

# International course: Training on strategies to foster solutions of undiagnosed rare disease cases

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Polyweb : a Framework to analyse resequencing data

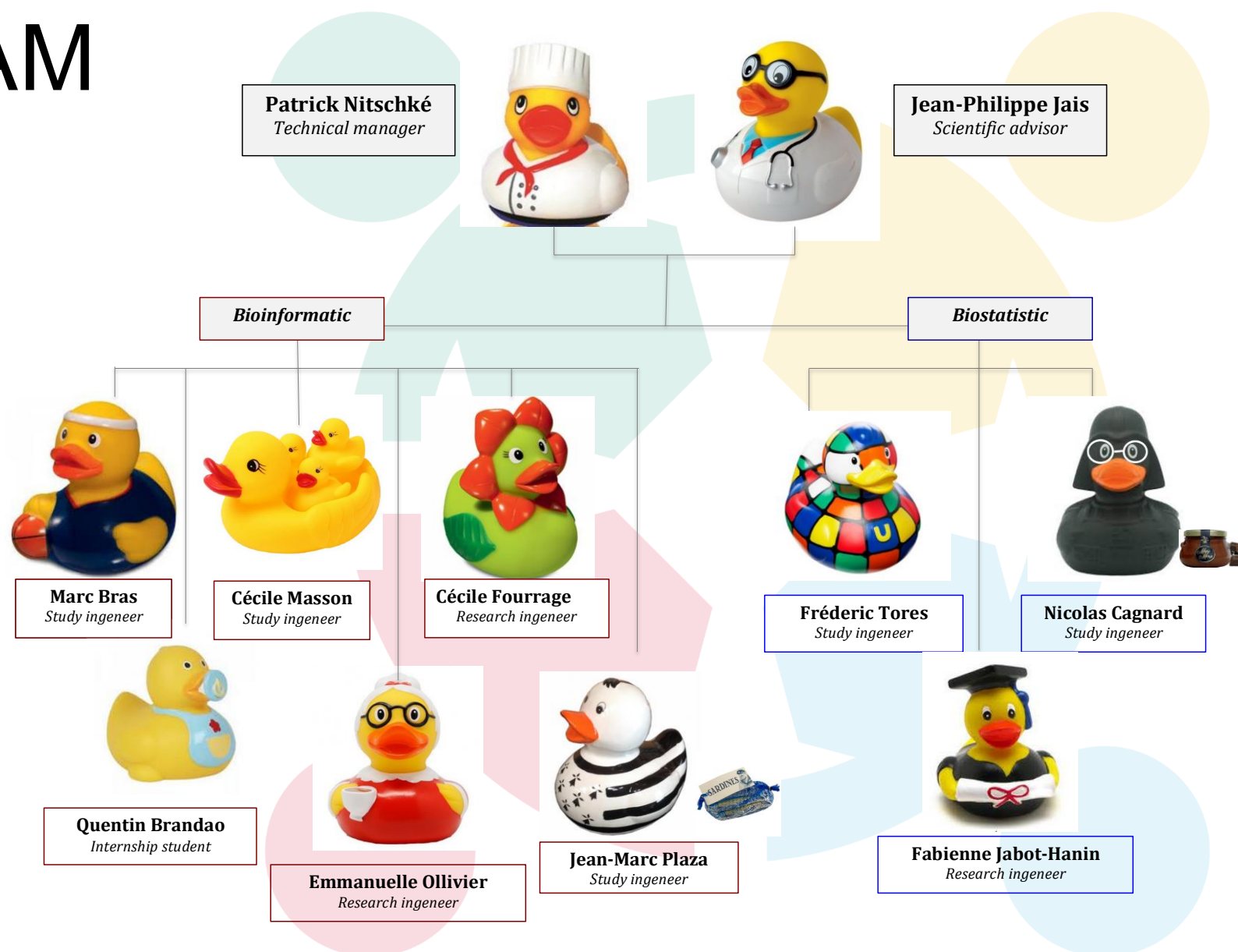
*Patrick Nitschké*



*Organised by National Centre for Rare Disease,  
Istituto Superiore di Sanità, Rome (Italy), April 27-29, 2020*

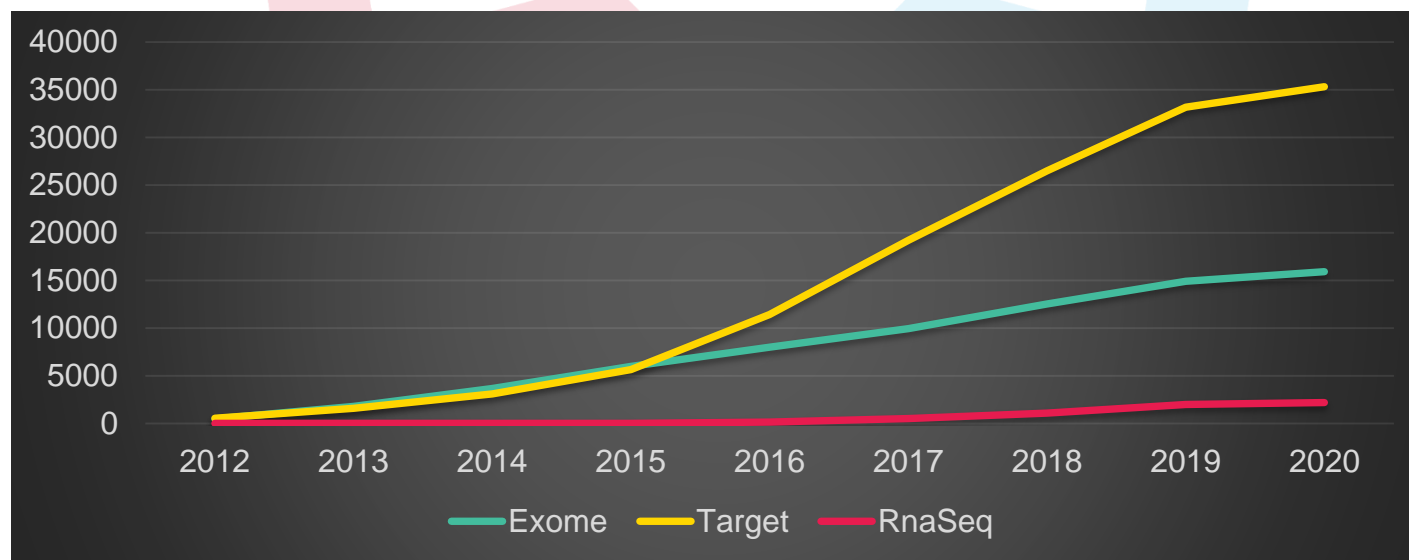


# TEAM

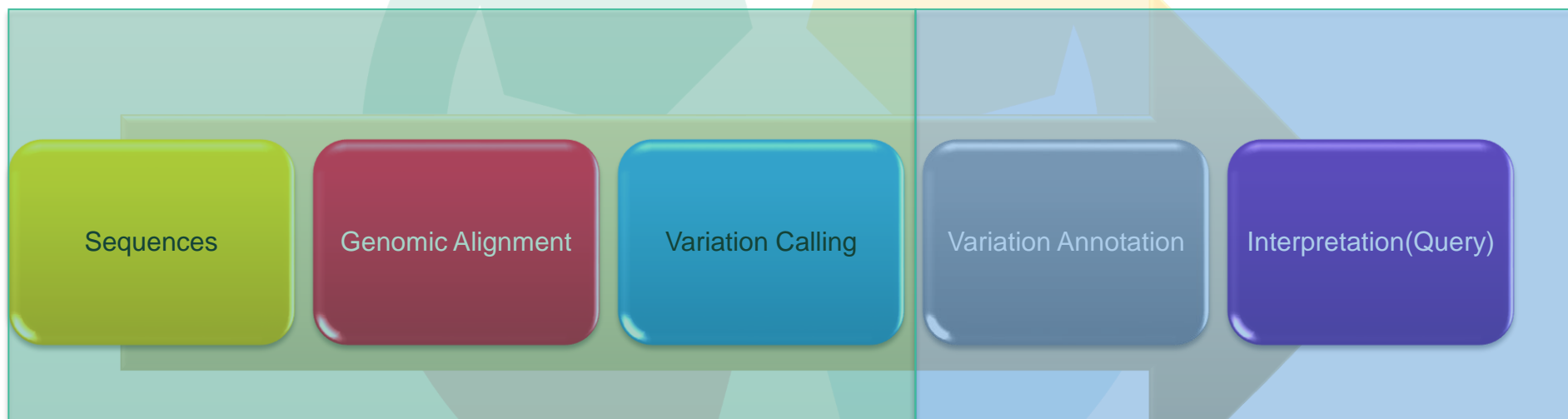


# Sequencing project

	2012	2013	2014	2015	2016	2017	2018	2019	2020	Total
Exomes	500	1300	1860	2325	2029	1945	2567	2405	1000	15932
Genomes				35	100(30)	225	124	228	405	1147
Target	556	1036	1519	2542	5764	7808	7257	6707	2354	33189
RnaSeq	-	-	-	-	151	370	573	913	200	2207



# Target resequencing Pipeline



# Polyweb

**imagine**  
INSTITUT DES MALADIES GÉNÉTIQUES

Welcome to PolyWeb  
Imagine – Paris Descartes

 UNIVERSITÉ  
PARIS DESCARTES



POLYQUERY

*Explore Exome/Genome  
(soon) project*



POLYDIAG

*Explore Genes target  
project*



POLYDEJAVU

*Explore "Dejavu"  
database*



POLYLINKAGE

*Explore "Linkage" project*



POLYPROJECTLINK






POLYRUN



POLYPROJECT



POLYMONOP

	 <b>POLYQUERY</b> <i>Explore Exome/Genome (soon) project</i>	 <b>POLYDIAG</b> <i>Explore Genes target project</i>	 <b>POLYDEJAVU</b> <i>Explore "Dejavu" database</i>
<b>Project Type</b>	Exomes and Full Genomes	Panels of genes	Variants Data Base
<b>Objective:</b>	Identification of new genes of interest related to a pathology → Approach by gene	Identification of causal mutations → Approach by patient	Query on all variants encountered in PolyWeb projects
<b>Purpose</b>	Research	Diagnostic	Minning

Déjà VU : 1500-16 000 – 35 000- 51 170 595

# PolyDiag

**imagine**  
INSTITUT DES MALADIES GÉNÉTIQUES

Welcome to PolyWeb  
Imagine – Paris Descartes

 UNIVERSITÉ  
PARIS DESCARTES



POLYQUERY

*Explore Exome/Genome  
(soon) project*



POLYDIAG

*Explore Genes target  
project*



POLYDEJAVU

*Explore "Dejavu"  
database*



POLYLINKAGE

*Explore "Linkage" project*



POLYPROJECTLINK

*Linkage project*



POLYRUN

*PolyRun*



POLYPROJECT

*Ngs project database*

POLYDIAG

1 SAMPLES

NGS1020\_1048

10-20-2020

AMPLIFICATION

1042043\_NG15

TRANSCRIPTS

572

RUN

1

SAMPLES

35

Project

Genes

Patients

Coverage

CNVs

Variations Editor

ToDo

refresh

report selected

print selected

Compose Report

clinvar

20191007

gnomad

2.1

hgms

2019.3

cds

1.4

gencode

19

run70\_IDEFIX-EDF-V3S31\_XTHS—IdFix-V3\_hg19—agilent

NOVASEQ

10/01/20

10/01/20

Cov :300.3 (300.3 ± 36)

15X :99.9% (99.9)

30X :99.9% (99.9)

HQ19

Print

Gender control 0

Quality Control 0

Mendelian Control

Control (Blanc)

Regions Dups 7

	Fun	view	Print	Patient	Cov	30x	validation
BUI		View	Print	BUI_Myr	335.5	99.7	-
		View	Print	BUI_Jea	277.8	99.5	-
		View	Print	BUI_Am	268.2	99.5	-
CRO		View	Print	CRO_Cec	299.5	99.5	-
		View	Print	CRO_Vin	229.1	99.4	-
		View	Print	CRO_Pau	353.5	99.7	-
ROT		View	Print	ROT_Mic	311.5	99.8	-
		View	Print	ROT_Jea	333.8	99.7	-
		View	Print	ROT_Mar	251.8	99.5	-
THO		View	Print	THO_Dom	289	99.5	-
		View	Print	THO_Pie	394.8	99.5	-
		View	Print	THO_Ben	271.2	99.5	-
		View	Print	ZIA_had	342	99.7	-



# Quality Control

♂/♀ Gender control 0

🚨 Quality Control 0

👤 Mendelian Control

✍ Control (Blanc)

📍 Regions Dups 7

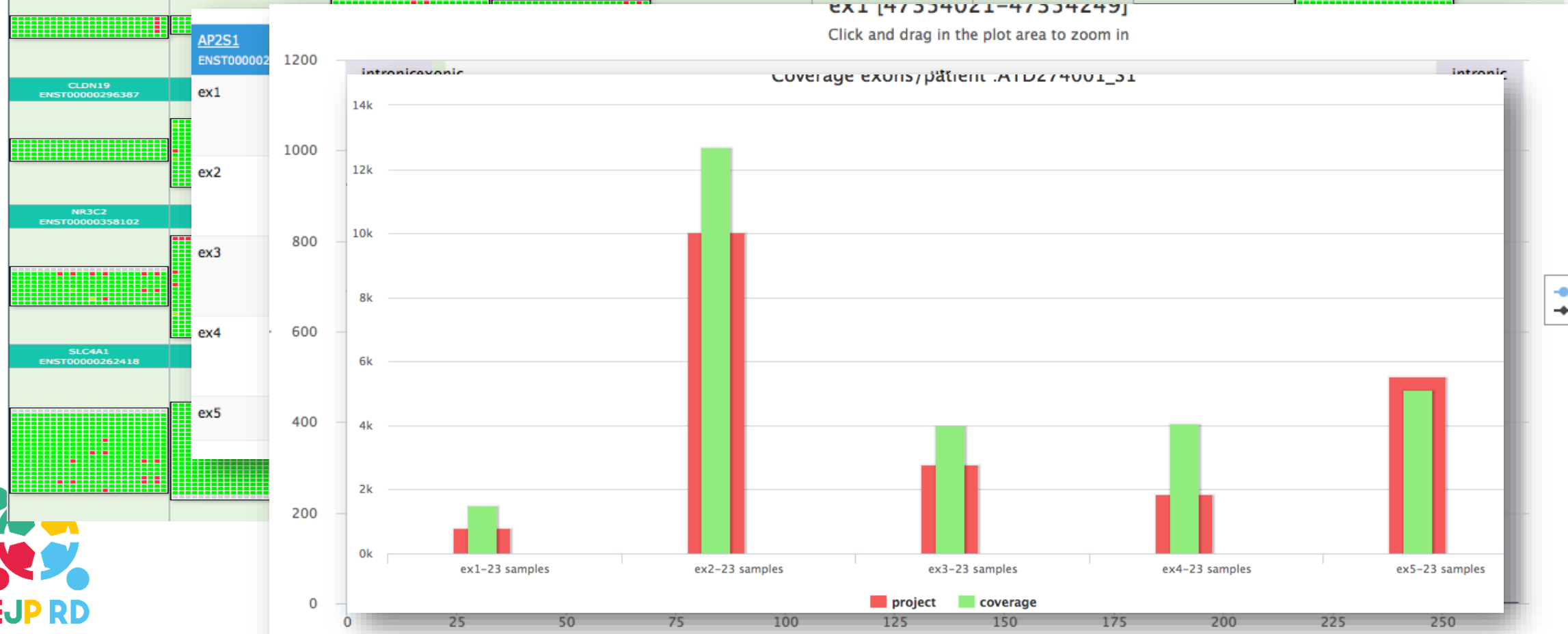
ALP1909218	ALP2000061	ALP2000134	ALP2000211	ALP2000260	ALP2000297	ALP2000306	ALP2000424	ALP2000433	ALP2000493	ALP2000499	ALP783	DYS261
<div><div>● mean 1016 (839.5)</div><div>● 15X 99.3 (99.3)</div><div>● 30X 99.2 (99.3)</div><div>● 100X 99.1 (99.1)</div><div>● snp 3914 (3848.5)</div><div>● indel 1160 (1128.4)</div><div>● %he 64 (61)</div><div>● %public 92 (92)</div></div>	<div>ALP1907098</div> <div><div></div><div>SRY : ● ♂ (485.7)</div><div>IV 233222113213312</div></div>	<div>ALP1907446</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 323121113231213</div></div>	<div>ALP1907553</div> <div><div></div><div>SRY : ● ♂ (527.5)</div><div>IV 112213221213231</div></div>	<div>ALP1907554</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 123231233313333</div></div>	<div>ALP1907620</div> <div><div></div><div>SRY : ● ♀ (0.4)</div><div>IV 311131323311233</div></div>	<div>ALP1907627</div> <div><div></div><div>SRY : ● ♂ (453.6)</div><div>IV 321333132323312</div></div>	<div>ALP1907745</div> <div><div></div><div>SRY : ● ♀ (0.2)</div><div>IV 223231123313333</div></div>	<div>ALP1907823</div> <div><div></div><div>SRY : ● ♂ (493.5)</div><div>IV 113332133233133</div></div>	<div>ALP1907997</div> <div><div></div><div>SRY : ● ♂ (498.5)</div><div>IV 122123112213332</div></div>	<div>ALP1908373</div> <div><div></div><div>SRY : ● ♀ (0.3)</div><div>IV 122213313313333</div></div>		
<div><div>● mean 600.1 (839.5)</div><div>● 15X 99.3 (99.3)</div><div>● 30X 99.2 (99.3)</div><div>● 100X 99.1 (99.1)</div><div>● snp 3695 (3848.5)</div><div>● indel 1106 (1128.4)</div><div>● %he 59 (61)</div><div>● %public 93 (92)</div></div>	<div>DYS1907348</div> <div><div></div><div>SRY : ● ♀ (2.2)</div><div>IV 331222333212311</div></div>	<div>DYS1907349</div> <div><div></div><div>SRY : ● ♂ (276.3)</div><div>IV 133322333212313</div></div>	<div>HYP1601784</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 333313322123233</div></div>	<div>HYP1906219</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 111123211133331</div></div>	<div>HYP1906220</div> <div><div></div><div>SRY : ● ♀ (0.4)</div><div>IV 113321231323331</div></div>	<div>HYP1906221</div> <div><div></div><div>SRY : ● ♂ (240.4)</div><div>IV 313323331111333</div></div>	<div>HYP1907065</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 323231122331331</div></div>	<div>HYP1907066</div> <div><div></div><div>SRY : ● ♂ (272.7)</div><div>IV 123232332213333</div></div>	<div>HYP1907157</div> <div><div></div><div>SRY : ● ♂ (483.3)</div><div>IV 321223322233133</div></div>	<div>HYP1907350</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 132332231313333</div></div>		
	<div>HYP1907590</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 12332332322212</div></div>	<div>HYP1907591</div> <div><div></div><div>SRY : ● ♂ (318.3)</div><div>IV 122321333332233</div></div>	<div>HYP1907592</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 121323233223333</div></div>	<div>HYP1907604</div> <div><div></div><div>SRY : ● ♀ (0.5)</div><div>IV 331323333223333</div></div>	<div>HYP1907989</div> <div><div></div><div>SRY : ● ♂ (454.4)</div><div>IV 112331333233331</div></div>	<div>HYP1907993</div> <div><div></div><div>SRY : ● ♂ (465.4)</div><div>IV 123123232332231</div></div>	<div>HYP1908004</div> <div><div></div><div>SRY : ● ♂ (508.5)</div><div>IV 113232221331313</div></div>	<div>HYP1908095</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 333323331313312</div></div>	<div>HYP1908096</div> <div><div></div><div>SRY : ● ♀ (0)</div><div>IV 333231333311312</div></div>	<div>HYP1908097</div> <div><div></div><div>SRY : ● ♂ (259.3)</div><div>IV 213231112111132</div></div>		
									<div><div>● mean 1000 (839.5)</div><div>● 15X 99.2 (99.3)</div><div>● 30X 99.2 (99.3)</div><div>● 100X 99.1 (99.1)</div><div>● snp 3522 (3848.5)</div><div>● indel 985 (1128.4)</div><div>● %he 57 (61)</div><div>● %public 92 (92)</div></div>	<div><div>● mean 564.3 (839.5)</div><div>● 15X 99.3 (99.3)</div><div>● 30X 99.3 (99.3)</div><div>● 100X 99.1 (99.1)</div><div>● snp 3476 (3848.5)</div><div>● indel 1010 (1128.4)</div><div>● %he 56 (61)</div><div>● %public 93 (92)</div></div>		

# Coverage

Project
Genes
Patients
**Coverage**
CNVs
Variations Editor
ToDo

ACMG-Defidiag
sort by name
save
refresh
☒ only genes below limit

AP2S1 ENST00000263270	AQP2 ENST00000199280	ATP6V0A4 ENST00000310018	ATP6V1B1 ENST00000234396	AVPR2 ENST00000337474	BSND ENST00000371265	CASR ENST00000490131	CLCN5 ENST00000376108	CLCNKB ENST00000375679	CLDN16 ENST00000264
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gnomAD Ho Allele Count

5

10

20

50

100

All

Impact

High

Medium

Low

☒ Mature miRNA
 ☒ Splice Acc/Don
 ☒ Frameshift
 ☒ Stop-gained
 ☒ (Start/Stop)-lost

☒ Splice Region
 ☒ Missense
 ☒ No-frameshift
 ☐ ncRNA
 ☐ Pseudogene

☐ Utr
 ☐ Synonymous
 ☐ Up/Downstream
 ☐ Intronic

% Ratio

80

40

20

10

all

☐ Strict-Denovo
 ☐ Denovo
 ☐ Recessif

☐ Father or Mother (Composite)
 ☐ Both Parents

All Genes

- GEF1900228

GEF2000050

GEF2000090

GEF2000104

GEF2000115

GEF2000040

GEF2000041

GEF2000091

GEF2000092

GEF2000105

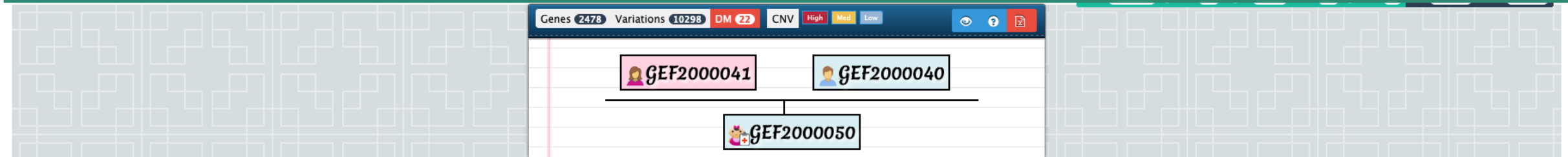
GEF2000106

GEF2000107

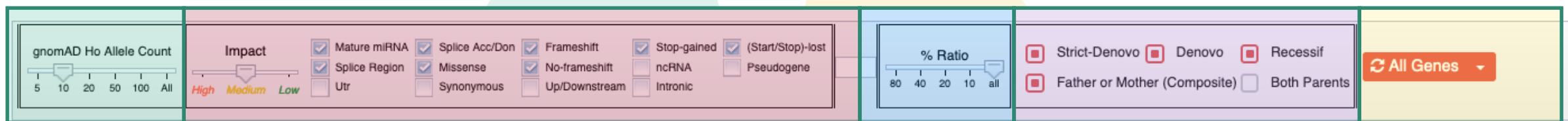
GEF2000108

GEF2000116

GEF2000117



# Variation filtering



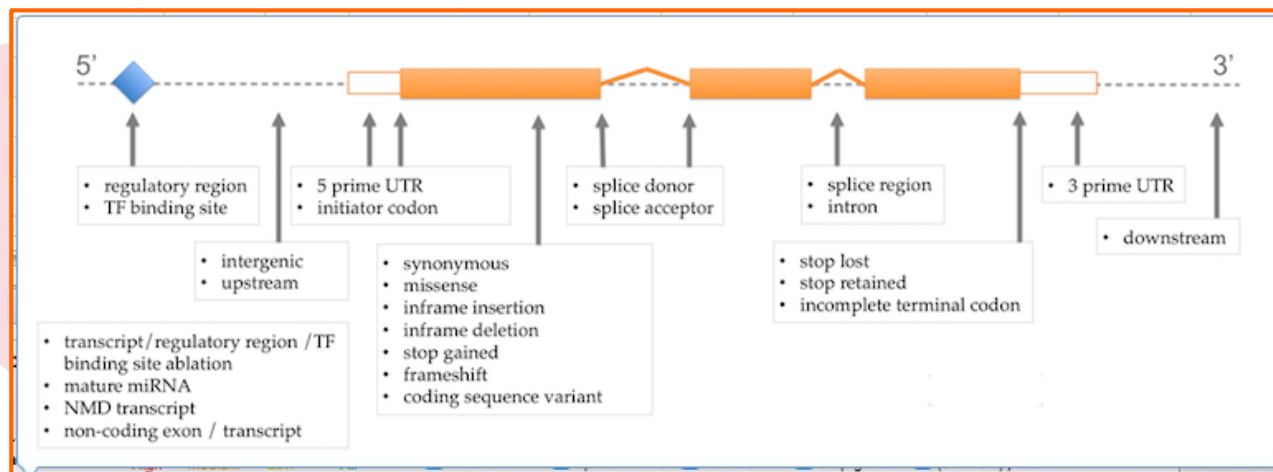
1- Frequency base on gnomad “homozygous allele count”

2-Impact

3-Allelique Ratio

4- Transmission Mode

5- Gene List



gnomAD Ho Allele Count



Impact



- ☒ Mature miRNA  
☒ Splice Region  
☐ Utr  
☒ Splice Acc/Don  
☒ Missense  
☐ Synonymous  
☒ Frameshift  
☒ No-frameshift  
☐ Up/Downstream  
☒ Stop-gained  
☐ ncRNA  
☐ Intronic  
☒ (Start/Stop)-lost  
☐ Pseudogene

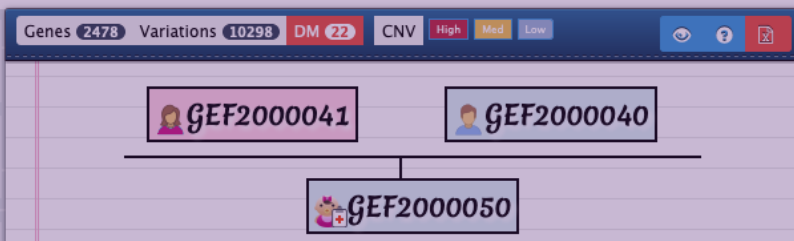
% Ratio



- ☐ Strict-Denovo  
☐ Denovo  
☐ Recessif  
☐ Father or Mother (Composite)  
☐ Both Parents

All Genes

GEF1900228 x GEF2000050 x GEF2000090 x GEF2000104 x GEF2000115 x GEF2000040 x GEF2000041 x GEF2000091 x GEF2000092 x GEF2000105 x GEF2000106 x GEF2000107 x GEF2000108 x GEF2000116 x GEF2000117

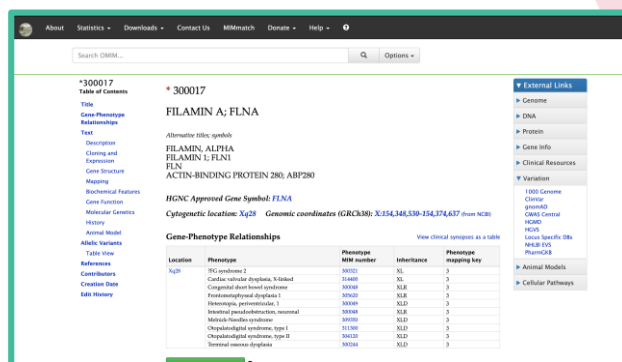


<div><div></div><div>RAB3GAP2</div><div>recessive</div></div>	Omim	Gtex	12.4	Panel : 12	● Ens: martsolf syndrome	<div><div></div><div>1</div><div></div><div></div><div></div><div>CNV</div></div>
<div><div></div><div>PC</div><div>recessive</div></div>	Omim	Gtex	12.1	Panel : 5	● Ens: pyruvate carboxylase deficiency	<div><div></div><div>2</div><div></div><div></div><div></div><div>CNV</div></div>
<div><div></div><div>ADPGK</div><div></div></div>	Omim	Gtex	11.7	Panel : 0	● ADP dependent glucokinase	<div><div></div><div>1</div><div></div><div></div><div></div><div>CNV</div></div>
<div><div></div><div>KMT2C</div><div>dominant</div></div>	Omim	Gtex	11.2	Panel : 6	● Ens: kleeftstra syndrome 2	<div><div></div><div>5</div><div></div><div></div><div></div><div>CNV</div></div>
<div><div></div><div>TDRD1</div><div></div></div>	Omim	Gtex	9.9	Panel : 0	● tudor domain containing 1	<div><div></div><div>1</div><div></div><div></div><div></div><div>CNV</div></div>
<div><div></div><div>BCL6</div><div></div></div>	Omim	Gtex	9.7	Panel : 0	● Ens: follicular lymphoma	<div><div></div><div>1</div><div></div><div></div><div></div><div>CNV</div></div>
<div><div></div><div>ADAMTSL3</div><div></div></div>	Omim	Gtex	9.7	Panel : 0	● ADAMTS like 3	<div><div></div><div>1</div><div></div><div></div><div></div><div>CNV</div></div>
<div><div></div><div>MEAK7</div><div></div></div>	—	Gtex	9.7	Panel : 0	● MTOR associated protein, eak-7 homolog	<div><div></div><div>1</div><div></div><div></div><div></div><div>CNV</div></div>

# Informations panel

The screenshot displays the GeneRanker interface with a list of genes. A red arrow points to the 'GPA1' gene entry, which is highlighted in green. The interface includes columns for gene names, inheritance patterns, and clinical significance, along with interactive icons for each entry.

Gene	Inheritance	Score	Panel	Ensembl ID
FLNA	X-linked	16.4	8	cardiac valvular dysplasia x-linked
TBL1XR1	dominant	15.6	8	mental retardation autosomal dominant 41
GPA1	recessive	15.1	5	glycosylphosphatidylinositol biosynthesis defect 15
FIG4	recessive dominant	14.4	5	amyotrophic lateral sclerosis 11



# Score

## Variation

- Transmission
- Frequency public + dejavu
- Clinvar + local DB + (HGMD)
- Impact
- Prediction Score

## Gene

- Phenotypes
  - Panels (DI: Imagine+PanelApp+SysID+Decipher)
  - Pli

# Variations Panels

▼ FLNA X-linked

16.4

Omim

Gtex

1

Panel : 8

● Ens: cardiac valvular dysplasia x-linked

⚠

1

☰

✎

CNV

varsome	igv	alamut	var_name	trio						gnomad						deja_vu			validations		transcripts																										
<div>V</div>			X-153578221-A-G	ABO_RAC	👤	he	60%	152	+	AC	Ho	♂	Max	Min	AN	other	Pr	Sa	Ho	HGMD	Clinvar	Defidiag	consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv											
				BOU_MOH	👤	-	-	96	-	-	-	-	-	-	0		0	0	Missense				ENST00000369850	NM_001110556	CCDS48194	P1	46	c.7348T>C	TTC/CTC	F2450L	0.959	0	29	0.91	-	-											
				BOU_SAM	👤	ho	100%	76	Recessive	-	-	-	-	-	DI		0	0	0				Missense	ENST00000422373	NM_001456	CCDS44021	-	45	c.7324T>C	TTC/CTC	F2442L	0.947	0	29	0.91	-	-										
																							Missense	ENST00000610817			-	42	c.6352T>C	TTC/CTC	F2118L	0.999	1	29	0.91	-	-										
																Missense	ENST00000369856			-	45	c.7267T>C	TTC/CTC	F2423L	0.959	0	29	0.91	-	-																	
																																+ view 1 Transcripts															

-

⬆

⬇

⬆

TBL1XR1 dominant

15.6

Omim

Gtex

0.99

Panel : 8

Ens: mental retardation autosomal dominant 41

1

≡

CNV

varsome	igv	alamut	var_name	trio					gnomad					deja_vu			validations			transcripts														
V			3-176763977-T-G	ABO_RAC		-	-	50	-	AC	Ho	Max	Min	AN	Pr	Sa	Ho	HGMD	Clinvar	Defidiag	consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv
				BOU_MOH		-	-	44	-	-	-	-	-	other	0	0	0				Splice Region, Missense	ENST00000430069	NM_001321195	CCDS46961	P1	10	c.865A>C	ACT/CCT	T289P	0.972	0	33	0.87	0.67
				BOU_SAM		he	50%	46	Strict Denovo	-	-	-	-	-	DI	0	0				0													
																					+ view 1 Transcripts													

-

⬇

▼

GPAA1

recessive

15.1

Omim

Gtex

0

Panel : 5

● Ens: glycosylphosphatidylinositol biosynthesis defect 15

1

# Variations Panels : External Viewer

varsome	igv	alamut	var_name	trio						gnomad						deja_vu			validations		transcripts																
<div>V</div> <div></div> <div></div> <div>X-153578221-A-G</div>				ABO_RAC		he	60%	152	+	AC	Ho	♂	Max	Min	AN	Pr	Sa	Ho	HGMD	Clinvar	Defdiag	consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv		
				BOU_MOH		-	-	96	-	-	-	-	-	-	-	-	0	0	0	-	-	-	Missense	ENST00000369850	NM_001110556	CCDS48194	P1	46	c.7348T>C	TTC/CTC	F2450L	0.959	0	29	0.91	-	-
				BOU_SAM		ho	100%	76	Recessive	-	-	-	-	-	-	-	0	0	0	-	-	-	Missense	ENST00000422373	NM_001456	CCDS44021	-	45	c.7324T>C	TTC/CTC	F2442L	0.947	0	29	0.91	-	-
																	0	0	0				Missense	ENST00000610817			-	42	c.6352T>C	TTC/CTC	F2118L	0.999	1	29	0.91	-	-
																	0	0	0				Missense	ENST00000369856			-	45	c.7267T>C	TTC/CTC	F2423L	0.959	0	29	0.91	-	-
+ view 1 Transcripts																																					

varsome X-153578221-A-G

chrX-153578221-A-G

varsomeclinical A clinical-grade Platform for Interpretation of NGS Data

Variant

Chromosome: chrX Position: 35,357,821 Ref Sequence: A ALT Sequence: G Variant type: SNV Cytosine: N/A HGVS: NM\_001110556.2:c.7348T>C (p.Pro1549Leu) Gene symbol: FLNA

This variant has been viewed 2 times on VarSome.

Connect with past and future viewers of this variant.

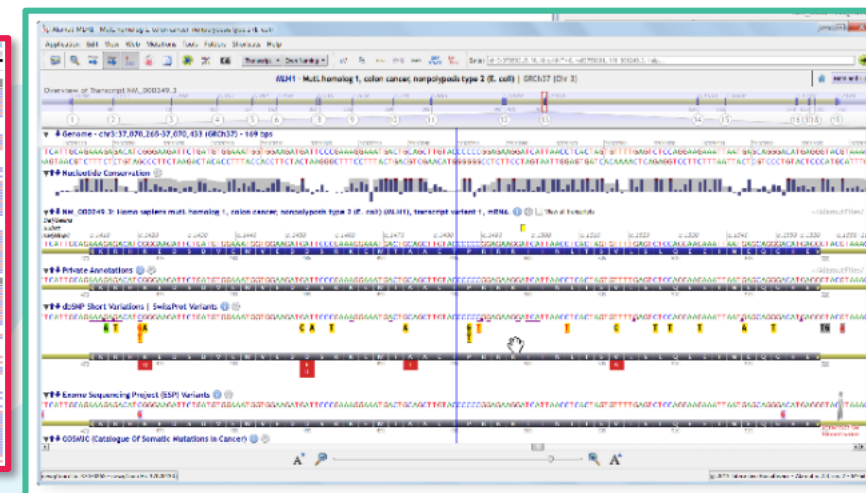
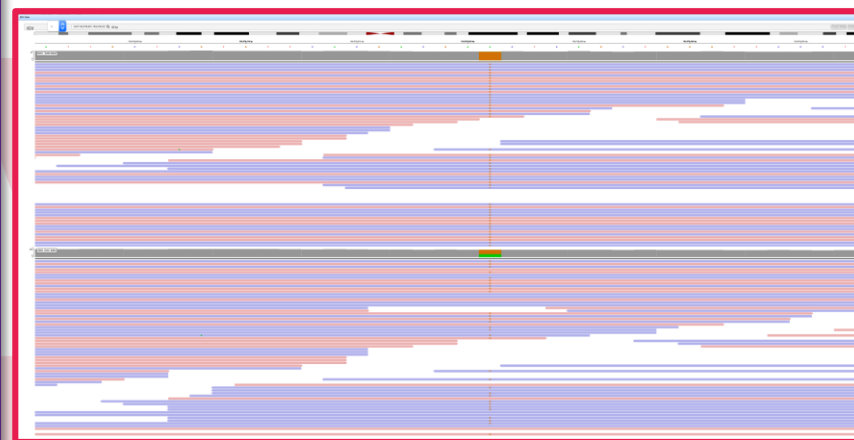
ACMG Classification - Educational use only. Version 4.2.1

Verdict: Uncertain Significance

Rules

Automated criteria

Rule	Pathogenicity	Explanation
PP2	Pathogenic	Variant not found in ClinVar
PP3	Pathogenic	Pathogenic computational prediction based on 9 pathogenic predictions from DANN, DEGENZ, FATMAN, FATHMM, FATHMM-MKL, FATHMM-PKL, FATHMM-RF, MutationAssessor, MutationTaster, REVEL, and SIFT
BP1	Benign	83 out of 127 non-VUS missense variants in gene FLNA are benign = 65.4% which is more than threshold of 50%, and 443 out of 1040 clinically reported variants in gene FLNA are benign = 42.6% which is more than threshold of 24.0%.



# Variations Panel : Transmission Mode

varsome	igv	alamut	var_name	trio	gnomad	deja_vu	validations	transcripts											
				<div><div>ABO_RAC</div><div>he60%152</div><div>+</div></div> <div><div>BOU_MOH</div><div>-96</div><div>-</div></div> <div><div>BOU_SAM</div><div>ho100%76</div><div>Recessive</div></div>	<div><div>C</div><div>Ho</div><div>♂</div><div>Max</div><div>Min</div><div>AN</div></div> <div><div>-</div><div>-</div><div>-</div><div>-</div><div>-</div><div>-</div></div>	<div><div>Pr</div><div>Sa</div><div>Ho</div></div> <div><div>other</div><div>000</div></div> <div><div>DI</div><div>000</div></div>	<div><div>HGMD</div><div>Clinvar</div><div>Defdiag</div></div> <div><div>-</div><div>-</div><div>-</div></div>	<div><div>consequence</div><div>enst</div><div>nm</div><div>ccds</div><div>appris</div><div>exon</div><div>nomenclature</div><div>codons</div><div>codons_AA</div><div>polyphen</div><div>sift</div><div>cadd</div><div>revel</div><div>dbcsnv</div></div> <div><div>Missense</div><div>ENST00000369850</div><div>NM_001110556</div><div>CCDS48194</div><div>P1</div><div>46</div><div>c.7348T&gt;C</div><div>TTC/CTC</div><div>F2450L</div><div>0.959</div><div>0</div><div>29</div><div>0.91</div><div>-</div><div>-</div></div> <div><div>Missense</div><div>ENST00000422373</div><div>NM_001456</div><div>CCDS44021</div><div>-</div><div>45</div><div>c.7324T&gt;C</div><div>TTC/CTC</div><div>F2442L</div><div>0.947</div><div>0</div><div>29</div><div>0.91</div><div>-</div><div>-</div></div> <div><div>Missense</div><div>ENST00000610817</div><div></div><div></div><div>-</div><div>42</div><div>c.6352T&gt;C</div><div>TTC/CTC</div><div>F2118L</div><div>0.999</div><div>1</div><div>29</div><div>0.91</div><div>-</div><div>-</div></div> <div><div>Missense</div><div>ENST00000369856</div><div></div><div></div><div>-</div><div>45</div><div>c.7267T&gt;C</div><div>TTC/CTC</div><div>F2423L</div><div>0.959</div><div>0</div><div>29</div><div>0.91</div><div>-</div><div>-</div></div> <div><div>+ view 1 Transcripts</div></div>											

## Recessive

GEF2000107		he	45%	131	+
GEF2000108		he	52%	102	+
GEF1900228		ho	99%	135	Recessive

## Denovo

GEF2000107		-	-	123	-
GEF2000108		-	-	95	-
GEF1900228		ho	94%	17	Denovo

## Mosaic Parental

835_M		he	13%	149	+
835_P		-	-	129	-
835		he	50%	119	mosaic mother

## Compound

GEF2000107		he	49%	179	+
GEF2000108		-	-	195	-
GEF1900228		he	53%	143	

GEF2000107		-	-	164	-
GEF2000108		he	52%	191	+
GEF1900228		he	46%	175	

## Strict-Denovo

NCR4635_BIEM_F		-	-	62	-
NCR4634_BIEM_3P		-	-	45	-
NCR4452_BIEM_PH		he	55%	63	Strict Denovo

## Unisomy Uniparental

MIL_Mam		he	44%	75	+
MIL_Pap		-	-	81	-
MIL_Pil		ho	100%	49	Uniparental

MIL_Mam		he	30%	129	+
MIL_Pap		he	35%	160	+
MIL_Pil		he	33%	118	

# Heterozygous Compound

10.5

GBA2 recessive

Omim

Gtex

0.01

Panel : 5

Ens: spastic paraplegia 46 autosomal recessive

2

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✎

CNV

varsome	igv	alamut	var_name	trio			gnomad					deja_vu			validations			transcripts																				
V			9-35737716-G-A	ABO_RAC	he	52%	164	AC	Ho	Max	Min	AN	Pr	Sa	Ho	HGMD	Clinvar	Defidiag	consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv						
				BOU_MOH	-	-	168	81	-	oth	afr	282706	20	27	1				-	-	-	Missense	ENST00000378088	-	-	-	-	2	c.437C>T	ACC/ATC	T146I	0.009	0.01	7	0.03	-		
				BOU_SAM	he	57%	129																															
												+ view 2 Transcripts																										
V			9-35738063-C-T	ABO_RAC	-	-	96	AC	Ho	Max	Min	AN	Pr	Sa	Ho	HGMD	Clinvar	Defidiag	consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv						
				BOU_MOH	he	50%	104																															
				BOU_SAM	he	44%	93																															
																								consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv	
																								Missense	ENST00000378103	NM_020944	CCDS6589	P3	15	c.2284G>A	GCC/ACC	A762T	0.999	0	31	0.33	-	
																								Missense	ENST00000378094	NM_001330660	CCDS83363	ALT2	15	c.2284G>A	GCC/ACC	A762T	0.988	0	31	0.33	-	
																								Missense	ENST00000378088				-	1	c.187G>A	GCC/ACC	A63T	0.917	0.14	31	0.33	-

varsome	igv	alamut	var_name	trio						gnomad					deja_vu			validations					
			<b>14-105846137-G-A</b>	ABO_RAC		-	-	100	-	AC	Ho	Max	Min	AN		Pr	Sa	Ho	HGMD	Clinvar	Defidiag	consequence	enst
				BOU_MOH		he	51%	115	+	354	3	afr	asj	281604	other	26	40	0				Missense	<a href="#">ENST00000325438</a>
				BOU_SAM		he	56%	123						DI	0	0	0	Missense				<a href="#">ENST00000547217</a>	
																	Missense	<a href="#">ENST00000430725</a>					
			<b>14-105859013-G-A</b>	ABO_RAC		he	52%	100	+	AC	Ho	Max	Min	AN		Pr	Sa	Ho	HGMD	Clinvar	Defidiag	consequence	enst
				BOU_MOH		-	-	118	-	123	1	oth	asj	278642	other	65	102	1				Synonymous	<a href="#">ENST00000325438</a>
				BOU_SAM		he	48%	105						DI	0	0	0						

# Heterozygous Coumpound



your Selected variation:

CLCN1 recessive dominant 8.2 Ovim Gtex Panel: 1 EMG disease 8.2 Myotonia%2C\_non-dystrophic

igv Alamut Var\_name Diag\_score Trio Gnomad Deja\_vu Table\_validation Table\_transcript

7-14309610-C-A 8.2

6002 6003 6001

AC Ho Max Min AN

Pr Sa Ho

HGMD Clinvar Defdiag

consequence ensi nm code appri exon nomenclature codone codons\_AA polyphen sift ncboost cadd reval discrv

ENST00000343257 NR\_046453 CCDS5881 P1 14 c.1478C>A GCA/GAA A493E 0.838 0 28 0.97

Variation(s) with Father Transmission or + 13 variations without father transmission

igv Alamut Var\_name Diag\_score Trio Gnomad Deja\_vu Table\_validation Table\_transcript

7-143018785-A-T -2.7

6002 6003 6001

AC Ho Max Min AN

Pr Sa Ho

HGMD Clinvar Defdiag

consequence ensi nm code appri exon nomenclature codone codons\_AA polyphen sift ncboost cadd reval discrv

ENST00000343257 NR\_046453 CCDS5881 P1 -23\_ex5 c.563-23A>T

7-143321110-G-A -2.7

6002 6003 6001

AC Ho Max Min AN

Pr Sa Ho

HGMD Clinvar Defdiag

consequence ensi nm code appri exon nomenclature codone codons\_AA polyphen sift ncboost cadd reval discrv

ENST00000343257 NR\_046453 CCDS5881 P1 -397\_ex7 c.775-397G>A

# Variation Panel

▼

LRP4 recessive dominant

9

Omim

Gtex

0

Panel : 3

● 46,XY disorder of sex development

1

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CNV

varsome	lgv	alamut	var_name	trio				gnomad					deja_vu			validations			transcripts													
				HYP2000146	he	45%	287	AC	Ho	Max	Min	AN	Pr	Sa	Ho	HGMD	Clinvar	Defidiag	consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv
<div>V</div>	<div></div>	<div></div>	<div><div>11-46897179-C-T</div></div>	HYP2000146	<div>he</div>	45%	287	32	-	asj 0.0011	fin 0.0000	282380	other	3	3	1	-	Likely benign	Synonymous	ENST00000378623	XM_005252923.1;NM_002334.3	CCDS31478.1	-	27	c.37536>A	CCG/CCA	P1251P	-	-	10	-	-
				HYP2000147	<div>he</div>	44%	339																									
				HYP2000142	<div>ho</div>	99%	453						DI	1	1	0																
							Recessive																									
																	+ view 1 Transcripts															

AC	Ho	Max	Min	AN
61	-	nfe 0.0004	afr 0.0000	276422

	Pr	Sa	Ho
other	1	1	0
DI	0	0	0

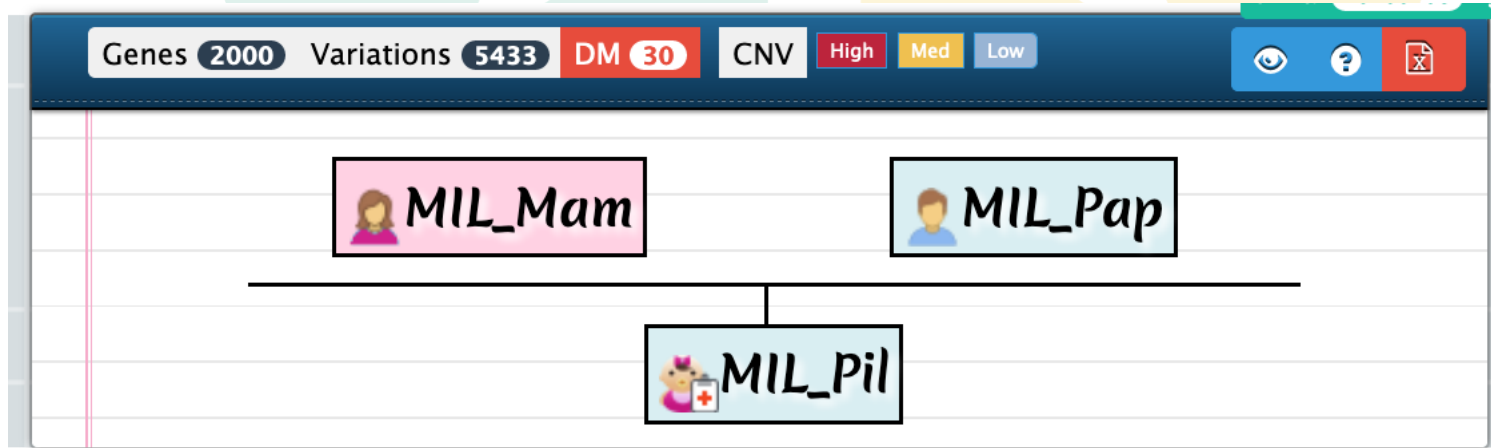
HGMD	Clinvar	Defidiag
DM?	Benign	-






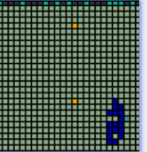
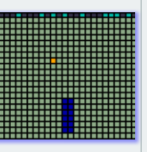
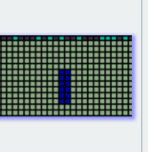
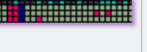
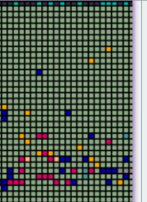
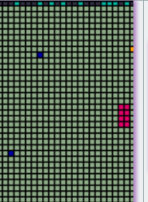
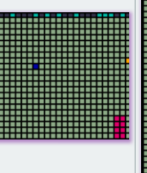
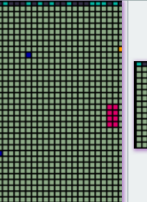
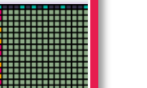
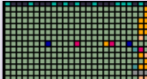
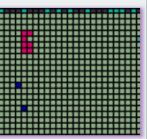
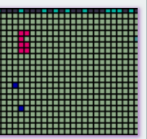
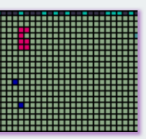
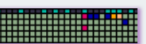
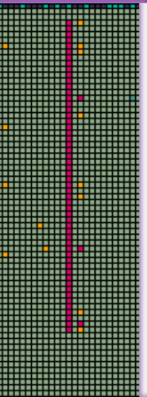
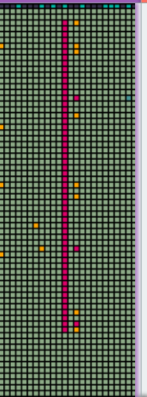

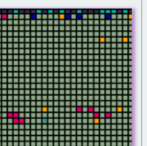






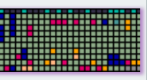
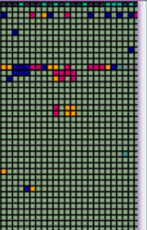
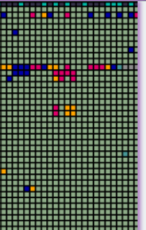

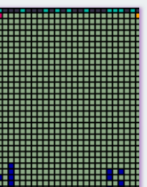

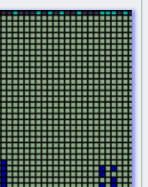
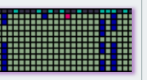
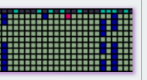
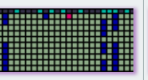

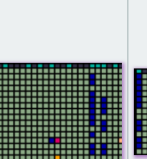

consequence	enst	nm	ccds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv
Missense	<a href="#">ENST00000391909</a>		<a href="#">CCDS12691</a>	P1	4	c.574G>A	GAC/AAC	D192N	0.066	0.55	14	0.42	-
+ view 1 Transcripts													

# Structural Variations CNV

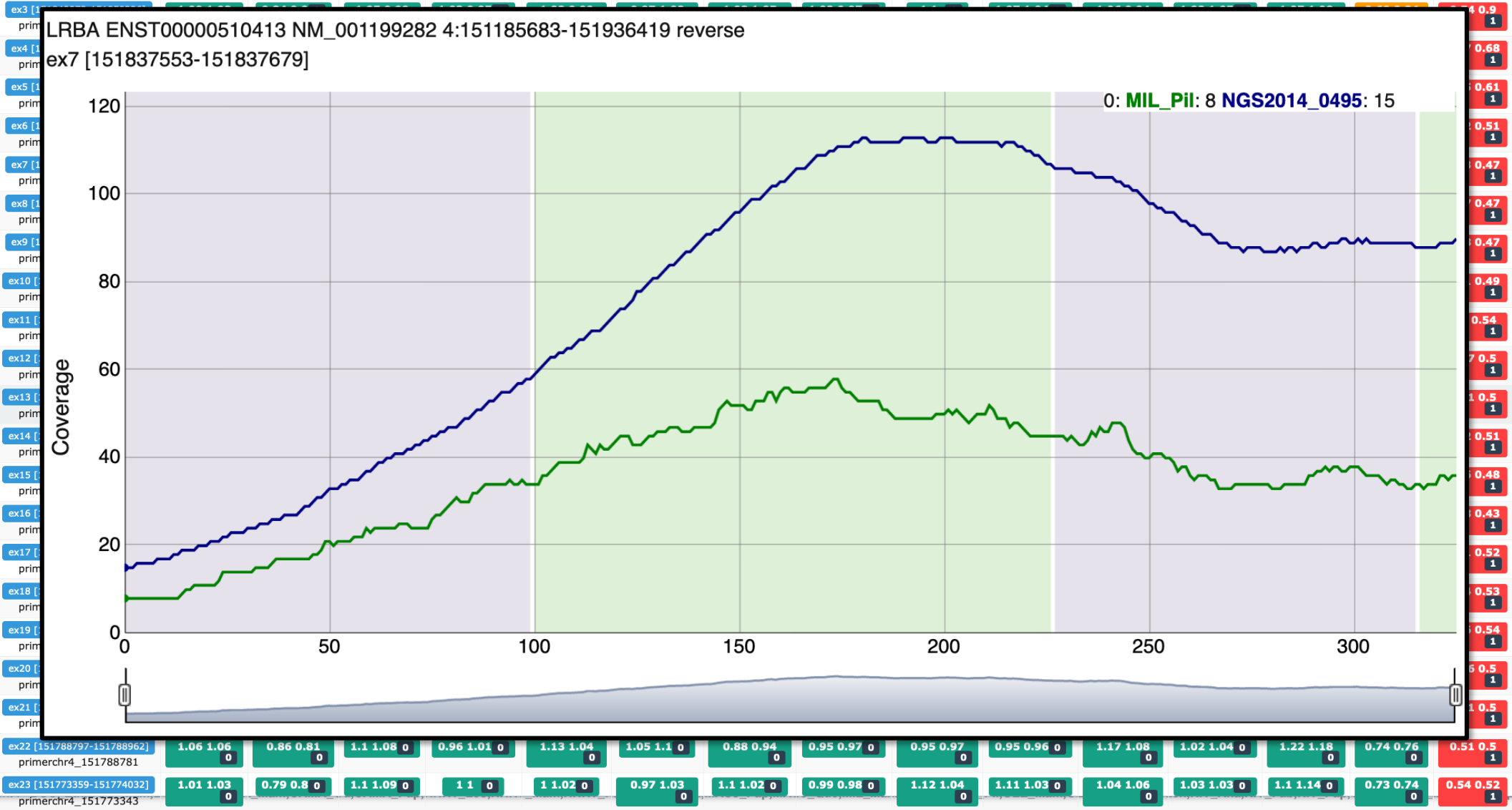
## Part 1 : Capture

# CNV (capture, exome and Panel)


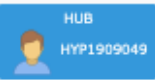
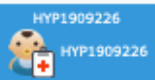
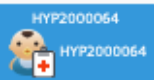
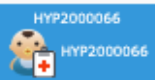
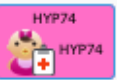


<p>FCGR3B ENST00000650385 1:161592986-161600966 Fc fragment of IgG receptor IIIb [Source:HGNC Symbol;Acc:HGNC:3620]</p> 	<p>FCGR3B ENST00000367964 1:161592986-161601753 Fc fragment of IgG receptor IIIb [Source:HGNC Symbol;Acc:HGNC:3620]</p> 	<p>FCGR3B ENST00000614870 1:161592990-161600837 Fc fragment of IgG receptor IIIb [Source:HGNC Symbol;Acc:HGNC:3620]</p> 	<p>FCGR3B ENST00000613418 1:161592990-161600837 Fc fragment of IgG receptor IIIb [Source:HGNC Symbol;Acc:HGNC:3620]</p> 	<p>FCGR3B ENST00000531221 1:161594305-161600992 Fc fragment of IgG receptor IIIb [Source:HGNC Symbol;Acc:HGNC:3620]</p> 	<p>TTC27 ENST00000317907 2:32853117-33046118 tetratricopeptide repeat domain 27 [Source:HGNC Symbol;Acc:HGNC:25986]</p> 	<p>AC013717.1 ENST00000649044 2:44395990-44547449 novel protein, PPM1B-SLC3A1 readthrough</p> 	<p>SLC3A1 ENST00000260649 2:44502599-44548633 solute carrier family 3 member 1 [Source:HGNC Symbol;Acc:HGNC:11025]</p> 	<p>IGKV1D-27 ENST00000453184 2:90007677-90008145 immunoglobulin kappa variable 1D-27 (pseudogene) [Source:HGNC Symbol;Acc:HGNC:5751]</p> 	<p>ANAPC1 ENST00000341068 2:112525217-112641770 anaphase promoting complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:19988]</p> 	<p>AGAP1 ENST00000304032 2:236402687-237040437 ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:HGNC Symbol;Acc:HGNC:16922]</p> 	<p>AGAP1 ENST00000409457 2:236402733-236761846 ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:HGNC Symbol;Acc:HGNC:16922]</p> 	<p>AGAP1 ENST00000336665 2:236402751-237035198 ArfGAP with GTPase domain, ankyrin repeat and PH domain 1 [Source:HGNC Symbol;Acc:HGNC:16922]</p> 	<p>LINC00960 ENST0000066814 3:75721451-75791 long intergenic non-pr oding RNA 960 [Source:HGNC Symbol;Acc:HGNC:48]</p> 
<p>UGT2B15 ENST00000338206 4:69512315-69536370 UDP glucuronosyltransferase family 2 member B15 [Source:HGNC Symbol;Acc:HGNC:12546]</p> 	<p>ABCG2 ENST00000650821 4:89011302-89152780 ATP binding cassette subfamily G member 2 (Junior blood group) [Source:HGNC Symbol;Acc:HGNC:74]</p> 	<p>ABCG2 ENST00000515655 4:89011416-89152474 ATP binding cassette subfamily G member 2 (Junior blood group) [Source:HGNC Symbol;Acc:HGNC:74]</p> 	<p>ABCG2 ENST00000237612 4:89011421-89079791 ATP binding cassette subfamily G member 2 (Junior blood group) [Source:HGNC Symbol;Acc:HGNC:74]</p> 	<p>PLA2G12A ENST00000243501 4:110631145-110651226 phospholipase A2 group XIIA [Source:HGNC Symbol;Acc:HGNC:18554]</p> 	<p>LRBA ENST00000357115 4:151185587-151936879 LPS responsive beige-like anchor protein [Source:HGNC Symbol;Acc:HGNC:1742]</p> 	<p>LRBA ENST00000510413 4:151185683-151936419 LPS responsive beige-like anchor protein [Source:HGNC Symbol;Acc:HGNC:1742]</p> 	<p>AC110813.1 ENST00000507934 4:151500241-151502697 novel transcript, antisense to LRBA</p> 	<p>AC021087.5 ENST00000651543 5:218413-315070 novel protein</p> 	<p>PDCD6 ENST00000618970 5:271736-315089 programmed cell death 6 [Source:HGNC Symbol;Acc:HGNC:8765]</p> 	<p>PDCD6 ENST00000614778 5:271736-315089 programmed cell death 6 [Source:HGNC Symbol;Acc:HGNC:8765]</p> 	<p>PDCD6 ENST00000264933 5:271761-315089 programmed cell death 6 [Source:HGNC Symbol;Acc:HGNC:8765]</p> 	<p>PDCD6 ENST00000505221 5:271762-314921 programmed cell death 6 [Source:HGNC Symbol;Acc:HGNC:8765]</p> 	<p>PDCD6 ENST0000050757 5:271772-31508 programmed cell dea [Source:HGNC Symbol;Acc:HGNC:87]</p> 
<p>CYP21A2 ENST00000644719 6:32006192-32009421 cytochrome P450 family 21 subfamily A member 2 [Source:HGNC Symbol;Acc:HGNC:2600]</p> 	<p>CYP21A2 ENST00000435122 6:32006192-32009419 cytochrome P450 family 21 subfamily A member 2 [Source:HGNC Symbol;Acc:HGNC:2600]</p> 	<p>EYS ENST00000503581 6:64429876-66417118 eyes shut homolog [Source:HGNC Symbol;Acc:HGNC:21555]</p> 	<p>EYS ENST00000370621 6:64430032-66417107 eyes shut homolog [Source:HGNC Symbol;Acc:HGNC:21555]</p> 	<p>NUS1 ENST00000368494 6:117996632-118031890 NUS1 dehydrodichyl diphosphate synthase subunit [Source:HGNC Symbol;Acc:HGNC:21042]</p> 	<p>AFDN ENST00000392112 6:168227671-168372700 afadin, adherens junction formation factor [Source:HGNC Symbol;Acc:HGNC:7137]</p> 	<p>AFDN ENST00000392108 6:168227671-168364976 afadin, adherens junction formation factor [Source:HGNC Symbol;Acc:HGNC:7137]</p> 	<p>AFDN ENST00000366806 6:168228315-168370912 afadin, adherens junction formation factor [Source:HGNC Symbol;Acc:HGNC:7137]</p> 	<p>KIF25 ENST00000643607 6:168398882-168445775 kinesin family member 25 [Source:HGNC Symbol;Acc:HGNC:6390]</p> 	<p>KIF25 ENST00000443060 6:168399772-168445743 kinesin family member 25 [Source:HGNC Symbol;Acc:HGNC:6390]</p> 	<p>KIF25 ENST00000351261 6:168418553-168445769 kinesin family member 25 [Source:HGNC Symbol;Acc:HGNC:6390]</p> 	<p>KIF25 ENST00000354419 6:168418553-168445769 kinesin family member 25 [Source:HGNC Symbol;Acc:HGNC:6390]</p> 	<p>FRMD1 ENST00000646385 6:168453846-168493692 FERM domain containing 1 [Source:HGNC Symbol;Acc:HGNC:21240]</p> 	<p>FRMD1 ENST0000028330 6:168456425-16847 FERM domain contain [Source:HGNC Symbol;Acc:HGNC:21]</p> 

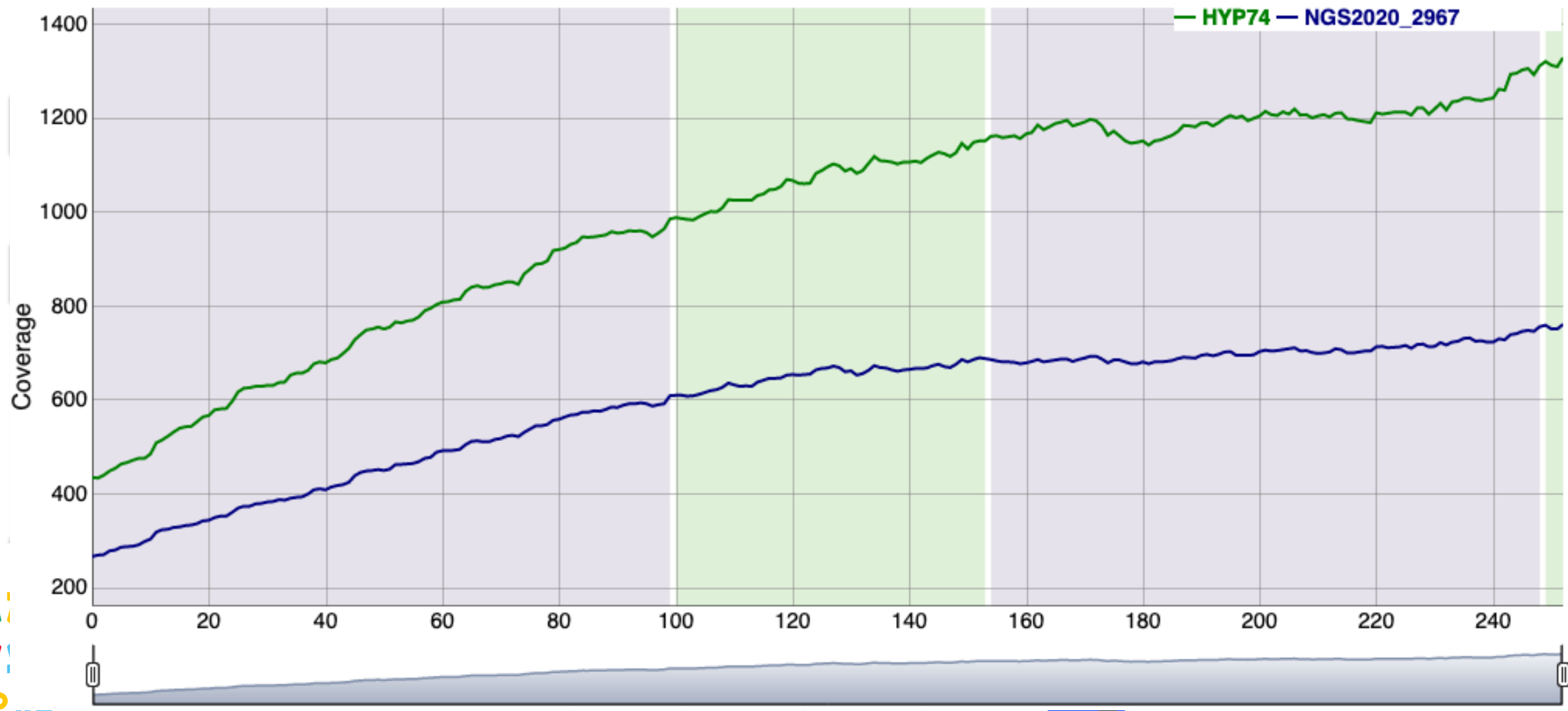
LRBA ENST00000510413 chr4:[151185683-151936419] (rev)	BOU BOU_Eth	BOU BOU_Mam	BOU BOU_Pap	CAMA CAMA_Mam	CAMA CAMA_Ou	CAMA CAMA_Pap	HNRT HNRT_Leo	HNRT HNRT_Mam	HNRT HNRT_Pap	MAUJ MAUJ_Mam	MAUJ MAUJ_Pap	MAUJ MAUJ_Que	MIL MIL_Mam	MIL MIL_Pap	MIL MIL_Pil
ex2 [151935707-151935825] primerchr4_151935691	1.14 1.14 0	0.96 0.96 0	0.9 0.9 0	0.8 0.8 0	0.98 0.98 0	1.02 1.02 0	1.02 1.02 0	0.9 0.9 0	1.03 1.03 0	1.13 1.13 0	0.75 0.75 0	1.17 1.17 0	1.11 1.11 0	1.09 1.09 0	1.29 1.29 0
ex2 [151935531-151935700] primerchr4_151935515	1.02 1.08 0	0.98 0.96 0	1 0.94 0	0.95 0.87 0	0.96 0.97 0	1.12 1.06 0	1.05 1.03 0	0.98 0.93 0	0.97 1 0	0.92 1.02 0	0.9 0.82 0	1.02 1.09 0	1.08 1.09 0	0.91 1 0	1.25 1.27 0



# Structural Va

 HYP1909048	 HYP1909049	 HYP1909226	 HYP2000064	 HYP2000066	 HYP74
1.11 1.11 0	1.02 1.02 0	1.02 1.02 0	0.97 0.97 0	1.13 1.13 0	1.94 1.94 2
0.93 1.01 0	0.88 0.94 0	0.99 1 0	1.04 1 0	1.02 1.07 0	1.92 1.92

COL4A5 ENST00000328300 XM\_005262070.1;NM\_033380.2 X:107683112-107940771 forward  
x14 [107823763-107823816]



1

▶

TRPM3

15

Omim

Gtex

0.03

Panel : 2

● Autism spectrum disorder

⚠

2

≡

✎

CNV

▶

LRBA recessive

14.4

Omim

Gtex

0

Panel : 2

● Antibody deficiency, primary

⚠

49

≡

✎

CNV

▶

FKRP recessive

12.6

Omim

Gtex

0

Panel : 8

● Cardiomyopathy, dilated

⚠

4

≡

✎

CNV

▶

MAB21L2 recessive dominant

12.1

Omim

Gtex

0.44

Panel : 9

● Bilateral anophthalmia, intellectual disability & rhizomelic skeletal dysplasia

⚠

2

≡

✎

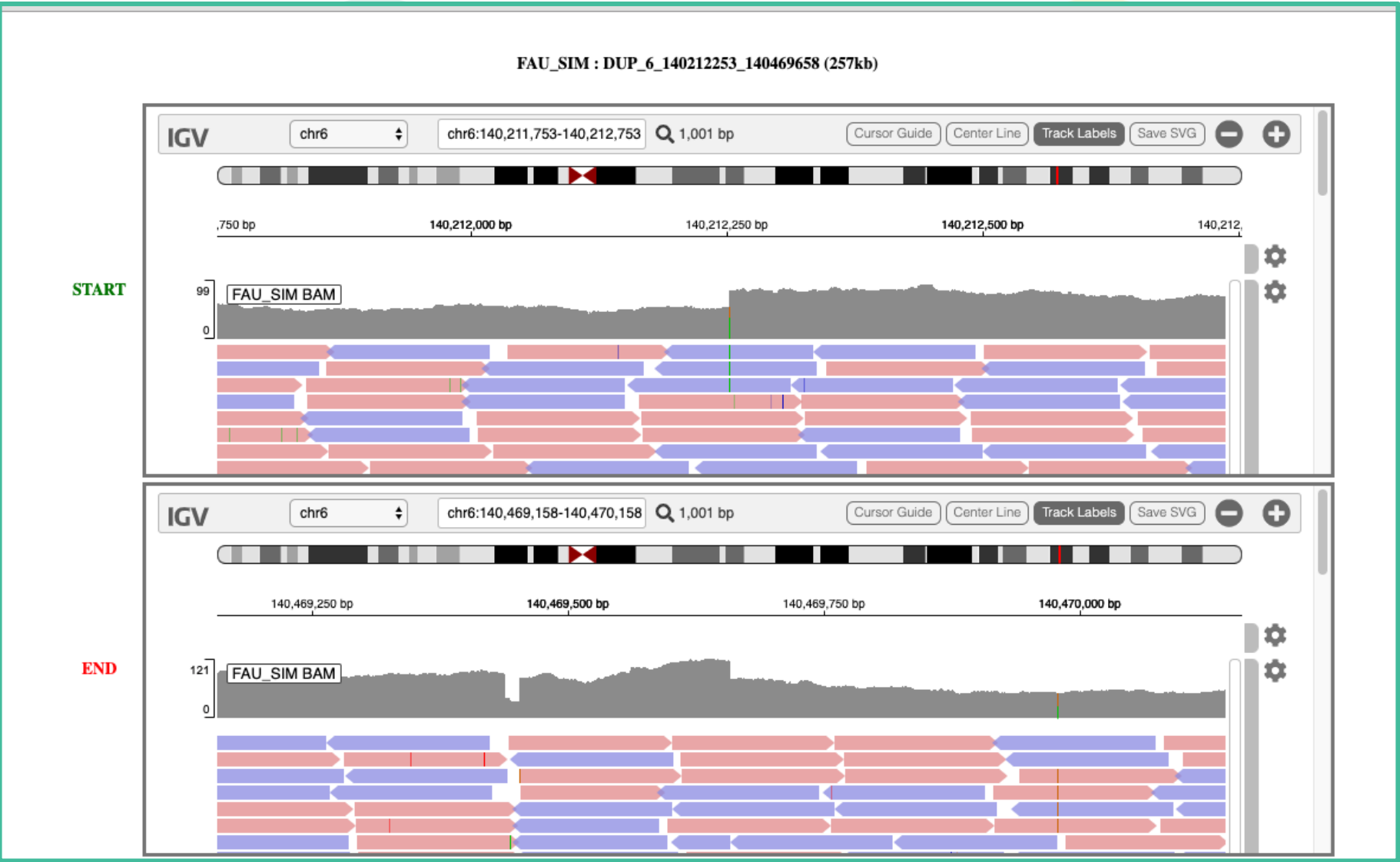
CNV

<div>LRBA</div> <div>ENST00000357115</div> <div>4:151185587-151936879</div> <div>LPS responsive beige-like anchor protein [Source:HGNC Symbol;Acc:HGNC:1742]</div> <div></div>	<div>LRBA</div> <div>ENST00000651943</div> <div>4:151185587-151936436</div> <div>LPS responsive beige-like anchor protein [Source:HGNC Symbol;Acc:HGNC:1742]</div> <div></div>	<div>LRBA</div> <div>ENST00000510413</div> <div>4:151185683-151936419</div> <div>LPS responsive beige-like anchor protein [Source:HGNC Symbol;Acc:HGNC:1742]</div> <div></div>	<div>LRBA</div> <div>ENST00000507224</div> <div>4:151235875-151936429</div> <div>LPS responsive beige-like anchor protein [Source:HGNC Symbol;Acc:HGNC:1742]</div> <div></div>
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# Structural Variations CNV

## Part 2 : Genome

# CNV



Gene	dBVar status
-	-
-	-
-	-
yes	*
yes	*
-	-
yes	*
-	-
yes	-
-	-

# Validations :

3 CNV

consequence	enst	nm	cds	appris	exon	nomenclature	codons	codons_AA	polyphen	sift	cadd	revel	dbcsnv
Frameshift	ENST00000304363	NM_017635	CCDS31623	P3	11	c.1555_1558delCAGA	cagaAT/AT	p.Q519fs	-	-	-	-	-

+ view 1 Transcripts

- pathogenic
- likely pathogenic
- Uncertain significance
- Likely benign
- benign
- False Positive
- ToDo

clinvar 20190211 | gnomad 2.1 | hgmd 2019.2 | cadd 1.4 | gencode v28

genome defdiag vcf — genome\_hg19 — other

SOLEXA | 04/02/19 | 04/02/19 | Cov : 33.3 (33.3 ± 0) | 15X : 89.2% (89.2) | 30X : 72.2% (72.2) | HG19c | Print

Gender control | Quality Control | Mendelian Control | Control (Blanc) | Regions Dups

Fam	view	Print	Patient	Cov	30x	validation
B00H6			B00H6XO	33.4	74.1	-
			B00H6XN	33.4	71.3	-
			B00H6XP	33.2	71.3	<div> <div>pathogenic</div> <div>pnitschk</div> <div>2019-Jun-26</div> <div></div> <div>11-118626975-A-G</div> <div> <div>B00H6XO</div> <div>B00H6XN</div> <div>B00H6XP</div> </div> <div> <div>45 reads</div> <div>45 reads</div> <div>40% Strict Denovo</div> </div> <div>DDX6</div> </div>

consequence	enst	nm	nomenclature
Misense	ENST00000534980	NM_004397	c.1168T>C

+ view 3 Transcripts

Rep

Patient Summary 2/2/2015	
name	
identifiant	IMB
Validation	-

## Run Summary

coverage limit=30 padding=20 1/4

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56

### Other detected Variations

Impact: [splice region - splice donor/acceptor - non coding transcript - stop gained - stop/start lost - missense - frameshift - inframe insertion/deletion - mature miRNA - ] frequency:[<=1%]

ADCK4 XM\_005259275.1;XM\_005259274;XM\_005259273;XM\_005259272;XM\_005259271;NM\_024876.3

gene	var_name	sanger	ngs	ratio	caller	genomique	transcript	exon	nomenclature	consequence	codons	codons_AA	freq	deja_vu	similar_projects	in_this_run	polyphen	sift
ADCK4	rs113871093	-	he(2116/2174)	50%	uni	19:41220518	ENST00000324464	2	c.20G>A	coding	GGC/GAC	G7D	0.0012	3:3	0:0	1/16	0.092	0.08

### CD151

gene	var_name	sanger	ngs	ratio	caller	genomique	transcript	exon	nomenclature	consequence	codons	codons_AA	freq	deja_vu	similar_projects	in_this_run	polyphen	sift
CD151	rs116211118	-	he(1350/1348)	49%	uni	11:836418	ENST00000397420	4	c.252G>T	coding	AAG/AAT	K84N	0.0029	12:18	2:2	1/16	0.081	0.09

### COQ6 NM\_182476.2

gene	var_name	sanger	ngs	ratio	caller	genomique	transcript	exon	nomenclature	consequence	codons	codons_AA	freq	deja_vu	similar_projects	in_this_run	polyphen	sift
COQ6	rs61743884	-	he(793/874)	52%	uni	14:74417180	ENST00000334571	1	c.145G>T	coding	GCC/TCC	A49S	0.0060	8:13	2:2	1/16	0.417	0.28

### EMP2 NM\_001424.4

gene	var_name	sanger	ngs	ratio	caller	genomique	transcript	exon	nomenclature	consequence	codons	codons_AA	freq	deja_vu	similar_projects	in_this_run	polyphen	sift
EMP2	rs140529660	-	he(2057/1982)	49%	uni	16:10641541	ENST00000359543	-7_ex2	c.-1-7T>A	splicing	T/A		0.0063	11:19	8:12	1/16	-	-

### TTC21B NM\_024753.4

gene	var_name	sanger	ngs	ratio	caller	genomique	transcript	exon	nomenclature	consequence	codons	codons_AA	freq	deja_vu	similar_projects	in_this_run	polyphen	sift
TTC21B	2_166810196_A_ACGCTCGCC	-	ho(74/273)	78%	uni	2:166810196	ENST00000243344	1	c.19_20insGGCGAGCG	splicing frameshift	AAG/AGGCGA	K7RR	-	0:0	17:58	2/16	0	0

TP53 NM\_001126114.2;NM\_001276696.1







gene	var_name	sanger	ngs	ratio	genomique	transcript	exon	nomenclature	consequence	codons	codons_AA	freq	deja_vu	similar_projects	in_this_project	polyphen	sift
TP53	rs1042522	confirmed (he)	ho(1/401)	99%	17:7579472	ENST00000420246	4	c.215C>G	coding	CCC/CGC	P72R	0.63	367:4081	0:0	5/6	0.189	0.55

# PolyQuery

**imagine**  
INSTITUT DES MALADIES GÉNÉTIQUES

Welcome to PolyWeb  
Imagine – Paris Descartes

 UNIVERSITÉ  
PARIS DESCARTES

 <b>POLYQUERY</b> <i>Explore Exome/Genome (soon) project</i>	 <b>POLYDIAG</b> <i>Explore Genes target project</i>	 <b>POLYDEJAVU</b> <i>Explore "Dejavu" database</i>	 <b>POLYLINKAGE</b> <i>Explore "Linkage" project</i>
 <b>POLYPROJECTLINK</b>	 <b>POLYRUM</b>	 <b>POLYPROJECT</b>	 <b>POLYMONOP</b>

# PolyQuery: the home page

Projects 67/1093

Exomes : 684/7769

Cillomes : 16/1257

Target Genes : 169/10872

Samples : 869/19898

Projects List

Université Paris Descartes, Institut Imagine

User/polyweb

Projects 67/1093

Exomes : 684/7769

Cillomes : 16/1257

Target Genes : 169/10872

Samples : 869/19898

Polyweb

filter by name,description,user

Interface Version ☐ OLD (Deprecated) ☒ NEW

Row	Name	description	capture	capture type	nb runs	Genes	Patient	sequencers	users
1	BACT2012_0001	Projet bacterie souche D344SRF	bacteria	...	...	...	4	...	christine.bole@inserm.fr
2	BACT2012_0002	Projet bacterie souche MG1655	bacteria	...	...	...	3	...	christine.bole@inserm.fr
3	BACT2012_0003	Projet bacterie souche OG1RF	bacteria	...	...	...	7	...	christine.bole@inserm.fr
4	DIAG2014	test_diag	test_diag	...	...	...	6	...	romain.gomez@institutimagine.org
5	NGS2010_0006	syndrome de Cornelia de Lange	agilent_v30	...	...	...	6	...	laurence.colleaux@inserm.fr helene.louis-dit-picard@inserm.fr karine.siquier-pernet@inserm.fr christine.bole@inserm.fr
6	NGS2010_0007	dysplasie acromicrique (DA)	agilent_v30	...	...	...	3	...	valerie.cormier-daire@inserm.fr carine.le-goff@inserm.fr christine.bole@inserm.fr
7	NGS2010_0009	j100xx	agilent_v30	...	...	...	6	...	laurent.abel@inserm.fr quentin.vincent@inserm.fr emjo558@mail.rockefeller.edu
8	NGS2010_0011	j10016-j10019	agilent_v30	...	...	...	6	...	avab473@mail.rockefeller.edu
9	NGS2010_0012	Ciliopathies	agilent_v30	...	...	...	2	...	tania.attie@inserm.fr avab473@mail.rockefeller.edu
10	NGS2010_0013	Hypertelorism	agilent_v30	...	...	...	3	...	jeanne.amiel@inserm.fr
11	NGS2010_0014	Geleophysic dysplasia	agilent_v30	...	...	...	2	...	valerie.cormier-daire@inserm.fr carine.le-goff@inserm.fr avab473@mail.rockefeller.edu
12	NGS2010_0015	Myhre Syndrome	agilent_v30	...	...	...	2	...	valerie.cormier-daire@inserm.fr carine.le-goff@inserm.fr avab473@mail.rockefeller.edu
13	NGS2010_0020	Usher syndrome type I	agilent_v30	...	...	...	1	...	sylvie.gerber@inserm.fr isabelle.perrault@inserm.fr jean-michel.rozet@inserm.fr brigitte.nedelec@inserm.fr
14	NGS2010_0021	exomes bunli	agilent_v50	...	...	...	2	...	quentin.vincent@inserm.fr

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User/polyweb

Projects 67/1093

Exomes : 684/7769

Cillomes : 16/1257

Target Genes : 169/10872

Samples : 869/19898

Interface Version ☐ OLD (Deprecated) ☒ NEW

Row	Name	description	capture	capture type	nb runs	Genes	Patient	sequencers	users
1	NGS2016_1094	CerID37-39-40	agilent_58_v6	...	...	...	5	...	laurence.colleaux@inserm.fr christine.bole@inserm.fr vincent.cantagrel@inserm.fr michael.nicouleau@inserm.fr

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NGS2014\_0357

Projects List

NGS2016\_1098  
"Famille EMM, HERR, E, HUE"

BIP&D  
Bioinformatics Paris Descartes

Samples 11 \* Chr 25 \* Genes 4720 \* Variations 32709 \* Uniq 8761 \* Filtration Level Variations \* Type Familial \* Model None

Graphical View

ChromosomesRegionFilter

Get AllXLS genesXLS variants

Chr	Genes	Sub	Del	Ins
1	460	660	34	31
2	274	411	23	32
3	259	531	40	31
4	165	251	14	15
5	206	261	20	10
6	240	646	25	42
7	236	435	19	34
8	157	208	8	9
9	224	383	23	22
10	178	266	10	15

FilterIntersectExcludeorIn the atticAt least

FamilialGenetic Model (None)

HomozygousHeterozygousAdd AllView allHide atticVariationExport VCF

Fam	Patients	Ped	St	Sub	Del	Ins	Ho	He	Genes	Cov	15x	30x	He	Ho	SI
EMM	EMM_OLI	♂	●	2584	157	147	400	2488	1415	170.1	98.3	96.5	✓	✓	●
EMM	EMM_STE	♀	●	2547	280	164	465	2526	1514	281.1	98.6	97.9	✓	✓	●
EMM	EMM_TOM	●	●	2622	166	152	390	2550	1437	290.9	98.8	98.1	✓	✓	●
EMM	EMM_ZOE	●	●	2610	164	162	357	2579	1437	158.2	98.2	96.5	✓	✓	●
HERR	HERR_GAB	●	●	2740	154	145	437	2602	1503	166	98.4	96.8	✓	✓	●
HERR	HERR_MIC	♂	●	2670	157	144	405	2566	1472	222.1	98.5	97.2	✓	✓	●
HERR	HERR_MYR	♀	●	2762	186	177	407	2718	1554	227.2	98.4	97.3	✓	✓	●
HERR	HERR_MAT	●	●	2668	160	140	410	2553	1454	188.1	98.4	96.0	✓	✓	●

FamiliesGroups

Fam	Pat	Sub	Del	Ins	Gene	SI	Model
EMM	4	4083	266	259	2383	●	
HERR	4	4214	284	269	2396	●	
HUE	3	4028	247	246	2271	●	

DB PublicOptions (All)Check Deja VuNoneOthers Projects: 1117AllHo / He

Impact FactorHighMediumLowAllImpactImpactImpactVariants

☒ Mature mRNA☒ Splice Acc/Don☒ Frameshift☒ Stop-gained☒ (Start/Stop)-lost  
☒ ncRNA☒ Splice Region☒ Missense☒ No-frameshift  
☐ Pseudogene☐ Utr☐ Synonymous☐ Intronic☐ Intergenic

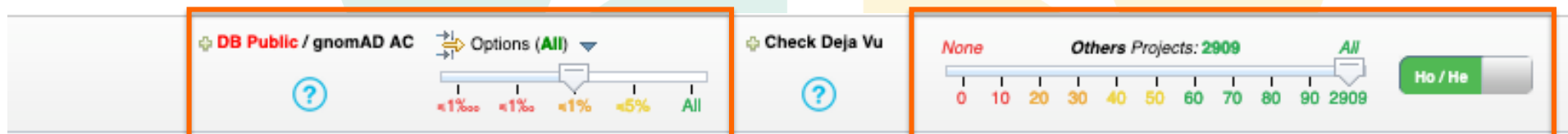
Run

Others Filters

Genes

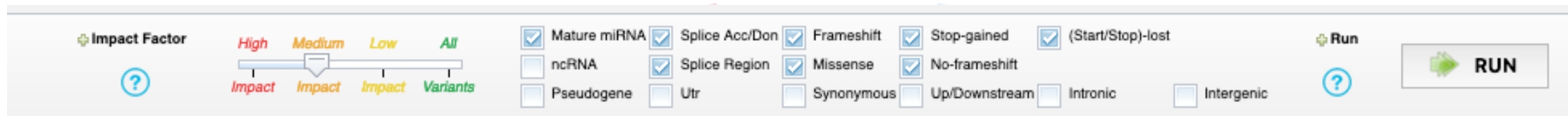
Name	xref	chr	Start	End	Description	PolyDiag Capture	All	Subs	Ins	Dels	With cons.	Syno	UTR	Splicing
							Pat.	Pat.	Pat.	Pat.	Pat.	Pat.	Pat.	Pat.
0	<a href="#">ENSG00000197530</a>	MB2	1	1550795	1565990	mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:30577]	...	1	1	0	0	1	0	0
1	<a href="#">ENSG00000157911</a>	PEX10	1	2336236	2345236	peroxisomal biogenesis factor 10 [Source:HGNC Symbol;Acc:8851]	★	1	1	0	0	1	0	0
2	<a href="#">ENSG00000131591</a>	C1orf159	1	1017198	1051741	chromosome 1 open reading frame 159 [Source:HGNC Symbol;Acc:26062]	...	2	2	0	0	1	0	1
3	<a href="#">ENSG00000189410</a>	SH2D5	1	21046225	21059330	SH2 domain containing 5 [Source:HGNC Symbol;Acc:28819]	...	5	5	0	0	2	0	3
4	<a href="#">ENSG00000127481</a>	UBR4	1	19401000	19536770	ubiquitin protein ligase E3 component n-recognin 4 [Source:HGNC Symbol;Acc:30313]	...	2	2	0	0	2	0	0
5	<a href="#">ENSG00000009724</a>	MASP2	1	11086580	11107290	mannan-binding lectin serine peptidase 2 [Source:HGNC Symbol;Acc:6902]	★	6	6	0	0	6	0	0
6	<a href="#">ENSG00000204479</a>	PRAMEF17	1	13716092	13719089	PRAME family member 17 [Source:HGNC Symbol;Acc:29485]	...	1	1	0	0	1	0	0
7	<a href="#">ENSG00000179840</a>	C1orf200	1	9712668	9714644	chromosome 1 open reading frame 200 [Source:HGNC	...	4	4	0	0	4	0	0

# Variations Filtering : Frequency



The screenshot shows two filter sections in the Variations Filtering interface. The first section, titled "DB Public / gnomAD AC", includes a dropdown menu set to "Options (All)" and a slider with markers at  $\leq 1\text{‰}$ ,  $\leq 1\%$ ,  $\leq 1\%$ ,  $\leq 5\%$ , and "All". The second section, titled "Check Deja Vu", includes a slider for "Others Projects: 2909" with markers from 0 to 90 and a final marker at 2909, and a "Ho / He" button.

# Variations Filtering : Annotation Impact



The screenshot shows the "Impact Factor" section of the Variations Filtering interface. It includes a slider with markers for "High", "Medium", "Low", and "All", with corresponding labels "Impact", "Impact", "Impact", and "Variants". Below the slider is a grid of checkboxes for various annotation categories: Mature miRNA, ncRNA, Pseudogene, Splice Acc/Don, Splice Region, Utr, Frameshift, Missense, Synonymous, Stop-gained, No-frameshift, Up/Downstream, (Start/Stop)-lost, Intronic, and Intergenic. A "Run" button is located to the right of the grid.

# Variant Annotation

DB Public ☐ Options (All) ☐ Check Deja Vu ☐ None ☐ Others Projects: 1117 ☐ All ☐ Ho / He ☐ Search gene or ontology...

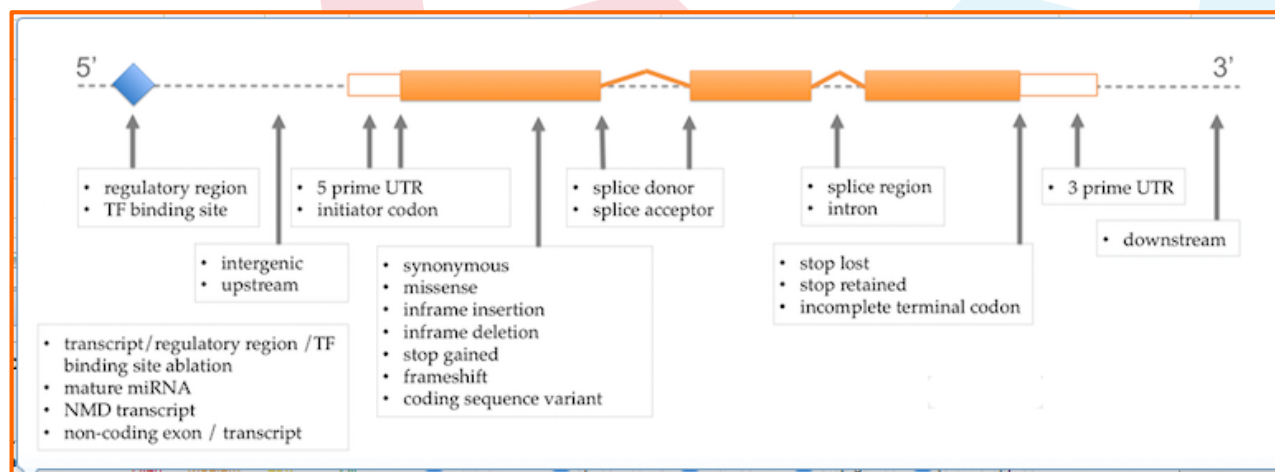
Impact Factor ☐ ? ☐ High ☐ Medium ☐ Low ☐ All ☐ Impact ☐ Impact ☐ Impact ☐ Variants

☒ Mature miRNA ☒ Splice Acc/Don ☒ Frameshift ☒ Stop-gained ☒ (Start/Stop)-lost ☐ Run ☐ ?




☒ ncRNA ☒ Splice Region ☒ Missense ☒ No-frameshift ☐ Pseudogene ☐ Utr ☐ Synonymous ☐ Intronic ☐ Intergenic



Impact Factor ☐ ? ☐ High ☐ Medium ☐ Low ☐ All ☐ Impact ☐ Impact ☐ Impact ☐ Variants



☒ Mature miRNA ☒ Splice Acc/Don ☒ Frameshift ☒ Stop-gained ☒ (Start/Stop)-lost ☒ ncRNA ☒ Splice Region ☒ Missense ☒ No-frameshift ☐ Pseudogene ☐ Utr ☐ Synonymous ☐ Intronic ☐ Intergenic







# More variations Filter



**Global**   Variants Type (All) 

**Predictions**  *Surely* *Probably* *Possibly*  
*Damaging* *Damaging* *Damaging* All 

**Confidence**  High Medium All 

**Ho Regions**  *Not Used*  
Extra Large Large Medium Short None 

**NCBoost**  High Medium Moderate All 

**Cadd Score**  30 25 20 15 10 5 All 

Predictions  
Score

Sift  
Polyphen  
CADD  
NCBoost

Variant  
Quality

Homozygous  
Region

# Samples Queries

Projects List

NGS2012\_0150  
"NGS"

BIPeD  
Bioinformatics Paris Descartes

★ Samples 15 ★ Chromosomes 24 ★ Genes 4908 ★ Variations 26698 ★ Uniq 8578 ★ He 7256 ★ Ho 1322 ★ Filtration Level Variations ★ Type Familial ★ Model None ★ pnitech

Filter | Intersect Exclude Or In The Attic | At Least  Pat | Individual | Genetic Model (None)

Add All | View ALL Hide attic | Variation | VCF | HGMD DejaVu

Fam	Patients	Ped	St	Sub	Del	Ins	Cnv	Ho	He	Genes	Cov	15x	30x	He	Ho	SI
1119TL000535	Workspace 535			4	3	0	0	1	6	4	792.7	100	100			
1119TL000569	1119TL000569			7	1	2	0	0	10	8	877.8	100	100			
1119TL000616	1119TL000616			5	6	1	0	4	8	7	737.4	100	100			
1119TL000636	1119TL000636			3	0	0	0	0	3	3	762.1	100	100			
1119TL000641	1119TL000641			1	1	0	0	1	1	2	801.7	100	100			

1	<a href="#">ENSG0000017757</a>	FAM87B	1	752751	755214	family with sequence similarity 87, member B [Source:HGNC Symbol;Acc:32236]	...	1	1	0	0	0	0	0	0	0
2	<a href="#">ENSG00000187583</a>	PLEKHN1	1	901877	911245	pleckstrin homology domain containing, family N member 1 [Source:HGNC Symbol;Acc:25284]	...	1	1	0	0	1	0	0	0	0
3	<a href="#">ENSG00000187642</a>	C1orf170	1	910579	917497	chromosome 1 open reading frame 170 [Source:HGNC Symbol;Acc:28208]	...	6	6	0	0	6	0	0	0	0
4	<a href="#">ENSG00000188290</a>	HES4	1	934342	935552	hairy and enhancer of split 4 (Drosophila) [Source:HGNC Symbol;Acc:24149]	...	1	1	0	0	1	0	0	0	0
5	<a href="#">ENSG00000131584</a>	ACAP3	1	1227756	1244989	ArtGAP with coiled-coil, ankyrin repeat and PH domains 3 [Source:HGNC Symbol;Acc:16754]	...	3	3	0	0	3	0	0	0	0
6	<a href="#">ENSG00000221978</a>	CCNL2	1	1321091	1334708	cyclin L2 [Source:HGNC Symbol;Acc:20570]	...	1	1	0	0	1	0	0	0	0
								1	1	0	0	1	0	0	1	1

01/04/2020

# Query By Sample : Variation Level

Same Variation 2 patients

Intersect ☒ Exclude ☒ or ☒ in the attic nb :  Genes ☒ Variations

Exclude : ☒ homozygous ☒ heterozygous ☒ Add All

N	Patients	Sub	Del	Ins	ho	he	Genes	Com p	Cov	5x	15x	he	ho	Sl.
0	TB1	191	29	40	80	180	248	13	10	63	22	✓	✓	+
1	TB2	191	29	40	70	190	248	13	23	83	54	✓	✓	+
2	TB3	60	13	18	56	35	81	8	21	80	49	✓	✓	•

Identical variation in 2 patients and never present in 1

Intersect ☒ Exclude ☒ or ☒ in the attic nb :  Genes ☒ Variations

Exclude : ☒ homozygous ☒ heterozygous ☒ Add All

N	Patients	Sub	Del	Ins	ho	he	Genes	Com p	Cov	5x	15x	he	ho	Sl.
0	TB1	131	16	22	26	143	172	2	10	63	22	✓	✓	+
1	TB2	131	16	22	13	158	172	2	23	83	54	✓	✓	+
2	TB3	0	0	0	0	0	0	0	21	80	49	✓	✓	-

heterozygous variation in 2 patient  
homozygous Variation in 1 data 1

Intersect ☒ Exclude ☒ or ☒ in the attic nb :  Genes ☒ Variations

Exclude : ☒ homozygous ☒ heterozygous ☒ Add All

N	Patients	Sub	Del	Ins	ho	he	Genes	Com p	Cov	5x	15x	he	ho	Sl.
0	TB1	6	1	1	0	8	8	0	10	63	22	✓	✗	+
1	TB2	6	2	1	0	9	8	1	23	83	54	✓	✗	+
2	TB3	5	2	1	8	0	8	0	21	80	49	✗	✓	+

All Variations present in at least «N» patients

Intersect ☒ Exclude ☒ or ☒ in the attic nb :  Genes ☒ Variations

Exclude : ☒ homozygous ☒ heterozygous ☒ Add All



# Familial Studies

**Projects List**

Université Paris Descartes, Institut Imagine

**NGS2012\_0150**  
"NGS"

BIP&D  
Bioinformatics Paris Descartes

Samples 15 \* Chromosomes 24 \* Genes 4908 \* Variations 26698 \* Uniq 8578 \* He 7256 \* Ho 7256 \* Variations \* Type Individual \* Model None \* pnitschk

Graphical View

Workspace

Chromosomes Region Diseases Filter

Select All

Chr	Genes	Sub	Del	Ins	he	ho
1	434	501	90	53	548	91
2	351	424	70	64	471	81
3	267	400	85	45	463	61
4	184	218	53	23	245	41
5	205	231	63	47	259	81
6	256	497	63	38	469	121
7	248	459	58	31	503	41
8	161	188	31	34	210	41
9	189	223	46	38	259	41
10	196	277	39	29	294	51

Filter Intersect Exclude or In the attic at least

Individual Familial Individual

homozygous heterozygous Add All view

N	fam	Patients	Ped	st	Sub	Del	Ins	Genes	Cov	Sx
0	BEN	BEN_ADA_EA			1526	26	22			
1	BEN	BEN_YOU_EA			1452	28	22	100	1402	1072 102 97 93
2	BEN	BEN_HAD_P			1504	25	21	87	1463	1108 102 97 93
3	BEN	BEN_CHA_M			1480	27	18	78	1447	1075 103 97 93
4	CAR	CAR_Flo			821	435	269	296	1229	1173 89 99 97
5	CAR	CAR_OE			874	443	264	300	1223	1153 72 99 96

variation

Fam	Pat	Sub	Del	Ins	Gene
LEF	4	2517	57	35	1579
SEB	1	604	74	75	522
CAR	3	1222	598	378	1564
BEN	4	2276	41	33	1633
DEN	3	2461	785	560	2400

Filter variations

DBSNP (clinical) EVS (None) 1KG (None) Deja vu 0 / 394 only ho variation type (All) Confidence (All) search : Run

Non Coding Consequence: Not exonic (None) No-Coding RNA (mature-miRNA ncRNA) UTR, Splicing (All)


Coding Consequences: with Consequence (All) Without Consequence (No-frameshift)


Predictions: Polyphen (All) sift (All) remove if filtered by Polyphen or and SIFT


Genes


# Famillial Studies : Intra-familial queries


Fam	Pat	Sub	Del	Ins	Gene	Sl.	Model
LEF	4	2517	57	35	1579	●	
SEB	1	604	74	75	522	●	
CAR	3	1222	598	378	1564	●	





 homozygous













 heterozygous

 Add All


 view all

 hide attic


 variation

N	fam	Patients	Ped	st	Sub	Del	Ins	ho	he	Genes	Cov	5x	15x	he
0	LEF	LEF_Jul			1841	31	23	90	1805	1143	58	90	81	
1	LEF	LEF_Emi			1819	36	25	86	1794	1146	54	90	80	
2	LEF	LEF_Fre			1728	35	20	89	1694	1092	41	88	75	
3	LEF	LEF_Isa			1824	34	21	94	1785	1144	50	89	79	


# “inter-familial” queries



Fam	Pat	Sub	Del	Ins	Gene	Sl.	Model
LEF	4	2517	57	35	1579	+	
SEB	1	604	74	75	522	•	
CAR	3	1222	598	378	1564	+	
BEN	4	2276	41	33	1633	•	
DEN	3	2461	785	560	2400	•	



		Sub	Del	Ins	Gene	Sl.	Model
		2517	57	35	1579	+	
SEB	1	604	74	75	522	•	
CAR	3	1222	598	378	1564	+	



		Sub	Del	Ins	Gene	Sl.	Model
		2517	57	35	1579	+	
SEB	1	604	74	75	522	•	
CAR	3	1222	598	378	1564	+	

at least

# Transimission Model

Filter | Intersect Exclude or In the attic at least  | familial | Genetic Model (None) ▼

## Recessive

Ho in affected child  
Not present in no affected  
He in mother and in father

## Compound

2 He in same gene in affected.  
1 from mother the other one from father

## Dominant

Same variation in affected patient

## De novo

Vairation only present in affected children

## Strict-denovo

Denovo +correct covergae on parent alignment.

- None
- Recessif ?
- Compound ?
- Recessif OR Compound ?
- Denovo ?
- Strict-denovo ?
- Dominant ?

# Textual search

er variations

DBSNP ( clinical) | EVS (None) | 1KG (None) | Deja vu 8 / 237 | variation type (All) | Confidence (All) | Genetic Model (None) | Text search :

Non Coding Consequence : Not exonic (None) | No-Coding RNA ( ) | Coding Consequences : Without Consequence ( No-frameshift)

Predictions : Polyphen (All) | sift (All) | remove if filtered b

search :

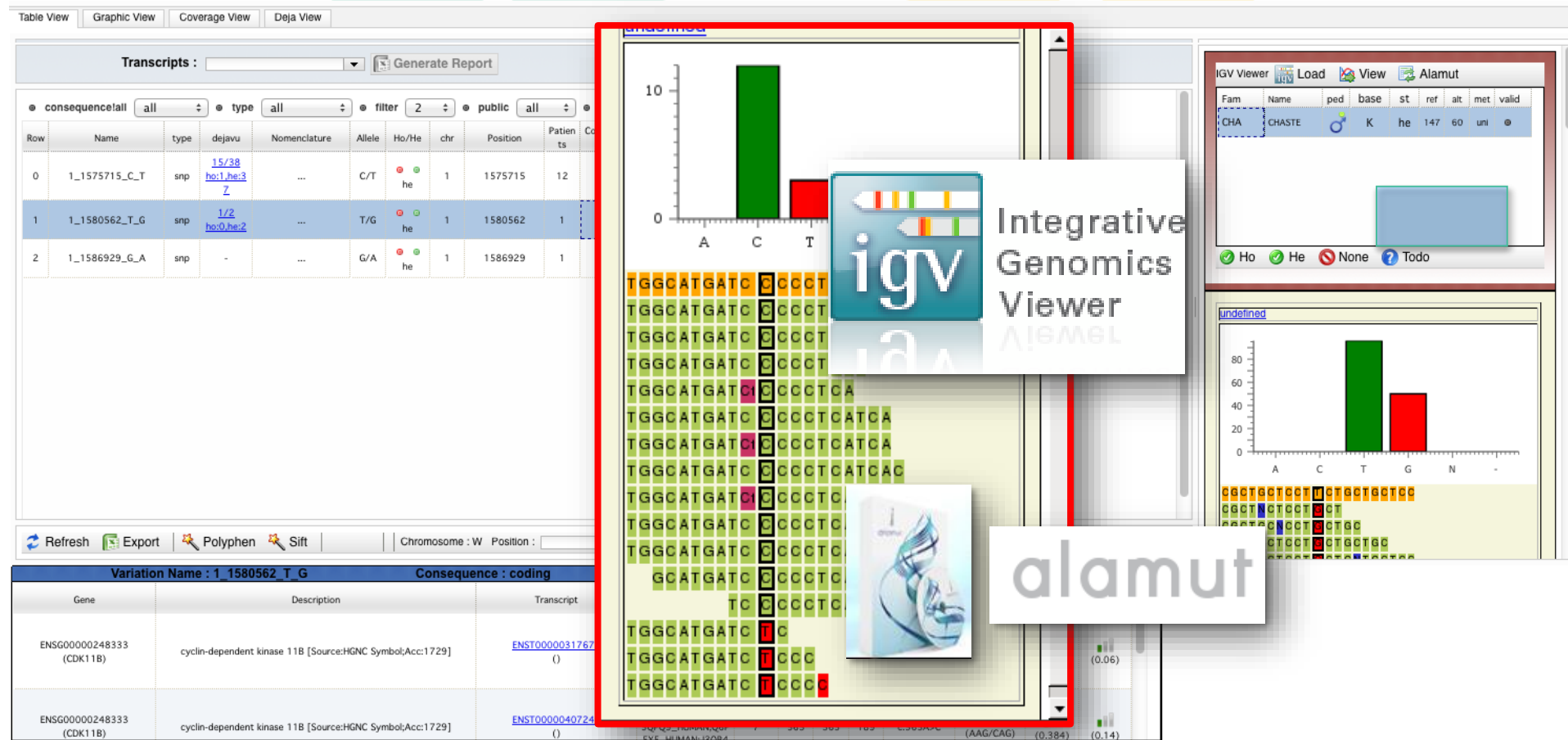
Nom de  
gène

Description

Gene  
Ontology

1	<a href="#">ENSG00000204463</a>	BAG6	6	3160680 5	3162048 2	BCL2-associated athanogene 6 [Source:HGNC Symbol;Acc:13919];kidney development	☆☆	1	1	0	0	1	0	2	0
								2	2	0	0	2	0	0	0
2	<a href="#">ENSG00000182580</a>	EPHB3	3	1842795 72	1843001 97	EPH receptor B3 [Source:HGNC Symbol;Acc:3394];kidney development	☆☆	2	2	0	0	2	0	1	1
								2	2	0	0	2	0	0	0
3	<a href="#">ENSG00000135100</a>	HNF1A	12	1214163 46	1214408 99	HNF1 homeobox A [Source:HGNC Symbol;Acc:11621];kidney development;renal absorption;renal glucose absorption	☆☆	2	2	0	0	2	0	2	0
								7	7	0	0	7	0	0	0
4	<a href="#">ENSG00000132130</a>	LHX1	17	3529408 4	3530191 7	LIM homeobox 1 [Source:HGNC Symbol;Acc:6593];nephron development;kidney development;renal absorption	☆☆	1	1	0	0	1	0	0	0
								1	1	0	0	1	0	0	0

# Variation Visualisation and tools



# Save Filters

The screenshot displays the EUPRD web application interface. A modal dialog box titled "Save Filters" is open, showing a table of saved filters. The background interface includes a "Filter variations" section with options like "DBSNP (clinical)", "EVS (None)", and "1KG (None)". It also has a "Genes" section with a list of genes and their coordinates. The "Save Filters" dialog box has a title bar with "Load Filter", "Save", and "Delete" buttons. The table inside the dialog has the following data:

id	Filter	date
597	filtre1	2013-10-14
598	filtre2	2013-10-14

01/04/2020

# Export data

Chromosomes Region Diseases

Intersect Exclude or In the attic Familial ☒ Individual nb : Genes ☒ Variations

Exclude : ☒ homozygous ☒ heterozygous ☒ Add All

Select All

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	
	type	consequen	dejavu	chr	position	allele	sequence	FEN_Emm	FEN_Isa	FEN_Luc	FEN_Pie	FEN_Hon	he	ho	gene	consequen	transcript	transcript x	description	exon	cdna pos	cds pos	protein	protein_xre	
11_617620_C_T	variations	coding	-	11	617620	C/T	AC[C/T]GC	enotyper : h						2	0	000099834	coding	IT000003397.1NM	cadherin-re	15	2434	2269	ENSP0000000000	CDHR5_H	
11_3249390_C_T	variations	coding	-	11	3249390	C/T	GC[C/T]CC	enotyper : h						2	0	0224513 (A	coding	IT000004341.00103918	MAS-relate	2	947	637	ENSP0000000000	393251_H	
11_9595956_C_T	variations	coding	-	11	9595956	C/T	GG[C/T]GC	enotyper : h						3	0	000166483	coding	IT00000445C.M_003390	MAS-relate	2	947	640	ENSP0000000000	J3KQB9_H	
11_9838494_C_T	variations	coding	-	11	9838494	C/T	TG[C/T]CA	enotyper : h						3	0	000133812	coding	IT00000445C.M_003390	WEE1 hom	1	729	476	ENSP0000000000	E9PRU3_H	
11_10585691_C_T	variations	coding	-	11	10585691	C/T	AA[C/T]AA	enotyper : h						2	0	000133800	coding	IT00000445C.M_003390	SET bindin	2	391		ENSP0000000000	H0VD21_H	
11_17485029_A_T	variations	coding	-	11	17485029	A/T	AT[A/T]GA	enotyper : h						3	0	000006071	coding	IT00000445C.M_003390	SET bindin	29	4009	3871	ENSP0000000000	H0VD21_H	
11_22646405_G_A	variations	coding	-	11	22646405	G/A	AG[G/A]GG	enotyper : h						2	0	000183161	coding	IT00000445C.M_003390	SET bindin	5	618	618	ENSP0000000000	432643_H	
11_47600645_T_A	variations	phase	-	11	47600645	T/A	A[T/A]GGC	enotyper : h						2	0	000133800	coding	IT00000445C.M_003390	MRV11 anti	22602_ex1	-1			ENSP0000000000	B2R672_H
11_57367424_G_A	variations	phase	-	11	57367424	G/A	AG[G/A]GG	enotyper : h						2	0	000133800	coding	IT00000445C.M_003390	MRV11 anti	-21883_ex2	-1			ENSP0000000000	B2R672_H
11_60501008_C_T	variations	phase	-	11	60501008	C/T	AC[C/T]GC	enotyper : h						2	0	000133800	coding	IT00000445C.M_003390	lymphatic v	59_ex2	-1			ENSP0000000000	B2R672_H
11_60538952_G_C	variations	coding	-	11	60538952	G/C	GG[G/C]AG	enotyper : h						2	0	000133800	coding	IT00000445C.M_003390	lymphatic v	-3344_ex2	-1			ENSP0000000000	F2Z296_H
11_62496472_A_G	variations	coding	-	11	62496472	A/G	TA[A/G]TCT	enotyper : h						3	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	578	535	ENSP0000000000	E9PK50_H	
11_6296712_G_A	variations	coding	-	11	6296712	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	604	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	661	535	ENSP0000000000	ABCC8_H	
11_63065342_G_A	variations	coding	-	11	63065342	G/A	AG[G/A]GG	enotyper : h						2	0	000162222	coding	IT00000445C.M_003390	ATP-bindin	4	566	661	ENSP0000000000	ABCC8_H	
11																									

# Example : 2 sporadic cases WES

Auriculocondylar syndrome (ACS) is a rare craniofacial disorder with mandibular hypoplasia and question-mark ears (QMEs) as major features.

Projects List

NGS2013\_0279  
"IQME"

Université Paris Descartes, Institut Imagine

Samples: 2 | Chr: 24 | Genes: 2537 | Variations: 4161 | Uniq: 3597 | Filtration Level: Variations | Type: Individual | Model: None | Annot Version: 31.5

Graphical View

Workspace

Chromosomes | Regions | Genes | Save/Load Filters

Get All | XLS genes | XLS variants

Chr	Genes	Sub	Del	Ins	Cnv
1	235	296	8	1	0
2	152	205	8	3	0
3	148	353	9	4	0
4	99	118	5	4	0
5	97	115	4	1	0
6	152	202	1	2	0
7	116	142	1	3	0
8	99	114	2	0	0
9	110	128	5	3	0
10	106	133	5	4	0

Filter: ☒ Homozygous ☒ Heterozygous ☒ Add All ☒ View ALL ☐ Hide altic ☒ Variation ☒ VCF ☒ HGMD Dejavu

Fam	Patients	Ped	St	Sub	Del	Ins	Cnv	Ho	He	Genes	Cov	15x	30x	He	Ho	SI
HAL_FAR	HAL_FAR			2674	84	44	0	90	2712	1990	102.4	97.8	91.7			
RUZ_QAN	RUZ_QAN			1307	36	16	0	53	1306	846	82.1	97.1	88.5			

Main Filters

DB Public / gnomAD AC ☒ Options (All) ☒ Check Dejavu ☒ Others Projects: 2918 ☒ Ho / He ☒ Search gene or ontology...

Impact Factor ☒ High ☒ Medium ☒ Low ☒ All ☒ Variants ☒ Mature miRNA ☒ Splice AcoDon ☒ Frameshift ☒ Stop-gained ☒ (Start/Stop)-lost ☒ ncRNA ☒ Splice Region ☒ Missense ☒ No-framehift ☒ Pseudogene ☒ Utr ☒ Synonymous ☒ Up/Downstream ☒ Intronic ☒ Intergenic ☒ Run ☒











Others Filters

Genes

Gene(s) Selection ☒ Individual ☒ Intersect ☒ Or ☒ Visualization ☒ View ALL Genes

Name	Xref	Chr	Start	End	Phenotype Description	PolyDiag Capture	Omin is Morbid	Gene HGMD DM	All Pat.	Subs Pat.	Ins/Del Pat.	Cnv Pat.	Low Pat.	Medium Pat.	High Pat.	HGMD Pat.
AKNAD1	AKNAD1	1	109358520	109506106	Diabetes, type 2, association with AKNAD domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28398]				1	1	0	0	0	1	0	0











Fam	Patients	Ped	St	Sub	Del	Ins	Cnv	Ho	He	Genes	Cov	15x	30x	He	Ho	SI
HAL_FAR	HAL_FAR			9	0	0	0	0	9	7	102.4	97.8	91.7			
RUZ_QAN	RUZ_QAN			7	0	0	0	0	7	7	82.1	97.1	88.5			

## REPORT

# Mutations in Endothelin 1 Cause Recessive Auriculocondylar Syndrome and Dominant Isolated Question-Mark Ears

Christopher T. Gordon,<sup>1,2,\*</sup> Florence Petit,<sup>3</sup> Peter M. Kroisel,<sup>4</sup> Linda Jakobsen,<sup>5</sup> Roseli Maria Zechi-Ceide,<sup>6</sup> Myriam Oufadem,<sup>1,2</sup> Christine Bole-Feysot,<sup>7</sup> Solenn Pruvost,<sup>7</sup> Cécile Masson,<sup>2,8</sup> Frédéric Torres,<sup>8</sup> Thierry Hieu,<sup>8</sup> Patrick Nitschké,<sup>2,8</sup> Pernille Lindholm,<sup>9</sup> Philippe Pellerin,<sup>10</sup> Maria Leine Guion-Almeida,<sup>6</sup> Nancy Mizue Kokitsu-Nakata,<sup>6</sup> Siulan Vendramini-Pittoli,<sup>6</sup> Arnold Munnich,<sup>1,2,11</sup> Stanislas Lyonnet,<sup>1,2,11</sup> Muriel Holder-Espinasse,<sup>12</sup> and Jeanne Amiel<sup>1,2,11,\*</sup>

Row	Name	Type	DejaVu	Allele	Ho/He	Chr	Position	Patients	Consequence	Gene	Gene Omim	Pathogenic status	Benign status	Score	DB Freq	Is Clinical	Ncboost
0	6_12292700_T_A	snp	-	T/A	  he	6	12292700	1	Missense	<a href="#">EDN1</a>	<a href="#">Omim</a>			33	0.000 %	Yes	-
1	6_12294189_T_G	snp	-	T/G	  he	6	12294189	1	Stop-gained	<a href="#">EDN1</a>	<a href="#">Omim</a>			41	0.000 %	Yes	-

	Medium	High	HGMD
	Pat.	Pat.	Pat.
	2	0	0
	2	0	0
	1	1	2

# Poly -BackToTheFuture

How to re-analyze data ? (DejaVu)



♥ Don't show me again

7457 New Pathogenic Variants in DataBases [HGMD: hgmd\_pro-2020.1, Clinvar: 20200407]  
We found 381 New Pathogenic Variants in your project(s) !

(with MAX DeJaVu: 100 projects)

(with MAX gnomAD AC: 300)

NGS2014_0480	CerID18-19-egy5-egy6-egy11	1	1		
NGS2015_0665	syndrome ADAM-OLMIER	1	3	1	1
NGS2013_0252	Projet Franck RM	1	1		
NGS2014_0527	RM set14	1	1	1	
NGS2018_1867	Exome-Diag-2017-Serie 1	1	1		
NGS2018_2090	Idefix_EDF_S23	1			
NGS2018_1866	THI BOU BESS MAR	1	1		
NGS2011_0061	neuropathie optique	1			
NGS2011_0084	quebec	1	12	8	
NGS2013_0310	MAR MET	1	1		
NGS2013_0327	Myocapture-J	1			
NGS2014_0381	Anemie de Blackfan-Diamond DBA	1	2	6	6

EOGT recessive 14.5 Ommi Gtex Panel : 4 Adams-Oliver syndrome

Varsome lgv Almut Var\_name Trio Gnomad Deja\_vu Table\_validation Table\_transcript

Fam AO\_13a18

Var	Sex	Age	Phenotype	AC	Ho	Max	Min	AN
AO_17	♀	he	43%	88	+			
AO_18	♂	he	50%	104	+			
AO_13	ho	100%	96	Recessive				
AO_14	-	-	-	-				

3-69050867-T-A

AC	Ho	Max	Min	AN
-	-	afr -0.0000	afr -0.0000	245056

Pr	Sa	Ho
0	0	0
0	0	0

other DI

HGMD	Clinvar	Local
DM	-	-

Adams-Oliver syndrome

consequence	ensl	nm	ccds	appr
Splice Acceptor/Donor	ENST00000383701	XM_005264744;XM_005264743;NM_001278689.1	CCDS63684.1	-
Splice Acceptor/Donor	ENST00000295571	NM_173654.2	CCDS2908.1	-
Splice Acceptor/Donor	ENST00000540764			-

## DM Adams-Oliver syndrome :

Ref : Expanding the phenotype in Adams-Oliver syndrome correlating with the genotype.

OMIM: 614789 dbSNP:rs1312622774 HGMD: CS200536 (2020-02-07)

3p14.1: chr3:69050867-69050867

EOGT: EGF domain specific O-linked N-acetylglucosamine transferase

## Expanding the phenotype in Adams-Oliver syndrome correlating with the genotype.

Dudoignon B<sup>1</sup>, Huber C<sup>2,3</sup>, Michot C<sup>1,2,3</sup>, Di Rocco F<sup>4</sup>, Girard M<sup>5</sup>, Lyonnet S<sup>1</sup>, Rio M<sup>1</sup>, Rabia SH<sup>6</sup>, Daire VC<sup>1,2,3</sup>, Baujat G<sup>1,2,3</sup>.

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# PolyBackToTheFuture : Perspectives



Push the  
information

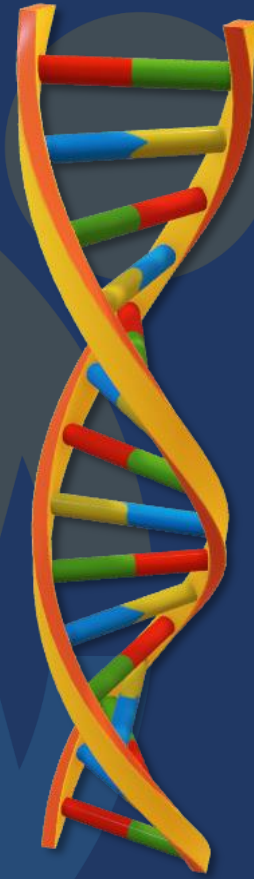


Update  
Gene  
phenotype



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# Thank You



imagine

INSTITUT DES MALADIES GÉNÉTIQUES



EUROPEAN JOINT PROGRAMME  
RARE DISEASES



