

GENETICS

1000 GENOMES QUICK BROWSER

6.01.2010

We did not anticipate that the first 1,000 human genomes could be such quickly browsed ;-) but this is what the [project website](#) says. By today 4 individuals are on display and I wonder how it will look like with 996 more lines??

Region in detail

Location: 8 : 62107544 - 62112543 Go>

THIS STYLE: Location of SNPs
THIS STYLE: Resequencing coverage

- Basepairs in secondary individuals matching the reference assembly
- ~ No resequencing coverage at this position

Homo_sapiens > [chromosome:NCBI36:8:62107544:62112543:1](#)

```
REF: 36      1 TGTGTCAGAGTCCTTTTTGGAAGCAATGCCTATCCTCCTATGTGA
LKG_NA12878_pilot2  1 .....
LKG_NA12891_pilot2  1 .....
LKG_NA12892_pilot2  1 .....
LKG_NA19240_pilot2  1 .....

REF: 36      121 TTACCAGTTAGGCCTTGGGGGCTTCAGGGAATATCCAGGCCTCTA
LKG_NA12878_pilot2  121 .....
LKG_NA12891_pilot2  121 .....
LKG_NA12892_pilot2  121 .....
LKG_NA19240_pilot2  121 .....
```

Nature has asked some people [about their forecast of personalized medicine 2020](#) - no idea why they asked this [guy](#)

... common genetic variation seems to have only a limited role in determining people's predisposition to many common diseases. Second, gene variants that are very rare in the general population can have outsized effects on predisposition.[...] If so, here's one confident but uncomfortable prediction of what personalized genomics could look like in 2020. The identification of major risk factors for disease is bound to substantially increase interest in embryonic and other screening programmes.

I am pleased to read that the community finally accepted the view that there is no value of current GWAs. We will see if rare variants will explain more although I have no idea how we can provide any statistical proof with N=1. At least the consequences are horrible if this will lead to embryonic screening programs.

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