

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 11:47:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008793.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_SRR6008793 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008793.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 11:47:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008793.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,482,329
Mapped reads	1,186,009 / 80.01%
Unmapped reads	296,320 / 19.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,462 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	156,696 / 10.57%
Duplication rate	10.12%
Clipped reads	638,394 / 43.07%

2.2. ACGT Content

Number/percentage of A's	20,315,926 / 26.53%
Number/percentage of C's	14,206,862 / 18.55%
Number/percentage of T's	24,160,686 / 31.55%
Number/percentage of G's	17,878,259 / 23.34%
Number/percentage of N's	28,128 / 0.04%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0248

Standard Deviation	0.2979
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.1
----------------------	------

2.5. Mismatches and indels

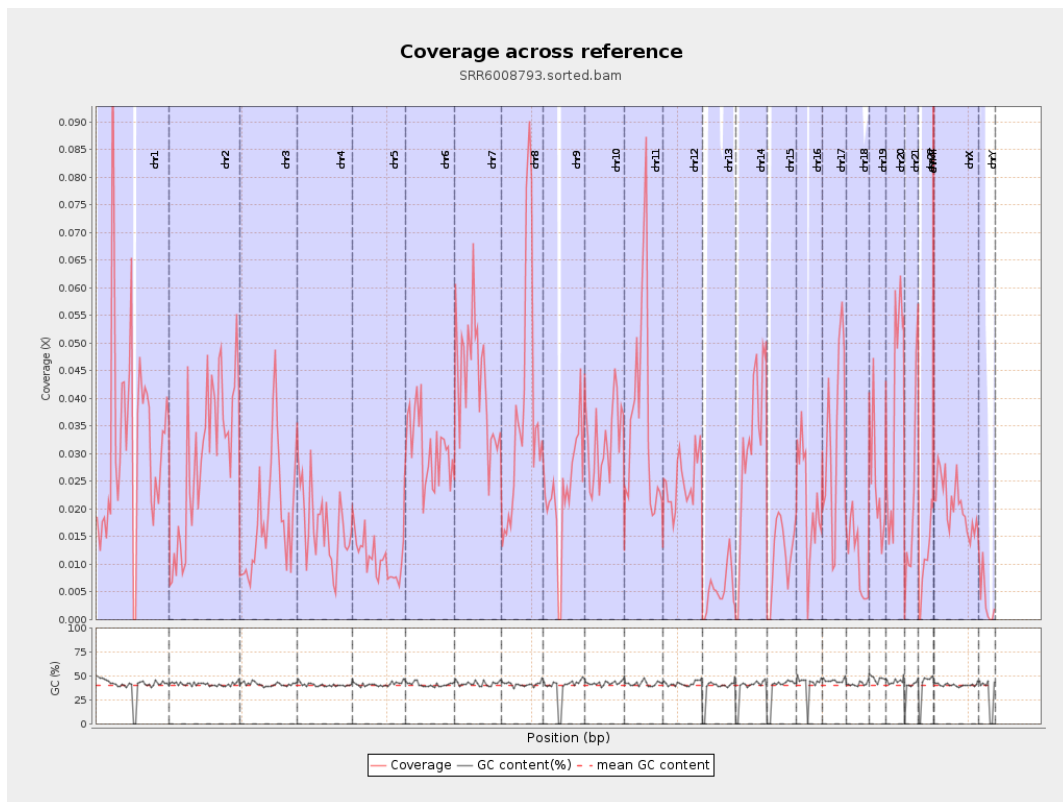
General error rate	0.87%
Mismatches	655,612
Insertions	5,637
Mapped reads with at least one insertion	0.47%
Deletions	21,967
Mapped reads with at least one deletion	1.83%
Homopolymer indels	45.21%

2.6. Chromosome stats

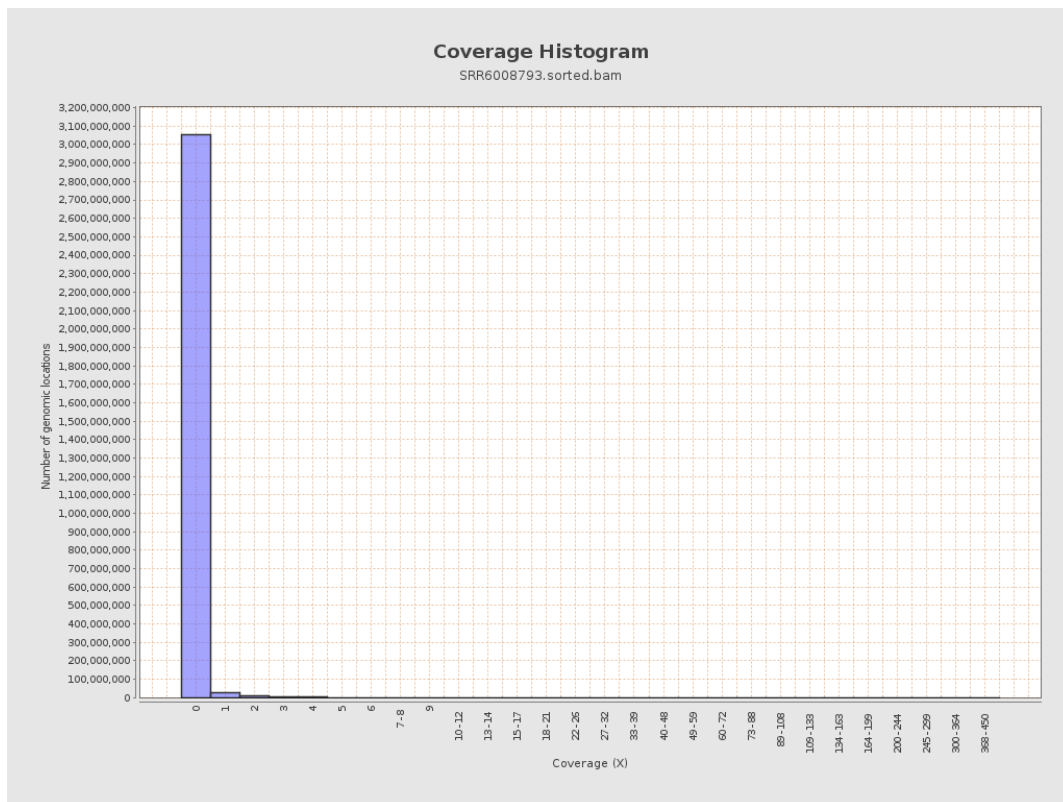
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7808593	0.0313	0.4134
chr2	243199373	7138112	0.0294	0.3546
chr3	198022430	3701543	0.0187	0.2135
chr4	191154276	3170351	0.0166	0.2245
chr5	180915260	2012284	0.0111	0.1596
chr6	171115067	5285201	0.0309	0.2948
chr7	159138663	6823853	0.0429	0.4629

chr8	146364022	5334646	0.0364	0.3695
chr9	141213431	3280144	0.0232	0.262
chr10	135534747	4345269	0.0321	0.3153
chr11	135006516	4894275	0.0363	0.3996
chr12	133851895	3338514	0.0249	0.249
chr13	115169878	624389	0.0054	0.1098
chr14	107349540	3311874	0.0309	0.2801
chr15	102531392	1213516	0.0118	0.1711
chr16	90354753	1915070	0.0212	0.2269
chr17	81195210	2625607	0.0323	0.3221
chr18	78077248	837673	0.0107	0.2563
chr19	59128983	1498125	0.0253	0.2985
chr20	63025520	2410173	0.0382	0.3145
chr21	48129895	1079680	0.0224	0.2485
chr22	51304566	546980	0.0107	0.1552
chrMT	16571	4316	0.2605	0.5451
chrX	155270560	3218847	0.0207	0.2349
chrY	59373566	208499	0.0035	0.1118

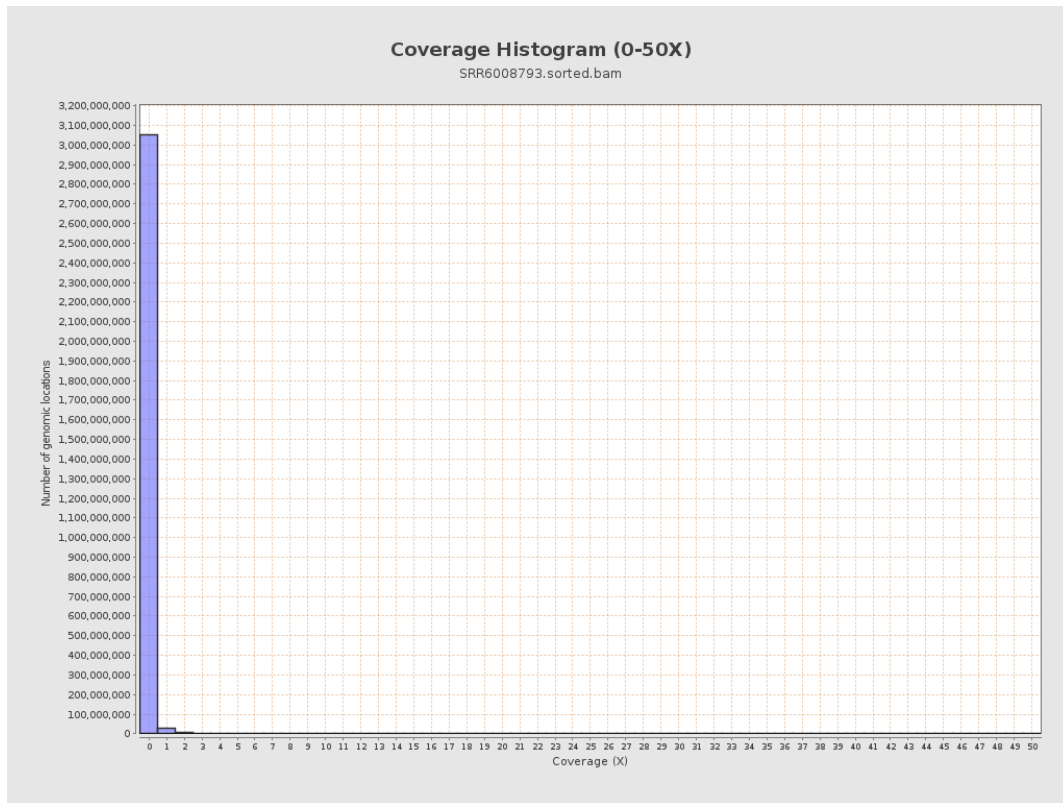
3. Results : Coverage across reference



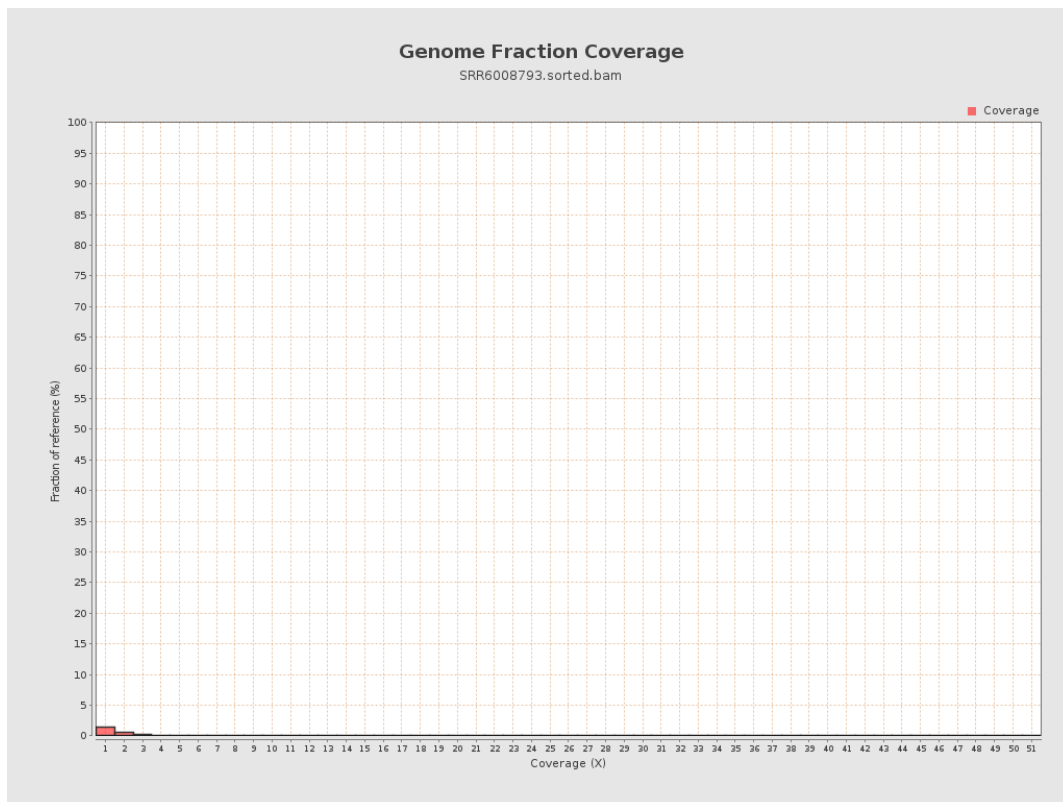
4. Results : Coverage Histogram



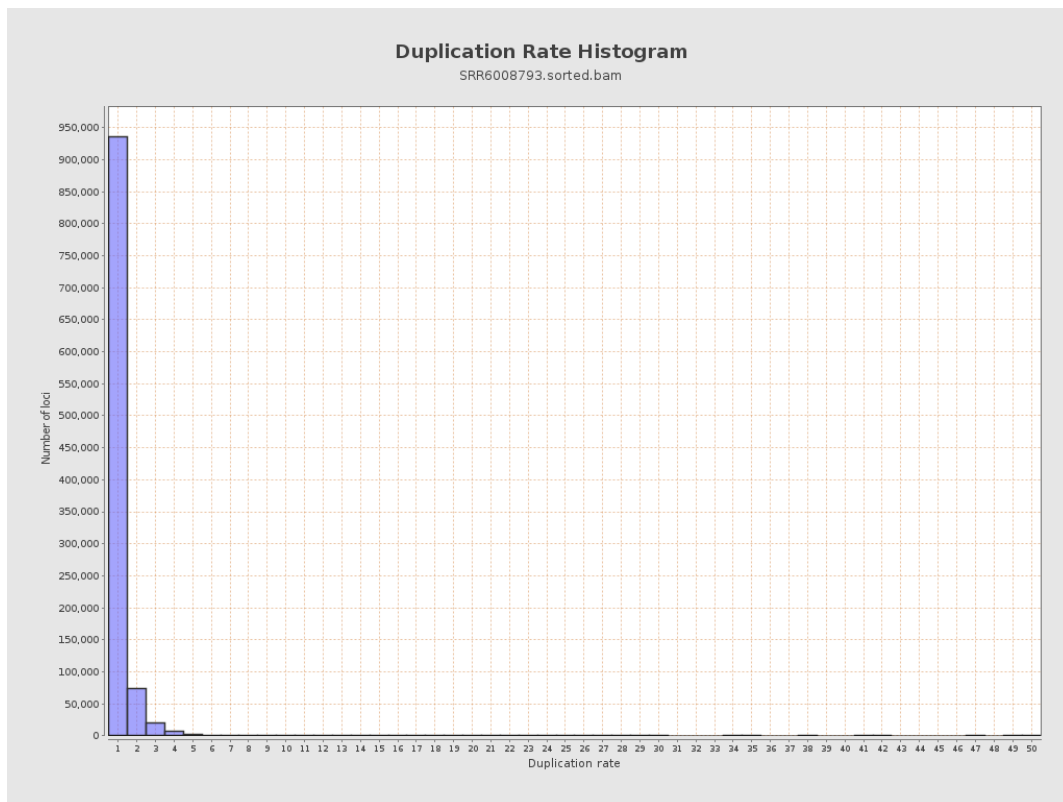
5. Results : Coverage Histogram (0-50X)



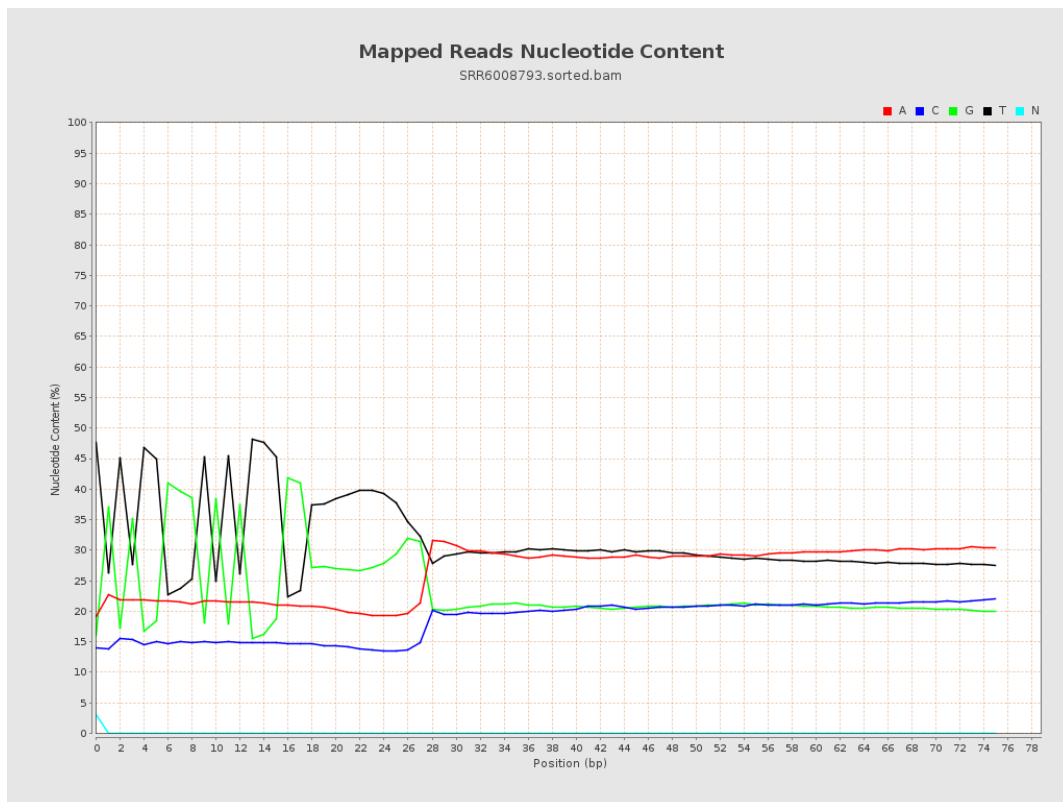
6. Results : Genome Fraction Coverage



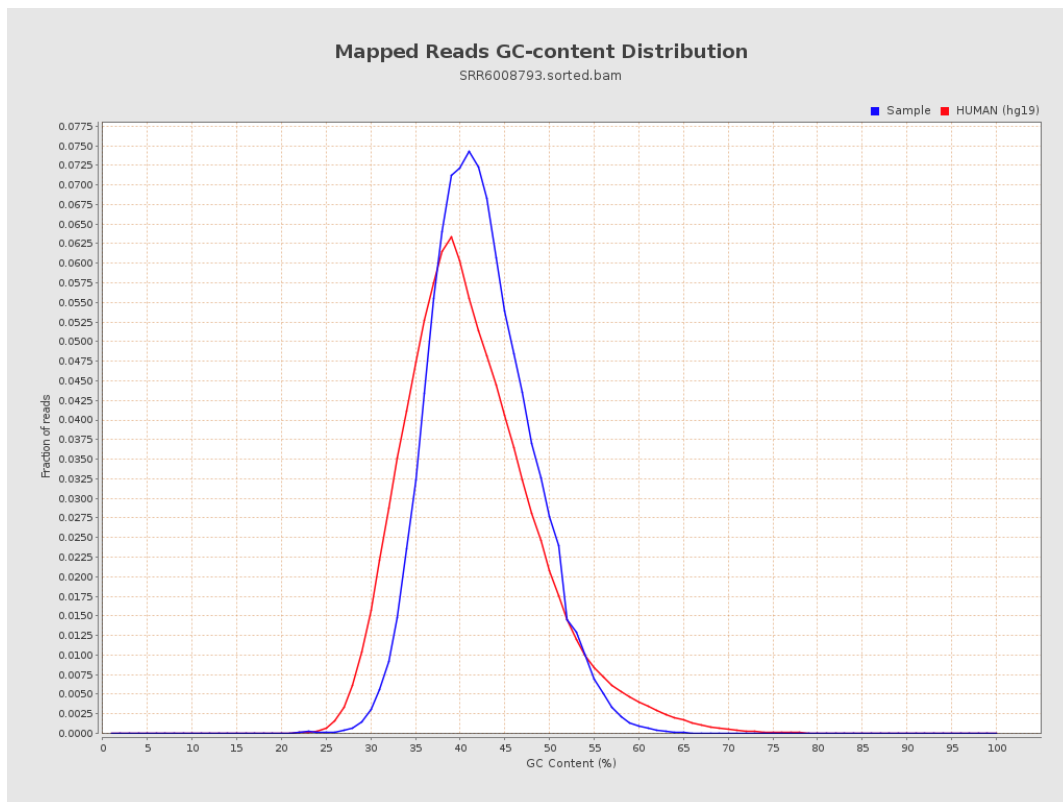
7. Results : Duplication Rate Histogram



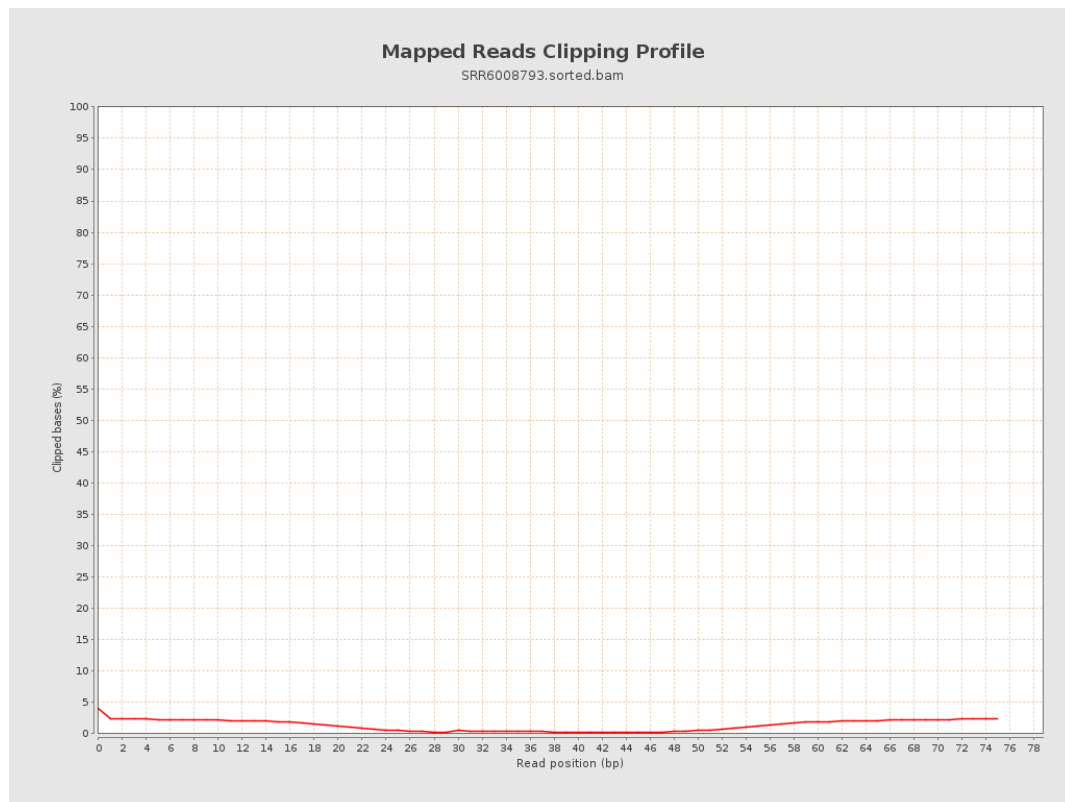
8. Results : Mapped Reads Nucleotide Content



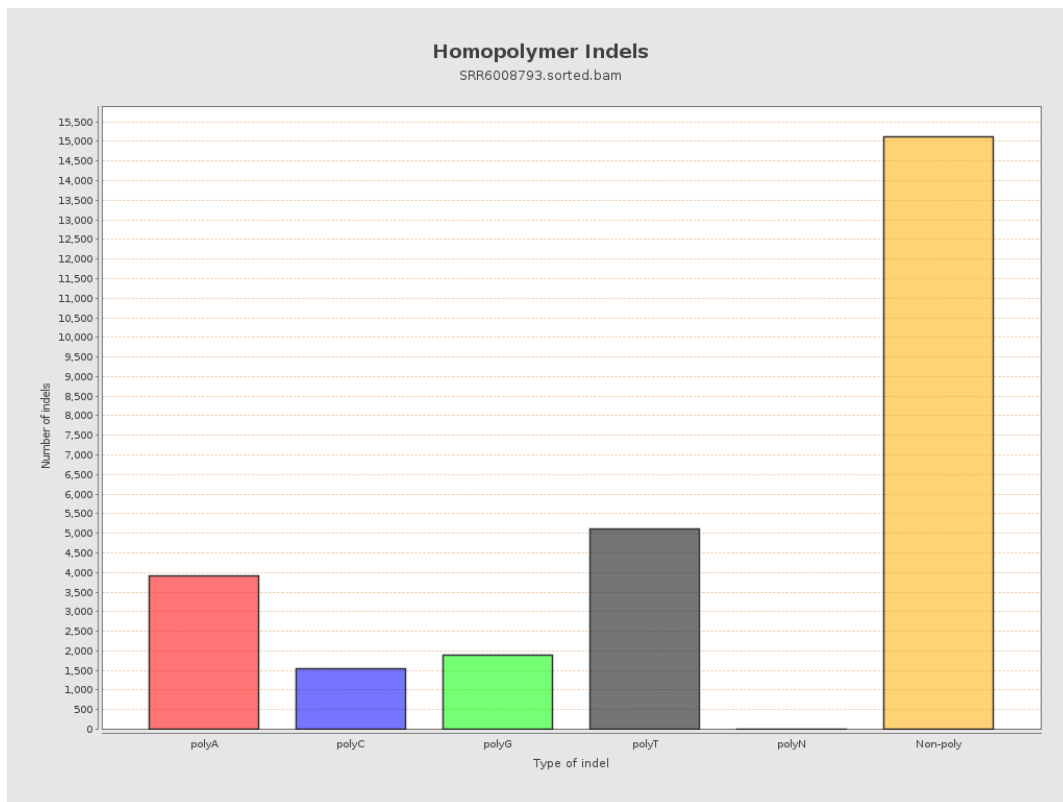
9. Results : Mapped Reads GC-content Distribution



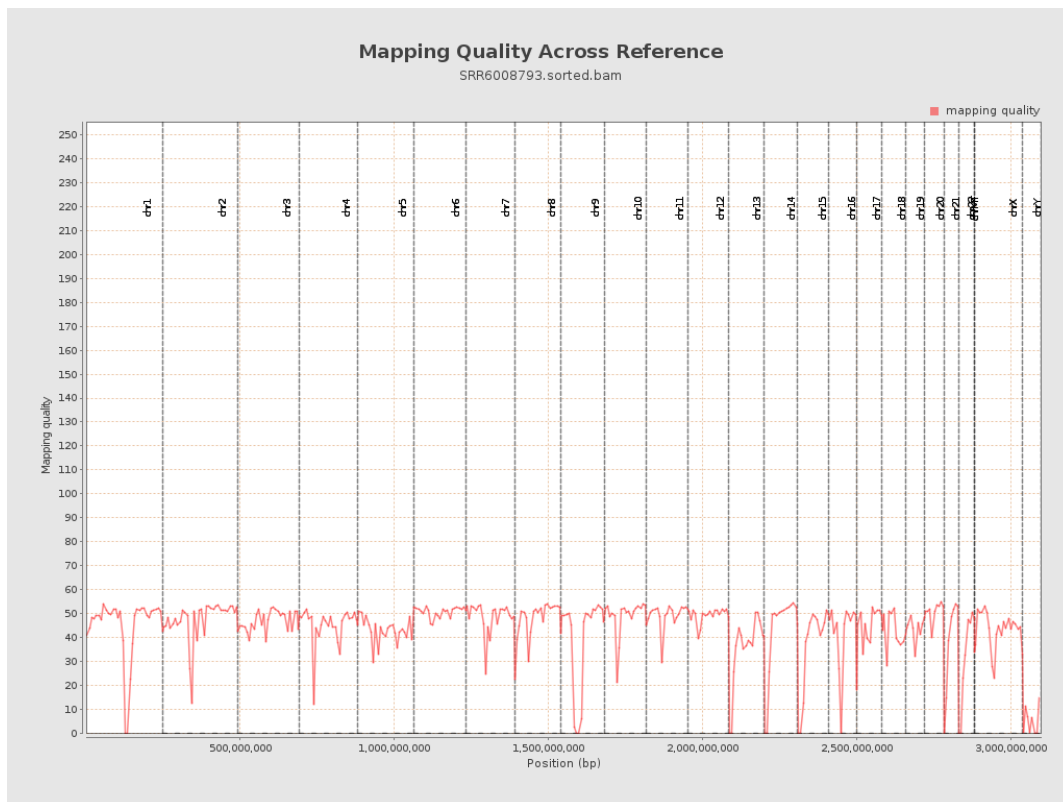
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

