

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:23:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068058.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_SRR6068058 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068058.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:23:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068058.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,697,652
Mapped reads	2,395,140 / 88.79%
Unmapped reads	302,512 / 11.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,992 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	227,815 / 8.44%
Duplication rate	7.08%
Clipped reads	1,064,947 / 39.48%

2.2. ACGT Content

Number/percentage of A's	44,229,769 / 27.76%
Number/percentage of C's	28,642,266 / 17.98%
Number/percentage of T's	51,220,516 / 32.15%
Number/percentage of G's	35,064,307 / 22.01%
Number/percentage of N's	176,452 / 0.11%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0515

Standard Deviation	0.7204
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	43.19
----------------------	-------

2.5. Mismatches and indels

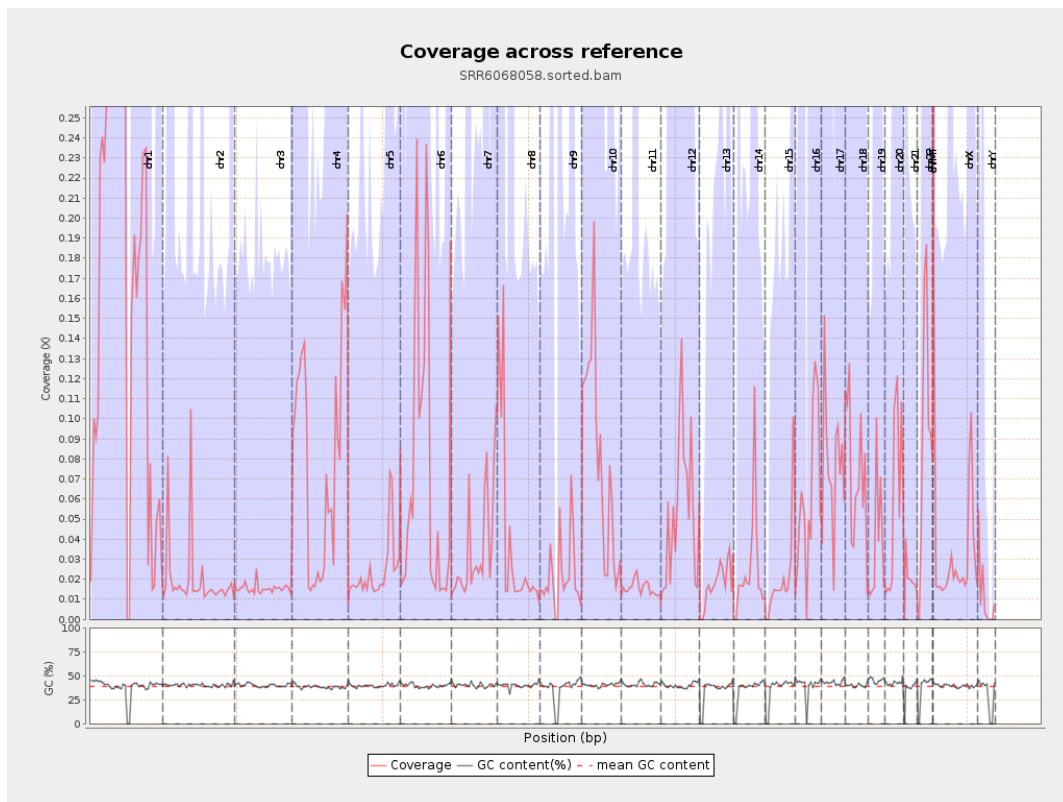
General error rate	0.9%
Mismatches	1,413,263
Insertions	11,924
Mapped reads with at least one insertion	0.49%
Deletions	41,070
Mapped reads with at least one deletion	1.7%
Homopolymer indels	47.15%

