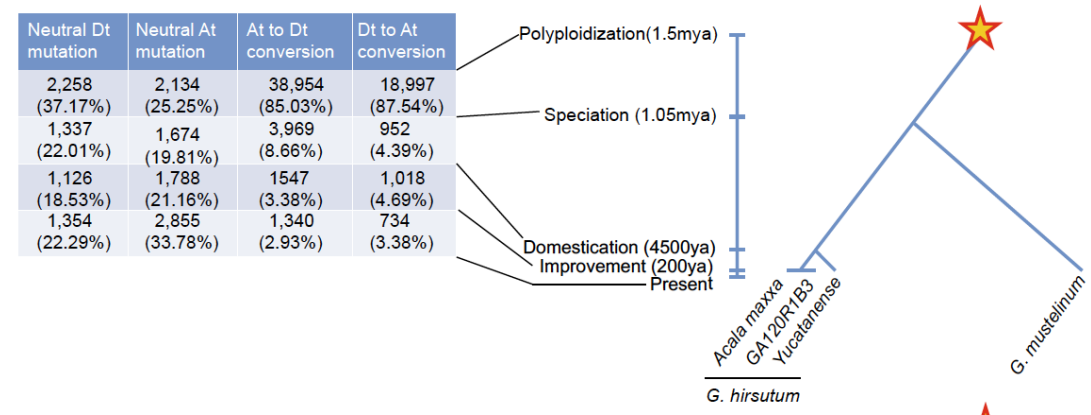
A

Neutral Dt mutation	Neutral At mutation	At to Dt conversion	Dt to At conversion
2,258 (37.17%)	2,134 (25.25%)	38,954 (85.03%)	18,997 (87.54%)
1,337 (22.01%)	1,674 (19.81%)	3,969 (8.66%)	952 (4.39%)
1,126 (18.53%)	1,788 (21.16%)	1547 (3.38%)	1,018 (4.69%)
1,354 (22.29%)	2,855 (33.78%)	1,340 (2.93%)	734 (3.38%)



B

Neutral Dt mutation	Neutral At mutation	At to Dt conversion	Dt to At conversion
2,066 (41.75%)	2,050 (27.5%)	28,446 (88.06%)	4,861 (87.54%)
1,218 (24.62%)	1,593 (21.37%)	3,146 (9.74%)	474 (7.53%)
837 (16.92%)	1,566 (21.01%)	546 (1.69%)	541 (8.59%)
827 (16.71%)	2,245 (30.12%)	166 (0.51%)	423 (6.72%)

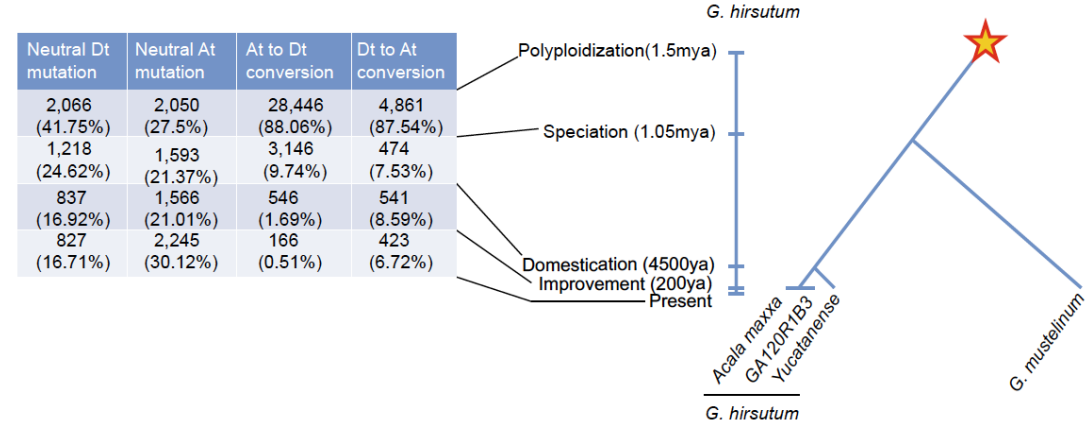


Figure S1 Timing of inter-genomic conversion. The star marks AD allopolyploidization occurring ~1-2 million years ago. (A) The numbers (proportion) of At, Dt neutral mutations (in intergenic region) and At to Dt conversions in both HC and LC are shown in each evolutionary time scale. (B) The numbers (proportion) of At, Dt neutral mutations (in intergenic region) and At to Dt conversions in HC are shown in each evolutionary time scale.

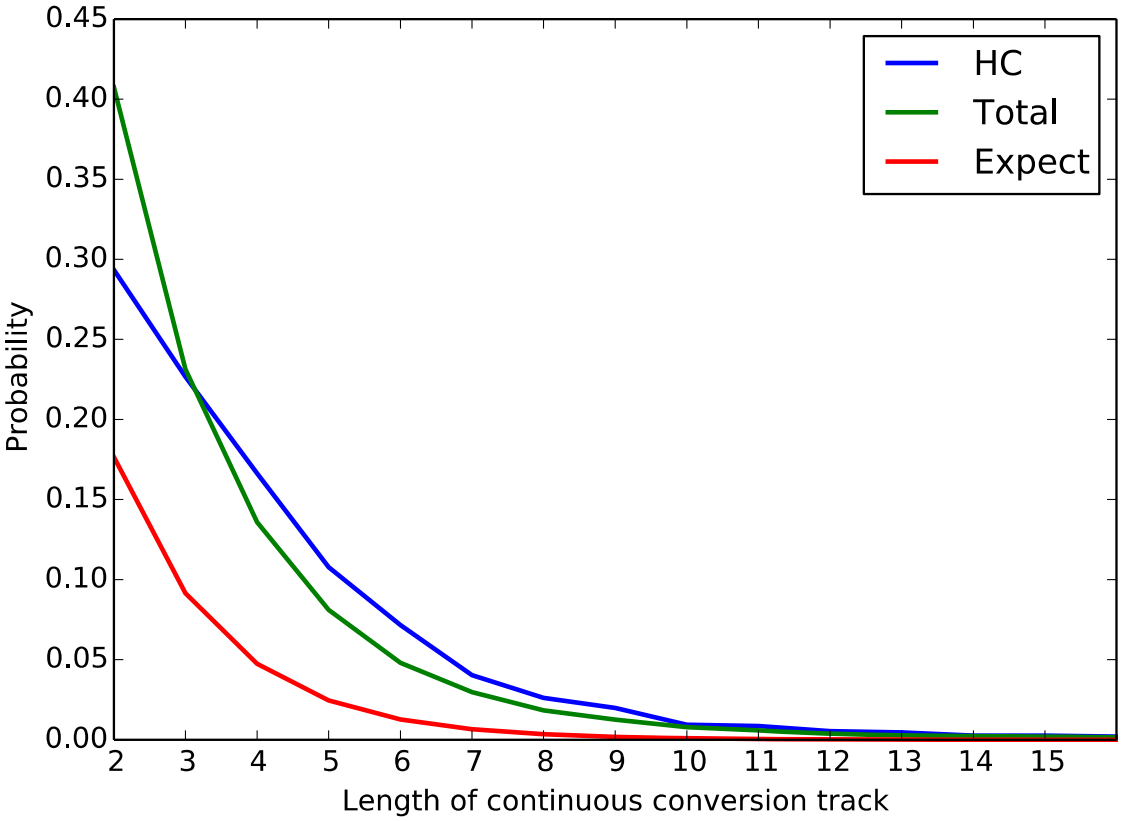
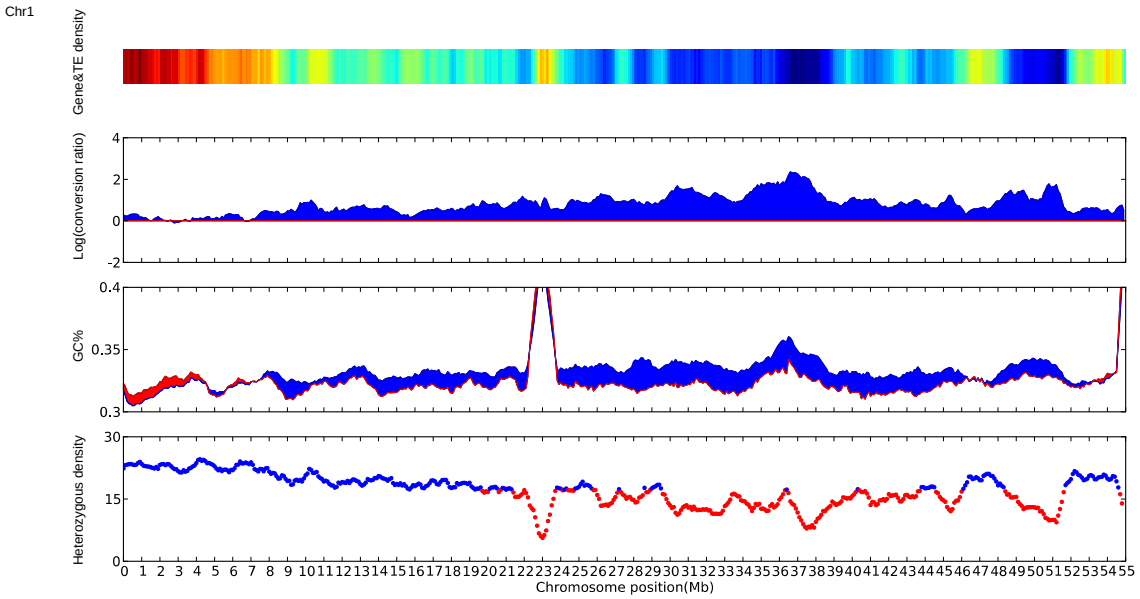
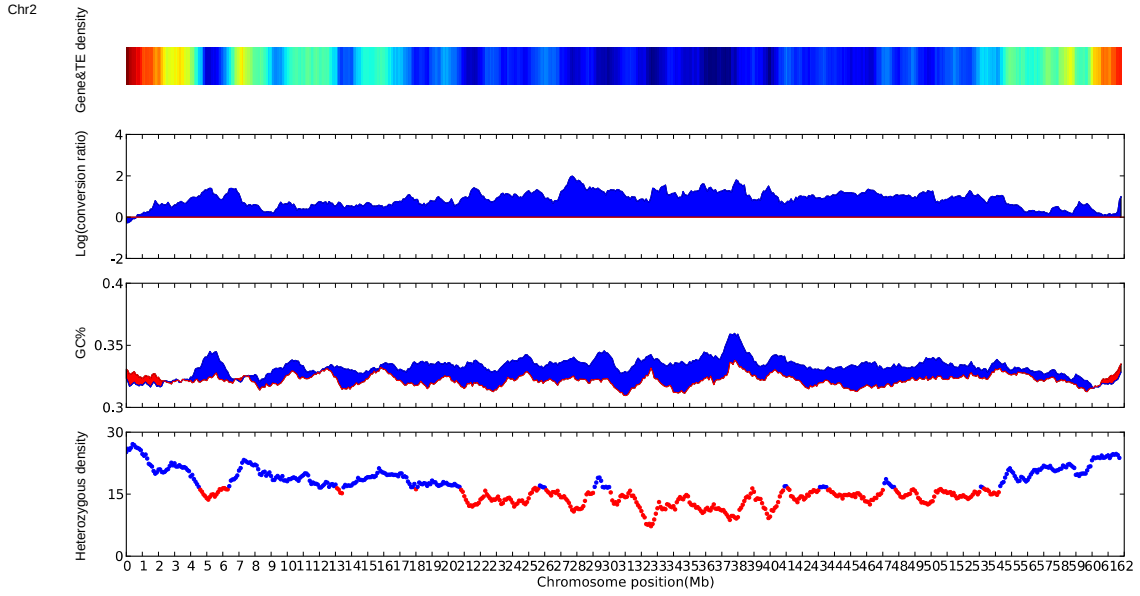
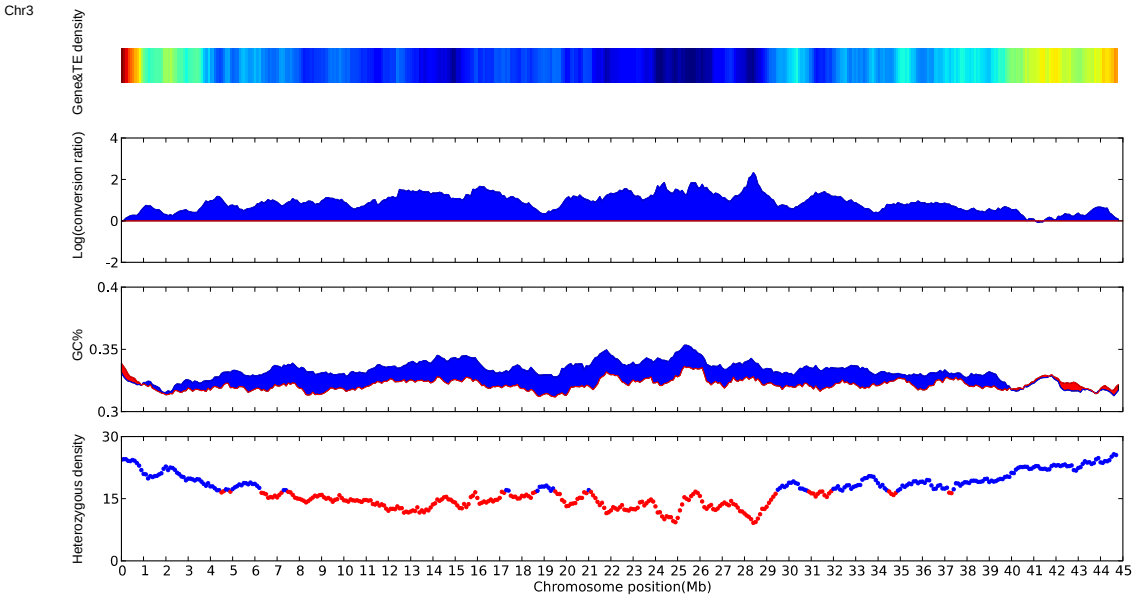
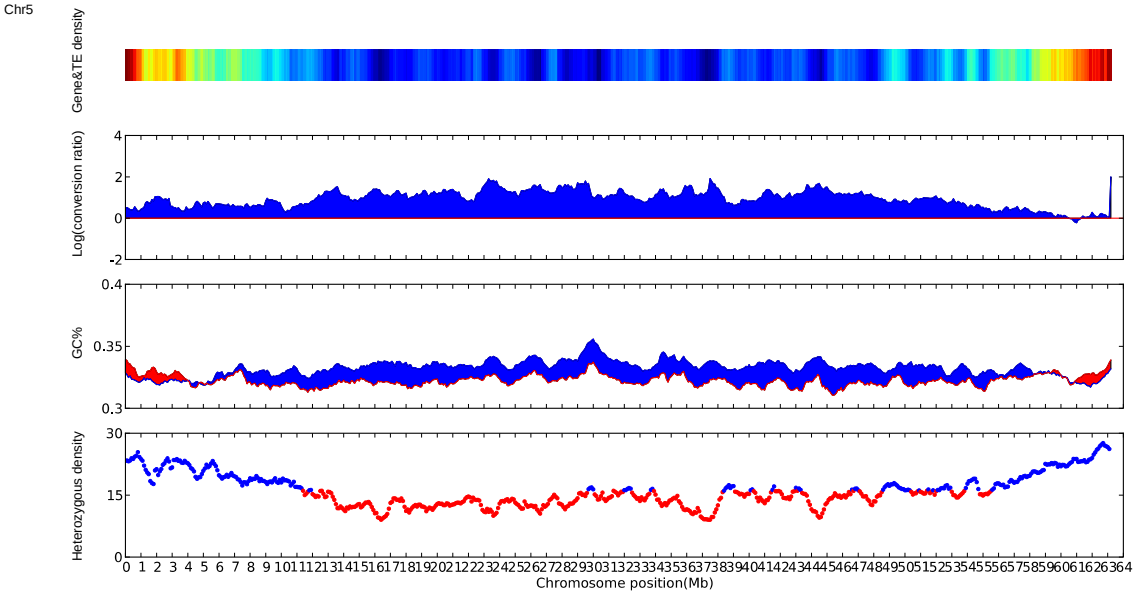


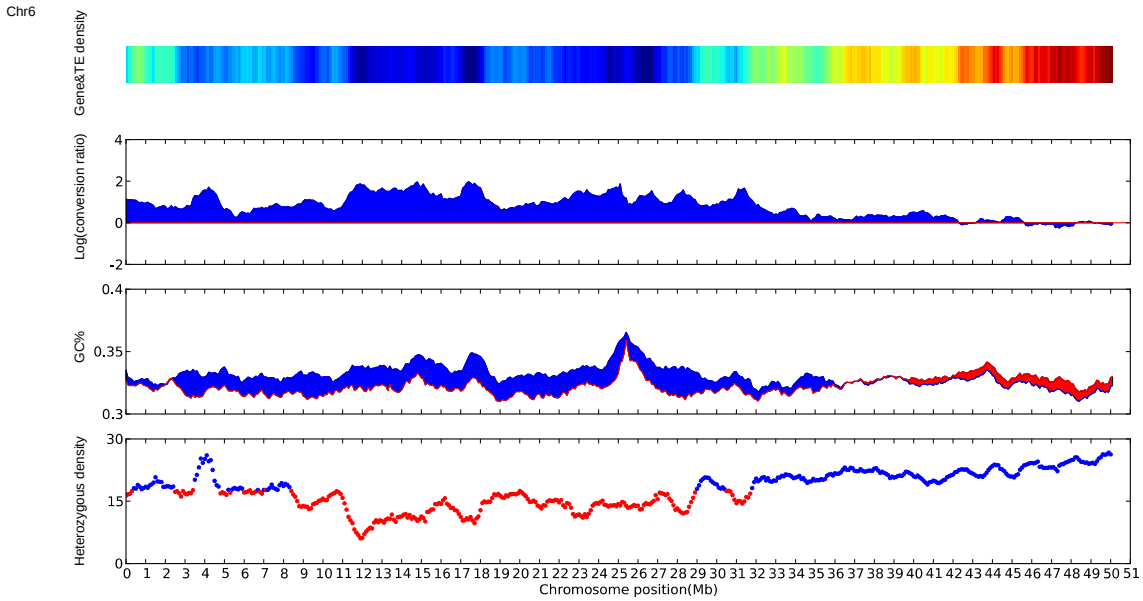
Figure S2 Frequency distribution of the length of conversion tracks measured by number of continuous converted alleles. Red line is expected distribution (exponential) of the length of continuous random mutations. Green line is the distribution of total number of conversions in the genome. Blue line is the distribution of conversions in HC.

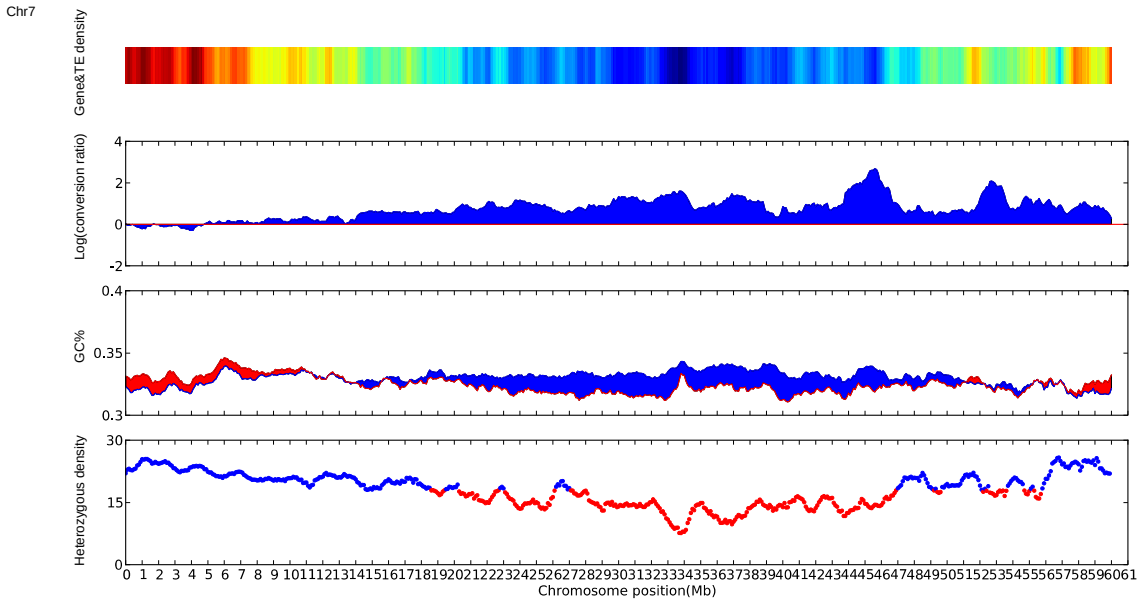

Chr1
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55
Chromosome position(Mb)

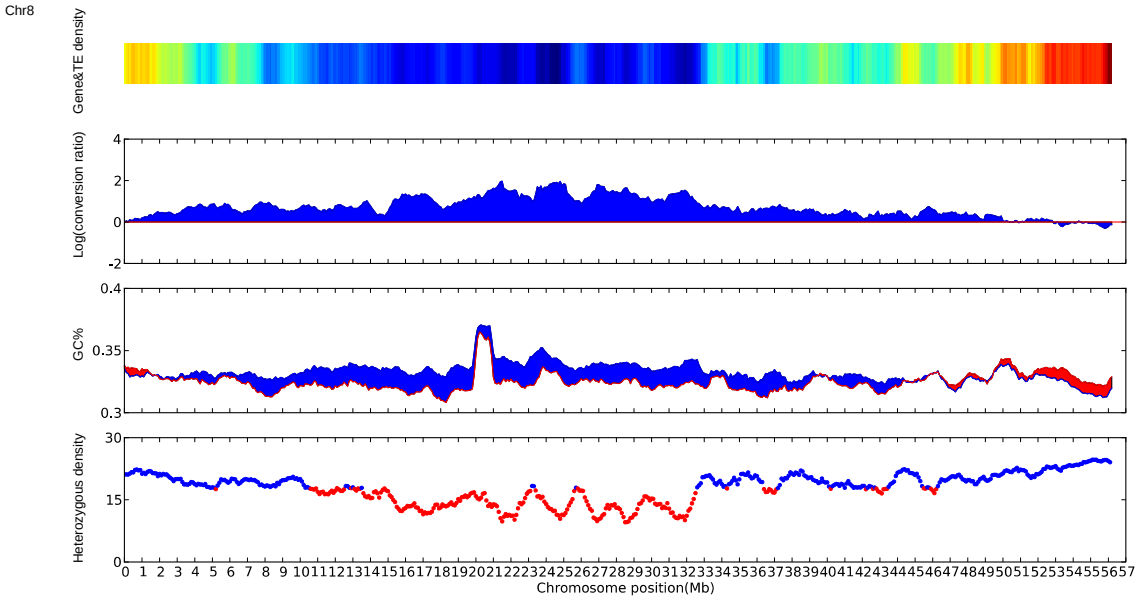

Chr2
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62
Chromosome position(Mb)

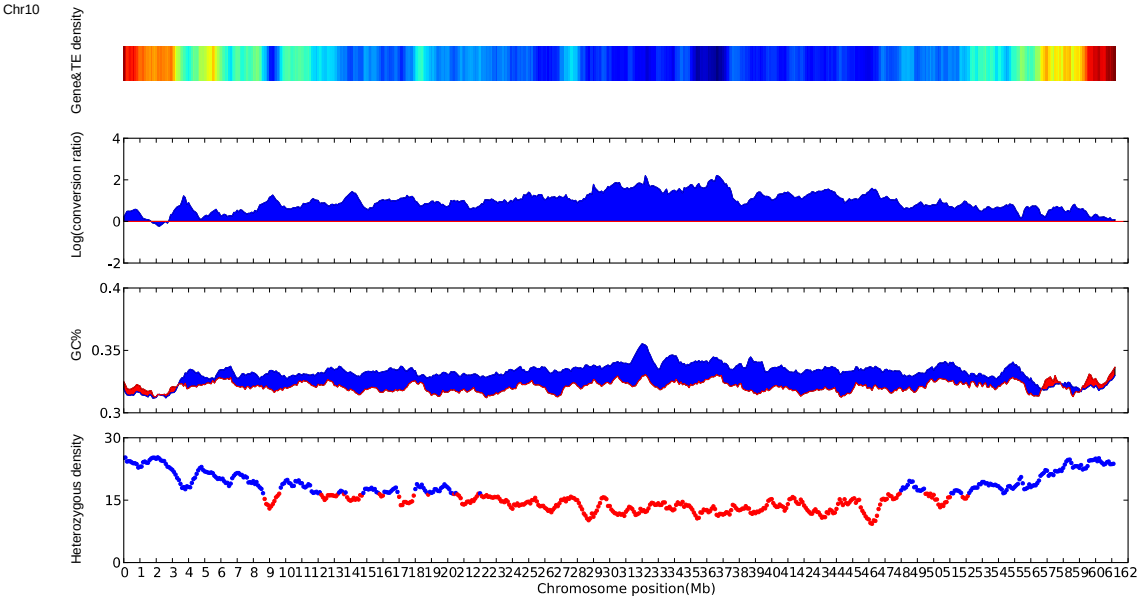

Chr3
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
Chromosome position(Mb)

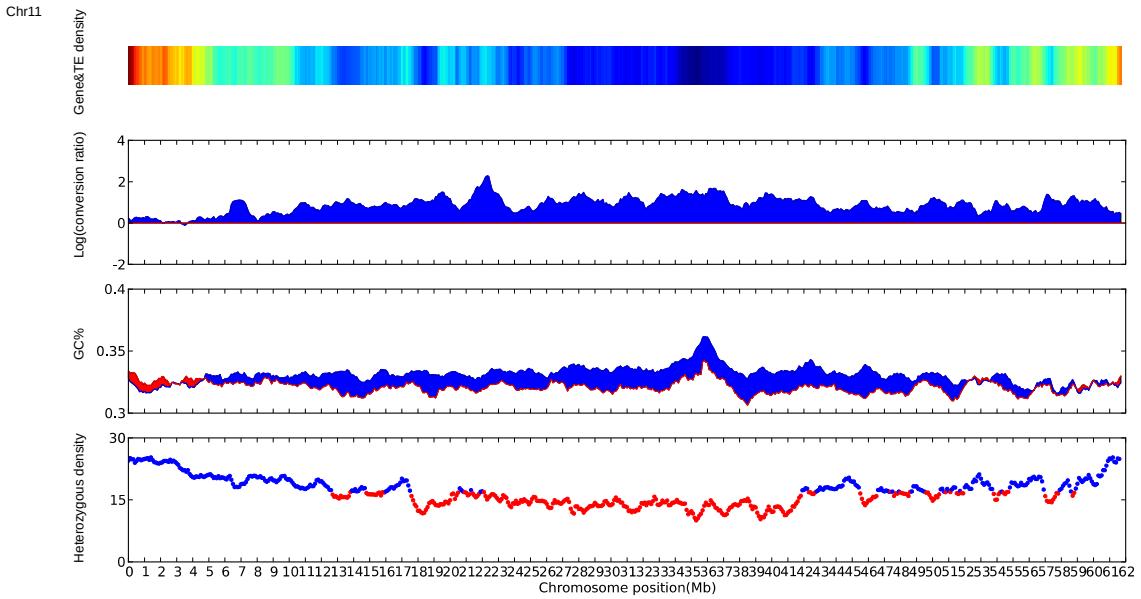

Chr5
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64
Chromosome position(Mb)

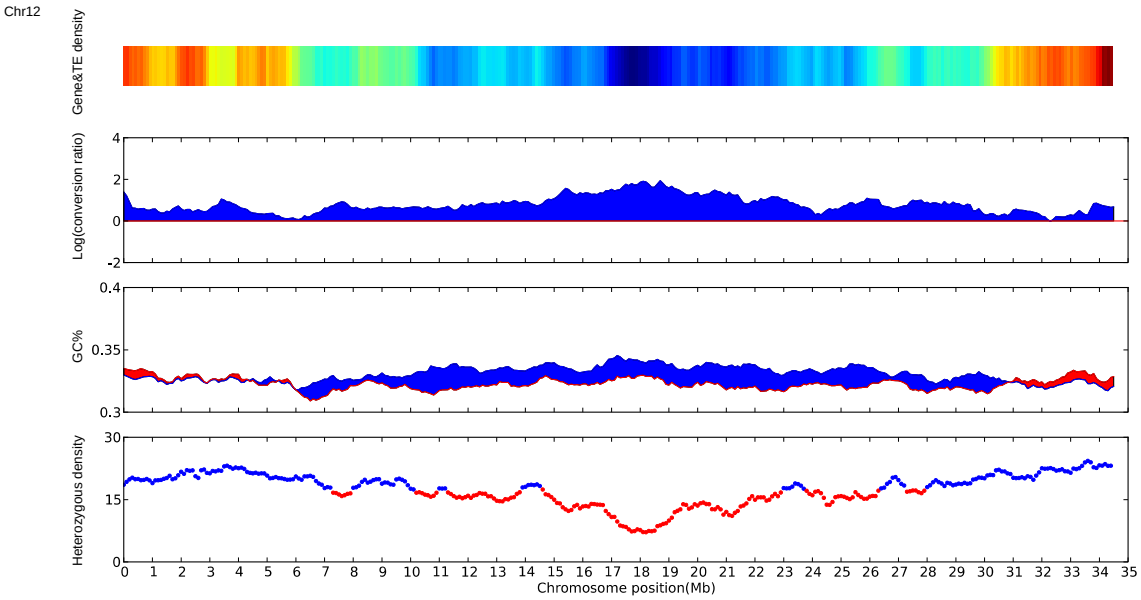

Chr6
Gene&TE density
Log(conversion ratio)
GC%
Heterozygous density
Chromosome position(Mb)


Chr7
Gene&TE density
Log(conversion ratio)
GC%
Heterozygous density
Chromosome position(Mb)


Chr8
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57
Chromosome position(Mb)


Chr10
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62
Chromosome position(Mb)


Chr11
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62
Chromosome position(Mb)


Chr12
Gene&TE density
Log(conversion ratio)
4
2
0
-2
GC%
0.4
0.35
0.3
Heterozygous density
30
15
0
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35
Chromosome position(Mb)

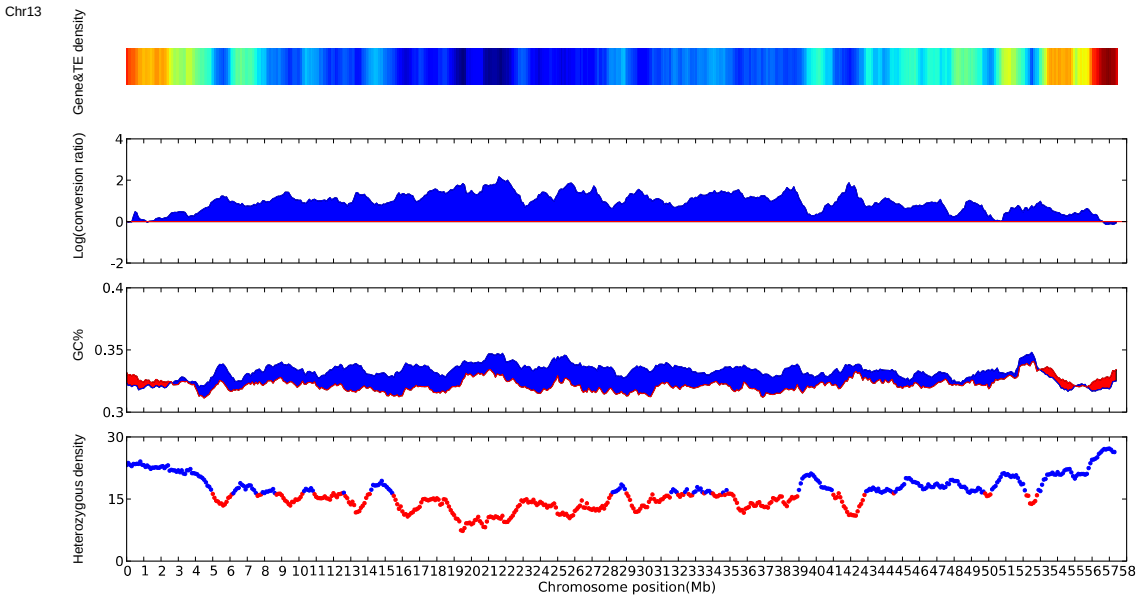


Figure S3 Genome distribution of biased conversion, heterozygosity and GC-content. See Fig. 2 for detailed legend.

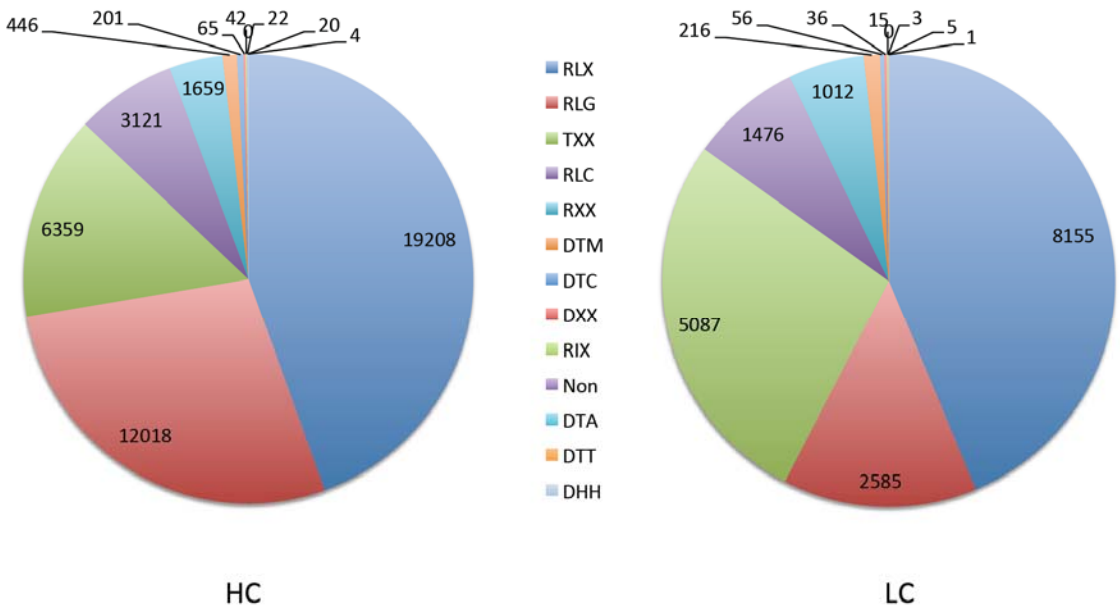


Figure S4 Number of each transposon types in HC and LC. Transposon types are: RLX, LTR-retrotransposon; RLG, Gypsy; TXX, transposon (either transposon or retrotransposon); RLC, Copia; RXX, retrotransposons; DTM, mutator; DTC, CACTA; DXX, DNA transposons; RIX, LINE; Non, others; DTA, hAT; DTT, Tc1-Mariner; DHH, Helitron.

	HC		LC	
	At -> Dt	Dt -> At	At -> Dt	Dt -> At
Polyploidization to speciation	735/472	338/263	1473/1116	1779/1733
Speciation to domestication	48/48	10/7	37/47	37/53
Domestication to improvement	12/1	8/5	11/17	12/12
Improvement to present	4/2	0/0	2/2	4/8

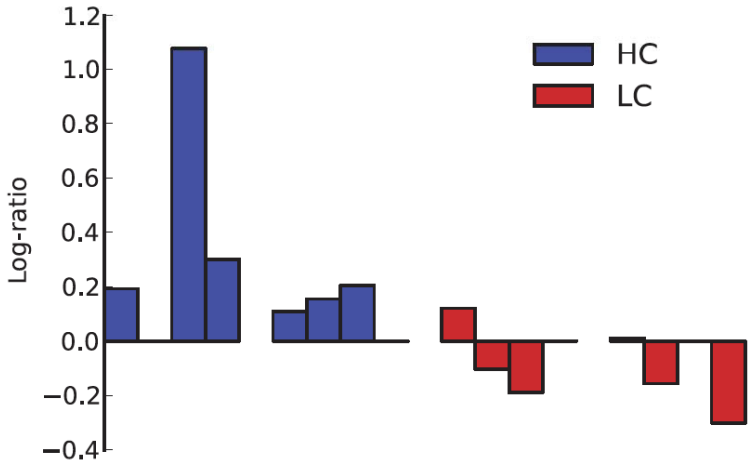


Figure S5 Phylogenetic distribution of the ratio of non-synonymous to synonymous conversions. Barplot shows logarithm of the ratio for each cell in the above table.

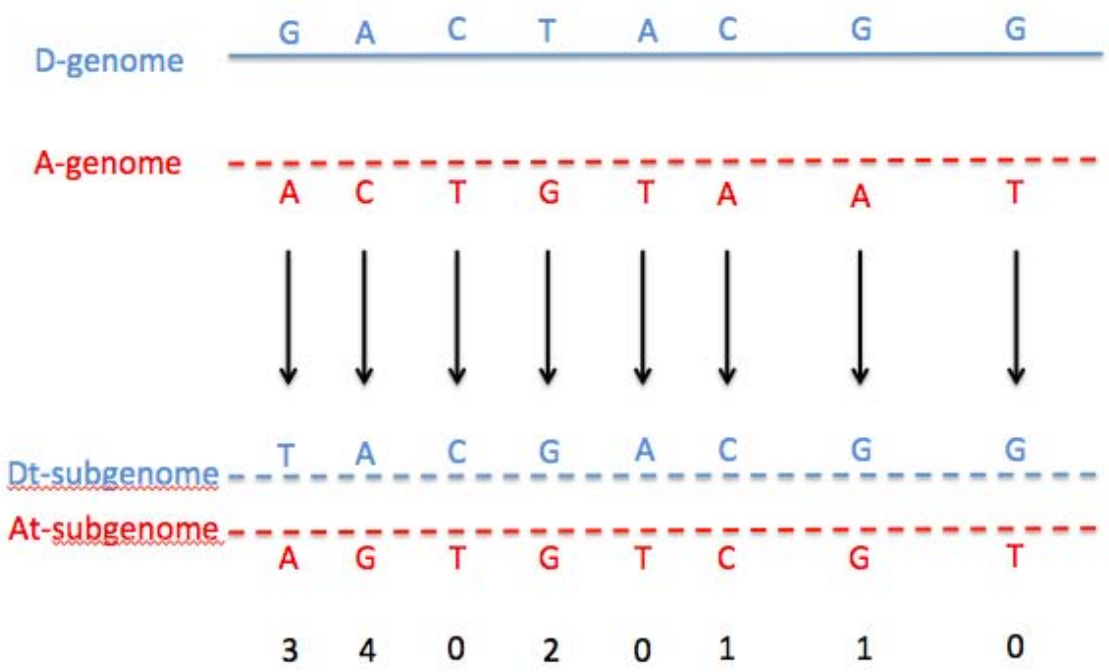
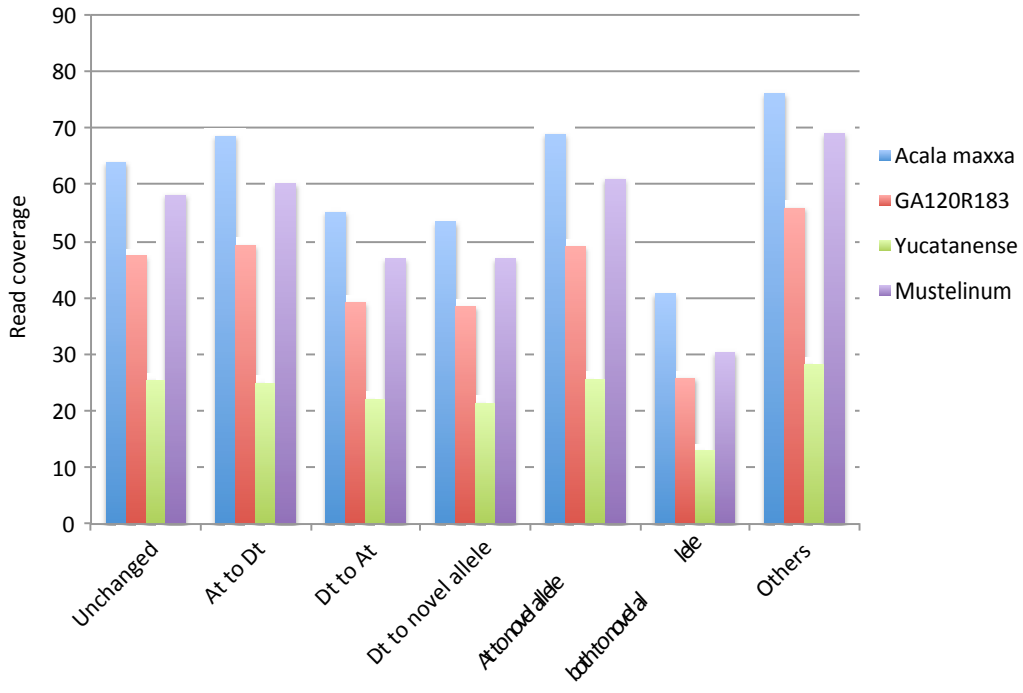
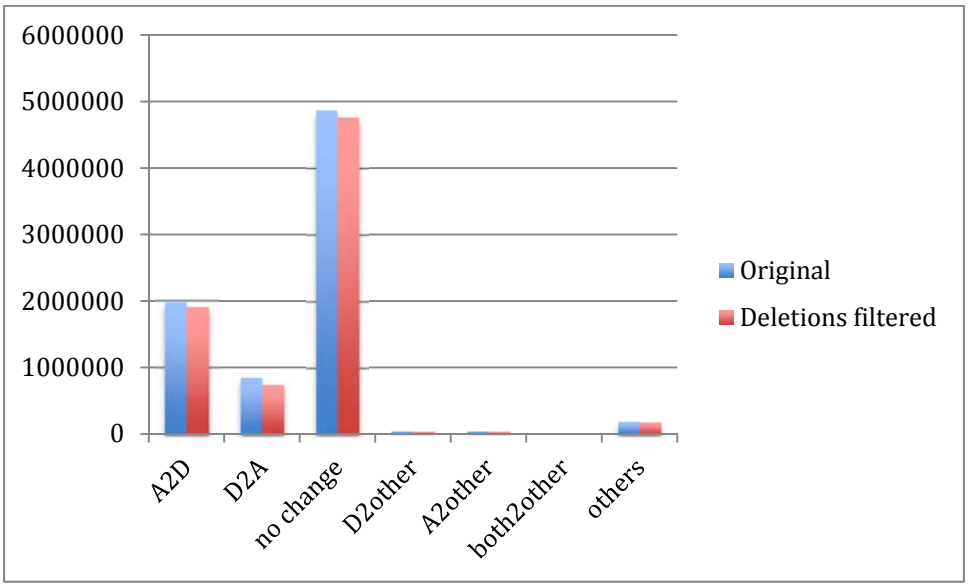


Figure S6 Identification of converted alleles. A-genome and D-genome are diploid progenitor genomes. At- and Dt-subgenome are tetraploid genomes with At-genome derived from A-genome and Dt-genome derived from D-genome. Solid line represents cotton reference genome and broken line indicates re-sequenced genomes. Sites with number “0” represents no allele changes in the tetraploid genomes, likewise, “1”: At to Dt conversion; “2”: Dt to At conversion; “3”: Dt mutation; “4”: At mutation.

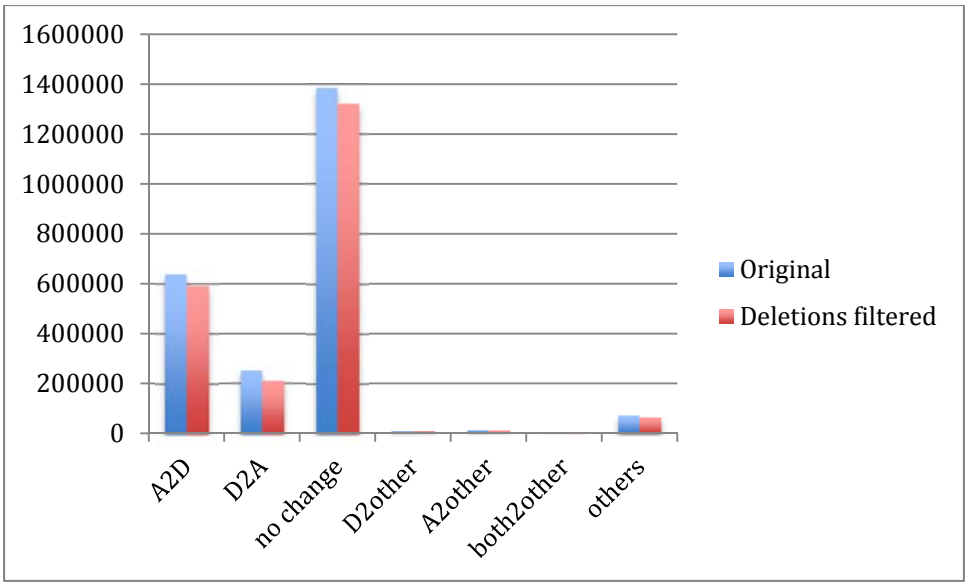
A


Read coverage
90
80
70
60
50
40
30
20
10
0
Unchanged
At to Dt
Dt to At
Dt to novel allele
At to novel allele
both to novel al
lele
Others
Acala maxxa
GA120R183
Yucatanense
Mustelinum

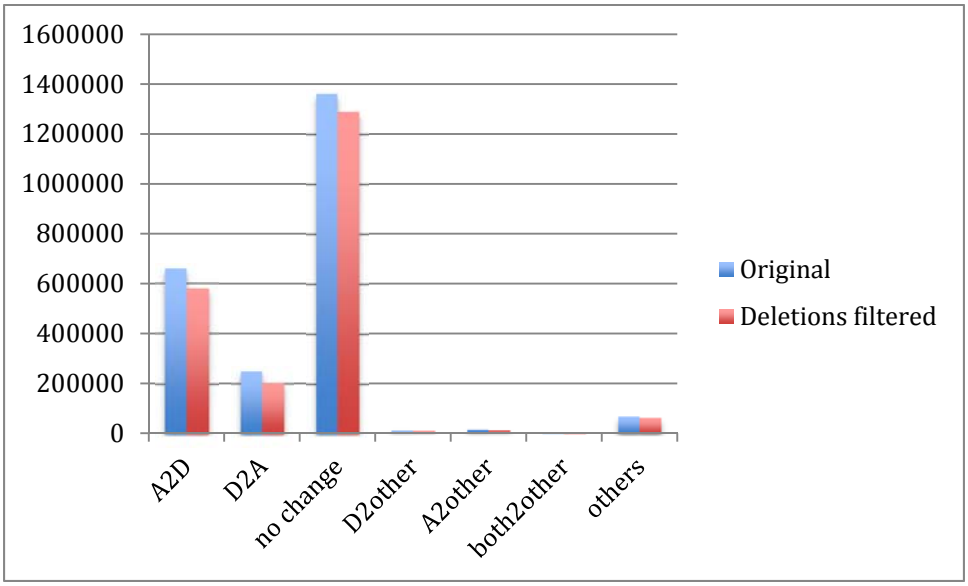
B


6000000
5000000
4000000
3000000
2000000
1000000
0
A2D
D2A
no change
D2other
A2other
both2other
others
Original
Deletions filtered

C


1600000
1400000
1200000
1000000
800000
600000
400000
200000
0
A2D
D2A
no change
D2other
A2other
both2other
others
Original
Deletions filtered

D


1600000
1400000
1200000
1000000
800000
600000
400000
200000
0
A2D
D2A
no change
D2other
A2other
both2other
others
Original
Deletions filtered

E

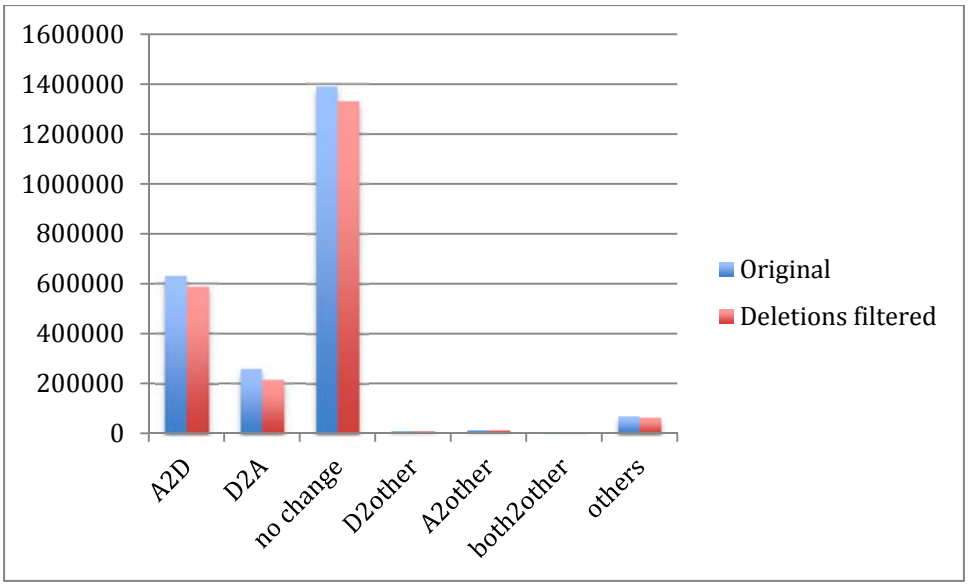


Figure S7 (A) Average mapped read coverage for different mutation categories in four cotton species. (B-E) Effects of deletion. Blue bar shows number of sites in each mutation category. Red bar shows number of sites after removal of the ones with reads coverage less than or equal to half of the average read coverage of each chromosome. (B) *Acala Maxxa*, (C) *GA120R183*, (D) *Yucatanense*, (E) *G. mustelinum*

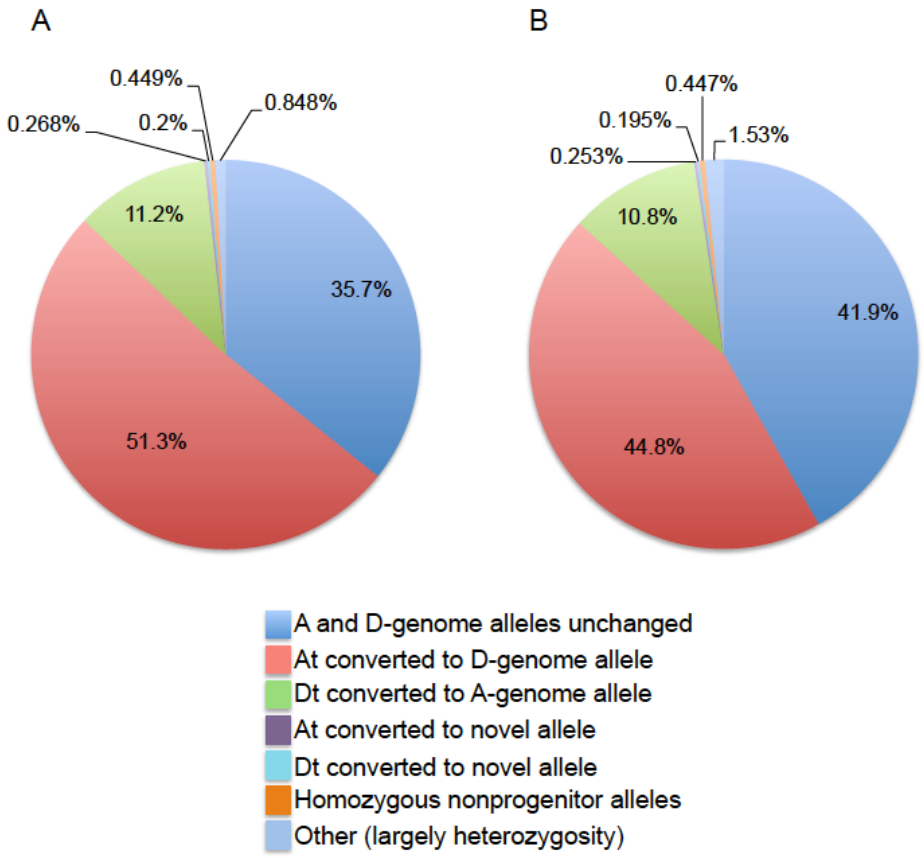


Figure S8 Allelic changes in polyploidy cotton using relaxed read editing distance (0.8). (A) Allelic changes with all other parameters unchanged. (B) Allelic changes with reduced frequency threshold to call heterozygous genotype.

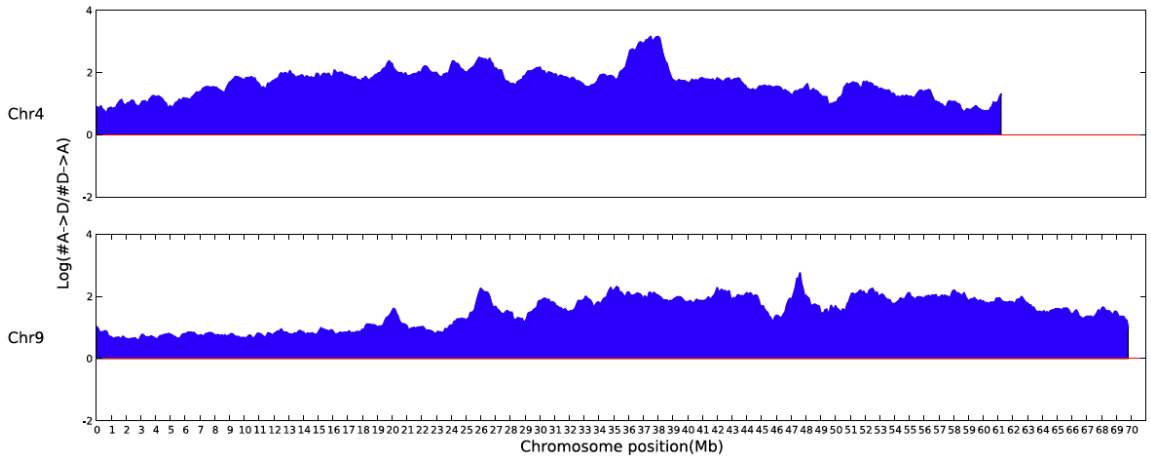
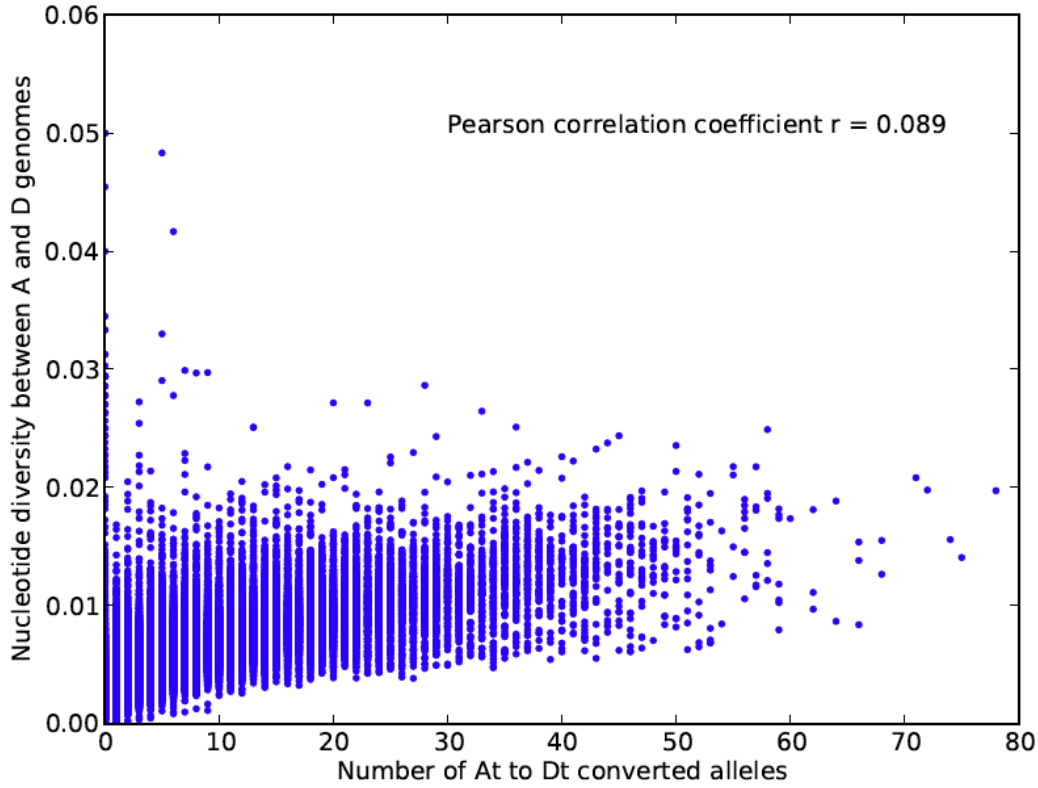
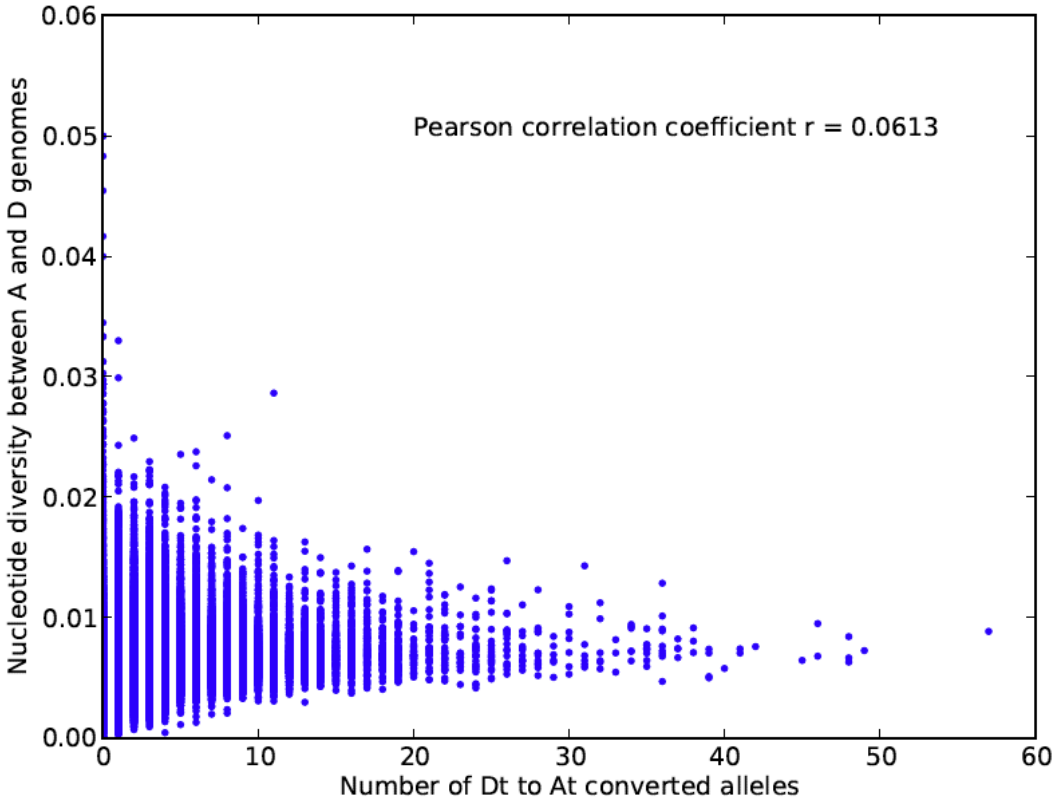


Figure S9 Genome distribution of conversion bias using relaxed read editing distance (0.8).

A


Pearson correlation coefficient r = 0.089
Nucleotide diversity between A and D genomes
Number of At to Dt converted alleles
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0
10
20
30
40
50
60
70
80

B


Pearson correlation coefficient r = 0.0613
Nucleotide diversity between A and D genomes
Number of Dt to At converted alleles
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0
10
20
30
40
50
60

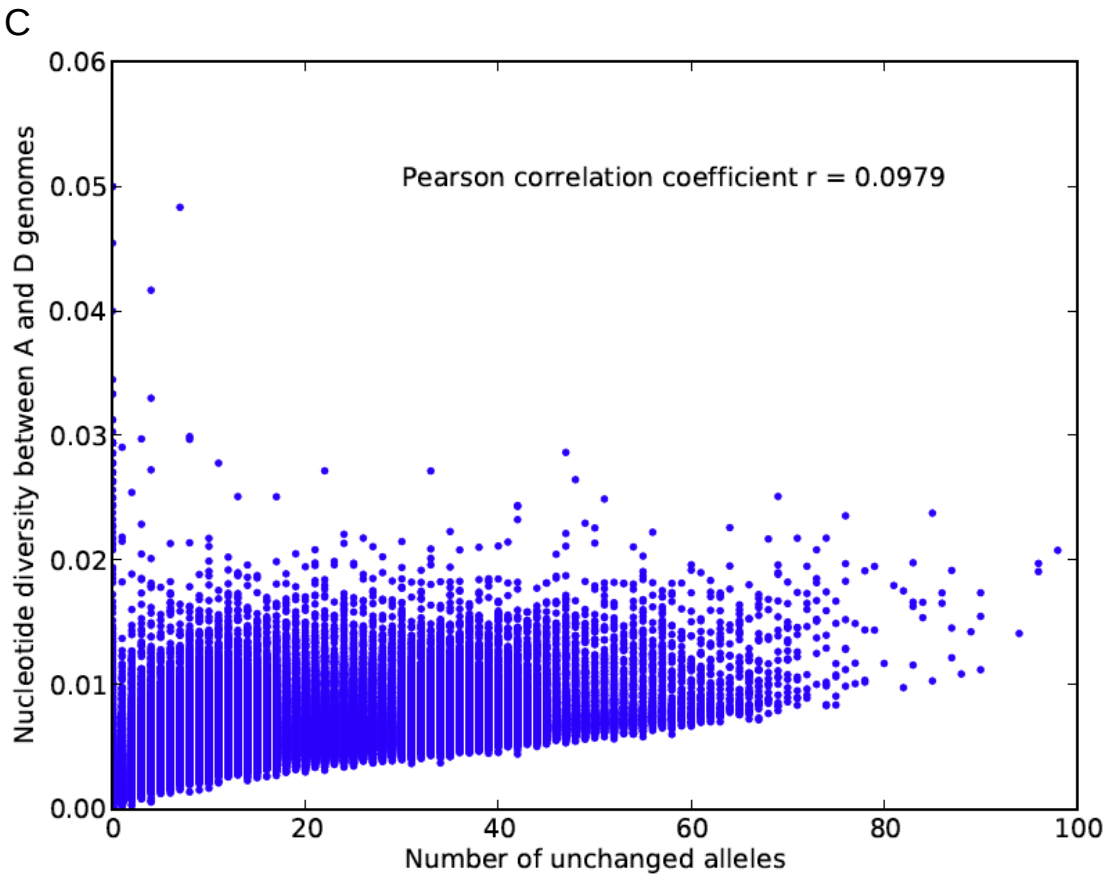


Figure S10 Correlation between number of allele changes and nucleotide divergence between A and D genomes. Genome is divided into non-overlap 10Kb bins. For each bins, the number of At to Dt converted alleles and the nucleotide divergence between the A and D genomes are calculated. (A) The number of At to Dt conversions and nucleotide divergence between A and D genomes. (B) The number of Dt to At conversions and nucleotide divergence between A and D genomes. (C) The number of unchanged alleles and nucleotide divergence between A and D genomes.

Table S1 is available for download as an Excel file at
http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.166124/-/DC1.