

\$anyexpress Combine :

This command combines multiple platform files into a single target-by-sample text file. Commonly used targets are 'gene' and 'isoform'.

-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*'.

-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*'

```
$anyexpress Combine \
```

```
-c U133A.BED 4samples.txt \
```

```
-o S5_ILMN.BED S6_ABI.BED \
```

```
-t RefGene2010 \
```

```
-e multiTarget dbsnp131 \
```

```
-s intersection
```

```
-p myProject
```

-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.

-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*'

-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.