

1 **Supplemental Table S1.** Number and percentage of sequencing reads mapped onto the
 2 allotetraploid cotton (AD) genome sequence.

Accession	Genome designation	Total reads	Clean reads	A	D	AD overlap	AD	
				Mapped reads	Mapped reads	overlap	Mapped reads	percent
TM-1_1R	AD	55,702,587	47,324,516	23,110,443	23,607,780	5,176,813	41,671,862	88.10%
TM-1_2R	AD	61,147,447	51,638,483	25,122,174	25,855,464	5,773,553	45,458,603	88.00%
TM-1_3R	AD	53,827,026	46,268,794	22,069,500	22,830,235	5,636,361	39,664,962	85.70%

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5 **Supplemental Table S2.** Number and expression levels of A and D homoeologous genomes
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Subgenome	Genes number	FPKM			
		R1	R2	R3	mean
A	16711	492777.76	466580.17	438941.09	466099.67
D	17400	514536.93	488100.39	457388.77	486675.36
total	34111	1007314.69	954680.57	896329.85	952775.04

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9 **Supplemental Table S3.** Correlation coefficients between immunostaining and gene
 10 densities of homoeologous A chromosomes in *G. hirsutum* (TM-1).

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Gene H3K4me3	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	A12	A13
	A01	0.846 ^{a,*}	0.514	0.648 ^a	0.148	0.549	0.734 ^a	0.730 ^a	0.721 ^a	0.366	0.682 ^a	0.716 ^a	0.334
A02	0.578	0.886 ^{b,*}	0.609 ^a	0.278	0.591	0.456	0.628 ^a	0.719 ^a	0.284	0.740 ^a	0.778 ^a	0.757 ^a	0.753 ^a
A03	0.802 ^a	0.720 ^a	0.824 ^{a,*}	0.047	0.692 ^a	0.767 ^a	0.080	0.730 ^a	0.278	0.804 ^a	0.812 ^a	0.532	0.232
A04	0.062	0.155	0.210	0.808 ^{b,*}	0.259	0.006	0.002	0.111	0.087	0.317	0.018 ^c	0.559	0.571
A05	0.832 ^a	0.506	0.645 ^a	0.101	0.943 ^{b,*}	0.801 ^a	0.747 ^a	0.690 ^a	0.307	0.608 ^a	0.840 ^a	0.218	0.096
A06	0.801 ^a	0.533	0.782 ^a	0.788 ^a	0.445	0.851 ^{b,*}	0.736 ^a	0.837 ^a	0.217	0.803 ^a	0.644 ^a	0.296	0.161
A07	0.790 ^a	0.898 ^a	0.728 ^a	0.090	0.767 ^a	0.703 ^a	0.949 ^{b,*}	0.787 ^a	0.027	0.818 ^a	0.869 ^a	0.759 ^a	0.666 ^a
A08	0.819 ^a	0.819 ^a	0.841 ^a	0.076	0.770 ^a	0.738 ^a	0.418	0.876 ^{b,*}	0.026	0.854 ^a	0.812 ^a	0.710 ^a	0.532
A09	0.398	0.218	0.292	0.700 ^a	0.519	0.483	0.244	0.211	0.894 ^{b,*}	0.067	0.384	0.352	0.456
A10	0.840 ^a	0.584	0.612 ^a	0.055	0.936 ^a	0.605 ^a	0.819 ^a	0.686 ^a	0.023	0.730 ^{b,*}	0.710 ^a	0.466	0.373
A11	0.598	0.458	0.622 ^a	0.124	0.801 ^a	0.829 ^a	0.694 ^a	0.664 ^a	0.410 ^a	0.585 ^a	0.842 ^{b,*}	0.131	0.005
A12	0.200	0.683 ^a	0.304	0.655 ^a	0.234	0.040	0.592	0.473	0.763 ^a	0.518 ^b	0.417	0.952 ^{b,*}	0.871 ^a
A13	0.393	0.645 ^a	0.422	0.505 ^a	0.319	0.234	0.729 ^a	0.507	0.657 ^a	0.677 ^a	0.517	0.942 ^a	0.919 ^{b,*}

12 ^a P<0.01; * designated pair

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14 **Supplemental Table S4.** Correlation coefficients between immunostaining and gene
 15 densities of homoeologous D chromosomes in *G. hirsutum* (TM-1).
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Gene H3K4me3	D01	D02	D03	D04	D05	D06	D07	D08	D09	D10	D11	D12	D13
D01	0.850 ^{a,*}	0.615	0.256	0.771	0.463	0.749 ^a	0.832 ^a	0.807 ^a	0.027	0.787 ^a	0.788 ^a	0.673	0.824 ^a
D02	0.743 ^a	0.801 ^{a,*}	0.700	0.318	0.260	0.616	0.747 ^a	0.599	0.305	0.761 ^a	0.772 ^a	0.782 ^a	0.624
D03	0.439	0.639	0.862 ^{a,*}	0.726	0.103	0.260	0.334	0.552	0.666 ^b	0.395	0.348 ^c	0.120	0.687
D04	0.821 ^a	0.727	0.743	0.940 ^{a,*}	0.452	0.740	0.808 ^a	0.838 ^a	0.086	0.737	0.827 ^a	0.854 ^a	0.841 ^a
D05	0.200	0.195	0.179	0.429	0.924 ^{a,*}	0.272	0.553	0.146	0.830 ^a	0.398	0.678 ^b	0.378	0.163
D06	0.726 ^a	0.429	0.342	0.248	0.675	0.795 ^{a,*}	0.654	0.591	0.508	0.706 ^a	0.673 ^b	0.208	0.579
D07	0.776 ^a	0.369	0.252	0.674	0.495	0.624	0.819 ^{a,*}	0.692	0.058	0.606	0.798 ^a	0.509	0.585
D08	0.763 ^a	0.612	0.668	0.893 ^a	0.219	0.562	0.738 ^a	0.767 ^{a,*}	0.312	0.682	0.700 ^a	0.792 ^a	0.794 ^a
D09	0.147	0.040	0.636	0.113	0.792 ^a	0.579	0.160	0.049	0.966 ^{a,*}	0.322	0.438 ^c	0.694	0.312
D10	0.714 ^a	0.535	0.089	0.498	0.884 ^a	0.776 ^a	0.749 ^a	0.631	0.653	0.753 ^{a,*}	0.885 ^a	0.020	0.424
D11	0.824 ^a	0.699 ^a	0.163	0.729 ^a	0.805 ^a	0.822 ^a	0.867 ^a	0.802 ^a	0.426	0.884 ^a	0.919 ^{a,*}	0.308	0.641
D12	0.298	0.192	0.859 ^a	0.455	0.531	0.010	0.153	0.357	0.940 ^a	0.147	0.079 ^c	0.895 ^{a,*}	0.685
D13	0.779 ^a	0.627	0.668	0.809 ^a	0.152	0.550	0.739 ^a	0.818 ^a	0.426	0.676	0.621 ^b	0.855 ^a	0.874 ^{a,*}

17 ^a P<0.01; * designated pair

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19 **Supplemental Table S5.** Number and percentage of sequencing reads of ChIP-seq mapped
20 onto the allotetraploid cotton (AD) genome sequence.

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Sample ID	Clean Reads	Mapped Reads	Mapped Rate (%)	Uniquely Mapped Reads	Uniquely Mapped Rate (%)
TM-1_1R-input	25,182,189	24,632,041	97.82	15,950,480	63.34
TM-1_1R-IP	25,028,831	24,219,563	96.77	15,854,549	63.35
TM-1_2R-input	26,470,323	25,861,008	97.70	16,764,139	63.33
TM-1_2R-IP	27,365,259	26,410,617	96.51	17,557,866	64.16

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23 **Supplemental Table S6.** Correlation coefficients of immunostaining densities (enriched with
 24 H3K4me3) in the distal portions between A and D homoeologous chromosomes in *G.*
 25 *hirsutum* (TM-1).

A \ D	A01	A02	A03	A04	A05	A06	A07	A08	A09	A10	A11	A12	A13
D01	0.938 ^{a,1}	0.898 ^a	0.855 ^a	0.760 ^a	0.446	0.737 ^a	0.658	0.878 ^a	0.512	0.892 ^a	0.413	0.735 ^a	0.829 ^a
D02	0.499	0.824 ^a	0.839 ^a	0.809 ^a	0.190	0.664 ^a	0.573	0.476	0.648	0.657	0.126	0.272	0.662 ^a
D03	0.791	0.962 ^{a,2}	0.867 ^a	0.728	0.211	0.849 ^a	0.725	0.852 ^a	0.097	0.763 ^a	0.108	0.543	0.892 ^{a,2}
D04	0.800 ^a	0.817 ^a	0.408	0.929 ^{a,1}	0.723	0.741	0.462	0.511	0.475	0.865 ^a	0.680	0.061	0.738
D05	0.559	0.334	0.013	0.196	0.955 ^{a,1}	0.351	0.683	0.121	0.721 ^a	0.593	0.600	0.428	0.101
D06	0.566	0.724 ^a	0.717 ^a	0.590	0.612	0.885 ^{a,1}	0.643	0.499	0.183	0.784	0.627	0.321	0.641
D07	0.760 ^a	0.808 ^a	0.803 ^a	0.655	0.617	0.821 ^a	0.681 ^{a,3}	0.610	0.134	0.828 ^a	0.599	0.377	0.722 ^a
D08	0.450	0.733 ^a	0.796 ^a	0.853 ^a	0.184	0.641	0.470	0.909 ^{a,1}	0.625	0.710 ^a	0.117	0.858 ^{a,2}	0.832 ^a
D09	0.035	0.301	0.681	0.800 ^a	0.671	0.228	0.177	0.730	0.974 ^{a,1}	0.061	0.712	0.920 ^a	0.529
D10	0.552	0.789 ^a	0.584	0.467	0.858 ^a	0.755	0.436	0.450	0.107	0.871 ^{a,1}	0.870 ^a	0.195	0.628
D11	0.893 ^a	0.930 ^a	0.892 ^{a,2}	0.630	0.692	0.827 ^a	0.835 ^{a,2}	0.812 ^a	0.350	0.947 ^{a,2}	0.958 ^{a,1}	0.634	0.885 ^a
D12	0.185	0.485	0.782 ^a	0.869 ^a	0.461	0.431	0.021	0.825 ^a	0.954	0.160	0.489	0.52 ^{a,1}	0.672
D13	0.582	0.807 ^a	0.617	0.516	0.142	0.758 ^a	0.482	0.492	0.700	0.682	0.094	0.249	0.876 ^{a,1}

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27 ^a P<0.01; ¹ designated pair (marked in yellow); ² highest value but not designated pair
 28 (green); ³ low correlation coefficients of the designated pair (pink).

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