins(c).

Figure S7 Length distribution of miRNA(a) and the distribution of clean reads (b:PF2, c:PF2S, d:PF4, e:PF4S) across the different chromosomes.

Figure S8 The correlation between transcriptome and proteome. Quantitative proteins and genes in PF2S vs PF2 (a1), PF4 vs PF2 (b1), PF4S vs PF2S(c1) and PF4S vs PF4 (d1); contrary expressional tendencies between proteins and genes in PF2S vs PF2 (a2), PF4 vs PF2 (b2), PF4S vs PF2S (c2) and PF4S vs PF4 (d2); same expressional tendencies between proteins and genes in PF2S vs PF2 (a3), PF4 vs PF2 (b3), (c3) PF4S vs PF2S and PF4S vs PF4 (d3).

Table S1 Statistics of each sample comparing with Paulownia genome.

Table S2 Top 20 up and down differentially expressed genes in PF2S vs PF2, PF4 vs PF2, PF4S vs PF4 and PF4S vs PF2S.

Table S3 The significantly enriched GO terms of PF2S vs PF2 and PF4S vs PF4.

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Table S6 Autotetraploid predominant salt response genes.

Table S7 The KEGG pathway enrichment distribution of Autotetraploid predominant salt response genes.

Table S8 The COG function classification and the KEGG pathway classification of all the proteins (a: COG function classification; b:KEGG pathway classification).

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Table S14 The sequence statistics of degradome comparing with Paulownia genome (a) and the predicted target genes of miRNA(b) .

Table S15 The statistics of miRNA-target mRNA/proteins in PF4S vs PF4 and PF2S vs PF2.

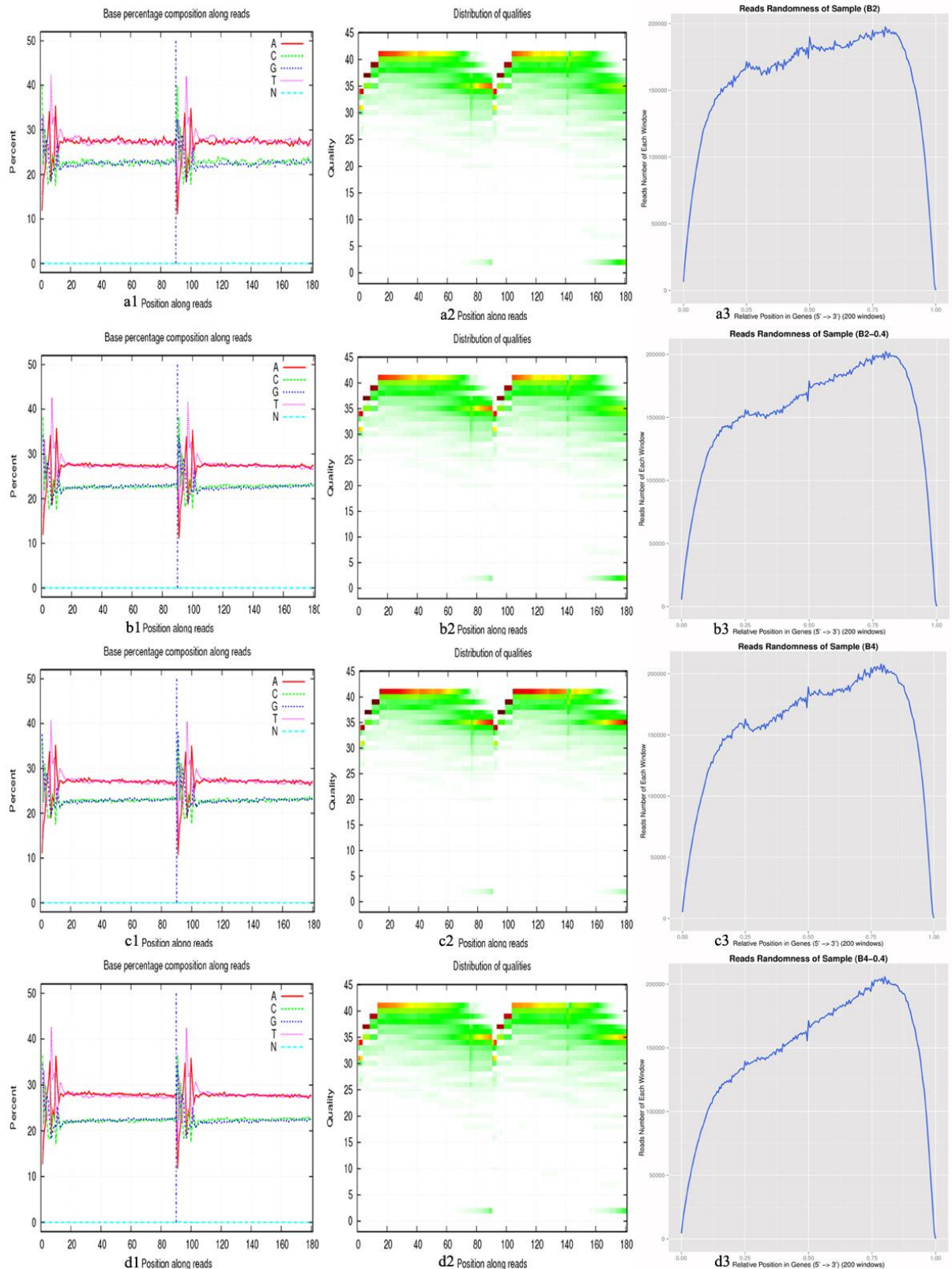


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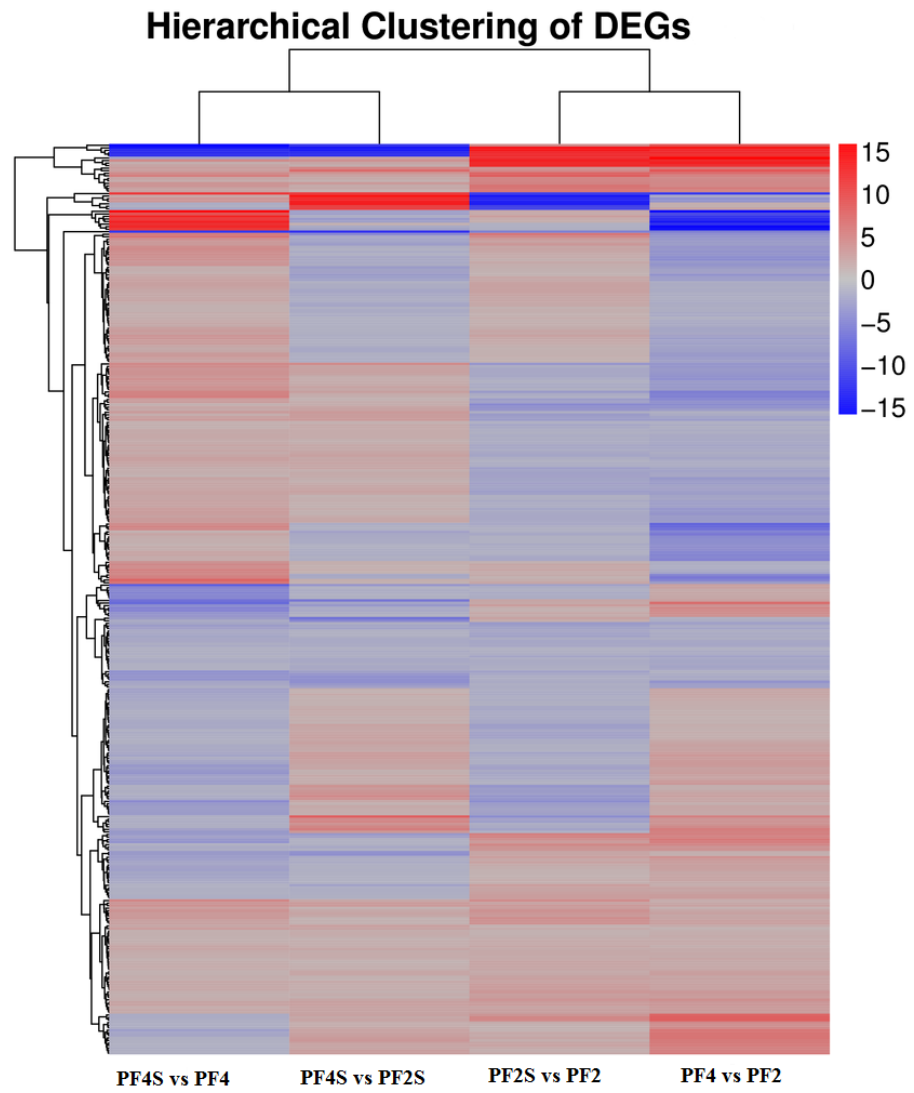


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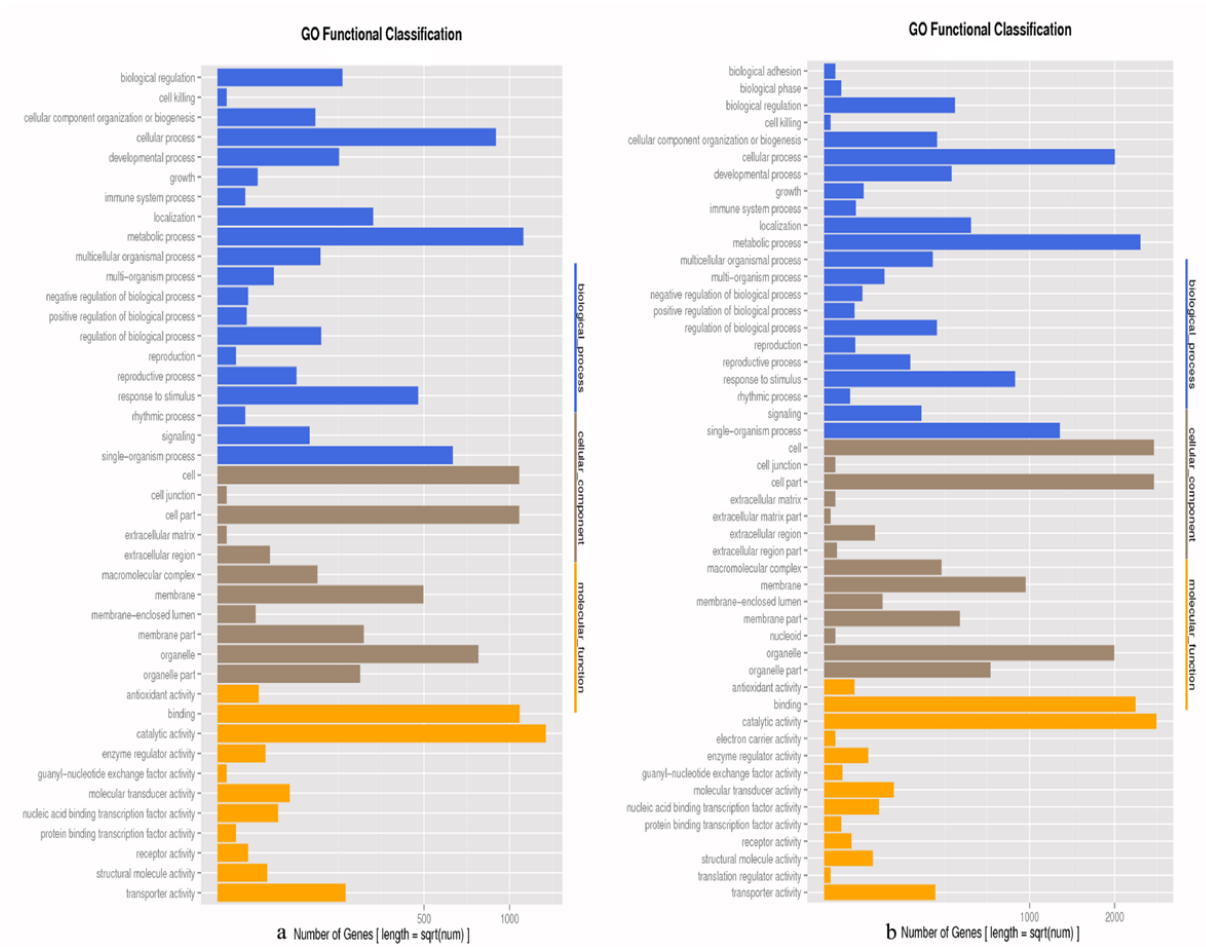
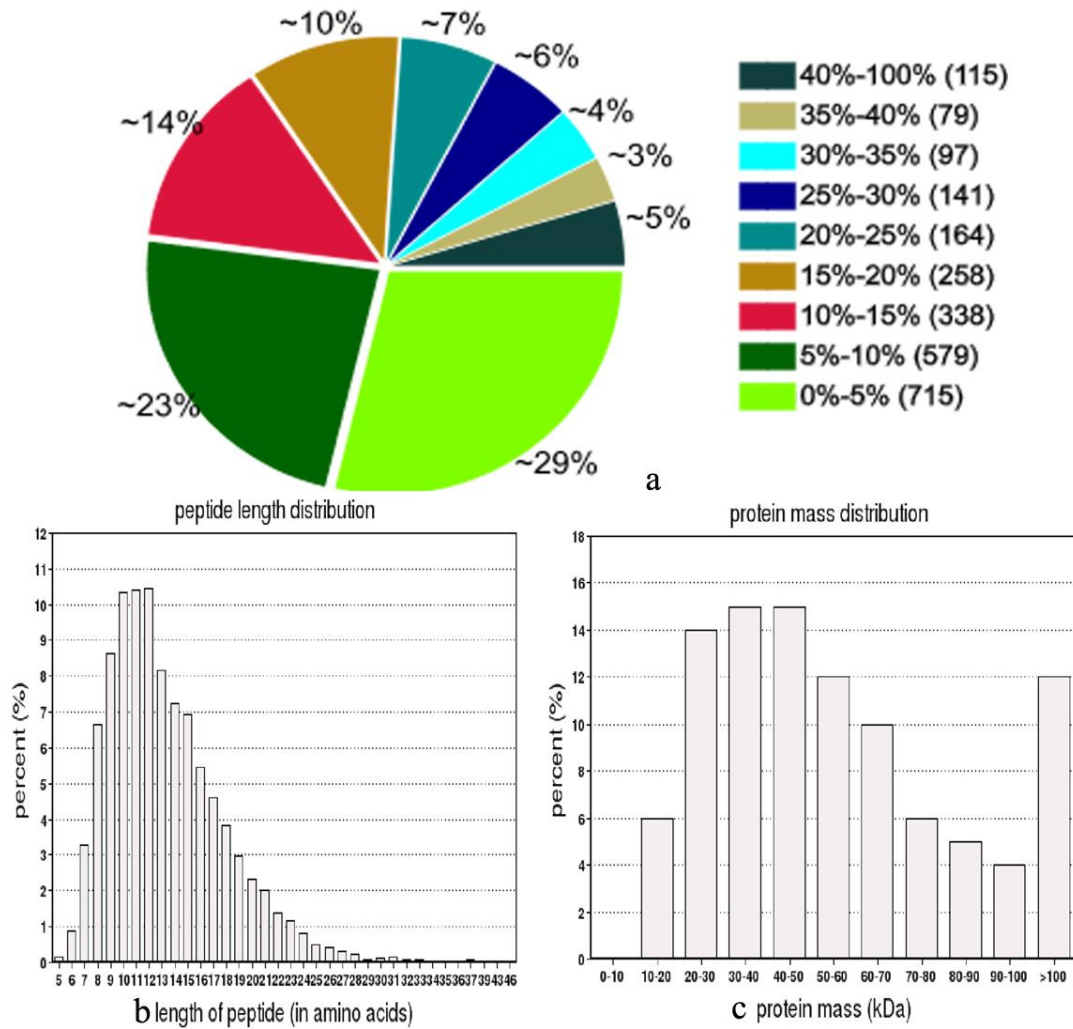


Figure S3 Gene ontology analysis of DEGs in PF2S vs PF2(a) and PF4S vs PF4 (b).

Figure S4 The detailed information of four samples' proteins. a: Distribution of Distribution of Protein's Sequences Coverage



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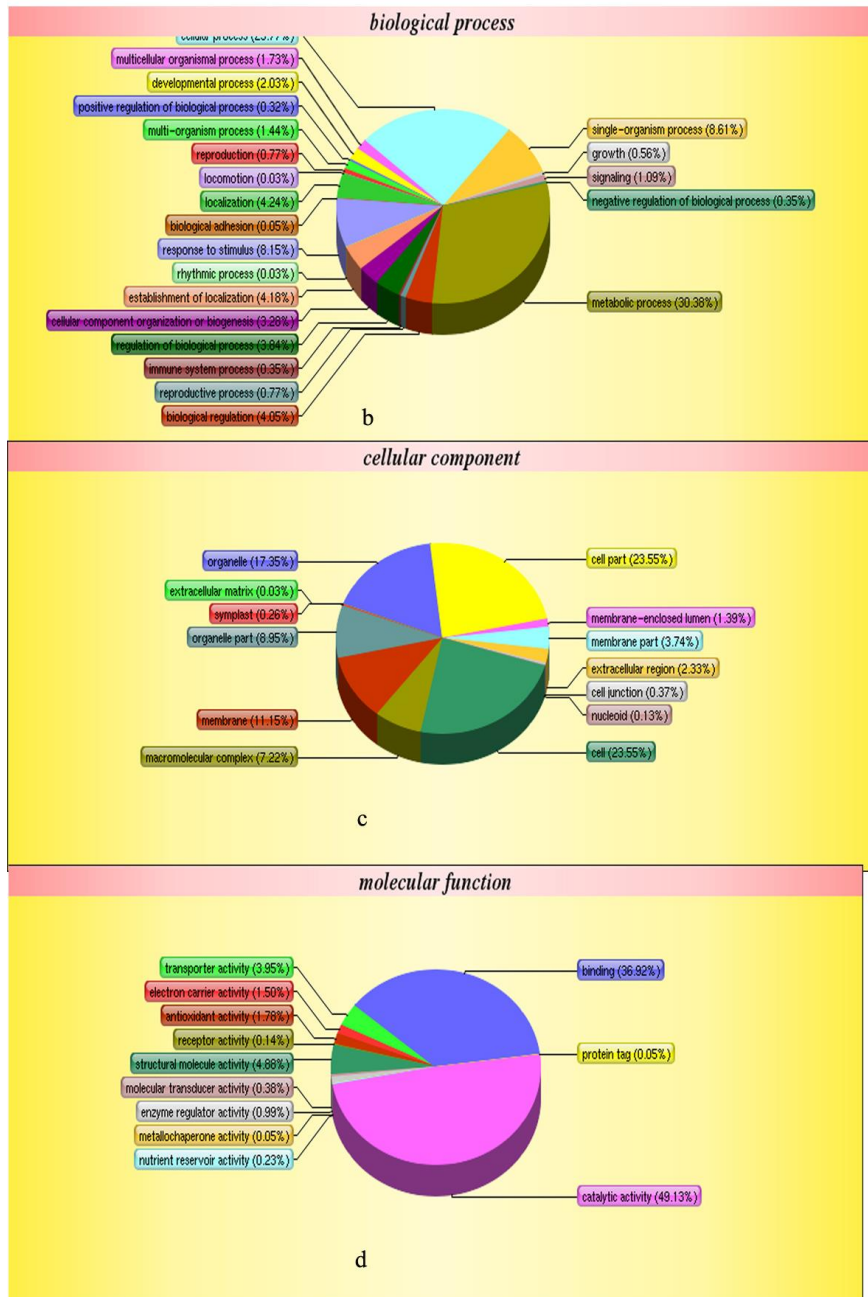
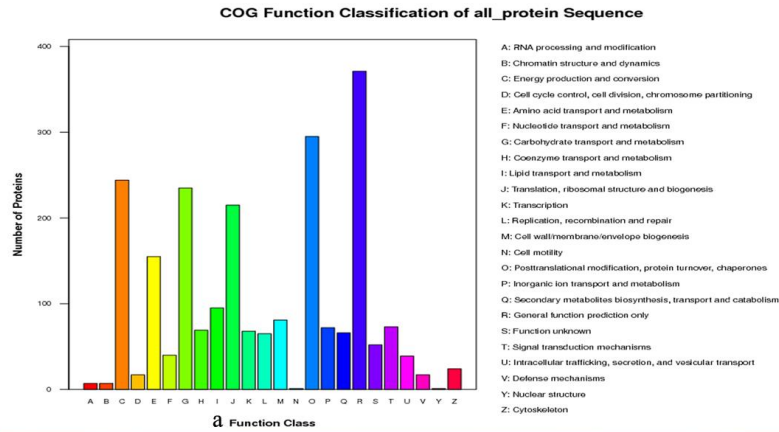


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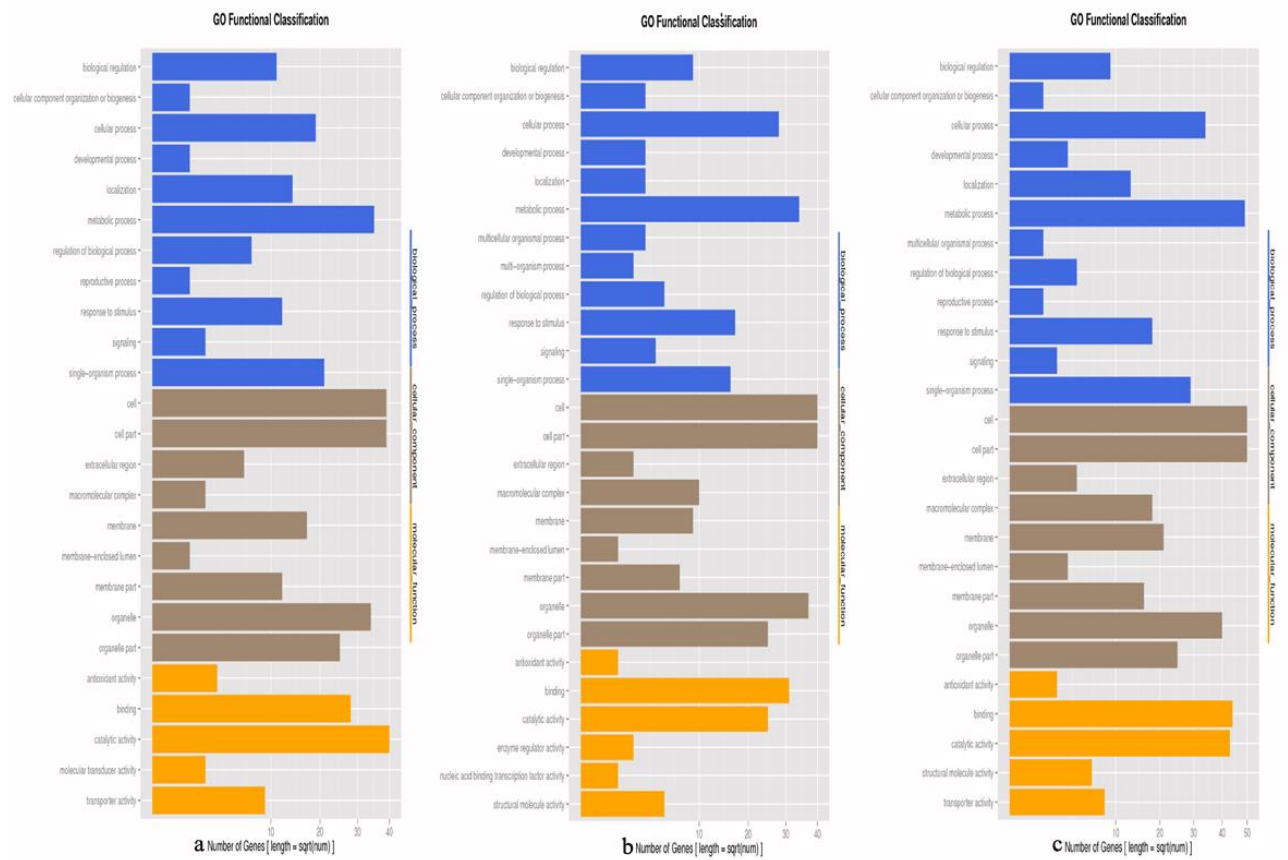


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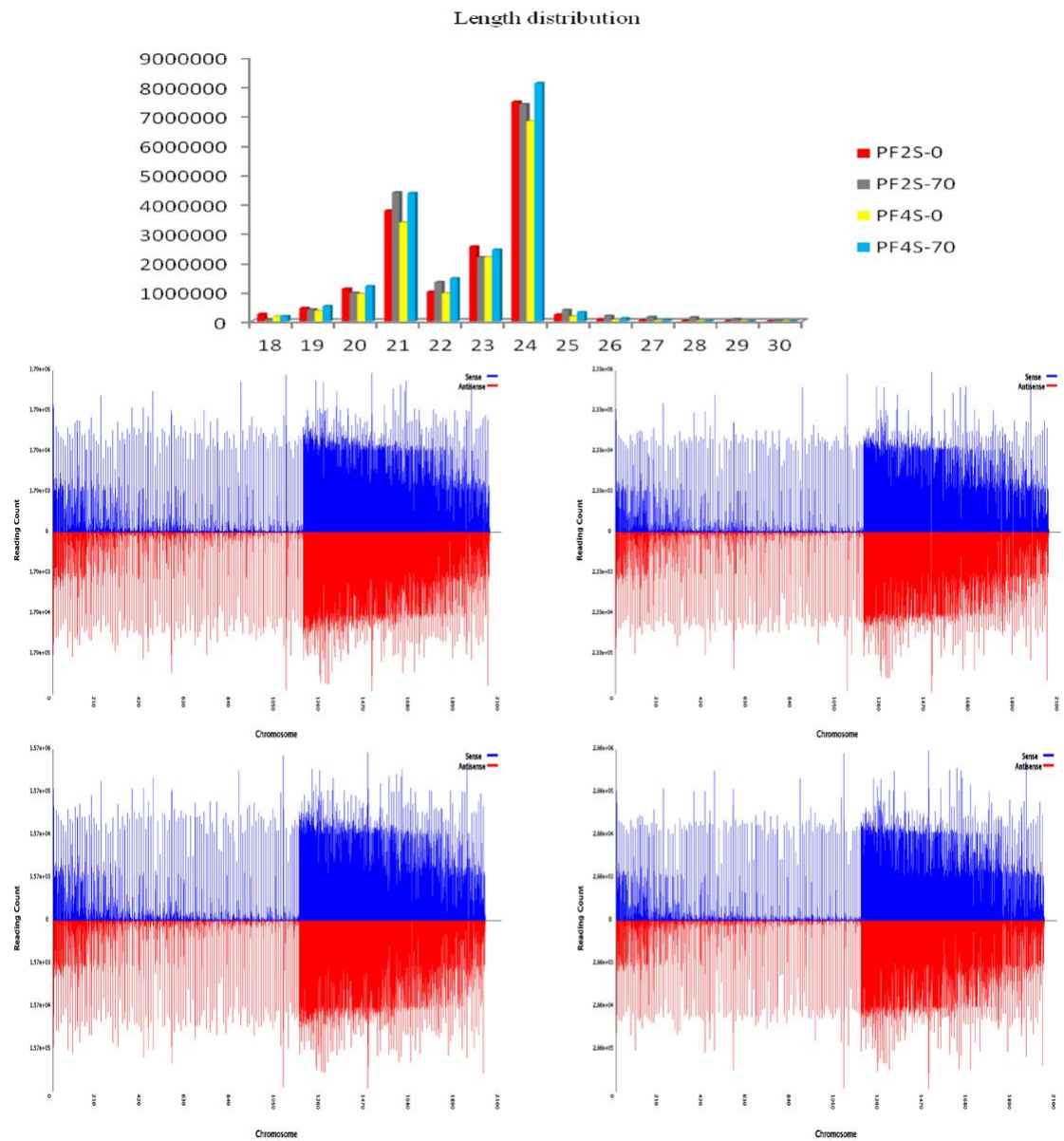


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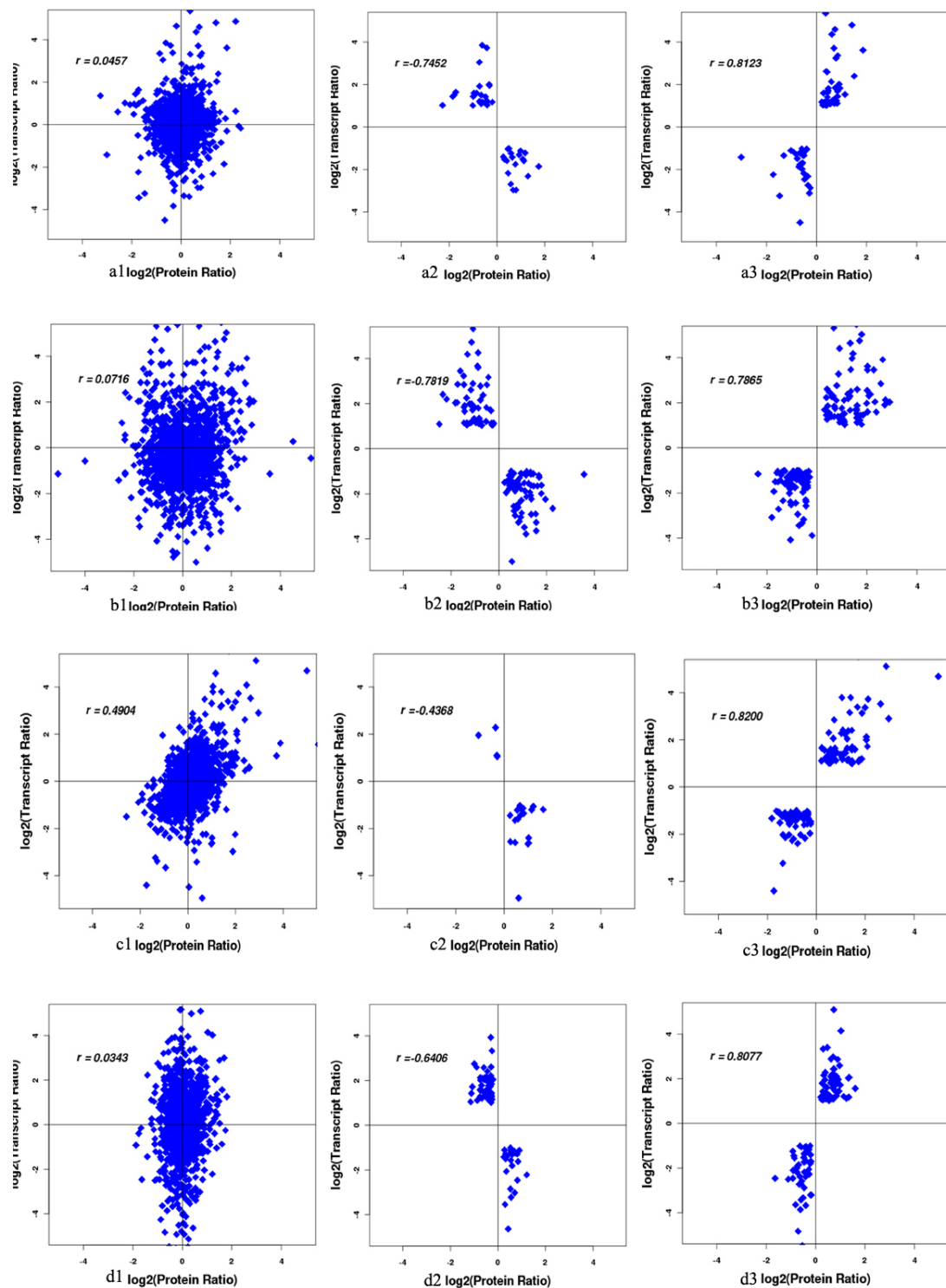


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