Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:41:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013163.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_SRR6013163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:41:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,326,647
Mapped reads	1,620,947 / 69.67%
Unmapped reads	705,700 / 30.33%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,306 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	457,467 / 19.66%
Duplication rate	16.42%
Clipped reads	938,178 / 40.32%

2.2. ACGT Content

Number/percentage of A's	27,018,392 / 26.41%
Number/percentage of C's	18,786,535 / 18.37%
Number/percentage of T's	32,320,229 / 31.6%
Number/percentage of G's	24,004,652 / 23.47%
Number/percentage of N's	156,773 / 0.15%
GC Percentage	41.83%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.5379

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

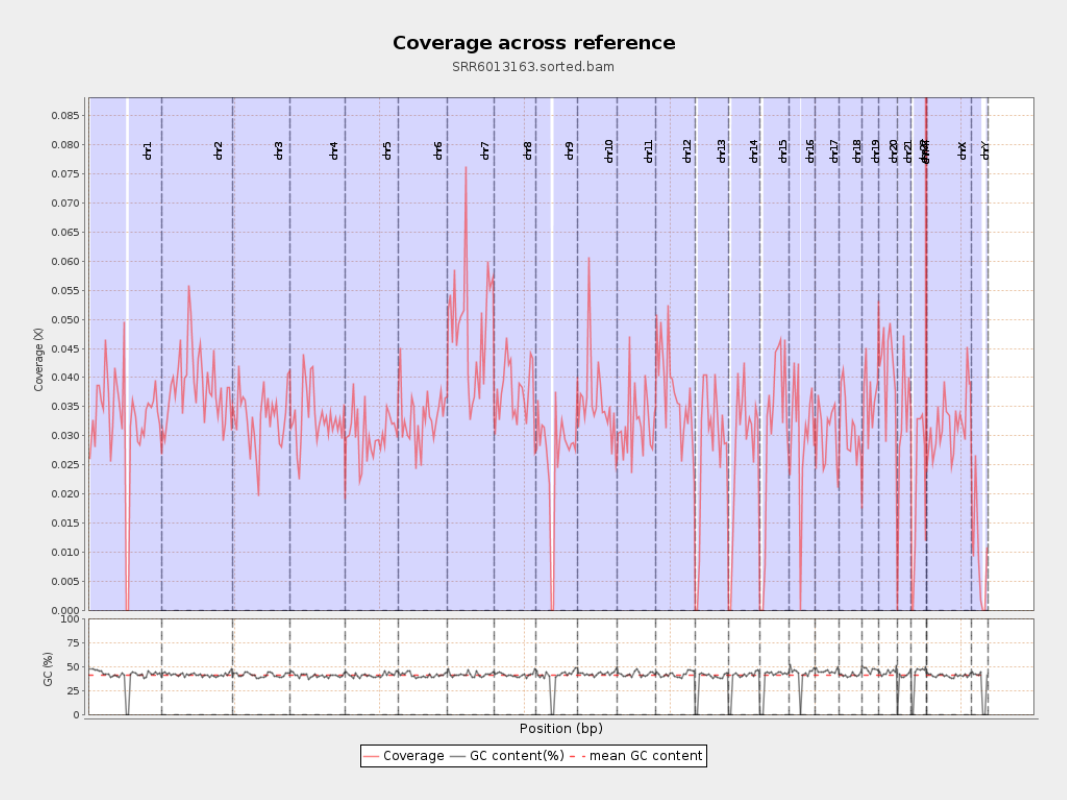
General error rate	0.93%
Mismatches	938,782
Insertions	7,060
Mapped reads with at least one insertion	0.43%
Deletions	29,967
Mapped reads with at least one deletion	1.82%
Homopolymer indels	45.08%

