Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:59:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080768.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_SRR3080768 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080768.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:59:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080768.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,392,789
Mapped reads	3,283,540 / 74.75%
Unmapped reads	1,109,249 / 25.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,082 / 0.55%
Read min/max/mean length	30 / 66 / 66.18
Duplicated reads (estimated)	423,379 / 9.64%
Duplication rate	9.49%
Clipped reads	464,426 / 10.57%

2.2. ACGT Content

Number/percentage of A's	65,542,698 / 31.17%
Number/percentage of C's	42,255,996 / 20.1%
Number/percentage of T's	54,461,594 / 25.9%
Number/percentage of G's	47,935,732 / 22.8%
Number/percentage of N's	70,026 / 0.03%
GC Percentage	42.89%

2.3. Coverage

Mean	0.0679

Standard Deviation	0.5406

2.4. Mapping Quality

Mean Mapping Quality	44.53

2.5. Mismatches and indels

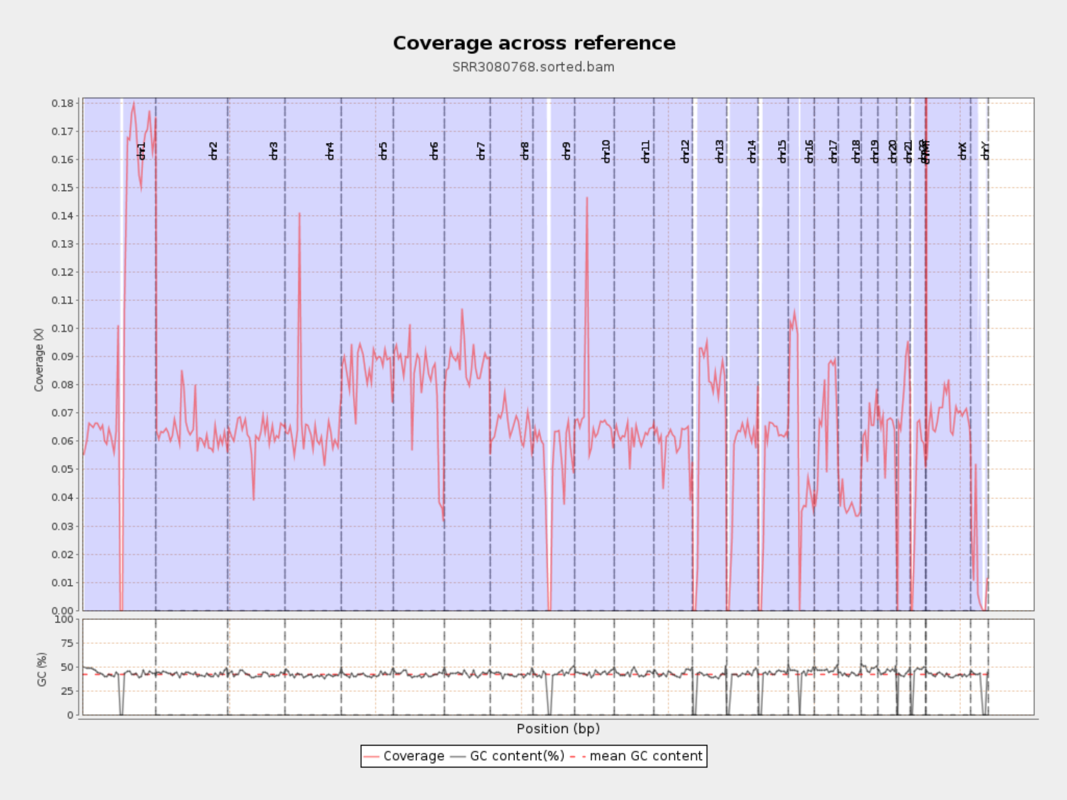
General error rate	0.79%
Mismatches	1,629,486
Insertions	16,362
Mapped reads with at least one insertion	0.49%
Deletions	38,669
Mapped reads with at least one deletion	1.16%
Homopolymer indels	42.61%

2.6. Chromosome stats

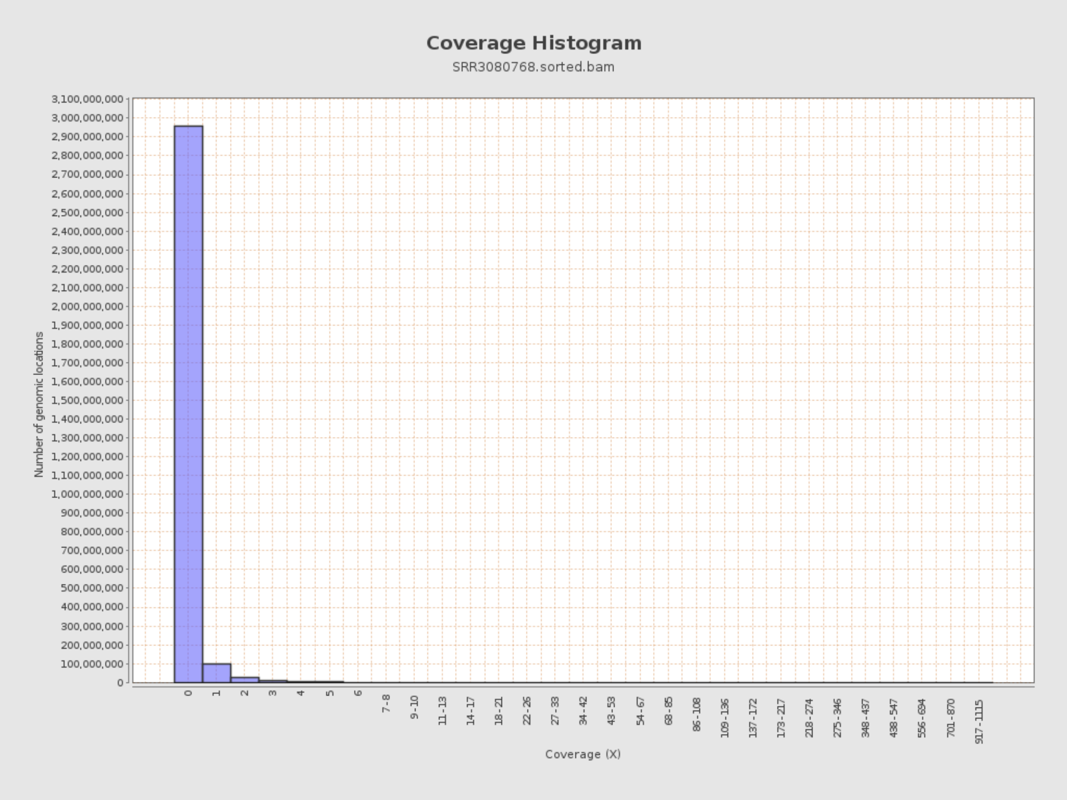
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26057142	0.1045	0.8277
chr2	243199373	15459667	0.0636	0.523
chr3	198022430	12378012	0.0625	0.3617
chr4	191154276	12417903	0.065	0.4884
chr5	180915260	15557687	0.086	0.4333
chr6	171115067	13781751	0.0805	0.5123
chr7	159138663	14070876	0.0884	0.7179

chr8	146364022	9581566	0.0655	0.8102
chr9	141213431	7211537	0.0511	0.3898
chr10	135534747	9375373	0.0692	0.7348
chr11	135006516	8359947	0.0619	0.4542
chr12	133851895	7985512	0.0597	0.3592
chr13	115169878	8195749	0.0712	0.3907
chr14	107349540	5598209	0.0521	0.3653
chr15	102531392	5293351	0.0516	0.3313
chr16	90354753	5290464	0.0586	0.3947
chr17	81195210	5653255	0.0696	0.4167
chr18	78077248	2921462	0.0374	0.5933
chr19	59128983	3858539	0.0653	0.7623
chr20	63025520	4023961	0.0638	0.3906
chr21	48129895	3446345	0.0716	0.4989
chr22	51304566	2236255	0.0436	0.3127
chrMT	16571	60153	3.63	3.6487
chrX	155270560	10751053	0.0692	0.4049
chrY	59373566	774404	0.013	0.459

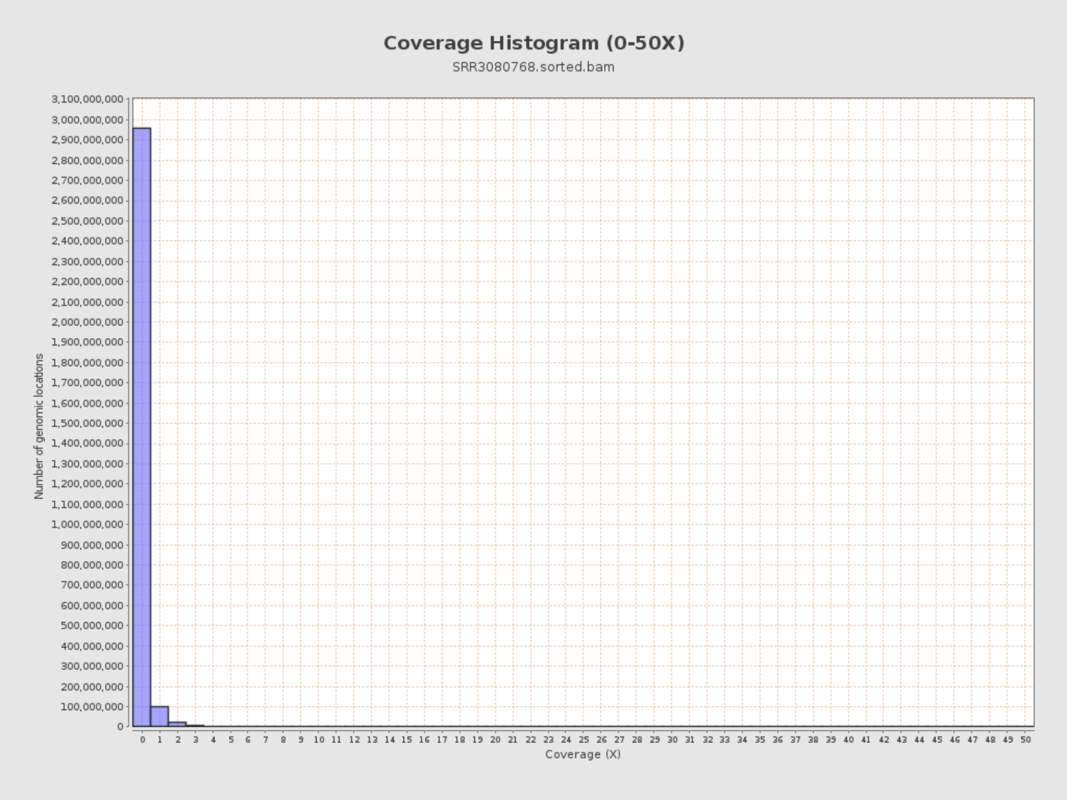
3. Results : Coverage across reference



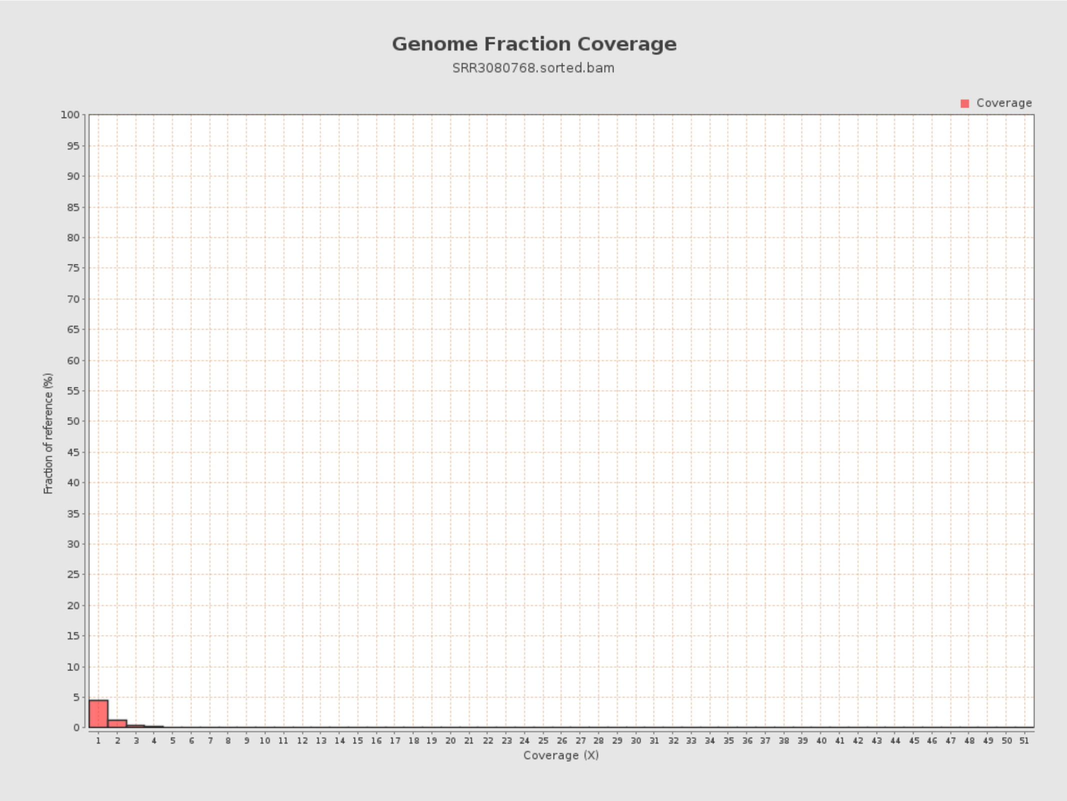
4. Results : Coverage Histogram



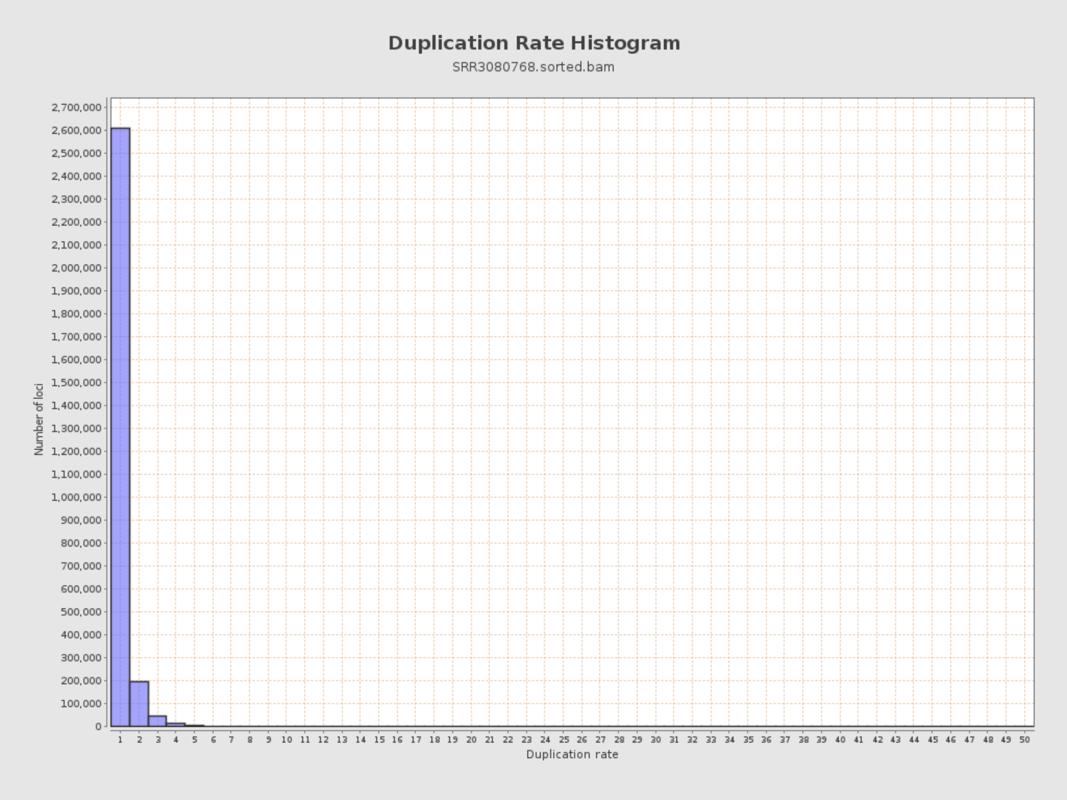
5. Results : Coverage Histogram (0-50X)



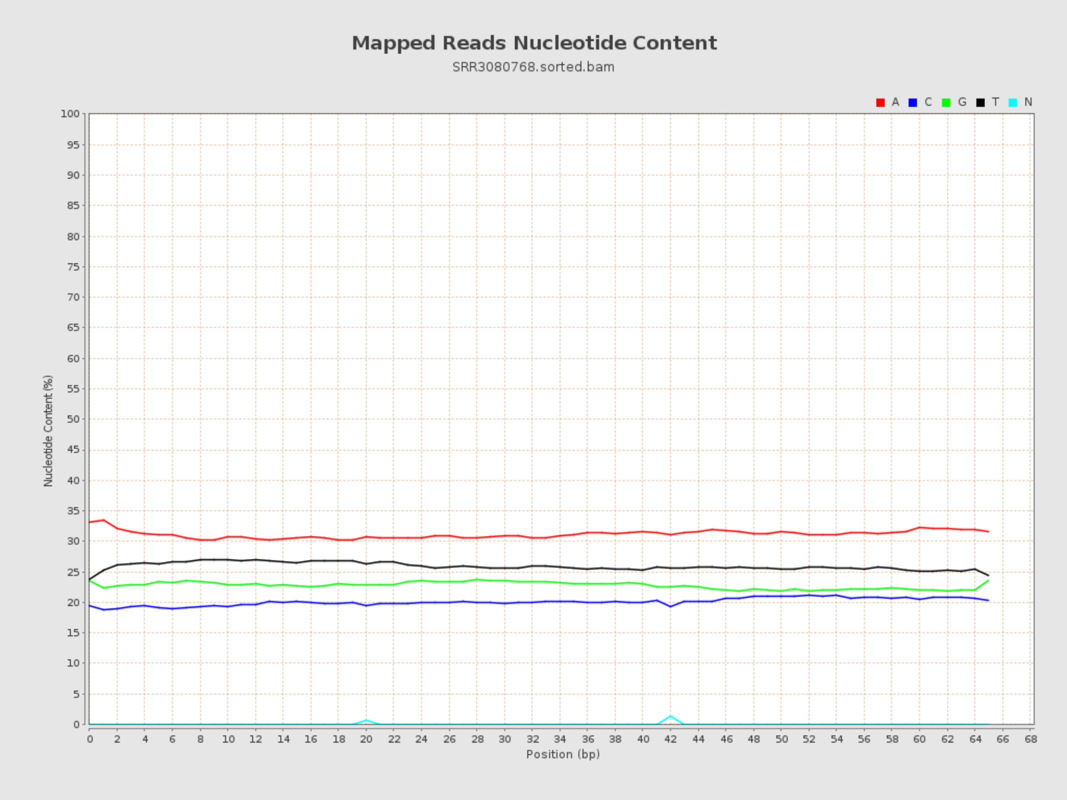
6. Results : Genome Fraction Coverage



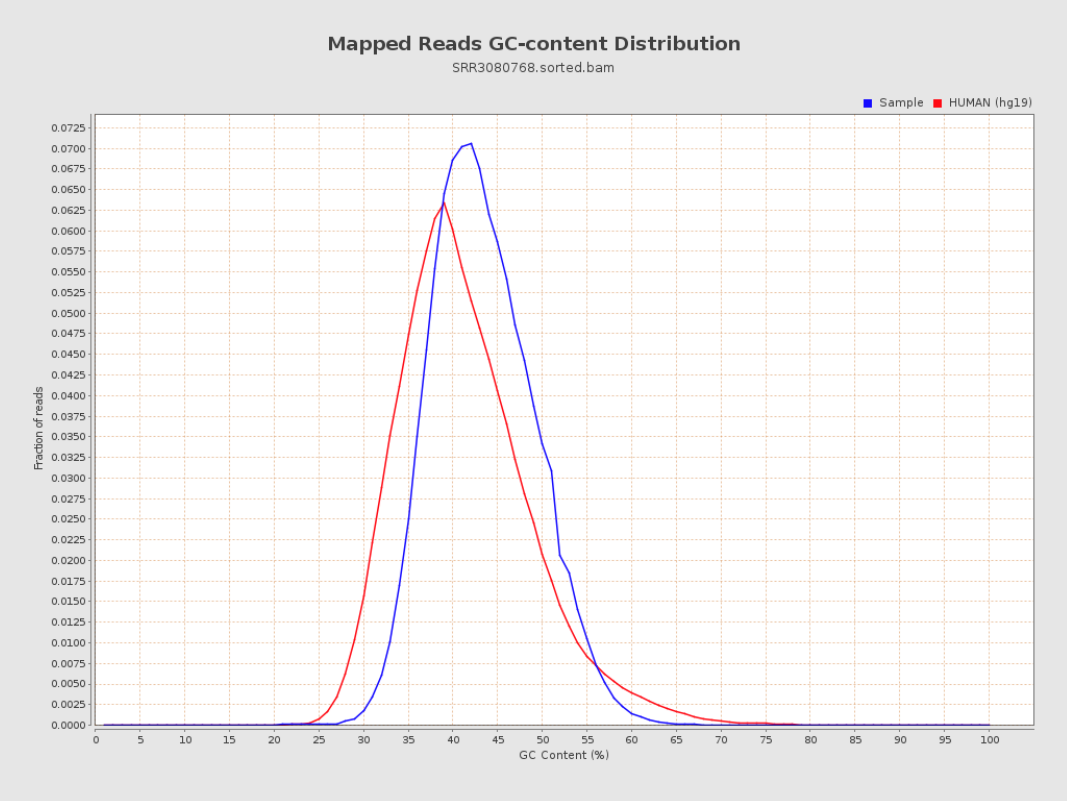
7. Results : Duplication Rate Histogram



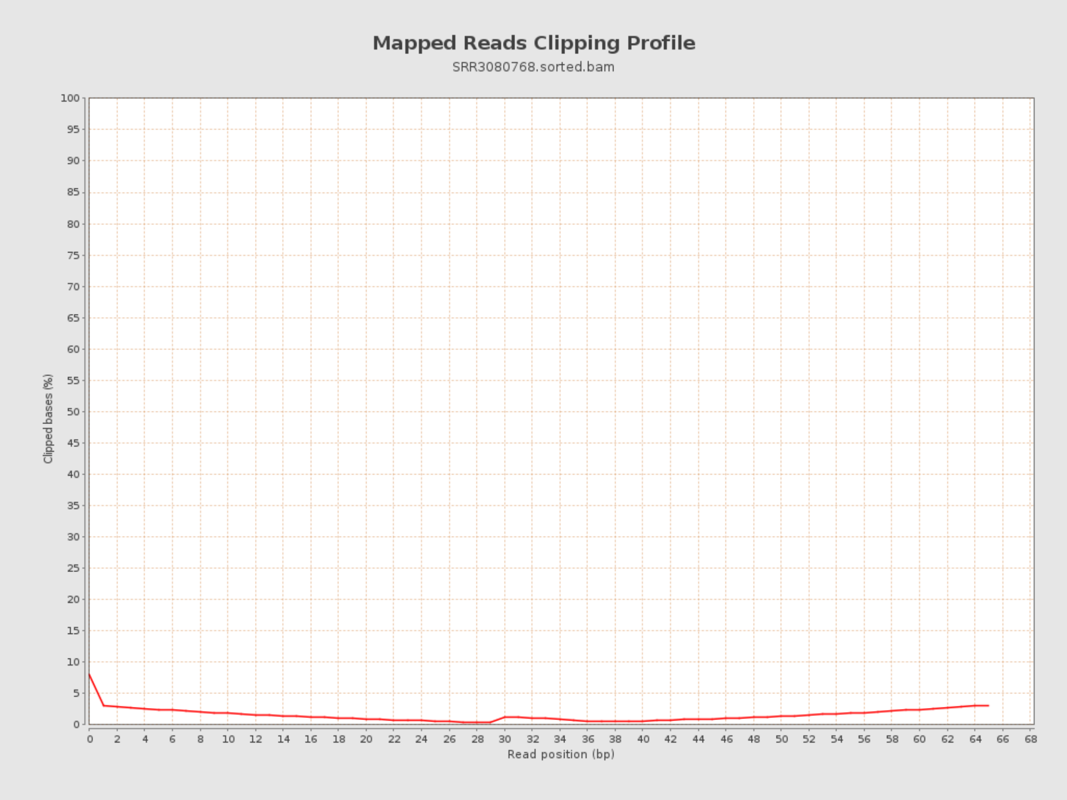
8. Results : Mapped Reads Nucleotide Content



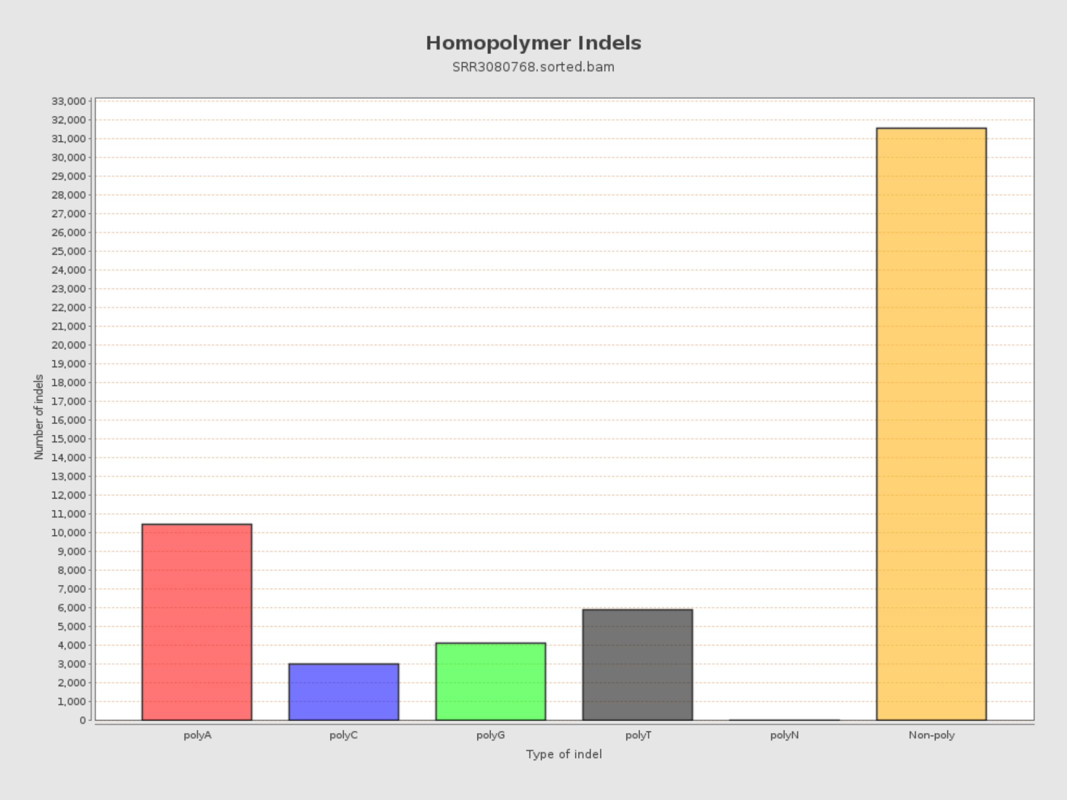
9. Results : Mapped Reads GC-content Distribution



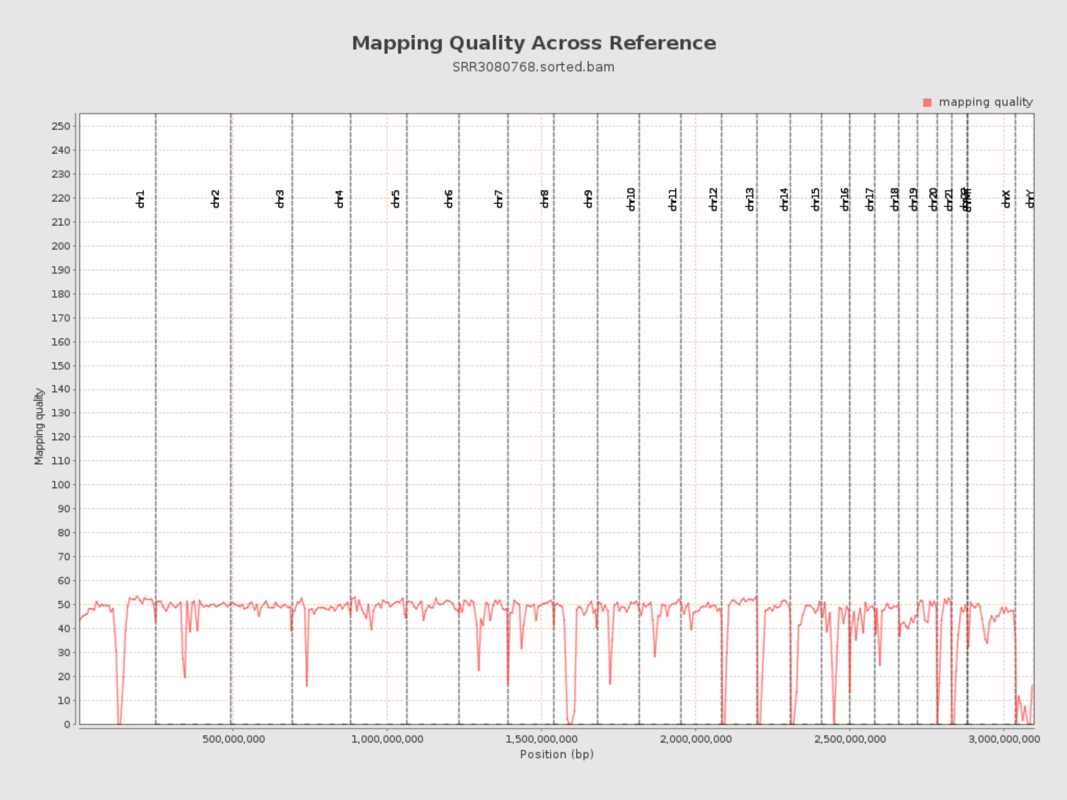
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram