

Identification of null alleles and deletions from SNP genotypes for an intercross between domestic and wild chickens

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File S1

Data Files

File S1 is available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.113.006643/-/DC1>.

pedigree.txt

File with one line per sample
Individuals grouped in families
First row for each family gives number of F₂ individuals in family
Second to fifth rows give data on grandparents
Sixth and seventh rows, data on parents
Remaining rows, data on F₂ individuals
Columns are id, sire id, dam id, sex and line (for founders)
Sex is recorded as 1 for males and 2 for females
Line is recorded as 1 for Red Junglefowl and 2 for White Leghorn

genotypes.txt

Data from the 10K SNPs
Header with SNP names
Ids in first column, genotypes in subsequent columns
One line per sample
Genotypes coded as 11, 12, 22; missing genotypes are represented by 00

intensity_data_region_x.txt

Data from the 60K SNPs in regions identified by 10K SNPs
Columns are SNP name, sample id, X raw intensity and Y raw intensity
For region 2, five SNPs in the interval determined from 10K SNPs are given
For regions 3 and 4, the SNP in the interval determined from 10K SNPs and the two flanking SNPs are given
There were no SNPs in the interval determined from 10K SNPs for region 1

###first_marker_per_chromosome.txt

File with the first marker on each chromosome, i.e. marker number 1 is the first marker on chromosome 1, marker number 1927 is the first marker on chromosome 2, marker number 3032 is the first marker on chromosome 3 and so on.