2.6. Chromosome stats

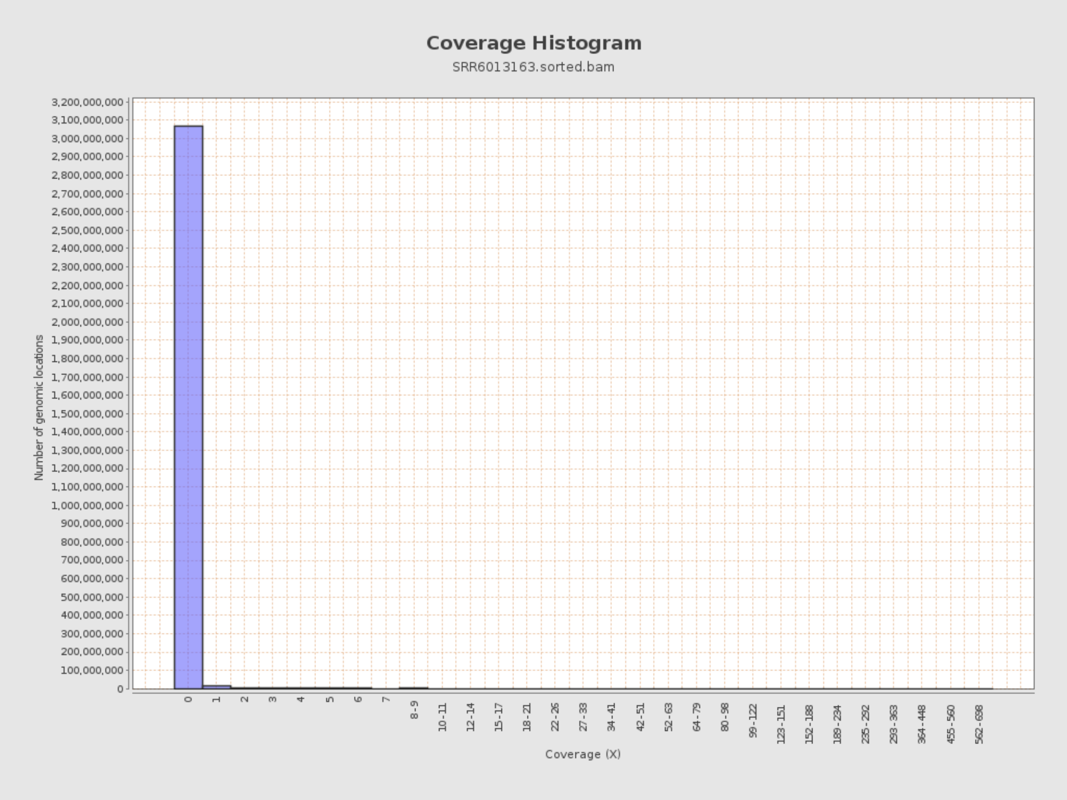
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8087647	0.0324	0.6358
chr2	243199373	9356555	0.0385	0.6266
chr3	198022430	6542980	0.033	0.5027
chr4	191154276	6331108	0.0331	0.4934
chr5	180915260	5466376	0.0302	0.4741
chr6	171115067	5706361	0.0333	0.5307
chr7	159138663	7709411	0.0484	0.7016

chr8	146364022	5452971	0.0373	0.556
chr9	141213431	3719306	0.0263	0.4723
chr10	135534747	4866809	0.0359	0.5769
chr11	135006516	4322279	0.032	0.5271
chr12	133851895	4996888	0.0373	0.5379
chr13	115169878	3165765	0.0275	0.4763
chr14	107349540	2967470	0.0276	0.4668
chr15	102531392	3093863	0.0302	0.4662
chr16	90354753	2747303	0.0304	0.4697
chr17	81195210	2419567	0.0298	0.4902
chr18	78077248	2473386	0.0317	0.6347
chr19	59128983	2150445	0.0364	0.5497
chr20	63025520	2611013	0.0414	0.5678
chr21	48129895	1537980	0.032	0.4726
chr22	51304566	1099889	0.0214	0.4059
chrMT	16571	50955	3.075	5.397
chrX	155270560	4962224	0.032	0.4667
chrY	59373566	500616	0.0084	0.2216

