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Analysis of Massively Parallel Sequencing Data Using the STR Allele Identification Tool – Razor (STRait Razor)

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Overview

- How STRait Razor works
- Starting your analysis
- Analysis workbook
- Customization potential
- Try it out

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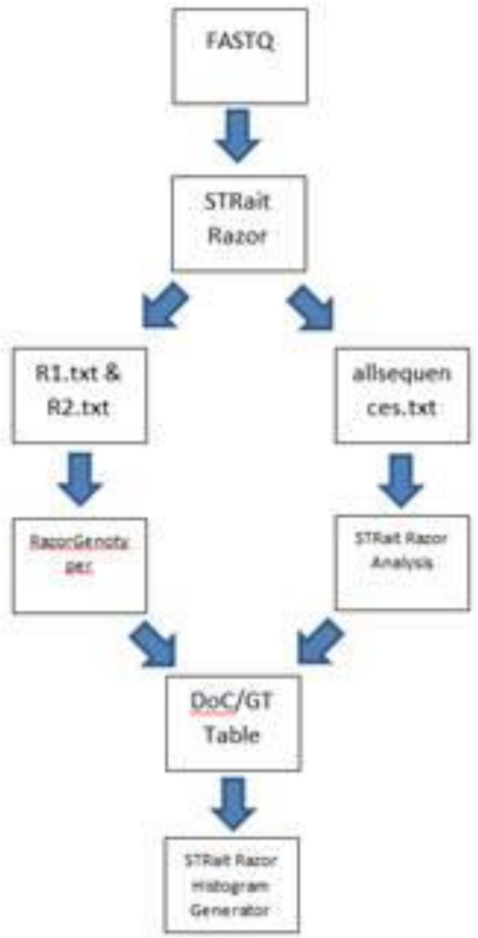
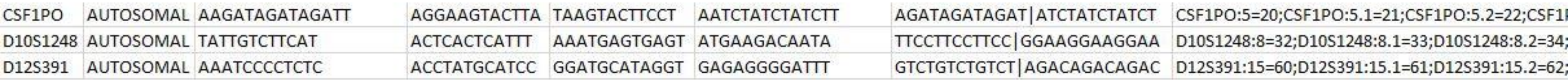


The Configuration File



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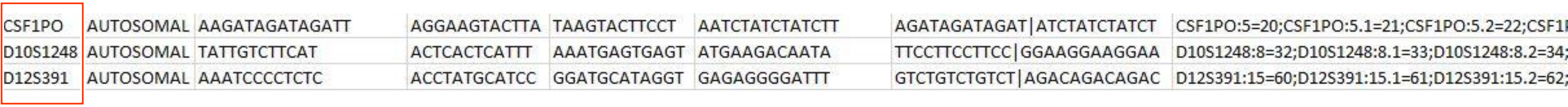
D10S1248	AUTOSOMAL	TATTGTCTTCAT	ACTCACTCATTT	AAATGAGTGAGT	ATGAAGACAATA	TTCCTTCCTTCC|GGAAGGAAGGAA	D10S1248:8=32;D10S1248:8.1=33;D10S1248:8.2=34;
D12S391	AUTOSOMAL	AAATCCCCTCTC	ACCTATGCATCC	GGATGCATAGGT	GAGAGGGGATTT	GTCTGTCTGTCT|AGACAGACAGAC	D12S391:15=60;D12S391:15.1=61;D12S391:15.2=62;

The Configuration File

- Locus



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<tr><td>CSF1PO</td><td>AUTOSOMAL</td><td>AAGATAGATAGATT</td><td>AGGAAGTACTTA</td><td>TAAGTACTTCCT</td><td>AATCTATCTATCTT</td><td>AGATAGATAGAT|ATCTATCTATCT</td><td>CSF1PO:5=20;CSF1PO:5.1=21;CSF1PO:5.2=22;CSF1</td></tr>
<tr><td>D10S1248</td><td>AUTOSOMAL</td><td>TATTGTCTTCAT</td><td>ACTCACTCATTT</td><td>AAATGAGTGAGT</td><td>ATGAAGACAATA</td><td>TTCCTTCCTTCC|GGAAGGAAGGAA</td><td>D10S1248:8=32;D10S1248:8.1=33;D10S1248:8.2=34;</td></tr>
<tr><td>D12S391</td><td>AUTOSOMAL</td><td>AAATCCCCTCTC</td><td>ACCTATGCATCC</td><td>GGATGCATAGGT</td><td>GAGAGGGGATTT</td><td>GTCTGTCTGTCT|AGACAGACAGAC</td><td>D12S391:15=60;D12S391:15.1=61;D12S391:15.2=62;</td></tr>
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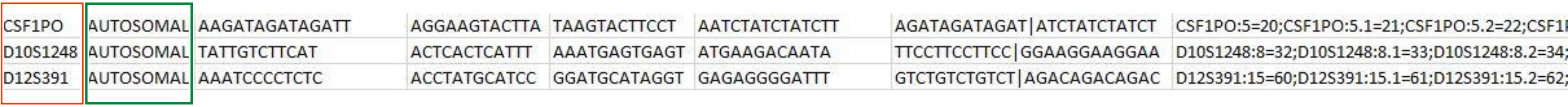
The Configuration File

- Locus
- Type of locus



CSF1PO	AUTOSOMAL	AAGATAGATAGATT	AGGAAGTACTTA	TAAGTACTTCCT	AATCTATCTATCTT	AGATAGATAGAT|ATCTATCTATCT	CSF1PO:5=20;CSF1PO:5.1=21;CSF1PO:5.2=22;CSF1
D10S1248	AUTOSOMAL	TATTGTCTTCAT	ACTCACTCATTT	AAATGAGTGAGT	ATGAAGACAATA	TTCCTTCCTTCC|GGAAGGAAGGAA	D10S1248:8=32;D10S1248:8.1=33;D10S1248:8.2=34;
D12S391	AUTOSOMAL	AAATCCCCTCTC	ACCTATGCATCC	GGATGCATAGGT	GAGAGGGGATTT	GTCTGTCTGTCT|AGACAGACAGAC	D12S391:15=60;D12S391:15.1=61;D12S391:15.2=62;

The Configuration File

- Locus
- Type of locus
- Flanking region sequences

CSF1PO	AUTOSOMAL	AAGATAGATAGATT	AGGAAGTACTTA	TAAGTACTTCCT	AATCTATCTATCTT	AGATAGATAGAT|ATCTATCTATCT	CSF1PO:5=20;CSF1PO:5.1=21;CSF1PO:5.2=22;CSF1
D10S1248	AUTOSOMAL	TATTGTCTTCAT	ACTCACTCATTT	AAATGAGTGAGT	ATGAAGACAATA	TTCCTTCCTTCC|GGAAGGAAGGAA	D10S1248:8=32;D10S1248:8.1=33;D10S1248:8.2=34;
D12S391	AUTOSOMAL	AAATCCCCTCTC	ACCTATGCATCC	GGATGCATAGGT	GAGAGGGGATTT	GTCTGTCTGTCT|AGACAGACAGAC	D12S391:15=60;D12S391:15.1=61;D12S391:15.2=62;

The Configuration File

- Locus
- Type of locus
- Flanking region sequences
- Unique sequence between the flanking regions

CSF1PO	AUTOSOMAL	AAGATAGATAGATT	AGGAAGTACTTA	TAAGTACTTCCT	AATCTATCTATCTT	AGATAGATAGAT|ATCTATCTATCT	CSF1PO:5=20;CSF1PO:5.1=21;CSF1PO:5.2=22;CSF1
D10S1248	AUTOSOMAL	TATTGTCTTCAT	ACTCACTCATTT	AAATGAGTGAGT	ATGAAGACAATA	TTCCTTCCTTCC|GGAAGGAAGGAA	D10S1248:8=32;D10S1248:8.1=33;D10S1248:8.2=34;
D12S391	AUTOSOMAL	AAATCCCCTCTC	ACCTATGCATCC	GGATGCATAGGT	GAGAGGGGATTT	GTCTGTCTGTCT|AGACAGACAGAC	D12S391:15=60;D12S391:15.1=61;D12S391:15.2=62;

The Configuration File

- Locus
- Type of locus
- Flanking region sequences
- Unique sequence between the flanking regions
- Allele designation based on length between flanks

CSF1PO	AUTOSOMAL	AAGATAGATAGATT	AGGAAGTACTTA	TAAGTACTTCCT	AATCTATCTATCTT	AGATAGATAGAT|ATCTATCTATCT	CSF1PO:5=20;CSF1PO:5.1=21;CSF1PO:5.2=22;CSF1
D10S1248	AUTOSOMAL	TATTGTCTTCAT	ACTCACTCATTT	AAATGAGTGAGT	ATGAAGACAATA	TTCCTTCCTTCC|GGAAGGAAGGAA	D10S1248:8=32;D10S1248:8.1=33;D10S1248:8.2=34
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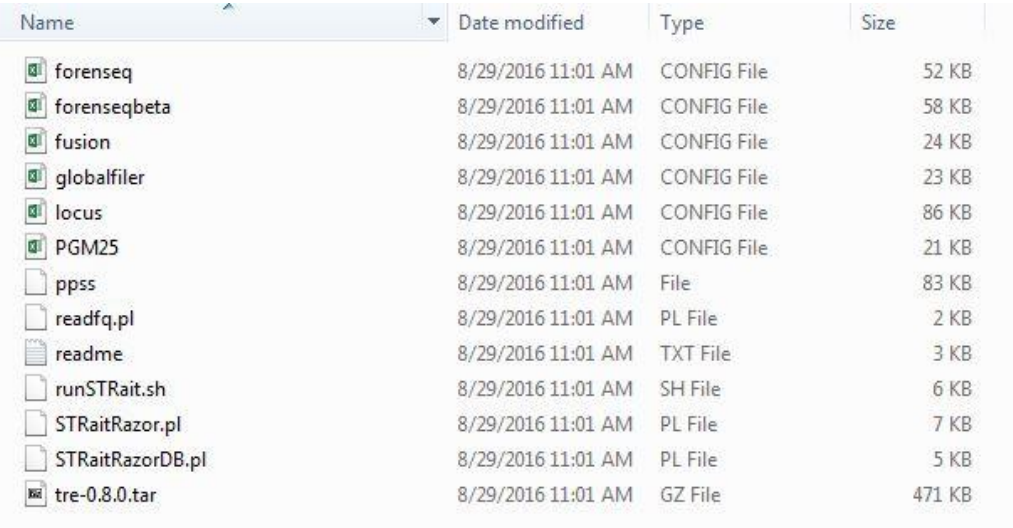
Download File

- https://www.unthsc.edu/graduate-school-of-biomedical-sciences/molecular-and-medical-genetics/laboratory-faculty-and-staff/strait-razor/
- Unzip the downloaded STRait Razor v2.5 zipped file
  - Important contents:



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fusion	8/29/2016 11:01 AM	CONFIG File	24 KB
globalfiler	8/29/2016 11:01 AM	CONFIG File	23 KB
locus	8/29/2016 11:01 AM	CONFIG File	86 KB
PGM25	8/29/2016 11:01 AM	CONFIG File	21 KB
ppss	8/29/2016 11:01 AM	File	83 KB
readfq.pl	8/29/2016 11:01 AM	PL File	2 KB
readme	8/29/2016 11:01 AM	TXT File	3 KB
runSTRait.sh	8/29/2016 11:01 AM	SH File	6 KB
STRaitRazor.pl	8/29/2016 11:01 AM	PL File	7 KB
STRaitRazorDB.pl	8/29/2016 11:01 AM	PL File	5 KB
tre-0.8.0.tar	8/29/2016 11:01 AM	GZ File	471 KB

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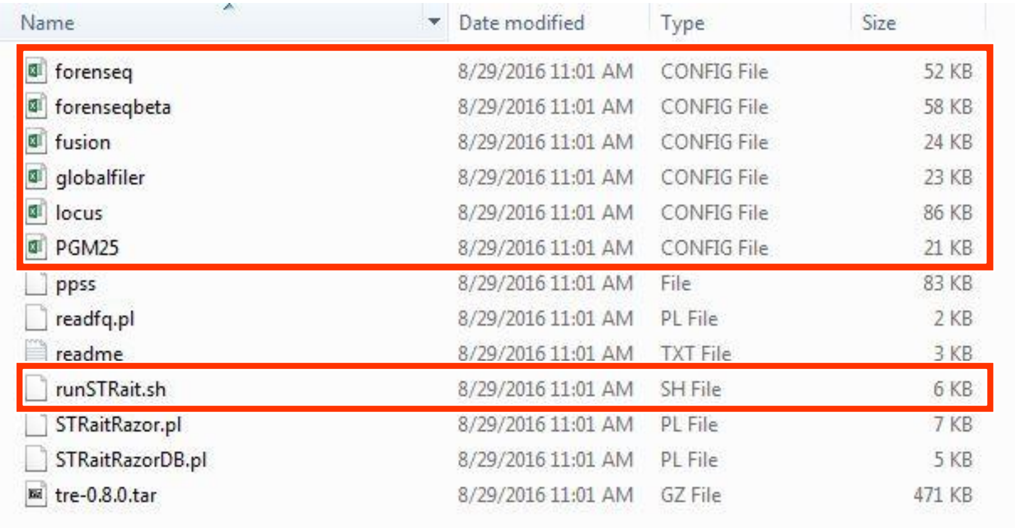
- https://www.unthsc.edu/graduate-school-of-biomedical-sciences/molecular-and-medical-genetics/laboratory-faculty-and-staff/strait-razor/
- Unzip the downloaded STRait Razor v2.5 zipped file
  - Important contents:



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forenseqbeta	8/29/2016 11:01 AM	CONFIG File	58 KB
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STRaitRazor.pl	8/29/2016 11:01 AM	PL File	7 KB
STRaitRazorDB.pl	8/29/2016 11:01 AM	PL File	5 KB
tre-0.8.0.tar	8/29/2016 11:01 AM	GZ File	471 KB

Creating Shell Script

- Open “runSTRait.sh” file in a text editor

```
#!/bin/bash
./STRaitRazor.pl -dir /illumina/data/FGx/Analyses -fastq /illumina/data/FGx/Analyses/1 - Copy (13)/R701-A501_S1_L001_R1_001.fastq -SampleNum R701-A501_S1_L001_R1_001 -typeselection ALL
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./STRaitRazor.pl -dir /illumina/data/FGx/Analyses -fastq /illumina/data/FGx/Analyses/1 - Copy (13)/R701-A507_S6_L001_R1_001.fastq -SampleNum R701-A507_S6_L001_R1_001 -typeselection ALL
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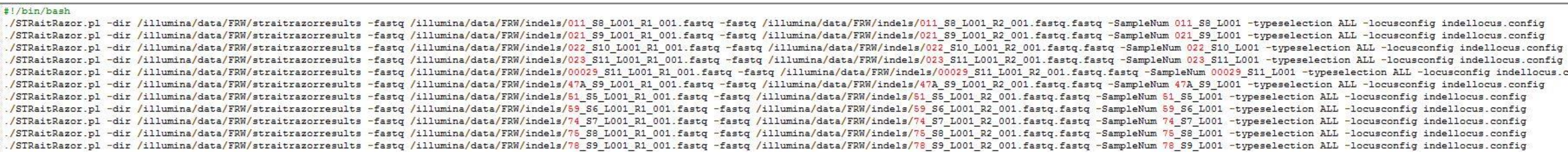

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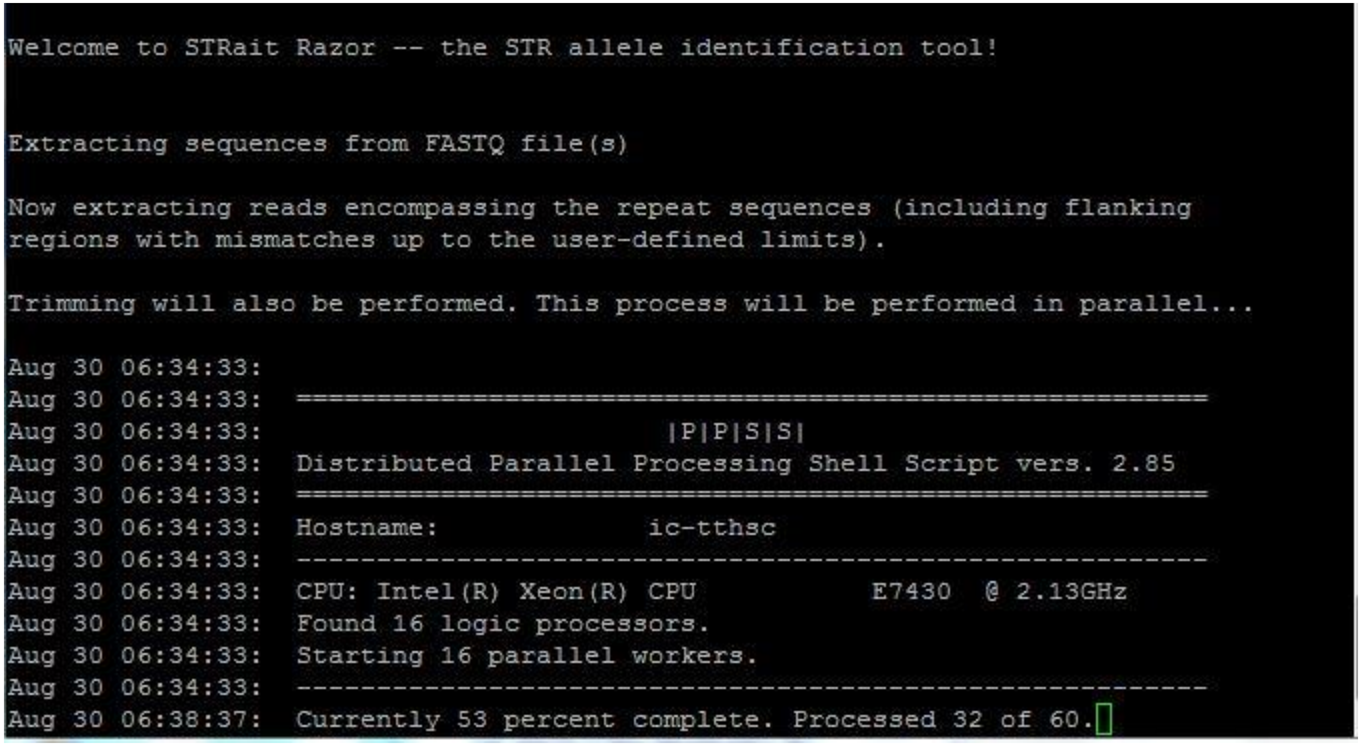
Executing Shell Script



```
Welcome to STRait Razor -- the STR allele identification tool!

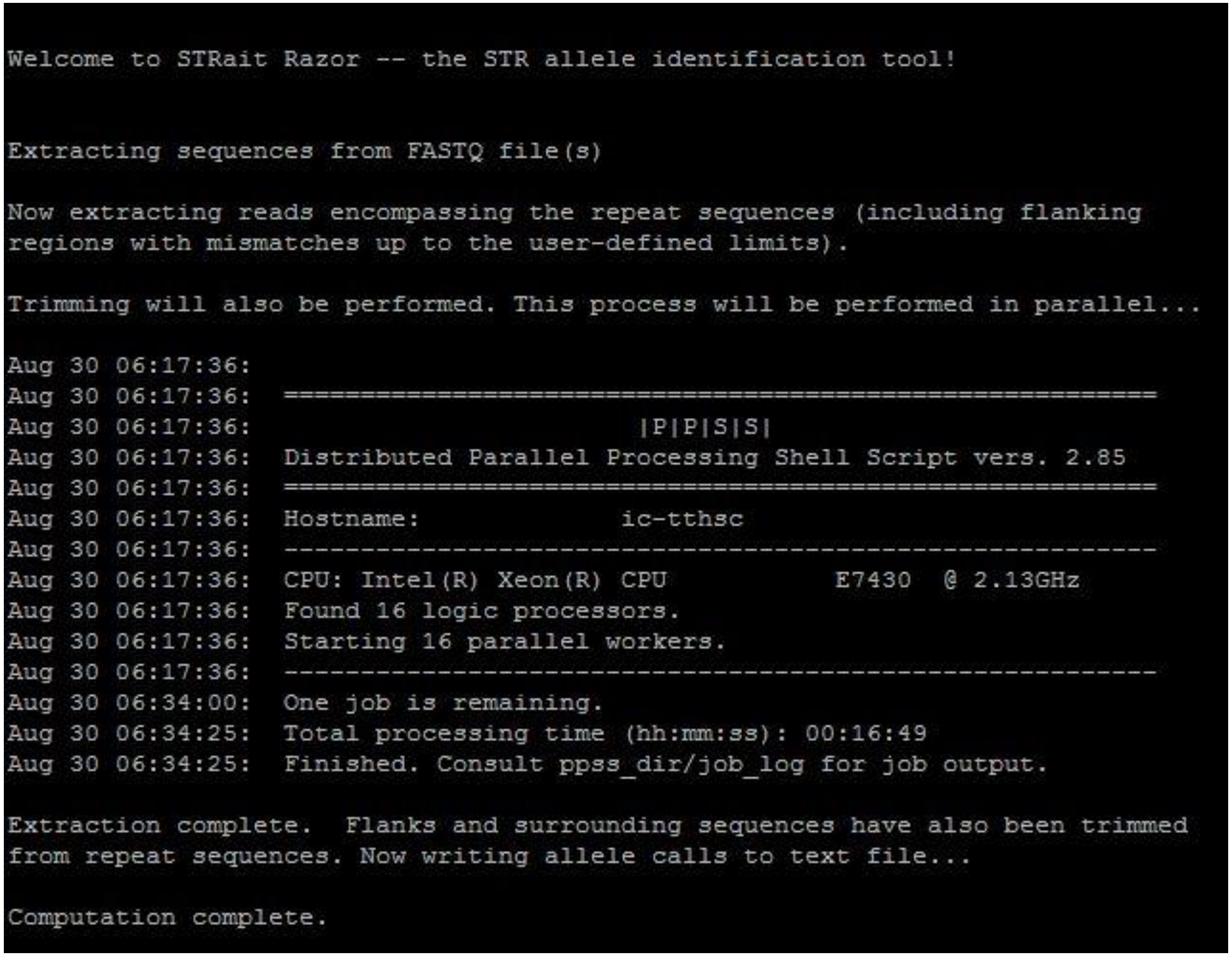

Extracting sequences from FASTQ file(s)

Now extracting reads encompassing the repeat sequences (including flanking
regions with mismatches up to the user-defined limits).

Trimming will also be performed. This process will be performed in parallel...

Aug 30 06:34:33:
Aug 30 06:34:33:  =========================================================
Aug 30 06:34:33:                         |P|P|S|S|
Aug 30 06:34:33:  Distributed Parallel Processing Shell Script vers. 2.85
Aug 30 06:34:33:  =========================================================
Aug 30 06:34:33:  Hostname:             ic-tthsc
Aug 30 06:34:33:  ---------------------------------------------------------
Aug 30 06:34:33:  CPU: Intel(R) Xeon(R) CPU           E7430  @ 2.13GHz
Aug 30 06:34:33:  Found 16 logic processors.
Aug 30 06:34:33:  Starting 16 parallel workers.
Aug 30 06:34:33:  ---------------------------------------------------------
Aug 30 06:38:37:  Currently 53 percent complete. Processed 32 of 60.
```

Executing Shell Script



```
Welcome to STRait Razor -- the STR allele identification tool!


Extracting sequences from FASTQ file(s)

Now extracting reads encompassing the repeat sequences (including flanking
regions with mismatches up to the user-defined limits).

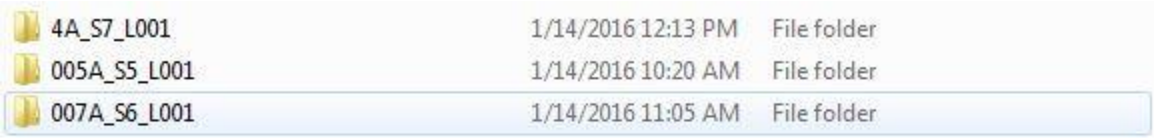
Trimming will also be performed. This process will be performed in parallel...

Aug 30 06:17:36:
Aug 30 06:17:36:  =========================================================
Aug 30 06:17:36:                         |P|P|S|S|
Aug 30 06:17:36:  Distributed Parallel Processing Shell Script vers. 2.85
Aug 30 06:17:36:  =========================================================
Aug 30 06:17:36:  Hostname:              ic-tthsc
Aug 30 06:17:36:  ---------------------------------------------------------
Aug 30 06:17:36:  CPU: Intel(R) Xeon(R) CPU           E7430  @ 2.13GHz
Aug 30 06:17:36:  Found 16 logic processors.
Aug 30 06:17:36:  Starting 16 parallel workers.
Aug 30 06:17:36:  ---------------------------------------------------------
Aug 30 06:34:00:  One job is remaining.
Aug 30 06:34:25:  Total processing time (hh:mm:ss): 00:16:49
Aug 30 06:34:25:  Finished. Consult ppss_dir/job_log for job output.

Extraction complete.  Flanks and surrounding sequences have also been trimmed
from repeat sequences. Now writing allele calls to text file...

Computation complete.
```

Output



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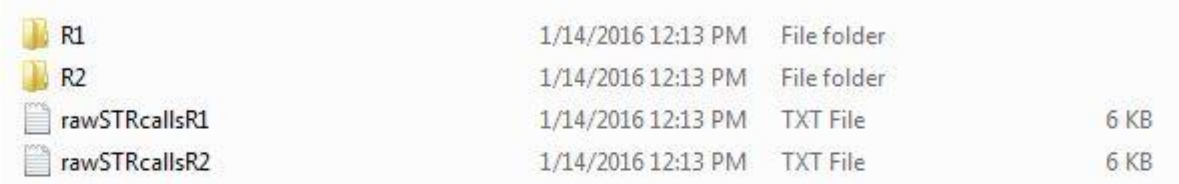
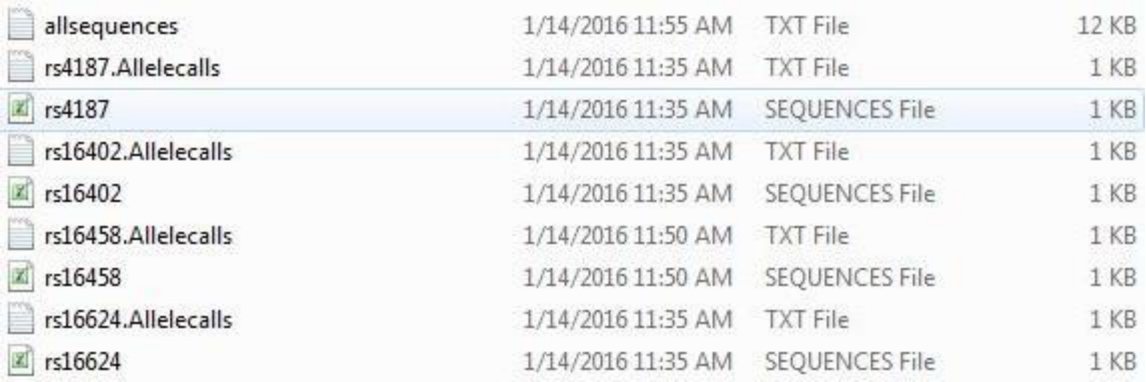
005A_S5_L001	1/14/2016 10:20 AM	File folder	
007A_S6_L001	1/14/2016 11:05 AM	File folder	



R1	1/14/2016 12:13 PM	File folder	
R2	1/14/2016 12:13 PM	File folder	
rawSTRcallsR1	1/14/2016 12:13 PM	TXT File	6 KB
rawSTRcallsR2	1/14/2016 12:13 PM	TXT File	6 KB



allsequences	1/14/2016 11:55 AM	TXT File	12 KB
rs4187.Allelecalls	1/14/2016 11:35 AM	TXT File	1 KB
rs4187	1/14/2016 11:35 AM	SEQUENCES File	1 KB
rs16402.Allelecalls	1/14/2016 11:35 AM	TXT File	1 KB
rs16402	1/14/2016 11:35 AM	SEQUENCES File	1 KB
rs16458.Allelecalls	1/14/2016 11:50 AM	TXT File	1 KB
rs16458	1/14/2016 11:50 AM	SEQUENCES File	1 KB
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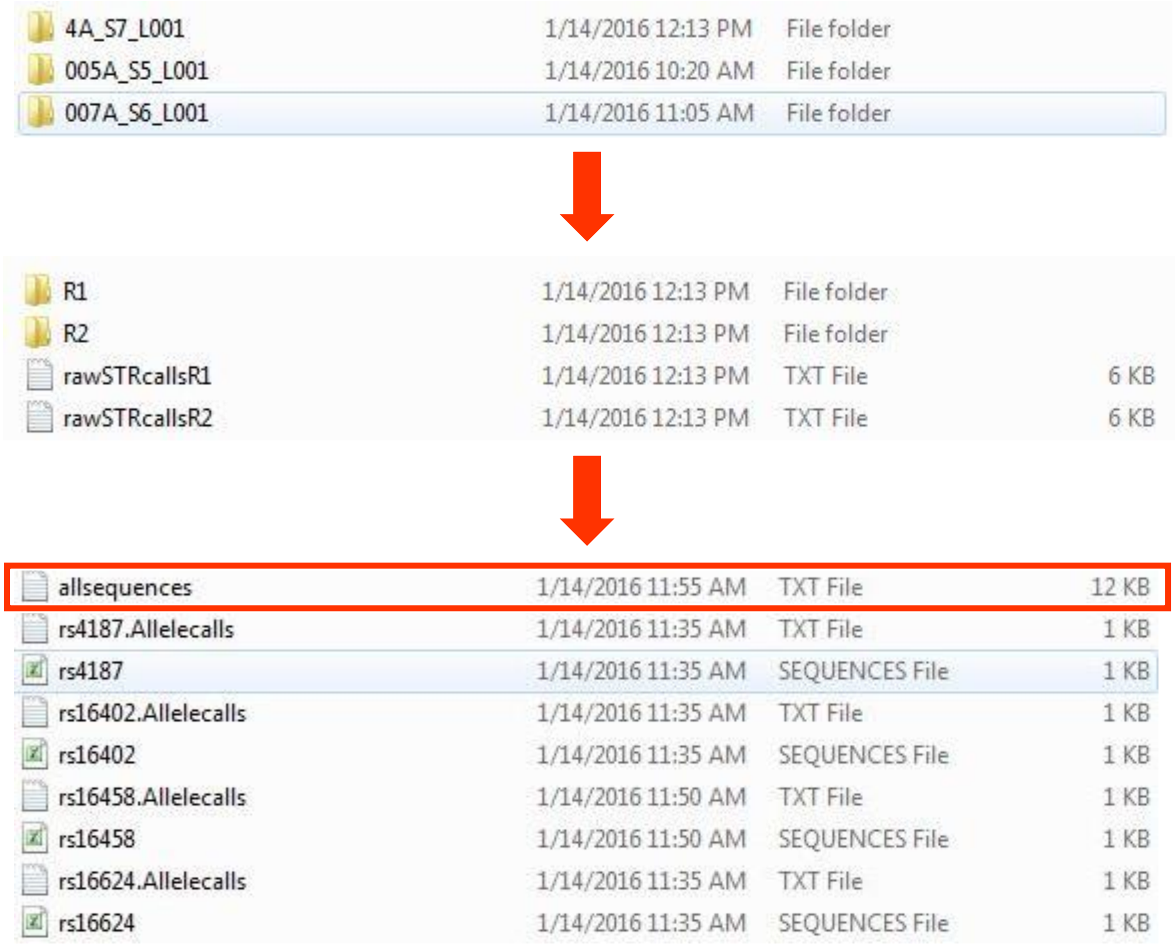
rs16624	1/14/2016 11:35 AM	SEQUENCES File	1 KB

Output



4A_S7_L001	1/14/2016 12:13 PM	File folder	
005A_S5_L001	1/14/2016 10:20 AM	File folder	
007A_S6_L001	1/14/2016 11:05 AM	File folder	

R1	1/14/2016 12:13 PM	File folder	
R2	1/14/2016 12:13 PM	File folder	
rawSTRcallsR1	1/14/2016 12:13 PM	TXT File	6 KB
rawSTRcallsR2	1/14/2016 12:13 PM	TXT File	6 KB

allsequences	1/14/2016 11:55 AM	TXT File	12 KB
rs4187.Allelecalls	1/14/2016 11:35 AM	TXT File	1 KB
rs4187	1/14/2016 11:35 AM	SEQUENCES File	1 KB
rs16402.Allelecalls	1/14/2016 11:35 AM	TXT File	1 KB
rs16402	1/14/2016 11:35 AM	SEQUENCES File	1 KB
rs16458.Allelecalls	1/14/2016 11:50 AM	TXT File	1 KB
rs16458	1/14/2016 11:50 AM	SEQUENCES File	1 KB
rs16624.Allelecalls	1/14/2016 11:35 AM	TXT File	1 KB
rs16624	1/14/2016 11:35 AM	SEQUENCES File	1 KB

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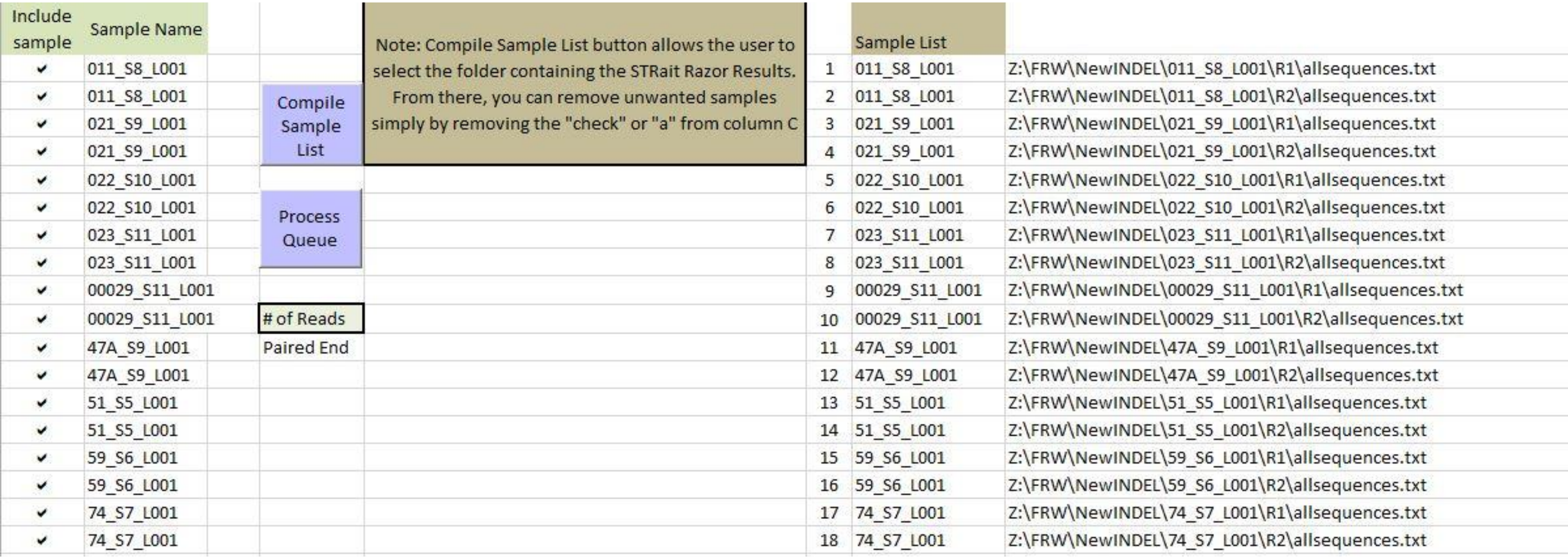


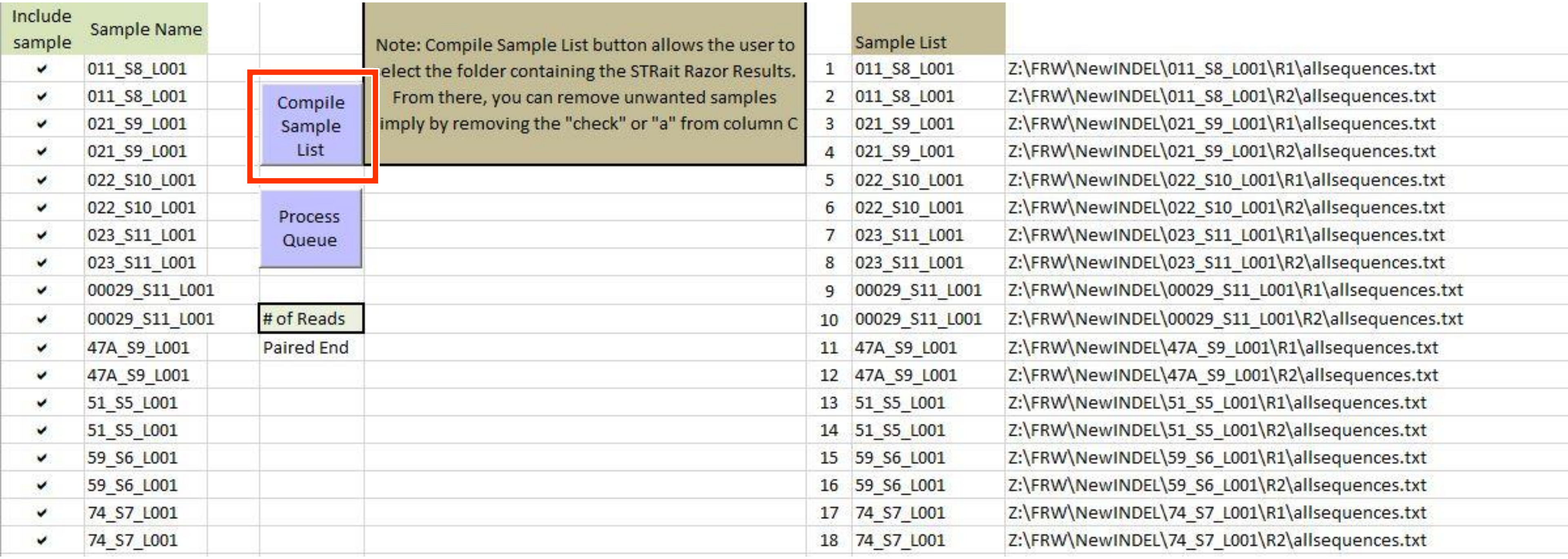
Note: Compile Sample List button allows the user to select the folder containing the STRait Razor Results. From there, you can remove unwanted samples simply by removing the "check" or "a" from column C

# of Reads
Paired End

Include sample	Sample Name
✓	011_S8_L001
✓	011_S8_L001
✓	021_S9_L001
✓	021_S9_L001
✓	022_S10_L001
✓	022_S10_L001
✓	023_S11_L001
✓	023_S11_L001
✓	00029_S11_L001
✓	00029_S11_L001
✓	47A_S9_L001
✓	47A_S9_L001
✓	51_S5_L001
✓	51_S5_L001
✓	59_S6_L001
✓	59_S6_L001
✓	74_S7_L001
✓	74_S7_L001

	Sample List	
1	011_S8_L001	Z:\FRW\NewINDEL\011_S8_L001\R1\allsequences.txt
2	011_S8_L001	Z:\FRW\NewINDEL\011_S8_L001\R2\allsequences.txt
3	021_S9_L001	Z:\FRW\NewINDEL\021_S9_L001\R1\allsequences.txt
4	021_S9_L001	Z:\FRW\NewINDEL\021_S9_L001\R2\allsequences.txt
5	022_S10_L001	Z:\FRW\NewINDEL\022_S10_L001\R1\allsequences.txt
6	022_S10_L001	Z:\FRW\NewINDEL\022_S10_L001\R2\allsequences.txt
7	023_S11_L001	Z:\FRW\NewINDEL\023_S11_L001\R1\allsequences.txt
8	023_S11_L001	Z:\FRW\NewINDEL\023_S11_L001\R2\allsequences.txt
9	00029_S11_L001	Z:\FRW\NewINDEL\00029_S11_L001\R1\allsequences.txt
10	00029_S11_L001	Z:\FRW\NewINDEL\00029_S11_L001\R2\allsequences.txt
11	47A_S9_L001	Z:\FRW\NewINDEL\47A_S9_L001\R1\allsequences.txt
12	47A_S9_L001	Z:\FRW\NewINDEL\47A_S9_L001\R2\allsequences.txt
13	51_S5_L001	Z:\FRW\NewINDEL\51_S5_L001\R1\allsequences.txt
14	51_S5_L001	Z:\FRW\NewINDEL\51_S5_L001\R2\allsequences.txt
15	59_S6_L001	Z:\FRW\NewINDEL\59_S6_L001\R1\allsequences.txt
16	59_S6_L001	Z:\FRW\NewINDEL\59_S6_L001\R2\allsequences.txt
17	74_S7_L001	Z:\FRW\NewINDEL\74_S7_L001\R1\allsequences.txt
18	74_S7_L001	Z:\FRW\NewINDEL\74_S7_L001\R2\allsequences.txt

Open Analysis Workbook



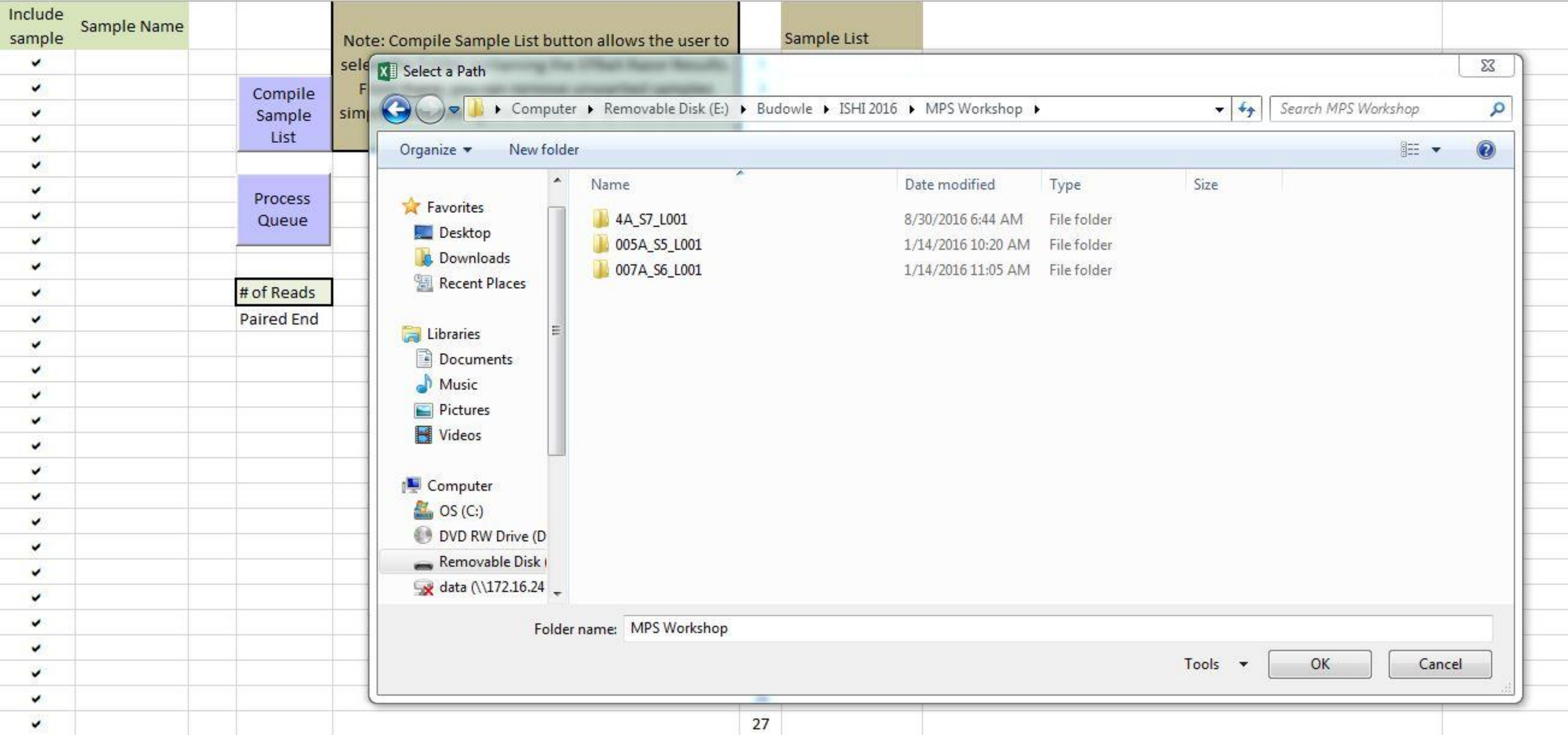
Include sample	Sample Name
✓	011_S8_L001
✓	011_S8_L001
✓	021_S9_L001
✓	021_S9_L001
✓	022_S10_L001
✓	022_S10_L001
✓	023_S11_L001
✓	023_S11_L001
✓	00029_S11_L001
✓	00029_S11_L001
✓	47A_S9_L001
✓	47A_S9_L001
✓	51_S5_L001
✓	51_S5_L001
✓	59_S6_L001
✓	59_S6_L001
✓	74_S7_L001
✓	74_S7_L001

# of Reads: Paired End

Note: Compile Sample List button allows the user to elect the folder containing the STRait Razor Results. From there, you can remove unwanted samples imply by removing the "check" or "a" from column C

	Sample List	
1	011_S8_L001	Z:\FRW\NewINDEL\011_S8_L001\R1\allsequences.txt
2	011_S8_L001	Z:\FRW\NewINDEL\011_S8_L001\R2\allsequences.txt
3	021_S9_L001	Z:\FRW\NewINDEL\021_S9_L001\R1\allsequences.txt
4	021_S9_L001	Z:\FRW\NewINDEL\021_S9_L001\R2\allsequences.txt
5	022_S10_L001	Z:\FRW\NewINDEL\022_S10_L001\R1\allsequences.txt
6	022_S10_L001	Z:\FRW\NewINDEL\022_S10_L001\R2\allsequences.txt
7	023_S11_L001	Z:\FRW\NewINDEL\023_S11_L001\R1\allsequences.txt
8	023_S11_L001	Z:\FRW\NewINDEL\023_S11_L001\R2\allsequences.txt
9	00029_S11_L001	Z:\FRW\NewINDEL\00029_S11_L001\R1\allsequences.txt
10	00029_S11_L001	Z:\FRW\NewINDEL\00029_S11_L001\R2\allsequences.txt
11	47A_S9_L001	Z:\FRW\NewINDEL\47A_S9_L001\R1\allsequences.txt
12	47A_S9_L001	Z:\FRW\NewINDEL\47A_S9_L001\R2\allsequences.txt
13	51_S5_L001	Z:\FRW\NewINDEL\51_S5_L001\R1\allsequences.txt
14	51_S5_L001	Z:\FRW\NewINDEL\51_S5_L001\R2\allsequences.txt
15	59_S6_L001	Z:\FRW\NewINDEL\59_S6_L001\R1\allsequences.txt
16	59_S6_L001	Z:\FRW\NewINDEL\59_S6_L001\R2\allsequences.txt
17	74_S7_L001	Z:\FRW\NewINDEL\74_S7_L001\R1\allsequences.txt
18	74_S7_L001	Z:\FRW\NewINDEL\74_S7_L001\R2\allsequences.txt

Navigate to STRait Razor Output



Note: Compile Sample List button allows the user to
sele
F
sim

# of Reads

Paired End

Select a Path

Computer ▸ Removable Disk (E:) ▸ Budowle ▸ ISHI 2016 ▸ MPS Workshop ▸

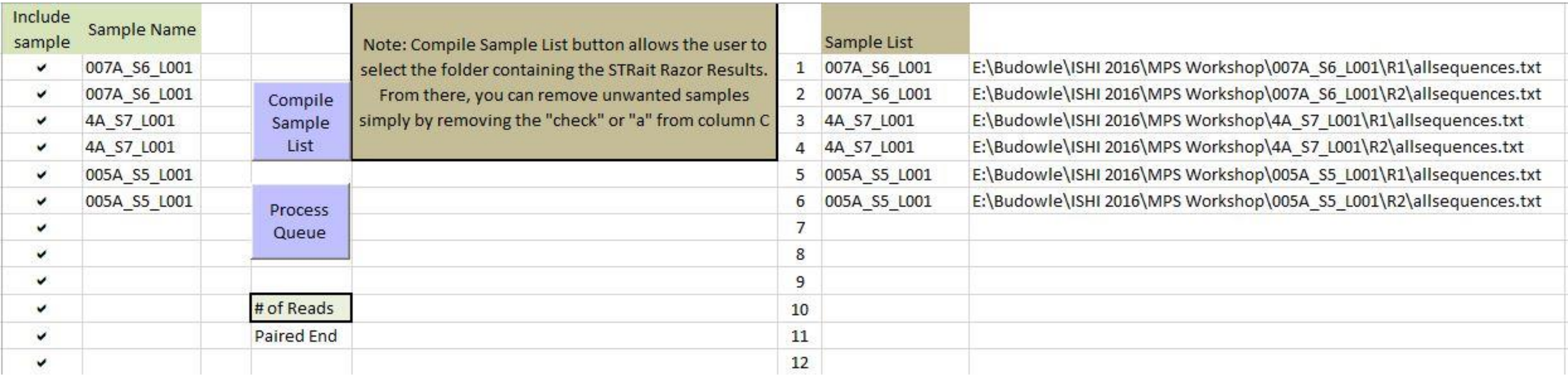
Search MPS Workshop

Name	Date modified	Type	Size
4A_S7_L001	8/30/2016 6:44 AM	File folder	
005A_S5_L001	1/14/2016 10:20 AM	File folder	
007A_S6_L001	1/14/2016 11:05 AM	File folder	

Folder name: MPS Workshop

27

Load allsequences.txt



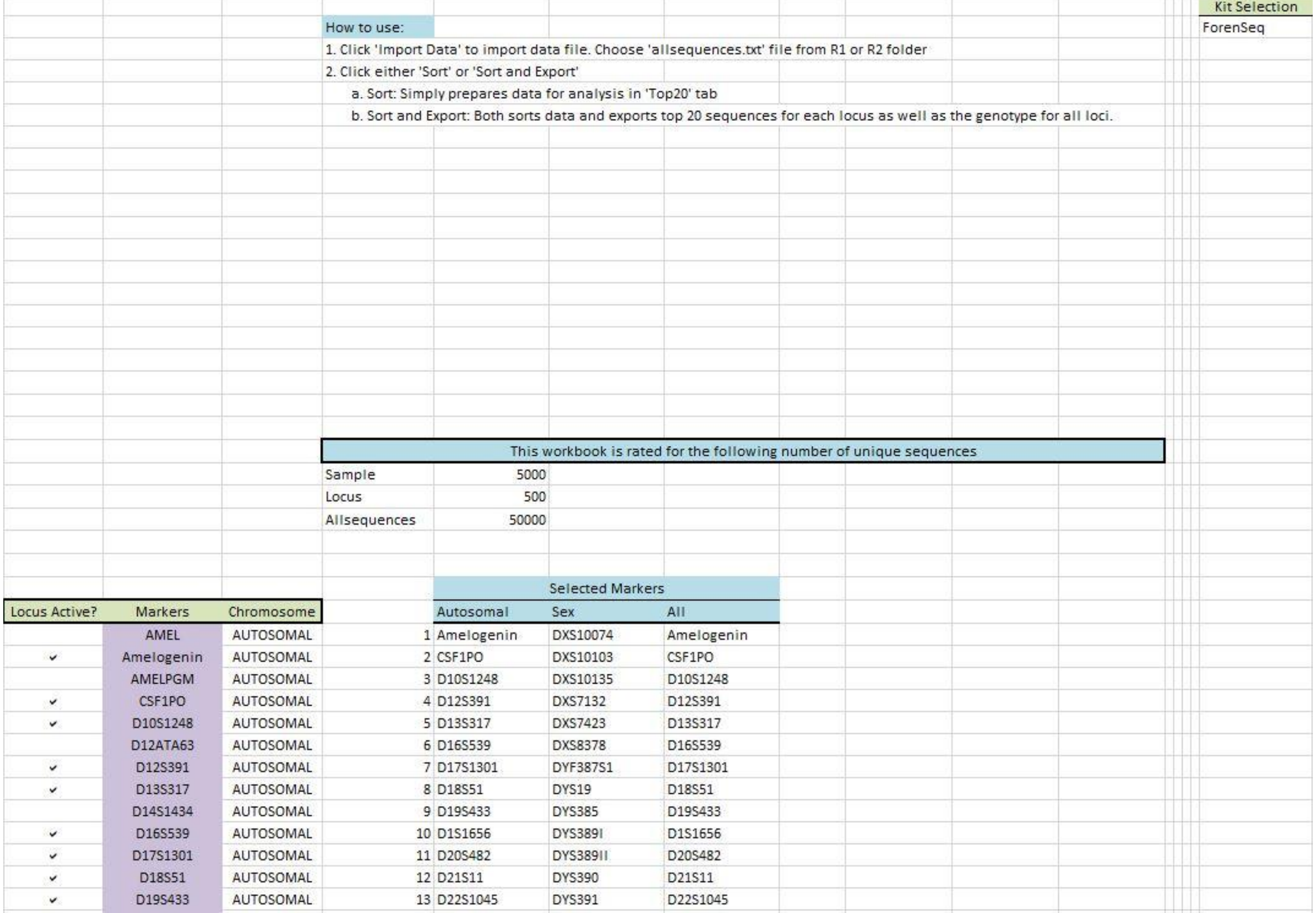
Note: Compile Sample List button allows the user to select the folder containing the STRait Razor Results. From there, you can remove unwanted samples simply by removing the "check" or "a" from column C

# of Reads
Paired End

Include sample	Sample Name
✓	007A_S6_L001
✓	007A_S6_L001
✓	4A_S7_L001
✓	4A_S7_L001
✓	005A_S5_L001
✓	005A_S5_L001
✓	
✓	
✓	
✓	
✓	
✓	

	Sample List	
1	007A_S6_L001	E:\Budowle\ISHI 2016\MPS Workshop\007A_S6_L001\R1\allsequences.txt
2	007A_S6_L001	E:\Budowle\ISHI 2016\MPS Workshop\007A_S6_L001\R2\allsequences.txt
3	4A_S7_L001	E:\Budowle\ISHI 2016\MPS Workshop\4A_S7_L001\R1\allsequences.txt
4	4A_S7_L001	E:\Budowle\ISHI 2016\MPS Workshop\4A_S7_L001\R2\allsequences.txt
5	005A_S5_L001	E:\Budowle\ISHI 2016\MPS Workshop\005A_S5_L001\R1\allsequences.txt
6	005A_S5_L001	E:\Budowle\ISHI 2016\MPS Workshop\005A_S5_L001\R2\allsequences.txt
7		
8		
9		
10		
11		
12		

Dropin Tab



Kit Selection
ForenSeq

How to use:

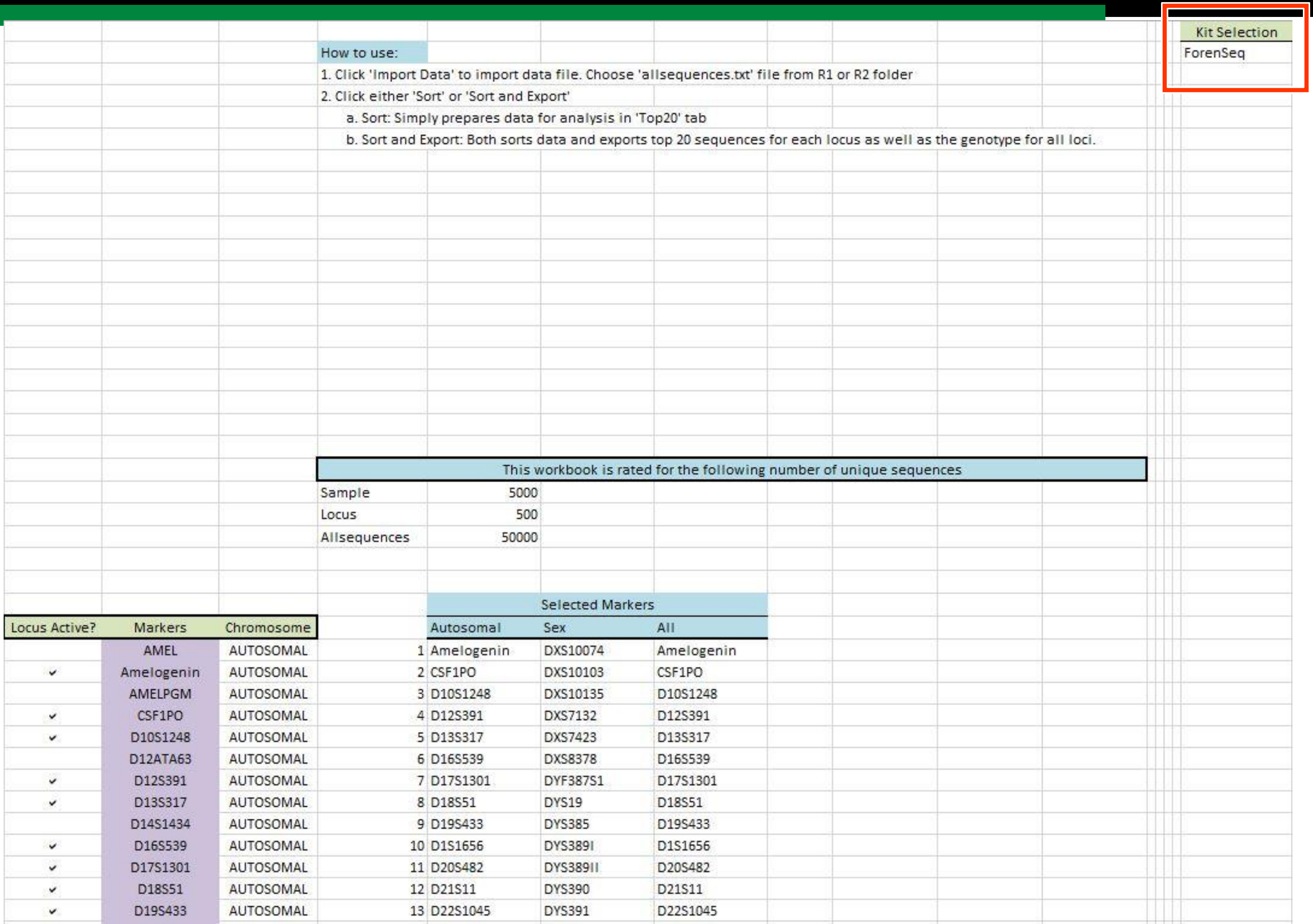
1. Click 'Import Data' to import data file. Choose 'allsequences.txt' file from R1 or R2 folder
2. Click either 'Sort' or 'Sort and Export'
   a. Sort: Simply prepares data for analysis in 'Top20' tab
   b. Sort and Export: Both sorts data and exports top 20 sequences for each locus as well as the genotype for all loci.

This workbook is rated for the following number of unique sequences	
Sample	5000
Locus	500
Allsequences	50000

Locus Active?	Markers	Chromosome
	AMEL	AUTOSOMAL
✓	Amelogenin	AUTOSOMAL
	AMELPGM	AUTOSOMAL
✓	CSF1PO	AUTOSOMAL
✓	D10S1248	AUTOSOMAL
	D12ATA63	AUTOSOMAL
✓	D12S391	AUTOSOMAL
✓	D13S317	AUTOSOMAL
	D14S1434	AUTOSOMAL
✓	D16S539	AUTOSOMAL
✓	D17S1301	AUTOSOMAL
✓	D18S51	AUTOSOMAL
✓	D19S433	AUTOSOMAL

	Selected Markers		
	Autosomal	Sex	All
1	Amelogenin	DXS10074	Amelogenin
2	CSF1PO	DXS10103	CSF1PO
3	D10S1248	DXS10135	D10S1248
4	D12S391	DXS7132	D12S391
5	D13S317	DXS7423	D13S317
6	D16S539	DXS8378	D16S539
7	D17S1301	DYF387S1	D17S1301
8	D18S51	DYS19	D18S51
9	D19S433	DYS385	D19S433
10	D1S1656	DYS389I	D1S1656
11	D20S482	DYS389II	D20S482
12	D21S11	DYS390	D21S11
13	D22S1045	DYS391	D22S1045

Dropin Tab



Kit Selection
ForenSeq

How to use:

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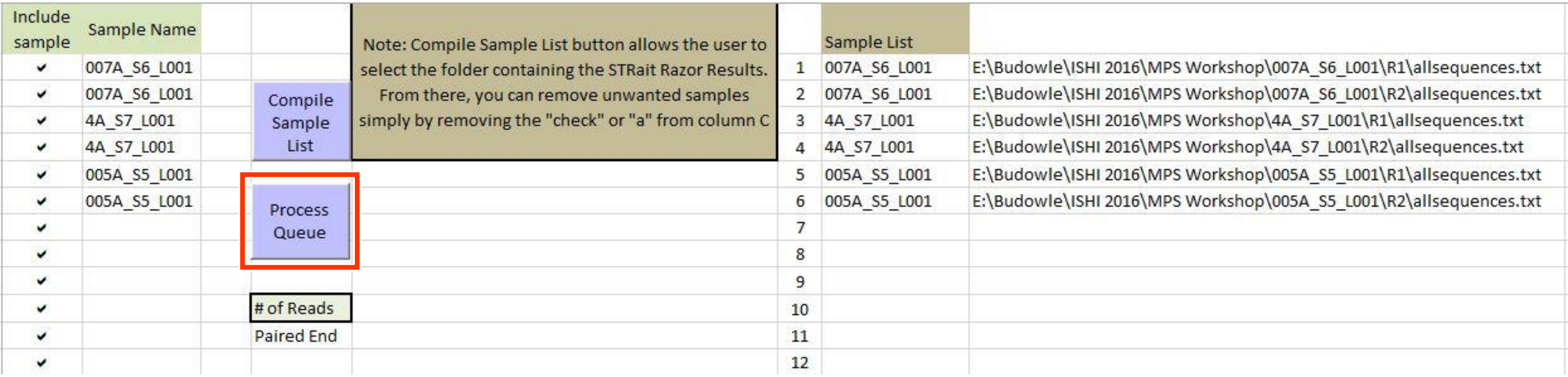
2. Click either 'Sort' or 'Sort and Export'
    a. Sort: Simply prepares data for analysis in 'Top20' tab
    b. Sort and Export: Both sorts data and exports top 20 sequences for each locus as well as the genotype for all loci.

This workbook is rated for the following number of unique sequences	
Sample	5000
Locus	500
Allsequences	50000

Locus Active?	Markers	Chromosome
	AMEL	AUTOSOMAL
✓	Amelogenin	AUTOSOMAL
	AMELPGM	AUTOSOMAL
✓	CSF1PO	AUTOSOMAL
✓	D10S1248	AUTOSOMAL
	D12ATA63	AUTOSOMAL
✓	D12S391	AUTOSOMAL
✓	D13S317	AUTOSOMAL
	D14S1434	AUTOSOMAL
✓	D16S539	AUTOSOMAL
✓	D17S1301	AUTOSOMAL
✓	D18S51	AUTOSOMAL
✓	D19S433	AUTOSOMAL

	Selected Markers		
	Autosomal	Sex	All
1	Amelogenin	DXS10074	Amelogenin
2	CSF1PO	DXS10103	CSF1PO
3	D10S1248	DXS10135	D10S1248
4	D12S391	DXS7132	D12S391
5	D13S317	DXS7423	D13S317
6	D16S539	DXS8378	D16S539
7	D17S1301	DYF387S1	D17S1301
8	D18S51	DYS19	D18S51
9	D19S433	DYS385	D19S433
10	D1S1656	DYS389I	D1S1656
11	D20S482	DYS389II	D20S482
12	D21S11	DYS390	D21S11
13	D22S1045	DYS391	D22S1045

Process



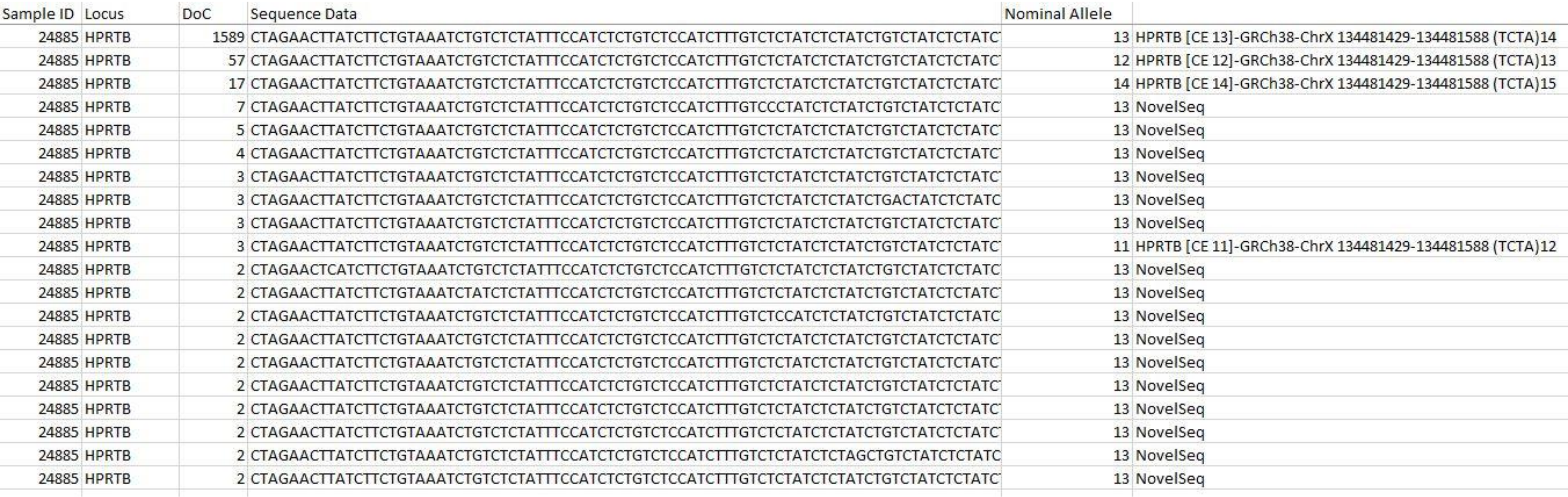
Note: Compile Sample List button allows the user to select the folder containing the STRait Razor Results. From there, you can remove unwanted samples simply by removing the "check" or "a" from column C

Include sample	Sample Name		Sample List	
✓	007A_S6_L001	1	007A_S6_L001	E:\Budowle\ISHI 2016\MPS Workshop\007A_S6_L001\R1\allsequences.txt
✓	007A_S6_L001	2	007A_S6_L001	E:\Budowle\ISHI 2016\MPS Workshop\007A_S6_L001\R2\allsequences.txt
✓	4A_S7_L001	3	4A_S7_L001	E:\Budowle\ISHI 2016\MPS Workshop\4A_S7_L001\R1\allsequences.txt
✓	4A_S7_L001	4	4A_S7_L001	E:\Budowle\ISHI 2016\MPS Workshop\4A_S7_L001\R2\allsequences.txt
✓	005A_S5_L001	5	005A_S5_L001	E:\Budowle\ISHI 2016\MPS Workshop\005A_S5_L001\R1\allsequences.txt
✓	005A_S5_L001	6	005A_S5_L001	E:\Budowle\ISHI 2016\MPS Workshop\005A_S5_L001\R2\allsequences.txt
✓		7		
✓		8		
✓		9		
✓		10		
✓		11		
✓		12		

# of Reads
Paired End

Useful Results Tabs

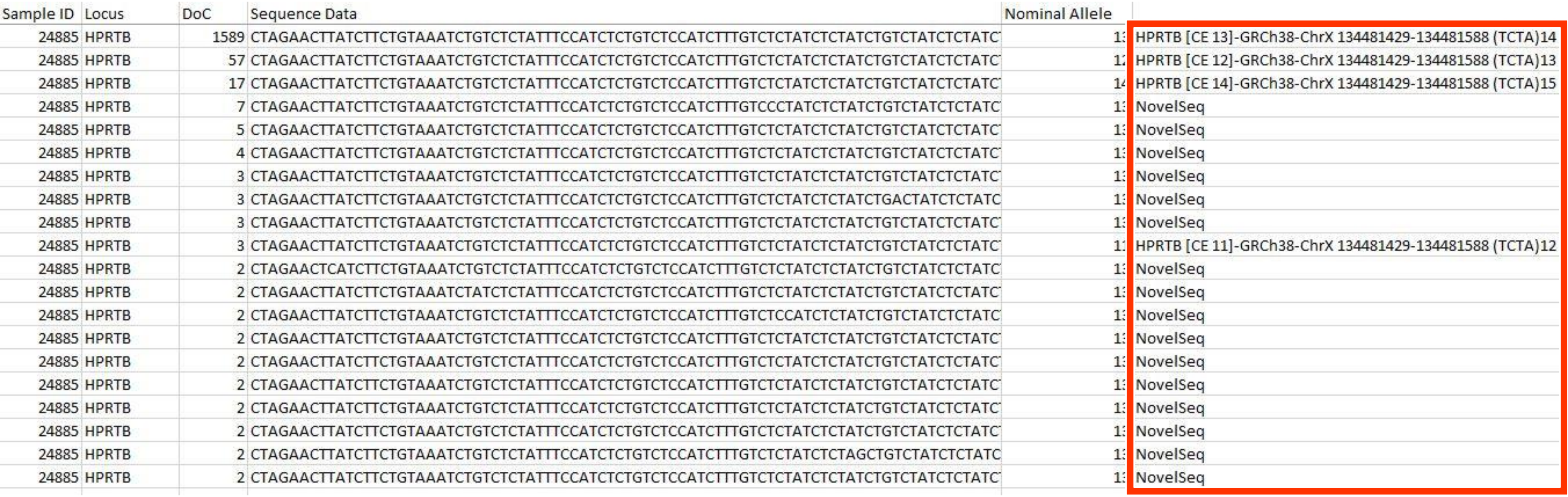
- Sequence Pileup



Sample ID	Locus	DoC	Sequence Data	Nominal Allele	
24885	HPRTB	1589	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	HPRTB [CE 13]-GRCh38-ChrX 134481429-134481588 (TCTA)14
24885	HPRTB	57	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	12	HPRTB [CE 12]-GRCh38-ChrX 134481429-134481588 (TCTA)13
24885	HPRTB	17	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	14	HPRTB [CE 14]-GRCh38-ChrX 134481429-134481588 (TCTA)15
24885	HPRTB	7	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCCCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	5	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	4	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGACTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	11	HPRTB [CE 11]-GRCh38-ChrX 134481429-134481588 (TCTA)12
24885	HPRTB	2	CTAGAACTCATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTATCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCCATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTAGCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq

Useful Results Tabs

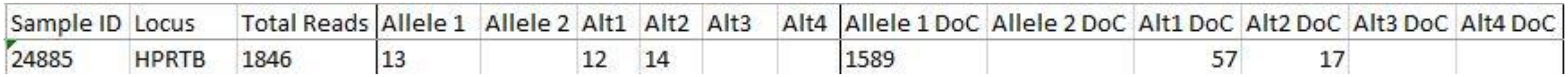
- Sequence Pileup



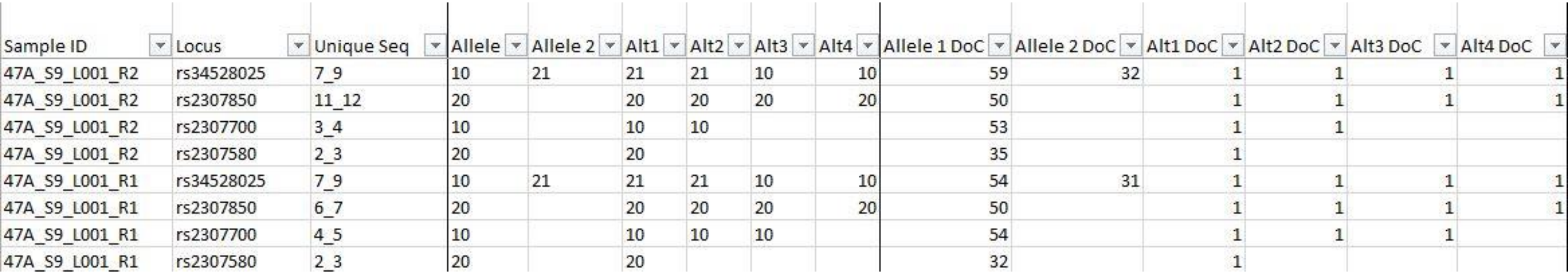
Sample ID	Locus	DoC	Sequence Data	Nominal Allele	
24885	HPRTB	1589	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	HPRTB [CE 13]-GRCh38-ChrX 134481429-134481588 (TCTA)14
24885	HPRTB	57	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	12	HPRTB [CE 12]-GRCh38-ChrX 134481429-134481588 (TCTA)13
24885	HPRTB	17	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	14	HPRTB [CE 14]-GRCh38-ChrX 134481429-134481588 (TCTA)15
24885	HPRTB	7	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCCCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	5	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	4	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGACTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	3	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	11	HPRTB [CE 11]-GRCh38-ChrX 134481429-134481588 (TCTA)12
24885	HPRTB	2	CTAGAACTCATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTATCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCCATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTAGCTGTCTATCTCTATC	13	NovelSeq
24885	HPRTB	2	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATC	13	NovelSeq

Useful Results Tabs

- Genotype Export



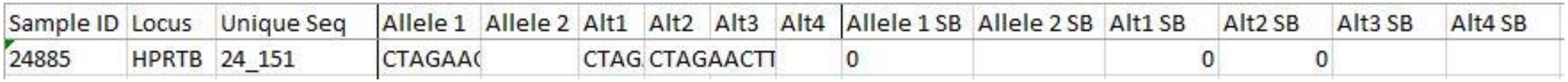
Sample ID	Locus	Total Reads	Allele 1	Allele 2	Alt1	Alt2	Alt3	Alt4	Allele 1 DoC	Allele 2 DoC	Alt1 DoC	Alt2 DoC	Alt3 DoC	Alt4 DoC
24885	HPRTB	1846	13		12	14			1589		57	17		



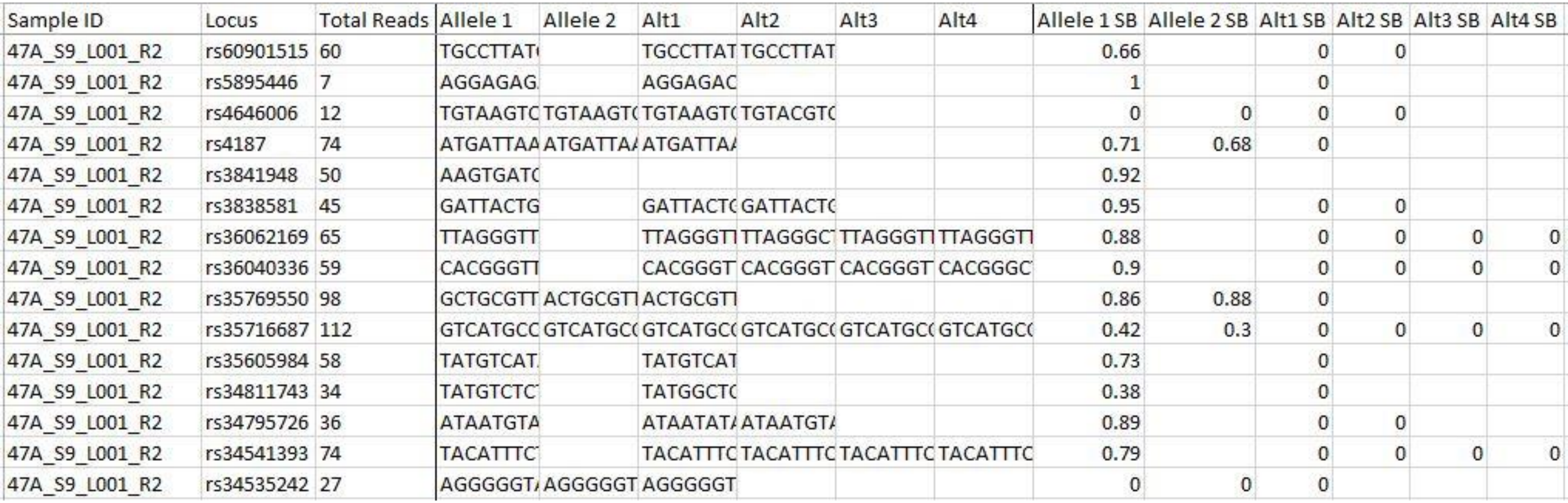
Sample ID	Locus	Unique Seq	Allele	Allele 2	Alt1	Alt2	Alt3	Alt4	Allele 1 DoC	Allele 2 DoC	Alt1 DoC	Alt2 DoC	Alt3 DoC	Alt4 DoC
47A_S9_L001_R2	rs34528025	7_9	10	21	21	21	10	10	59	32	1	1	1	1
47A_S9_L001_R2	rs2307850	11_12	20		20	20	20	20	50		1	1	1	1
47A_S9_L001_R2	rs2307700	3_4	10		10	10			53		1	1		
47A_S9_L001_R2	rs2307580	2_3	20		20				35		1			
47A_S9_L001_R1	rs34528025	7_9	10	21	21	21	10	10	54	31	1	1	1	1
47A_S9_L001_R1	rs2307850	6_7	20		20	20	20	20	50		1	1	1	1
47A_S9_L001_R1	rs2307700	4_5	10		10	10	10		54		1	1	1	
47A_S9_L001_R1	rs2307580	2_3	20		20				32		1			

Useful Results Tabs

- Allele Export



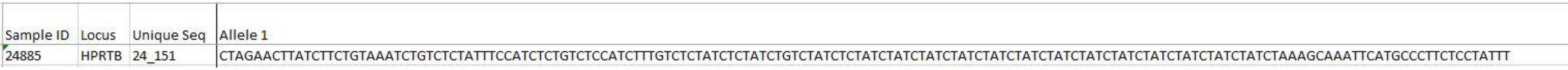
Sample ID	Locus	Unique Seq	Allele 1	Allele 2	Alt1	Alt2	Alt3	Alt4	Allele 1 SB	Allele 2 SB	Alt1 SB	Alt2 SB	Alt3 SB	Alt4 SB
24885	HPRTB	24_151	CTAGAA		CTAG	CTAGAACTT			0		0	0		



Sample ID	Locus	Total Reads	Allele 1	Allele 2	Alt1	Alt2	Alt3	Alt4	Allele 1 SB	Allele 2 SB	Alt1 SB	Alt2 SB	Alt3 SB	Alt4 SB
47A_S9_L001_R2	rs60901515	60	TGCCTTAT		TGCCTTAT	TGCCTTAT			0.66		0	0		
47A_S9_L001_R2	rs5895446	7	AGGAGAG		AGGAGAC				1		0			
47A_S9_L001_R2	rs4646006	12	TGTAAGTC	TGTAAGT	TGTAAGT	TGTACGT			0	0	0	0		
47A_S9_L001_R2	rs4187	74	ATGATTAA	ATGATTA	ATGATTA				0.71	0.68	0			
47A_S9_L001_R2	rs3841948	50	AAGTGAT						0.92					
47A_S9_L001_R2	rs3838581	45	GATTACTG		GATTACT	GATTACT			0.95		0	0		
47A_S9_L001_R2	rs36062169	65	TTAGGGTT		TTAGGGT	TTAGGGC	TTAGGGT	TTAGGGT	0.88		0	0	0	0
47A_S9_L001_R2	rs36040336	59	CACGGGTT		CACGGGT	CACGGGT	CACGGGT	CACGGGC	0.9		0	0	0	0
47A_S9_L001_R2	rs35769550	98	GCTGCGTT	ACTGCGTT	ACTGCGTT				0.86	0.88	0			
47A_S9_L001_R2	rs35716687	112	GTCATGCC	GTCATGC	GTCATGC	GTCATGC	GTCATGC	GTCATGC	0.42	0.3	0	0	0	0
47A_S9_L001_R2	rs35605984	58	TATGTCAT		TATGTCAT				0.73		0			
47A_S9_L001_R2	rs34811743	34	TATGTCTC		TATGGCT				0.38		0			
47A_S9_L001_R2	rs34795726	36	ATAATGTA		ATAATAT	ATAATGT			0.89		0	0		
47A_S9_L001_R2	rs34541393	74	TACATTTC		TACATTTC	TACATTTC	TACATTTC	TACATTTC	0.79		0	0	0	0
47A_S9_L001_R2	rs34535242	27	AGGGGGT	AGGGGGT	AGGGGGT				0	0	0			

Useful Results Tabs

- Allele Export (expanded)



Sample ID	Locus	Unique Seq	Allele 1
24885	HPRTB	24_151	CTAGAACTTATCTTCTGTAAATCTGTCTCTATTTCCATCTCTGTCTCCATCTTTGTCTCTATCTCTATCTGTCTATCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTAAAGCAAATTCATGCCCTTCTCCTATTT

Sample ID	Locus	Total Reads	Allele 1
47A_S9_L001_R2	rs60901515	60	TGCCTTATGCAATTTAAGCAACAATAGAAGACAAGTCAGGAACTGAGACTTATCTATTGAAACTCAGGAGTGCTTGGTATCCACAGTGGCAGATAAATTC
47A_S9_L001_R2	rs5895446	7	AGGAGAGATATAGAGTTACTTTGTATCCTGCCACTATCACTGGGGAGATATGTTGGACACAGAGTTCTATCGTGCAAAGTTAAGTGAAAGAGGTTCTAAGGAGATTGTTC
47A_S9_L001_R2	rs4646006	12	TGTAAGTCTAAACAATCAGGCACGTGGGCAGCAATGGAGCTGCAGGTGCACTGTGTGCCATTTACCAGCCTTTGCTGATCTGTTCATTATTTTGCAGGGC
47A_S9_L001_R2	rs4187	74	ATGATTAACAAAAAAACAAGTAGAAAAATAAGAGAGTGTATTTAAAAAAAATAAAGATAATCAAATGCTTTTTGAAAGACCTGTTCTCTTCACTGCCACACATATT
47A_S9_L001_R2	rs3841948	50	AAGTGATCCAGATTTGGTCTTTTACTGTGAAAATGCTTTTATACAATTTAGTAGAGATGTTATGCAATTGTACTATATCCTTTGCACACTGGAAT
47A_S9_L001_R2	rs3838581	45	GATTACTGGTGTTTACTTTTAATTCCAATAAATTAAAAGTTCTACTGTTTGTTATTCTACTTCCTCATACAAATCTTGAGCAAGACAAACTTTAACATTC
47A_S9_L001_R2	rs36062169	65	TTAGGGTTTCCTGTCAACTATTCTACTGCCATTTACCACAGGGTCACCACATTCTAATAAGTCCATCCTTCTGAGATATCCTCTTCCTAACATG
47A_S9_L001_R2	rs36040336	59	CACGGGTTAACAGATGCAGTTATTATGCCCATTTAACACGAGGGAAACTGAGGCCCAGAGAGGTTGAGGTTCACAGGTTGCAGCAGGG
47A_S9_L001_R2	rs35769550	98	GCTGCGTTTCTGTAGAGGAGTAAATGTACTAAGACTATTAAATAACTTACTGACACCTTAACTAAAACTTTTAGGTGGAAACAAAAGACTGGTTAGAAAAAATG
47A_S9_L001_R2	rs35716687	112	GTCATGCCATCATTAGGGGACTAAATGTGTTAATATCCTGAAAATTATAAGTAATCAATAATTTCTCTTTCGTGATACACCTTGTTTTGAAATATTT
47A_S9_L001_R2	rs35605984	58	TATGTCATAGTAAAAACTTGGAAATAATAAGATGTTGAATAATTGACATTATTAAATTATGCTACATTAGCATAATAAAATATTAGGTAGTTATTTTTAA
47A_S9_L001_R2	rs34811743	34	TATGTCTCTACATCCCACCCCAACTACAACACTTCGTACCCAGGATGCAACTGAGATCAAAGTAGTTGCTTACTATGGGTTGAACAAAAAGGAGAGGCACAC
47A_S9_L001_R2	rs34795726	36	ATAATGTAGAGTTATTCAAAAAAAAGGTCTTTCTTTTAGAAATTCTTTTTAAATTATTTGCTACCTATCCATGTTTTCTCCAAATCTATCAGCAGCACAGAGTA
47A_S9_L001_R2	rs34541393	74	TACATTTCTAGATGTGTCAGGAGTCTAGAAACTTCAGTTTGGAGAATAAAACTCTACTTCCCTCACATCATTGTTCATACTGTTTTGGTTTTTATTATAA
47A_S9_L001_R2	rs34535242	27	AGGGGGTACTACAGACAGGTTTAAAATGAGCAAACCTAGCTGGTAGGTAGTGTCCTTAGAAGAGTTTTAAGTGAAAAAGGACATGATAAAATATGGCTTT

Overview

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