Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:57:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080787.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_SRR3080787 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080787.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:57:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080787.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,007,469
Mapped reads	2,546,551 / 84.67%
Unmapped reads	460,918 / 15.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,173 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	112,725 / 3.75%
Duplication rate	3.7%
Clipped reads	1,453,839 / 48.34%

2.2. ACGT Content

Number/percentage of A's	47,364,279 / 28.99%
Number/percentage of C's	32,694,071 / 20.01%
Number/percentage of T's	48,290,595 / 29.56%
Number/percentage of G's	35,026,537 / 21.44%
Number/percentage of N's	3,370 / 0%
GC Percentage	41.45%

2.3. Coverage

Mean	0.0528

Standard Deviation	0.351

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

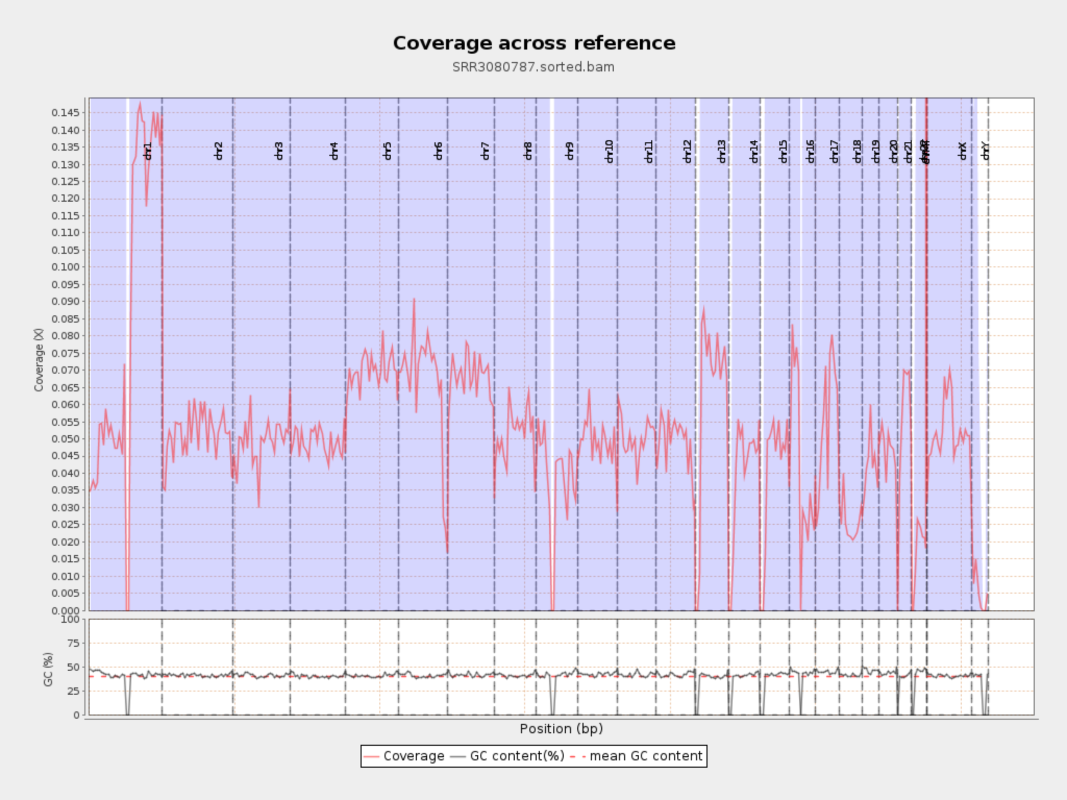
General error rate	0.78%
Mismatches	1,250,185
Insertions	11,959
Mapped reads with at least one insertion	0.47%
Deletions	34,458
Mapped reads with at least one deletion	1.34%
Homopolymer indels	46.26%

