

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 21:54:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004036.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_SRR6004036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 21:54:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,232,348
Mapped reads	1,938,334 / 86.83%
Unmapped reads	294,014 / 13.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,955 / 0.54%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	77,291 / 3.46%
Duplication rate	2.94%
Clipped reads	1,073,497 / 48.09%

2.2. ACGT Content

Number/percentage of A's	33,666,243 / 26.92%
Number/percentage of C's	22,945,848 / 18.35%
Number/percentage of T's	38,960,437 / 31.15%
Number/percentage of G's	29,461,565 / 23.56%
Number/percentage of N's	19,844 / 0.02%
GC Percentage	41.91%

2.3. Coverage

Mean	0.0404

Standard Deviation	0.3793
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2.4. Mapping Quality

Mean Mapping Quality	43
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2.5. Mismatches and indels

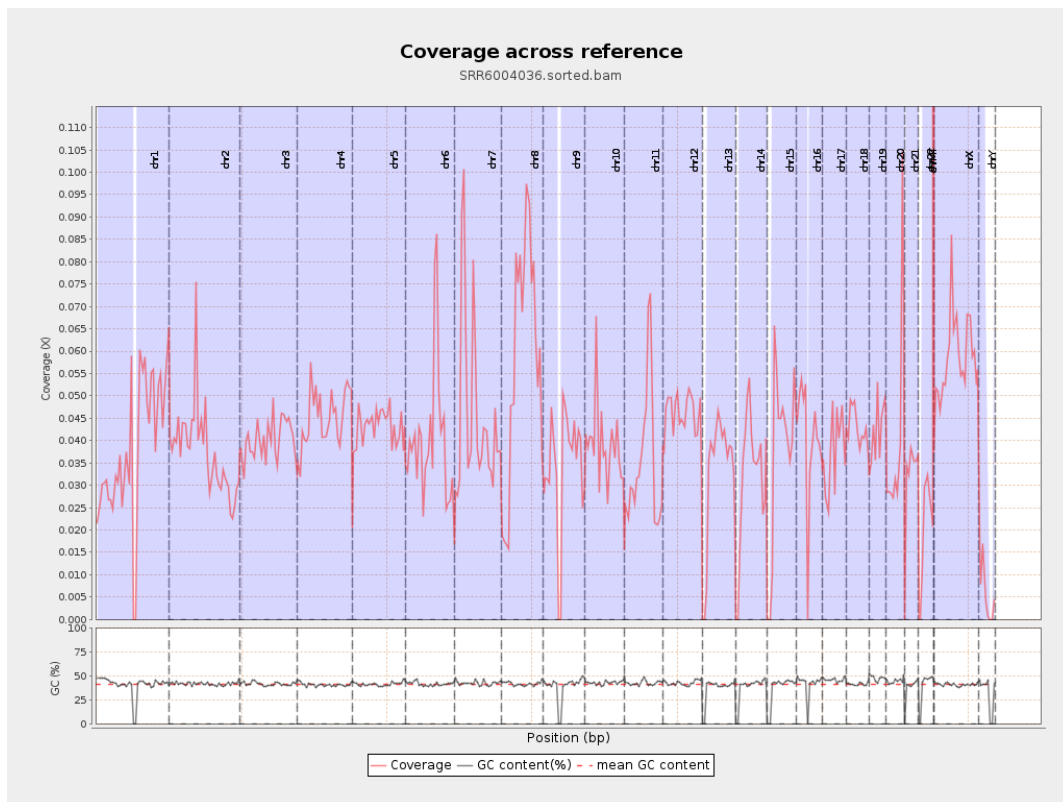
General error rate	0.97%
Mismatches	1,195,625
Insertions	10,266
Mapped reads with at least one insertion	0.52%
Deletions	41,087
Mapped reads with at least one deletion	2.09%
Homopolymer indels	44.01%

2.6. Chromosome stats

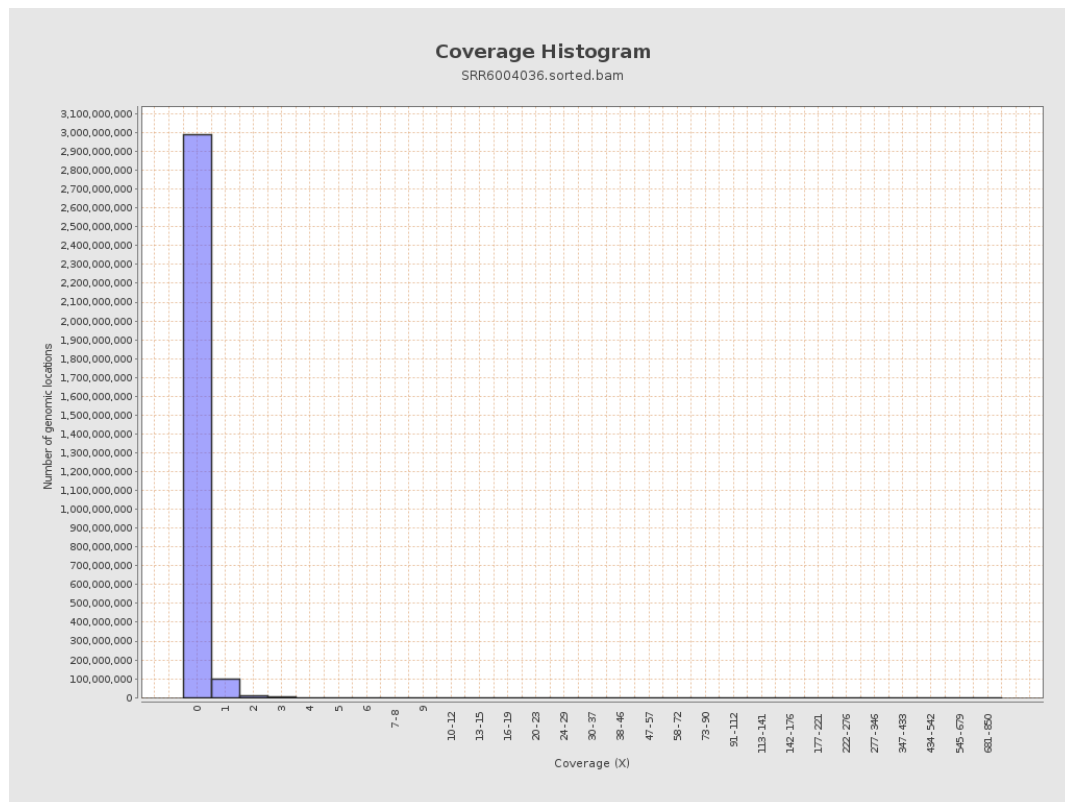
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9472757	0.038	0.6756
chr2	243199373	9081089	0.0373	0.4994
chr3	198022430	7968835	0.0402	0.2231
chr4	191154276	8658232	0.0453	0.2538
chr5	180915260	7822772	0.0432	0.2376
chr6	171115067	6855470	0.0401	0.2564
chr7	159138663	7382098	0.0464	0.5826

chr8	146364022	8562422	0.0585	0.4244
chr9	141213431	4884719	0.0346	0.3572
chr10	135534747	5284477	0.039	0.3459
chr11	135006516	4768581	0.0353	0.2757
chr12	133851895	6167430	0.0461	0.2503
chr13	115169878	3772601	0.0328	0.2088
chr14	107349540	3406735	0.0317	0.2417
chr15	102531392	3875190	0.0378	0.232
chr16	90354753	3649723	0.0404	0.2604
chr17	81195210	3048358	0.0375	0.2333
chr18	78077248	3354339	0.043	0.5862
chr19	59128983	2501511	0.0423	0.5139
chr20	63025520	2615754	0.0415	0.2429
chr21	48129895	1544676	0.0321	0.2215
chr22	51304566	1006767	0.0196	0.1538
chrMT	16571	32549	1.9642	1.8659
chrX	155270560	9046010	0.0583	0.3166
chrY	59373566	358807	0.006	0.1248

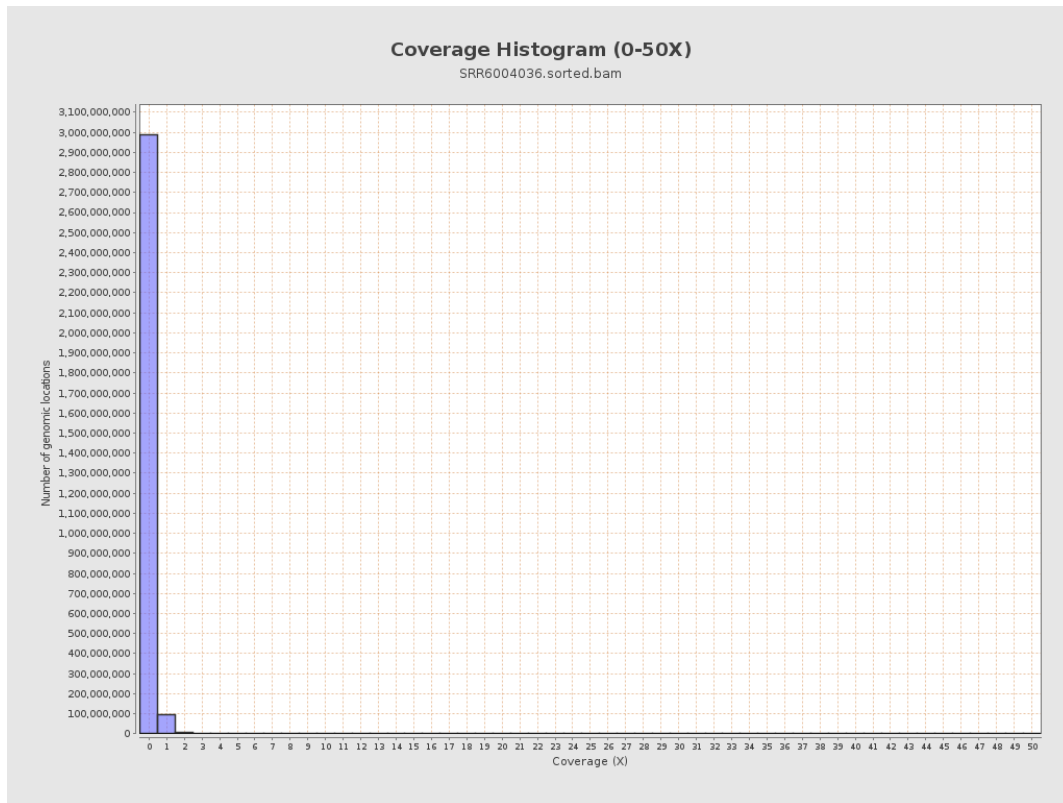
3. Results : Coverage across reference



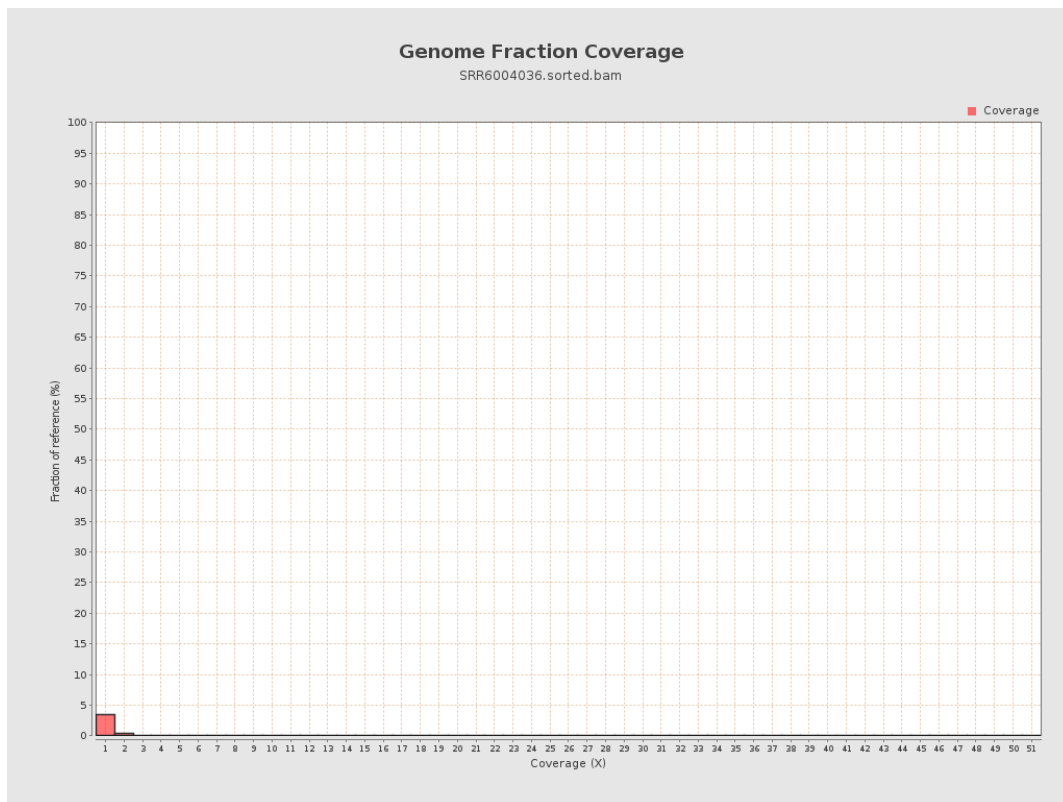
4. Results : Coverage Histogram



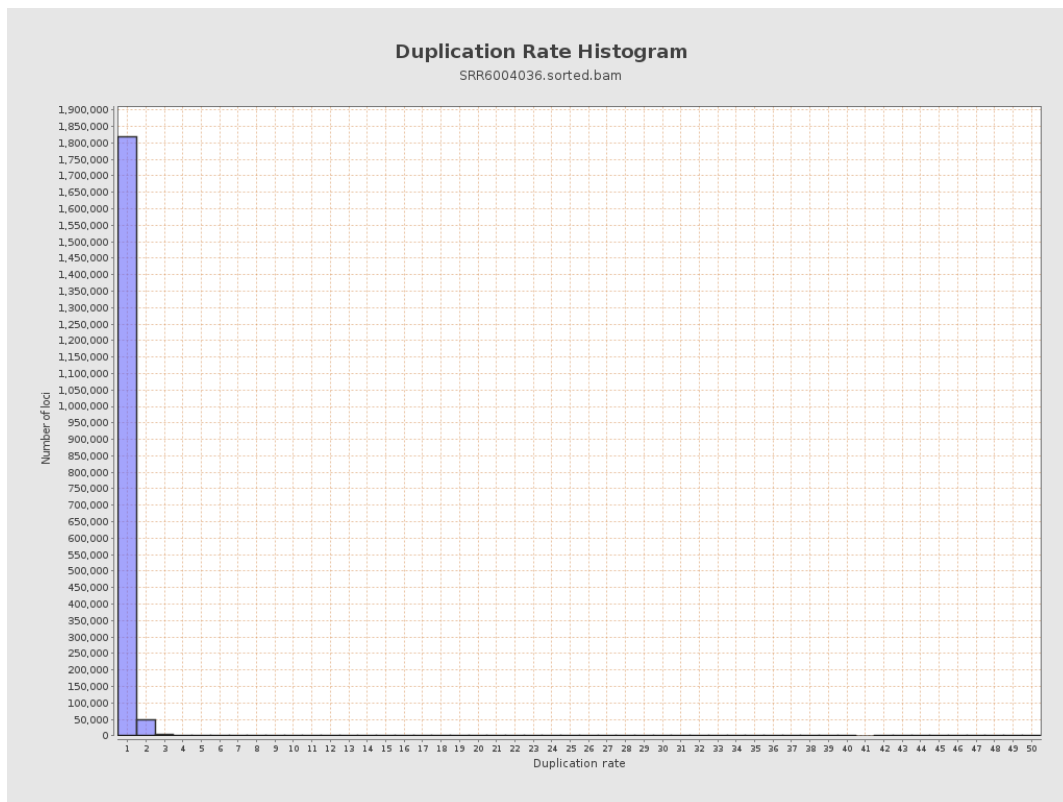
5. Results : Coverage Histogram (0-50X)



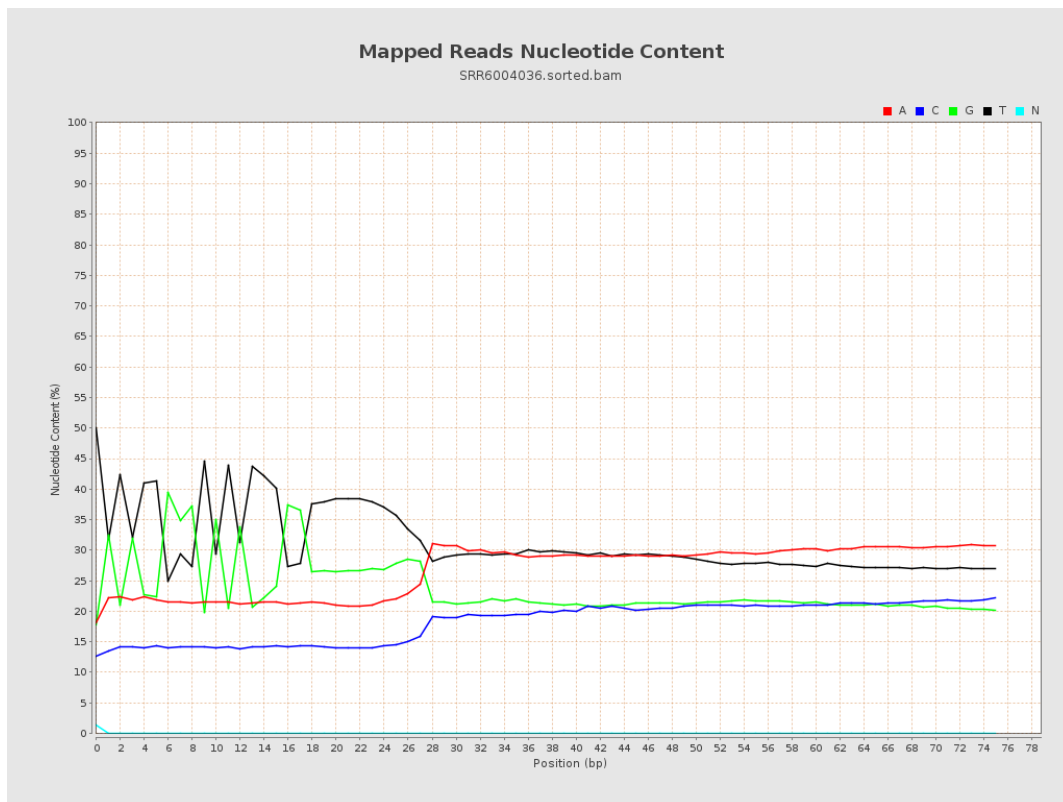
6. Results : Genome Fraction Coverage



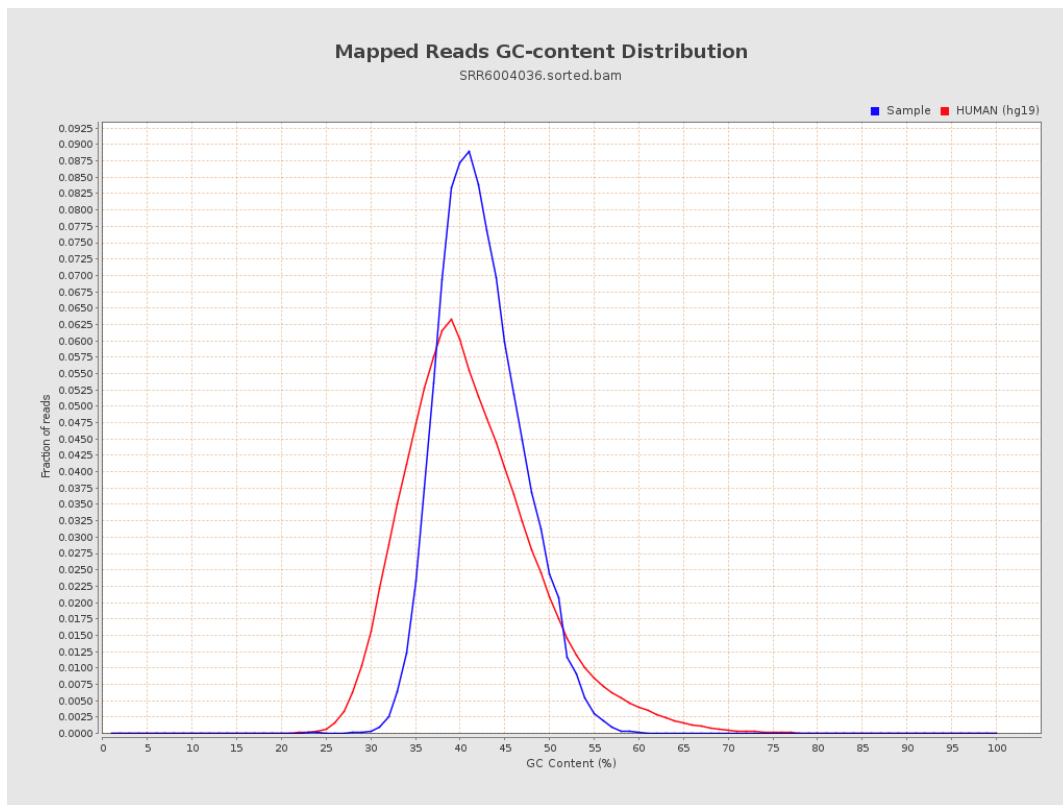
7. Results : Duplication Rate Histogram



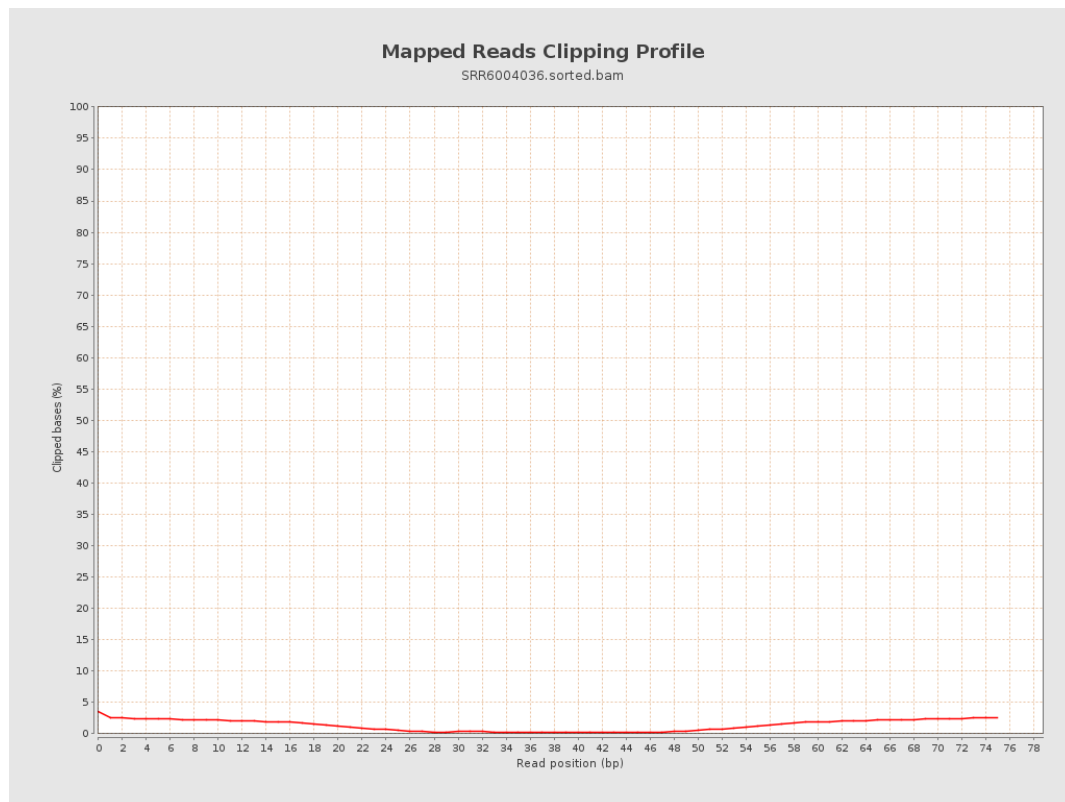
8. Results : Mapped Reads Nucleotide Content



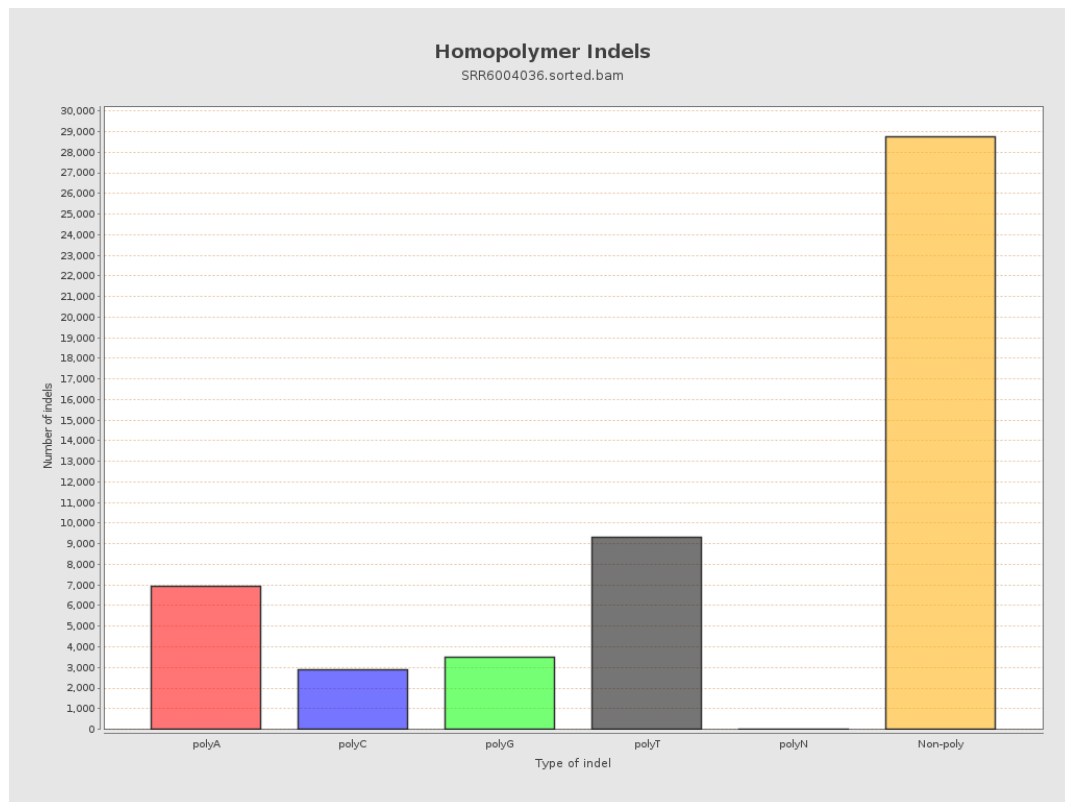
9. Results : Mapped Reads GC-content Distribution



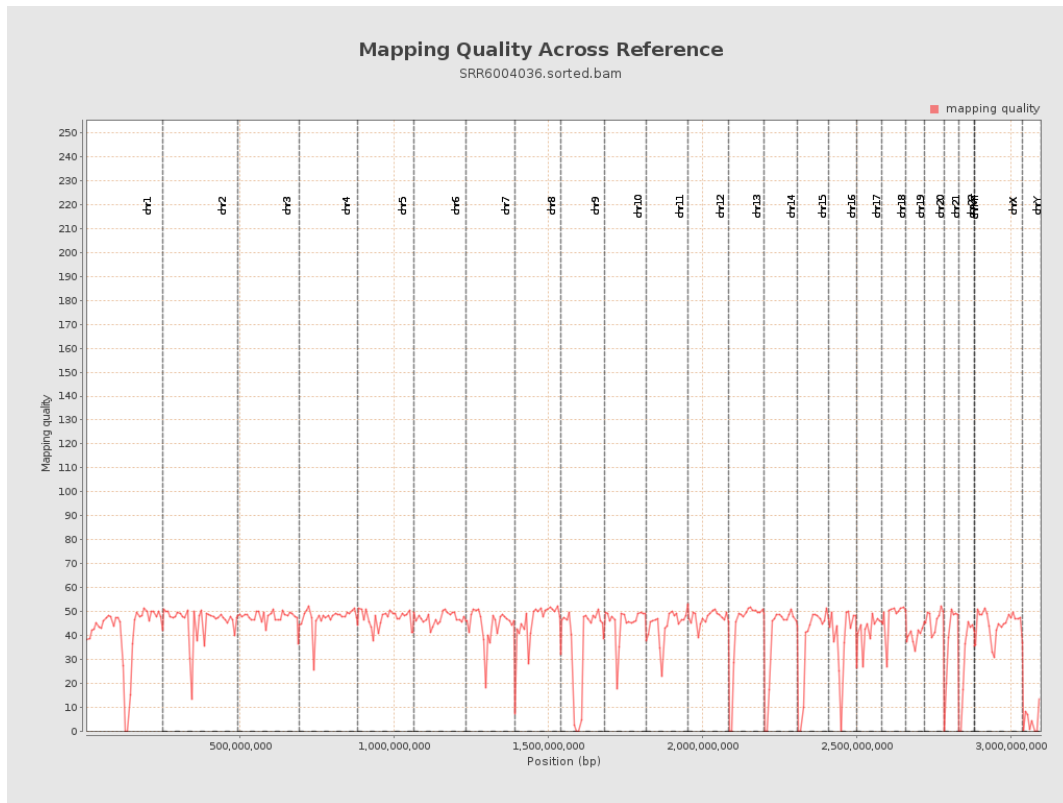
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