2.6. Chromosome stats

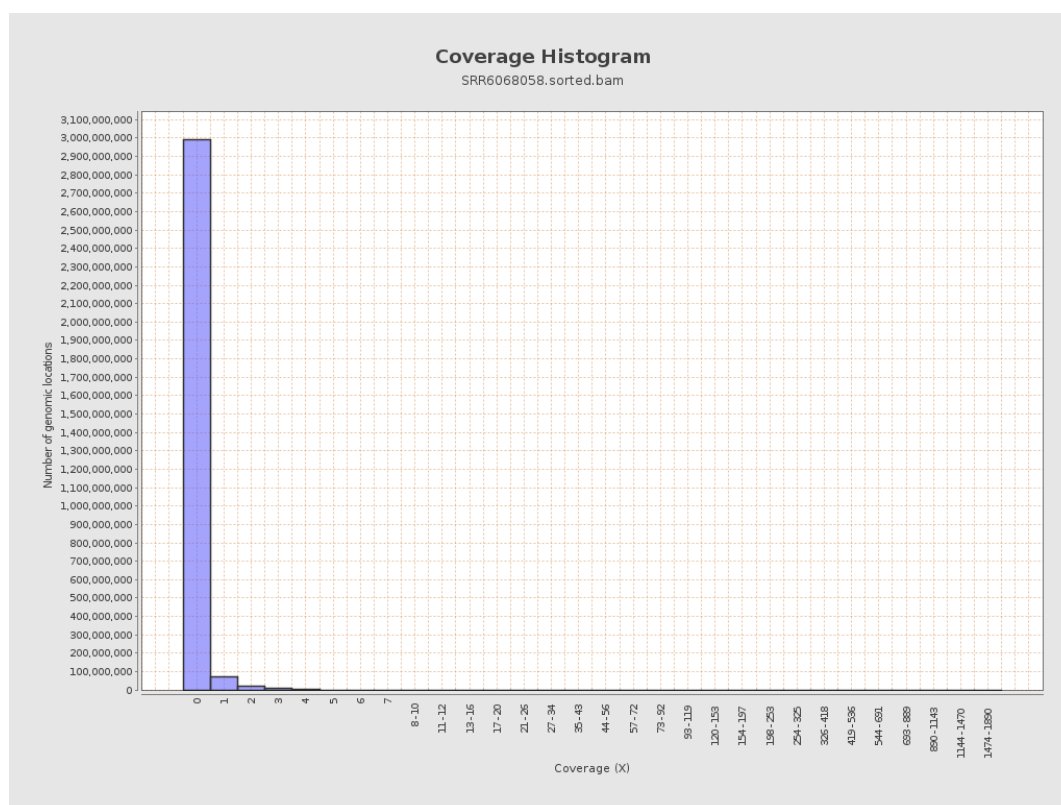
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	42575688	0.1708	1.7182
chr2	243199373	4890723	0.0201	0.7103
chr3	198022430	3094822	0.0156	0.2854
chr4	191154276	15116662	0.0791	0.412
chr5	180915260	4486272	0.0248	0.2219
chr6	171115067	12679644	0.0741	0.5786
chr7	159138663	5674833	0.0357	0.7102

chr8	146364022	5429675	0.0371	0.9862
chr9	141213431	3180075	0.0225	0.4654
chr10	135534747	10713431	0.079	1.1121
chr11	135006516	2111534	0.0156	0.2533
chr12	133851895	7225739	0.054	0.3447
chr13	115169878	2073735	0.018	0.1908
chr14	107349540	2751933	0.0256	0.249
chr15	102531392	2292981	0.0224	0.2093
chr16	90354753	5395806	0.0597	0.3756
chr17	81195210	6284441	0.0774	0.4297
chr18	78077248	5708106	0.0731	0.7429
chr19	59128983	2167123	0.0367	0.9645
chr20	63025520	3693442	0.0586	0.3476
chr21	48129895	967188	0.0201	0.2087
chr22	51304566	4754030	0.0927	0.4282
chrMT	16571	284950	17.1957	9.7504
chrX	155270560	5212247	0.0336	0.298
chrY	59373566	636001	0.0107	0.1815

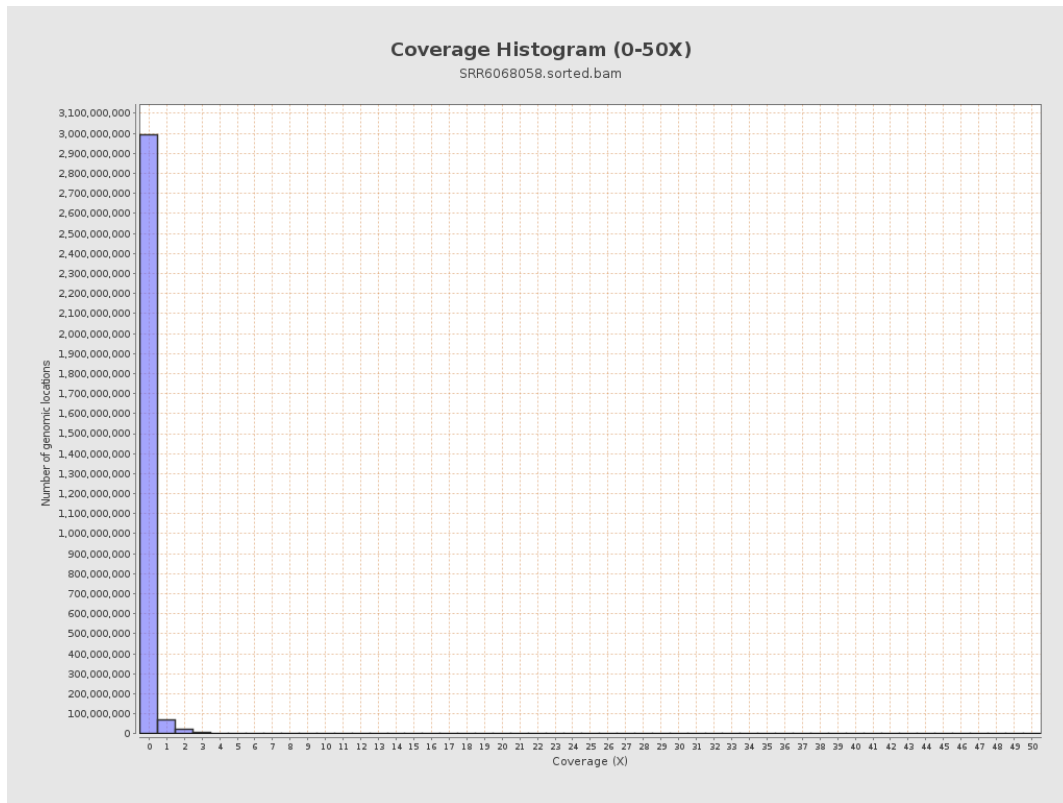
3. Results : Coverage across reference



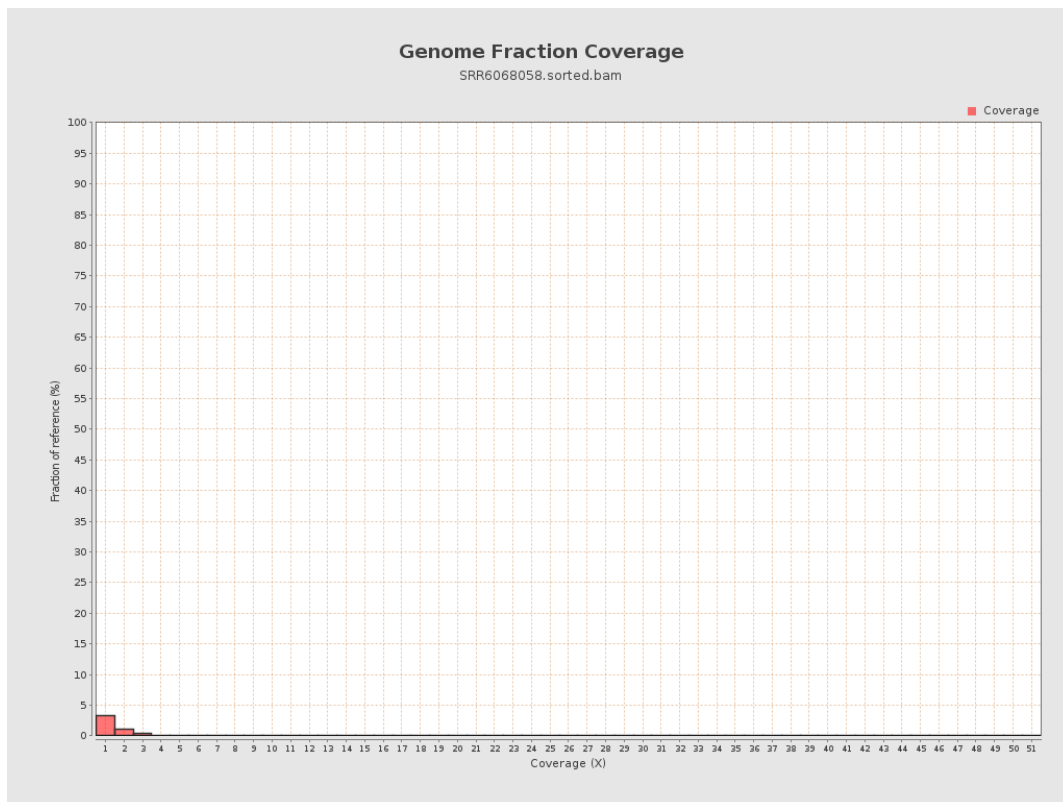
4. Results : Coverage Histogram



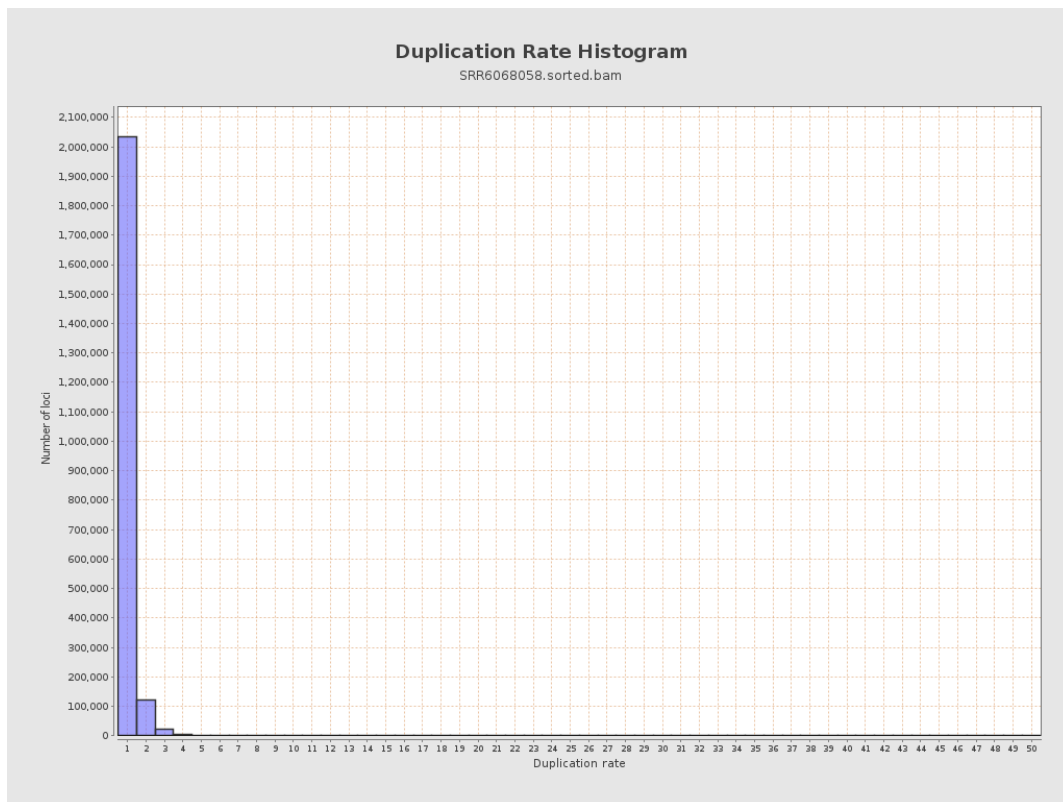
5. Results : Coverage Histogram (0-50X)



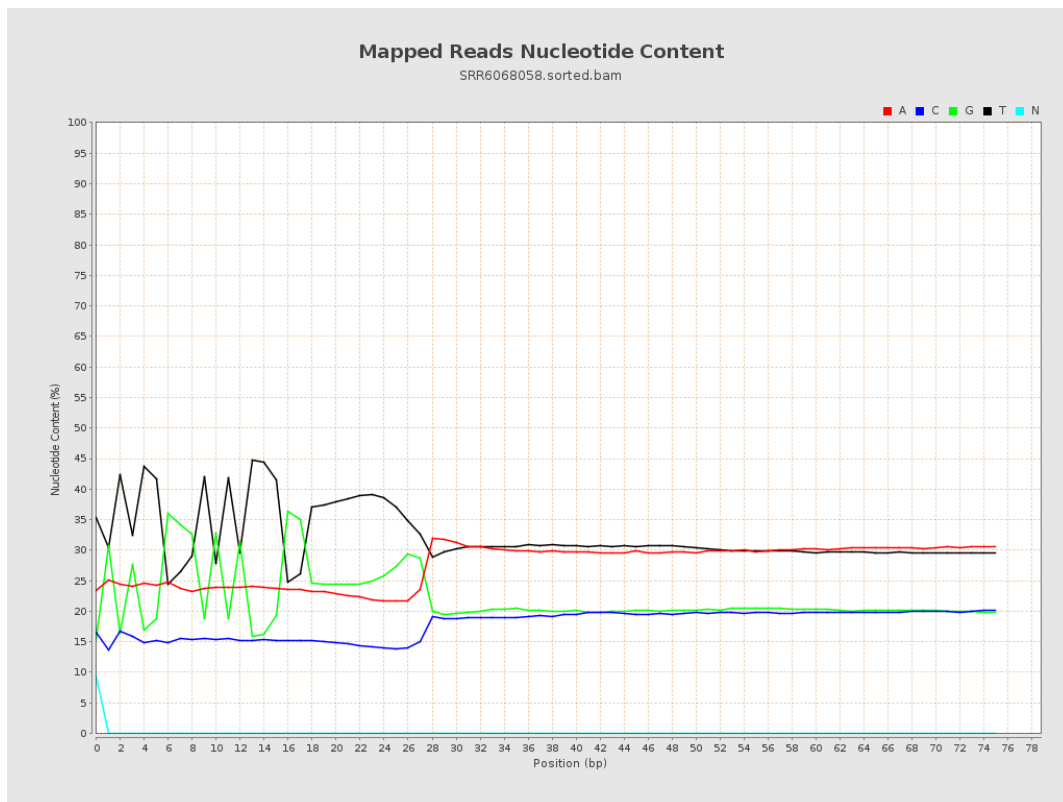
6. Results : Genome Fraction Coverage



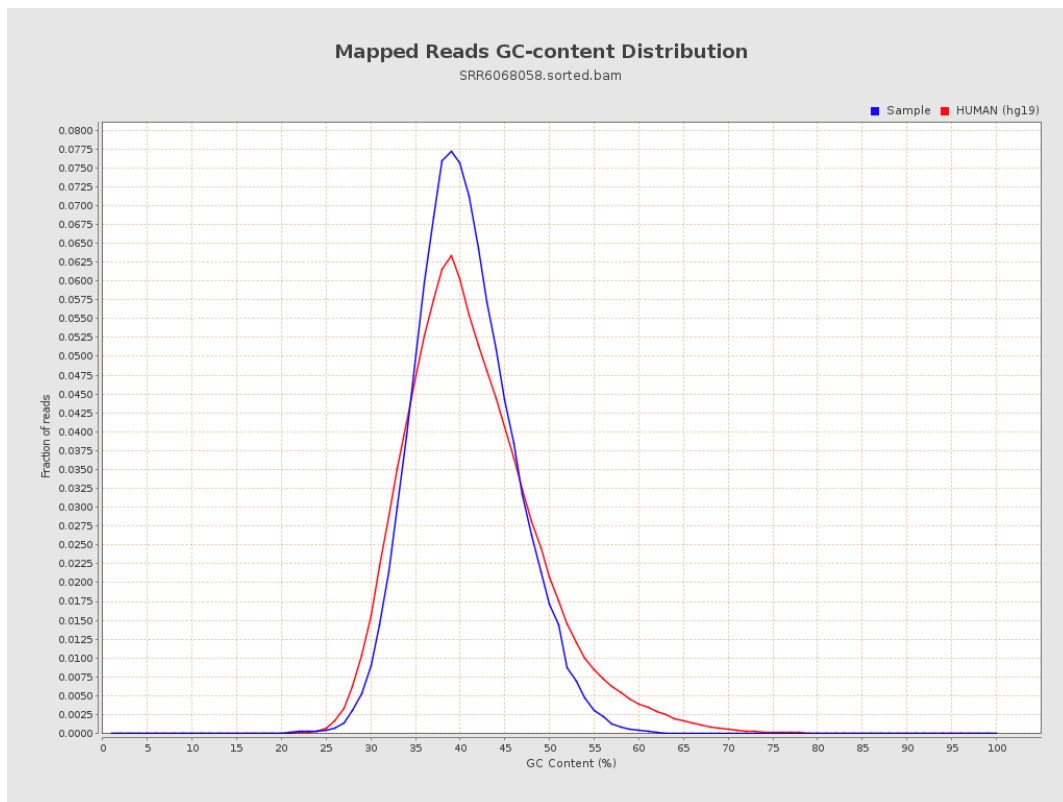
7. Results : Duplication Rate Histogram



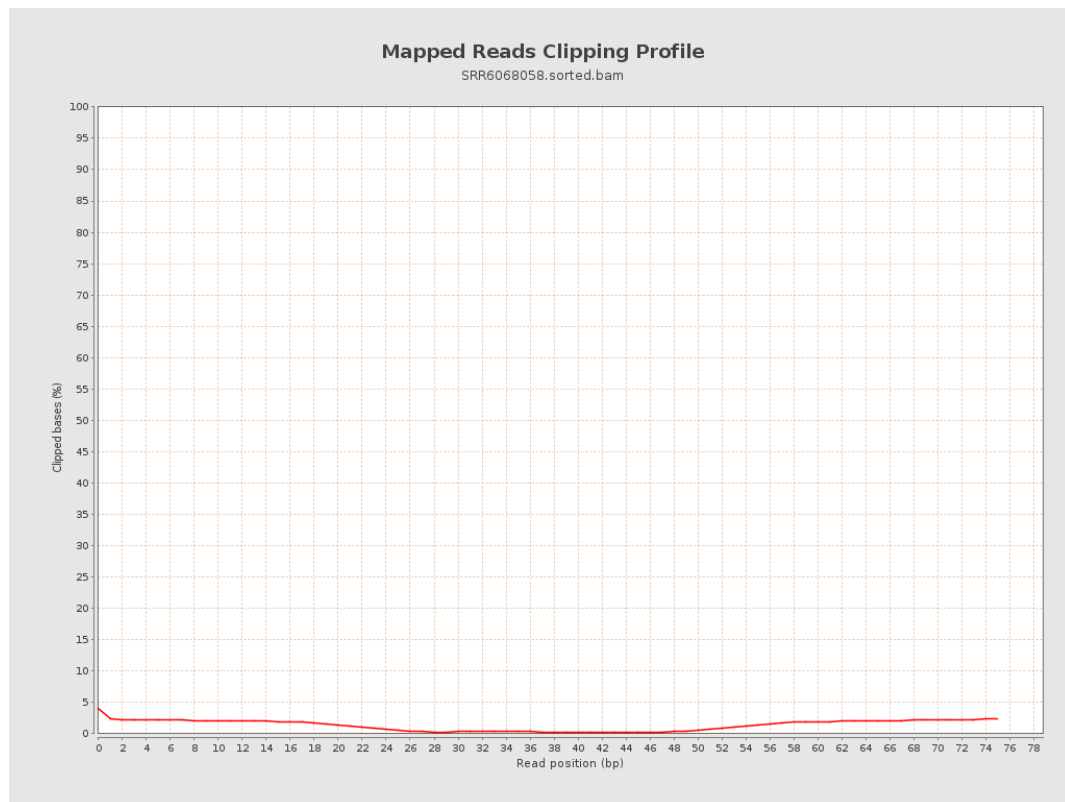
8. Results : Mapped Reads Nucleotide Content



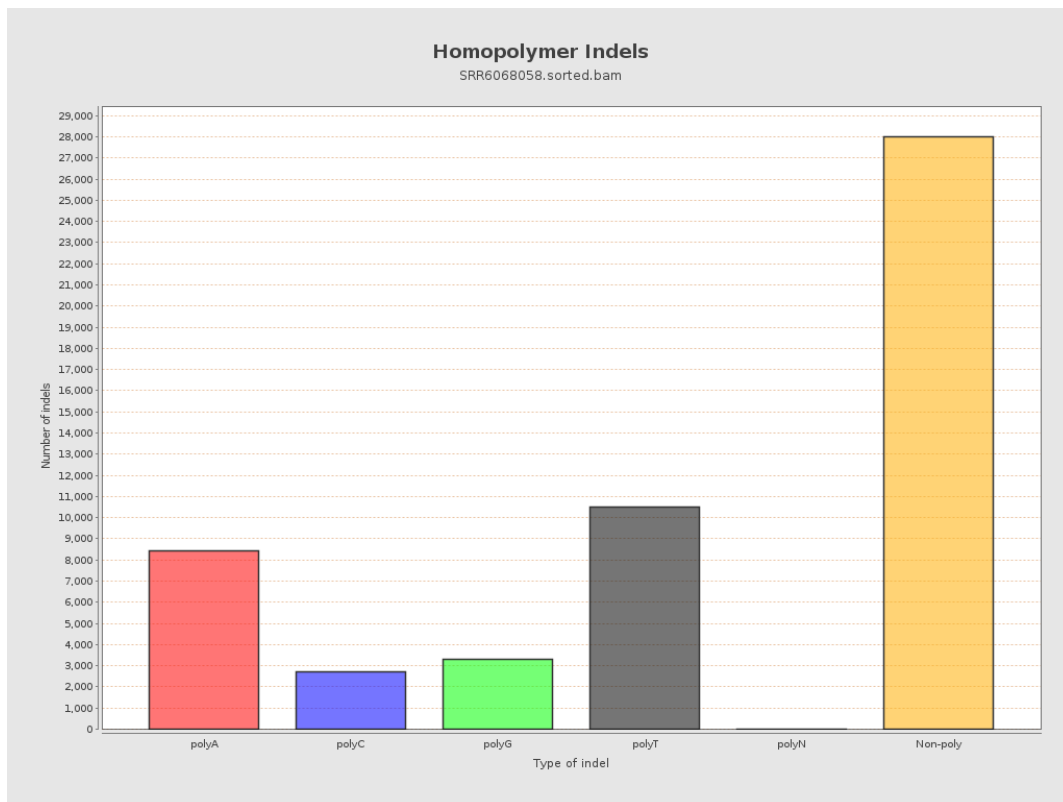
9. Results : Mapped Reads GC-content Distribution



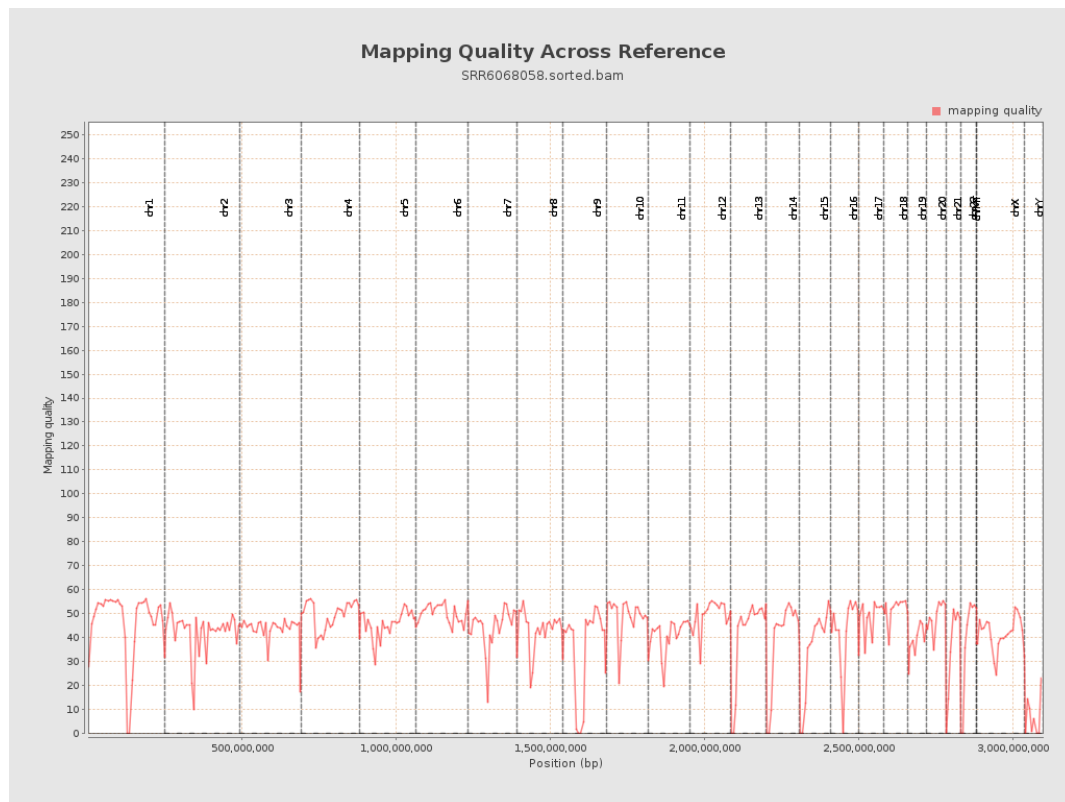
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

