

Illumina Seminar Series

Munich 6. July 2009

Tim M Strom
Helmholtz Zentrum München &
Technische Universität München

Outline

- Introduction
 - Setup, Projects
 - Error rates
 - Data management

Tim M Strom

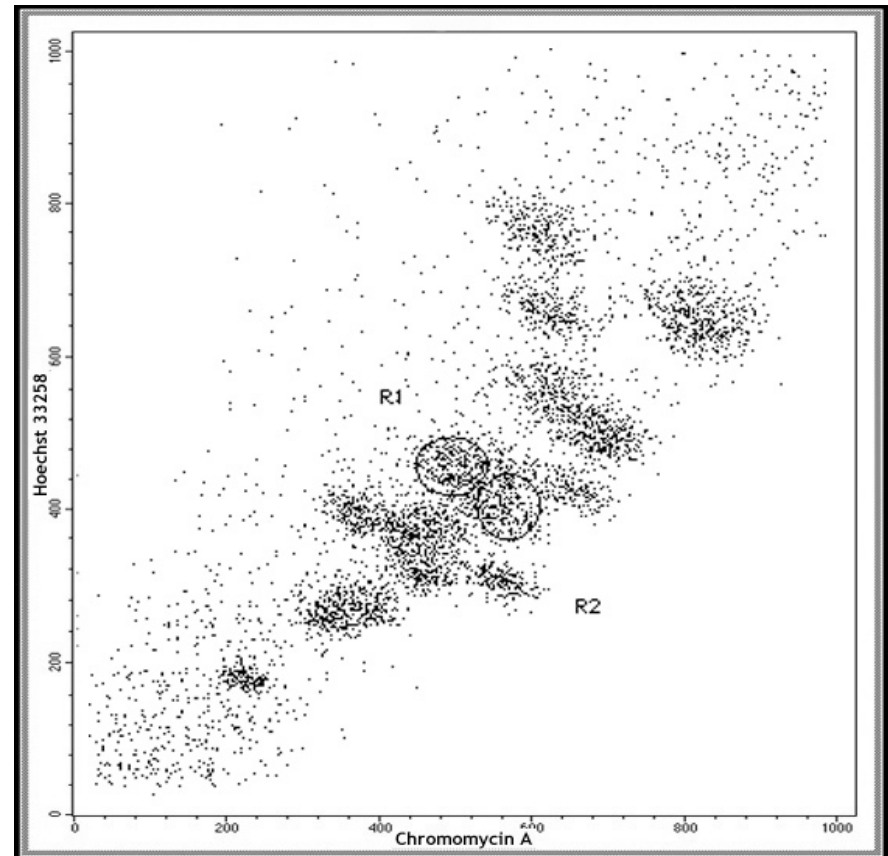
- Somatic mutations in Acute Myeloid Leukemia
- Sebastian Eck

Setup

- 2 GA II (30 runs, 100 GB mappable raw data)
(Storage 100 TB, 2 Servers 40 cores)
- Service at the Helmholtz Zentrum Munich and for external customers
- Synbreed: Whole-genome re-sequencing of cattle, chicken and maize -> SNP detection -> SNP arrays
- Mutation detection in ENU mutagenized mice
- Somatic mutations in AML and CLL

ENU mutagenized mice

- Linkage in 50 mice
- Chromosome sorting



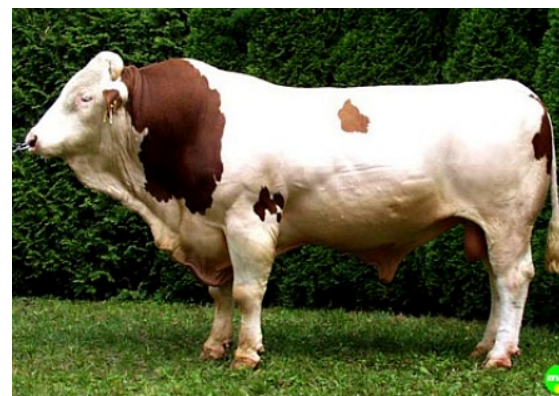
- Chromosome-specific library (~100ng)
- Sequencing of mutant and background strain

Chromosome sorting, Johannes Wienberg, Chrombios

SNP detection in cattle (genomic selection)

- Whole-genome resequencing of a single breeding bull

(50.000 inseminations in 2008)



- 24 GB, 7.4-fold read depth
- Comparison with the reference (bosTau4)
- 2.4 million SNPs, 2 million novel
- 9.318 coding SNPs
- False-positive detection rate 1%,
determined by genotyping 190 randomly selected SNPs
- Detection rate (homozygous) 74%, (heterozygous) 30%
determined by comparison with 50k SNP array

Error rate

Reads \longleftrightarrow Reference sequence

Sequencing errors (0.5-1.5%)
(depending on cluster density)

+

Genomic variability (0.1% in humans)

+

Alignment errors

!=

False-positive SNP detection rate (1-4%)

Wanted: tuning of the trade-off between error rate
and sequence output

Error rate

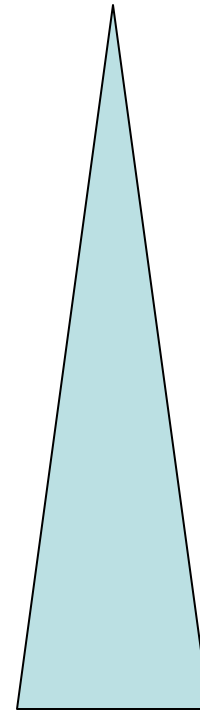
ChIP-Seq

Expression analysis

SNP detection

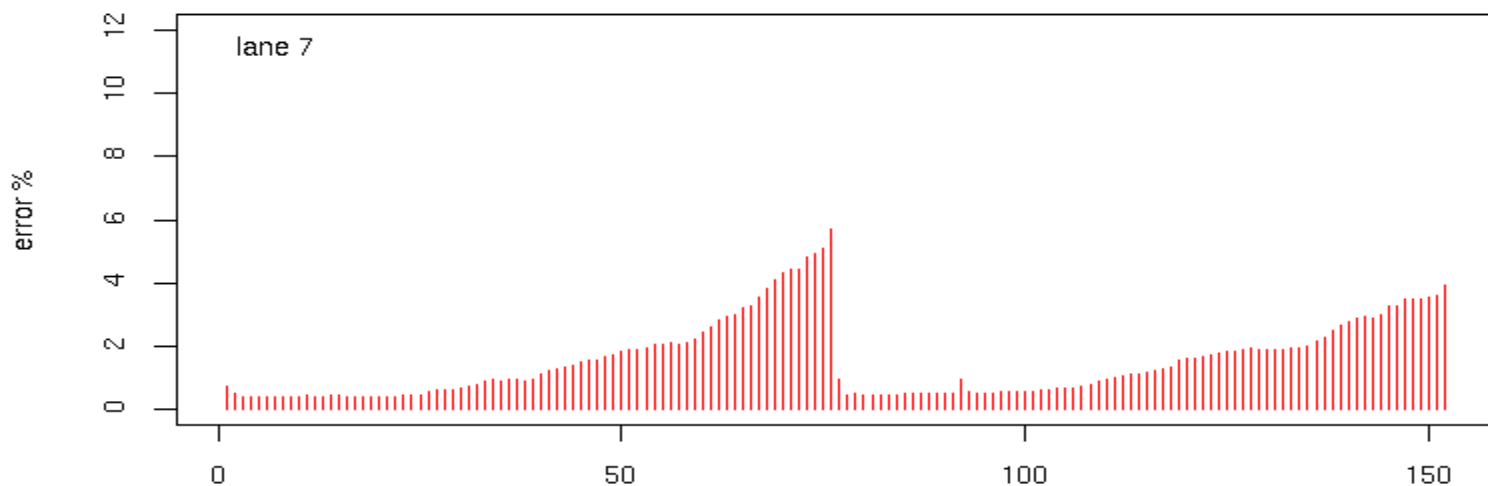
Mutation detection

De novo assembly

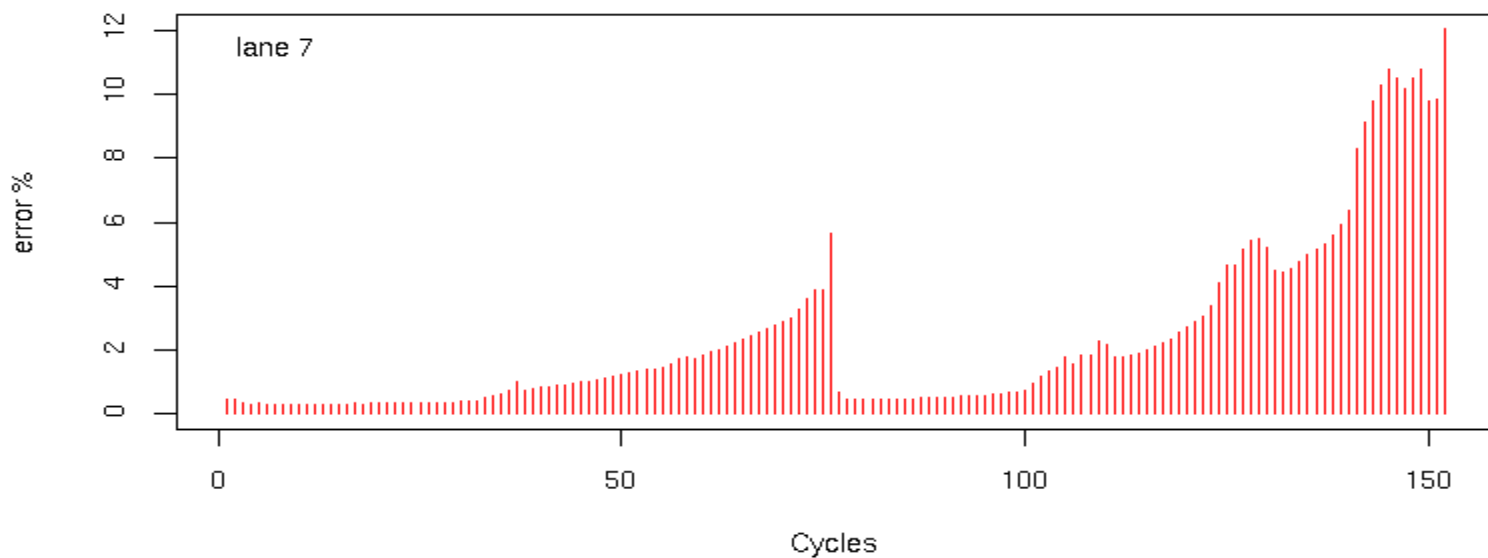


Error rate: Sequencing error

At least 10-fold higher than in capillary sequencing



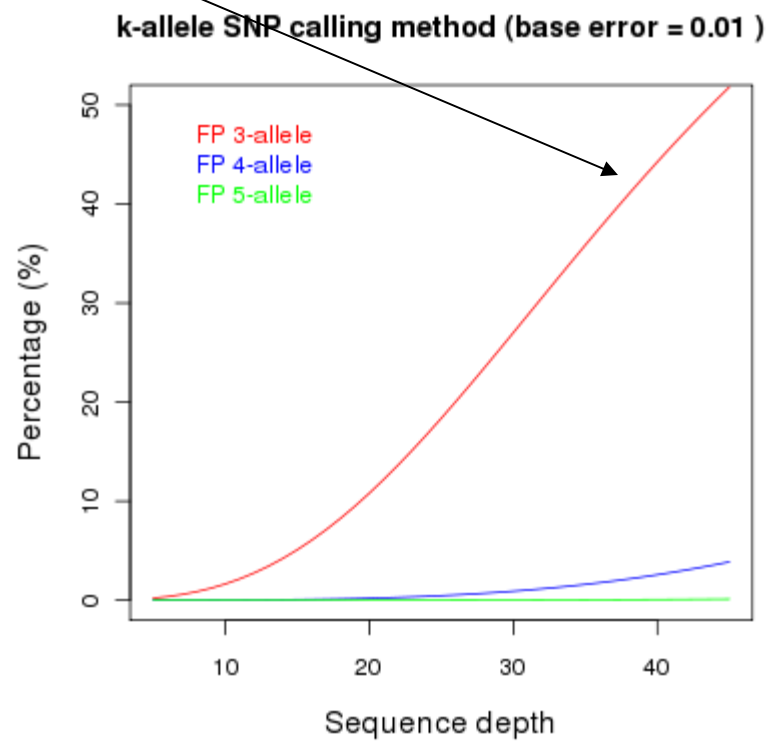
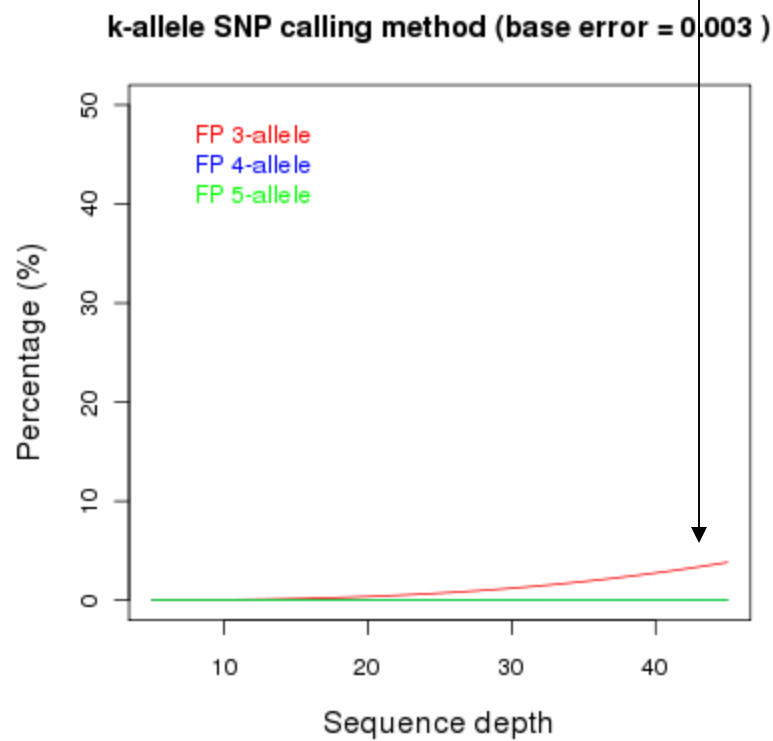
Read 1
1.21%
Read 2
1.12%



Read 1
0.89%
Read 2
2.61%

Error rate: false positive detection rate

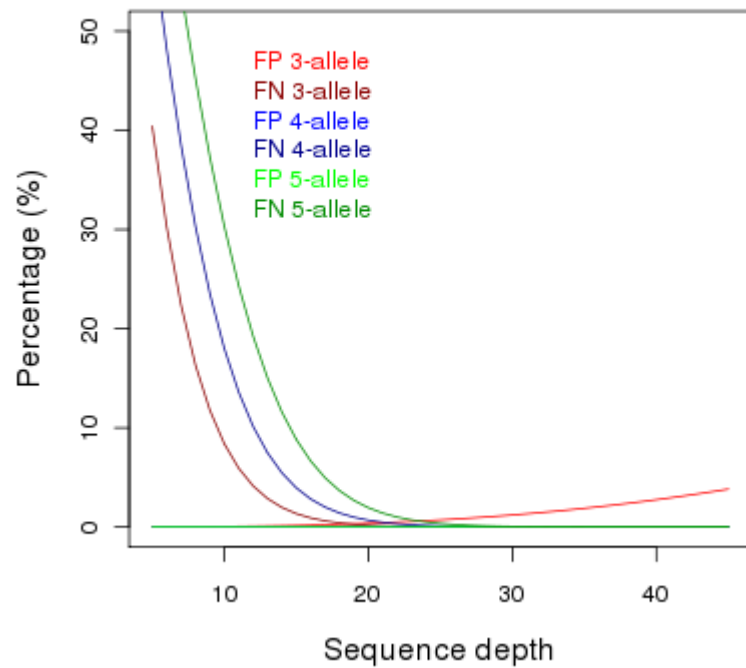
SNPs covered by at least 3 alleles



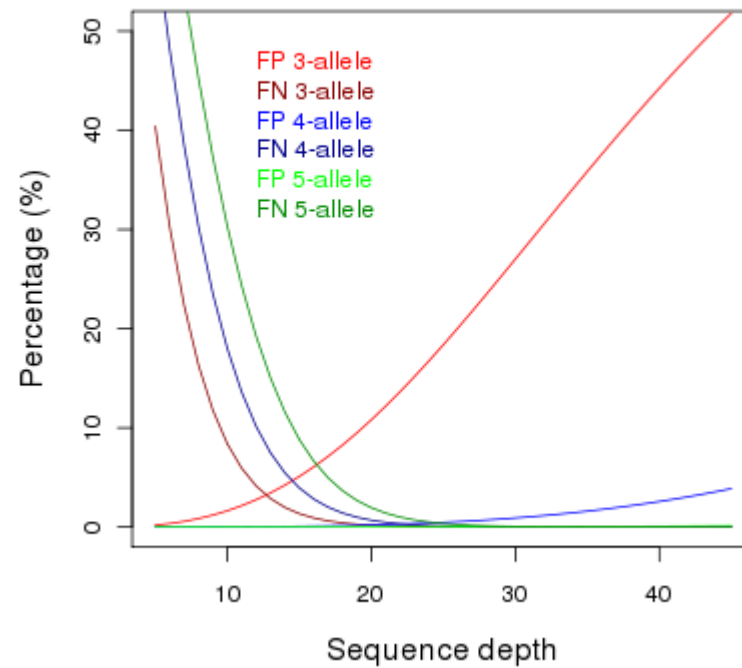
According to H Li, J Ruan and R Durbin, Genome Research, 2008

Error rate: false negative detection rate

k-allele SNP calling method (base error = 0.003)



k-allele SNP calling method (base error = 0.01)



-> Sequence depth ≥ 30

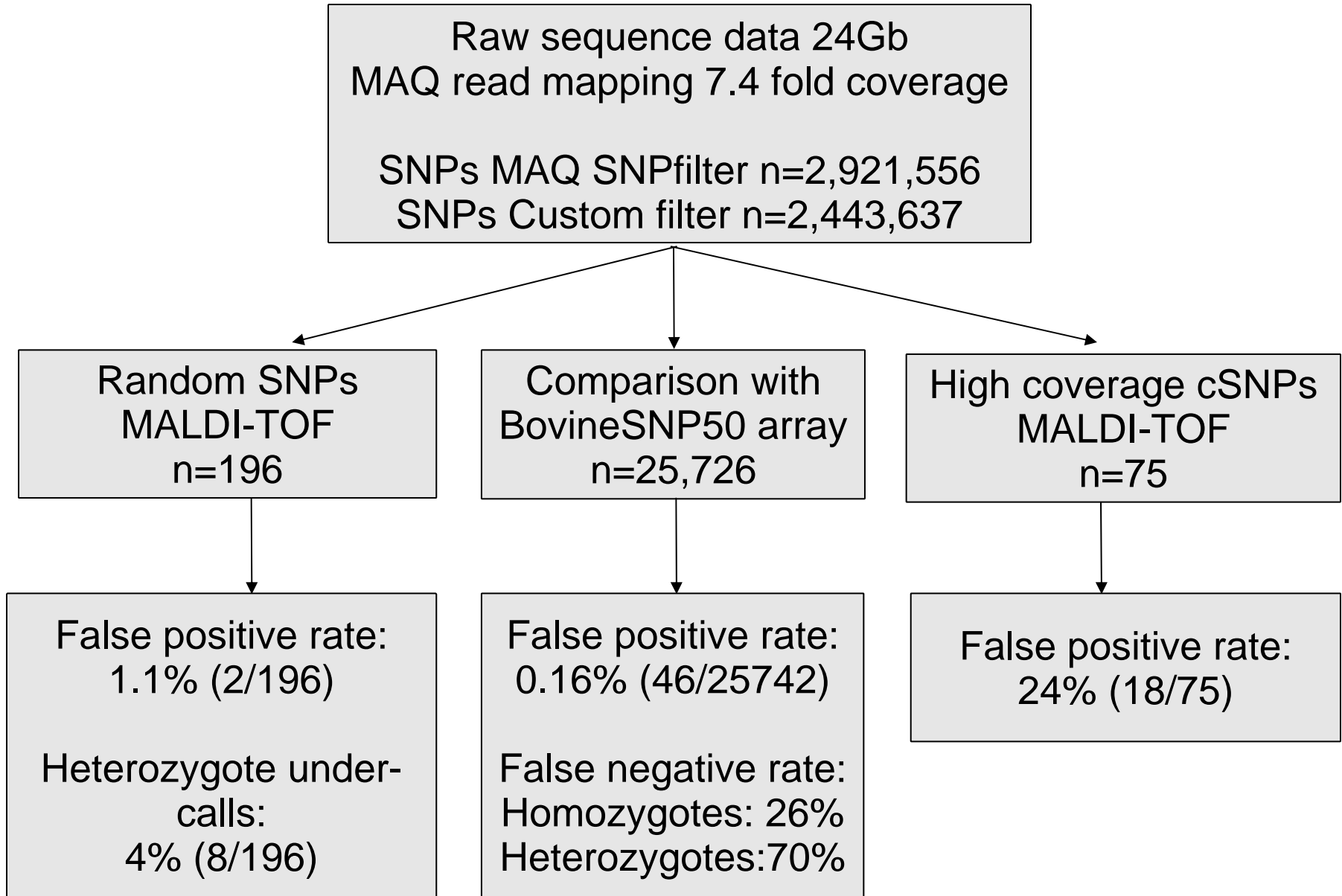
-> Error rate $< 1\%$ or Pred-like quality score ≥ 25

According to H Li, J Ruan and R Durbin, Genome Research, 2008

Error rate: Systematic error

```
M.A.Q Viewer
GGCTTCCTCCCTCTTTGGGTAGCCCTCAAGCCACTGGACTTTGAAGTCAGCAGGTAATTCTCCAAATGGAAGAACTTTTTTTTTTTTTTTTAAAGGCAGA
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Read: 173930241-1_Index_Read1:5:29:1059:496#ATCACG/1[30]IG 29
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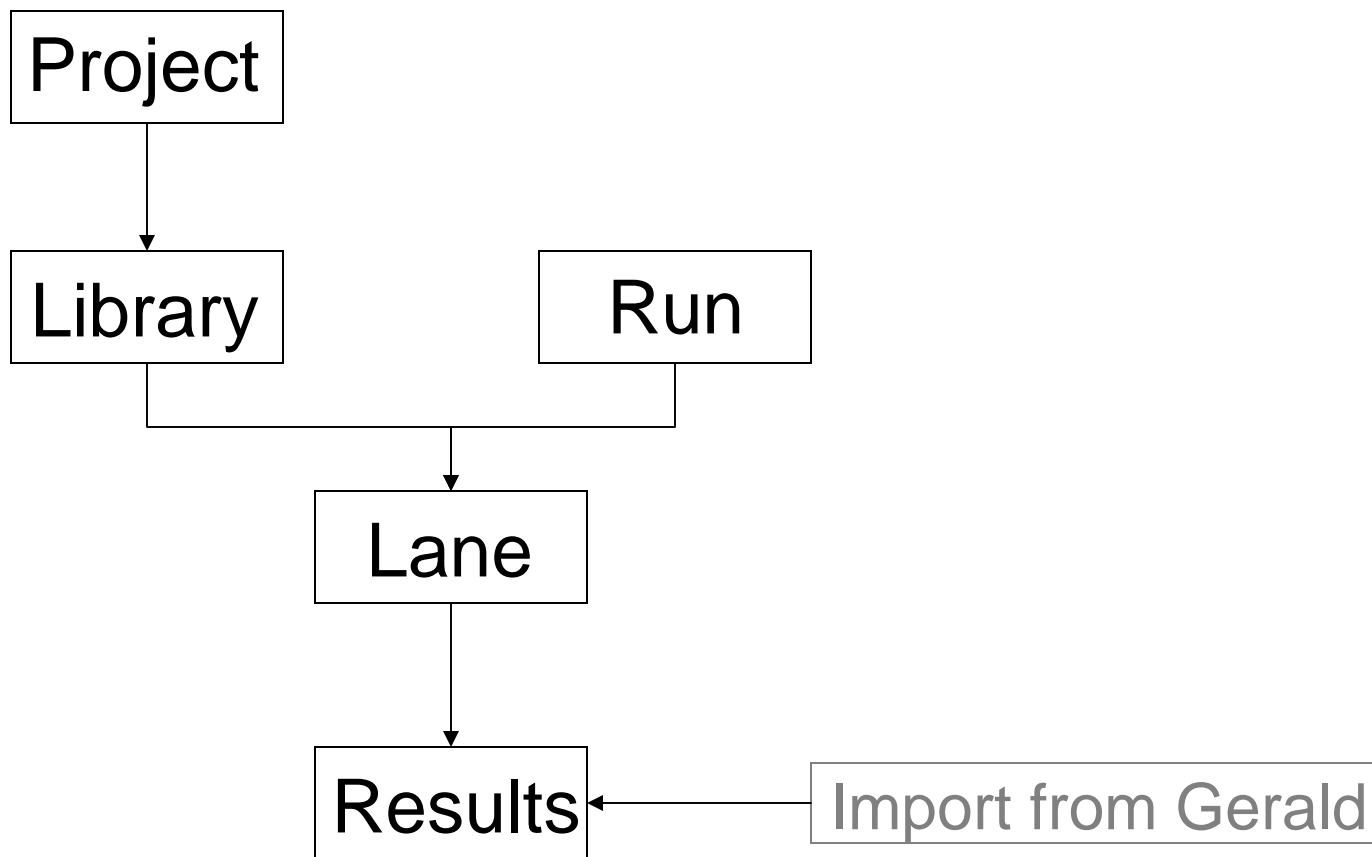
Error rate: Alignment error



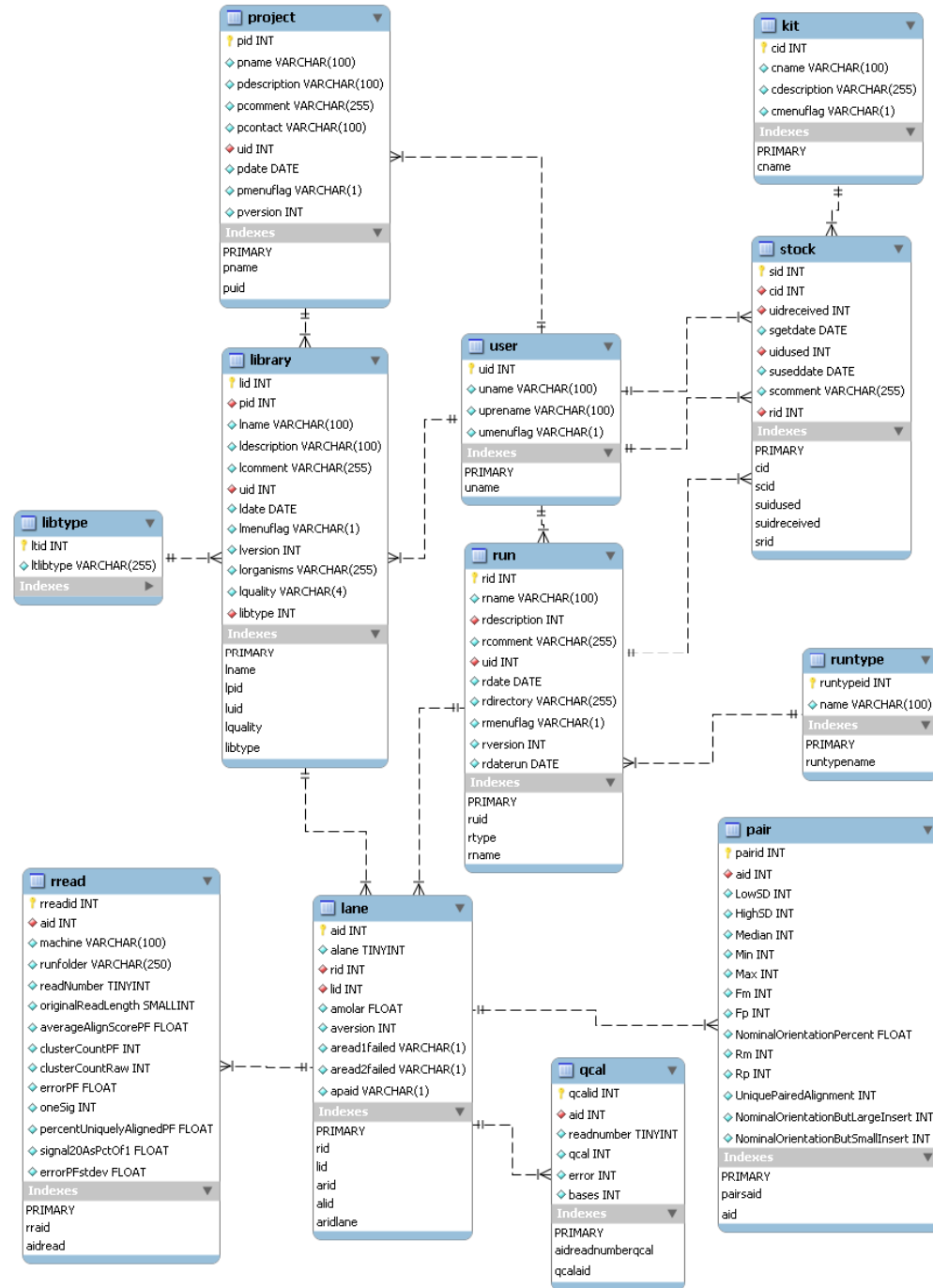
Exome non-synonymous SNPs

- Synonymous SNPs 10413 (novel 649)
- Non-synony. SNPs 10389 (novel 769)
 - 1600-2000 MAF < 0.05
- ~1500 (14% of 10389) may affect protein function (SIFT)
- 105 premature stop codon
 - 31 duplicated regions
 - 31 hypothetical genes
 - 22 members of gene families
 - 9 unique members
- 739 coding indels (52% tandem repeats)
- 632 nsSNPs in 443 OMIM disease genes

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All runs and lanes (including failed)

Runs 13
 Lanes 88
 Read1 failed 28
 Read2 failed 16

Summary

n Reads	Yield (Gb)	Sum Clusters (PF)	Mean Clusters (raw)	Mean Clusters (PF)	Mean 1st Cycle Int (PF)	Mean % Error Rate (PF)
9+ Reads, % Error Rate <= 2	23.815	6615771	119903	72700	224	1.14

n	Project	Library	Description	Machine	Run	Lane	Read	Length	pMol	Yield (Mbases)	Clusters (raw)	Clusters (PF)	1st Cycle Int (PF)	% PF C
1	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	1	1	36	2	260	120580	72459	240	60
2	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	1	2	36	2	260	120580	72459	152	60
3	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	2	1	36	2	272	122683	75632	247	61
4	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	2	2	36	2	272	122683	75632	145	61
5	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	3	1	36	2	271	123040	75482	245	61
6	Rind Vanstein	42563_IB2	paired end	HWI-CAS106	307FYAAXX	3	2	36	2	271	123040	75402	143	61
7	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	5	1	36	1	187	70149	52027	236	74
8	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	5	2	36	1	187	70149	52027	138	74
9	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	6	1	36	1	187	69845	52069	239	74
10	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	6	2	36	1	187	69845	52069	138	74
11	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	7	1	36	1	189	71117	52745	239	74
12	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	7	2	36	1	189	71117	52745	138	74
13	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	8	1	36	1	183	69332	50966	246	73
14	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307FYAAXX	8	2	36	1	183	69332	50966	149	73
15	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307J5AAXX	7	1	36	3	305	150488	84989	264	56
16	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307J5AAXX	7	2	36	3	305	150488	84989	245	56
17	Rind Vanstein	42563_IB2	paired end	HWI-EAS186	307J5AAXX	8	1	36	3	301	148202	83740	252	56
18	Rind Vanstein	42563_IB2	paired end	HWI-FAS186	307J5AAXX	8	2	36	3	301	148202	83740	237	56

Thank you!

Anna Benet-Pagès, Sebastian Eck and
Kerstin Schwerdtner