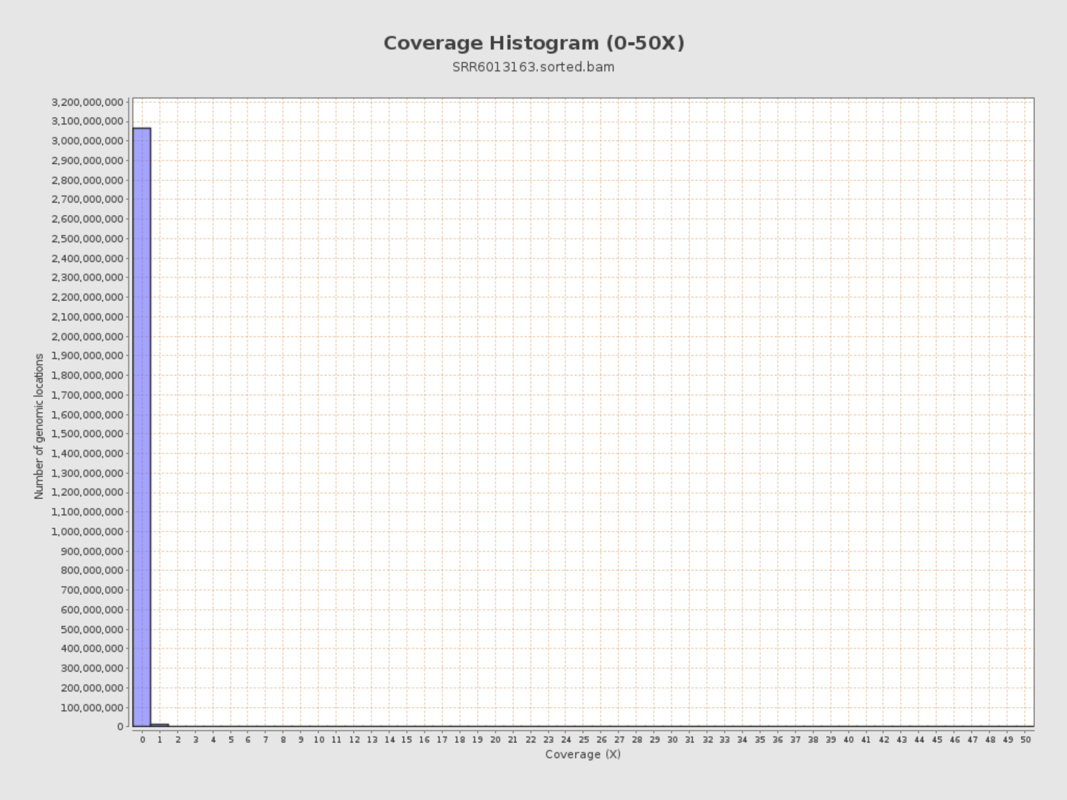
3. Results : Coverage across reference



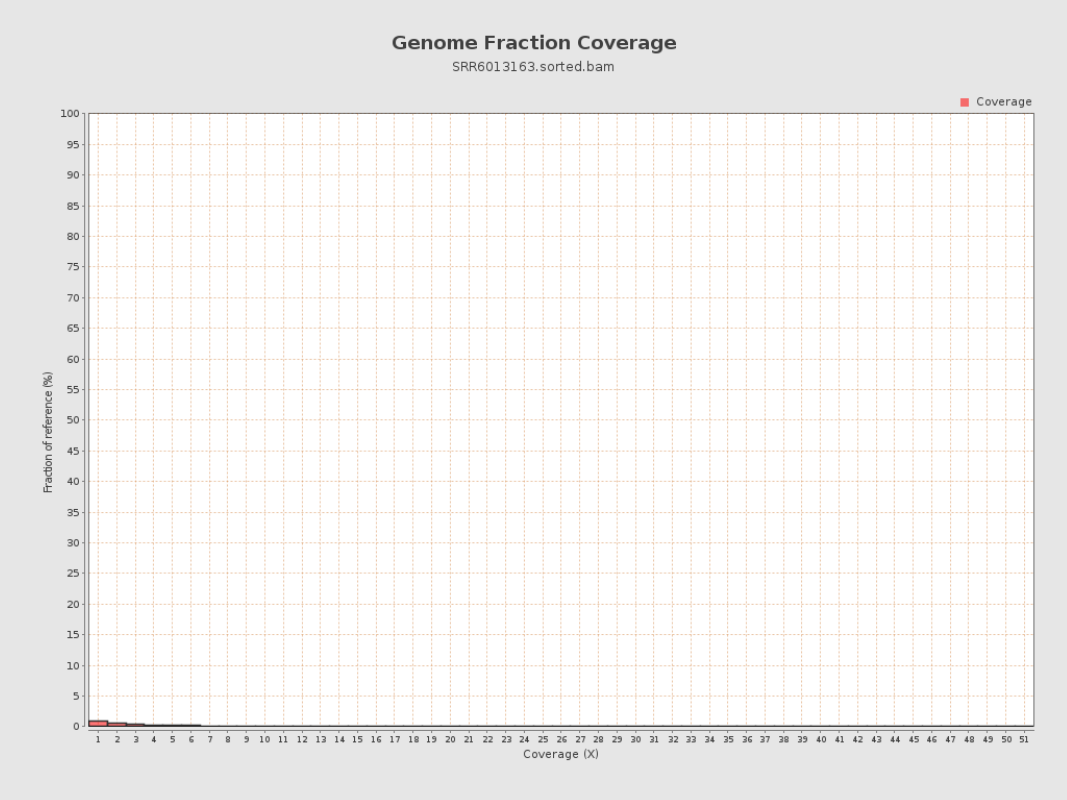
