

Future developments



Johan den Dunnen

Warning

- I am born optimist
- I am a researcher
- I stress possibilities
esp. the positive sides
- I do understand choices made so far
*do not criticize current choices,
but do think we can do even better*

Your genome

who knows his genome sequence ?

who had a DNA test ?

do you have the DRD4 7R gene ?

...future !?

...your grand children will not believe you dared to live without knowing your genome,

...nor your partner's genome



maybe good to start trying to understand what info your DNA contains

Eerst een DNA-test, dan pas bevruchten

Geneeskunde

Een baby zonder ernstige erfelijke ziekte. Stellen die dat willen, kunnen hun DNA op tientallen ziekten laten testen. Nog vóór ze het kind maken.

Wim Köhler 23 september 2016



*first a
DNA test,
then sex*

nrc.nl

...future !?

*nowadays nobody would start surgery
without an X-ray,*

*why do we start treatment without
knowing the genome ?*

Olaf Rieß

... for the hospital

...a patient will not be treated when the basics, the DNA, is not known

...why risk undesired effects from treatment, when these can be determined beforehand ?

...why risk treating a problem for which the origin lies elsewhere (has a genetic component) ?

Your genome

"preventive medicine"



European Journal of Human Genetics

Article | Published: 05 October 2018

1 in 38 individuals at risk of a dominant medically actionable disease

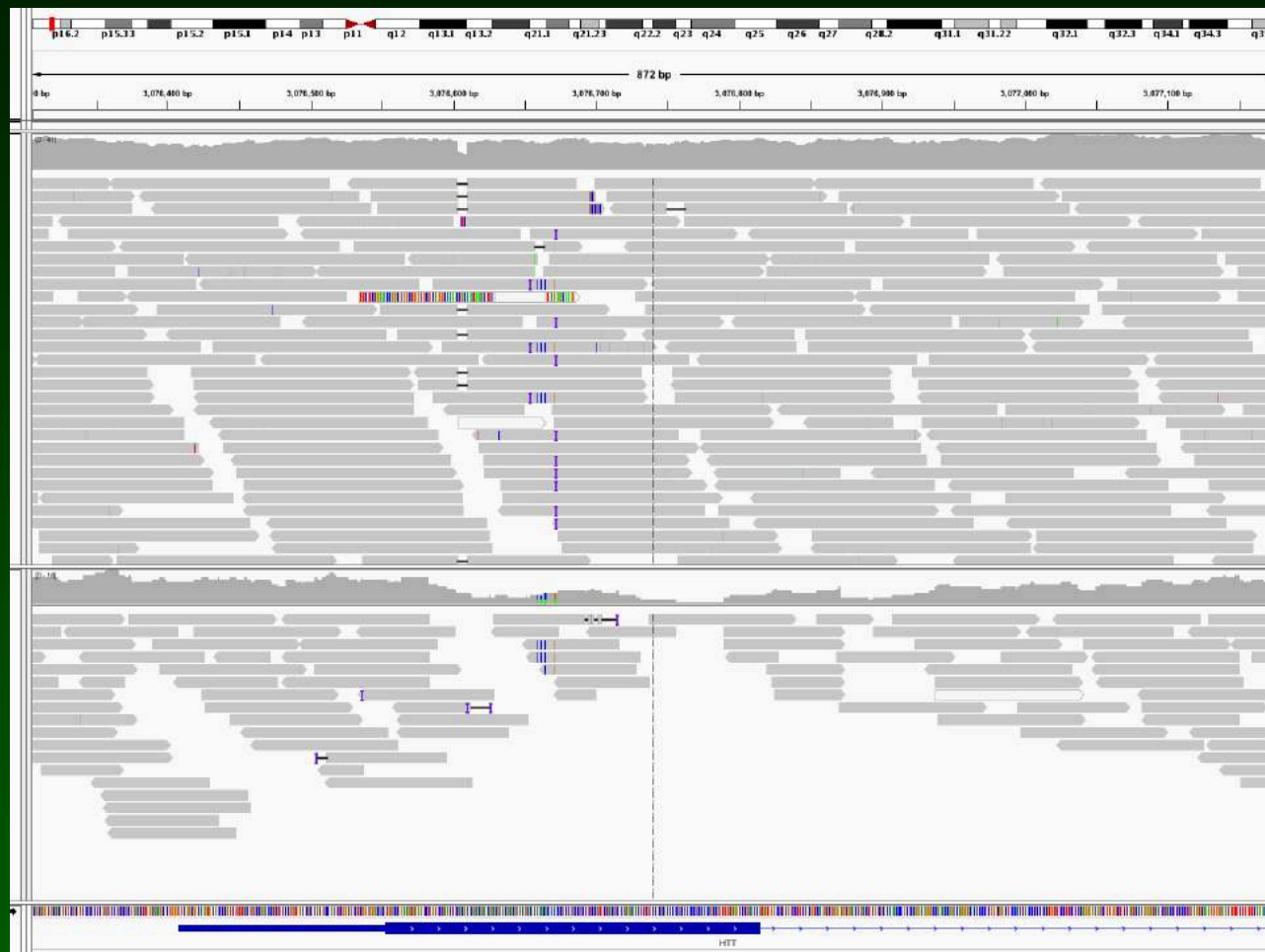
Lonneke Haer-Wigman, Vyne van der Schoot, Ilse Feenstra, Anneke T. Vulto-van Silfhout, Christian Gilissen, Han G. Brunner, Lisenka E. L. M. Vissers & Helger G. Yntema

...and from pharmacogenetic information to fun (bitter taste, m/paternal origin, ...)

