

Figure S1. Schematic representation of the production of genetic materials for this study.

A. ipaënsis
KG30076 (2x)

X

A. Correntina
9530 (2x)



Sterile diploid hybrid of *IpaCor*^{2x}



Chromosome doubling
through
Colchicine treatment



X



cultivated peanut

IpaCor^{4x} _S0



Fertile cultivated peanut x *IpaCor*^{4x}
F₁ hybrids

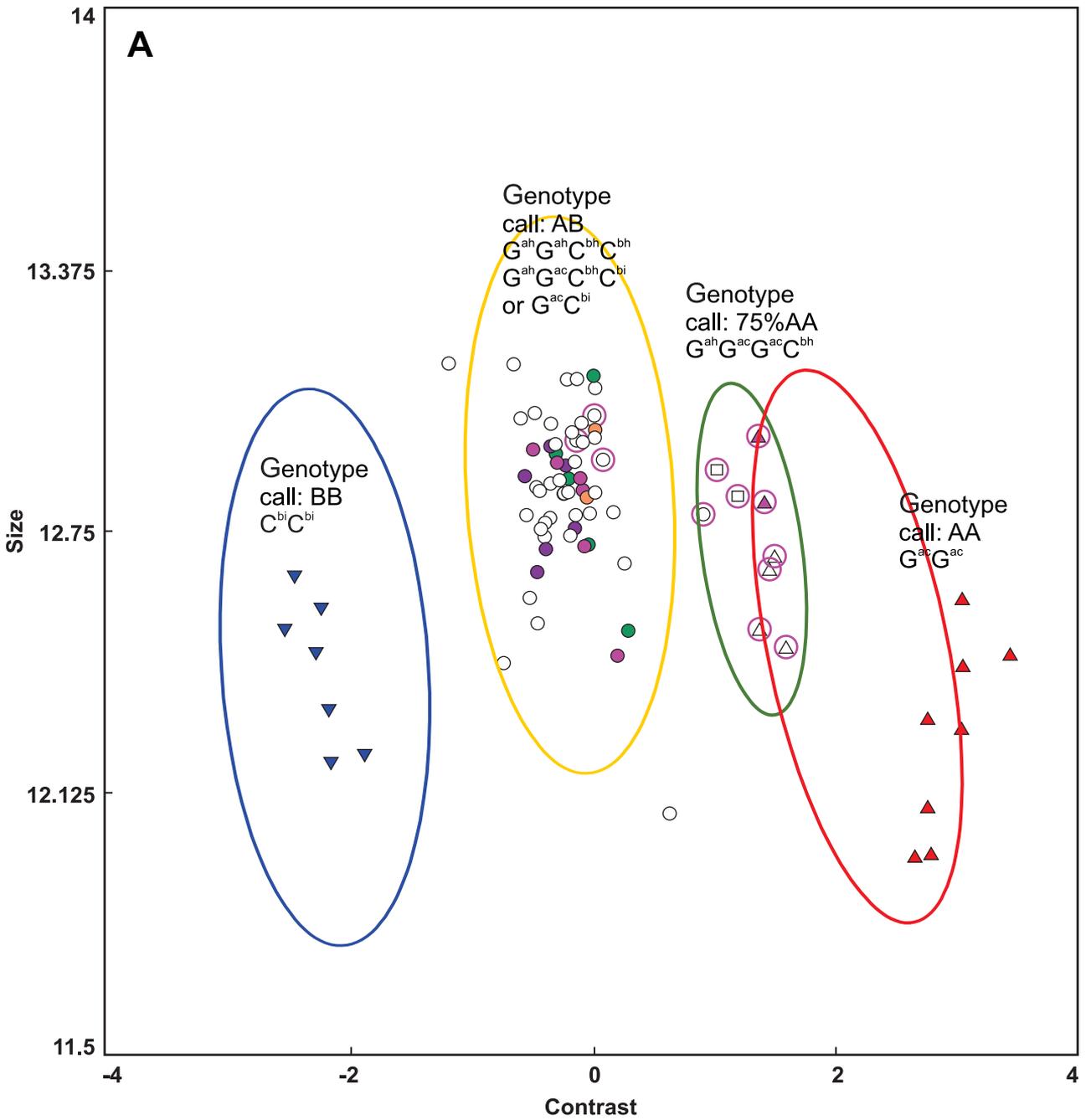


Selfing

F₂ population of cultivated peanut x *IpaCor*^{4x}

Figure S1.

Figure S2. The F₁ progenies from *A. hypogaea* x *IpaCor*^{4x}_{S0:6} cross demonstrated expected segregation of the existing subgenome recombination in *IpaCor*^{4x}_{S0:6} when the *A. hypogaea* parent has the homeologous polymorphism. The ancestral origin of the *A. hypogaea* parents is unclear at this locus, therefore, ah is used to denote their genome composition. Panel A) Genotyping profile from the SNP array. The *A. hypogaea* parents (G^{ah}G^{ah}C^{bh}C^{bh}; golden circles) are homeologous at this locus and *IpaCor*^{4x}_{S0:6} parent (G^{ac}G^{ac}G^{ac}C^{bi}; circled magenta triangles) has one allele from *Ipa* replaced by *Cor*. It is expected to produce two types of F₁ hybrids (panel B) i.e. G^{ah}G^{ac}C^{bh}C^{bi} (genotype call AB) and G^{ah}G^{ac}G^{ac}C^{bh} (genotype call 75%AA). Indeed, three of the F₁ progenies (circled white circles) were in the AB group and seven were in the 75%AA group (circled four white triangles and three white squares).



- *A. hypogaea* parent
- ◻ *IpaCor*^{4x}_{S_{0.6}} parent
- *IpaCor*^{4x}_{S₀}

- *IpaCor*^{2x}
- ▲ *Cor*
- ▼ *Ipa*

Unfilled shapes:
A. hypogaea x *IpaCor*^{4x}_{S₀}_{F₁}

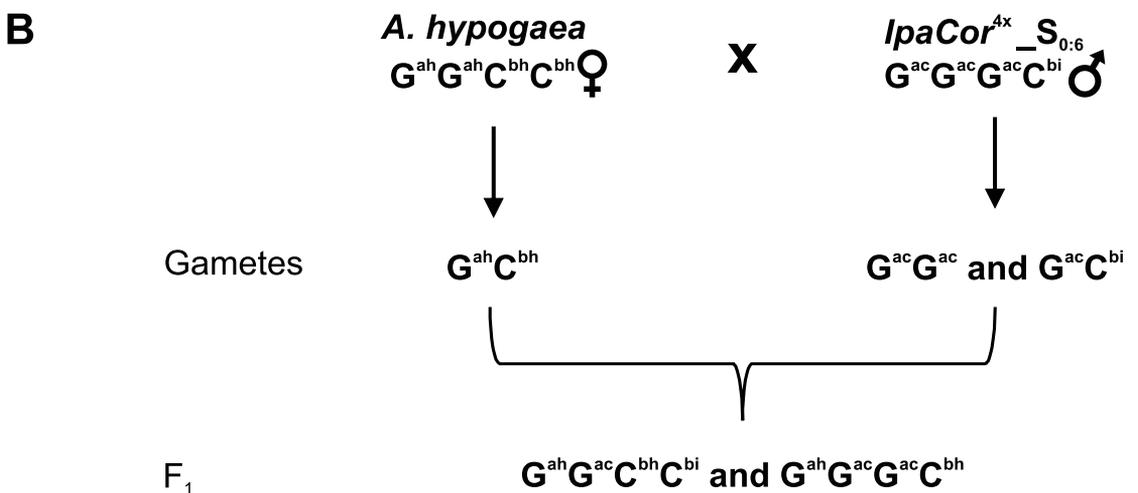
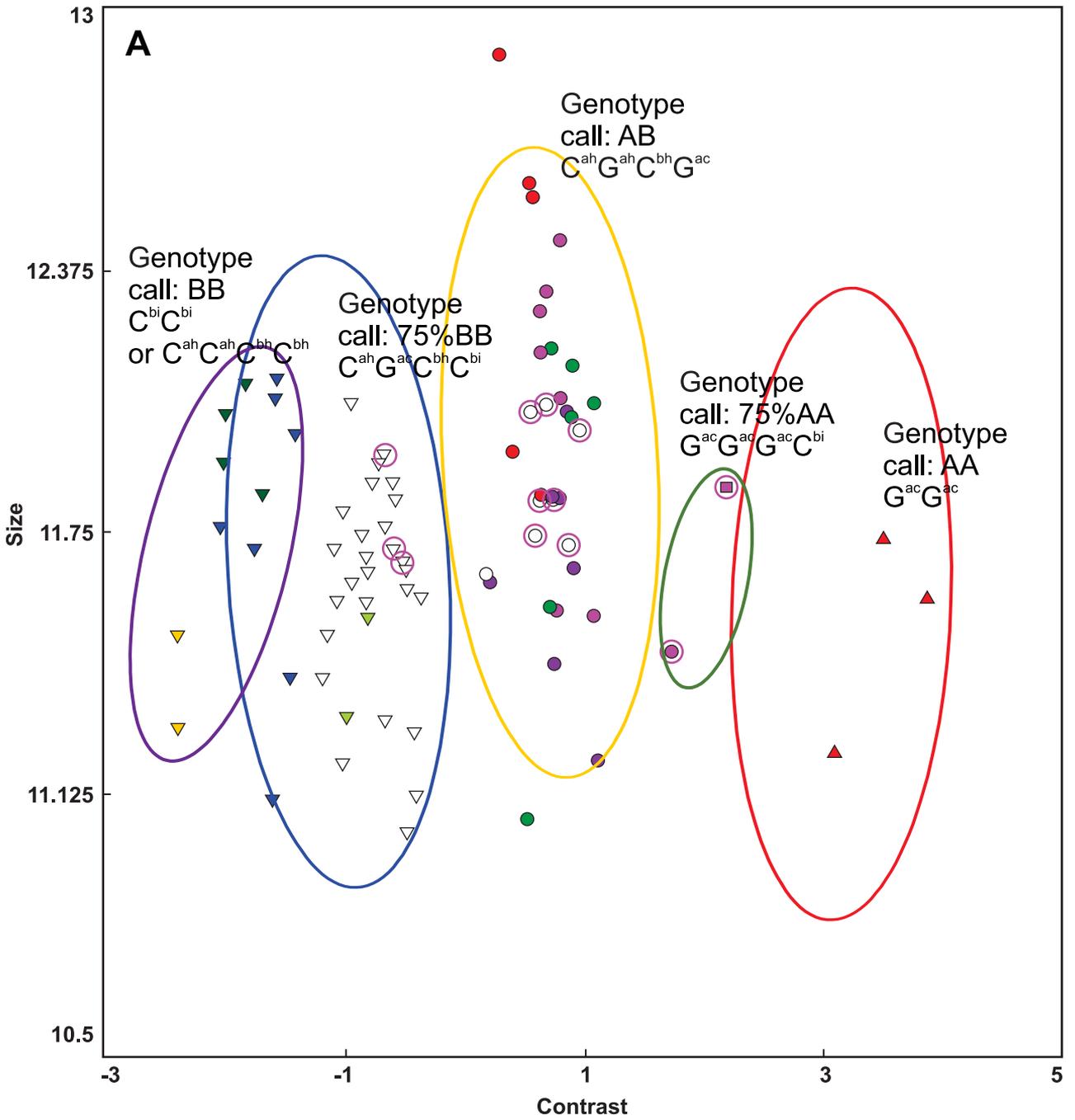


Figure S2.

Figure S3. The F₁ progenies from *A. hypogaea* x *IpaCor*^{4x}_{S0:6} cross demonstrated expected segregation of the inherited subgenome recombination from *IpaCor*^{4x}_{S0:6} when the *A. hypogaea* parent has the homologous call. ac superscript indicates A subgenome from *Cor*, bi superscript denotes B sub genome from *Ipa*. The ancestral origin of the *A. hypogaea* parents is unclear at this locus, therefore, ah is used to denote their genome composition. Panel A) Genotyping profile from the SNP array. The *A. hypogaea* parents (C^{ah}C^{ah}C^{bh}C^{bh}; golden triangles) were homologous at this locus and *IpaCor*^{4x}_{S0:6} parent (G^{ac}G^{ac}G^{ac}C^{bi}; circled magenta square and circle) has one allele from *Ipa* replaced by *Cor*. It is expected to produce two types of F₁ hybrids (panel B) i.e. C^{ah}G^{ac}C^{bh}G^{ac} (genotype call AB) and C^{ah}G^{ac}C^{bh}C^{bi} (genotype call 75%BB). Indeed, seven of the F₁ hybrids (circled white circles) were in the AB group and three (circled white triangles) were in the 75%BB group. It is noteworthy, that the two *Cor* samples are heterogeneous at this locus. Based on the genotype call of *IpaCor*^{4x}_{S0:6}, the *Cor* sample with genotype call of AA shared the allele of the actual parent of *IpaCor*^{4x}_{S0:6}.



▼ *A. hypogaea* parent

○ □ *IpaCor*^{4x}_{S_{0.6} parent}

● *IpaCor*^{4x}_{S₀}

● *IpaCor*^{2x}

▲ ● *Cor*

▼ *Ipa*

Unfilled shapes:

A. hypogaea x *IpaCor*^{4x}_{S₀_{F₁}}

B

A. hypogaea ♀
 $C^{ah}C^{ah}C^{bh}C^{bh}$

×

IpaCor^{4x}<sub>S_{0.6} ♂
 $G^{ac}G^{ac}G^{ac}C^{bi}$</sub>

Gametes

$C^{ah}C^{bh}$

$G^{ac}G^{ac}$ and $G^{ac}C^{bi}$

F₁

$C^{ah}G^{ac}C^{bh}G^{ac}$ and $C^{ah}G^{ac}C^{bh}C^{bi}$

Figure S3.

Figure S4. Overview of the new subgenome recombination events captured in F₂ populations from 13-1014 x *IpaCor*^{4x}_{S0:2}_{F1:4} (brown background) and 13-1014 x *IpaCor*^{4x}_{S0:5}_{F1:4} (grey background). The first row of the table contains name of each line. The following rows represent genetic markers exhibiting subgenome recombination among the populations. B01 to B10 stand for chromosomes. All of the markers were ordered based on chromosomal positions in ascending order which were indicated by the gradually enhancing color of the first column on the left. From the second column to the sixth column listed five control lines including *IpaCor*^{4x}_{S0:2}, 13-1014, 13-1014 x *IpaCor*^{4x}_{S0:2}_{F1:4}, *Ipa* and *Cor*. The F₂ individuals followed the controls. Genotype calls of “AB” recoded as “1” in the table were colored brown and grey for the 13-1014 x *IpaCor*^{4x}_{S0:2}_{F1:4} and 13-1014 x *IpaCor*^{4x}_{S0:5}_{F1:4} populations respectively forming the background colors. Light blue highlighted the events when one strand of *Ipa* replaced the *Cor* subgenome. Pink highlighted the events when one strand of *Cor* replaced the *Ipa* subgenome. Dark pink highlighted the tetrasomic regions for *Cor* subgenome. Dark blue highlighted the tetrasomic region for *Ipa* subgenome.

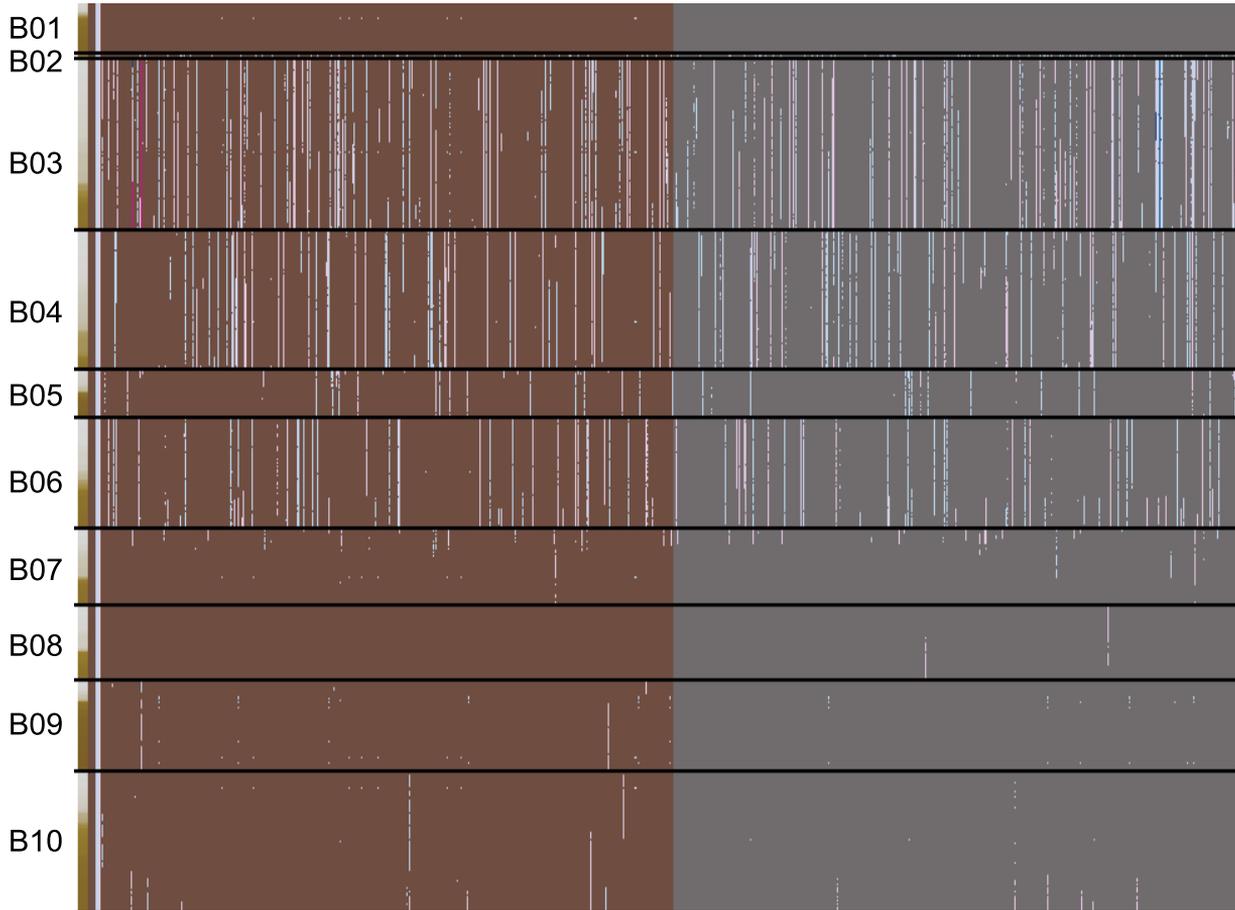


Figure S4.