

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:24:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004162.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_SRR6004162 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004162.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:24:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004162.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,230,665
Mapped reads	1,936,543 / 86.81%
Unmapped reads	294,122 / 13.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,795 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	84,319 / 3.78%
Duplication rate	3.52%
Clipped reads	996,092 / 44.65%

2.2. ACGT Content

Number/percentage of A's	34,971,310 / 27.73%
Number/percentage of C's	22,970,311 / 18.21%
Number/percentage of T's	40,033,992 / 31.74%
Number/percentage of G's	28,115,677 / 22.29%
Number/percentage of N's	20,504 / 0.02%
GC Percentage	40.51%

2.3. Coverage

Mean	0.0408

Standard Deviation	0.3357
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	45.29
----------------------	-------

2.5. Mismatches and indels

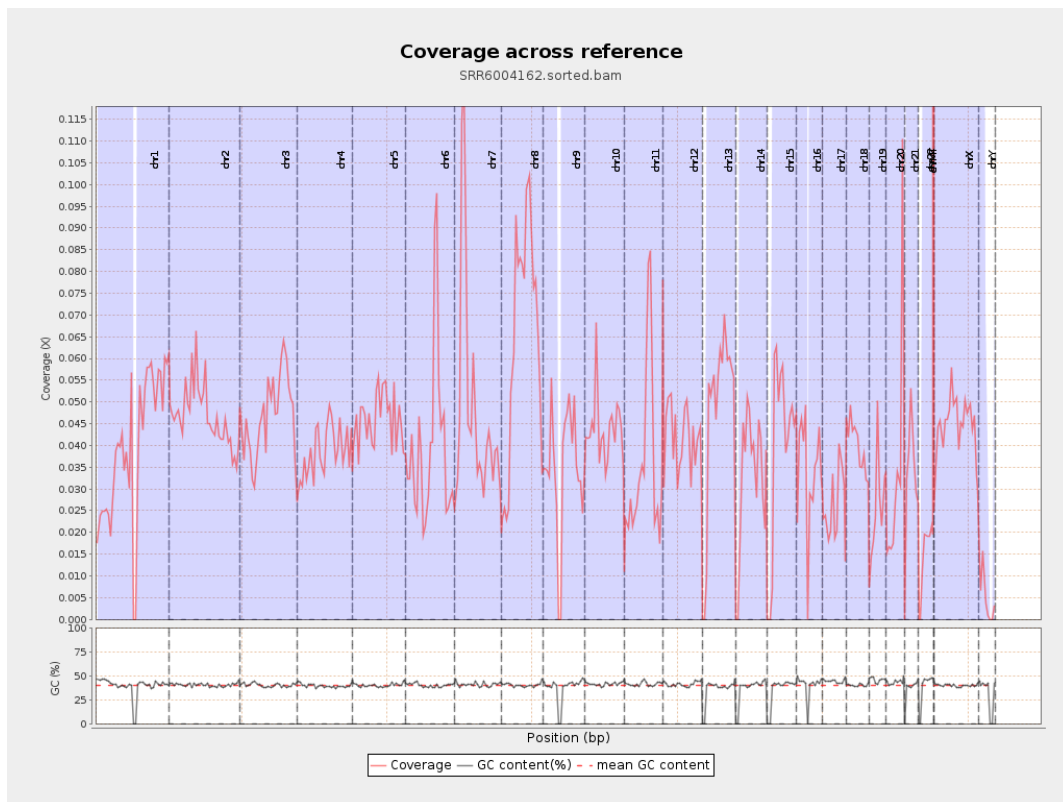
General error rate	0.93%
Mismatches	1,157,300
Insertions	9,281
Mapped reads with at least one insertion	0.48%
Deletions	37,701
Mapped reads with at least one deletion	1.92%
Homopolymer indels	44.6%

2.6. Chromosome stats

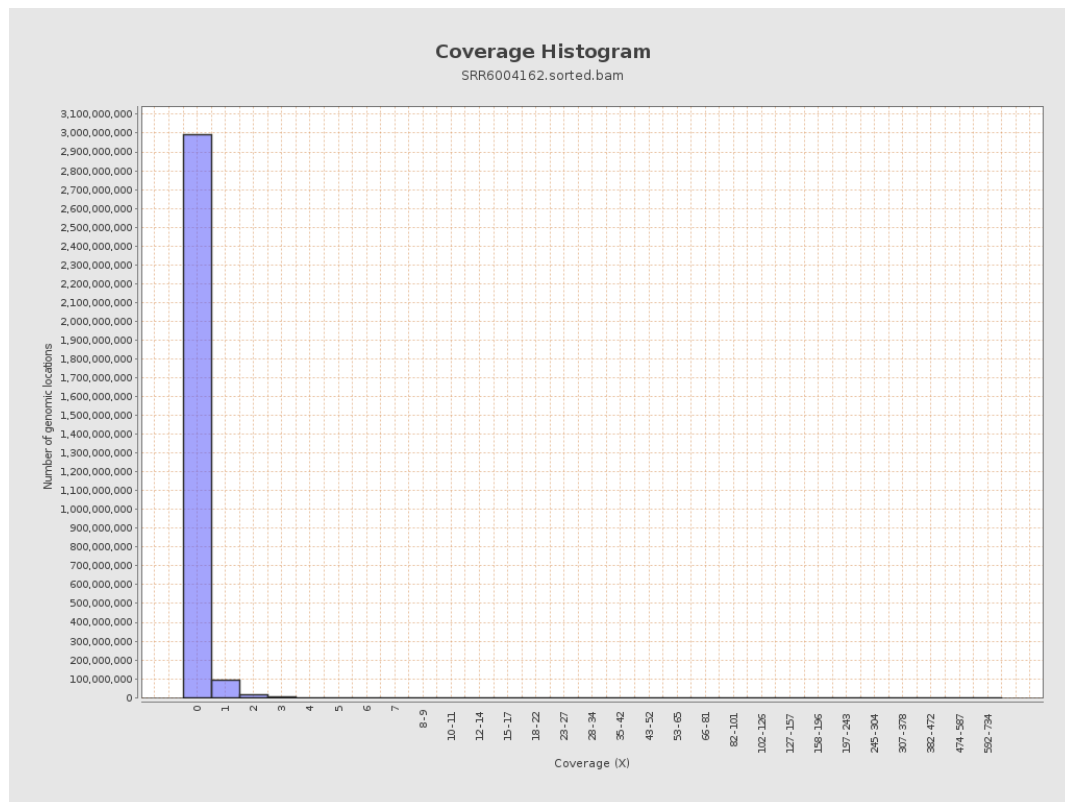
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9779012	0.0392	0.5975
chr2	243199373	11379201	0.0468	0.3737
chr3	198022430	9304850	0.047	0.248
chr4	191154276	7376454	0.0386	0.2355
chr5	180915260	8309664	0.0459	0.2475
chr6	171115067	6743799	0.0394	0.2485
chr7	159138663	7813570	0.0491	0.4207

chr8	146364022	9465903	0.0647	0.4347
chr9	141213431	4891785	0.0346	0.2932
chr10	135534747	5908012	0.0436	0.3375
chr11	135006516	4870918	0.0361	0.2869
chr12	133851895	5528612	0.0413	0.2377
chr13	115169878	5471117	0.0475	0.254
chr14	107349540	3481665	0.0324	0.2212
chr15	102531392	4130942	0.0403	0.2346
chr16	90354753	3095433	0.0343	0.2391
chr17	81195210	2098257	0.0258	0.2008
chr18	78077248	3116443	0.0399	0.5337
chr19	59128983	1557425	0.0263	0.4372
chr20	63025520	2249736	0.0357	0.2328
chr21	48129895	1599840	0.0332	0.2218
chr22	51304566	740852	0.0144	0.1345
chrMT	16571	67137	4.0515	3.068
chrX	155270560	6892055	0.0444	0.2646
chrY	59373566	302425	0.0051	0.1119

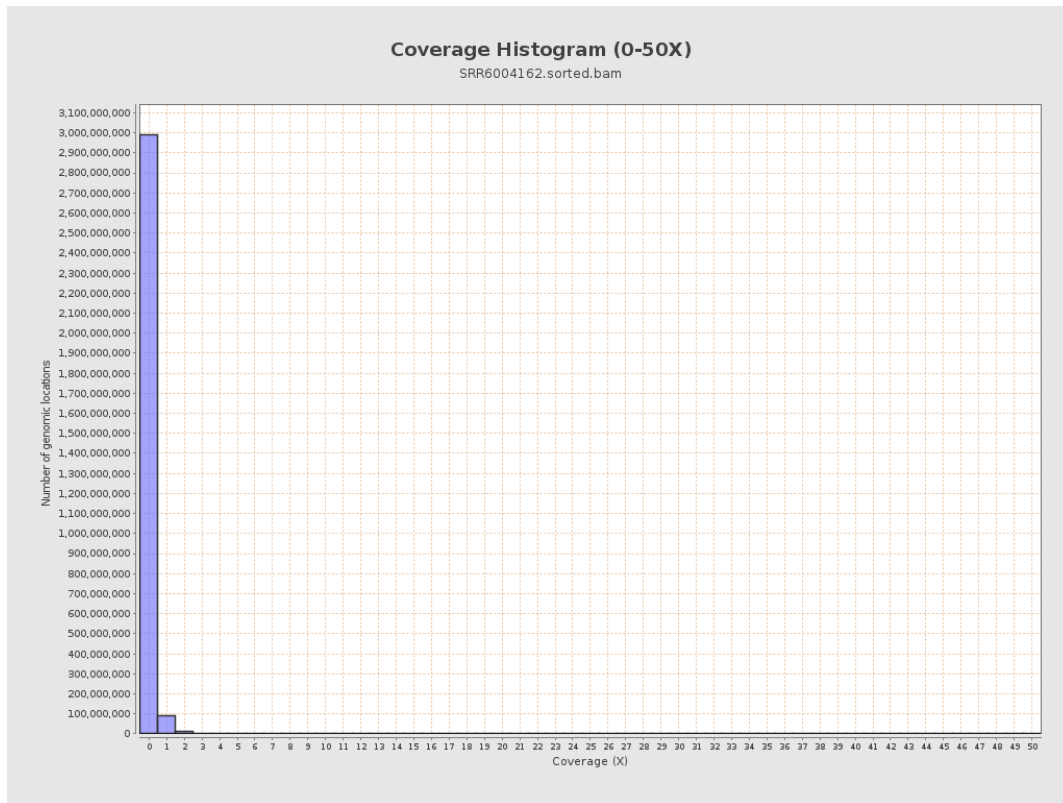
3. Results : Coverage across reference



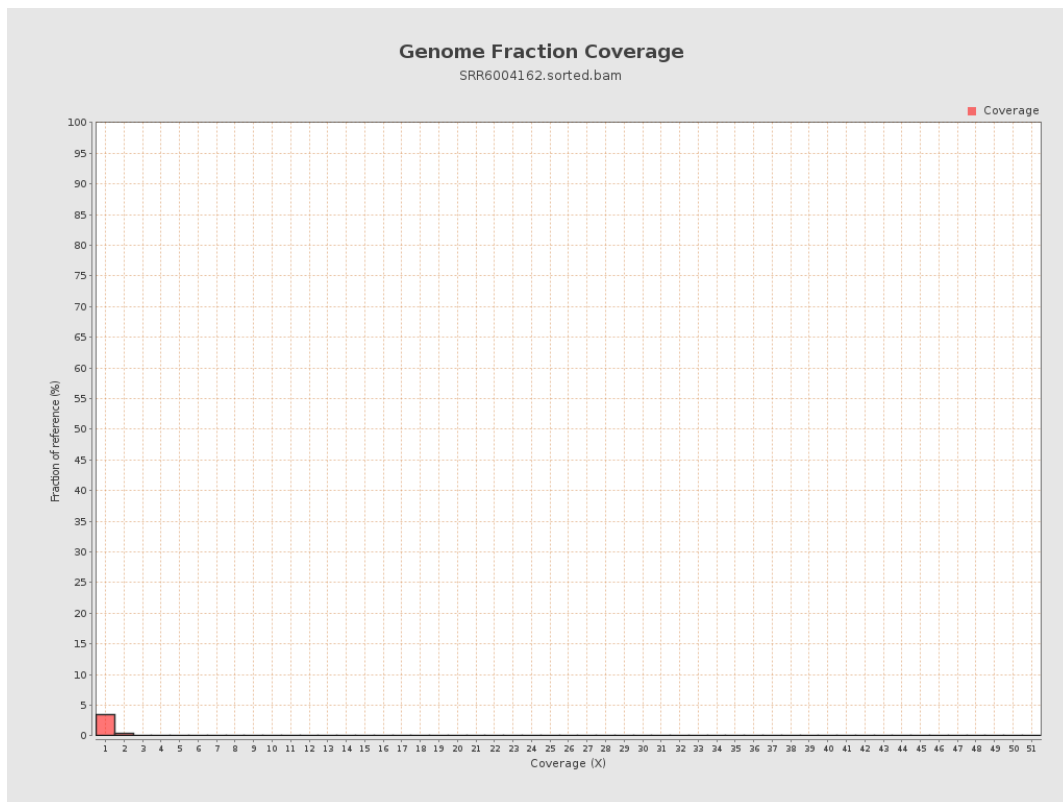
4. Results : Coverage Histogram



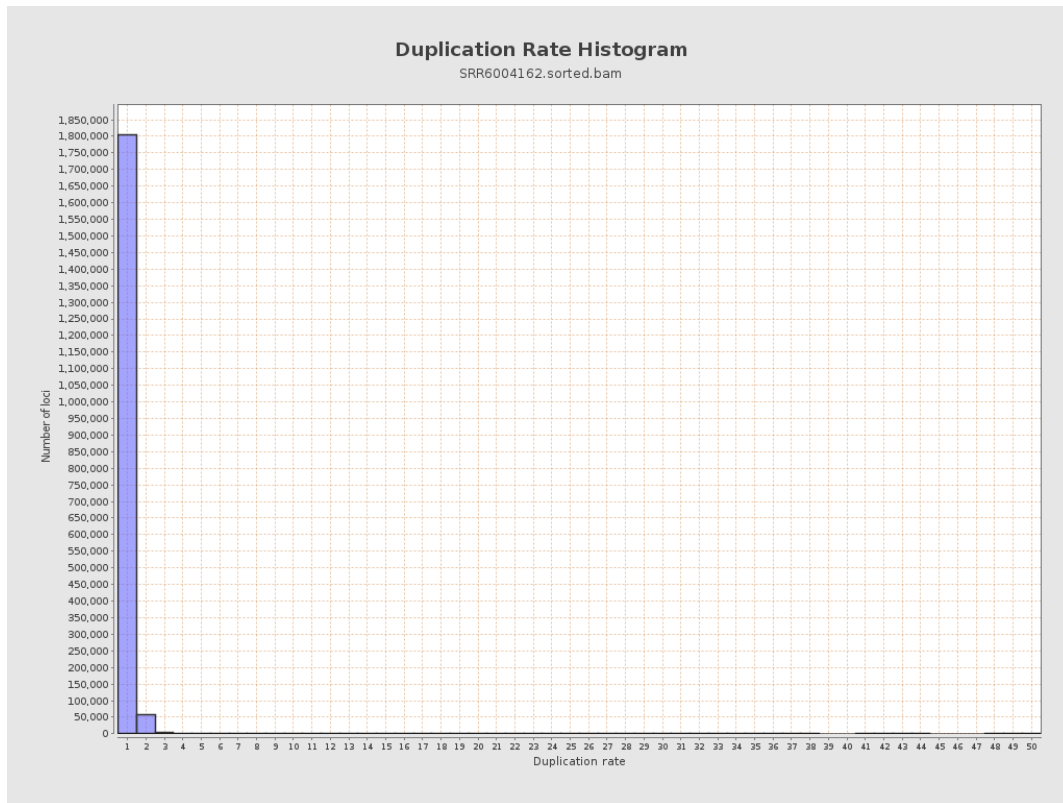
5. Results : Coverage Histogram (0-50X)



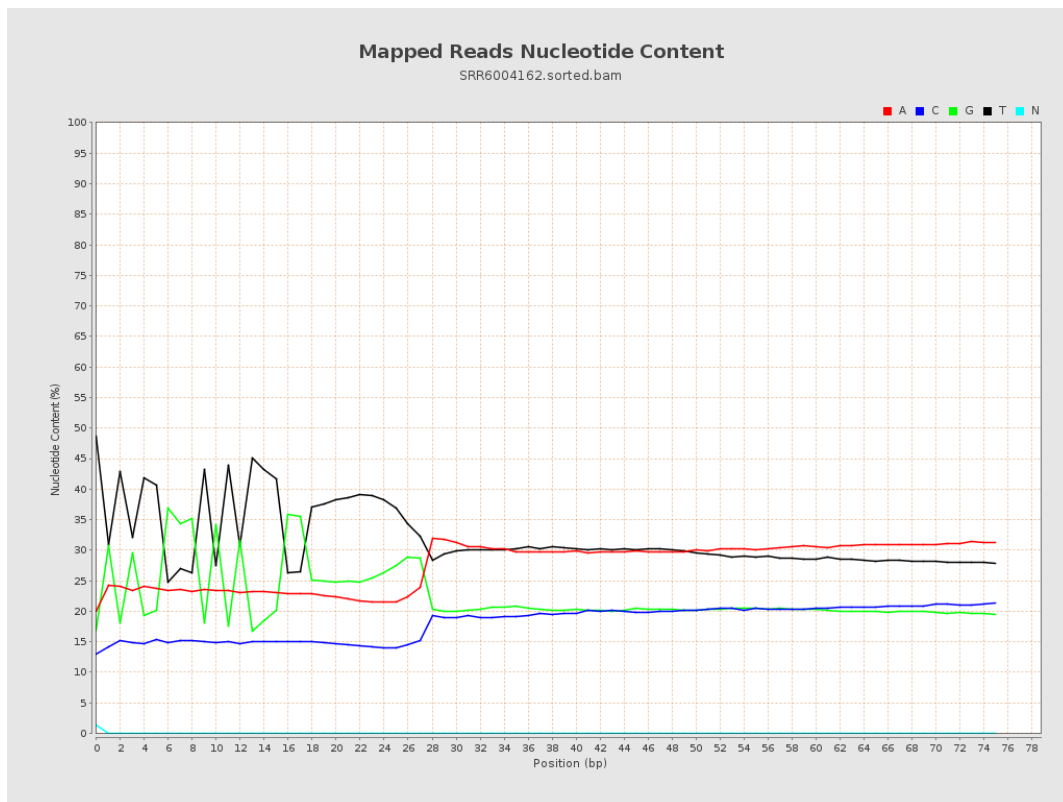
6. Results : Genome Fraction Coverage



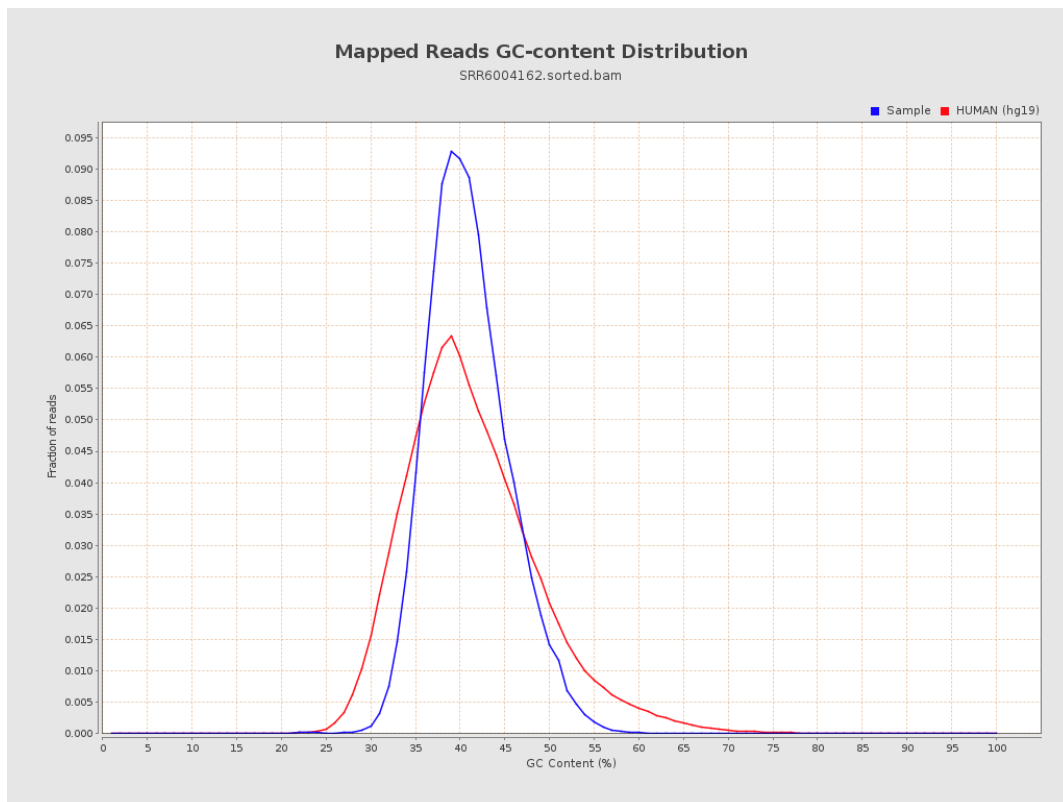
7. Results : Duplication Rate Histogram



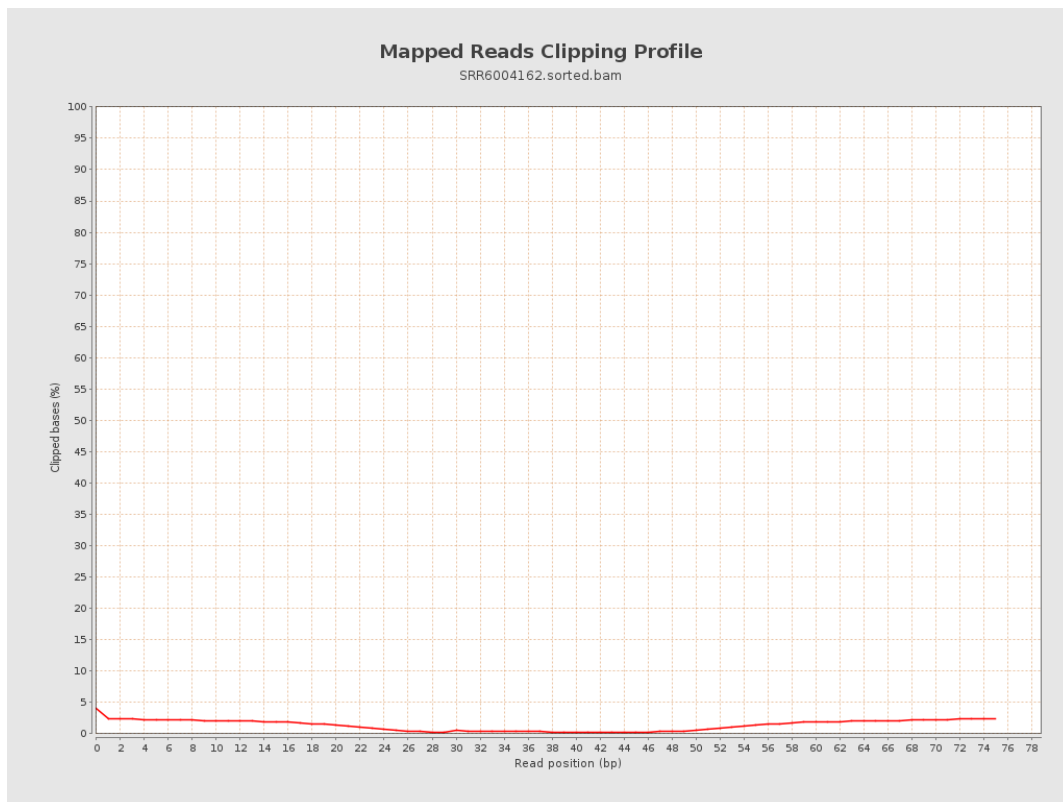
8. Results : Mapped Reads Nucleotide Content



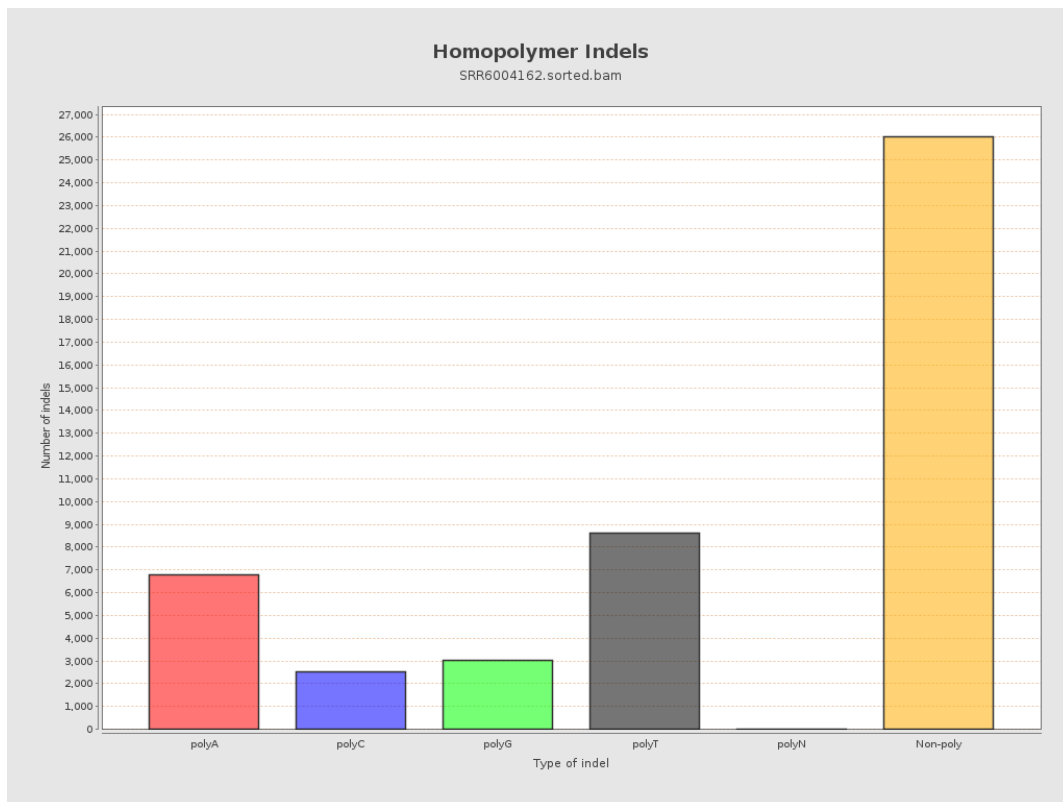
9. Results : Mapped Reads GC-content Distribution



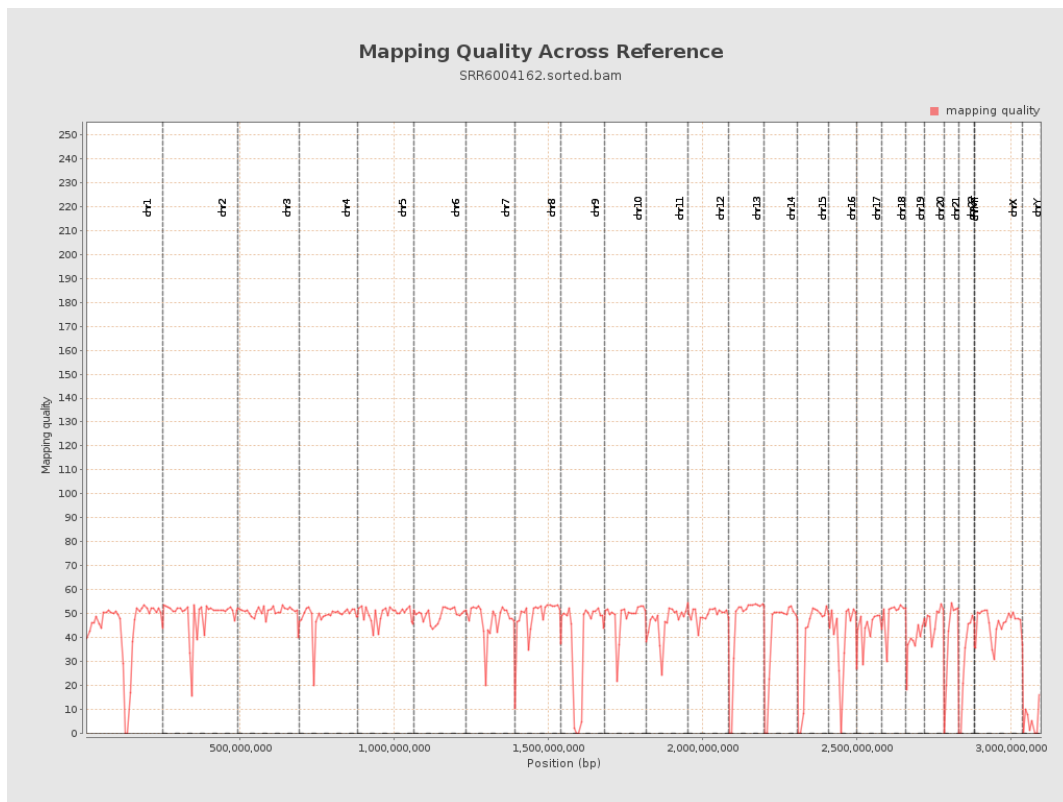
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

