

Alyssa

Bonnes idées

- Graphe de filtres = stratégie : suite d'opération (briques en drag and drop)
- Flagger les opérations manuelles dans le graphe (expertise utilisateur ajoutée ou en attente)
- Valider une stratégie (fige la config)
- Partager une stratégie (publique)
- Etiqueter une stratégie (clinical domains : à quoi sert cette stratégie)
- Représentation de l'ACMG
- Représentations des overlaps en % d'une boîte
- Gestion des d'identifiants entre les manip (CGH034 <-> VCF18)
- Waiting analyses

Accueil de l'analyse

Les informations sont très similaires à celles qu'on avait décrites :
Statut de l'analyse, date, génome, stratégie de filtres utilisées, input types (VCF, CNV, CGH...)

Agilent Technologies | Alissa Interpret Manuel Leburrier

Files | Patients | Analyses | Gene Profiles | MVL | Configuration | Search | Help Administration

Patient: 36228 > Analysis: A_36228 Assign Lock/Edit Request Sign-off

Click the 'Lock/Edit' button at the top right of the screen to perform actions on this analysis and its variants and reports. Click [here](#) for more information.

General | Variant triage | Variant review | Reports

Status

Status	In Progress	Assigned to	jimages
Updated on	mars 5, 2021 3:53 PM CET	Assigned on	mars 5, 2021 3:53 PM CET
Updated by	jimages	Comments	

Analysis Details


Reference	A_36228	# Molecular variants	64 137	Created on	mars 5, 2021 3:53 PM CET
Domain	Default	# CNVs	19	Created by	jimages
Genome build	GRCh37	# Translocations	0	Last updated on	mars 16, 2021 2:39 PM CET
Target Panels	None	Summary		Last updated by	jtaminau
Classification Tree	Manual	Description			

1501 variants created with annotation warnings. Click [here](#) to download warning file.

232 variant positions excluded with errors. Click [here](#) to download error file.

Accueil de l'analyse

Les informations sont très similaires à celles qu'on avait décrites :
Fichiers et contenus.
Phénotype.
Structure familiale.

Lab Results						
Status	Source	Regions of low coverage	File Type	# Var. pos. in Lab Result	# Var. pos. used in Analysis	# Variants in Analysis
Ready	 DI_WESA_20-36228.gatk.haplotype.snp_indel.filtred2.vcf (20-36228-A-02-00)		VCF File	57 721	57 721	64 137
Ready	IntervalBasedReport_20488.xls (20-20488-252206093341_1_2)		Cytogenomics Interval File	19	19	19

Phenotype			
Code	Phenotype Trait	Modifiers	Actions
No phenotype traits found.			

Family Members				
Patient	Affected status	Lab Results	# Var. pos. in Lab Result	# Var. pos. used in Analysis
37647 (Mother)	unaffected	DI_WESA_20-36228.gatk.haplotype.snp_indel.filtred2.vcf (20-37647-A-02-00)	57 701	62 077
37917 (Father)	unaffected	DI_WESA_20-36228.gatk.haplotype.snp_indel.filtred2.vcf (20-37917-A-02-00)	57 661	62 303

Accueil de l'analyse

Les informations sont très similaires à celles qu'on avait décrites :
Sources de BDD utilisées (nécessaire uniquement dans le rapport)

Sources

Platform Dataset

33, RefSeq Transcripts v96 + RefSeqGene released 2019-10-22
OMIM® Copyright © 1966-2019 Johns Hopkins University - All rights reserved.
GRCh37.p13

Genome build

Annotation Sources

Name

Description

[1000Genomes](#)

1000 Genomes Phase1 release v3.20101123

[1000GenomesPhase3](#)

1000 Genomes Phase 3 release v5 (10 September 2014), including GRCh38 data

[CGA](#)

ClinGen CNV Atlas 2019-10-07

[CGDS](#)

ClinGen Dosage Sensitivity Map 2019-08-12

[CGDS_GENE](#)

ClinGen Gene Curation Dosage Sensitivity Map - 2019-07-15

[CIViC](#)

CIViC - Clinical Interpretations of Variants in Cancer - release 01-Oct-2019

[COSMIC](#)

COSMIC release v90

[ClinVar](#)

NCBI ClinVar 2019-10

[DGV](#)

Database of Genomic Variants 2016-05-15

[DPOP](#)

DECIPHER population CNVs v9.23

[DSYN](#)

DECIPHER syndromes 2019-10-05

[ESP6500](#)

Variants in the ESP6500SI-V2 dataset of the exome sequencing project (ESP), annotated with SeattleSeqAnnotation137.

[ExAC](#)

ExAC release 1.0 - including GRCh38 from liftover data

[JAX](#)

Somatic gene variant annotations and related content powered by The Jackson Laboratory Clinical Knowledgebase (JAX-CKB™) - version 20200124

[OMIM](#)

OMIM 2019-10-25

[dbNSFP](#)

dbNSFP v3.0b2: Database of functional predictions for non-synonymous SNPs

[dbSNP](#)

dbSNP build 151

[gnomAD](#)

gnomAD release 2.0.2 - with additional multi-allelic insertions and GRCh38 statistics from the lift-over vcf files

Accueil de l'analyse

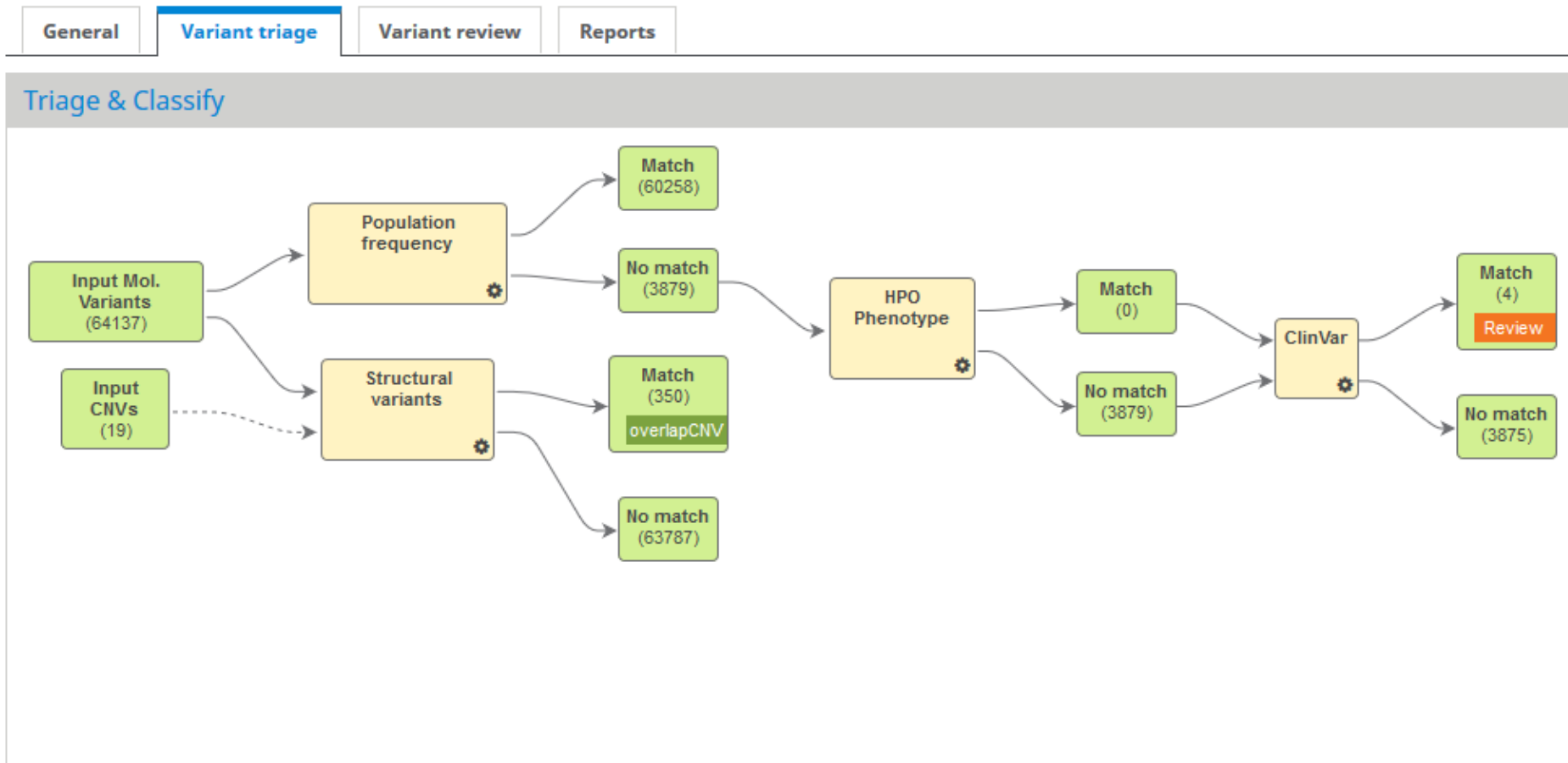
Les informations sont très similaires à celles qu'on avait décrites :

Audit trail

Change History			
Updated on	Updated by	Scope of change	Action
mars 16, 2021 4:47 PM CET	mlebeurrier	Analysis access	Analysis has been accessed
mars 16, 2021 2:37 PM CET	jtaminau	Filtering	Filtered Molecular variants using classification tree bin: ClinVar () Match
mars 16, 2021 2:19 PM CET	jtaminau	Analysis access	Analysis has been accessed
mars 12, 2021 10:36 AM CET	jtaminau	Analysis access	Analysis has been accessed
mars 8, 2021 9:46 AM CET	jimages	Analysis access	Analysis has been accessed
mars 5, 2021 3:53 PM CET	jimages	Analysis status	In Progress
mars 5, 2021 3:53 PM CET	jimages	Analysis access	Analysis has been accessed
mars 5, 2021 3:53 PM CET	system	Analysis status	Available For Analysis
mars 5, 2021 3:53 PM CET	jimages	Analysis details	Created analysis with reference: A_36228, summary: '' and description: '' and target panels: None

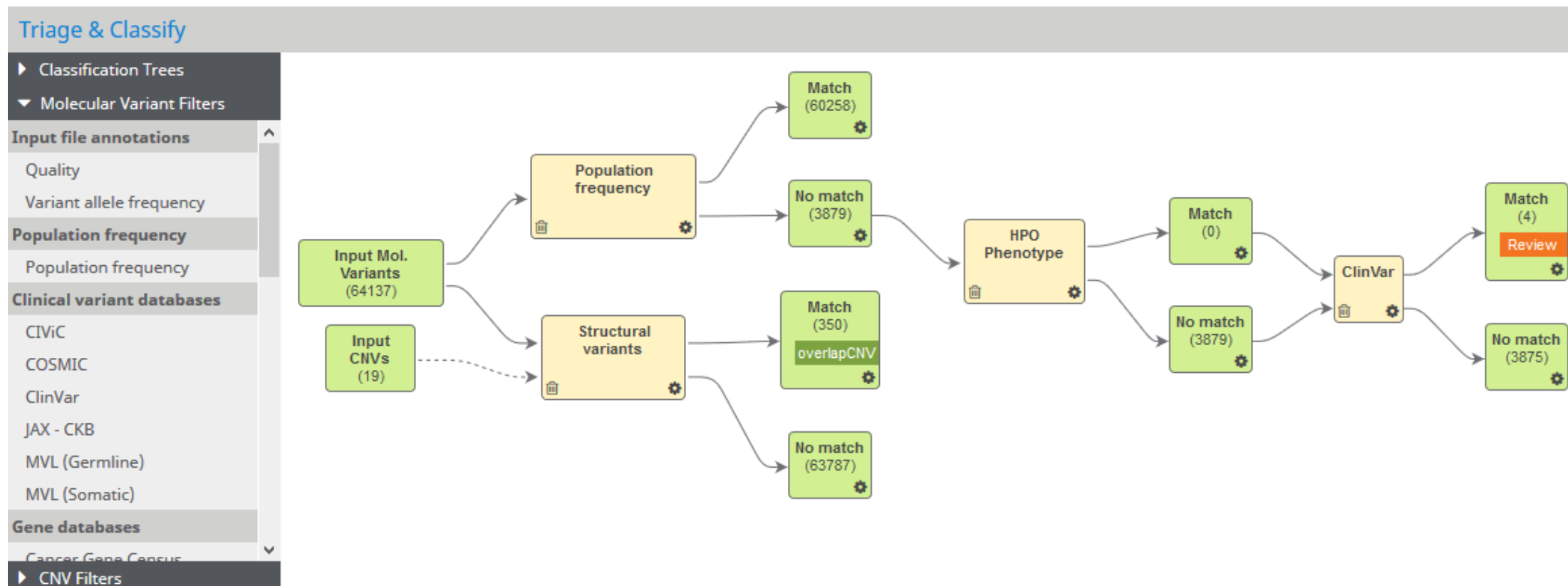
Variant triage = tableau de variants

Graphe de filtre interactif avec les étapes filtrages et les comptages associés.



Editer le graphe

Drag and drop une étape (depuis la liste accessible) de filtrage puis la relier aux data.



Voir le tableau de variants d'une étape

Triage & Classify ▶ Run Classification Tree 📄 Save Classification Tree 🔍 🔍 🔍 🔍

Classification Trees
 Molecular Variant Filters

Input file annotations

- Quality
- Variant allele frequency

Population frequency

- Population frequency

Clinical variant databases

- CIViC
- COSMIC
- ClinVar
- JAX - CKB
- MVL (Germline)
- MVL (Somatic)

Gene databases

- Cancer Gene Census
- ▶ CNV Filters

Molecular variants | **CNVs**

Variant List: 64 137 variants (total) ▶ 4 variants (1 classification tree bin)

clinical significance

overlapCNV

	Gene	Position	Ref	Patient	Read Depth	Inheritance mode	Inh. from	Family		Read Depth		CNV	Type	Transcript	cDNA	Location	Exon	Effect	Protein	CT Labels	External Databases	Simil.	Info	Classification	Assessr	
								Mother	Father	Mother	Father															
<input type="checkbox"/>	PNPT1	2:55,874,559	C	T C	48	Comp. Het. cand.	♀	C	T	C	C	47	41	snp	NM_033109.5	c.1525G>A	exonic	19	nonsynonymous	p.Val509Ile						
<input type="checkbox"/>	INTU	4:128,608,927	G	G A	76	Comp. Het. cand.	♂	G	G	G	A	36	92	snp	NM_015693.4	c.1354G>A	exonic	8	nonsynonymous	p.Ala452Thr						
<input type="checkbox"/>	MC1R	16:89,986,546	G	C G	108	Comp. Het. cand.	♀	G	C	G	G	111	45	snp	NM_002386.3	c.880G>C	exonic	1	nonsynonymous	p.Asp294His						
<input type="checkbox"/>	TANGO2	22:20,049,207	G	A / A	32	Mend. viol.	.	G	G	G	A	37	74	snp	NR_136211.1	n.784G>A	ncRNA_exonic	7			overlapC					

Actions on selection

Show 20 results Page: 1 of 1

Où retrouver un variant dans la stratégie

Triage & Classify ▶ Run Classification Tree 📄 Save Classification Tree 🔍 🔍 🗑️

▶ Classification Trees
 ▼ Molecular Variant Filters
 Input file annotations
 Quality
 Variant allele frequency
 Population frequency
 Population frequency
 Clinical variant databases
 CIVIC
 COSMIC
 ClinVar
 JAX - CKB
 MVL (Germline)
 MVL (Somatic)
 Gene databases
 Ensembl
 CNV Filters

Input Mol. Variants (64137)
 Input CNVs (19)
 Population frequency
 Structural variants
 Match (60258)
 No match (3879)
 Match (350) overlapCNV
 No match (63767)
 HPO Phenotype
 Match (0)
 No match (3879)
 ClinVar
 Match (4) Review
 No match (3875)

Molecular variants | CNVs
 Variant List: 64 137 variants (total) ▶ 4 variants (1 classification tree bin) ⌕
⚠ Show warning list 👁 Show all 📄 Export 📊 Summary ⏴ Filter

clinical significance
 overlapCNV

Gene	Position	Ref	Patient	Read Depth	Inheritance mode	Inh. from	Family		Read Depth		CNV	Type	Transcript	cDNA	Location	Exon	Effect	Protein	CT Labels	External Databases	Simil.	Info	Classification	Assessment	
							Mother	Father	Mother	Father															
<input type="checkbox"/> PNPT1	2:55,874,559	C	T C	48	Comp. Het. cand.	♀	C	T	C	C	47	41	snp	NM_033109.5	c.1525G>A	exonic	19	nonsynonymous	p.Val509Ile						
<input type="checkbox"/> INTU	4:128,608,927	G	G A	76	Comp. Het. cand.	♂	G	G	G	A	36	92	snp	NM_015693.4	c.1354G>A	exonic	8	nonsynonymous	p.Ala452Thr						

Voir les annotations pour un variant

External databases		HGVS nomenclature		Quality	
dbSNP	rs146571352	RefSeqGene	NG_033012.1	Observed allele 1 depth	18
dbSNP validated	yes	HGVS cDNA-level nomenclature	NM_033109.5:c.1525G>A	Observed allele 2 depth	30
dbSNP average heterozygosity	0.001	HGVS genomic-level nomenclature	NC_000002.11:g.55874559C>T	Allelic depth	C = 18
dbSNP suspect false snp	no	HGVS protein-level nomenclature	NP_149100.2:p.Val509Ile		T = 30
dbSNP clinical significance	Likely pathogenic			Call quality	1376.16
ClinVar Id	209185, 209185, 209185, 209185			Genotype quality	99
ClinVar clinical significance	probable-pathogenic, other, other, unknown			Filter status	PASS
ClinVar disease	Combined oxidative phosphorylation deficiency 13, not specified, not provided, Hypermetropia	Population		Conservation	
COSMIC Id	COSM7384835	ESP6500 allele frequency	15/13006=0.001	GERP++ neutral rate	5.53
COSMIC sample count	2	ESP65000 genotype frequency	15/6503=0.002	GERP++ RS score	5.53
COSMIC tumor type (sample count)	Pulmonary adenocarcinoma - non-small cell lung cancer (NSCLC) (1)	ExAC allele frequency	91/121358=0.001	PhyloP score	0.871
		gnomAD allele frequency	262/276804=0.001	SiPhy score	19.811
		gnomAD genotype frequency	258/138402=0.002		
Substitution		Coding		Missense	
MutationTaster score	1	LRT score	0	BLOSUM45	3
MutationTaster prediction	Disease causing	LRT prediction	Deleterious	BLOSUM62	3
MutationAssessor score	0.625	LRT omega	0	BLOSUM80	3
MutationAssessor prediction	Neutral			SIFT score	0.136
FATHMM Score	0.56			PolyPhen2 score HumDiv	0.992
				PolyPhen2 score HumVar	0.867
				PolyPhen2 prediction HumDiv	Probably damaging
				PolyPhen2 prediction HumVar	Possibly damaging
				PROVEAN Score	-0.83
				PROVEAN prediction	Neutral
Splice		Custom fields		Repetitive regions	
Positions from nearest splice site	30	No annotations found.		No annotations found.	

Voir les infos pour un gene

Gene	Position	Ref	Patient	Read Depth	Inheritance mode	Inh. from	Family		Read Depth		CNV	Type	Transcript	cDNA	Location	Exon	Effect	Protein	CT Labels	External Databases	Simil.	Info	Classification	Asses
							Mother	Father	Mother	Father														
<input type="checkbox"/> PNPT1	2:55,874,559			48	Comp. Het. cand.	♀			47	41		snp	NM_033109.5	c.1525G>A	exonic	19	nonsynonymous	p.Val509Ile						

Gene Info		Gene-Disease Relationships		HPO phenotype traits	
HGNC Symbol	PNPT1	OMIM® Morbid gene MIM	610316	Abnormal corpus callosum morphology	
Gene name	polyribonucleotide nucleotidyltransferase 1	OMIM® Morbid phenotype	Combined oxidative phosphorylation deficiency 13, 614932 (3), Autosomal recessive	Abnormal corpus striatum morphology	
Synonyms	PNPase, OLD35, old-35		Deafness, autosomal recessive 70, 614934 (3), Autosomal recessive	Absent speech	
Ensembl ID	ENSG00000138035	NCBI gene ID	87178	Ankle flexion contracture	
Chromosomal location	2p16.1	ClinVar disease	Deafness, autosomal recessive 70 C1824925, NCBI curation	Autosomal recessive inheritance	
Genomic location	2:55 861 196-55 920 980		Combined oxidative phosphorylation deficiency 13 C3554129, NCBI curation	Cataract	
Strand	-		Combined oxidative phosphorylation deficiency CN228601, OMIM (PS609060)	Show all	
Biotype	gene with protein product	Cancer Gene Census		ClinGen Dosage Sensitivity Map	
				No annotations found.	

Flag human annotation

Cliquer sur n'importe quelle étape de la stratégie permet d'ajouter une catégorie, d'ajouter ces variants aux panier. Permet d'identifier où l'utilisateur intervient.

Output bin: No match (HPO Phenotype) ✕

Labels

Category Label ✕

Category Label ✕

Category Label ✕

Category Label ✕

✕ Clear all

Scoring

Score contribution

✕ Clear

Review

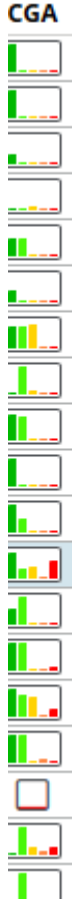
Mark for review

Save Cancel



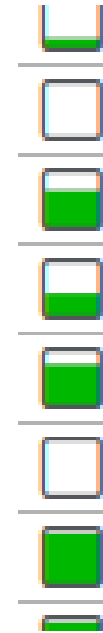
ACMG representation

Proportion of ACMG classes in th regions :
Benign : 10%
Likely benign : 10 %
...
Pathogenic : 50%



Coverage of regions

- % of coverage of the element :
- Not only 0, 50, 100%



Interface de filtre pas top

Configure filter [X]

Location

- exonic
- UTR5
- UTR3
- intronic
- upstream
- downstream
- intergenic
- ncRNA_exonic
- ncRNA_UTR5
- ncRNA_UTR3
- ncRNA_intronic
- Not specified

Read Depth >=

Marked for review

Included in report

Type

- snp
- deletion
- insertion
- substitution
- reference
- Not specified

Effect

- frameshift
- stopgain
- stoploss
- startloss
- inframe
- nonsynonymous
- synonymous
- Not specified

Zygosity

- Homozygous var / var
- Heterozygous wt / var
- Heterozygous var x / var y
- Hemizygous

Classification

- Benign
- Likely benign
- VOUS
- Likely pathogenic
- Pathogenic
- Not classified

Inheritance mode

- Dominant
- Recessive
- Compound Heterozygous candidate
- Inherited - Unresolved
 - Exclude variants that are present as homozygous (*) in an unaffected parent or sibling (*including hemizygous for non-PAR X-linked or Y-linked variants in an unaffected father*)
 - Exclude variants that are not present in an affected parent or sibling
- Mendelian Violation
 - Exclude variants that are present in an unaffected parent or sibling
- Uncertain

Parent genotype

- Only display variants for which the genotype of both parents is available in the input data

[Apply filter] [Clear filter] [Cancel]

Le panier = variant review

Affiner la définition du panier. Ici human manageable variant list. Ajout d'informations tel que la classification les commentaires l'interprétation.

Mais surtout ajout au rapport du variant classification finale.

The screenshot displays a web interface for variant review, organized into several sections:

- Navigation:** Tabs for "General", "Variant triage", "Variant review" (active), and "Reports".
- Variant List:** A sidebar with a "Filter" icon and a list of variants. The selected variant is "c.1354G>A p.Ala452Thr" under the "INTU" gene. Other variants include "c.880G>C p.Asp294His" (MC1R), "c.1525G>A p.Val509Ile" (PNPT1), and "n.784G>A" (TANGO2).
- Variant Details:** Shows "INTU c.1354G>A p.Ala452Thr" with a "Variant change history" link. It includes dropdown menus for "Classification" and "Include in report".
- Gene Information:** A tabbed section with "Gene information" selected. It lists:
 - HGNC Symbol:** INTU
 - Gene name:** inturned planar cell polarity protein
 - Synonyms:** KIAA1284, CPLANE4
 - Ensembl ID:** ENSG00000164066
 - Chromosomal location:** 4q28.1
 - Genomic location:** 4:128 554 112-128 647 893
 - Strand:** +
 - Biotype:** gene with protein product
- Report Abstract:** A section with an "Edit" icon.
- Analysis assessment:** A section with tabs for "Findings", "Recommendations" (active), and "Remarks". It includes an "Analysis assessment change history" link.