2.6. Chromosome stats

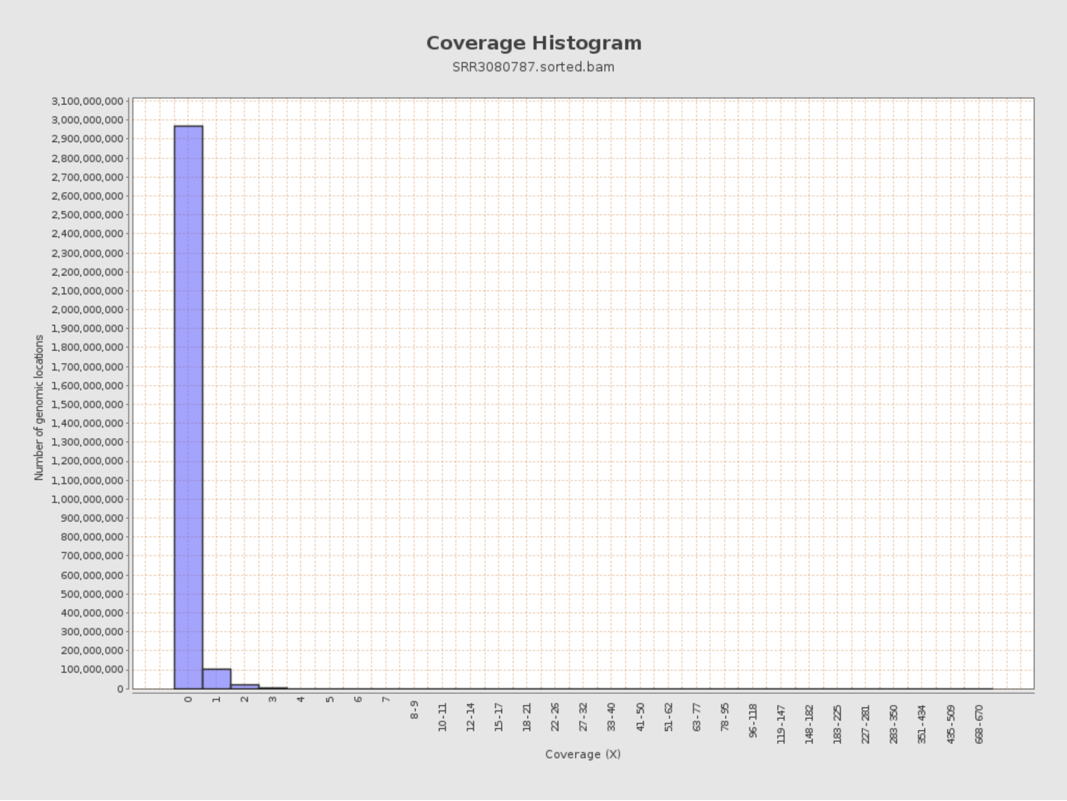
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20761293	0.0833	0.5645
chr2	243199373	12497869	0.0514	0.419
chr3	198022430	9677402	0.0489	0.2703
chr4	191154276	9384321	0.0491	0.2777
chr5	180915260	12625109	0.0698	0.3234
chr6	171115067	11506700	0.0672	0.3878
chr7	159138663	10929574	0.0687	0.4446

chr8	146364022	7601974	0.0519	0.4015
chr9	141213431	5323138	0.0377	0.2767
chr10	135534747	6728773	0.0496	0.3221
chr11	135006516	6718555	0.0498	0.3018
chr12	133851895	6561454	0.049	0.2725
chr13	115169878	7138925	0.062	0.3084
chr14	107349540	4232634	0.0394	0.2531
chr15	102531392	4135475	0.0403	0.2613
chr16	90354753	3818671	0.0423	0.2646
chr17	81195210	4500274	0.0554	0.3076
chr18	78077248	1998181	0.0256	0.3683
chr19	59128983	2523730	0.0427	0.3921
chr20	63025520	2925058	0.0464	0.2659
chr21	48129895	2582942	0.0537	0.2895
chr22	51304566	846986	0.0165	0.1561
chrMT	16571	52095	3.1437	2.5992
chrX	155270560	8021838	0.0517	0.2916
chrY	59373566	340081	0.0057	0.1085

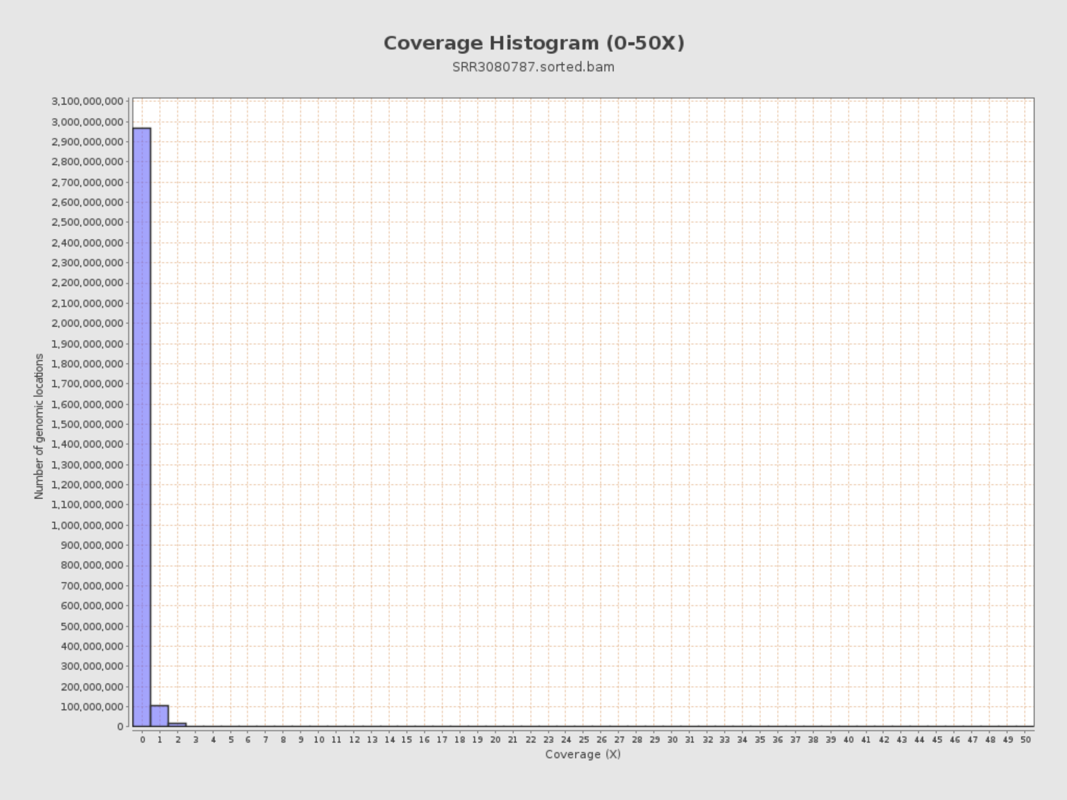
3. Results : Coverage across reference



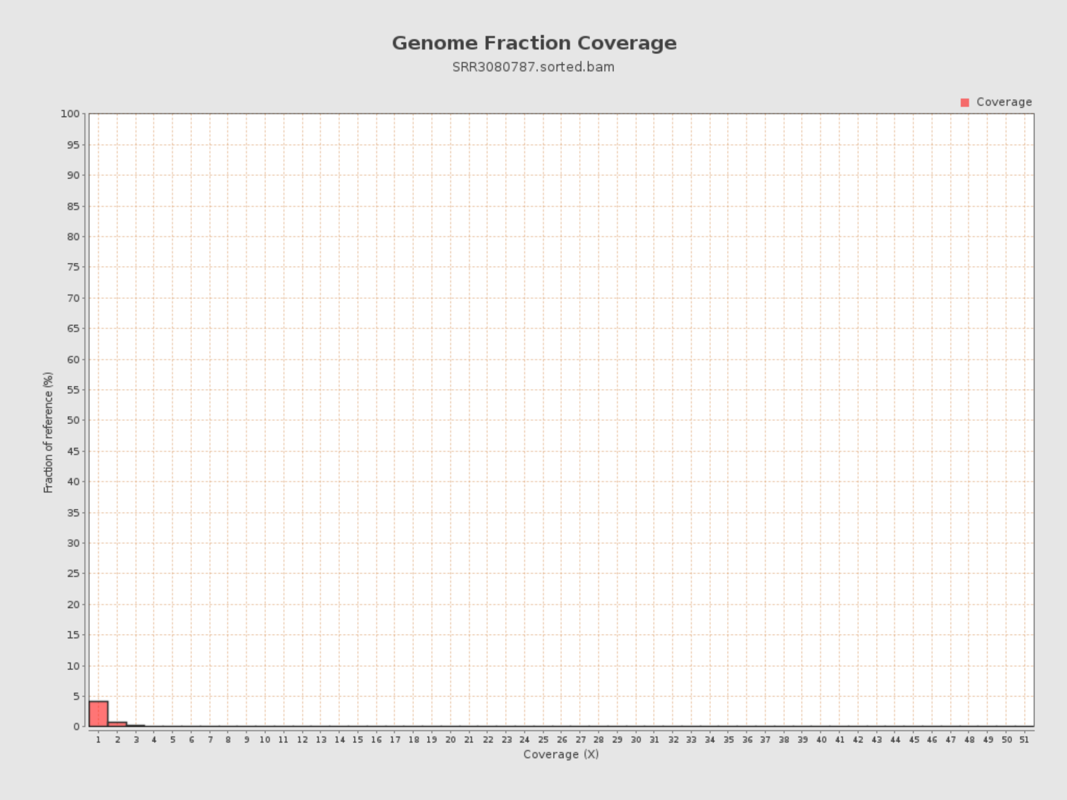
