Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:19:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080761.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_SRR3080761 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080761.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:19:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080761.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,003,006
Mapped reads	4,388,387 / 73.1%
Unmapped reads	1,614,619 / 26.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,011 / 0.47%
Read min/max/mean length	30 / 66 / 66.15
Duplicated reads (estimated)	650,401 / 10.83%
Duplication rate	10.89%
Clipped reads	588,712 / 9.81%

2.2. ACGT Content

Number/percentage of A's	87,021,529 / 30.92%
Number/percentage of C's	56,601,385 / 20.11%
Number/percentage of T's	73,543,338 / 26.13%
Number/percentage of G's	64,175,649 / 22.8%
Number/percentage of N's	90,627 / 0.03%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0909

Standard Deviation	0.6037

2.4. Mapping Quality

Mean Mapping Quality	45.15

2.5. Mismatches and indels

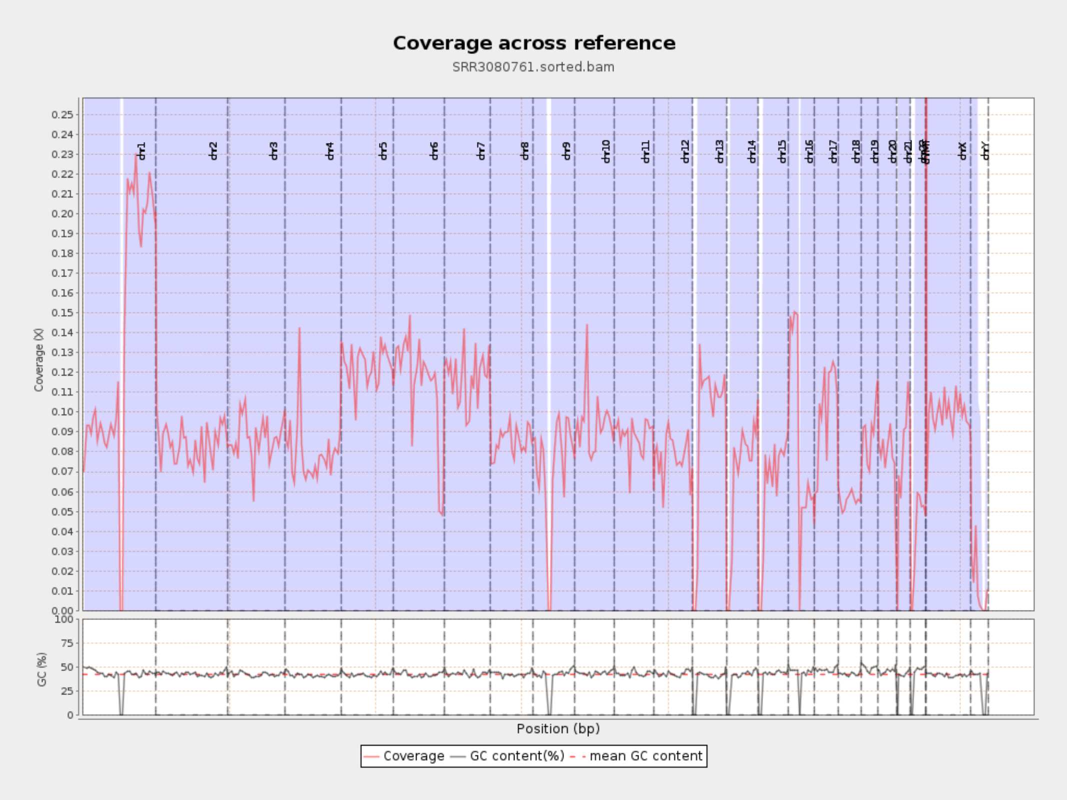
General error rate	0.8%
Mismatches	2,214,714
Insertions	19,962
Mapped reads with at least one insertion	0.45%
Deletions	53,801
Mapped reads with at least one deletion	1.21%
Homopolymer indels	43.44%

2.6. Chromosome stats

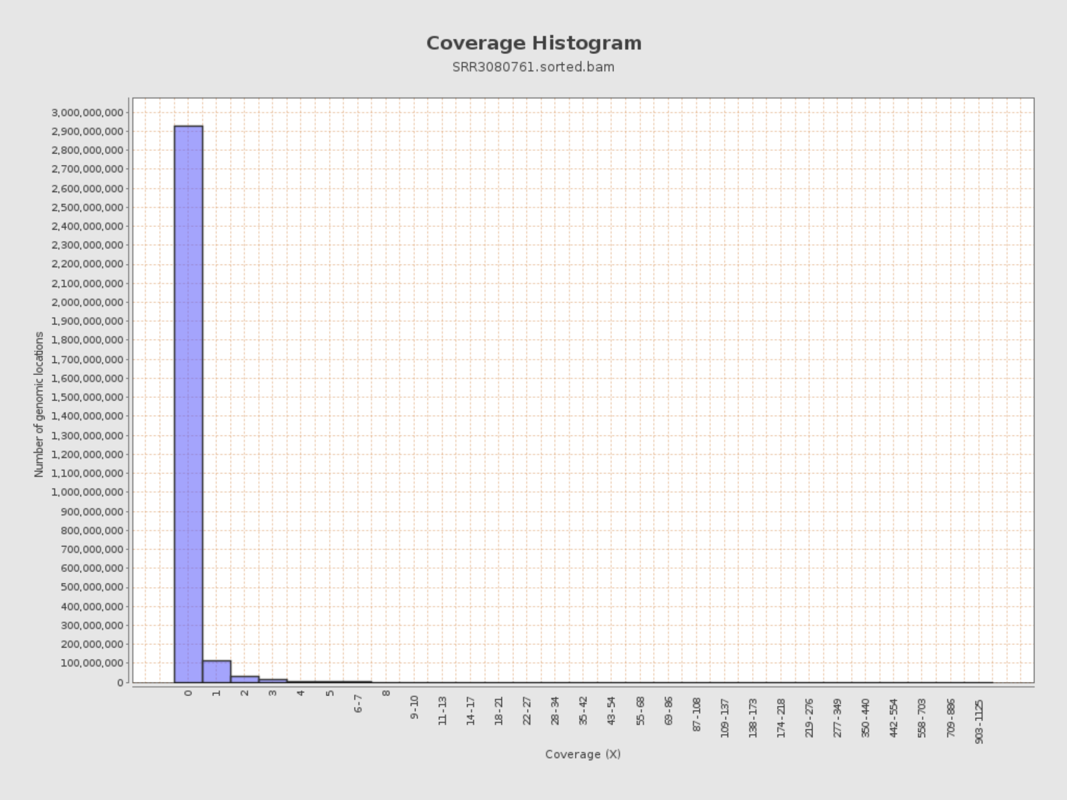
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33625721	0.1349	0.8741
chr2	243199373	20439929	0.084	0.5625
chr3	198022430	17198205	0.0868	0.4652
chr4	191154276	15207202	0.0796	0.5047
chr5	180915260	22352525	0.1236	0.5606
chr6	171115067	19665404	0.1149	0.7039
chr7	159138663	18772411	0.118	0.8343

chr8	146364022	12513813	0.0855	0.838
chr9	141213431	10106604	0.0716	0.4441
chr10	135534747	12715511	0.0938	0.7167
chr11	135006516	11834621	0.0877	0.5198
chr12	133851895	10488298	0.0784	0.4408
chr13	115169878	10889614	0.0946	0.4881
chr14	107349540	7264098	0.0677	0.4475
chr15	102531392	6210833	0.0606	0.383
chr16	90354753	7591940	0.084	0.4944
chr17	81195210	8226961	0.1013	0.5291
chr18	78077248	4338748	0.0556	0.5034
chr19	59128983	5269942	0.0891	0.8765
chr20	63025520	4967227	0.0788	0.4657
chr21	48129895	3754682	0.078	0.5089
chr22	51304566	1962312	0.0382	0.3021
chrMT	16571	65175	3.9331	4.1405
chrX	155270560	15333505	0.0988	0.5101
chrY	59373566	738137	0.0124	0.3346

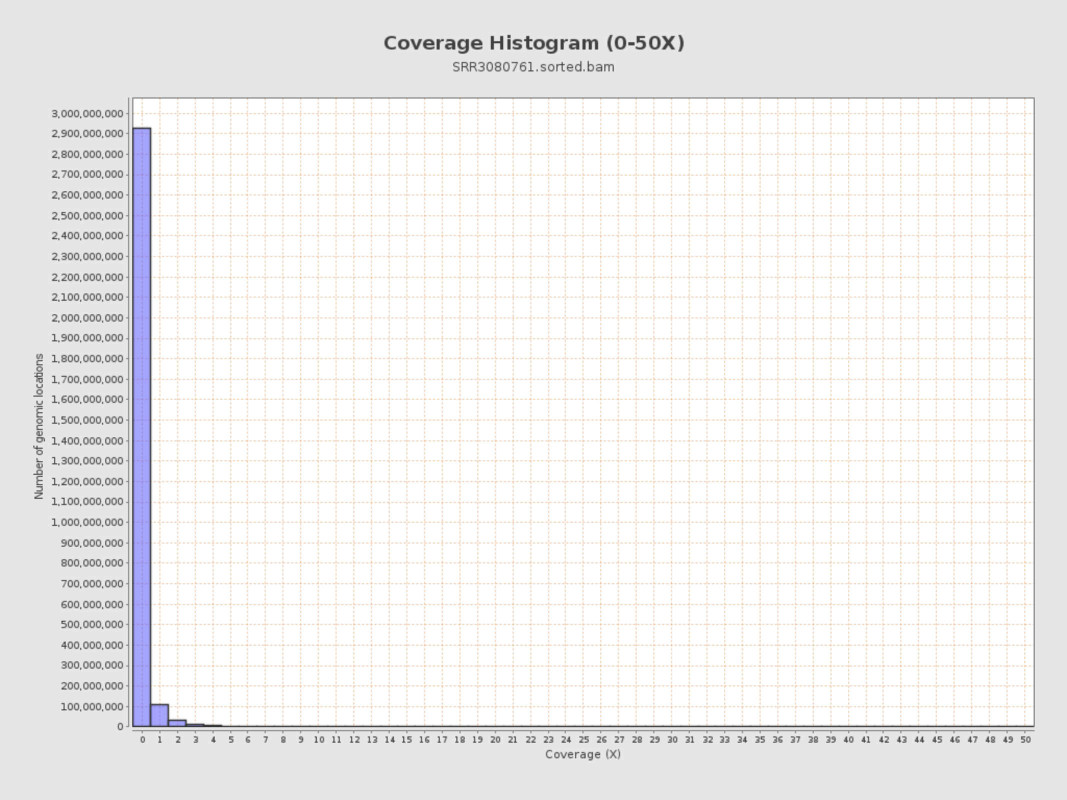
3. Results : Coverage across reference



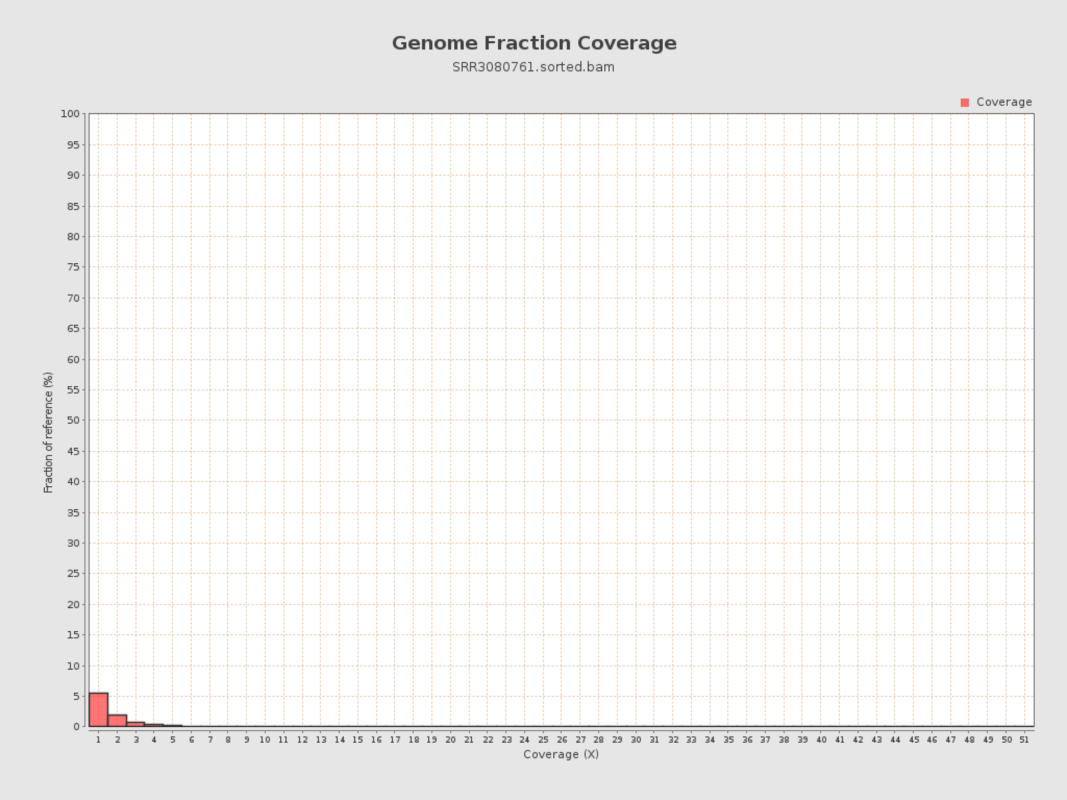
4. Results : Coverage Histogram



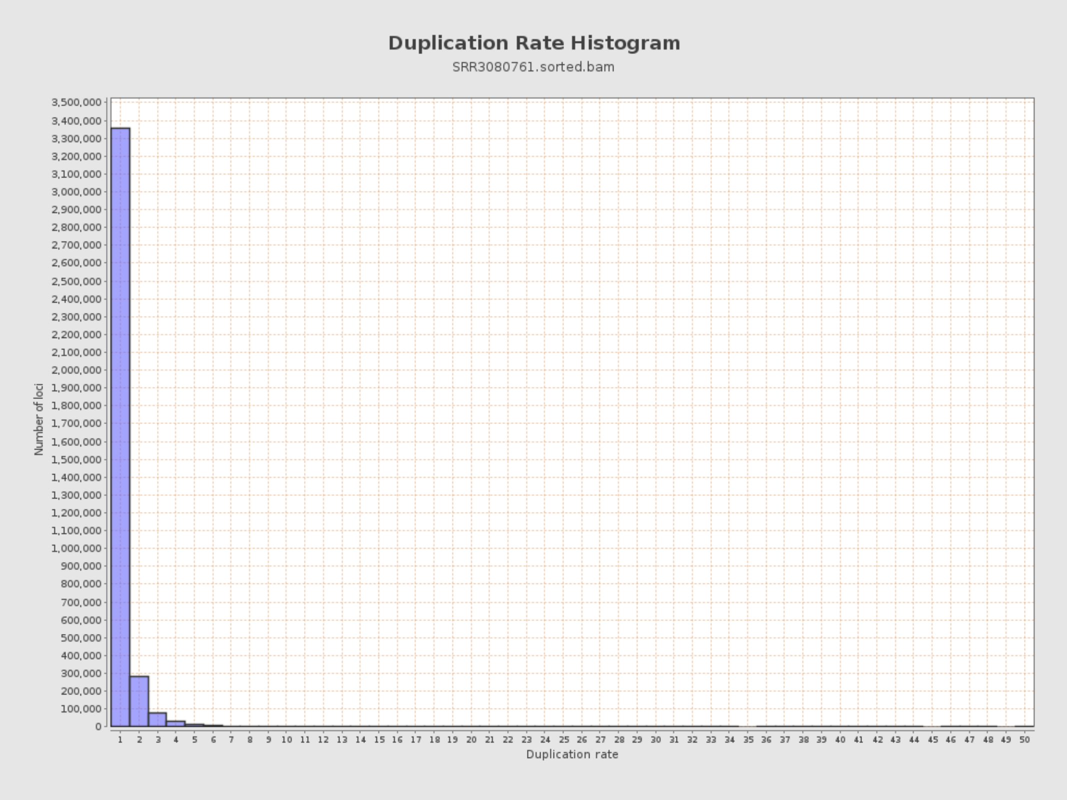
5. Results : Coverage Histogram (0-50X)



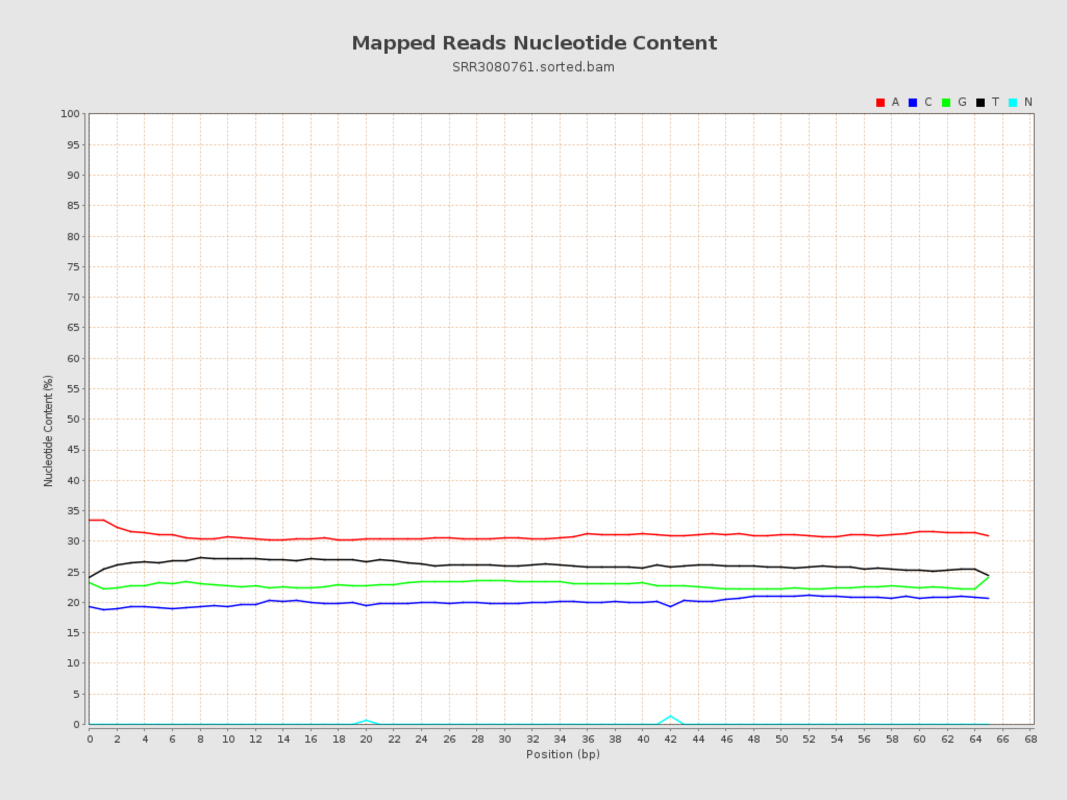
6. Results : Genome Fraction Coverage



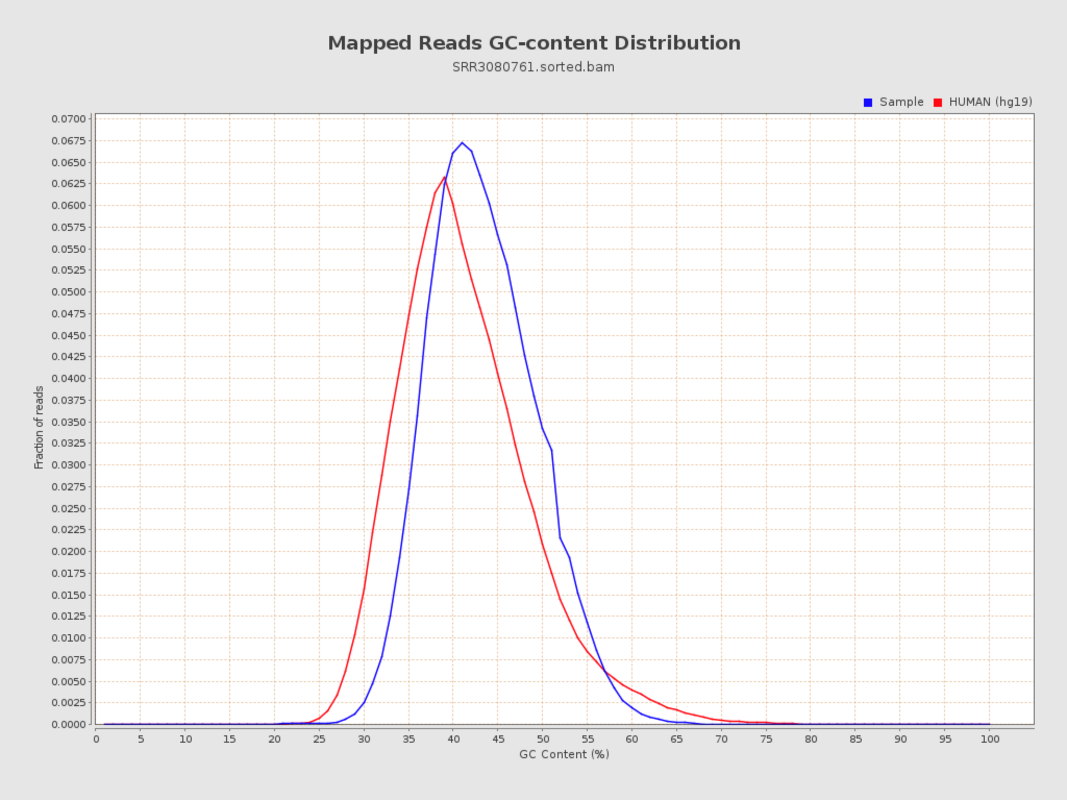
7. Results : Duplication Rate Histogram



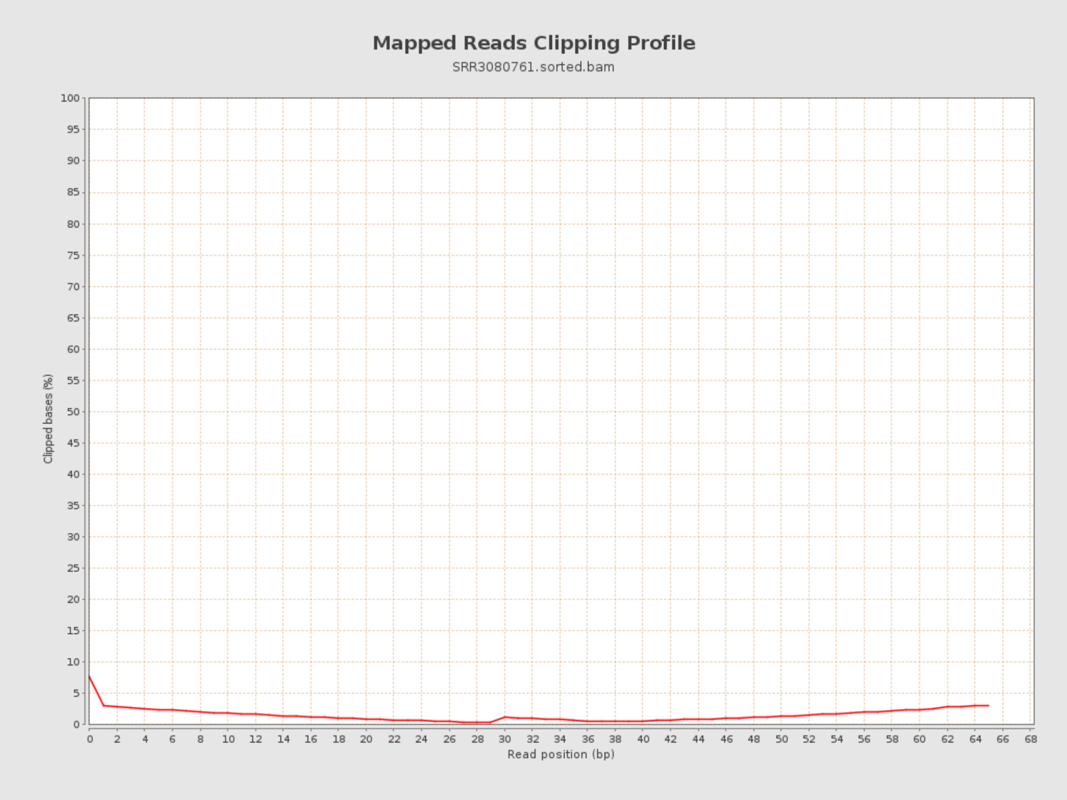
8. Results : Mapped Reads Nucleotide Content



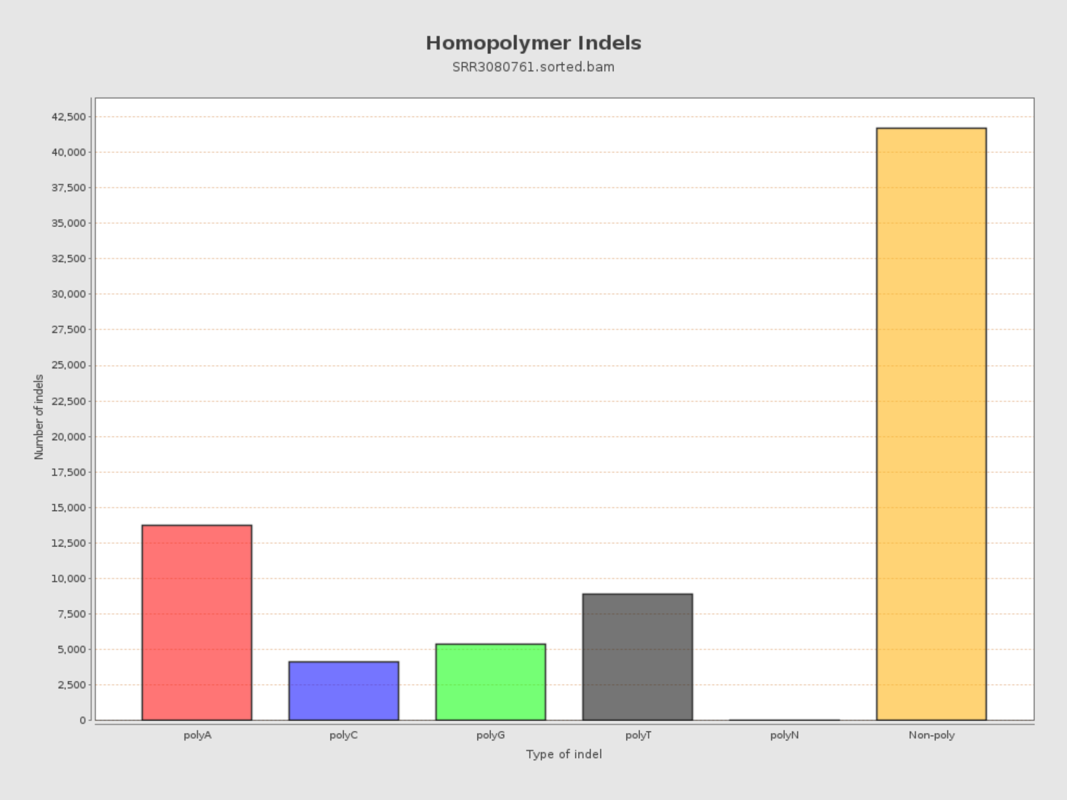
9. Results : Mapped Reads GC-content Distribution



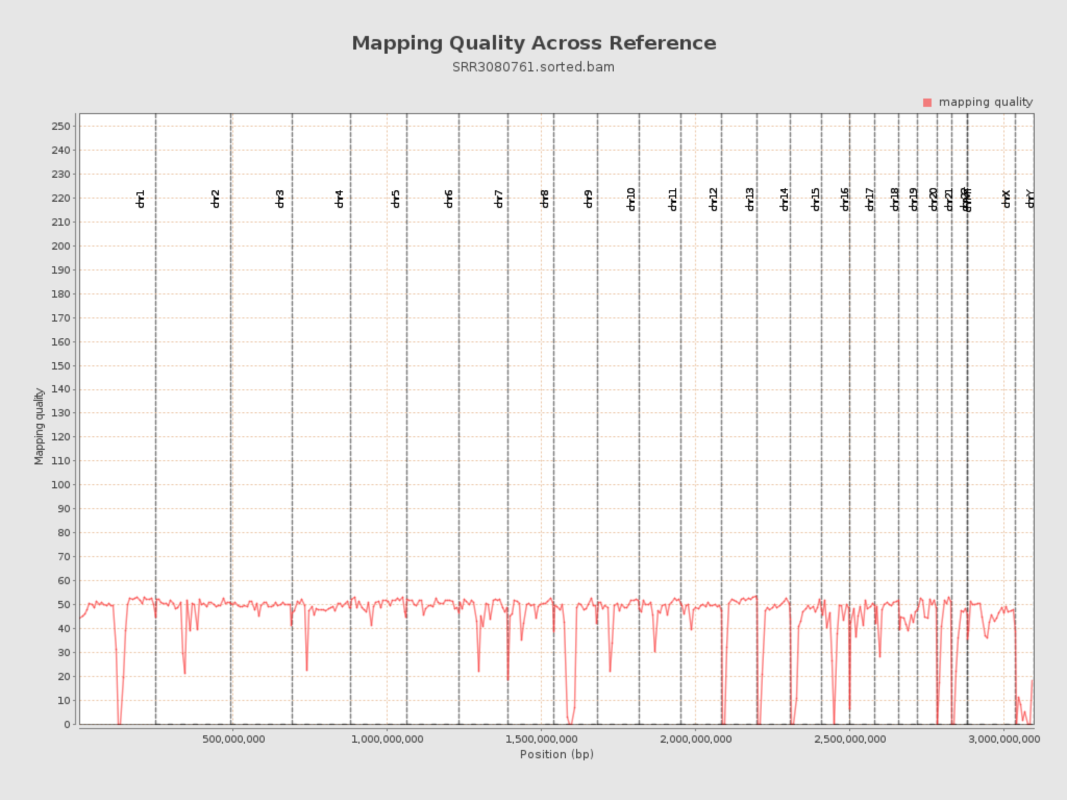
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram