Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 08:44:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008727.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_SRR6008727 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008727.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 08:44:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008727.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,294,175
Mapped reads	1,858,823 / 81.02%
Unmapped reads	435,352 / 18.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,009 / 0.61%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	315,579 / 13.76%
Duplication rate	12.18%
Clipped reads	993,026 / 43.28%

2.2. ACGT Content

Number/percentage of A's	32,034,907 / 26.67%
Number/percentage of C's	22,911,369 / 19.08%
Number/percentage of T's	37,292,506 / 31.05%
Number/percentage of G's	27,795,121 / 23.14%
Number/percentage of N's	76,629 / 0.06%
GC Percentage	42.22%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.4124

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

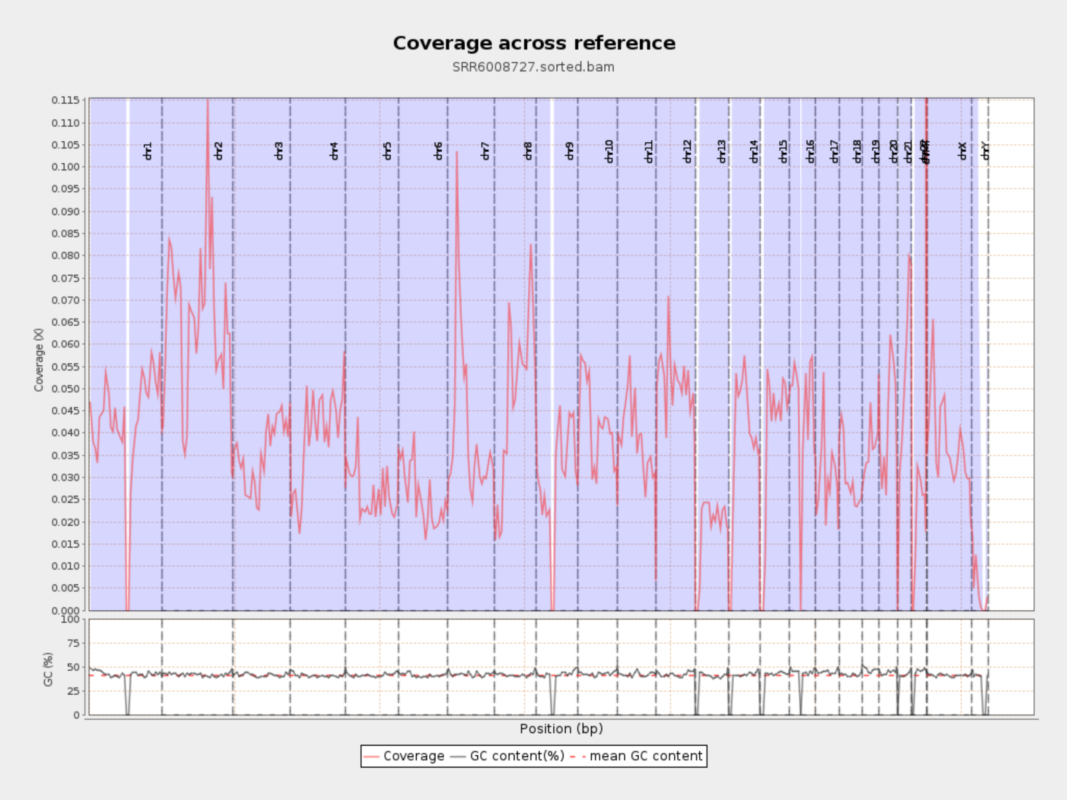
General error rate	0.92%
Mismatches	1,091,001
Insertions	8,884
Mapped reads with at least one insertion	0.47%
Deletions	39,307
Mapped reads with at least one deletion	2.09%
Homopolymer indels	49%

2.6. Chromosome stats

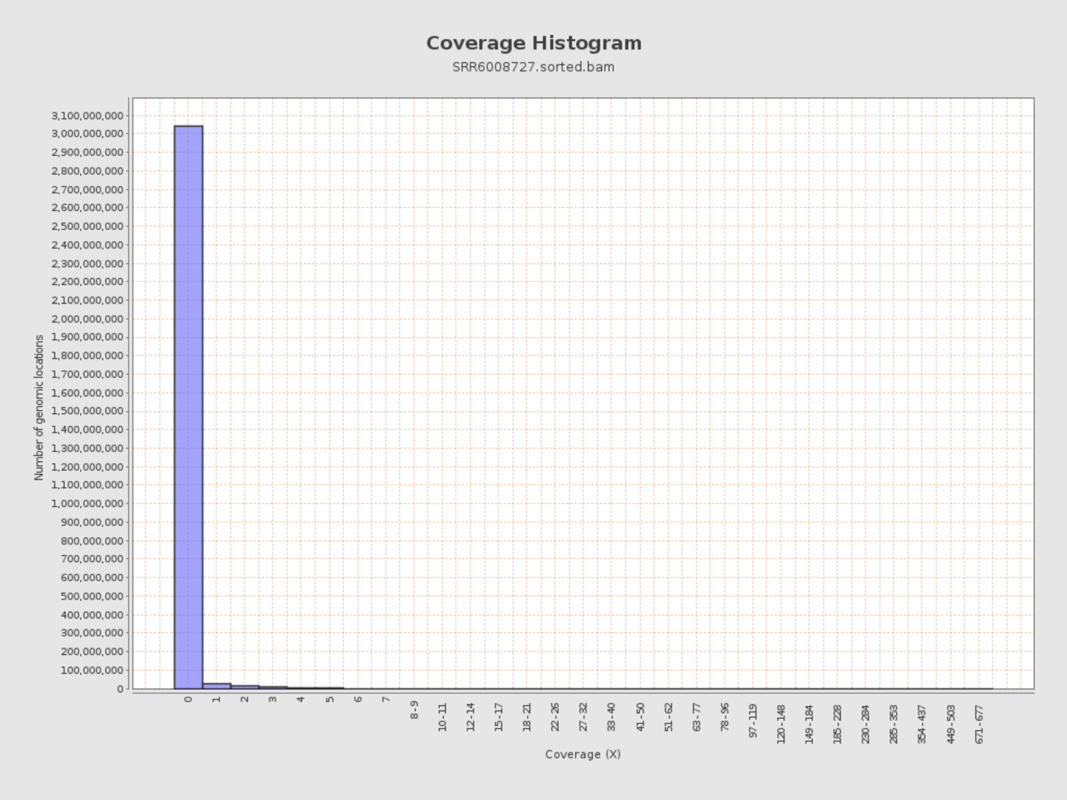
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10537457	0.0423	0.5166
chr2	243199373	15985468	0.0657	0.5774
chr3	198022430	7020267	0.0355	0.3333
chr4	191154276	7474853	0.0391	0.3641
chr5	180915260	4821857	0.0267	0.2867
chr6	171115067	4453001	0.026	0.3075
chr7	159138663	6651752	0.0418	0.516

chr8	146364022	7155514	0.0489	0.435
chr9	141213431	4200072	0.0297	0.3545
chr10	135534747	5771236	0.0426	0.4127
chr11	135006516	5232708	0.0388	0.4111
chr12	133851895	6962065	0.052	0.4143
chr13	115169878	2118527	0.0184	0.2366
chr14	107349540	4087377	0.0381	0.3725
chr15	102531392	3940017	0.0384	0.376
chr16	90354753	4031039	0.0446	0.3847
chr17	81195210	2460279	0.0303	0.3192
chr18	78077248	2354742	0.0302	0.4679
chr19	59128983	2185405	0.037	0.4173
chr20	63025520	2683505	0.0426	0.3753
chr21	48129895	2391342	0.0497	0.4109
chr22	51304566	1016075	0.0198	0.2471
chrMT	16571	441668	26.6531	19.2234
chrX	155270560	5924477	0.0382	0.3547
chrY	59373566	276205	0.0047	0.1233

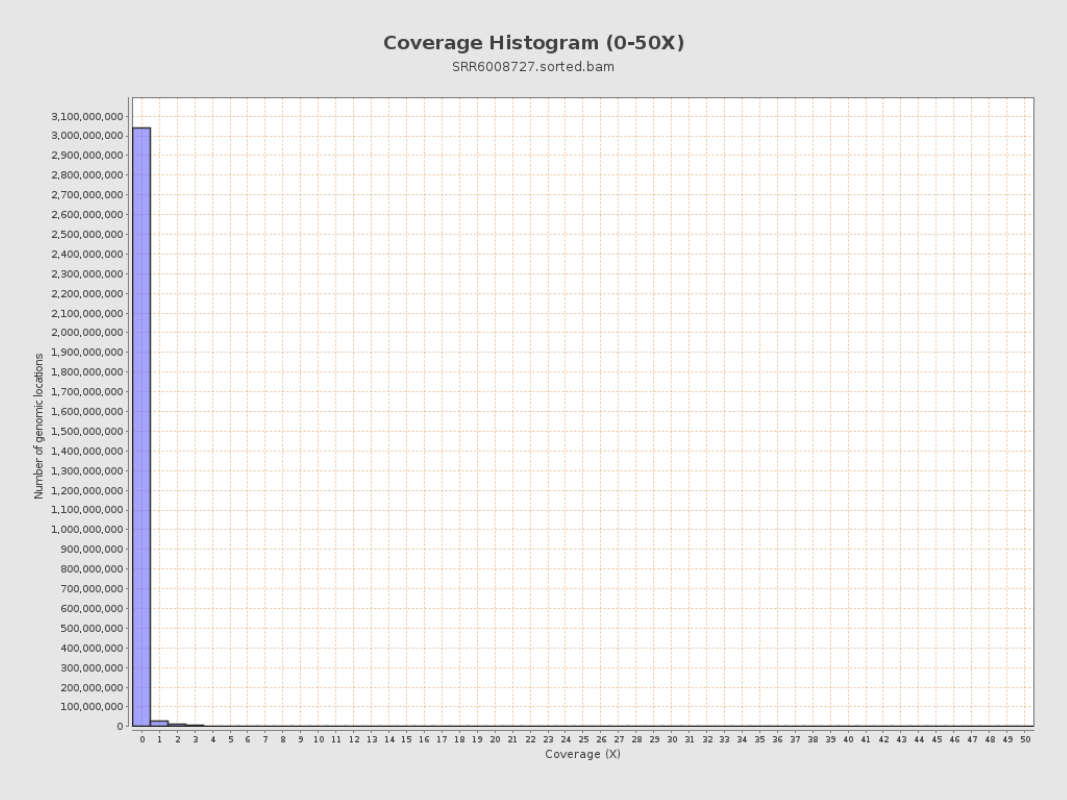
3. Results : Coverage across reference



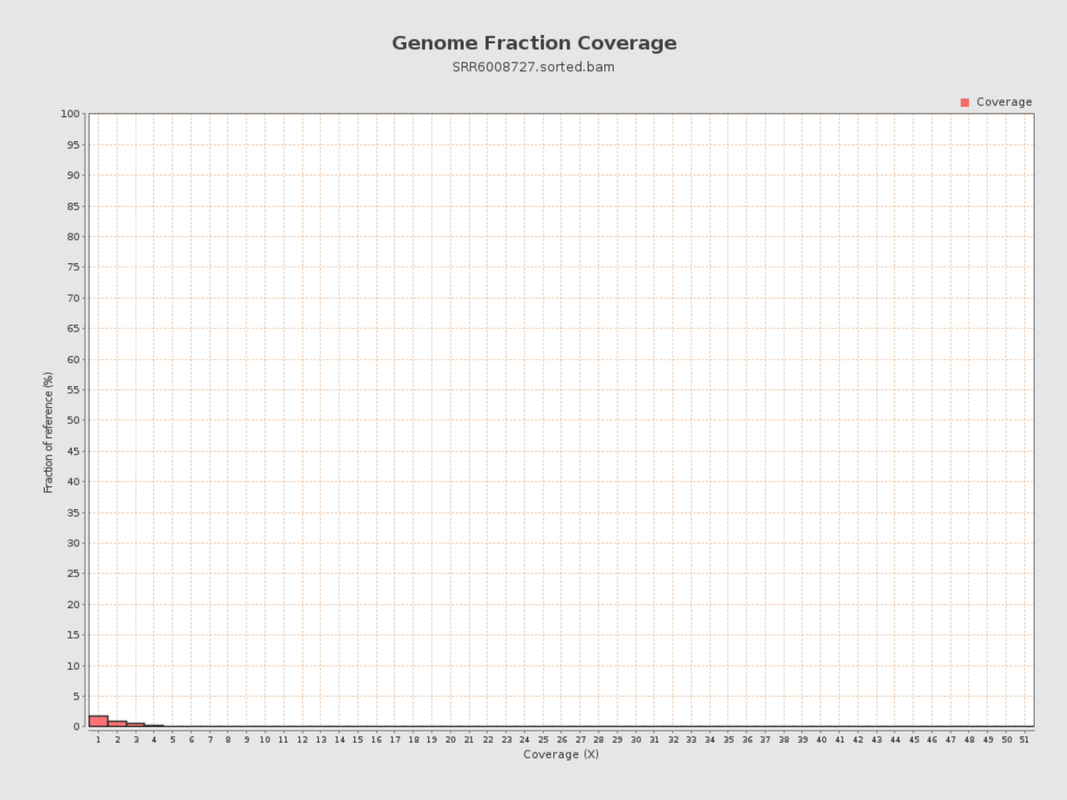
4. Results : Coverage Histogram



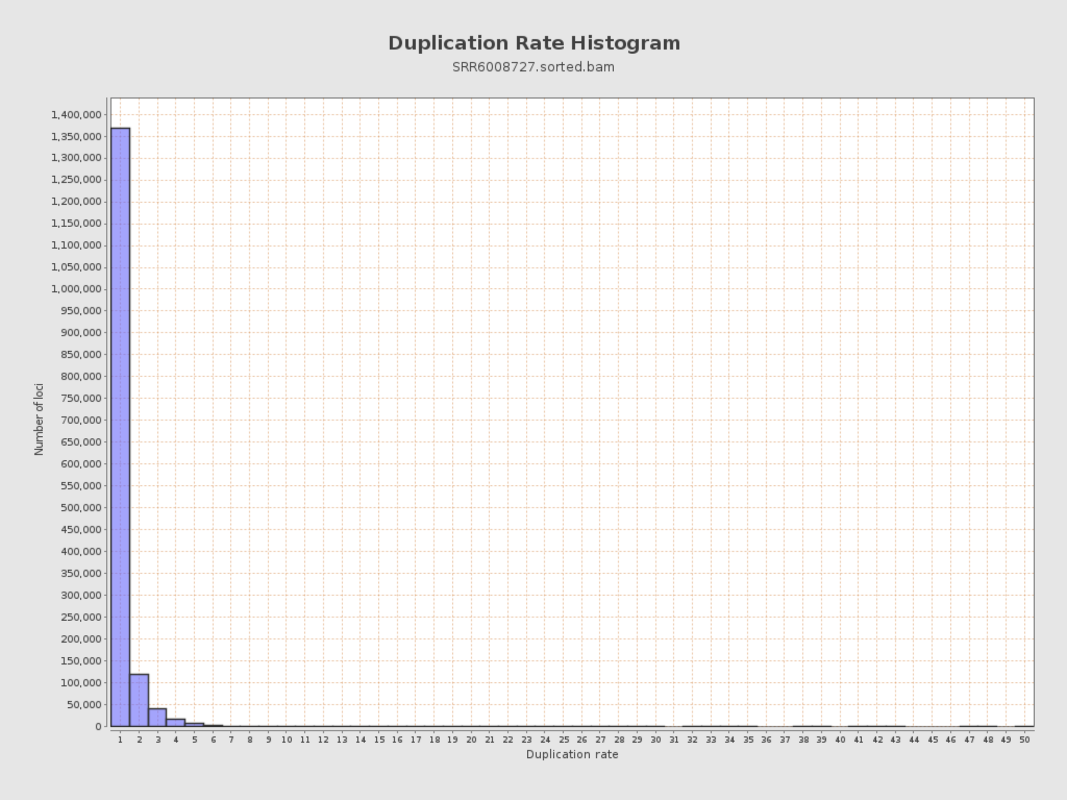
5. Results : Coverage Histogram (0-50X)