My genome

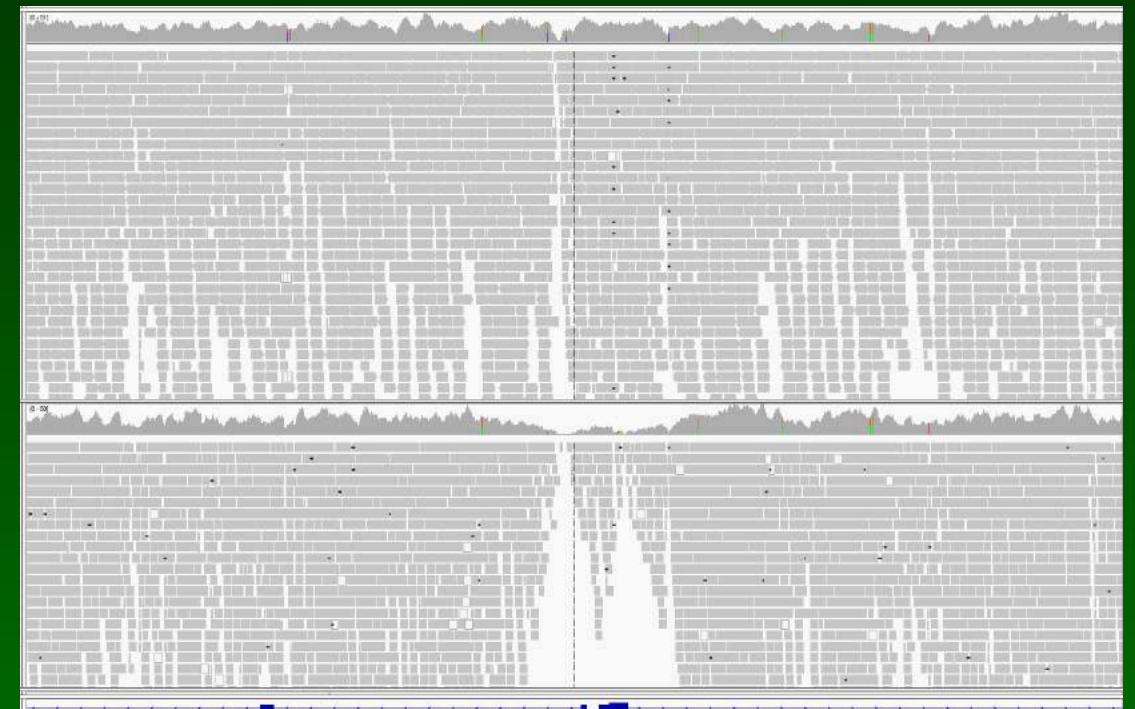
sequenced it twice

*(best way to
determine quality)*



HTT gene

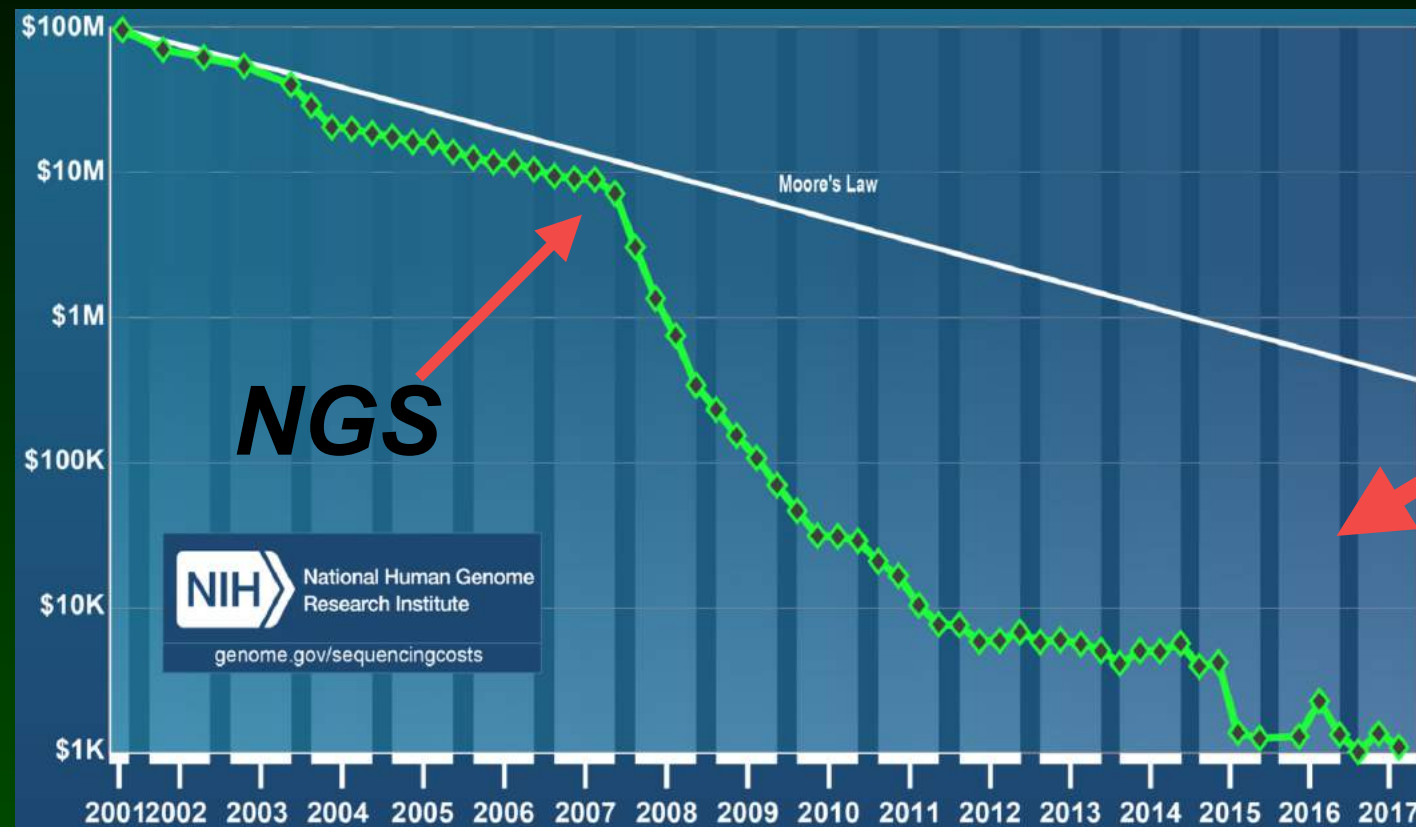
FMR1 gene



*GC-bias
(WGS)*

*top: no PCR (2013)
bottom: few cycles (2017)*

Sequencing revolution



to a €1000 genome

now a reality !



*more sequence
longer reads
faster
cheaper*

GAATTAAGTTCAGGATACAGCCCAATCCTATTCTAGAGTCCATATCAGCAATAGGGTTAT
TCTATCTACNTTCAAATTTCCTCCCTGTACGAAAGGACAAGAGAAATAAGGGCTACTTCACAAA
GTGACAGGTTCAATTTCCTCTTTTAAACAACATACCCATGCCCAAGCTCTACTCTCTATTCTAI
TGACGCCATAAAATCTCTTACCAAGAGCCCTTAAACCCGCCATCTACCATCAGCCCTCTAI
GGCTAGCCGTTTACTCAATCTCTGTATCAGGCTGAGCATCAAACTCAAACTAGCCCTCATCGI
GAACAGCTCTGATTACTCTGCTGCTCATGACCTTGGCCATAATATGATTTATCTCCACACTAI
AAACATTATTATAATAAACACCTCACCACCTNCAATCTTCTAGGAAACATATGAGCCACTI
TATGAAAAAATCTCTACCACTCACTTACTTATATGATATGCTCCATACCCATTAI
CATCCCTGAGAAATCCAAATTTCTCCGTGCCACCTATCACACCCATCTTAAAGTAAGGTCAGC
GGGCTAAGCTCGCACTGATTTTTTACCTGAGTAGGCTAGAAATAAACATGCTAGCTTTTTATTI
CTCCGGACAATGAAACATAACCAATACTACCAATCAATACTCATCATTAAATCATATAGC
CAATCATATACCAATCTCTCTCTCACTAAAGCTAAGGCTTCTCTCACTCTCTCAATCTTAT
ATAACCATTTCTTAATTTAACTATTATATTATGCTAACTACTACCGCATTCCTACTACTCAAC
CTTTTTGGCCAAATGGGCCATTATCGAAGAAATTCACAAAAACAATAGGCTCATCATCCCCACI
ATACAAAAACCCACCCCATTTCTCTCCACACTCATCGCCCTTACCAAGCTACTCTACTATCTI
CACTCTGCATCACTGAAACGCAATCAGCCACTTTAATTAAGCTAAGGCTTACTAGACCAAT
GCTTCTTGGAAATTTGCAATTCAATATGAAATCAGCTCGAGCTGGTAAAAAGAGGCCATAACCI
TATTATTGGGGCATGAGCTGGAGTCTTAGGACAGCTCTAAGGCTCTTATTCTGAGCCGAGC
AACTCACTAGTTCCGCTAATAATCGGTGCCCCCGATATGCGCTTTCCCGGCATAAACCAACATA
TGGAGCTTCCGTAGAGCTAAGCATCTTCTCTTACACCTAGCAAGCTGCTCTCTATCTTACG
TCCAGTCTAGCTGCTGGCATCACTATCTACTAACAGACCGCAACCTCAACACCCCTTCT
ACTTACTACTCCGAAAAAAGAACCATTTGGATACATAGCTATGGTCTGAGCTATCATATCA
CAAGTATTTAGCTGACTCGCCCACTCCACGGAGCAATATGAATGATCTGCTGCACTGCT
ACTATGCTCATCAATAGGAGCTGATTTGCCATCATAGGAGGCTTCATTCACTGATTTCCCT
CGACGTTACTCGGACTACCCGATGCATACCCACATGAACATCTCATCTGTAGGCTCA
ATGCCCCCACCCTACCAACATTCGAAGAACCGTANACATAAAATCTAGACAGAAAGGAAI
CCTATATATCTTAATGCCATATGCAGCGCAAGTAGGTCTACAGAGCTACTTCCCTATCAT

*...single molecule
...label-free*

World record



Kingsmore Has Done it Again: Rady Children's Set Guinness World Record for Genetic Diagnosis

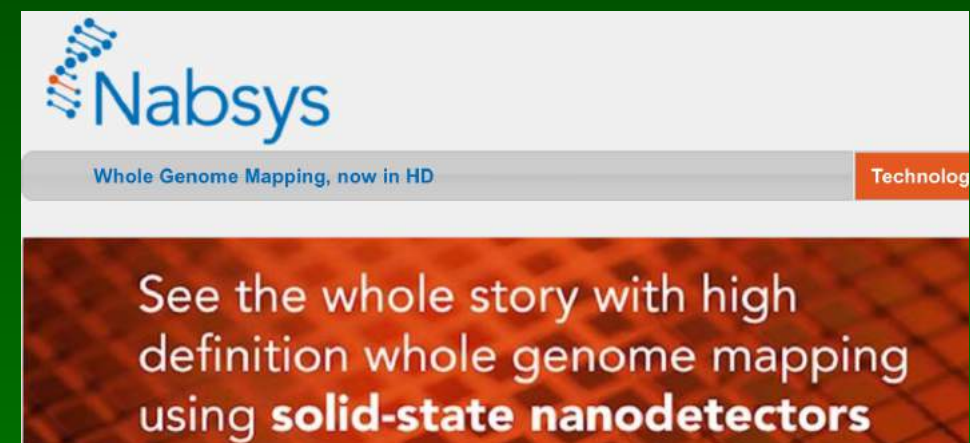
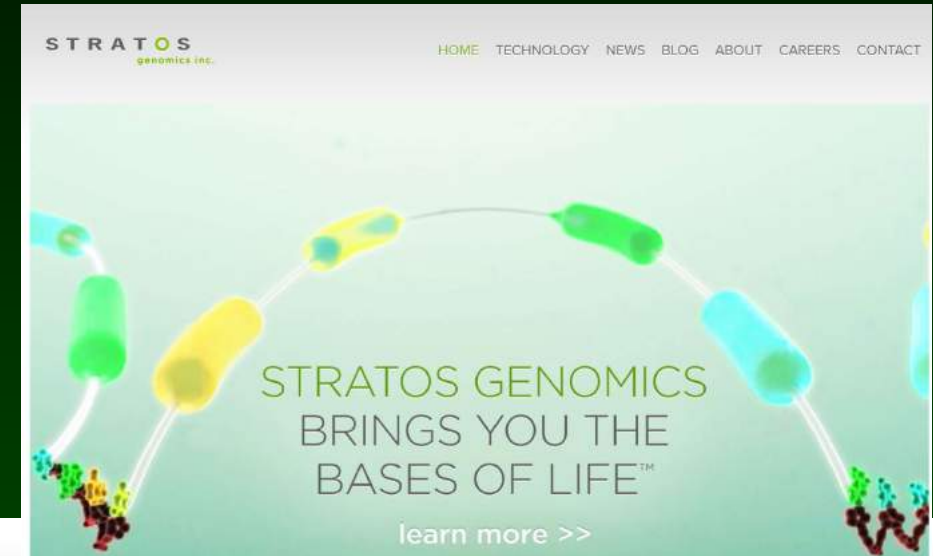
*19.5 h
incl. diagnosis*

Front Line
Genomics
Unzipping genes for the good of humanity



Single molecule sequencing

nanopore technology

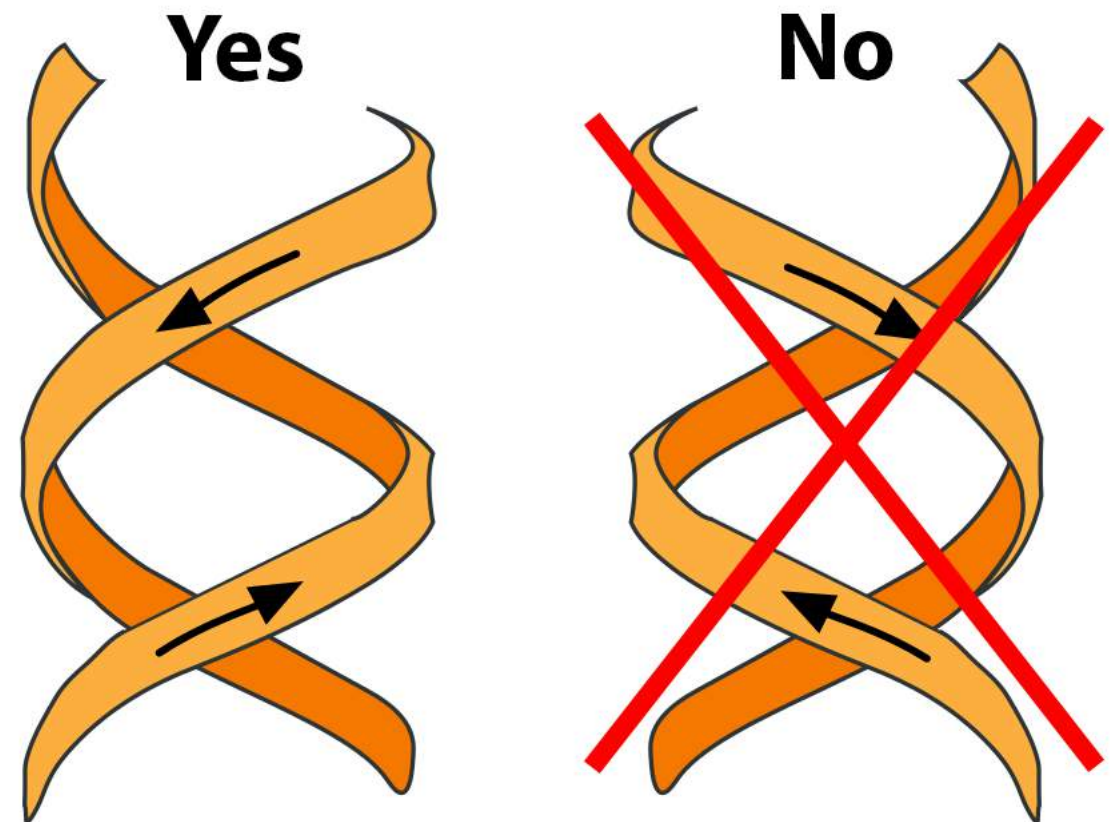


DNA



will the system work?

***...YOU did pay
attention at school***



ESHG 2019

Future technology



twoporeguys

Meet the Guys...



..and then



SmidgION



*sequence
@home*

Long-read seq


nature
COMMUNICATIONS

Article | OPEN | Published: 30 June 2016

Long-read sequencing and *de novo* assembly of a Chinese genome


Lingling Shi, Yunfei Guo [...] Kai Wang 

Nature Communications **7**, Article number: 12065 (2016) | [Download Citation](#) 

Journal of
Human Genetics

Article | Published: 13 February 2019

A 12-kb structural variation in progressive myoclonic epilepsy was newly identified by long-read whole-genome sequencing


Takeshi Mizuguchi, Takeshi Suzuki, Chihiro Abe, Ayako Umemura, Katsushi Tokunaga, Yosuke Kawai, Minoru Nakamura, Masao Nagasaki, Kengo Kinoshita, Yasunobu Okamura, Satoko Miyatake, Naomichi Matsumoto 

Genome Biology

Menu 

Research | Open Access

Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight

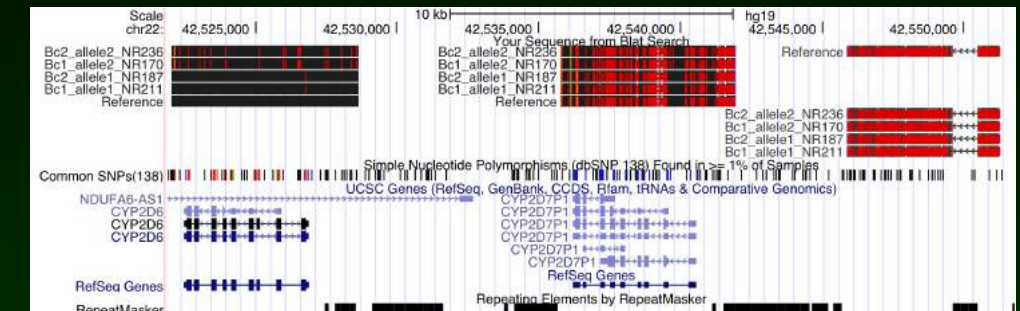
Mark T. W. Ebbert [†], Tanner D. Jensen [†], Karen Jansen-West, Jonathon P. Sens, Joseph S. Reddy, Perry G. Ridqe,

Long-read seq

(*phasing*)

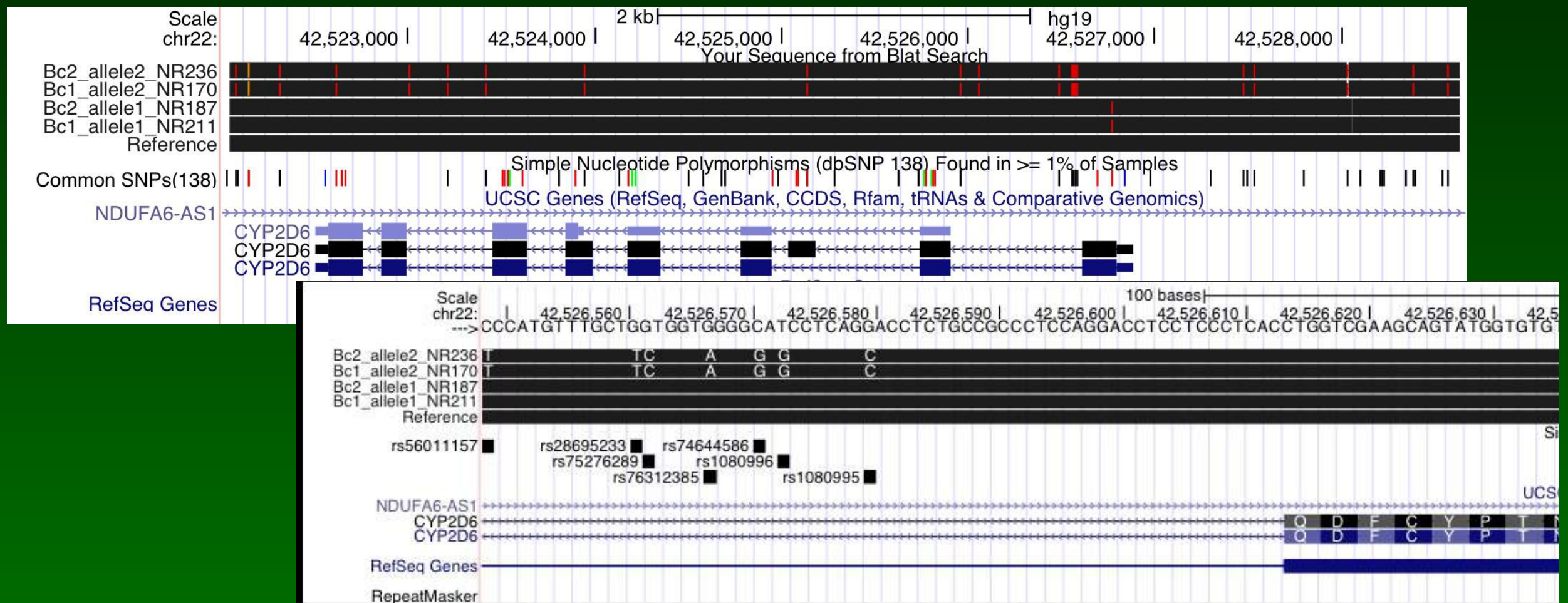
• CYP2D6

long-range PCR > PacBio seq
2 alleles clearly separated



CYP2D6

CYP2D6-like



PacBio allele-seq

- **PKD1 gene**
unique 3' end, repetitive 5' end
long-range PCR far into repetitive region
- **PMS2 gene**
several pseudogenes
specific long-range PCR and/or
discriminate based on sequence
get & load long molecules
- **...other genes**
CYP-genes
discriminate maternal/paternal
long-range cDNA-seq

MYL6 cDNA



Rare cases ?

- many mono-genic diseases solved

*where are the di-genic diseases ??
I would expect many more*

NATURE GENETICS VOLUME 44 | NUMBER 12 | DECEMBER 2012

Digenic inheritance of an *SMCHD1* mutation and an FSHD-permissive D4Z4 allele causes facioscapulohumeral muscular dystrophy type 2

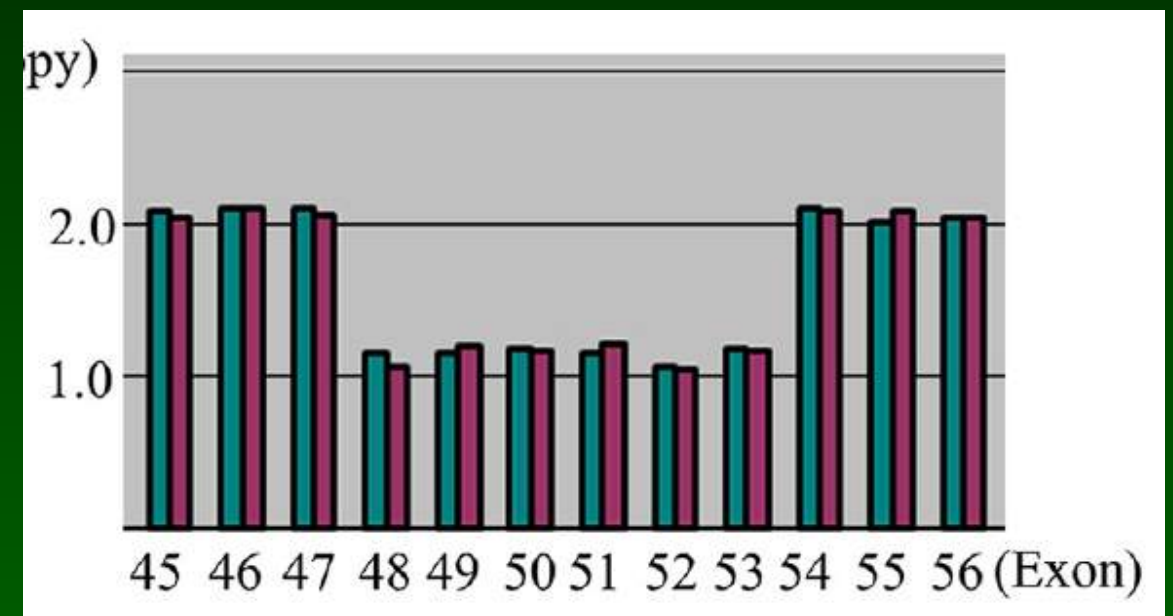
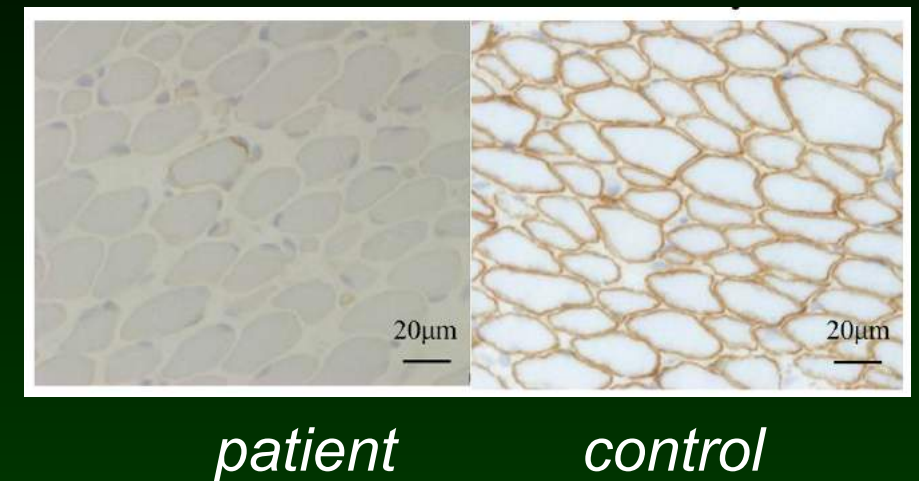
Richard J L F Lemmers^{1,13}, Rabi Tawil^{2,13}, Lisa M Petek³, Judit Balog¹, Gregory J Block³, Gijs W E Santen⁴, Amanda M Amell³, Patrick J van der Vliet¹, Rowida Almomani⁴, Kirsten R Straasheijm¹, Yvonne D Krom¹, Rinse Klooster¹, Yu Sun¹, Johan T den Dunnen^{1,4}, Quinta Helmer⁵, Colleen M Donlin-Smith², George W Padberg⁶, Baziell G M van Engelen⁶, Jessica C de Greef^{1,12}, Annemieke M Aartsma-Rus¹, Rune R Frants¹, Marianne de Visser⁷, Claude Desnuelle^{8,9}, Sabrina Sacconi^{8,9}, Galina N Filippova¹⁰, Bert Bakker⁴, Michael J Bamshad^{3,11}, Stephen J Tapscott¹⁰, Daniel G Miller^{3,11} & Silvere M van der Maarel¹

*clear phenotype
unsolved FSHD cases*

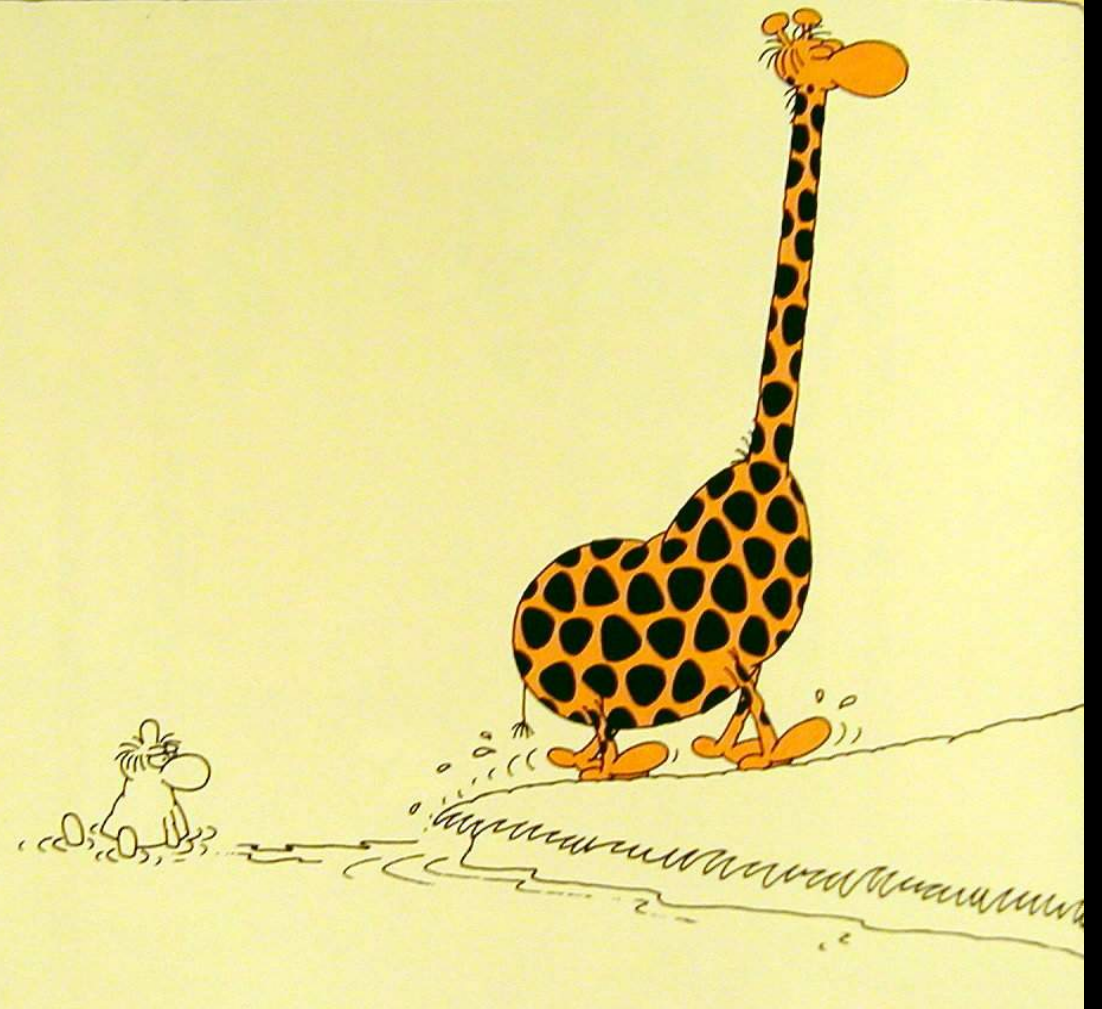
*WES analysis several families
shared SMCHD1 variants*

Female DMD

- muscle biopsy
no dystrophin staining
- MLPA
*deletion exons 48-53
in-frame*
- sequencing
no deleterious variants
- X-inactivation
random



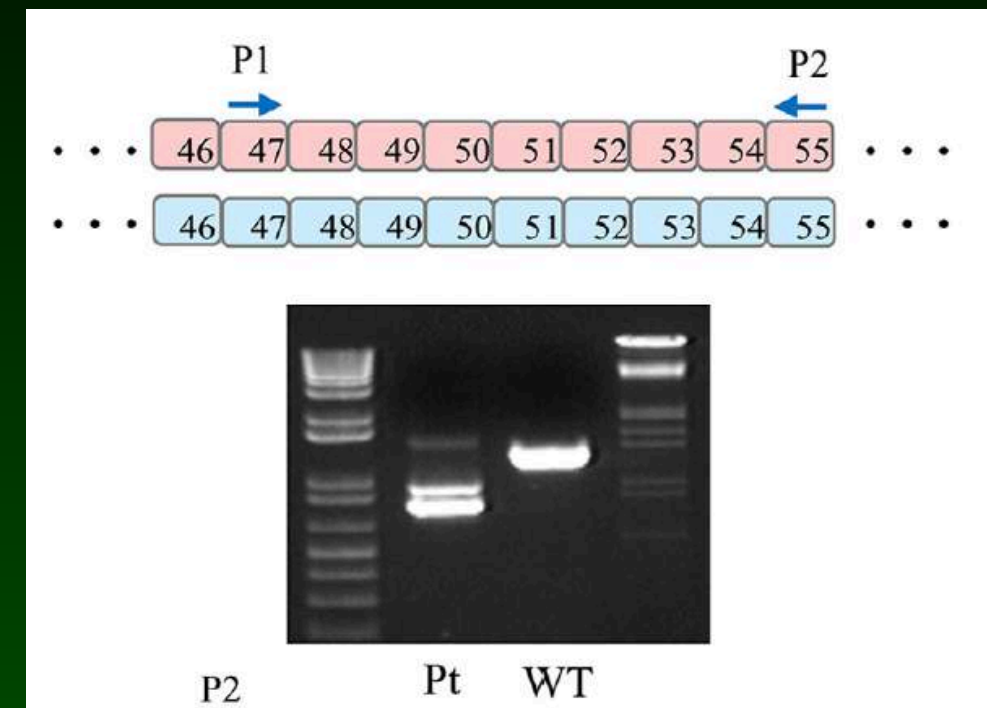
*Is my
conclusion
right ?*



Female DMD

- RNA analysis

RNA analysis



Available online at www.sciencedirect.com

ScienceDirect

Neuromuscular Disorders 27 (2017) 569–573

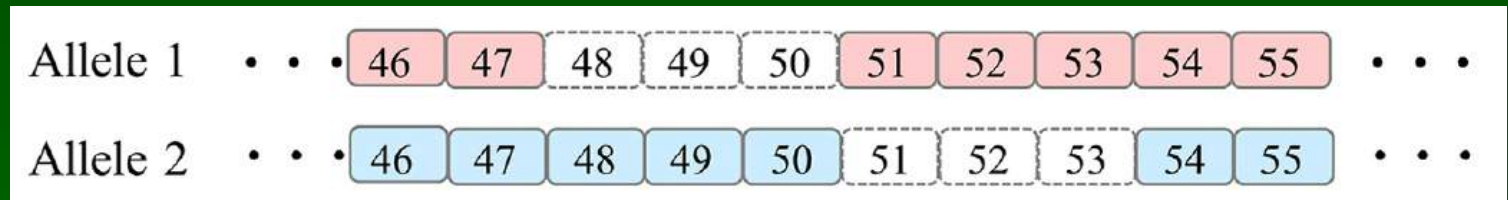
Case report

Duchenne muscular dystrophy in a female with compound heterozygous contiguous exon deletions

Eri Takeshita ^{a,*}, Narihiro Minami ^{b,c}, Kumiko Minami ^c, Mikiya Suzuki ^d, Takeya Awashima ^a, Akihiko Ishiyama ^a, Hirofumi Komaki ^a, Ichizo Nishino ^{c,e}, Masayuki Sasaki ^a

^a Department of Cellular Neurology, National Center for Child Health and Development, Tokyo, Japan; ^b Department of Pediatrics, National Center for Child Health and Development, Tokyo, Japan; ^c Department of Pediatrics, National Center for Child Health and Development, Tokyo, Japan; ^d Department of Pediatrics, National Center for Child Health and Development, Tokyo, Japan; ^e Department of Pediatrics, National Center for Child Health and Development, Tokyo, Japan

*two different deletions,
both frame shifting*



RNA, it exists !

..the neglected molecule

under-appreciated

most go blindly DNA > protein

..there is much more

Describe ?


NOTE: reference sequences can be assumed to be known, spaces in descriptions used for clarity only.


MLPA shows all exons are present except exons 3 to 6 (nucleotide c.411 to 1428). Which description(s) is/are correct ?

- c.411-?_1428+?del
- c.(411-?_1428+?)del
- c.(410+1_411-1)_(1428+1_1429-1)del **correct**
- c.411_?_1428del
- none of these

NOTE: using probe-based positions would be even better

MILPA variants

LOVD³ Leiden Open Variation Database  **Global Variome shared LOVD** LOVD is supported by the Human Variome Project

CAPN3 (calpain 3, (p94)) 

Curators: [Johan den Dunnen](#) and [Jacqui Beckmann](#)

[Genes](#) [Transcripts](#) [Variants](#) [Individuals](#) [Diseases](#) [Screenings](#) [Submit](#)

CAPN3 gene homepage

This database is one of the gene variant databases from the [Leiden Muscular Dystrophy pages](#)

General information	
Gene symbol	CAPN3
Gene name	calpain 3, (p94)
Chromosome	15
Chromosomal band	q15.1
Imprinted	Unknown
Genomic reference	NG_008660.1
Transcript reference	NM_000070.2
Exon/intron information	NM_000070.2 exon/intron table
Associated with diseases	LGMD-2 , LGMD-2A
Citation reference(s)	-
Refseq URL	Genomic reference sequence
Curators (2)	Johan den Dunnen and Jacqui Beckmann
Total number of public variants reported	2791
Unique public DNA variants reported	635
Individuals with public variants	2263
Hidden variants	445

exon	c.startExon	c.endExon	g.startExon	g.endExon	lengthExon	lengthIntron
1	-306	309	16398	17012	615	24368
2	310	379	41381	41450	70	1614
3	380	498	43065	43183	119	1467
4	499	632	44651	44784	134	1041
5	633	801	45826	45994	169	856
6	802	945	46851	46994	144	2542
7	946	1029	49537	49620	84	1533
8	1030	1115	51151	51238	86	3458

calpain 3, (p94) (CAPN3) - 313 nt intron 11

(intronic numbering for coding DNA Reference Sequence)

```

gtgtgcagtcctgattggctccagccaggaaacatactttccaggaggacgcttcca g.58768
c.1524+60
ggggcttctagagggggccctctggttcctcaatacccagtgacccacagagctcctggt g.58828
c.1524+120
atcaggaccacttggtgtttgtaacaagcaaaaaatac g.58865
c.1524+157
----- middle of intron -----
g.58866
c.1525-156 cagggggggcattagagagcagtgaggcgggctcg g.58901
c.1525-121
gcagaacagggtgctgggggtcaggcttcgcgcgcgggctgcagttgctggcattgcct g.58961
c.1525-61
tcgcaggctcctcatcctcattcacatctgaagcatcttcttctgtttcttctcaag g.59021
c.1525-1

```

Graphical displays and utilities

Graphs

Reading frame checker

Graphs displaying summary information of all variants in the database »
The Reading-frame checker generates a prediction of the effect of whole-exon changes. Active for: [NM_000070.2](#).

UCSC Genome Browser

Show variants in the UCSC Genome Browser ([full view](#), [compact view](#))

Ensembl Genome Browser

Show variants in the Ensembl Genome Browser ([full view](#), [compact view](#))

NCBI Sequence Viewer

Show distribution histogram of variants in the [NCBI Sequence Viewer](#)

MILPA variants

Graphical displays and utilities

Graphs	Graphs displaying summary information of all variants in the database »
Reading frame checker	The Reading-frame checker generates a prediction of the effect of whole-exon changes. Active for: NM_000070.2 .
UCSC Genome Browser	Show variants in the UCSC Genome Browser (full view , compact view)
Ensembl Genome Browser	Show variants in the Ensembl Genome Browser (full view , compact view)
NCBI Sequence Viewer	Show distribution histogram of variants in the NCBI Sequence Viewer

Currently viewing gene/transcript: **CAPN3 / NM_000070.2**

Deletion or Duplication

Deletion ▼

From exon

6 ▼

To exon

11 ▼

Check

Deleting exon 6 to exon 11 leads to ... an IN-FRAME deletion.

According to the CAPN3_NM_000070.2 reference sequence in the LOVD database,
ex06ex11del -> c.802-?_1524+?del

...will be modified to report HGVS correct

c.(801+1_802-1)_(1524+1_1525-1)del

LOVD queries

queries

- | = or
A>T | T>A
- ! = not
> !>T

4997 entries on 50 pages. Showing entries 1001 - 1100.

100 per page **Legend** << First < Prev 1 2 3 4 5

Effect	Reported	Exon	DNA change (cDNA)
+/.		1 6	c.484dup
+/.		1 6	c.484_493delinsTGGCTTTGAAT
+/.		1 6	c.485_486dup
+/.		1 6	c.487T>G
+/.		2 6	c.488G>A
+?/.		1 6	c.488G>C
+/.		1 6	c.489G>A
-?/., +?/., ?/.		3 6	c.494A>T

sort

Search terms	Field	Result
>	Variant/DNA	Show only substitutions
A>T T>A	Variant/DNA	Show only A to T or T to A substitutions
c.328 >	Variant/DNA	Show only substitutions at position c.328
p.(Arg X)	Variant/Protein	Show only arginine to stopcodon changes
Asian	Patient/Origin/Ethnic	Shows "Asian", but also "Caucasian" entries
Asian !Caucasian	Patient/Origin/Ethnic	Shows "Asian", but no "Caucasian" entries
Asian African !Caucasian	Patient/Origin/Ethnic	Shows "Asian" or "African", but no "Caucasian" entries
"South Asian"	Patient/Origin/Ethnic	Shows "South Asian", but no "South East Asian" entries



c.62G>A lovd

Search

[Advanced Search](#)
[Preferences](#)



Web [Show options...](#)

Essayez avec cette orthographe : [c.62G>A love](#)

Did you mean: [c.62G>A loved](#)

[Search unique variants - LOVD - Leiden Open Variation Database ...](#)

02, c.62G>A, -, r.(?) p.(Arg21Gln), ARG1_00001, -, -, Mitchell 2009, DNA, HRMA ... Powered by LOVD v.2.0 Build 18. Enabled modules: showmaxdbid, chromium.liacs.nl/LOVD2/variants.php?select_db=ARG1&unique&search_pathogenic_=- - 28k - [Cached](#) - [Similar pages](#)

[View unique variants - LOVD - Leiden Open](#)

01, 1-62G>A (Reported 10 times), -, -, GCK_00037, Leu20Pro, GCK_00063, -. 02, 106C>T (Reported 2 times) chromium.liacs.nl/LOVD2/variants.php?action=view_ [Cached](#) - [Similar pages](#)

[More results from chromium.liacs.nl »](#)

[Variants - NGRL, Manchester LOVD - Leiden Open](#)

NGRL, Manchester LOVD. ubiquitin protein ligase E3A (UBE3A) RNA change. Protein, p.Cys21Tyr (predicted) ... ngrl.man.ac.uk/lovd2/variants.php?select_db=UBE3A&action=view_0000082%2C0000082%2C21 - [Similar pages](#)



c.1A>G LOVD

[ALL](#)

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[BOOKS](#)

Did you mean: [c.1A>G LOVE](#)

[HBB:c.1A>G - bx.psu.edu\).](#)

<https://lovd.bx.psu.edu> › variants › DNA...

HBB homepage View unique variants Public list of submitters Submit new data View unique variants · Search unique ... LOVD - Variant listings for HBB. Unhide

[All transcript variants in gene FANCA - Global Variome shared LOVD](#)

<https://databases.lovd.nl> › shared › FANCA



c.62G>A lovd

Search

[Advanced Search](#)
[Preferences](#)



Web [Show options...](#)

Essayez avec cette orthographe : [c.62G>A love](#)

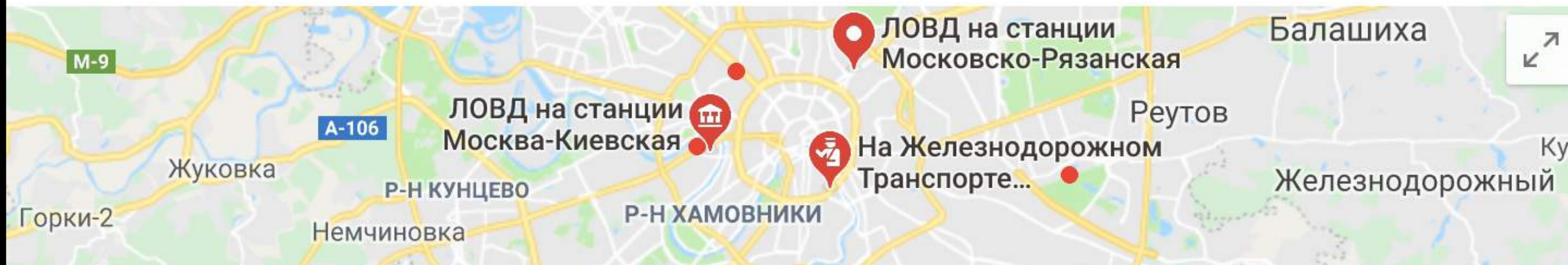
Did you mean: [c.62G>A loved](#)

[Search unique variants - LOVD - Leiden Open Variation Database ...](#)

02, c.62G>A, - , r.(?) p.(Arg21Gln), ARG1, 00001, - , - , Mitchell 2009, DNA, HRMA ... Powered

Lovd

Москва [Обновить местоположение](#)



<https://lovd.bx.psu.edu/variants/DNA/...>

HBB homepage View unique variants Public list of submitters Submit new data
View unique variants · Search unique ... LOVD - Variant listings for HBB. Unhide

[All transcript variants in gene FANCA - Global Variome shared LOVD](#)
<https://databases.lovd.nl/shared/FANCA>

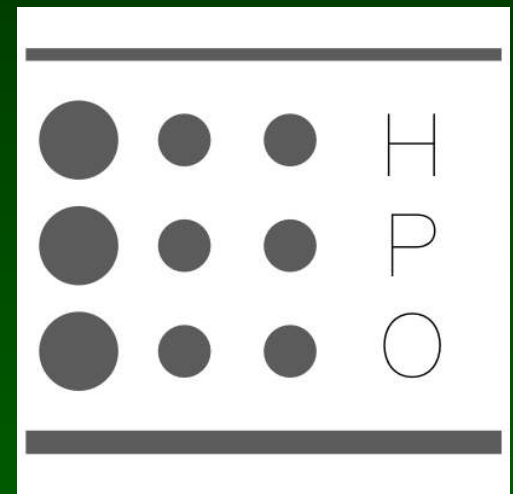
Standards

- annoying, ...but
we need them
...and use without errors



- variants
HGVS nomenclature

- phenotypes
Human Phenotype Ontology (HPO)



- classification
ACMG

Variant classification

standards for classification

ACMG recommendations

labs start sharing classifications

ACMG:

"beware of variants that may impact splicing"

Variant Annotation Integrator

Select Genome Assembly and Region

clade: Mammal genome: Human assembly: Feb. 2009 (GRCh37/hg19)

region to annotate: genome

Select Variants



varsome

Verdict: Likely Pathogenic

Rules

<input checked="" type="checkbox"/> PVS1	<input checked="" type="checkbox"/> PS1	<input checked="" type="checkbox"/> PS2	<input checked="" type="checkbox"/> PS3	<input type="checkbox"/> PS4	<input checked="" type="checkbox"/> PM1	<input checked="" type="checkbox"/> PM2	<input type="checkbox"/> PM3
<input checked="" type="checkbox"/> PM4	<input checked="" type="checkbox"/> PM5	<input checked="" type="checkbox"/> PM6	<input checked="" type="checkbox"/> PP1	<input checked="" type="checkbox"/> PP2	<input checked="" type="checkbox"/> PP3	<input type="checkbox"/> PP4	<input checked="" type="checkbox"/> PP5
<input checked="" type="checkbox"/> BA1	<input type="checkbox"/> BS1	<input type="checkbox"/> BS2	<input checked="" type="checkbox"/> BS3	<input checked="" type="checkbox"/> BS4			
<input checked="" type="checkbox"/> BP1	<input type="checkbox"/> BP2	<input checked="" type="checkbox"/> BP3	<input checked="" type="checkbox"/> BP4	<input type="checkbox"/> BP5	<input checked="" type="checkbox"/> BP6	<input checked="" type="checkbox"/> BP7	

Gene panels

- 20,000 protein coding
60,000 total
- which gene should be in a specific panel
- which transcript to use
preferred reference transcript



New rare disease gene tool launched
PanelApp

standards for analysis, agreement on what to analyse

Databases

...all these databases

DNA diagnostics is based on:

***SHARING** what we know on the **relation**
between **variants in genes** & **phenotypes***

without sharing, no DNA diagnostics

***Variant of Uninsufficient Sharing**
(VUS)*

A good idea ?

*you are only allowed to perform
clinical diagnosis when you have
sequenced your own genome*

(what about a VUS in your genome ?)



my data

- **LOVD (Global Variome sha...** 08:48
LOVD submission (TASP1)
Curator: LOVD-team, but with Curator vacancy Managers: Johan den Dunnen...
- **LOVD (Global Variome sha...** 08:47
LOVD submission update (TASP1)
Curator: LOVD-team, but with Curator vacancy Dear Curator, Ayman El-Hatta...
- **LOVD (Global Variome sha...** 08:40
LOVD submission update (TASP1)
Curator: LOVD-team, but with Curator vacancy Dear Curator, Ayman El-Hatta...
- **LOVD (Global Variome s...** 08:38 >>
LOVD submission (THOC6)
Curator: LOVD-team, but with Curator vacancy Dear Curator, MedGenome_d...
- **LOVD (Global Variome sha...** 08:37
LOVD submission update (TASP1)
Curator: LOVD-team, but with Curator vacancy Dear Curator, Ayman El-Hatta...
- **LOVD (Global Variome sha...** 08:29
LOVD submission (TASP1)
Curator: LOVD-team, but with Curator vacancy Managers: Johan den Dunnen...
- **LOVD (Global Variome shar...** 08:16
LOVD submission

The DNA bank

you in control of your data

INVITED COMMENTARY

Human Mutation

OFFICIAL JOURNAL

HGVS

HUMAN GENOME
VARIATION SOCIETY

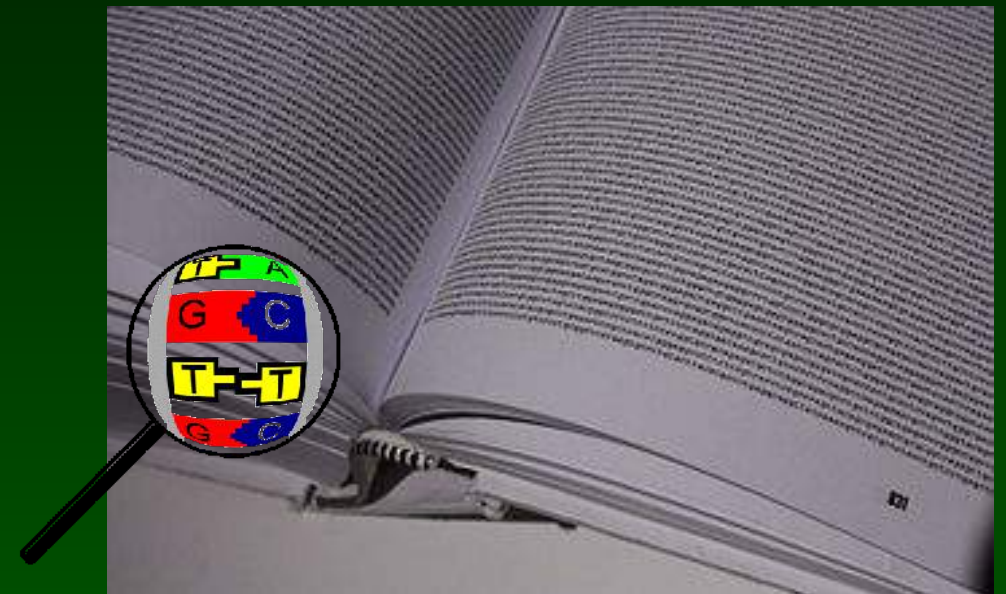
www.hgvs.org

**The DNA Bank: High-Security Bank Accounts to Protect
and Share Your Genetic Identity**

Johan T. den Dunnen*

Human Mutation (2015) 36: 657

*everybody should own
all their genetic data*



when you do not agree, who should?

(the state, hospital, GP, insurance company, ..)

Adopt a gene !

become a
foster parent
database curator



*claim your child at
gene.LOVD.nl*



*essential on your CV
...only ~15,000 available*



*with 7,000,000,000 people
chance 1/400,000*

ru.LOVD.org

[Home](#)
[Variants in individuals from Russian Federation](#)
[Variant](#)

126 entries on 6 pages. Showing entries 1 - 25.

25 per page

Legend

« First

< Prev

1

2

3

4

5

6

Gene	Transcript	Effect	DNA change (cDNA)
APC	NM_000038.5	+/.	c.218_219insTA
APC	NM_000038.5	+/.	c.694C>T
APC	NM_000038.5	+/.	c.712C>T

Country node

Nodo mexicano del Varioma Humano
Based on:
LOVD
Leiden Open Variation Database

[Home](#) [Variants in individuals from Mexico](#) [Variants by submitters from Mexico](#) [Registrarse](#) [Log in](#)


sharing data • reducing disease

Proyecto del Varioma Humano
El HVP es una Organización Internacional No Gubernamental que exhorta a reducir las enfermedades genéticas a través de compartir gratuitamente el conocimiento derivado del estudio de las variantes en el genoma humano.

HVP es auspiciado por la Organización para la Educación, la Ciencia y la Cultura de las Naciones Unidas (UNESCO) para asegurar y garantizar que la información de variantes genéticas y su efecto sobre la salud humana pueda captarse, ser curada, interpretada y compartida libre y abiertamente.

Para coleccionar las variantes genéticas de una población, un país o una región y revisar esta información para hacerla confiable para su uso en la práctica clínica, se requiere de un repositorio electrónico al cual se le ha denominado "nodo" y se compone de un conjunto de bases de datos de genes relevantes a estudiar para cada país, un comité científico/académico y reglas de operación.

GV shared LOVD offers access to country home page

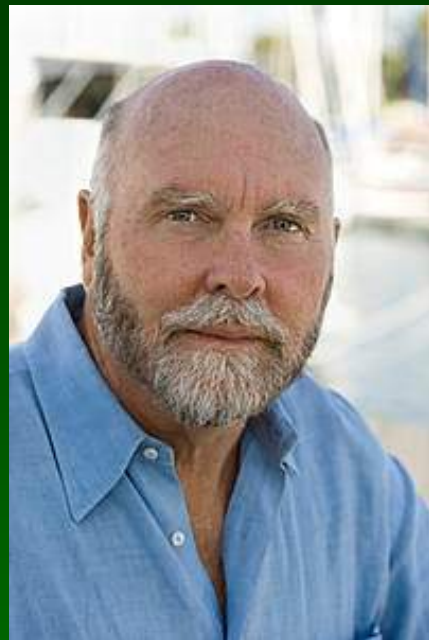
Focus on disease

(individual genomes sequenced)



James Watson

*JLupsky, Kim,
GChurch, DTutu, JFlattery,
MSnyder,
....*



Craig Venter

Marjolein Kriek



A rumour

female DNA finally sequenced



© 2008 Lectrr.be - Eerder verschenen in Metro.

"here the defective gene for parking a car backwards"

From: **Pastafarian** ®

Subject: **re: Scientists claim to understand women
Nobel Prize for them**

27/05/2008 3:15:32 PM

post id: 3604572

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Scientists crack women's DNA code

FINALLY, men may be able to understand women,
it seems. Dutch scientists said they have mapped
the full genetic sequence of an individual
woman's DNA for the first time.

Researchers at Leiden University Medical Centre said they had sequenced the genome of one of their researchers, geneticist Marjolein Kriek, and plan to publish it after review.

Focus on disease

(individual genomes sequenced)



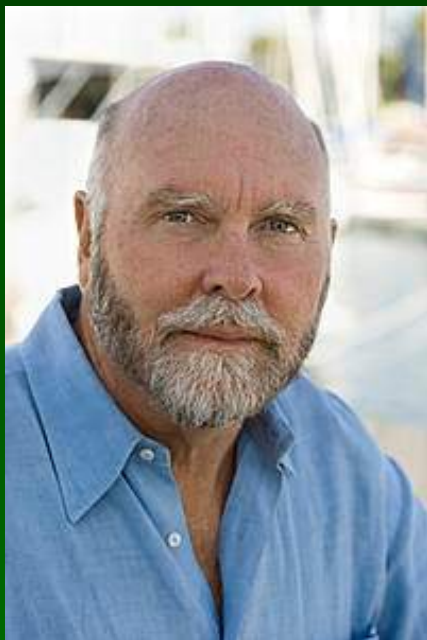
James Watson

*JLupsky, Kim,
GChurch, DTutu, JFlattery,
MSnyder,
....*

Marjolein Kriek



***conclusion 'sick' much
easier than 'healthy'***



Craig Venter

Do you have the DRD4 7R gene ?

1 in 4 has the
DRD4 7R gene



VEHICLES ▾

APPROVED PRE-OWNED

FLEET & BUSINESS

OWNERSHIP

EXPERIENCES

ABOVE AND BEYOND

ABOVE AND BEYOND OVERVIEW

RESPONSIBILITY

UNSTOPPABLE SPIRIT

25 YEARS OF DISCOVERY

CELEBRATE DEFENDER

THE ADVENTURE GENE

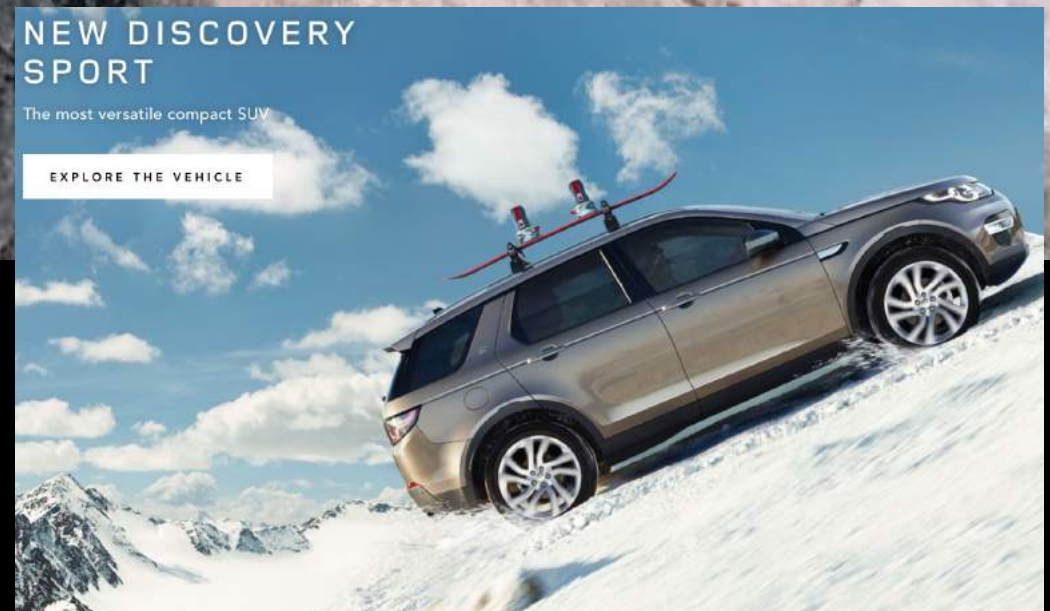
Are you hard-wired to go Above and Beyond?

WATCH THE FILM

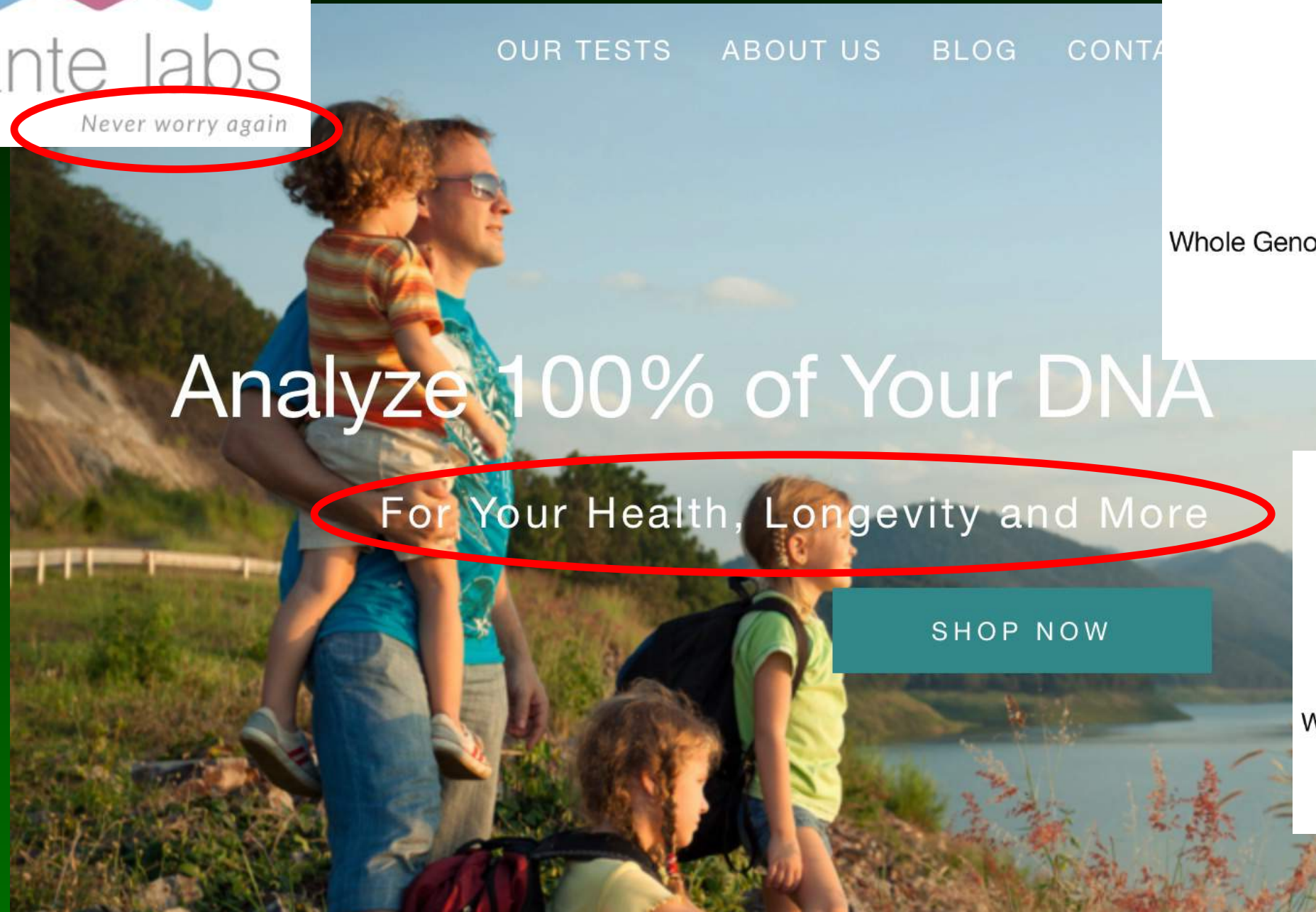
NEW DISCOVERY SPORT

The most versatile compact SUV

EXPLORE THE VEHICLE



Commercial DNA test



Whole Genome Sequencing (WGS) - Full
DNA Analysis

£399



Whole Exome Sequencing (WES) -
Sequence all Your Genes

£299

Special offer



HALLOWEEN SPECIAL: €399 WHOLE
GENOME SEQUENCING

ND 31 ONLY



Sequencing
your genome

Whole Genome Sequencing Test

€199

[SHOP NOW](#)

ER →

Halloween Special

SALE



Whole Genome Sequencing
(WGS) - Full DNA Analysis

€399.00 ~~€850.00~~
YOU SAVE €451.00



Whole Exome Sequencing (WES)
- Sequence all Your Genes

€299.00 ~~€549.00~~
YOU SAVE €250.00

*maybe offer on Halloween
because it is a scary thing to do ?*

Test the baby



Het leukste en meest originele kraamcadeau!

Vijf leuke weetjes over je baby op basis van zijn of haar DNA in een gepersonaliseerde animatievideo.

the nicest and most original present

Dna-test voor baby's voorlopig van de markt

© VRIJDAG, 17:33 BINNENLAND



Dna-test voor je baby: leuk kraamcadeau of risico?

© WO 20 FEBRUARI, 18:34 BINNENLAND, TECH

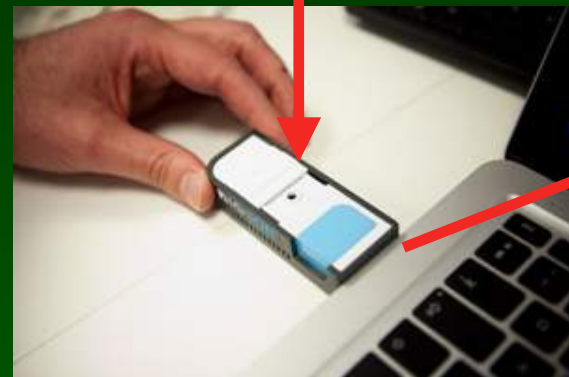


Predictions

***...it is good we can not yet trust
predictions***

*(dangerous tools, eventually they will
take over your job)*

Future VEP



FINAL



GENOME REPORT

(complete error free)

