

Figure S1 Images of 2-DE gels

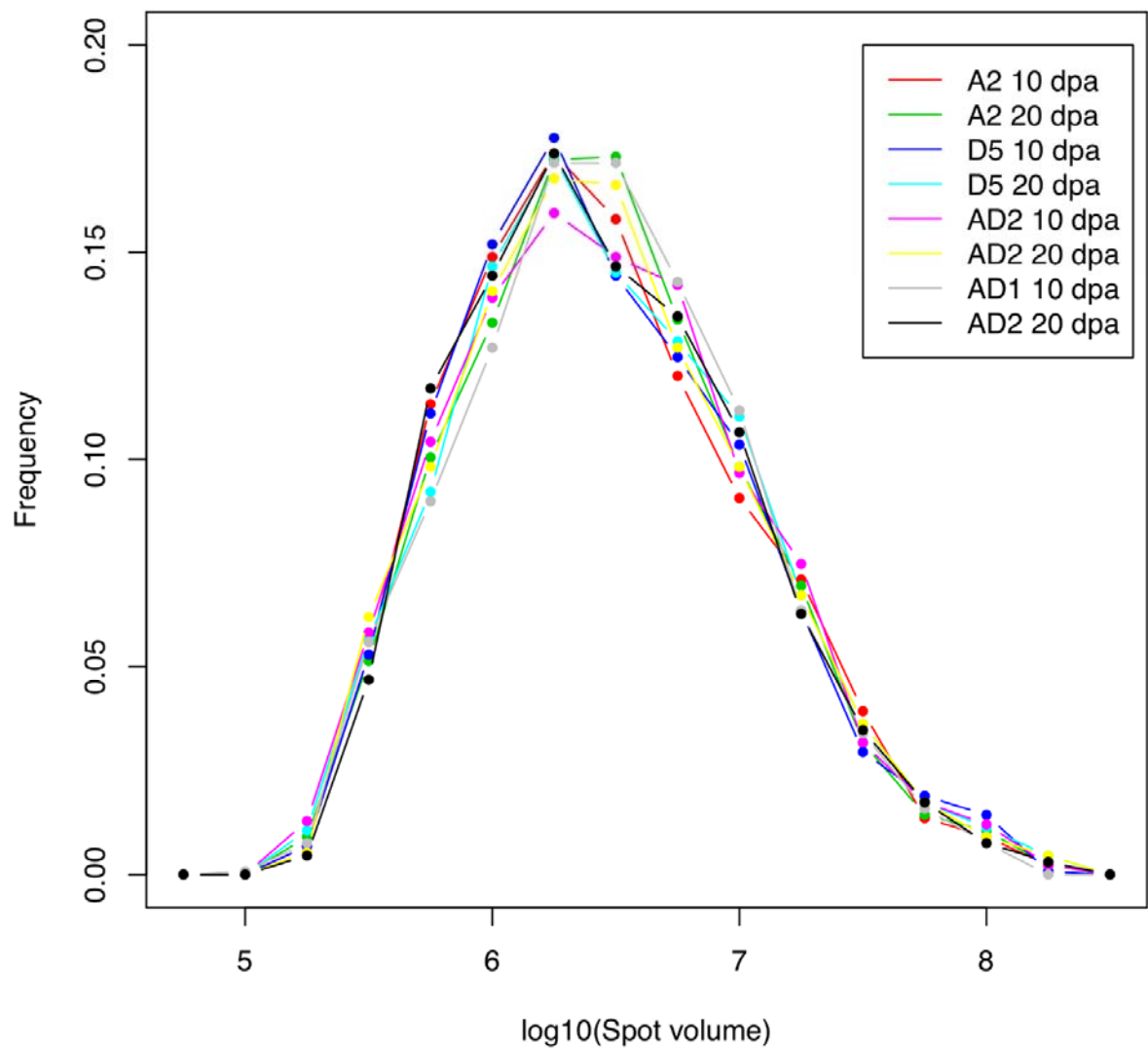


Figure S2 Frequency distribution plots for 2-DE spot volume

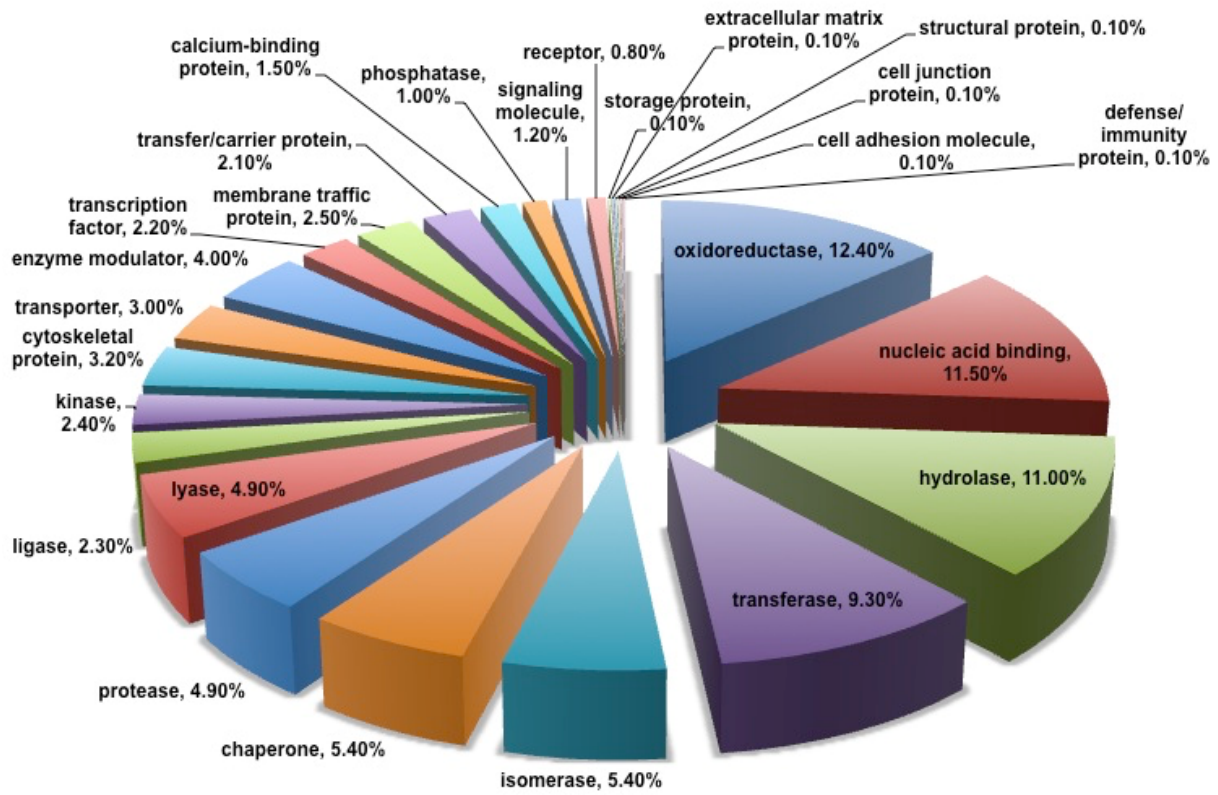


Figure S3 Panther classification of identified fiber proteins by iTRAQ

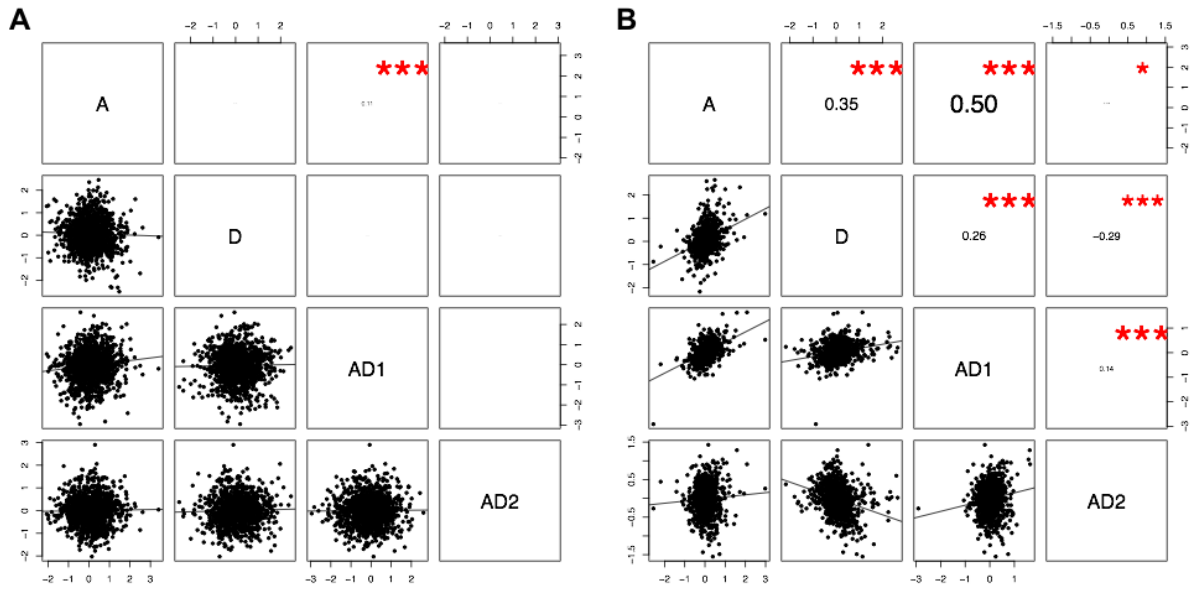


Figure S4 Pairwise comparison of developmental expression changes among diploid and polyploid cotton. Log₂ expression ratios were calculated for 20 dpa versus 10 dpa within each genome using 2-DE (A) and iTRAQ datasets (B). Lower-left panels of the comparison matrix show scatterplots while upper-right panels give Pearson's correlation coefficients, with the font size proportional to the absolute value of the correlation. Asterisks indicate significance of the adjacent correlation coefficient: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

Table S1 Protein identification and false discovery rate (FDR) analysis

a. Number of proteins identified at 95% confidence level

	run 1	run 2	run 3	Total
Total Spectra	114654	83352	110173	
Spectra Identified	54020 (47.1%)	29555 (35.5%)	46871 (42.5%)	
Distinct Peptides	19652	10749	17250	
Proteins	1483	886	1339	1652

b. Number of proteins estimated according to FDR analysis

Critical FDR	Local FDR	Global FDR	Global FDR from Fit
1.0%	1388 836 1085	1539 935 1359	1543 918 1367
5.0%	1449 853 1270	1683 1014 1562	1689 1025 1552
10.0%	1490 887 1331	1817 1102 1687	1830 1111 1699

Protein numbers from triplicated experiments were listed; numbers in bold are close to that from protein identification with above 95% confidence level.

Files S1-S6

Available for download as Excel files at

<http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.115.174367/-/DC1>

- File S1** Normalized spot volumes of 2-DE gels
- File S2** Significant expression changes profiled by 2-DE
- File S3** Protein identification and quantification by ProteinPilot iTRAQ analyses
- File S4** Significant expression changes profiled by iTRAQ
- File S5** GO enrichment analysis
- File S6** Homoeolog-specific peptides and expression changes