target$_{c}aptur e_{b}ed$

Nov 09, 2020

Panel details

Repository to collect and share bed files for each bait set. This repository does not contain any bait information. There is also plan to add annotations for each bed file.

Source code	https://github.com/Clinical-Genomics/target_capture_bed
Build status	
Version	
Repository size	
Development model	Github Flow
Maintainers	Hassan Foroughi, Anna Lyander, Keyvan Elhami

id	short name	file name	designer
CG2.1	lymphomatic_2.1	lymphomatic_2.1_hg19_design.bed	Christian Brieghel
CG3.1	gi_cfdna_3.1	gicfdna_3.1_hg19_design.bed	Emma Tham
CG4.1	gmck_solid_4.1	gmcksolid_4.1_hg19_design.bed	Johan Lindberg
CG5.1	gms_myeloid_5.1	gmsmyeloid_5.1_hg19_design.bed	Christina Orsmark Pietras
CG5.2	gms_myeloid_5.2	gmsmyeloid_5.2_hg19_design.bed	Christina Orsmark Pietras
CG6.1	lymphoma_6.1	lymphoma_6.1_hg19_design.bed	Valtteri Wirta
CG7.1	gms_lymphoid_7.1	gmslymphoid_7.1_hg19_design.bed	Christina Orsmark Pietras
CG8.1	exome_8.1	twistexome_8.1_hg19_design.bed	Twist Bioscience
CG9.1	exome_refseq_9.1	twistexomerefseq_9.1_hg19_design.bed	Twist Bioscience
CG10.1	exome_comp_10.1	twistexomecomprehensive_10.1_hg19_design.bed	Twist Bioscience
CG11.1	agilent_sureselect_cre_11.1	agilentsureselectcre_11.1_hg19_design.bed	Agilent
CG12.1	agilent_sureselect_v5_12.1	agilentsureselectv5_12.1_hg19_design.bed	Agilent
CG13.1	agilent_sureselect_v1_13.1	agilentsureselectv1_13.1_hg19_design.bed	Agilent

CHAPTER 1

lymphomatic_2.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	26548 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independandant segments	000
Version	v1
Control sample in library prep	•

CHAPTER 2

gi_cfdna_3.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	76261 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independandant segments	000
Version	v1
Control sample in library prep	•

CHAPTER 3

gmck_solid_4.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	1705152 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v1
Control sample in library prep	HD832 (OncoSpan FFPE, Horizon Discovery)

CHAPTER 4

gms_myeloid_5.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	712494 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v1
Control sample in library prep	HD829 (Myeloid DNA Reference Standard, Horizon Discovery)

CHAPTER 5

gms_myeloid_5.2

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	728436 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v2
Control sample in library prep	HD829 (Myeloid DNA Reference Standard, Horizon Discovery)

CHAPTER 6

lymphoma_6.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	159268 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independandant segments	000
Version	v1
Control sample in library prep	•

CHAPTER 7

gms_lymphoid_7.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	1957492 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v1
Control sample in library prep	HD829 (Myeloid DNA Reference Standard, Horizon Discovery)

CHAPTER 8

exome_8.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	33053262 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v1
Control sample in library prep	NA24143 (Coriell Institute)

CHAPTER 9

exome_refseq_9.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	36339084 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v1
Control sample in library prep	NA24143 (Coriell Institute)

CHAPTER 10

exome_comp_10.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	36363631 bp
Genome version	hg19
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v1
Control sample in library prep	NA24143 (Coriell Institute)

CHAPTER 11

agilent_sureselect_cre_11.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	54098923 bp
Genome version	
COSMIC SNPs	000
Non-genic regions	000bp
Number of independandant segments	000
Version	v1
Control sample in library prep	•

CHAPTER 12

agilent_sureselect_v5_12.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	50390601 bp
Genome version	
COSMIC SNPs	000
Non-genic regions	000bp
Number of independendant segments	000
Version	v1
Control sample in library prep	•

CHAPTER 13

agilent_sureselect_v1_13.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	51542852 bp
Genome version	
COSMIC SNPs	000
Non-genic regions	000bp
Number of independandant segments	000
Version	v1
Control sample in library prep	•

CHAPTER 14

agilent_sureselect_focused_exome_v1_14.1

Feature type	Count
Genes	000
Unique Transcripts	000
Transcripts with all exons covered	000
Transcripts with at least one exon covered	000
Design Padding	000bp
Panel size	17846036 bp
Genome version	
COSMIC SNPs	000
Non-genic regions	000bp
Number of independandant segments	000
Version	v1
Control sample in library prep	•

CHAPTER 15

Calculate panel size

Target bed file in data_files:

Bed file in production:

CHAPTER 16

Prepare for UCSC tracks

Create bigBed files from data files:

Create trackDb.txt

CHAPTER 17

Filename convention

{project_name}_{project_number.version}_{genome_version}_{application/purpose}.{file_extension}

example1: GMCKsolid_4.1_hg19_design.bed

example2: GMCKsolid_4.1_hg38_design.bed

example3: TwistExome_8.1_hg19_design.bed

example4: TwistExomeRefSeq_9.1_hg19_design.bed

17.1 project_name

Name will reflect company or project name for the bed. Examples: GMCKsolid or TwistExomeRefSeq

17.2 project_number

Integer starting from 1 and new projects will get a new number.

17.3 version

Any change to regions or features in the original design file.

17.4 genome_version

hg19, hg38

17.5 application/purpose

1. target: original target file that was sent to Twist
2. design: all_target_segments_covered_by_probes file received from Twist
3. dropout: all_target_segments_not_covered_by_probes file received from Twist
4. ucsctrack: file is suitable to upload to ucsc as track file. Same file as target but with a header suitable to upload to UCSC genome browser

17.6 file_extension

- bed: bed can be bed3, 4, 6, 12 columns
- bedgraph/bigwig: standard bedgraph and bigwig format from ucsc

CHAPTER 18

Versioning Schema

This change log will document the notable changes to this project in this file and it is following Semantic Versioning. The version numbering consists of three digits: major.minor.patch:

- major: addition, updating, or removing following items from a bed file:
  - Genome version
  - Region size (even 1bp) (e.g. chr:Start-End)
  - Target bed name (not file name). (e.g. GMCKSolid to GMCKsolid or GMCKsolidtumor)
- minor: addition, updating, or removing following items:
  - External URLs
  - annotations and features
  - file name (i.e. not panel name)
- patch: addition, updating, or removing following items:
  - README (designer, description, typo)

CHAPTER 19

Build Doc

Following steps explains how to build documents locally.

19.1 Container

You can pull latest container via:

19.2 Conda

Create a conda environment:

Install Sphinx and extensions:

Build docs:

View docs (`open` or similar command from your OS):