4. Results : Coverage Histogram



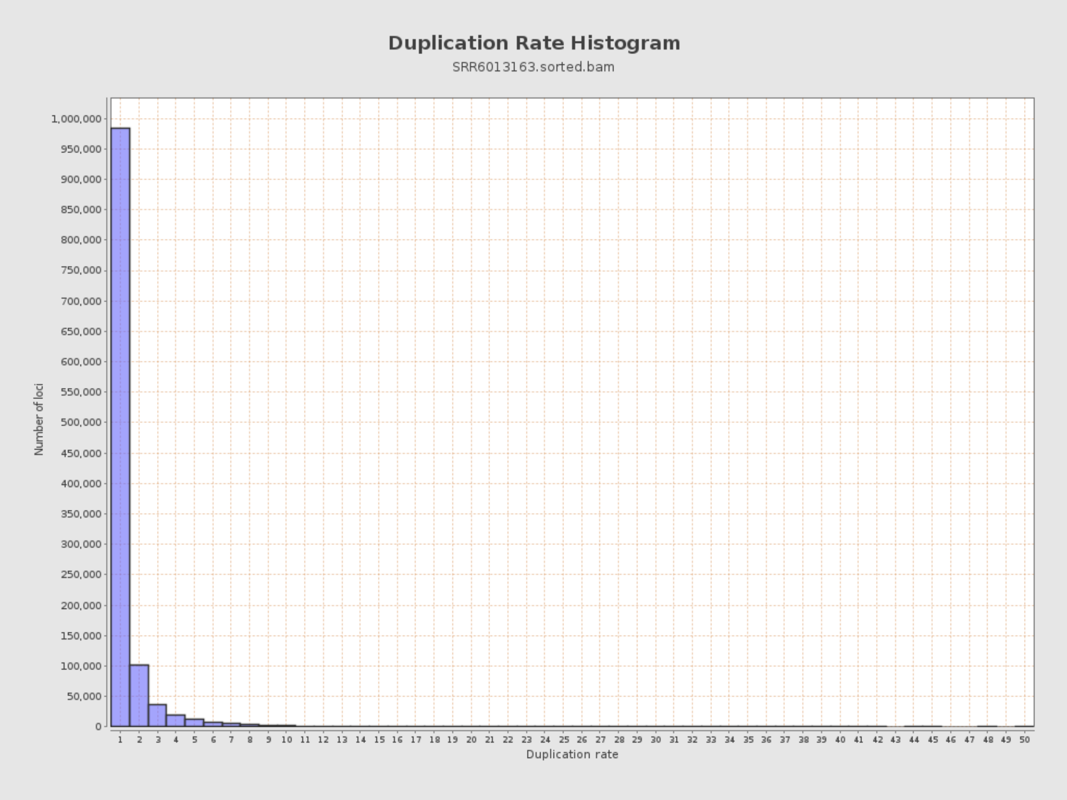
5. Results : Coverage Histogram (0-50X)



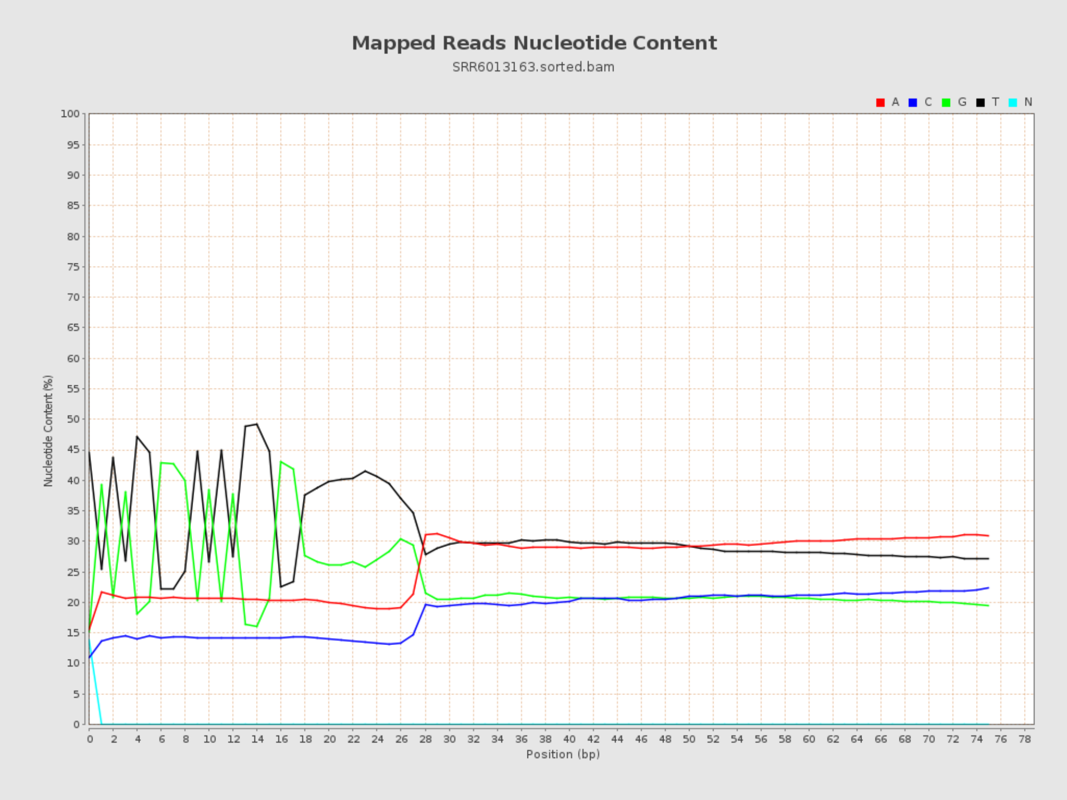
6. Results : Genome Fraction Coverage



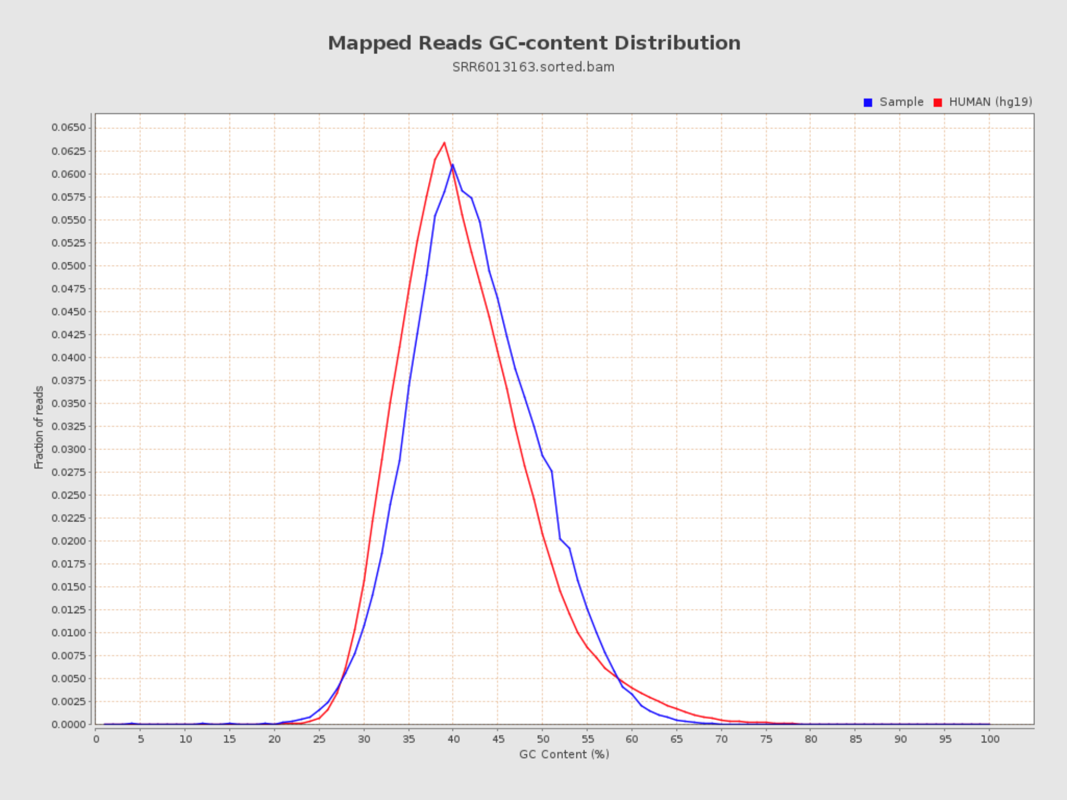
7. Results : Duplication Rate Histogram



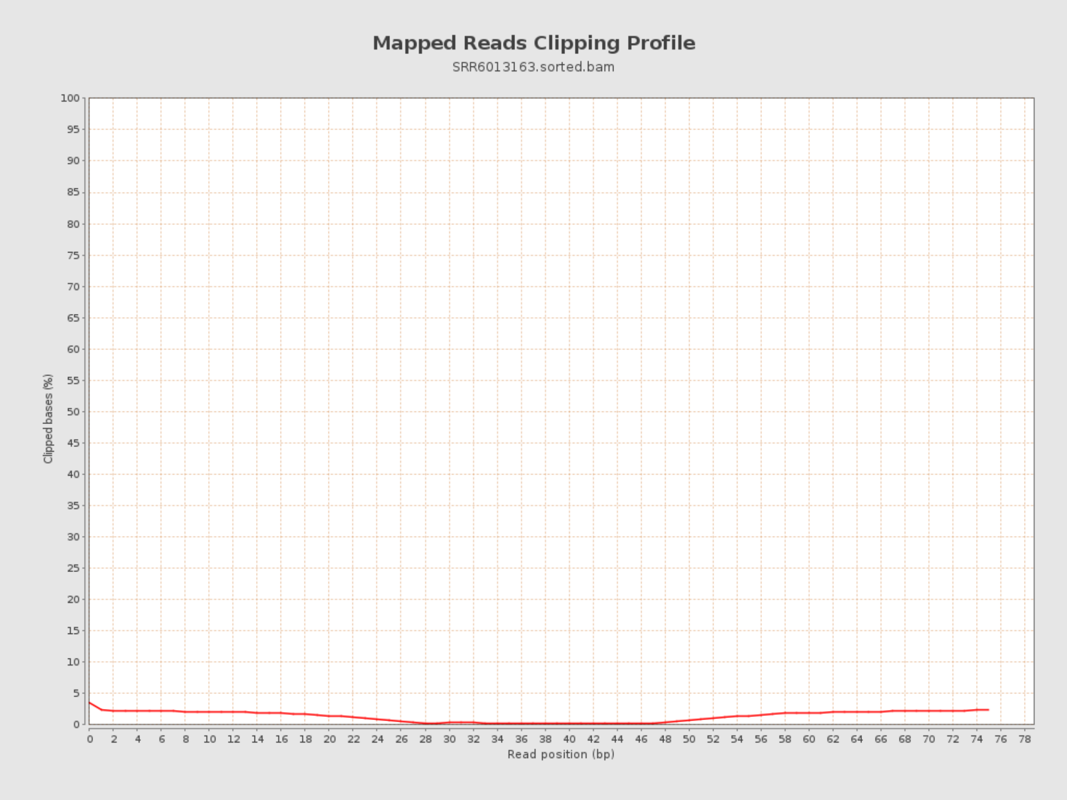
8. Results : Mapped Reads Nucleotide Content



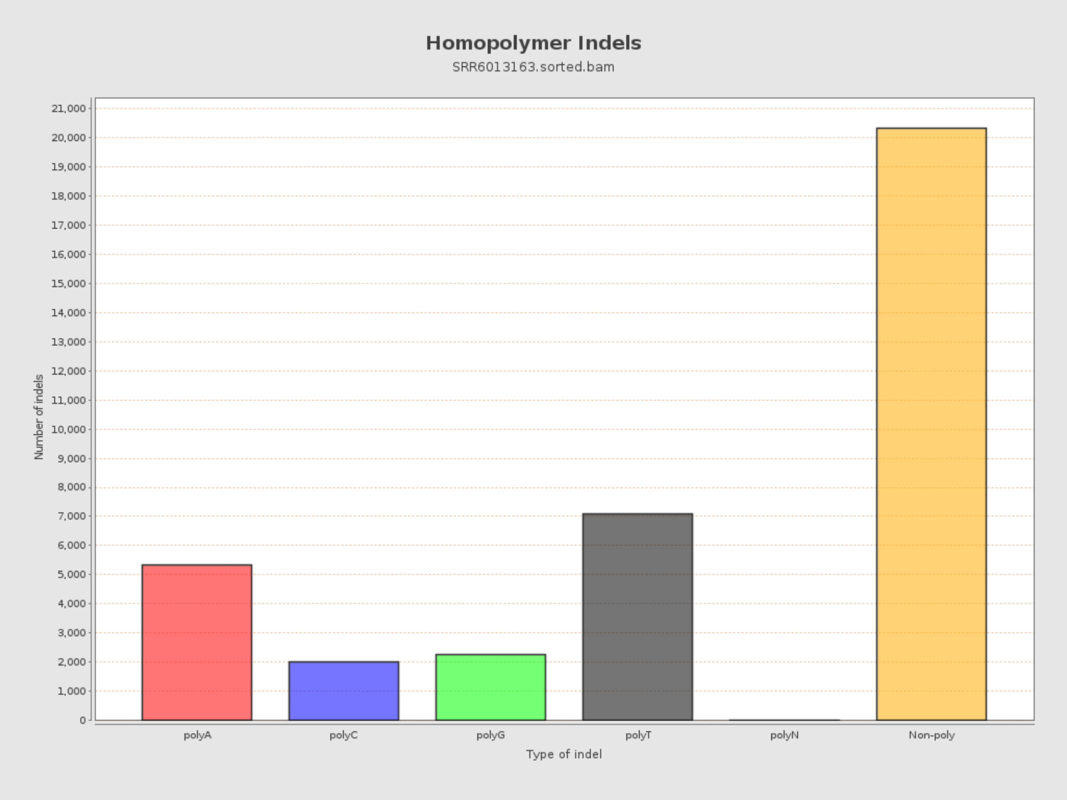
9. Results : Mapped Reads GC-content Distribution



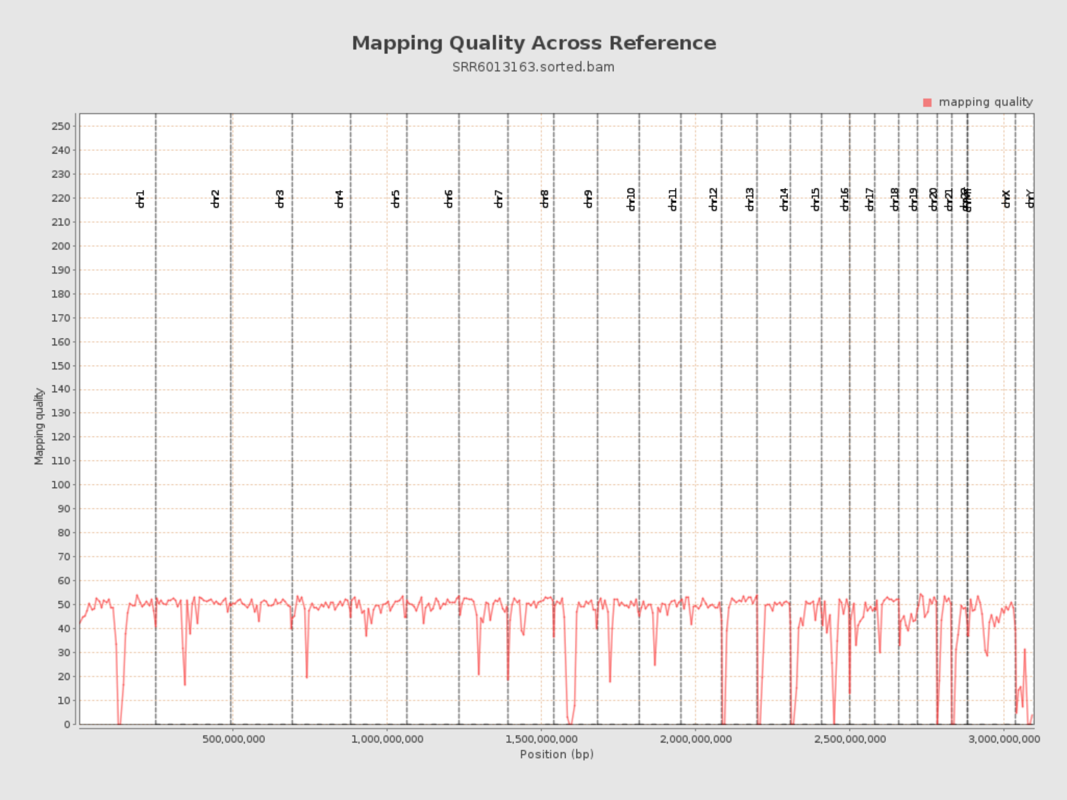
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram