**anyexpress Combine**:
This command combines multiple platform files into a single target-by-sample text file. Commonly used targets are ‘gene’ and ‘isoform’.  

-c (closed-platform):
Each closed-platform needs two parameters: (1) the file name with a full path to the genomic position file (.BED file), and (2) a probe-by-sample text file. Multiple platforms are allowed, each described by two parameters.

-o (open-platform):
One .BED file per platform. There can be multiple .BED files. In this example, ‘S5_ILMN.BED’ is an Illumina GA file and ‘S6_ABI.BED’ is an ABI SOLiD file. The .BED file results from external alignment software (e.g., Bowtie) and is necessary before running ‘anyexpress Combine’.

-t (target):
Reference target used for entire project. The user has to run ‘anyexpress BuildTarget’ in advance. Available reference targets can be listed with the command ‘anyexpress DisplaySys’.

-e (exclusion feature):
These are criteria for filtering out undesirable tags. The user has to run ‘anyexpress BuildExclusionFeature’ in advance. Available exclusion features can be listed with the command ‘anyexpress DisplaySys’.

-s (set operation):
This option indicates whether the user wants to use ‘intersection’ or ‘union’ set operation to combine data.

-p (project workspace):
This is the directory to which all the results will be written.