Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 16:30:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080687.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_SRR3080687 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080687.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 16:30:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080687.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,394,519
Mapped reads	2,184,796 / 91.24%
Unmapped reads	209,723 / 8.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,124 / 1.01%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	93,095 / 3.89%
Duplication rate	3.5%
Clipped reads	523,833 / 21.88%

2.2. ACGT Content

Number/percentage of A's	48,560,289 / 30.88%
Number/percentage of C's	29,246,730 / 18.6%
Number/percentage of T's	48,484,272 / 30.83%
Number/percentage of G's	30,968,243 / 19.69%
Number/percentage of N's	2,464 / 0%
GC Percentage	38.29%

2.3. Coverage

Mean	0.0508

Standard Deviation	0.5131

2.4. Mapping Quality

Mean Mapping Quality	48.65

2.5. Mismatches and indels

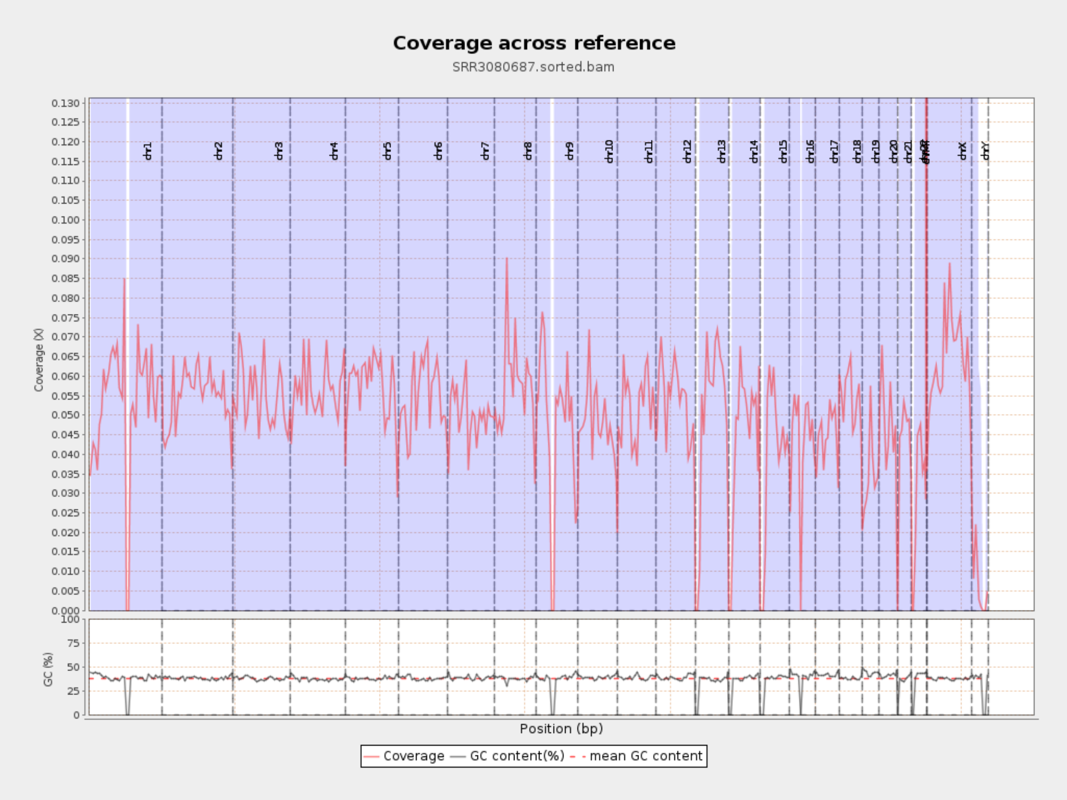
General error rate	0.81%
Mismatches	1,251,990
Insertions	12,481
Mapped reads with at least one insertion	0.57%
Deletions	32,922
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.13%

2.6. Chromosome stats

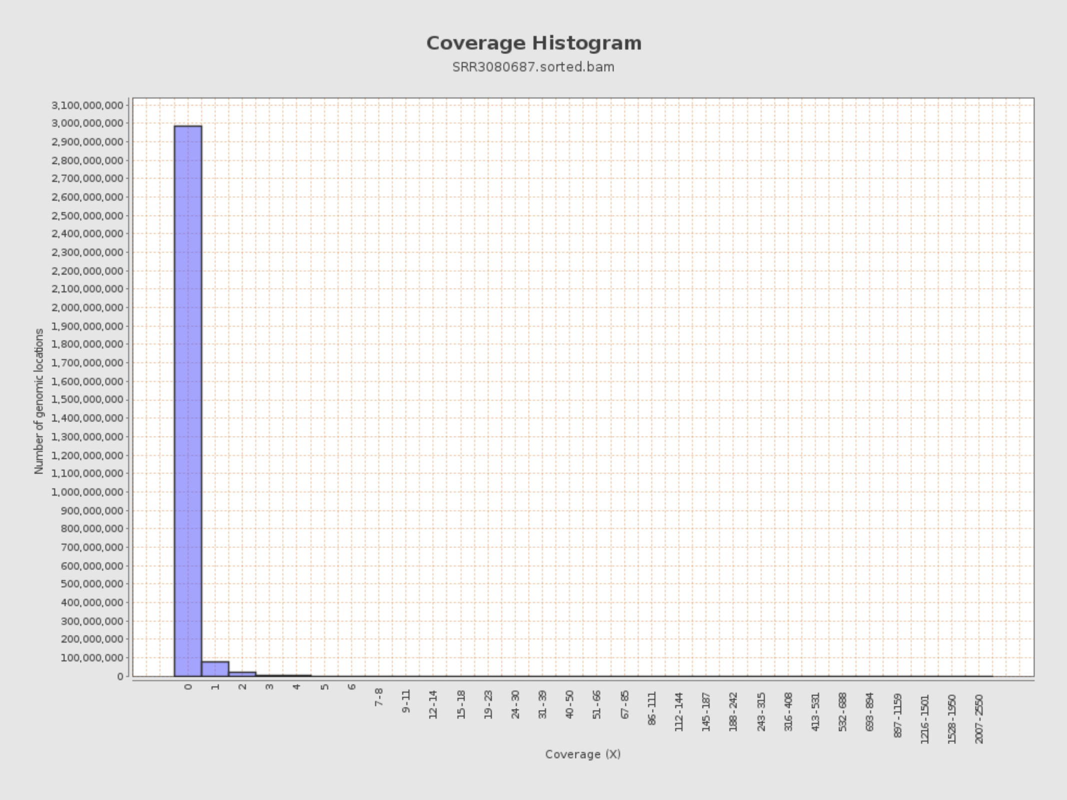
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13332442	0.0535	0.6952
chr2	243199373	13385150	0.055	0.3768
chr3	198022430	10821503	0.0546	0.3153
chr4	191154276	10856698	0.0568	0.3449
chr5	180915260	10430373	0.0577	0.323
chr6	171115067	9340763	0.0546	0.3302
chr7	159138663	8001772	0.0503	0.4427

chr8	146364022	8385301	0.0573	1.6029
chr9	141213431	6742684	0.0477	0.3399
chr10	135534747	6566341	0.0484	0.4007
chr11	135006516	6984857	0.0517	0.3242
chr12	133851895	7228214	0.054	0.3145
chr13	115169878	5714792	0.0496	0.3018
chr14	107349540	4695424	0.0437	0.2904
chr15	102531392	4077208	0.0398	0.2668
chr16	90354753	3883502	0.043	0.283
chr17	81195210	3575602	0.044	0.2952
chr18	78077248	4264525	0.0546	0.4894
chr19	59128983	2068485	0.035	0.4683
chr20	63025520	3026109	0.048	0.2968
chr21	48129895	2038974	0.0424	0.2959
chr22	51304566	1470236	0.0287	0.2203
chrMT	16571	81217	4.9012	3.8423
chrX	155270560	9959657	0.0641	0.3511
chrY	59373566	390214	0.0066	0.1869

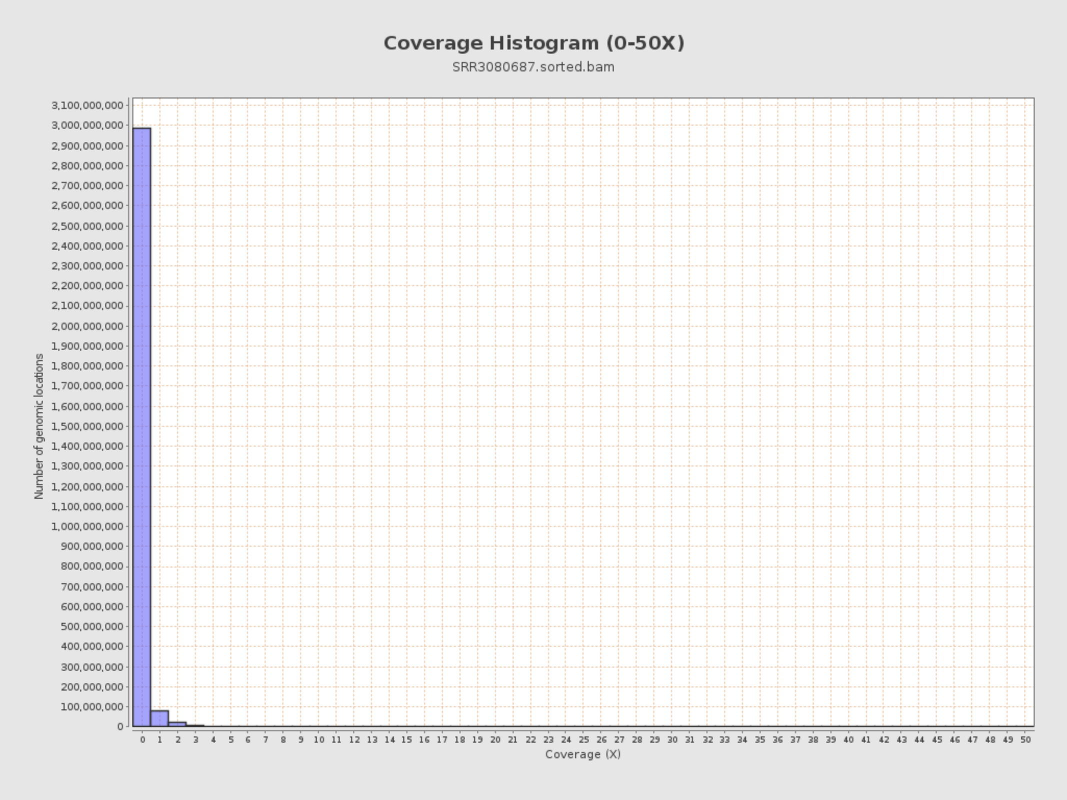
3. Results : Coverage across reference



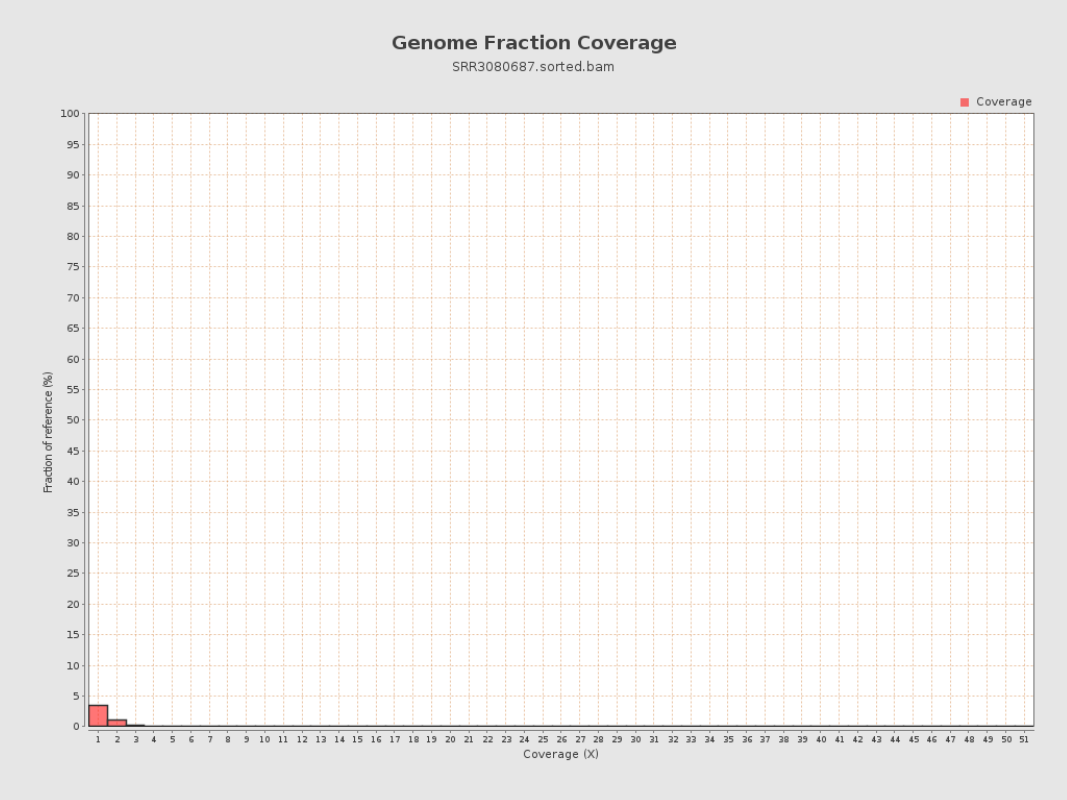
