

Additional file 2. Parameters used for exonerate analysis of the Agilent-016047 maize microarray reporters and ESTs against the B73 maize genome sequence

| Exonerate parameter | Value | Description |
|----------------------------|-----------------------------|---|
| alignment model | est2genome | This model is similar to the affine:local model, but it also includes intron modelling on the target sequence to allow alignment of spliced to unspliced coding sequences for both forward and reversed genes |
| bestn | 1 | Report the best N results for each query (only results scoring better than the score threshold will be reported) |
| minintron | 30 (default) | Minimum intron length limit |
| maxintron | 100000 | Maximum intron length limit |
| raw score | 100 (default minimum score) | The sum of transition scores used in the dynamic programming. The maximum score depends on the query sequence length. |
| gapopen | -12 (default) | This is the gap open penalty |
| gapextend | -4 (default) | This is the gap extension penalty |
| mismatch | -9 (default) | Mismatch penalty |