These files are the output of the Bayesian model for detection of allelic imbalance.

bayesian\_out\_dmYYYYY\_XXZ.csv: output file measuring AI in one condition

bayesian\_out\_dmYYYYY\_01h\_vs\_dmZZZZZ\_38d.csv: output file measuring AI between different timepoints in the same line

bayesian\_out\_dmYYYYY\_XXX\_vs\_dmZZZZZ\_WWW\_01h.csv: output file measuring AI between different lines at the same timepoint

Description of field for files of the type bayesian\_out\_dmYYYYY\_XXZ.csv

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| --- | --- |
| **Column name** | **Column meaning** |
| Comparison | name of the comparison |
| FEATURE\_ID | name of the gene |
| dm11037\_01h\_num\_reps | number of replicates |
| counts\_dm11037\_01h\_g1 | Number of reads assigned to haplotype 1 (g1) |
| counts\_dm11037\_01h\_g2 | Number of reads assigned to haplotype 2 (g2) |
| counts\_dm11037\_01h\_both | Number of reads not assigned to haplotypes |
| prior\_dm11037\_01h\_g1 | Prior probability of a read mapping to haplotype 1 |
| prior\_dm11037\_01h\_g2 | Prior probability of a read mapping to haplotype 2 |
| H3\_independence\_Bayes\_evidence | pvalue for H3 violation (not used for one condition) |
| dm11037\_01h\_sampleprop | Proportion of reads assigned to haplotype 1: g1/(g1+g2) |
| dm11037\_01h\_theta | Estimated proportion of reads assigned to haplotype 1 |
| dm11037\_01h\_q025 | LCL for proportion of reads assigned to haplotype 1 |
| dm11037\_01h\_q975 | UCL for proportion of reads assigned to haplotype 1 |
| dm11037\_01h\_Bayes\_evidence | pvalue for AI |
| dm11037\_01h\_AI\_decision | Was AI detected? 1 = Yes, 0= No |
| alpha1\_postmean | Posterior mean of alpha |
| flaganalyze | Should this gene be analyzed? 1 = Yes, 0= No |

Description of field for files of the type bayesian\_out\_sample\_1\_vs\_ sample\_2.csv

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| --- | --- |
| **Column name** | **Column meaning** |
| comparison | name of the comparison |
| FEATURE\_ID | name of the gene |
| sample\_1\_num\_reps | number of replicates in sample1 |
| sample\_2\_num\_reps | number of replicates in sample2 |
| counts\_sample\_1\_g1 | Number of reads assigned to haplotype 1 (g1) in sample 1 |
| counts\_sample\_1\_g2 | Number of reads assigned to haplotype 2 (g2) in sample 1 |
| counts\_sample\_1\_both | Number of reads not assigned to haplotypes in sample 1 |
| counts\_sample\_2\_g1 | Number of reads assigned to haplotype 1 (g1) in sample 2 |
| counts\_sample\_2\_g2 | Number of reads assigned to haplotype 2 (g2) in sample 2 |
| counts\_sample\_2\_both | Number of reads not assigned to haplotypes in sample 2 |
| prior\_sample\_1\_g1 | Prior probability of a read mapping to haplotype 1 in sample 1 |
| prior\_sample\_1\_g2 | Prior probability of a read mapping to haplotype 2 in sample 1 |
| prior\_sample\_2\_g1 | Prior probability of a read mapping to haplotype 1 in sample 2 |
| prior\_sample\_2\_g2 | Prior probability of a read mapping to haplotype 2 in sample 2 |
| H3\_independence\_Bayes\_evidence | pvalue for H03 violation (if <0.05 H03 is violated) |
| sample\_1\_sampleprop | Proportion of reads assigned to haplotype 1 in sample 1: g1/(g1+g2) |
| sample\_1\_theta | Estimated proportion of reads assigned to haplotype 1 in sample 1 |
| sample\_1\_q025 | LCL for proportion of reads assigned to haplotype 1 in sample 1 |
| sample\_1\_q975 | UCL for proportion of reads assigned to haplotype 1 in sample 1 |
| sample\_1\_Bayes\_evidence | pvalue for AI in sample 1 |
| sample\_1\_AI\_decision | Was AI detected in sample 1? 1 = Yes, 0= No |
| sample\_2\_sampleprop | Proportion of reads assigned to haplotype 1 in sample 2: g1/(g1+g2) |
| sample\_2\_theta | Estimated proportion of reads assigned to haplotype 1 in sample 2 |
| sample\_2\_q025 | LCL for proportion of reads assigned to haplotype 1 in sample 2 |
| sample\_2\_q975 | UCL for proportion of reads assigned to haplotype 1 in sample 2 |
| sample\_2\_Bayes\_evidence | pvalue for AI in sample 2 |
| sample\_2\_AI\_decision | Was AI detected in sample 2? 1 = Yes, 0= No |
| alpha1\_postmean | Posterior mean of alpha in sample 1 |
| alpha2\_postmean | Posterior mean of alpha in sample 2 |
| flaganalyze | Should this gene be analyzed? 1 = Yes, 0= No |
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