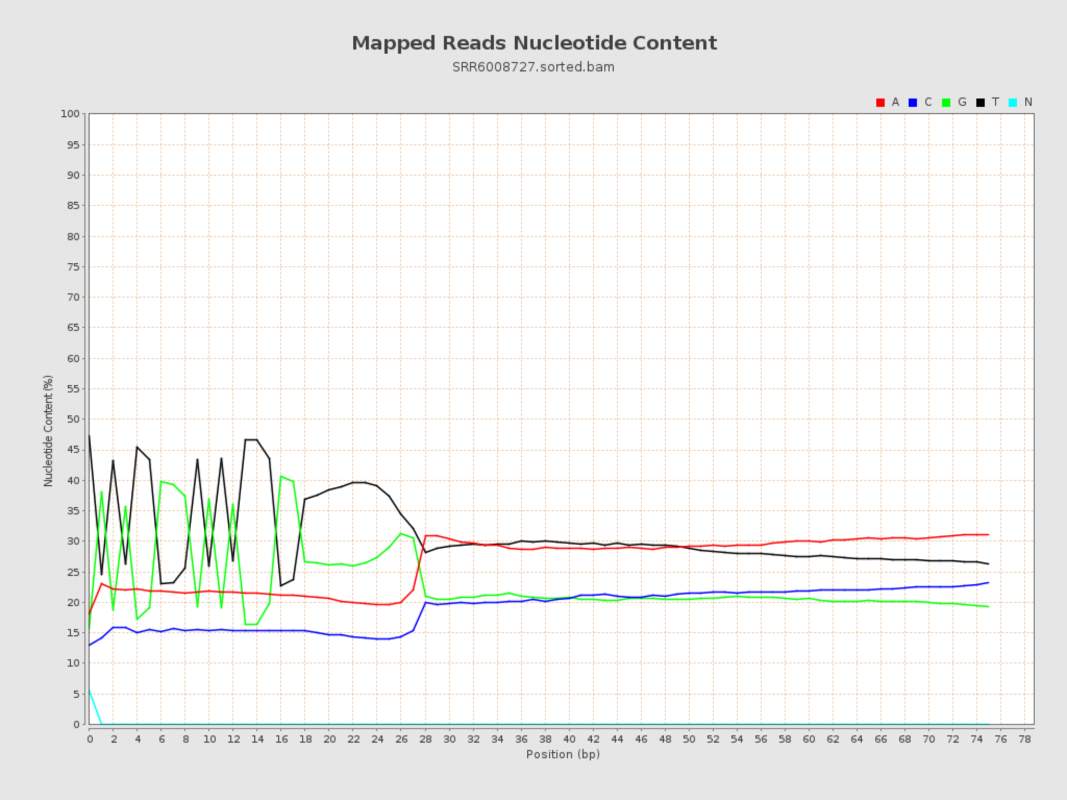
6. Results : Genome Fraction Coverage



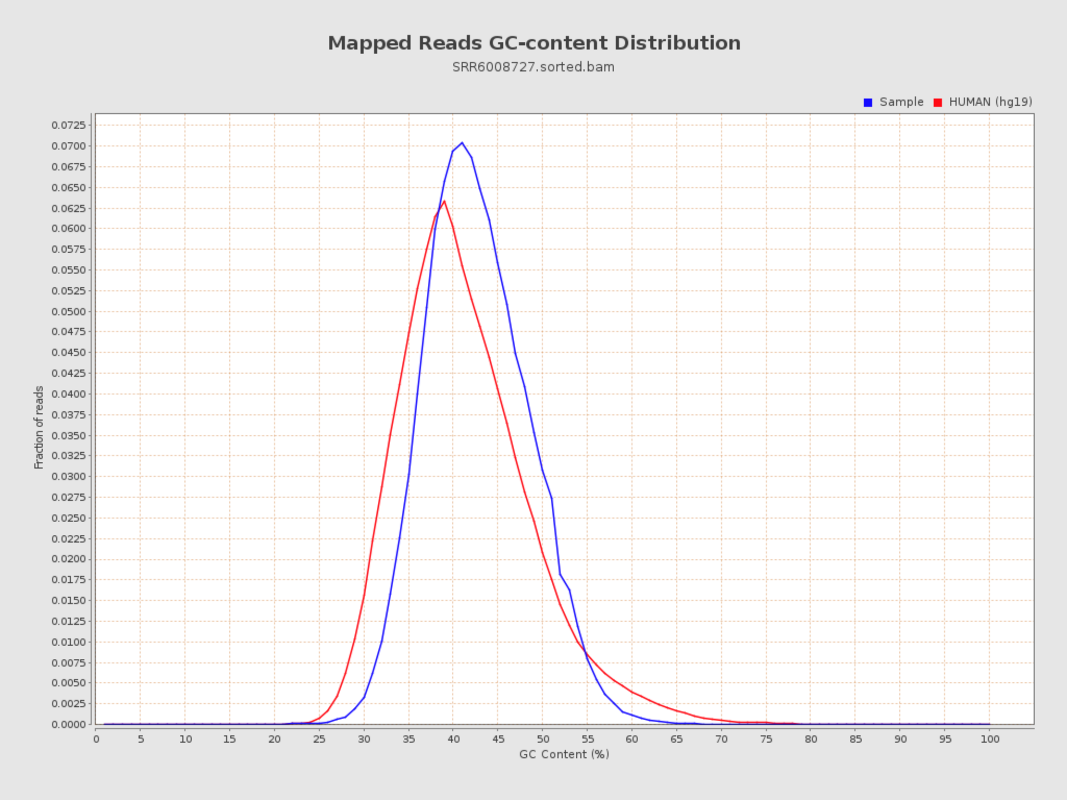
7. Results : Duplication Rate Histogram



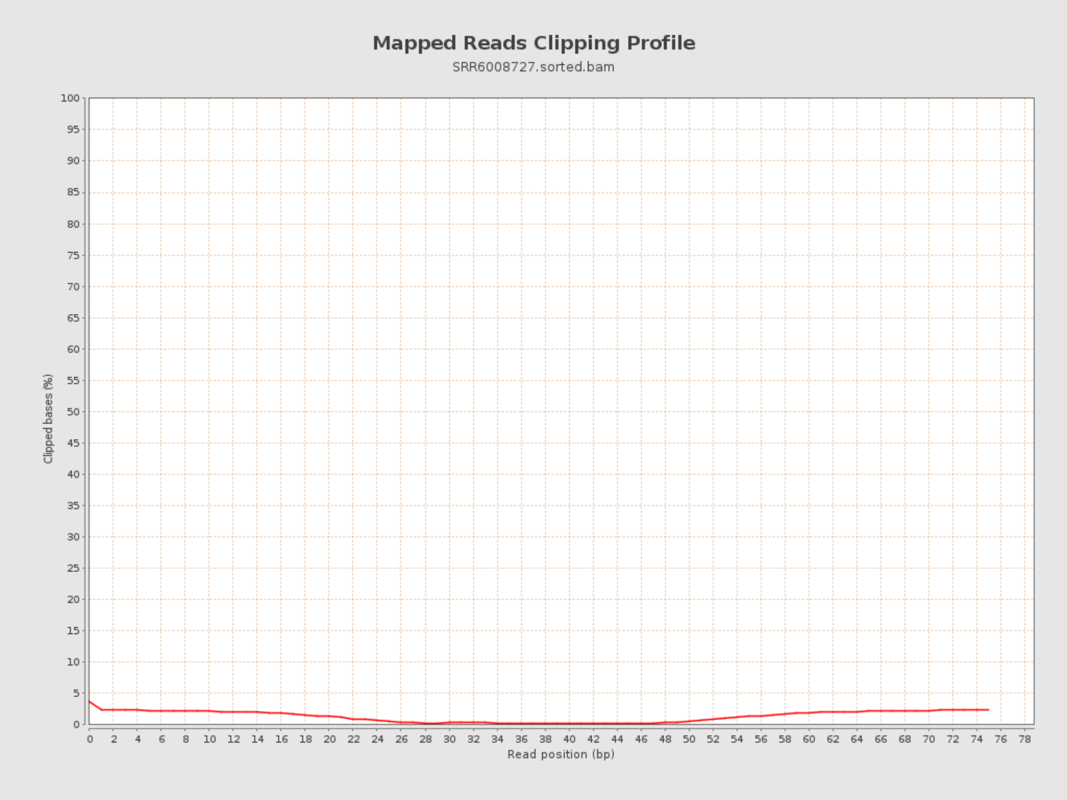
8. Results : Mapped Reads Nucleotide Content



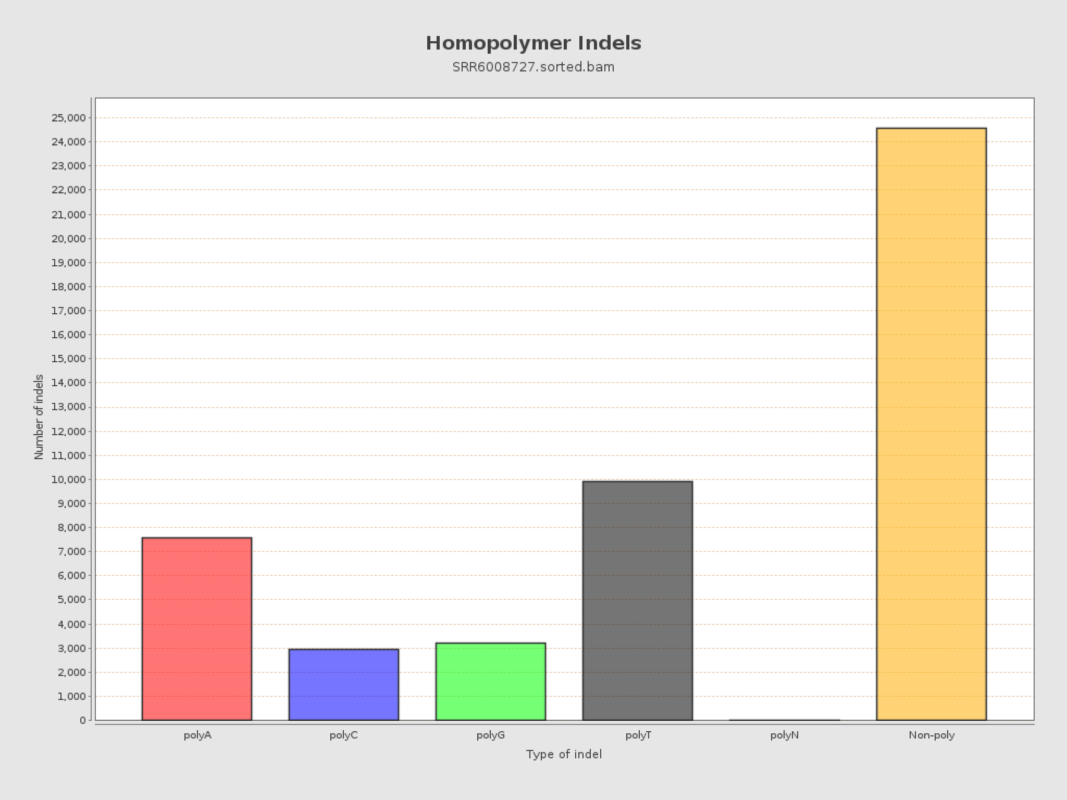
9. Results : Mapped Reads GC-content Distribution



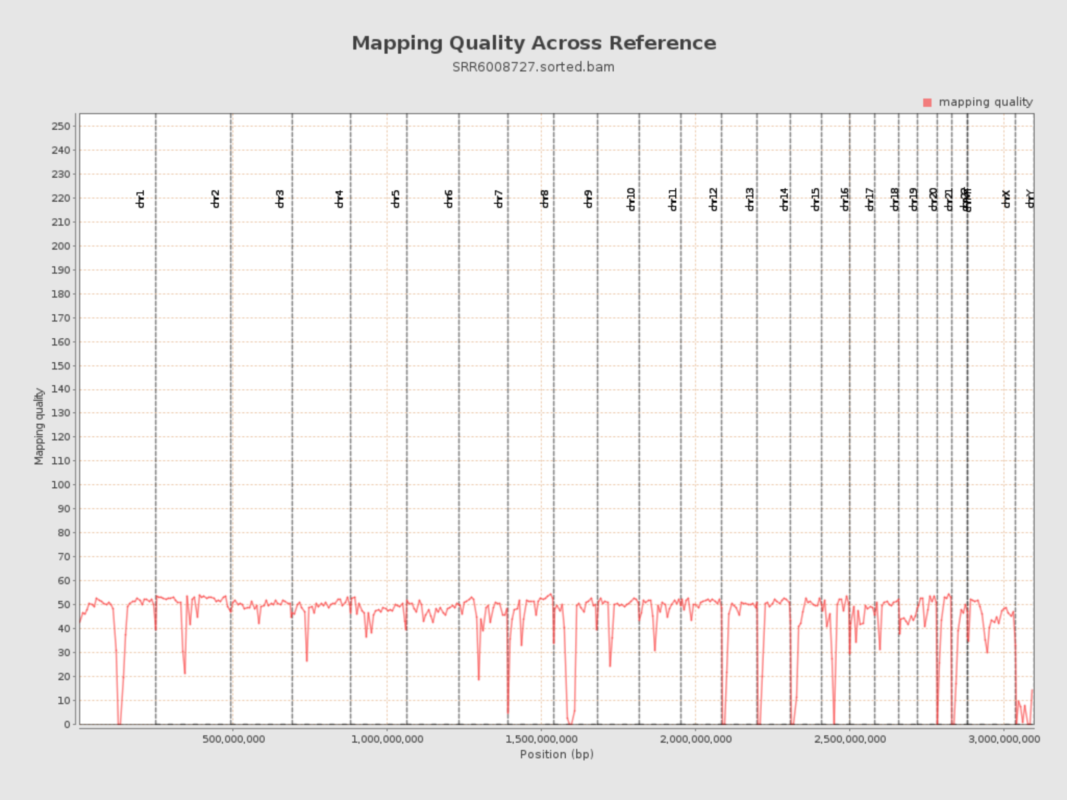
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram