Interpreting Results.INF

"Results.INF" is a tab-delimited text file split into ten columns with the following headers:

Table 1. Column headers for "Results.INF" file and the associated description and data.

Header	Description	Data shown
FLAG	-	+
POS	Base Position in consensus sequence	1,2,3,4,5… …
ID	Clone Number Analysed	Clone_1, Clone_2, Clone_3, etc…
MT	Types of Mutation	WT, SUB, INS, DEL
TMPSEQ	Base on the Template Sequence	T, A, C, G
QRYSEQ	Base on the Query Consensus Sequence	T, A, C, G
ORITMP	Original base from the raw AB1 / FASTQ file	('T/A/C/G/<Blank>', 'T/A/C/G/<Blank>')
ORIPHRED	Phred score obtained from the Raw AB1	(61,58)
ORIPOS	Original position of base in the raw AB1 / FASTQ file	(335, 6), (336, 5), (337, 4), etc…
ORIID	Filename of Raw Sequence	('Filename1', 'Filename2')

Bases are numbered according to the consensus sequence. Any base mutations are highlighted under the "MT" column and can be traced back to the raw sequencing file to verify the base from the reads.

YAQAAT detects if the base is reversed complemented or read in the forward direction. If the sequence is reverse complemented, the ORIPOS number corresponding to the sequence decreases down the row. But if the sequence is read in the forward direction, the ORIPOS number increases down the row.

Table 2: First five lines of a sample Results.INF

FLAG	POS	ID	MT	TMPSEQ	QRYSEQ	ORITMP	ORIPHRED	ORIPOS	ORIID
+	1	Clone_1	WT	T	T	('T',)	(10,)	(1,)	('1x',)
+	2	Clone_1	WT	A	A	('A',)	(10,)	(2,)	('1x',)
+	3	Clone_1	WT	A	A	('A',)	(20,)	(3,)	('1x',)
+	4	Clone_1	WT	G	G	('G',)	(7,)	(4,)	('1x',)
+	5	Clone_1	WT	T	T	('T',)	(7,)	(5,)	('1x',)

Interpreting Summary.csv

“Results.INF” is a comma-separated CSV file split into six columns with the following headers:

Table 3. Column headers for “Summary.csv” file and the associated description and data.

Header	Description	Data shown
ID	Clone Number Analysed	Clone_1, Clone_2, Clone_3, etc…
Sequence	Consensus sequence of analysed pair	AAGTTAATCCTATT…
Sequence_Length	Length of consensus sequence (integer)	794
SUB	Base substitution at base position 1 from “T/A/C/G” to “T/A/C/G”, if any	398A>G
INS	Base Insertion at base position 1 from “-“ to “T/A/C/G”, if any	398->G
DEL	Base Deletion from base position 1 to base position 2, if any	794_799del

All clones analysed are displayed in the Summary.csv file indicating presence or absence of mutations. If mutations are absent, the columns are left blank. Otherwise, the mutations are as described in Table 3.

Table 4. Sample data of “Summary.csv”

ID	Sequence	Sequence_Length	SUB	INS	DEL
Clone_1	TAAGTTAATCCTATT…	794			

Interpreting Skipped.csv

"Skipped.csv" is a comma-delimited text file split into six columns with the following headers:

Table 5. Column headers for "Skipped.csv" file and the associated description and data.

Header	Description	Data shown
Skipped_Clone	Clone Number skipped	Clone_1, Clone_2, Clone_3, etc…
Skipped_low_quality_file	Low quality file	N/A
Quality_score	Quality score sequence	N/A
Ab1_Quality_score_Cutoff	Cutoff score of AB1	N/A
Reason	Reason for skipping	Unallignable/Assembly error

All skipped clones are displayed in the Skipped.csv file indicating reason for skipping as described in Table 5.

Table 6: Sample data of "Skipped.csv"

Skipped_Clone	Skipped_low_quality_file	Quality_score	Ab1_Quality_score_Cutoff	Reason
Clone_2	N/A	N/A	N/A	Unallignable/Assembly error
Clone_3	N/A	N/A	N/A	Unallignable/Assembly error