

Additional File 1. BLAST parameters used for annotation of the Agilent-016047 maize microarray

BLAST parameter	reporters vs (i) ESTs; (ii) WGS transcripts; (iii) gDNA	ESTs vs WGS transcripts	WGS transcripts vs GenBank (functional annotation)
Program name	BLASTN	BLASTN	BLASTX
Word size	23	11 (default)	3 (default)
Filter query sequence for low-complexity subsequences	TRUE (default)	TRUE (default)	TRUE (default)
Gapped alignment	FALSE	TRUE (default)	TRUE (default)
Initial penalty for opening a gap	NA (no gaps allowed)	5 (default)	11 (default)
Penalty for each gap character	NA (no gaps allowed)	2 (default)	1 (default)
Threshold expectation value for keeping alignments	10 (default); own filtering on identity out of 60	10^{-10}	10^{-10}
Protein similarity matrix	not used in BLASTN	not used in BLASTN	BLOSUM62 (default)