4. Results : Coverage Histogram



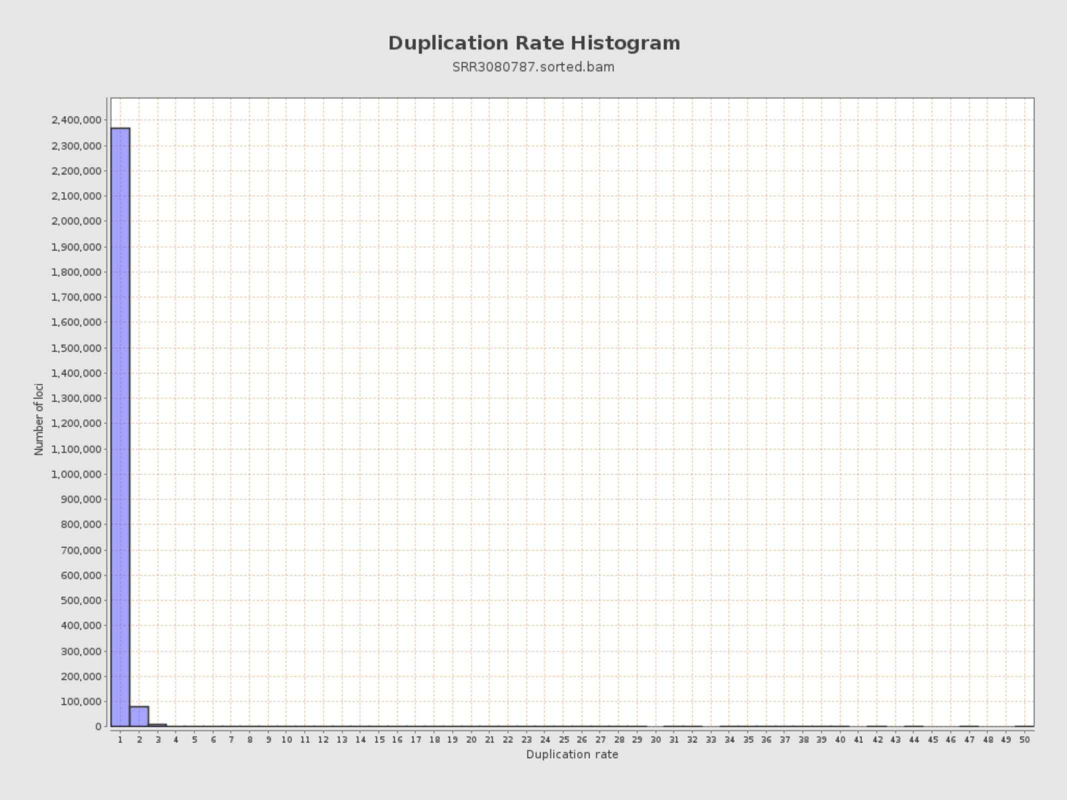
5. Results : Coverage Histogram (0-50X)



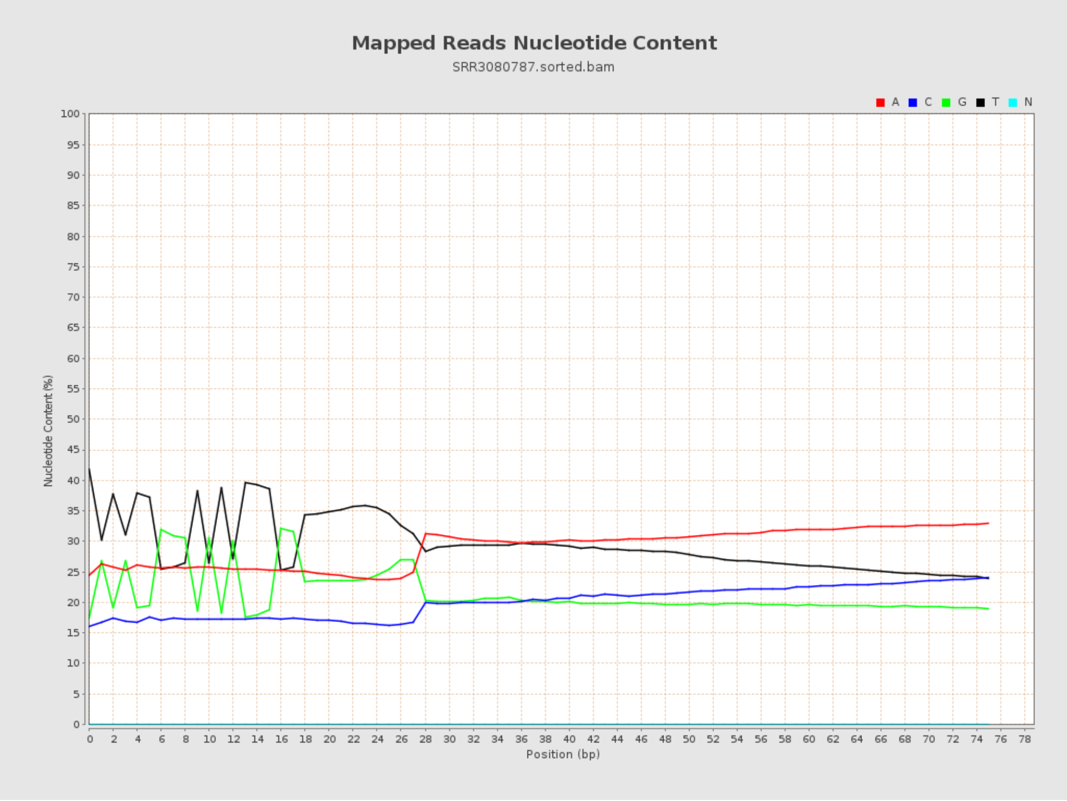
6. Results : Genome Fraction Coverage



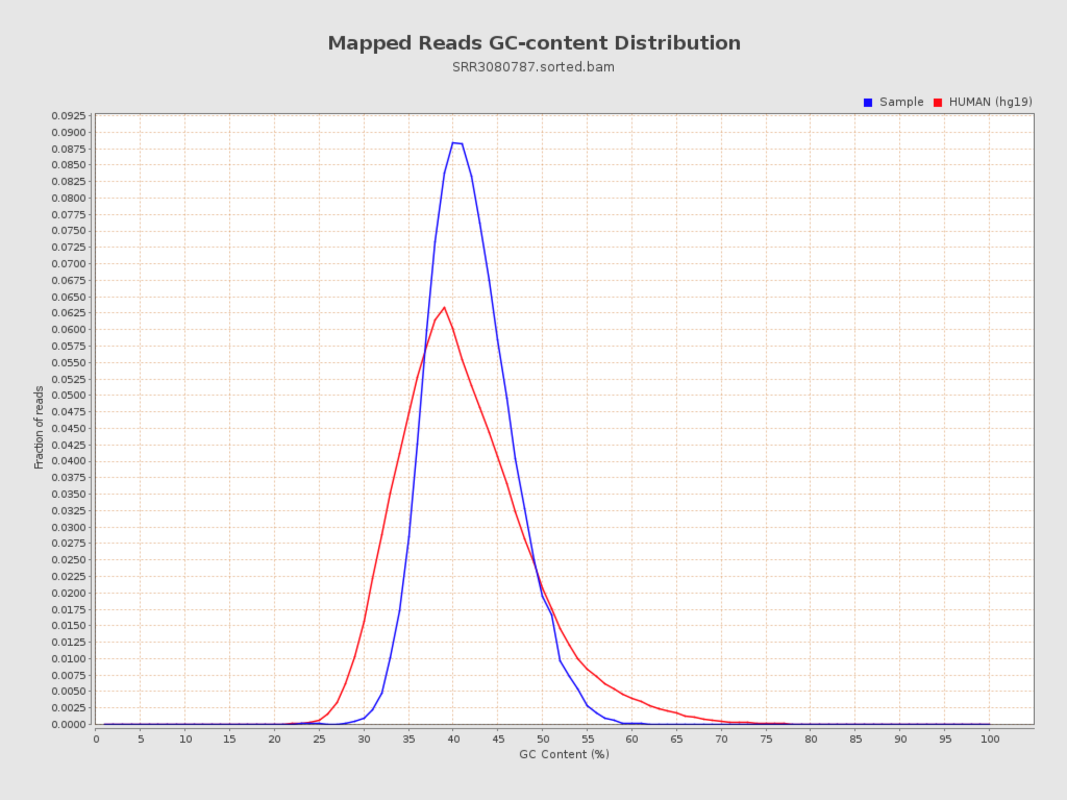
7. Results : Duplication Rate Histogram



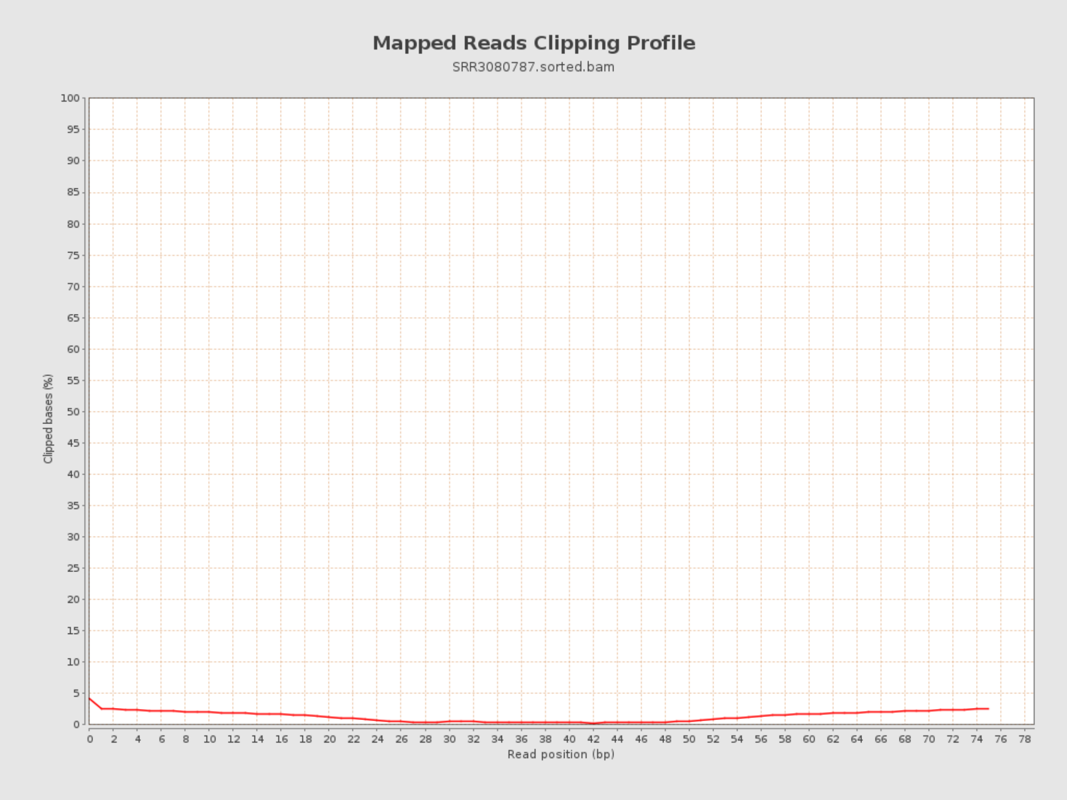
8. Results : Mapped Reads Nucleotide Content



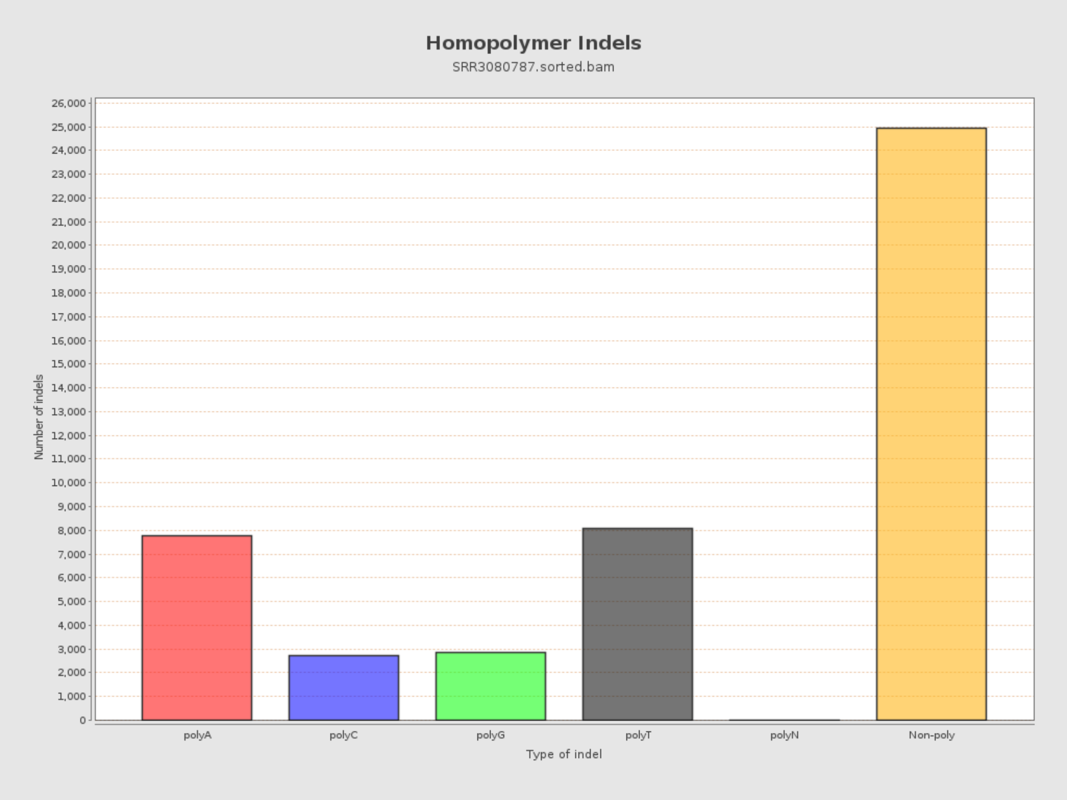
9. Results : Mapped Reads GC-content Distribution



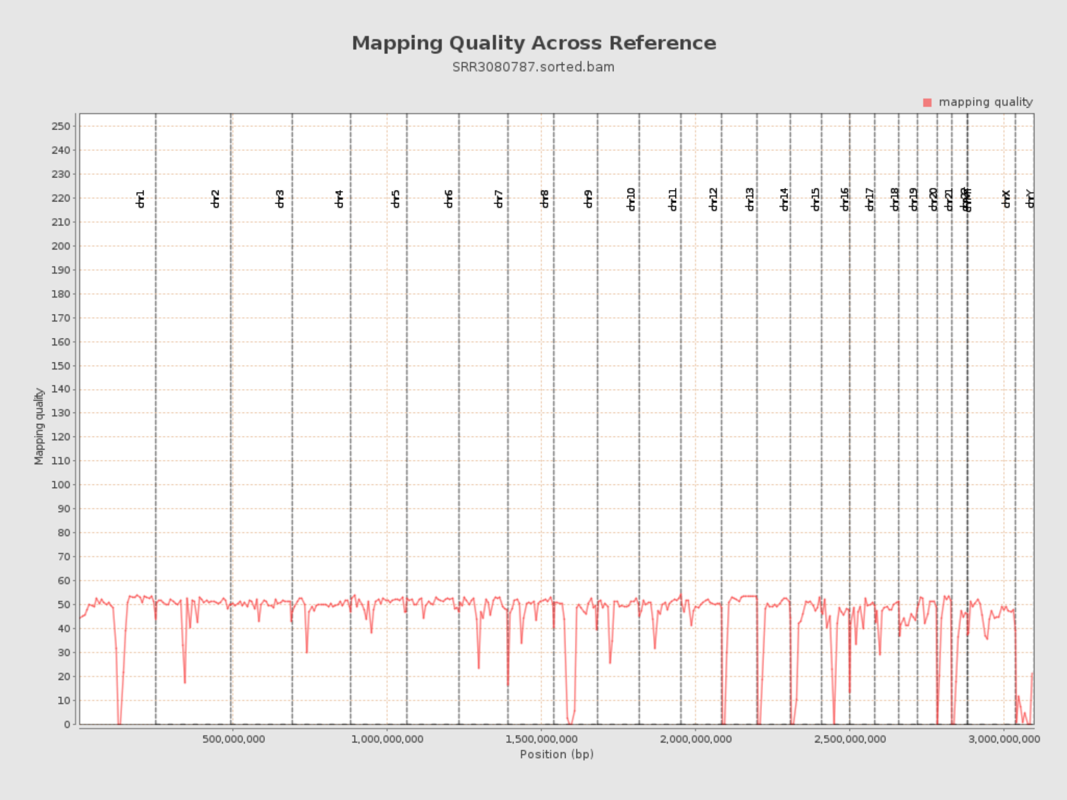
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram