

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:13:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003987.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6003987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003987.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:13:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,108,228
Mapped reads	2,364,076 / 76.06%
Unmapped reads	744,152 / 23.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,112 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	323,919 / 10.42%
Duplication rate	10.53%
Clipped reads	1,242,670 / 39.98%

2.2. ACGT Content

Number/percentage of A's	41,253,261 / 27.02%
Number/percentage of C's	26,605,768 / 17.43%
Number/percentage of T's	51,184,834 / 33.53%
Number/percentage of G's	33,600,320 / 22.01%
Number/percentage of N's	14,991 / 0.01%
GC Percentage	39.44%

2.3. Coverage

Mean	0.0493

Standard Deviation	0.5577
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.73
----------------------	-------

2.5. Mismatches and indels

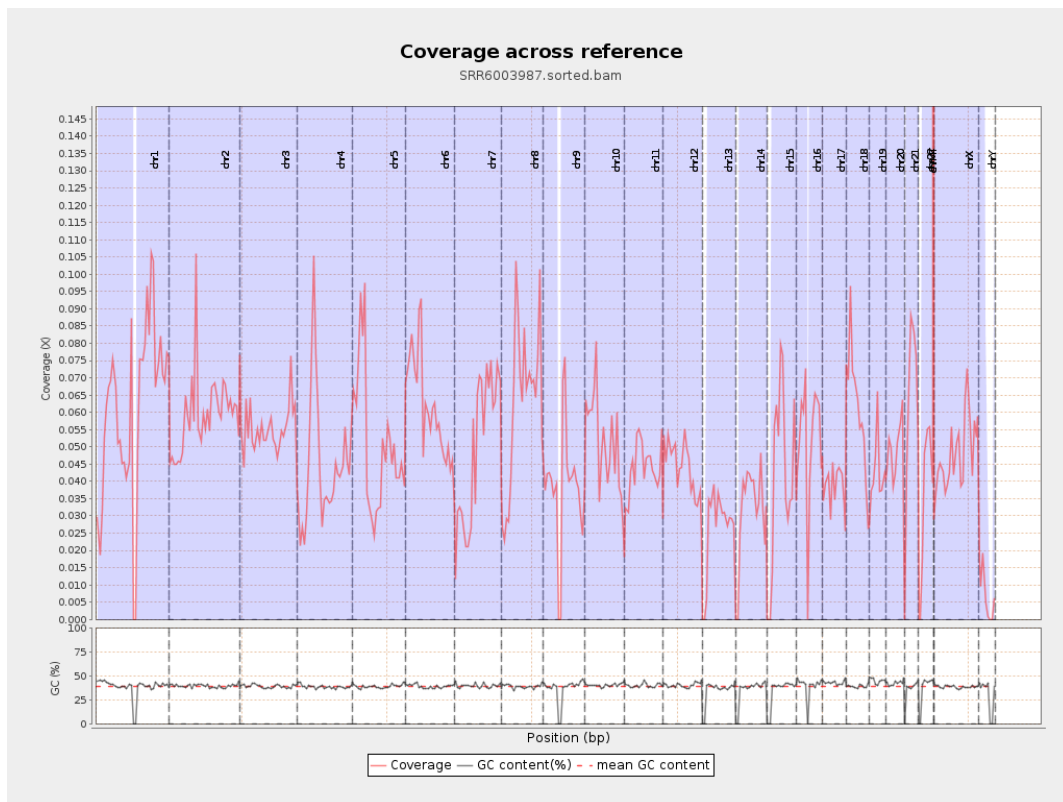
General error rate	1.05%
Mismatches	1,580,508
Insertions	13,954
Mapped reads with at least one insertion	0.59%
Deletions	46,549
Mapped reads with at least one deletion	1.95%
Homopolymer indels	49.31%

2.6. Chromosome stats

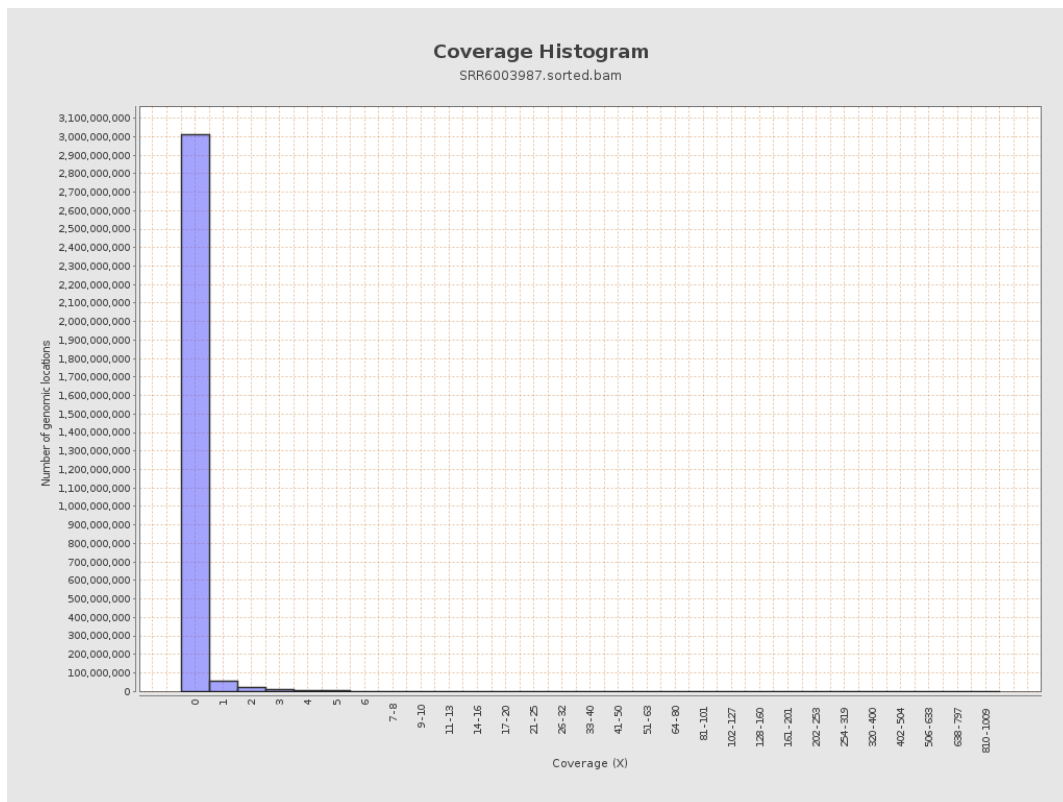
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15221938	0.0611	0.9507
chr2	243199373	14399628	0.0592	0.6677
chr3	198022430	11004740	0.0556	0.3899
chr4	191154276	8437627	0.0441	0.3464
chr5	180915260	9183552	0.0508	0.3688
chr6	171115067	10517663	0.0615	0.4594
chr7	159138663	7955708	0.05	0.5007

chr8	146364022	9233247	0.0631	0.7636
chr9	141213431	5390373	0.0382	0.4892
chr10	135534747	7001707	0.0517	0.4585
chr11	135006516	5913413	0.0438	0.4572
chr12	133851895	5910240	0.0442	0.3467
chr13	115169878	3009533	0.0261	0.2642
chr14	107349540	3387524	0.0316	0.3171
chr15	102531392	4262507	0.0416	0.3328
chr16	90354753	4737549	0.0524	0.3961
chr17	81195210	3098358	0.0382	0.3463
chr18	78077248	4834816	0.0619	1.0069
chr19	59128983	2542134	0.043	0.6256
chr20	63025520	3087096	0.049	0.3653
chr21	48129895	3026723	0.0629	0.4296
chr22	51304566	1798455	0.0351	0.2919
chrMT	16571	1015659	61.2914	33.4766
chrX	155270560	7369137	0.0475	0.3869
chrY	59373566	397152	0.0067	0.1425

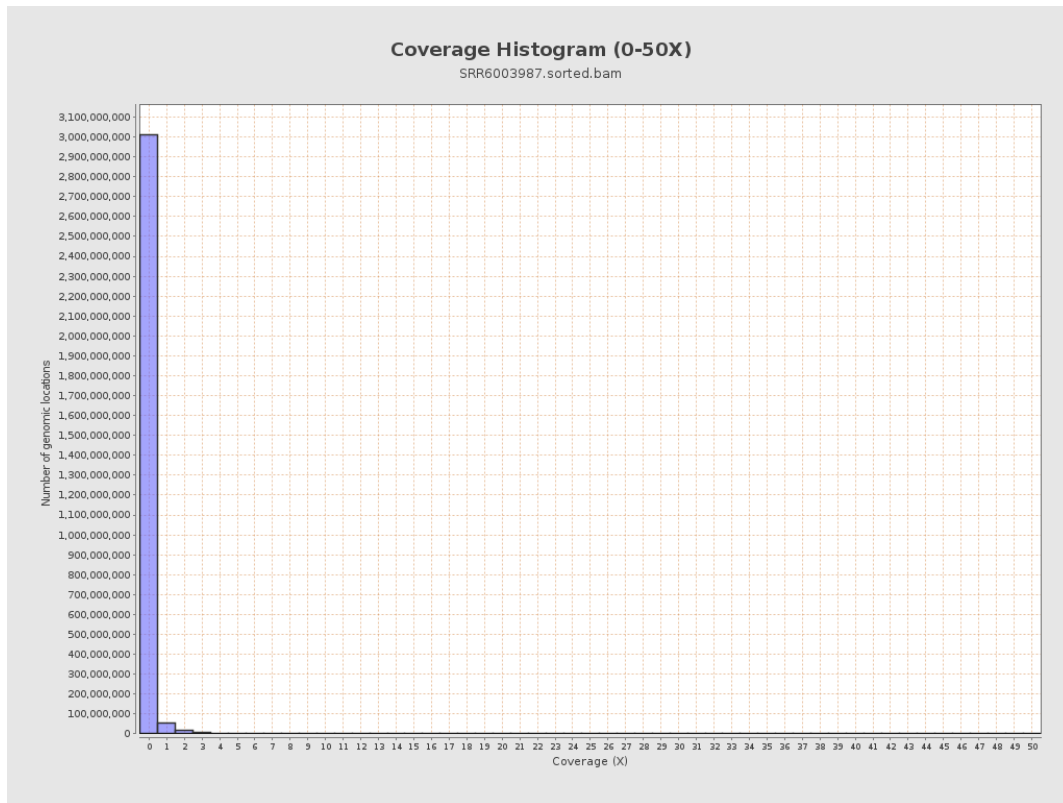
3. Results : Coverage across reference



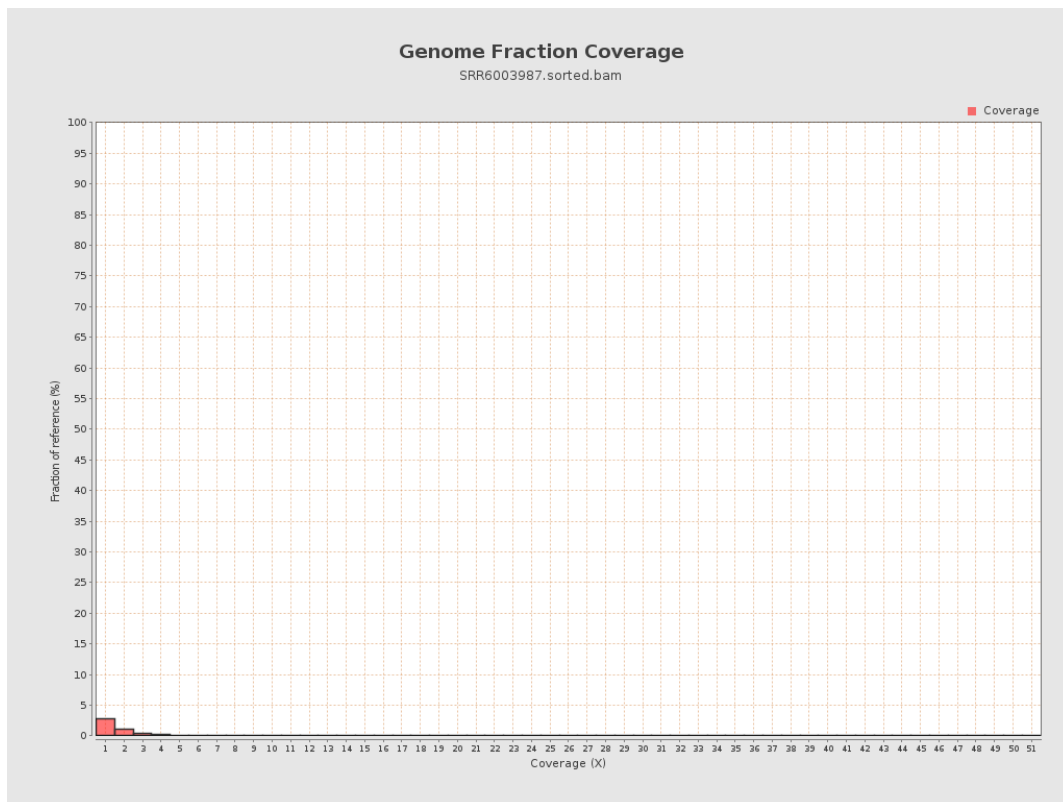
4. Results : Coverage Histogram



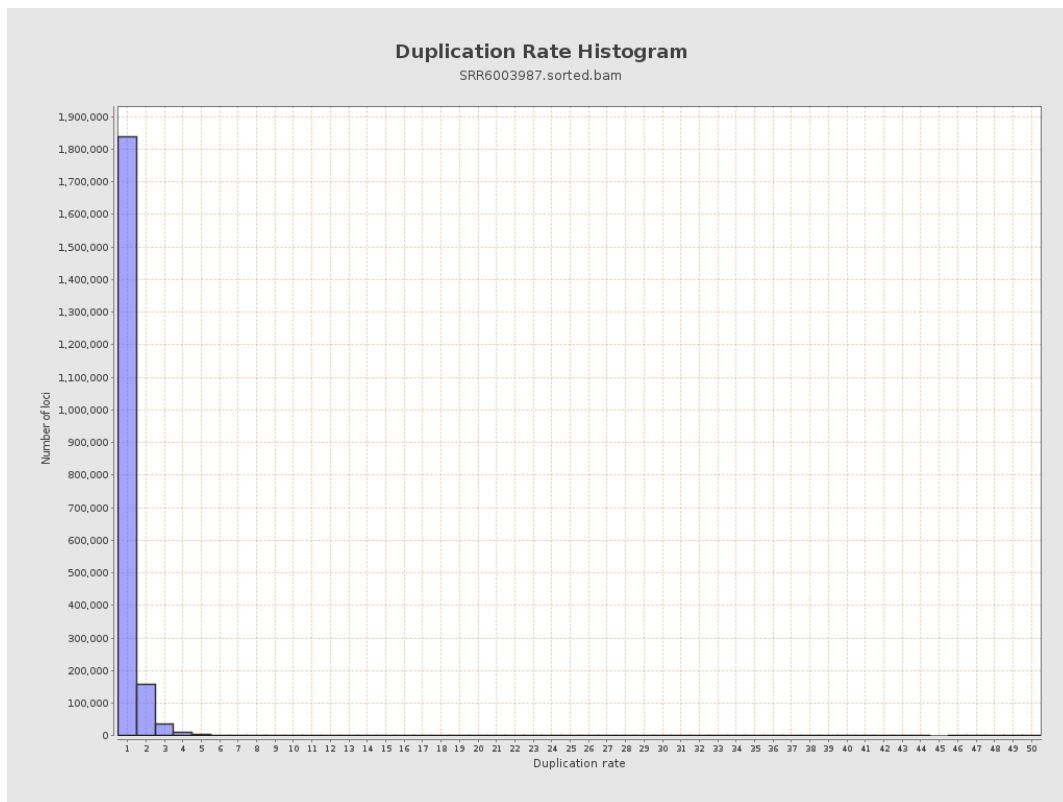
5. Results : Coverage Histogram (0-50X)



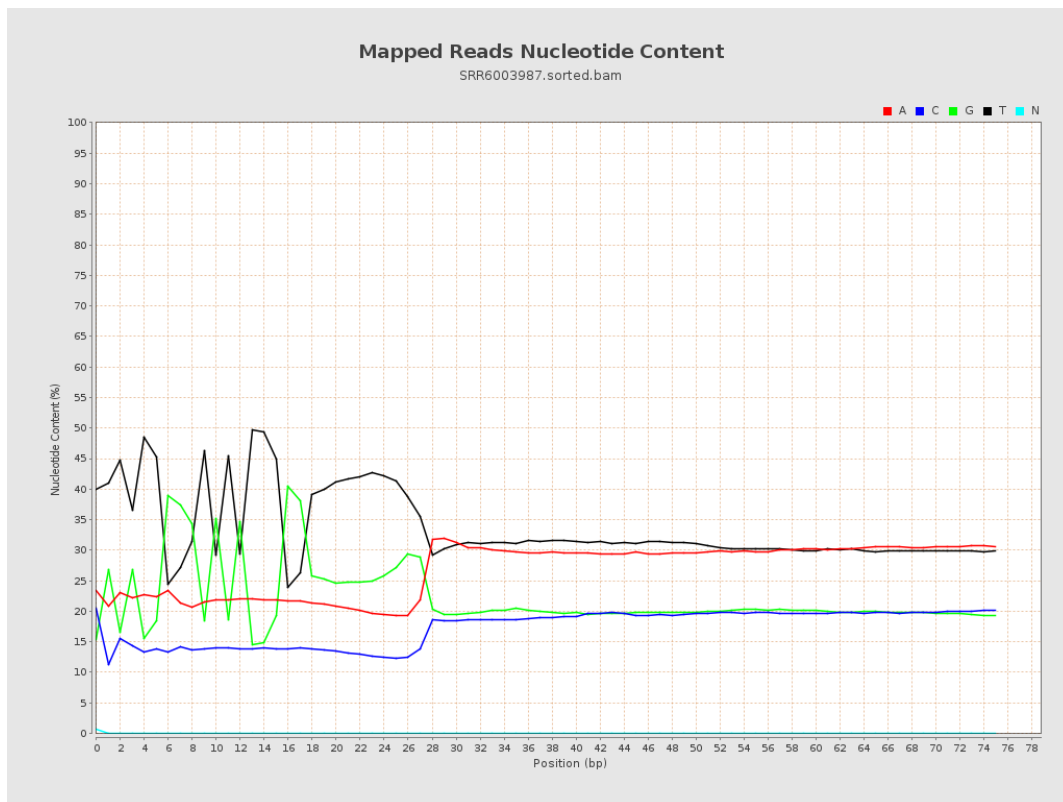
6. Results : Genome Fraction Coverage



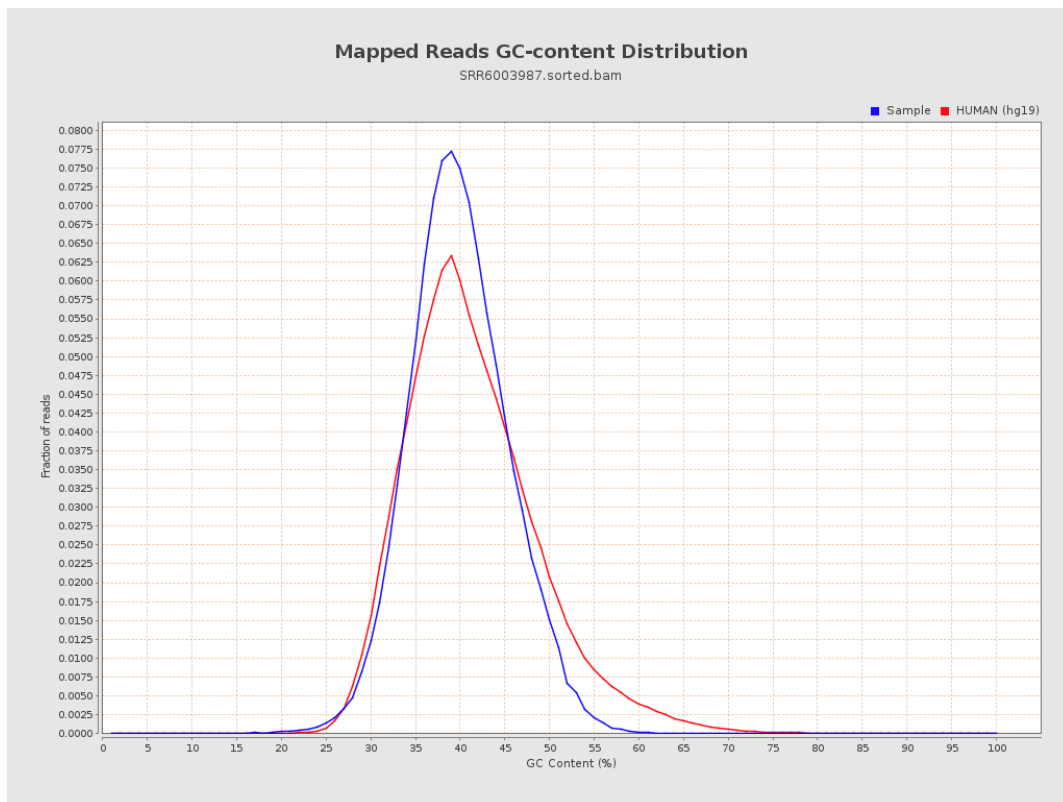
7. Results : Duplication Rate Histogram



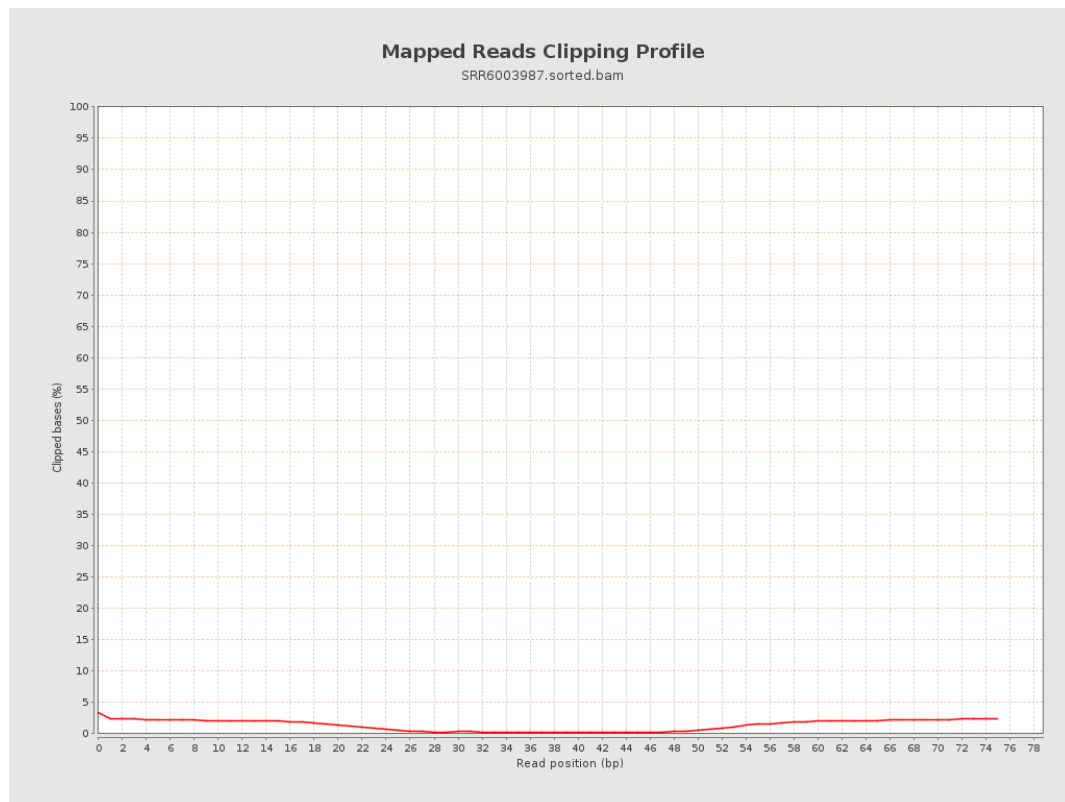
8. Results : Mapped Reads Nucleotide Content



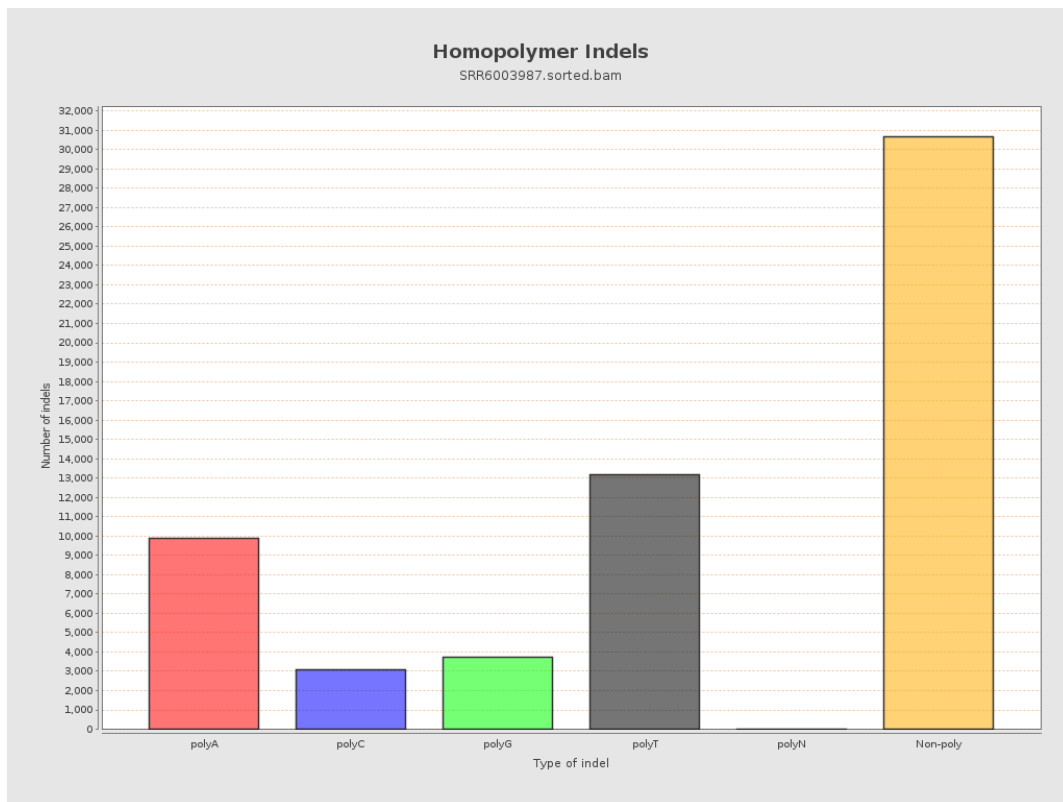
9. Results : Mapped Reads GC-content Distribution



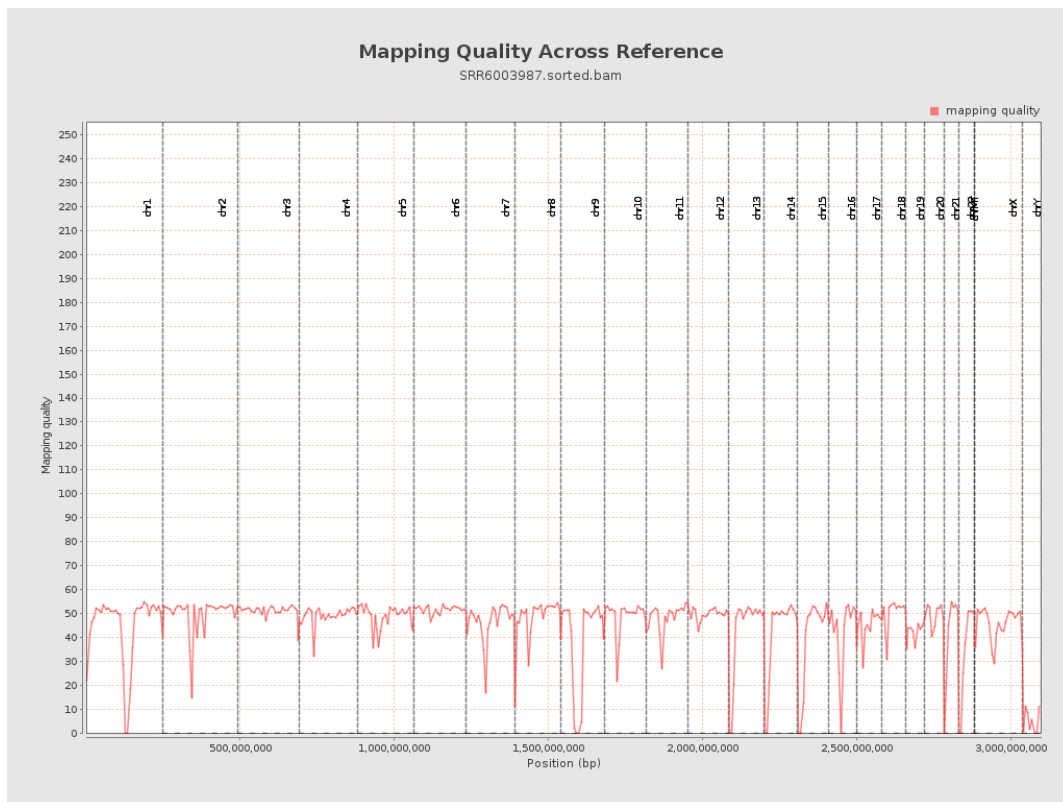
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