4. Results : Coverage Histogram



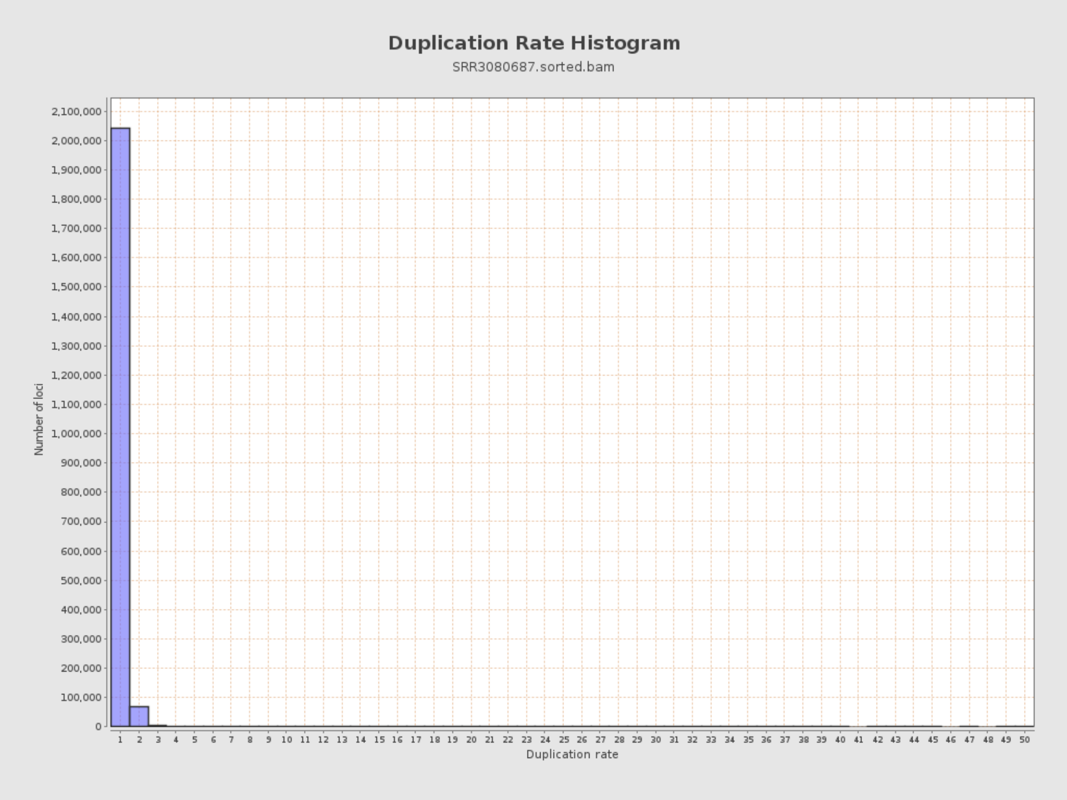
5. Results : Coverage Histogram (0-50X)



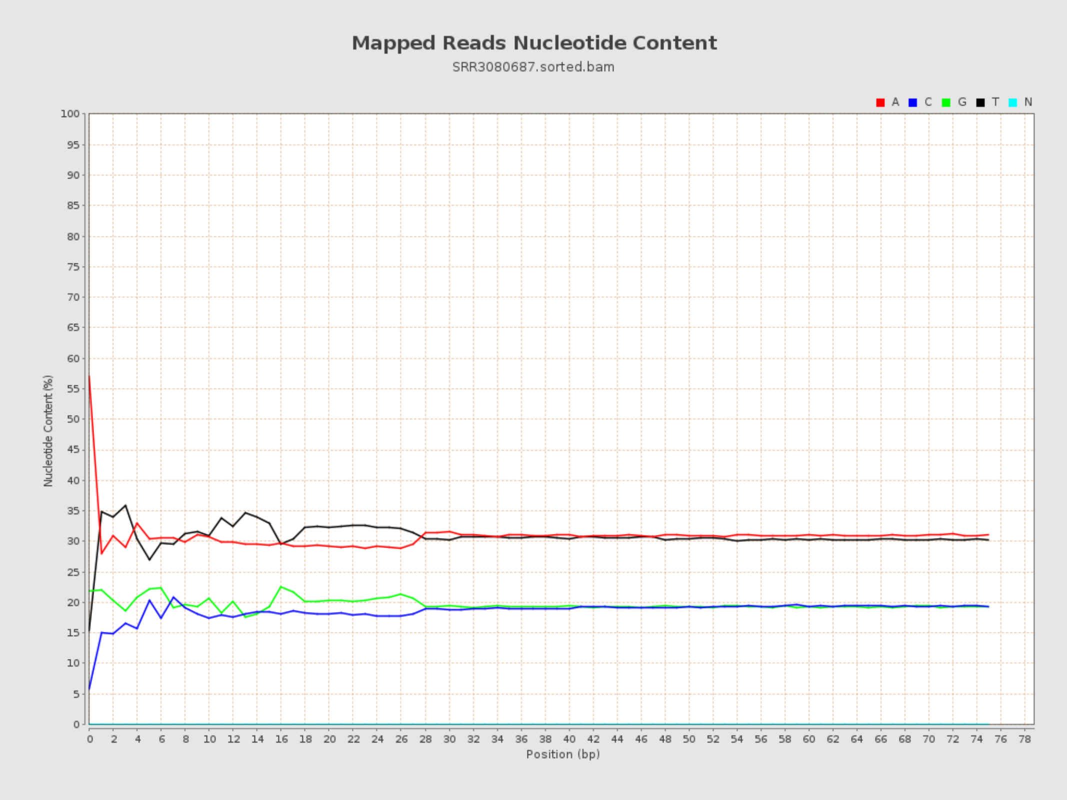
6. Results : Genome Fraction Coverage



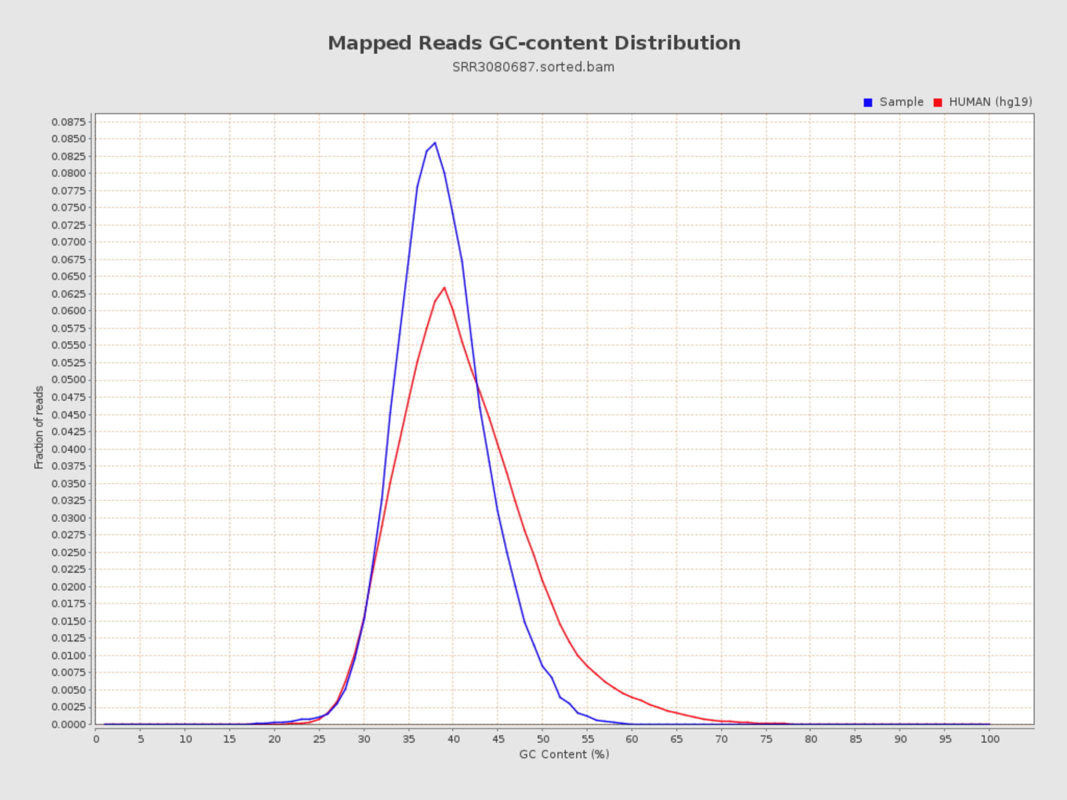
7. Results : Duplication Rate Histogram



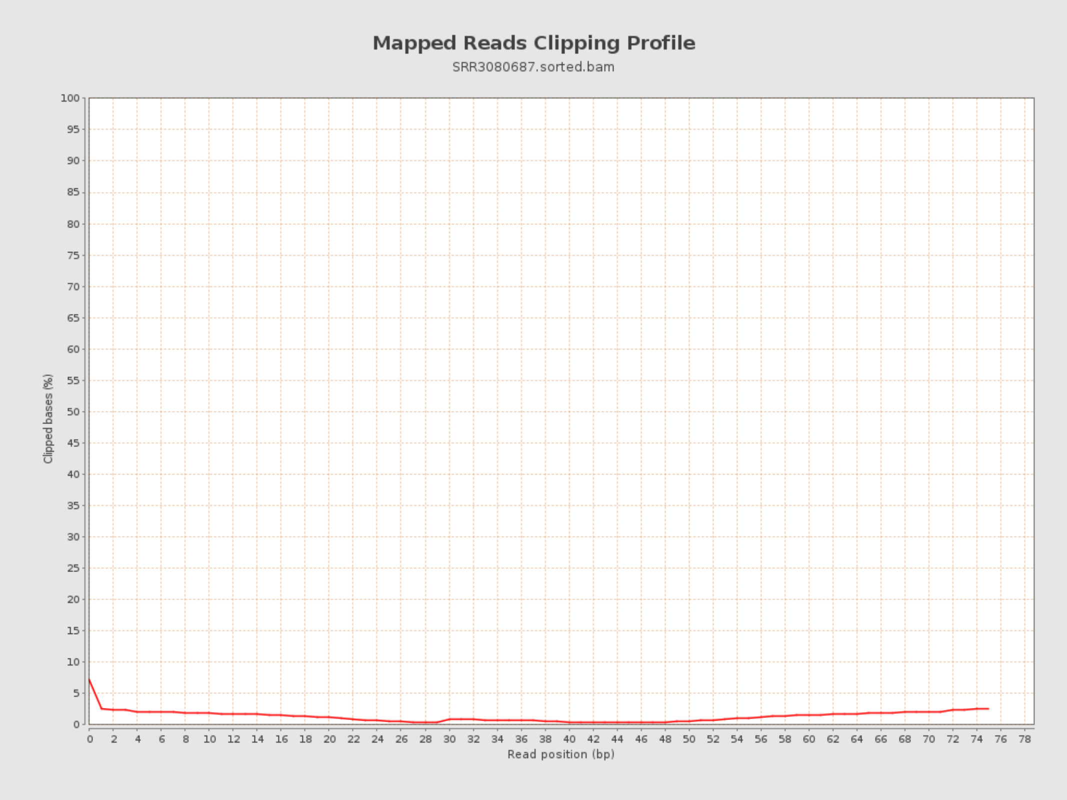
8. Results : Mapped Reads Nucleotide Content



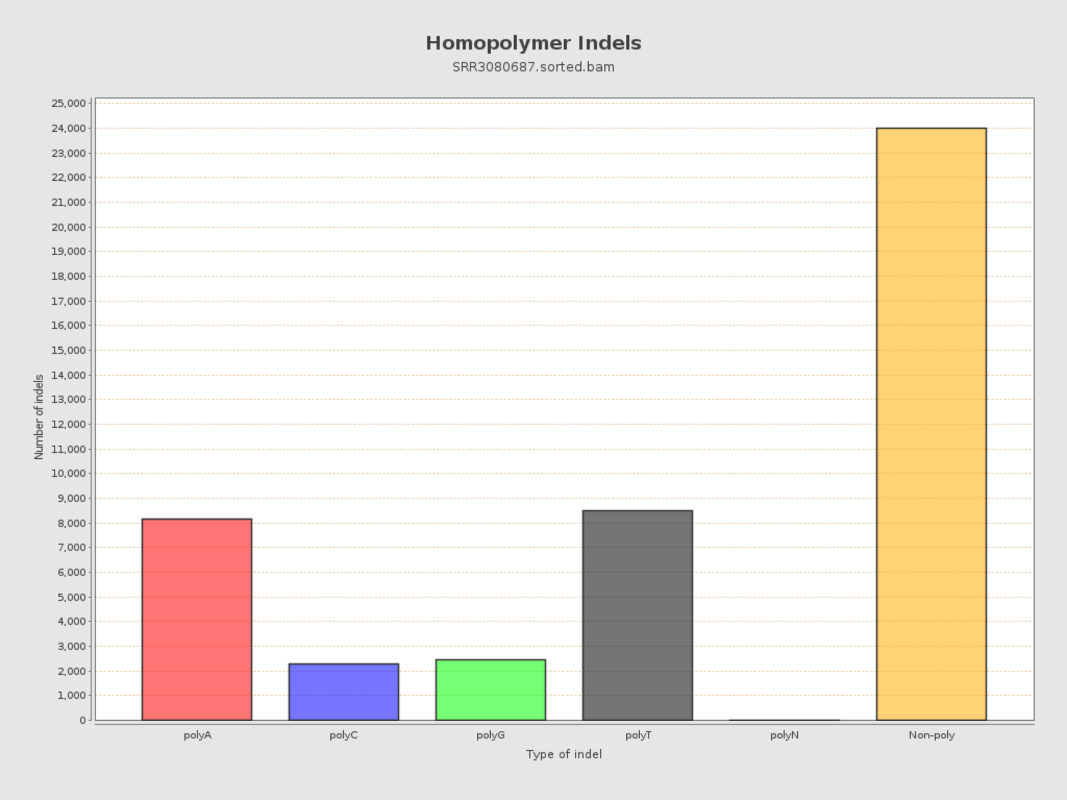
9. Results : Mapped Reads GC-content Distribution



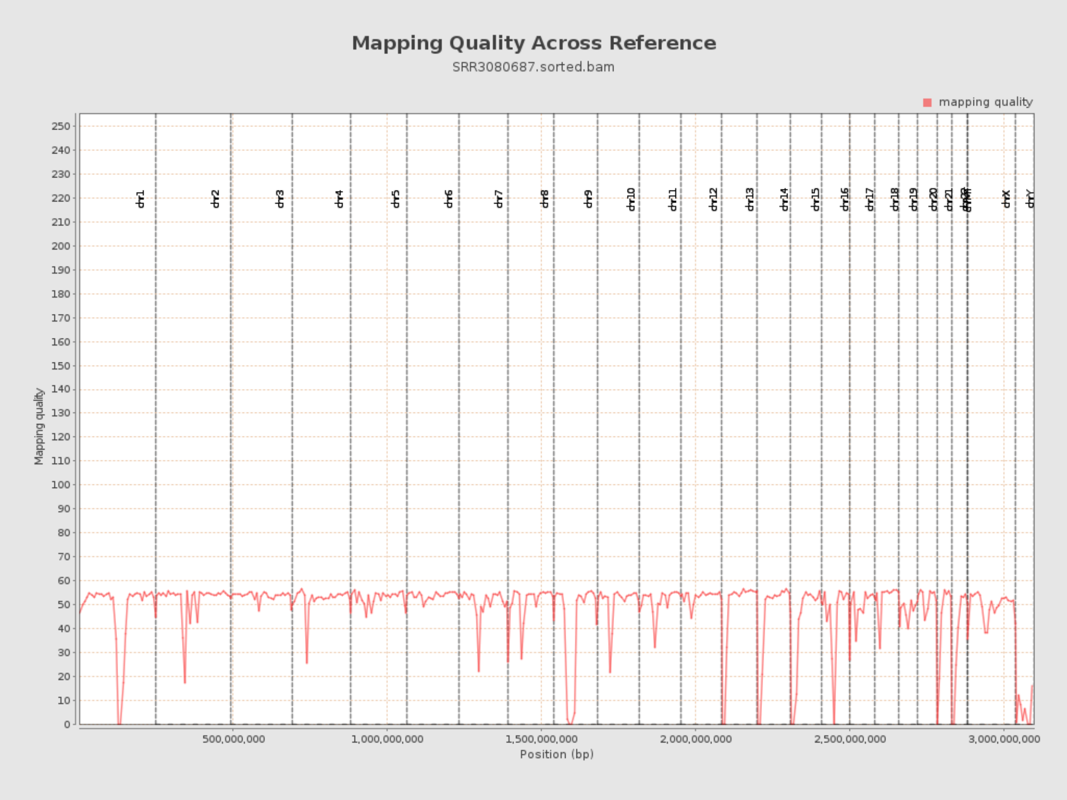
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram