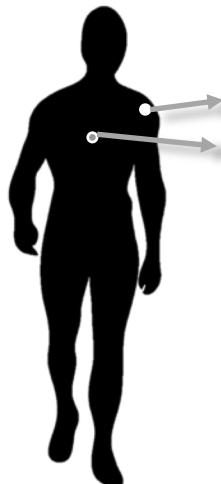


Réalisation d'un Pipeline d'analyse d'exome

Les données



Normal tissue (blood)
Tumor tissue (non small cell lung cancer)

Ju et al. Genome Res. 22:436–445, 2012
100bp paired-end reads, Illumina HiSeq 2000
SRA (Sequence Read Archive): ERA148528

- Mean depth higher for the tumor sample (~100X) than for the normal sample (~30X) to detect somatic variant with a low allelic frequency
- Aligned Exome size: ~15 Go tumor ; ~7 Go blood
Complete analysis processing Time: ~20h
- **Fastq files restricted to a few regions (~112kb) to limit processing time**

Galaxy server

- <https://usegalaxy.eu>

Chargez vos données

Galaxy / Europe Analyse de données Workflow Visualize Données partagées Aide Utilisateur Using 0%

Tools search tools

FILE AND META TOOLS
[Get Data](#)
[Send Data](#)
[Convert Formats](#)
[Collection Operations](#)

GENERAL TEXT TOOLS
[Text Manipulation](#)
[Filter and Sort](#)
[Join, Subtract and Group](#)

GENOMICS, NGS
[Extract Features](#)
[BED Tools](#)
[Fetch Alignments](#)

"Anyone, anywhere in the world should have free, unhindered access to not just my research, but to the research of every great and enquiring mind across the spectrum of human understanding." – Prof. Stephen Hawking

News

- Jan 18, 2019 ! Queue cleared
- Jan 11, 2019 ⚡ Another European CVMFS mirror is online
- Jan 10, 2019 🧑 The European Galaxy Team has open positions!
- Jan 8, 2019 💾 New hardware: 8x1TB memory nodes

Events

- Jul 1, 2019 - Jul 6, 2019 🎓 2019 Galaxy Community Conference (GCC2019)
- Mar 6, 2019 - Mar 8, 2019 🎓 Galaxy for linking Bisulfite sequencing with RNA sequencing 06.-08.03.2019 in Rostock
- Feb 25, 2019 - Mar 1, 2019 🎓 Galaxy HTS data analysis workshop in Freiburg
- Jan 28, 2019 - Feb 1, 2019 🎓 2019 Galaxy Admin Training

History Rechercher des données

exome test 2
(empty)

Cet historique est vide. You can [Charger vos propres données](#) or [Charger des données depuis une source externe](#)

Fera apparaître:

- 6: exome_regions.bed
- 5: known_sites_regions.vcf
- 4: normal_R1.fastq
- 3: normal_R2.fastq
- 2: tumor_R2.fastq
- 1: tumor_R1.fastq

(alternativement: à partir de données partagées)

- Menu « Données partagées »
- Histories
- Choisir History « ... IFSBM ...»
- Click on history, then "+"

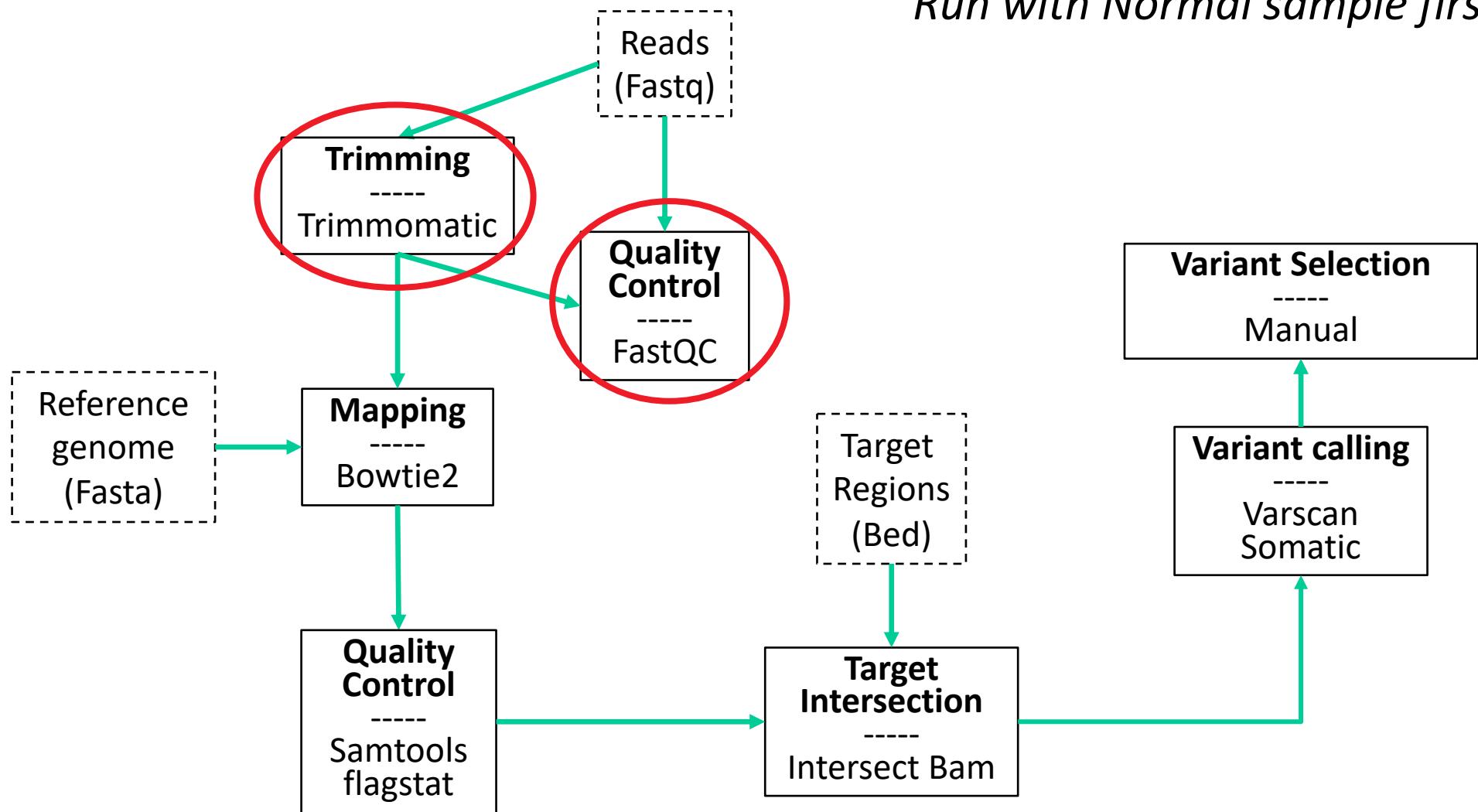
The screenshot shows a user interface for managing genomic data. On the left, a modal window titled "About this History" is open, featuring a "Switch to this history" button and a large red arrow pointing to a "+" button. Below the modal, the word "Author" is visible. To the right, a vertical list of files is displayed, each with edit and delete icons:

6: exome_regions.bed			
5: known_sites_regions.vcf			
4: normal_R1.fastq			
3: normal_R2.fastq			
2: tumor_R2.fastq			
1: tumor_R1.fastq			

Fera apparaître:

A simplified Variant Pipeline

Run with Normal sample first



fastqc

Galaxy / Europe Analyse de données Workflow Visualize Données partagées Aide Utilisateur Using 0%

Tools

fastqc

FASTA/FASTQ manipulation

Combine FASTA and QUAL into FASTQ

Manipulate FASTQ reads on various attributes

fastp – fast all-in-one preprocessing for FASTQ files

FastQC Read Quality reports

Quality Control

FastQC Read Quality reports

Mapping

Map with PerM for SOLiD and Illumina

FastQC Read Quality reports (Galaxy Version 0.71)

Short read data from your current history

4: normal_R1.fastq
3: normal_R2.fastq
2: tumor_R2.fastq
1: tumor_R1.fastq

This is a batch mode input field. Separate jobs will be triggered for each dataset selection.

Contaminant list

Nothing selected

tab delimited file with 2 columns: name and sequence. For example: Illumina Small RNA RT Primer
CAAGCAGAAGACGGCATACGA

Submodule and Limit specifying file

Nothing selected

a file that specifies which submodules are to be executed (default=all) and also specifies the thresholds for the each submodules warning parameter

Execute

History

Rechercher des données

exome test 2

6 shown

45.53 MB

6: exome_regions.bed

5: known_sites_regions.vcf

4: normal_R1.fastq

3: normal_R2.fastq

2: tumor_R2.fastq

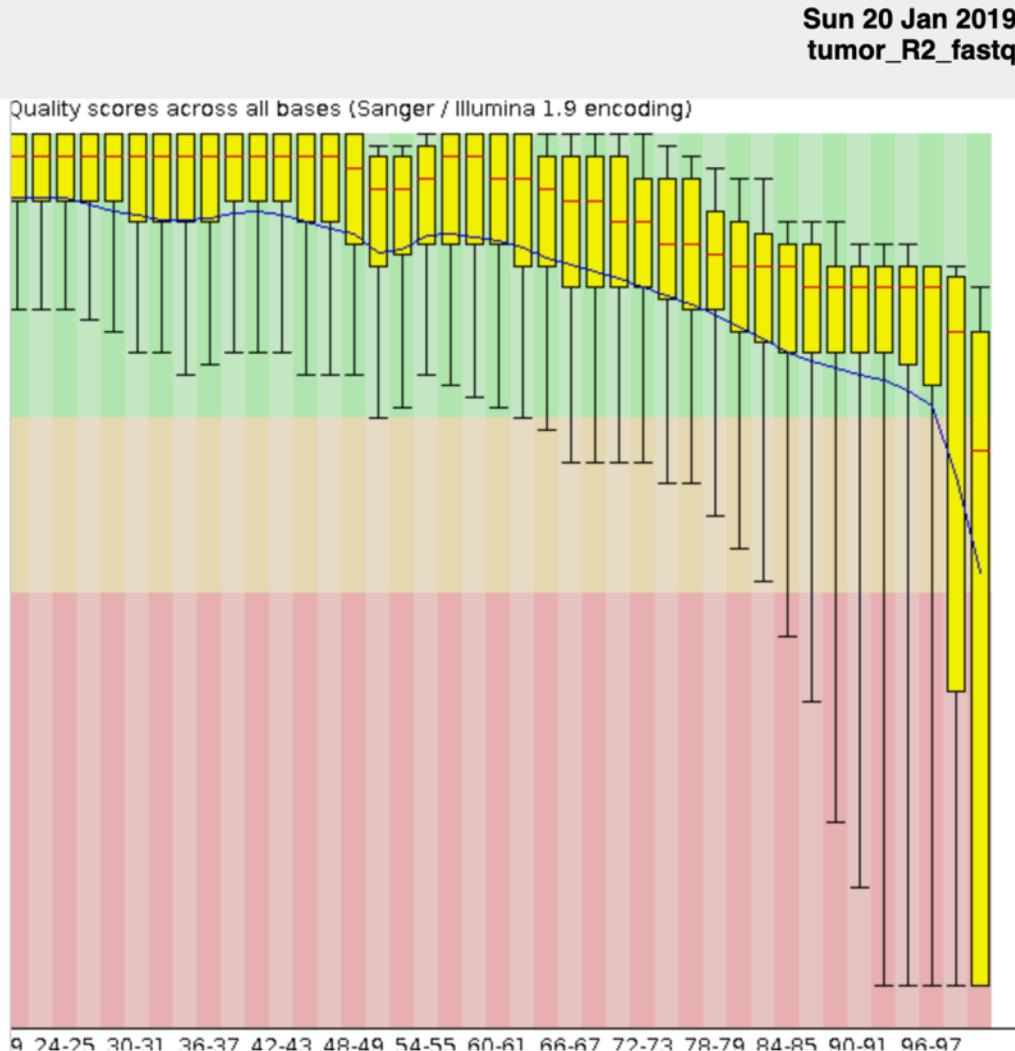
1: tumor_R1.fastq

Fastqc results

FastQC Report

Summary

- ✓ [Basic Statistics](#)
- ✗ [Per base sequence quality](#)
- ✓ [Per sequence quality scores](#)
- ! [Per base sequence content](#)
- ! [Per sequence GC content](#)
- ✓ [Per base N content](#)
- ✓ [Sequence Length Distribution](#)
- ✓ [Sequence Duplication Levels](#)
- ✓ [Overrepresented sequences](#)
- ✓ [Adapter Content](#)



History	Rechercher des données
exome test 2	
14 shown	<input checked="" type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>
49.67 MB	<input checked="" type="checkbox"/> <input type="checkbox"/> <input type="checkbox"/>
14: FastQC on data 4: Ra wData	
13: FastQC on data 4: We bpage	
12: FastQC on data 3: Ra wData	
11: FastQC on data 3: We bpage	
10: FastQC on data 2: Ra wData	
9: FastQC on data 2: We bpage	
8: FastQC on data 1: Raw Data	
7: FastQC on data 1: Web page	
6: exome_regions.bed	
5: known_sites_regions.vcf	

- Look at the different metrics for both reads
- **Problem:** the per base sequence quality of the Read2 are quite low towards the end

Trimmomatic

Galaxy / Europe Analyse de données Workflow Visualize Données partagées Aide Utilisateur History Using 0%

Tools

trimmomatic

FASTA/FASTQ manipulation

fastp – fast all-in-one preprocessing for FASTQ files

Trimmomatic flexible read trimming tool for Illumina NGS data

Quality Control

Trimmomatic flexible read trimming tool for Illumina NGS data

Assembly

Shovill Faster SPAdes assembly of Illumina reads

Workflows

All workflows

Trimmomatic flexible read trimming tool for Illumina NGS data (Galaxy Version 0.36.0)

Versions Options

Paired end data?

Yes No

Input Type

Pair of datasets

Input FASTQ file (R1/first of pair)
4: normal_R1.fastq

Input FASTQ file (R2/second of pair)
3: normal_R2.fastq

Perform initial ILLUMINACLIP step?

Yes No

Cut adapter and other illumina-specific sequences from the read

Trimmomatic Operation

1: Trimmomatic Operation

Select Trimmomatic operation to perform

Sliding window trimming (SLIDINGWINDOW)

Number of bases to average across
4

Average quality required
20

+ Insert Trimmomatic Operation

Execute

History

Rechercher des données

ExomeTest

27 shown, 31 deleted, 1 hidden

242.36 MB

Binary bam alignments file

27: BWA NORMAL

24: Trimmomatic on normal_R2.fastq (R2 paired)

23: Trimmomatic on normal_R1.fastq (R1 paired)

22: BWA TUMOR

18: Trimmomatic on tumor_R2.fastq (R2 paired)

17: Trimmomatic on tumor_R1.fastq (R1 paired)

6: exome_regions.bed

5: known_sites_regions.vcf

4: normal_R1.fastq

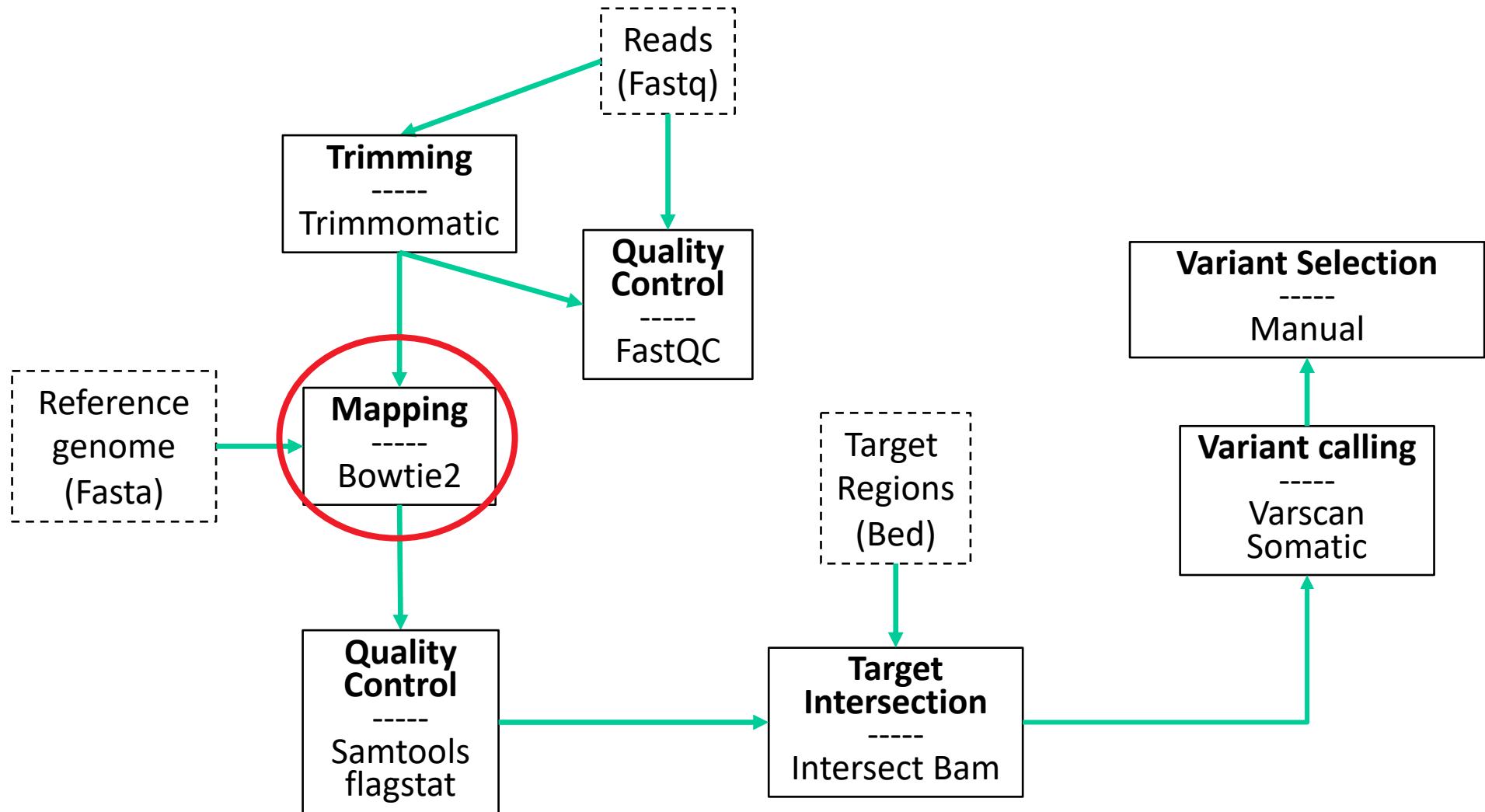
3: normal_R2.fastq

2: tumor_R2.fastq

Vérifiez à nouveau les fichiers corrigés avec fastqc

Trimmomatic (fin)

- Vérifiez le gain de qualité (fastqc d'un fastq)
- Eliminez les données « unpaired »



Bowtie

Galaxy / Europe Analyse de données Workflow Visualize ▾ Données partagées ▾ Aide ▾ Utilisateur ▾ Grid

Using 0%

Tools

bowtie

FASTA/FASTQ manipulation

AB-SOLID DATA

Convert SOLiD output to fastq

FASTA/FASTQ manipulation

Trim Galore! Quality and adapter trimmer of reads

Assembly

SOPRA with prebuilt contigs for Illumina libraries

Mapping

Bowtie2 – map reads against reference genome

Map with Bowtie for Illumina

Bismark Mapper Bisulfite reads mapper

Bismark bisulfite mapper (bowtie)

HISAT2 A fast and sensitive alignment program

Map with minimap2 A fast pairwise aligner for genomic and spliced nucleotide sequences

TopHat Gapped-read mapper for RNA-seq data

Map with Bowtie for SOLiD

RNA Analysis

Bowtie2 – map reads against reference genome (Galaxy Version 2.3.4.2)

Is this single or paired library

Paired-end

FASTA/Q file #1
23: Trimmomatic on normal_R1.fastq (R1 paired)
Must be of datatype "fastqsanger" or "fasta"

FASTA/Q file #2
24: Trimmomatic on normal_R2.fastq (R2 paired)
Must be of datatype "fastqsanger" or "fasta"

Write unaligned reads (in fastq format) to separate file(s)
Yes No
--un/--un-conc (possibly with -gz or -bz2); This triggers --un parameter for single reads and --un-conc for paired reads

Write aligned reads (in fastq format) to separate file(s)
Yes No
--al/--al-conc (possibly with -gz or -bz2); This triggers --al parameter for single reads and --al-conc for paired reads

Do you want to set paired-end options?
No
See "Alignment Options" section of Help below for information

Will you select a reference genome from your history or use a built-in index?

Use a built-in genome index
Built-ins were indexed using default options. See 'Indexes' section of help below

Select reference genome
Human (Homo sapiens): hg19
If your genome of interest is not listed, contact the Galaxy team

Set read groups information?
Do not set
Specifying read group information can greatly simplify your downstream analyses by allowing combining multiple datasets.

History

Rechercher des données

ExomeTest
26 shown, 32 deleted, 1 hidden
242.36 MB

data 6 and data 30

56: Samtools flagstat on data 27

55: VarScan somatic on data 42

48: VarScan mpileup on BWA

47: VarScan mpileup on bowtie

46: samtools mpileup on bwa

45: samtools mpileup on Bowtie

42: Samtools sort BWA tumor

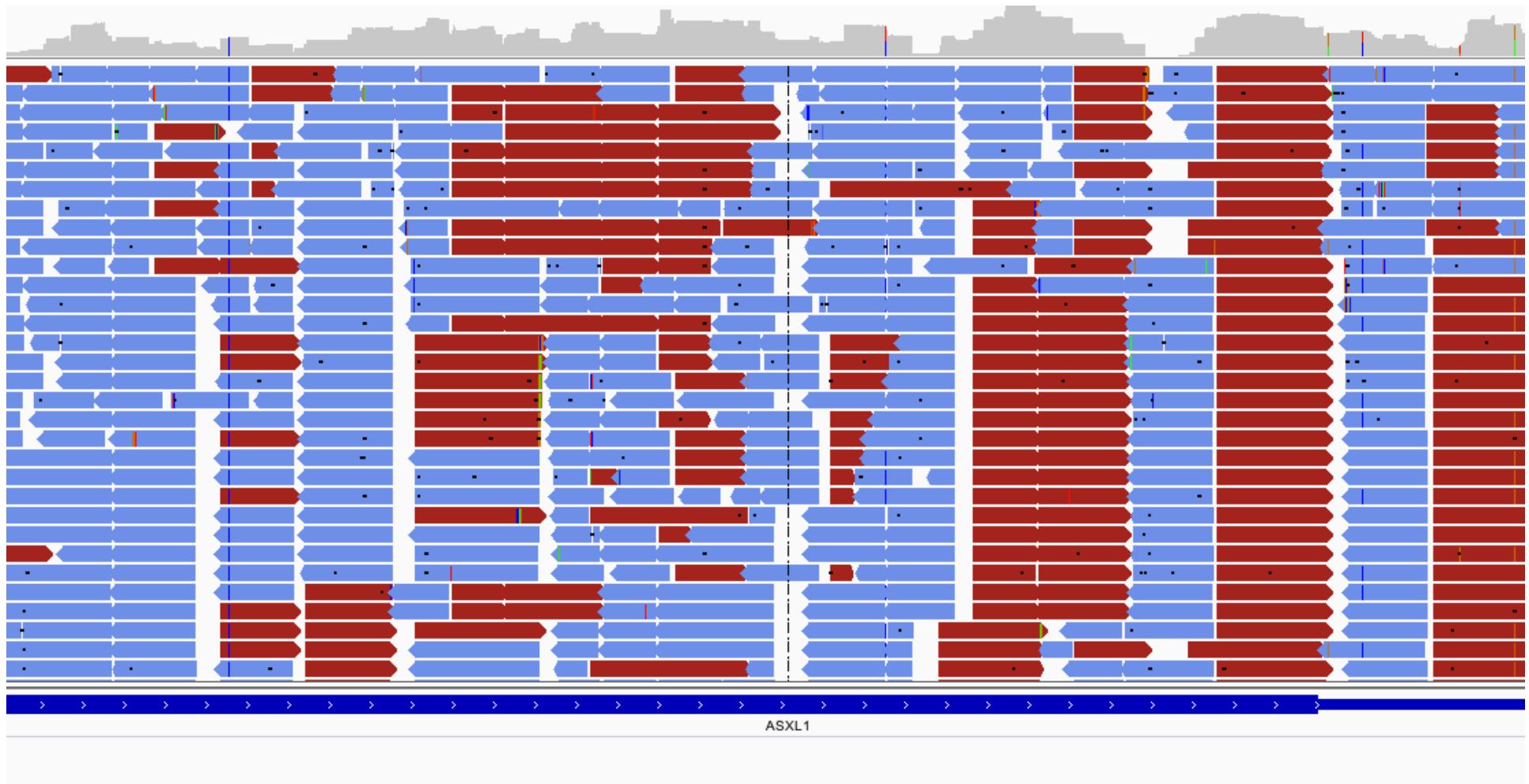
41: Samtools sort BWA normal

40: Samtools sort Bowtie TUMOR

39: Samtools sort Bowtie NORMAL

Check Bowtie result: what type of file is it?

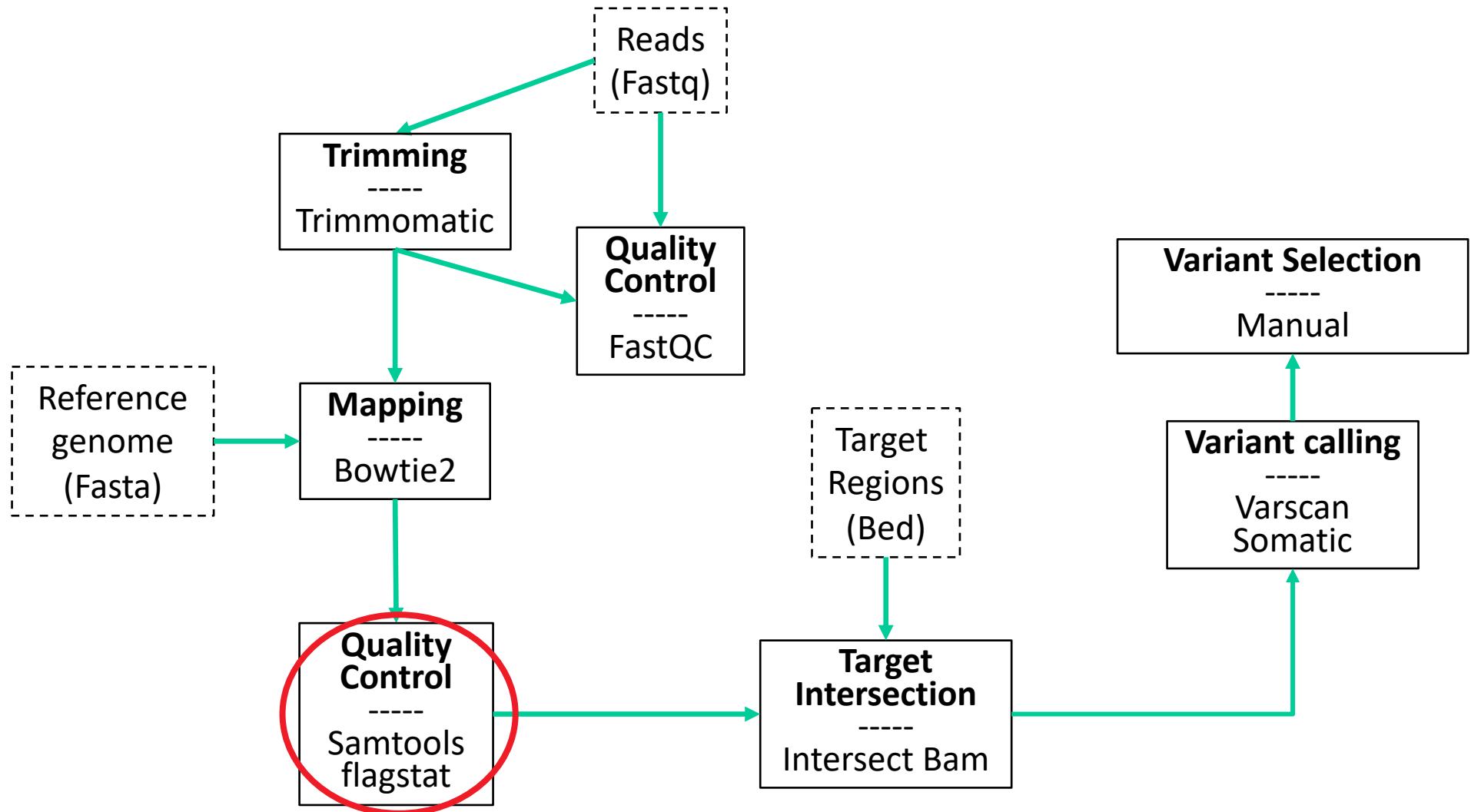
Reads alignés: le format BAM/SAM



BAM format

Rappel BAM:

```
@RG  ID:group1  SM:1425_CD34  PL:ILLUMINA  LB:lib1 PU:unit1
@PG  ID:bwa  PN:bwa  VN:0.7.12-r1039 CL:bwa mem -M -t 2 -A 2 -E 1 -R @RG\tID:group1\tSM:1425_CD34\tPL:ILLUMINA\tLB:lib1\tPU:unit1 /root/myd
ERR166338.13782800  83  chr13  32890449  60  101M  =  32890343  -207  GGGACTGAATTAGAACAAATTTCAGCGCTT
ERR166338.13782800  163  chr13  32890343  60  75M  =  32890449  207  CACTAGCCACGTTCGAGTGCTTAATGTGGCTAGTGGC
ERR166338.26716588  99  chr13  32890406  60  101M  =  32890553  222  AATGTTCCCACCTCACAGTAAGCTGTTACCGTTCCAG
ERR166338.26716588  147  chr13  32890553  60  75M  =  32890406  -222  TTGCAGACTTACCAAGCATTGGAGGAATATCGTAAG
ERR166338.27259961  99  chr13  32890496  60  101M  =  32890558  137  ACCTCAGTCACATAATAAGGAATGCATCCCTGTGTAAG
ERR166338.27259961  147  chr13  32890558  60  75M  =  32890496  -137  GACTTACCAAGCATTGGAGGAATATCGTAGGTAAG
ERR166338.63037998  99  chr13  32890496  60  101M  =  32890558  137  ACCTCAGTCACATAATAAGGAATGCATCCCTGTGTAAG
ERR166338.63037998  147  chr13  32890558  60  75M  =  32890496  -137  GACTTACCAAGCATTGGAGGAATATCGTAGGTAAG
```



Samtools

- La boîte à outils pour traiter les BAMs/SAMs
 - BAM <-> SAM
 - BAM <-> FASTQ
 - Tri de BAM
 - Indexation du BAM (création fichier .bai)
 - Obtenir un rapport sur le BAM (flagstat)

Samtools flagstats

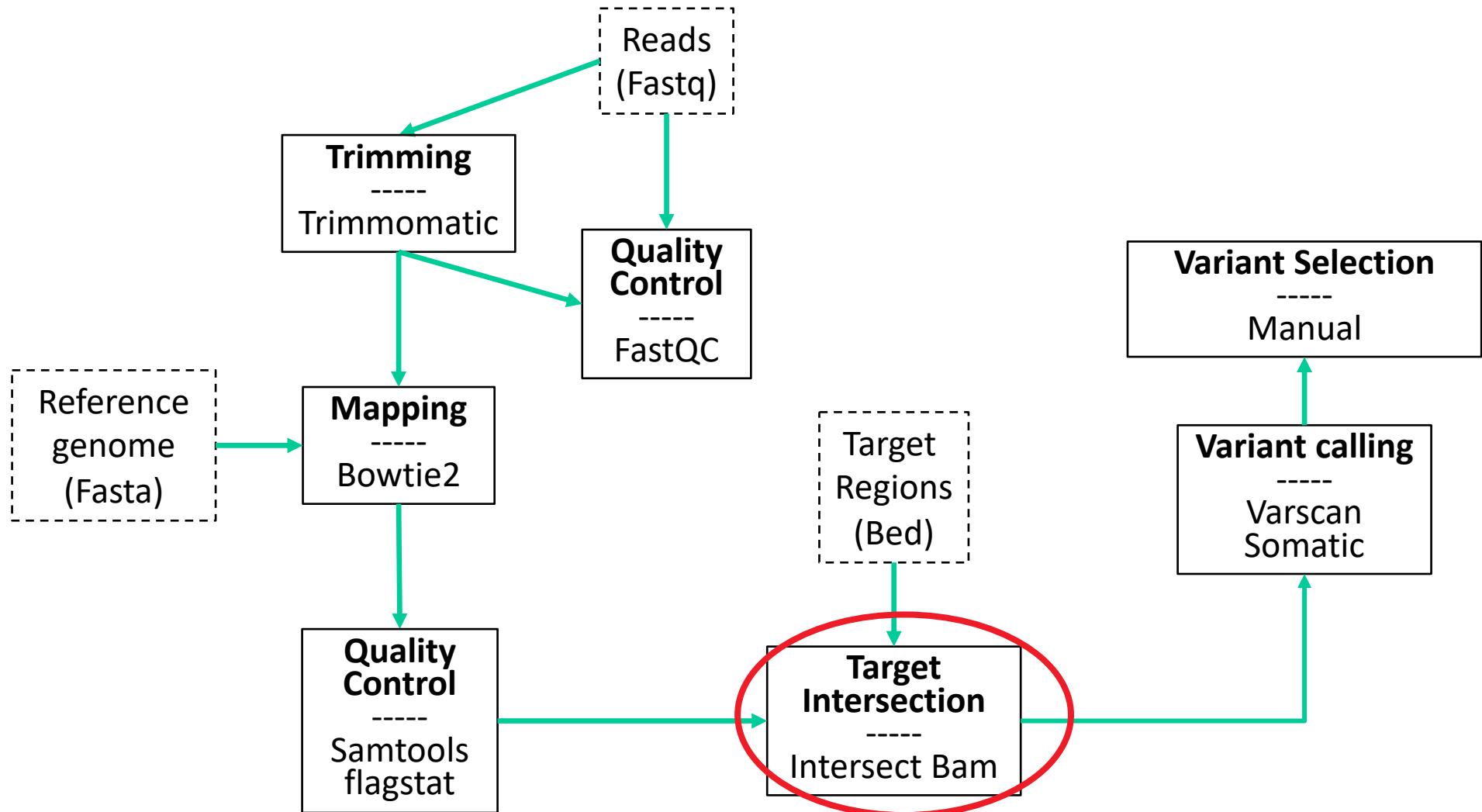
After renaming "Bowtie Normal"

The screenshot shows the Galaxy Europe interface. On the left, the 'Tools' panel has 'flagstat' selected. The main area displays the 'Samtools flagstat tabulate descriptive stats for BAM dataset (Galaxy Version 2.0.2)' tool. The 'BAM File to report statistics of' dropdown is set to '80: Bowtie2 NORMAL (BAM)', which is highlighted with a red arrow. Below it is a 'Execute' button. To the right, the 'History' panel shows a pipeline named 'Pipe1' with three steps: '83: VarScan somatic on data 82', '96.68 MB', and '82: Bowtie2 TUMOR (BAM)'. The last step is highlighted with a green background.

résultat

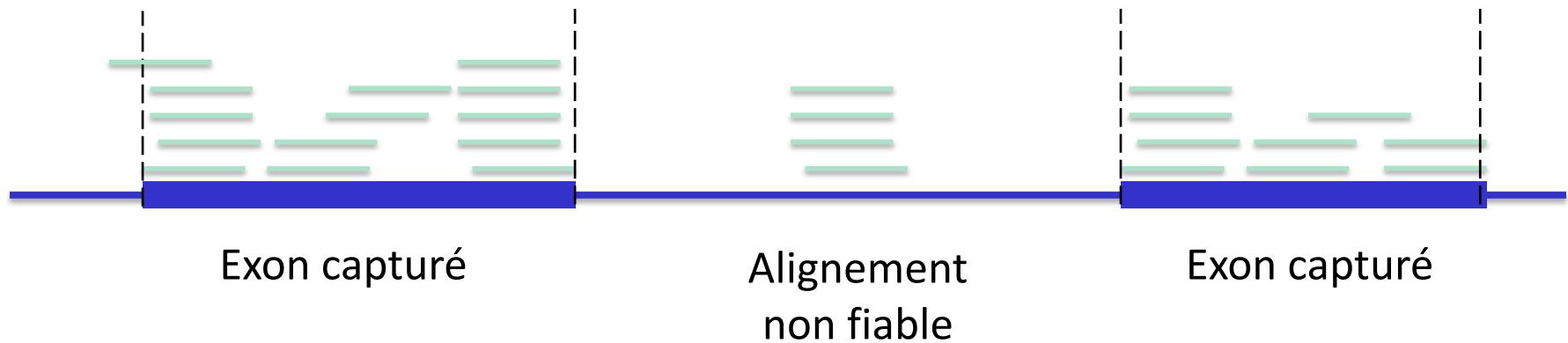
```
86796 + 0 in total (QC-passed reads + QC-failed reads)
0 + 0 secondary
0 + 0 supplementary
0 + 0 duplicates
86738 + 0 mapped (99.93% : N/A)
86796 + 0 paired in sequencing
43398 + 0 read1
43398 + 0 read2
86152 + 0 properly paired (99.26% : N/A)
86706 + 0 with itself and mate mapped
32 + 0 singletons (0.04% : N/A)
76 + 0 with mate mapped to a different chr
19 + 0 with mate mapped to a different chr (mapQ>=5)
```

The screenshot shows the Galaxy Europe interface with the results of the Samtools flagstat tool. In the 'History' panel, the last step is highlighted with a green background and labeled '84: Samtools flagstat on data 80'. A red arrow points to this step. The pipeline 'Pipe1' is shown with 14 steps, 71 deleted, and a total size of 96.68 MB.



Target intersection

- Comparer l'alignement obtenu à la liste des positions visées par le protocole de capture



Bedtools intersect intervals

Screenshot of the Galaxy Europe interface showing the "bedtools intersect" tool configuration.

The main panel displays the "bedtools Intersect intervals find overlapping intervals in various ways (Galaxy Version 2.27.1)" tool configuration. Two red arrows point to specific input fields:

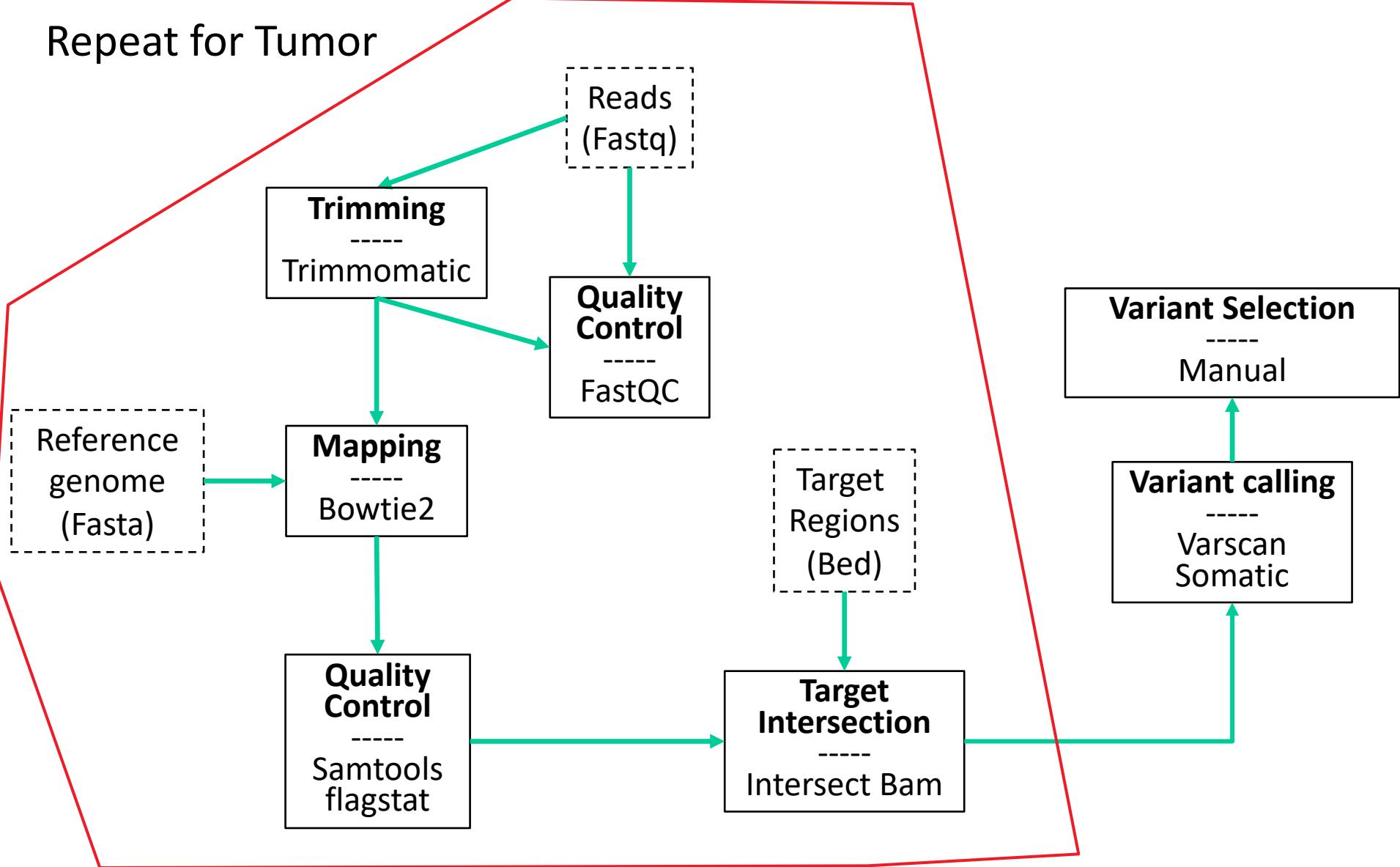
- A red arrow points to the "File A to intersect with B" field, which contains "39: Samtools sort Bowtie NORMAL".
- A red arrow points to the "File(s) B to intersect with A" field, which contains "6: exome_regions.bed".

The right sidebar shows a history of previous analyses, including:

- ExomeTest (31 shown, 34 deleted)
- 242.39 MB
- 57: Intersect intervals on data 6 and data 30
- 56: Samtools flagstat on data 27
- 55: VarScan somatic on data 42
- 48: VarScan mpileup on BWA
- 47: VarScan mpileup on bowtie
- 46: samtools mpileup on bwa
- 45: samtools mpileup on Bowtie
- 42: Samtools sort BWA tumor
- 41: Samtools sort BWA normal

Vérifiez la réduction de taille du fichier BAM!

Repeat for Tumor



Extraire un workflow



- Extraire workflow
- Le nommer
- Editer le workflow
- Choisir les données pertinentes (juste 2 fastq et regions.bed)
- Choisir les étapes de Trimmomatic à Intersect bed
- Enlever les data inutilisées (fastq tumor)
- Renommer les objets de façon générique (« sample » plutot que « normal »)
- Puis save workflow

Tools

search tools

Inputs

FILE AND META TOOLS

Get Data

Send Data

Convert Formats

Collection Operations

GENERAL TEXT TOOLS

Text Manipulation

Filter and Sort

Join, Subtract and Group

GENOMICS, NGS

Extract Features

BED Tools

Fetch Alignments

Operate on Genomic Intervals

FASTA/FASTQ manipulation

Multiple Alignments

FASTA/FASTQ manipulation

Picard

Quality Control

Assembly

Mapping

Variant Calling

Genome editing

GATK Tools

Gemini Tools

RNA Analysis

Workflow Canvas | OneSample



Details

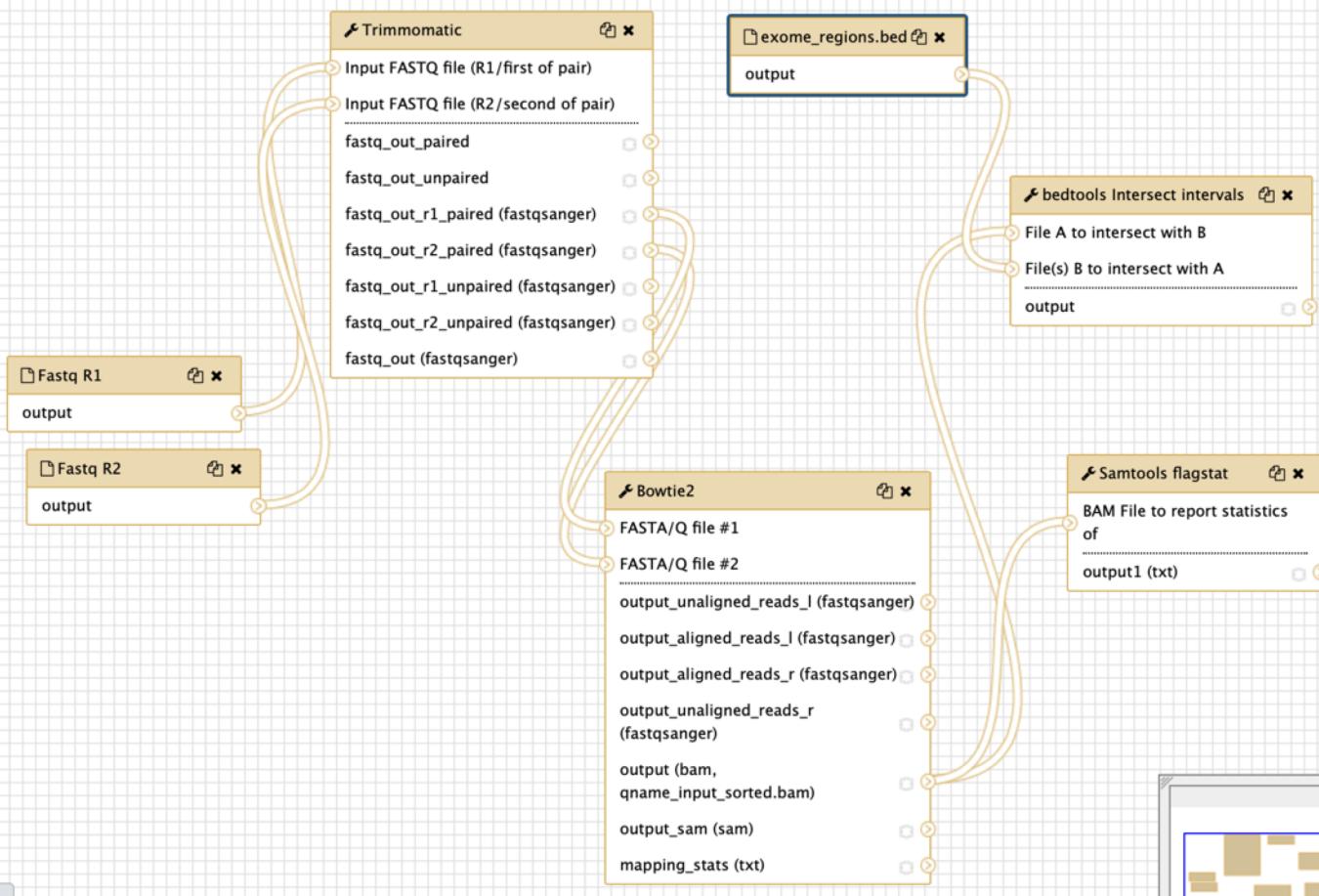
Input dataset

Label

exome_regions.bed

Add a step label.

Annotation

Add an annotation or notes to this step.
Annotations are available when a workflow is viewed.

Maintenant lancez le workflow sur les données Tumor (run workflow)

Screenshot of the Galaxy web interface showing a workflow named "Workflow: OneSample".

The interface includes a top navigation bar with tabs: Analyse de données, Workflow (selected), Visualize, Données partagées, Aide, Utilisateur, and a grid icon.

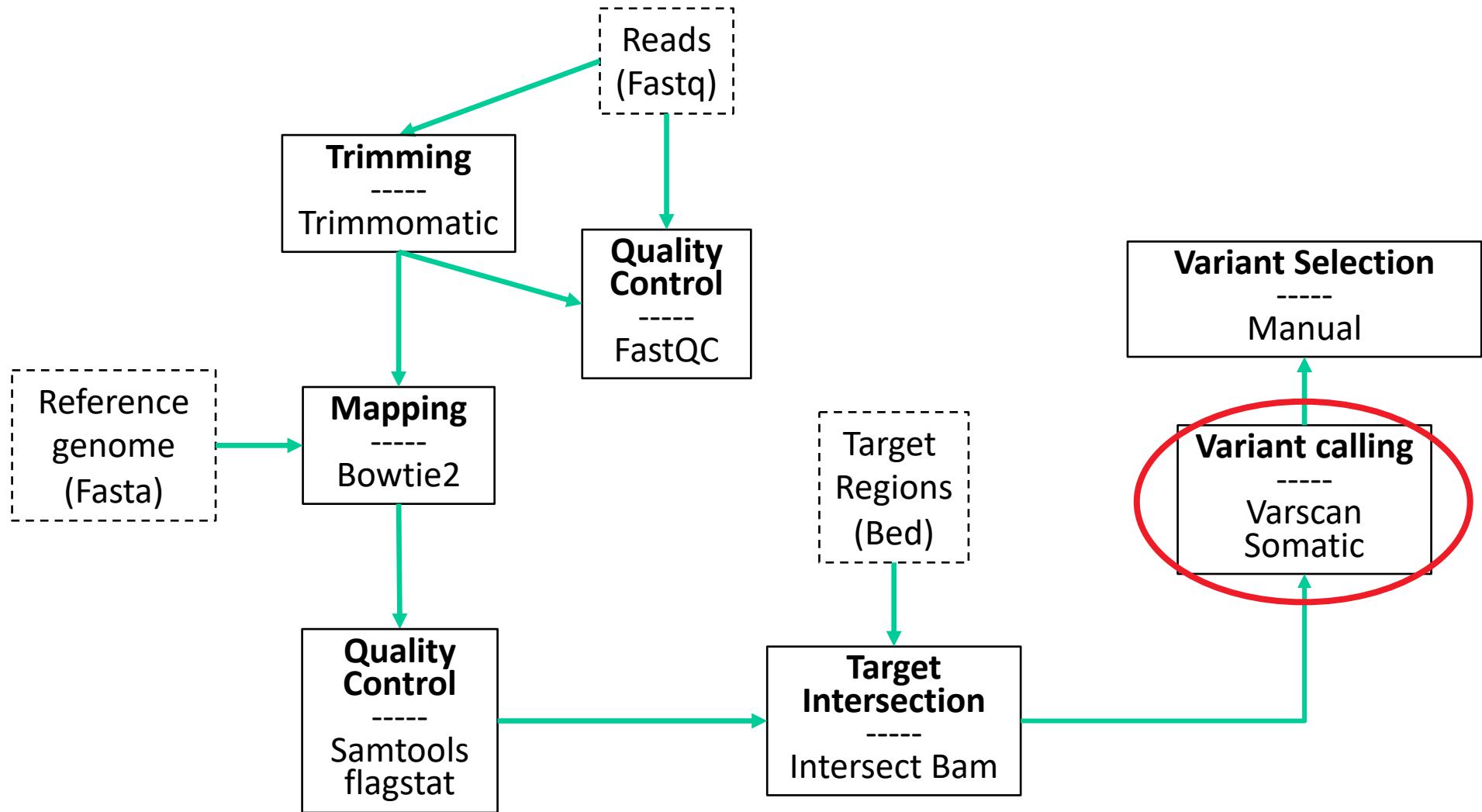
The left sidebar lists various tool categories under "META TOOLS".

The main workspace displays the "Workflow: OneSample" configuration. It shows a list of inputs and tools:

- History Options:** Send results to a new history (Yes or No). A red arrow points to the "No" button.
- 1: Fastq R1:** Input file 1: tumor_R1.fastq. A red arrow points to the dropdown menu.
- 2: Fastq R2:** Input file 2: tumor_R2.fastq. A red arrow points to the dropdown menu.
- 3: exome_regions.bed:** Input file 6: exome_regions.bed. A red arrow points to the dropdown menu.
- 4: Trimmomatic (Galaxy Version 0.36.0):** A tool step.
- 5: Bowtie2 (Galaxy Version 2.3.4.2):** A tool step.
- 6: bedtools Intersect intervals (Galaxy Version 2.27.1):** A tool step.
- 7: Samtools flagstat (Galaxy Version 2.0.2):** A tool step.

A "Run workflow" button is located at the top right of the configuration area.

The right side of the interface shows a "History" panel with a list of pipeline steps and their details, including log messages and file outputs. A red arrow points to the "6: exome_regions.bed" entry in the history list.



Somatic variant calling: VarScan

Attention: étape de 30min!

Galaxy / Europe Analyse de données Workflow Visualize Données partagées Aide Utilisateur Using 0%

Tools

VarScan somatic

Variant Calling

VarScan somatic Call germline/somatic and LOH variants from tumor-normal sample pairs

Workflows

- All workflows

VarScan somatic Call germline/somatic and LOH variants from tumor-normal sample pairs (Galaxy Version 2.4.3.3)

Versions Options

Will you select a reference genome from your history or use a built-in genome?

Use a built-in genome

reference genome

Human (Homo sapiens): hg19

The fasta reference genome that variants should be called against.

aligned reads from normal sample

44: NORMAL BAM intersect

aligned reads from tumor sample

54: TUMOR BAM intersect

Estimated purity (non-tumor content) of normal sample

1

(--normal-purity)

Estimated purity (tumor content) of tumor sample

1

(--tumor-purity)

Generate separate output datasets for SNP and indel calls?

Yes No

Settings for Variant Calling

Use default values

Settings for Posterior Variant Filtering

Do not perform posterior filtering

Execute

History

Rechercher des données

exome test 2

29 shown, 26 deleted

170.08 MB

55: Samtools flagstat on data 53

54: TUMOR BAM intersect

5.5 MB

format: bam, génome de référence: hg19

display at UCSC main
display at Ensembl Current
display with IGV local Human hg19
display in IGB View

Binary bam alignments file

53: Bowtie2 on data 46 and data 45: aligned reads (BAM)

52: FastQC on data 46: R awData

51: FastQC on data 46: W ebpage

50: FastQC on data 45: R awData

49: FastQC on data 45: W ebpage

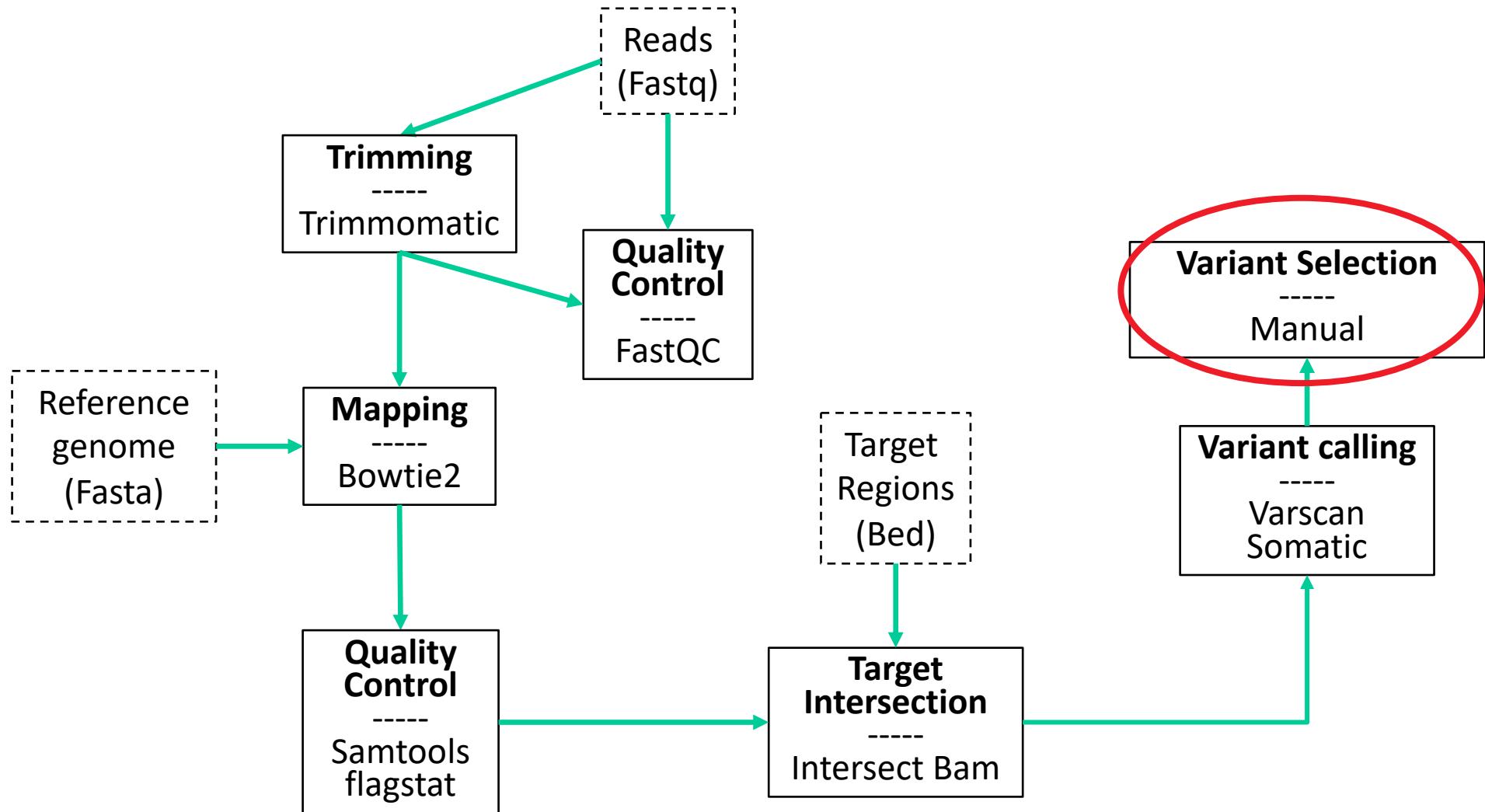
48: Trimmomatic on tumor R2.fastq (R2 unpaired)

Check Varscan output

FILE AND META TOOLS
Get Data
Send Data
Convert Formats
Collection Operations
GENERAL TEXT TOOLS
Text Manipulation
Filter and Sort
Join, Subtract and Group
GENOMICS, NGS
Extract Features
BED Tools
Fetch Alignments
Operate on Genomic Intervals
FASTA/FASTQ manipulation
Multiple Alignments
FASTA/FASTQ manipulation
Picard
Quality Control
Assembly
Mapping
Variant Calling
Genome editing

chr17	18874685	.	C	CGGT	.	PASS	DP=32;SS=3;SSC=16;GPV=1;SPV=0.022989;INDEL	Pipeline1
chr17	18874720	.	C	G	.	PASS	DP=33;SS=1;SSC=0;GPV=1.3852e-19;SPV=1	24 shown, 72 deleted
chr17	18882991	.	T	A	.	PASS	DP=60;SS=1;SSC=0;GPV=1.035e-35;SPV=1	151.47 MB
chr17	41256074	.	C	CA	.	PASS	DP=81;SS=1;SSC=1;GPV=0.0015196;SPV=0.63343;INDEL	
chr17	73759304	.	G	T	.	PASS	DP=36;SS=1;SSC=0;GPV=2.2598e-21;SPV=1	
chr19	6374813	.	T	C	.	PASS	DP=33;SS=1;SSC=0;GPV=2.8029e-05;SPV=0.8425	
chr19	7550844	.	G	A	.	PASS	DP=44;SS=1;SSC=4;GPV=2.3358e-10;SPV=0.35332	
chr19	36504365	.	C	T	.	PASS	DP=34;SS=1;SSC=1;GPV=5.1914e-07;SPV=0.63966	
chr1	10596341	.	C	T	.	PASS	DP=44;SS=1;SSC=2;GPV=7.4746e-10;SPV=0.53262	
chr1	160251792	.	A	G	.	PASS	DP=37;SS=1;SSC=0;GPV=5.1339e-06;SPV=0.87856	
chr1	167082869	.	G	A	.	PASS	DP=71;SS=1;SSC=8;GPV=2.0173e-19;SPV=0.13252	
chr1	167095163	.	G	C	.	PASS	DP=52;SS=1;SSC=5;GPV=6.8522e-13;SPV=0.28624	
chr1	167097739	.	C	A	.	PASS	DP=64;SS=1;SSC=3;GPV=4.3049e-14;SPV=0.44587	
chr1	214788427	.	C	T	.	PASS	DP=45;SS=1;SSC=1;GPV=8.5784e-10;SPV=0.66234	
chr1	214802553	.	CT	C	.	PASS	DP=83;SOMATIC;SS=2;SSC=18;GPV=1;SPV=0.015148;INDEL	
chr1	214803969	.	G	C	.	PASS	DP=111;SOMATIC;SS=2;SSC=35;GPV=1;SPV=0.00029013	
chr1	214804041	.	C	A	.	PASS	DP=65;SS=1;SSC=0;GPV=2.7963e-08;SPV=0.9934	
chr1	214811174	.	G	A	.	PASS	DP=76;SS=1;SSC=0;GPV=3.6183e-12;SPV=0.99124	
chr1	214811244	.	C	G	.	PASS	DP=120;SS=1;SSC=0;GPV=1.7875e-19;SPV=0.92629	
chr1	214813487	.	A	G	.	PASS	DP=291;SS=1;SSC=3;GPV=1.3526e-38;SPV=0.47444	
chr1	214813782	.	A	G	.	PASS	DP=108;SS=1;SSC=0;GPV=1.7692e-19;SPV=0.98472	
chr1	214813941	.	C	G	.	PASS	DP=86;SS=1;SSC=4;GPV=8.038e-16;SPV=0.34707	
chr1	214814125	.	G	A	.	PASS	DP=80;SS=1;SSC=0;GPV=1.2414e-11;SPV=0.85982	
chr1	214814582	.	G	A	.	PASS	DP=226;SS=1;SSC=5;GPV=3.0361e-32;SPV=0.28302	
chr1	214814733	.	T	G	.	PASS	DP=244;SS=1;SSC=0;GPV=2.27499e-40;SPV=0.97323	

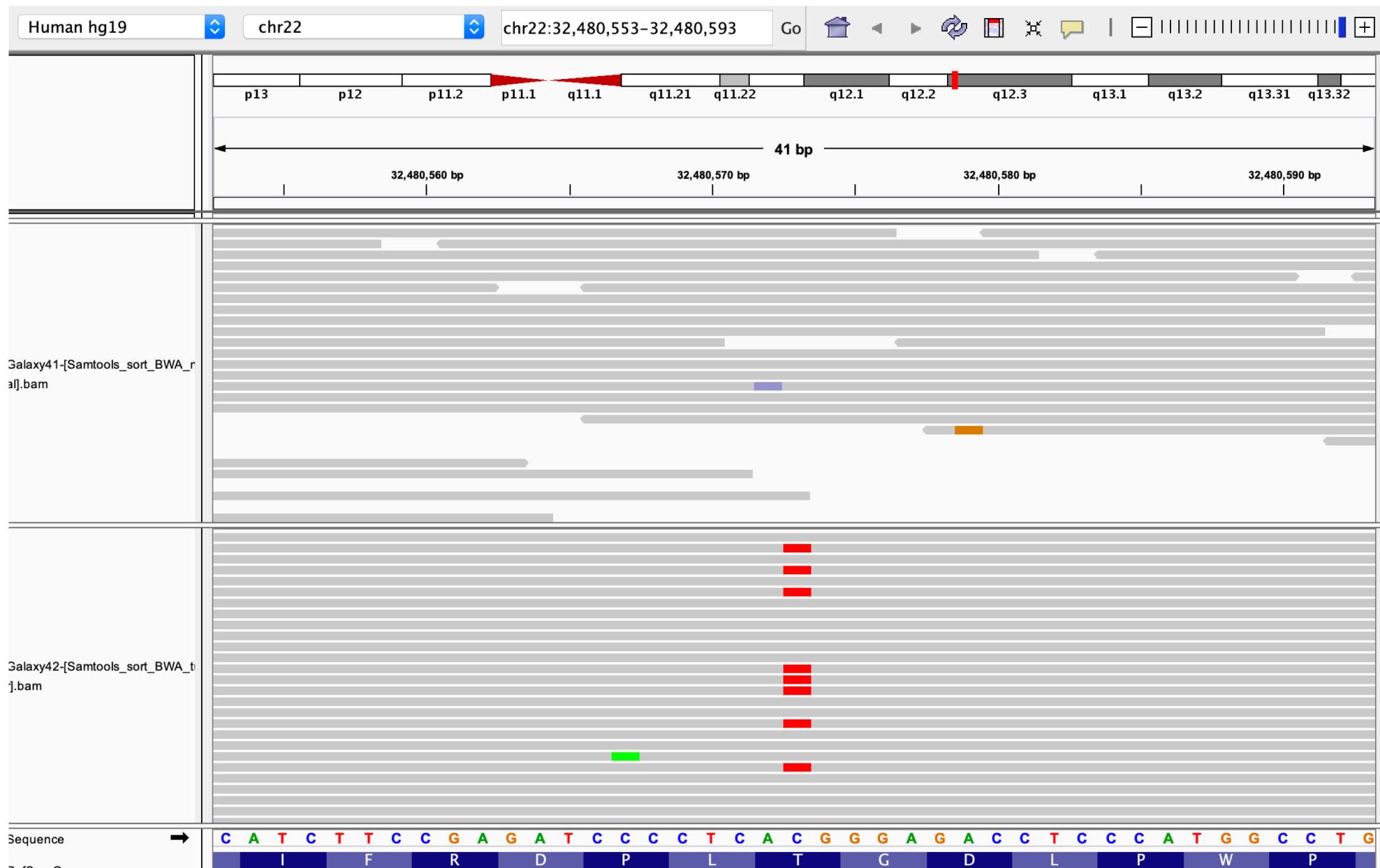
Somatic variants found?
Check "NORMAL" and "TUMOR" sample stats



Filter and visualize somatic variants

- Run the *grep* filter on the Varscan output with regular expression « somatic ». Check the result
- Launch IGV with hg19 reference
- Then 2 possibilities:
 - Download Normal and Tumor BAM files on your local computer (select option « download bam_index ») and load these files in IGV (« load from file »)
 - In Galaxy, click on « display with IGV local ». (will automatically connect with our local IGV session)
- Visualize somatic events.

IGV view



Variant annotation with VEP

- Download the Varscan VCF file
- Go to <https://www.ensembl.org/Tools/VEP>
- Select GRCh37.p13 (=hg19)
- Launch VEP
- Display column "impact" and sort results by impact

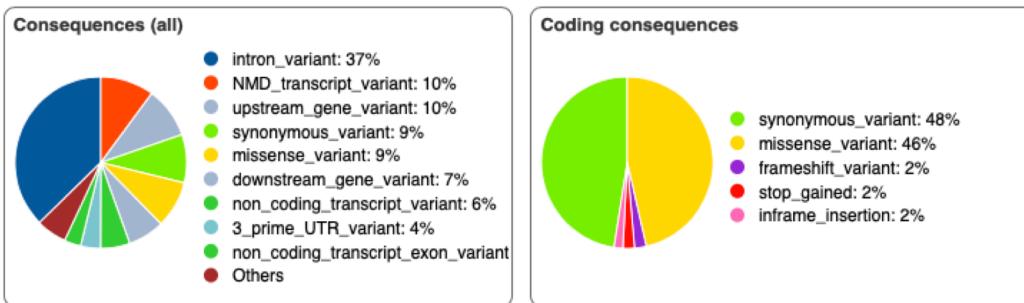
Note: the highest impact variants are not necessarily somatic!

Variant Effect Predictor results

Job details

Summary statistics

Category	Count
Variants processed	153
Variants filtered out	0
Novel / existing variants	6 (3.9) / 147 (96.1)
Overlapped genes	55
Overlapped transcripts	318
Overlapped regulatory features	23



Results preview

 Navigation (per variant)
 Filters
 Download

Show: [1](#) [5](#) [10](#) [50](#) [All](#) variants
Uploaded variant Add

All: [VCF](#) [VEP](#) [TXT](#)
BioMart: [Variants](#) [Genes](#)

Show/hide columns (2 hidden)

Uploaded variant	Location	Allele	Consequence	Impact	Symbol	Gene	Feature type	Feature	Biotype	Exon	Intron	cDNA position
.	1:248059779-248059779	A	frameshift_variant	HIGH	OR2W3	ENSG00000238243	Transcript	ENST00000360358	protein_coding	1/1	-	891-8
.	1:248059779-248059779	A	frameshift_variant	HIGH	OR2W3	ENSG00000238243	Transcript	ENST00000537741	protein_coding	3/3	-	1148-
.	3:121416308-121416308	T	stop_gained	HIGH	GOLGB1	ENSG00000173230	Transcript	ENST00000340645	protein_coding	13/22	-	3173
.	3:121416308-121416308	T	stop_gained	HIGH	GOLGB1	ENSG00000173230	Transcript	ENST00000393667	protein_coding	13/22	-	3173
.	3:121416308-121416308	T	stop_gained	HIGH	GOLGB1	ENSG00000173230	Transcript	ENST00000489400	protein_coding	9/9	-	2659

Annexes

Galaxy: partager ses données



- Partager et publier
- Make History Accessible via Link
 - Cocher « also make all objects within the History accessible »

Galaxy: récupérer des données partagées

- Menu « Données partagées »
- Histories
- Choisir History « ... IFSBM ... dgauth»
- Import History