Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 05:31:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080762.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_SRR3080762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 05:31:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,801,876
Mapped reads	5,056,439 / 74.34%
Unmapped reads	1,745,437 / 25.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,326 / 0.43%
Read min/max/mean length	30 / 66 / 66.14
Duplicated reads (estimated)	703,408 / 10.34%
Duplication rate	10.64%
Clipped reads	627,232 / 9.22%

2.2. ACGT Content

Number/percentage of A's	100,791,560 / 31%
Number/percentage of C's	65,142,617 / 20.04%
Number/percentage of T's	84,806,942 / 26.09%
Number/percentage of G's	74,253,129 / 22.84%
Number/percentage of N's	104,641 / 0.03%
GC Percentage	42.88%

2.3. Coverage

Mean	0.1051

Standard Deviation	0.6758

2.4. Mapping Quality

Mean Mapping Quality	45.16

2.5. Mismatches and indels

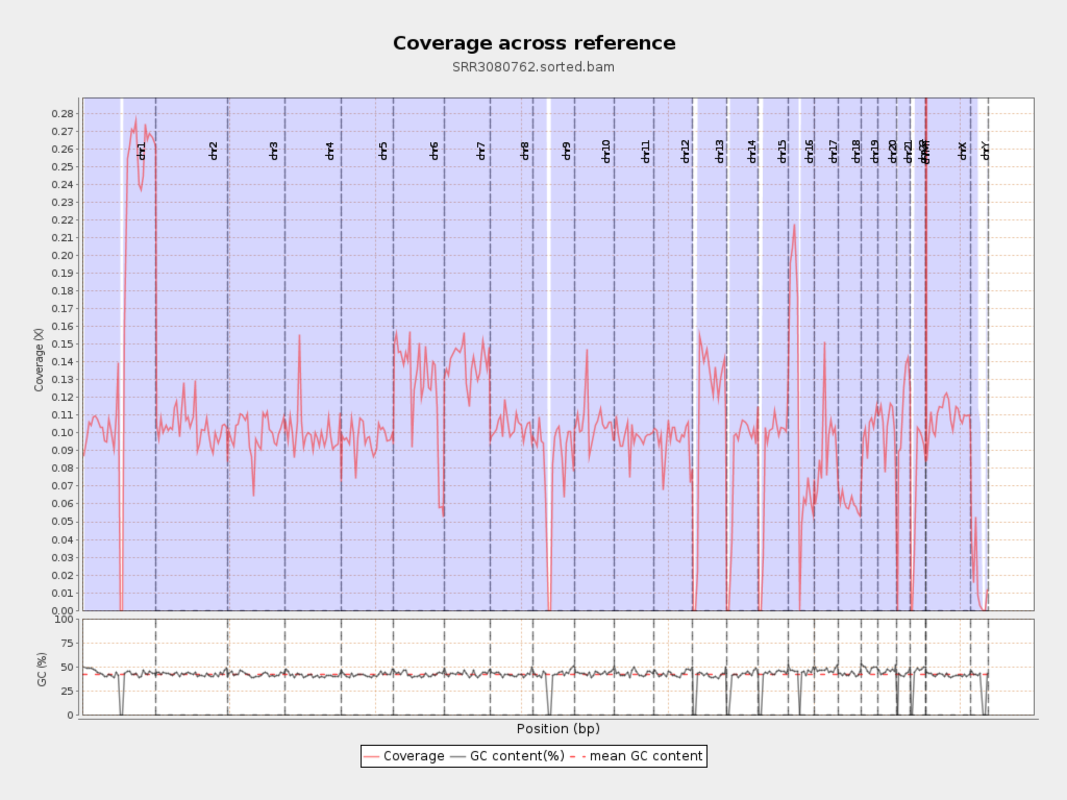
General error rate	0.81%
Mismatches	2,575,012
Insertions	22,847
Mapped reads with at least one insertion	0.45%
Deletions	61,520
Mapped reads with at least one deletion	1.2%
Homopolymer indels	44.36%

2.6. Chromosome stats

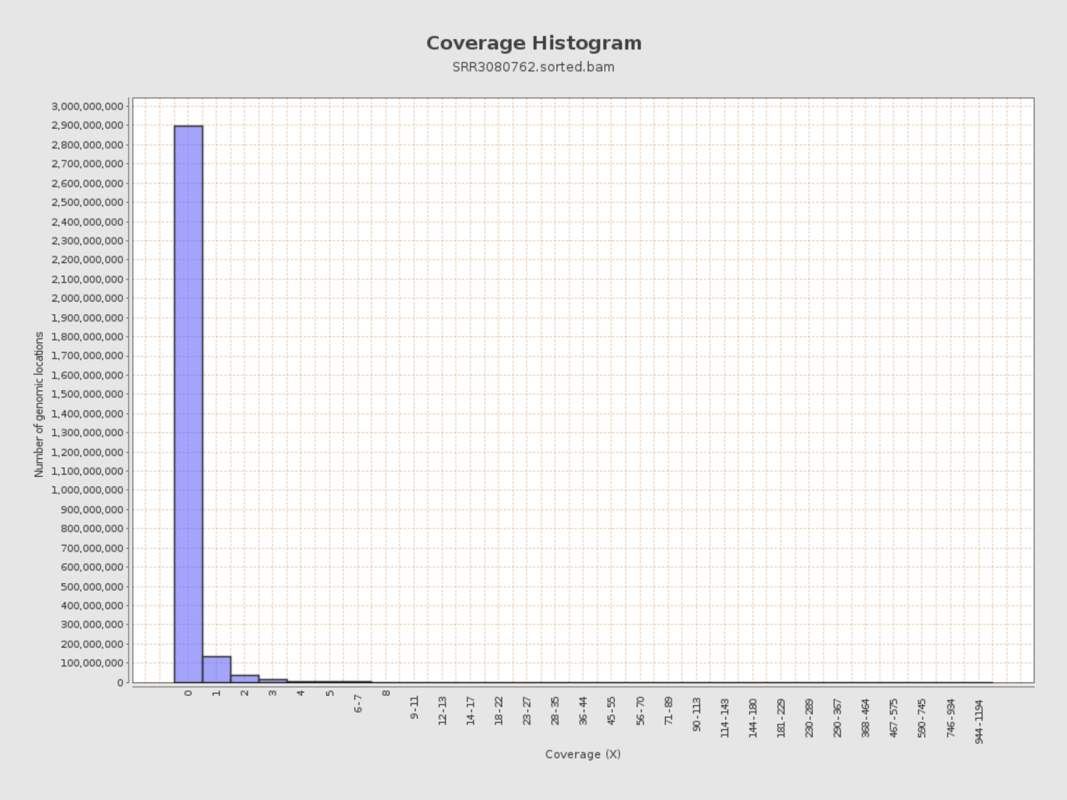
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	40806018	0.1637	1.0174
chr2	243199373	25296549	0.104	0.6428
chr3	198022430	19708710	0.0995	0.4855
chr4	191154276	19254389	0.1007	0.5559
chr5	180915260	17589113	0.0972	0.4821
chr6	171115067	21777598	0.1273	0.7697
chr7	159138663	22254685	0.1398	1.0327

chr8	146364022	15117598	0.1033	0.9175
chr9	141213431	11522928	0.0816	0.5307
chr10	135534747	14299391	0.1055	0.6897
chr11	135006516	13150894	0.0974	0.6383
chr12	133851895	12842079	0.0959	0.4833
chr13	115169878	13114629	0.1139	0.528
chr14	107349540	8986626	0.0837	0.5016
chr15	102531392	8481971	0.0827	0.4464
chr16	90354753	9620279	0.1065	0.5441
chr17	81195210	7462460	0.0919	0.4903
chr18	78077248	4705551	0.0603	0.7424
chr19	59128983	5998376	0.1014	0.9321
chr20	63025520	6577226	0.1044	0.5204
chr21	48129895	5166935	0.1074	0.5934
chr22	51304566	3480027	0.0678	0.4095
chrMT	16571	158343	9.5554	8.043
chrX	155270560	16927485	0.109	0.5386
chrY	59373566	912433	0.0154	0.4184

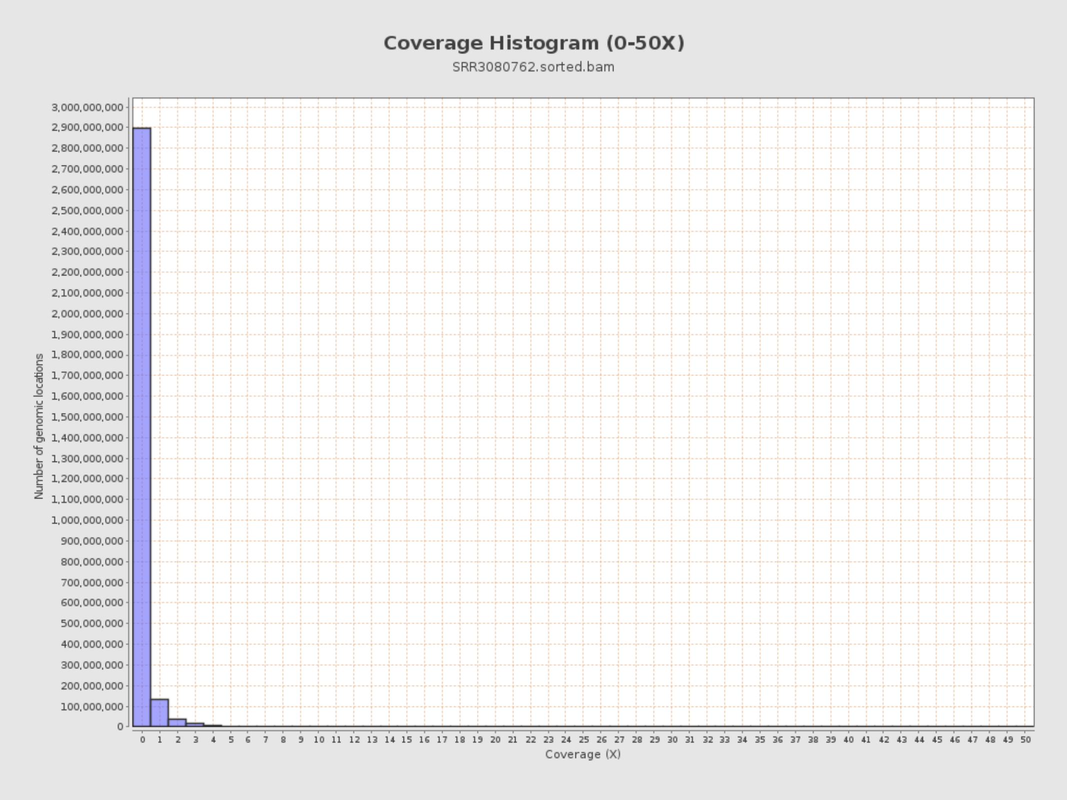
3. Results : Coverage across reference



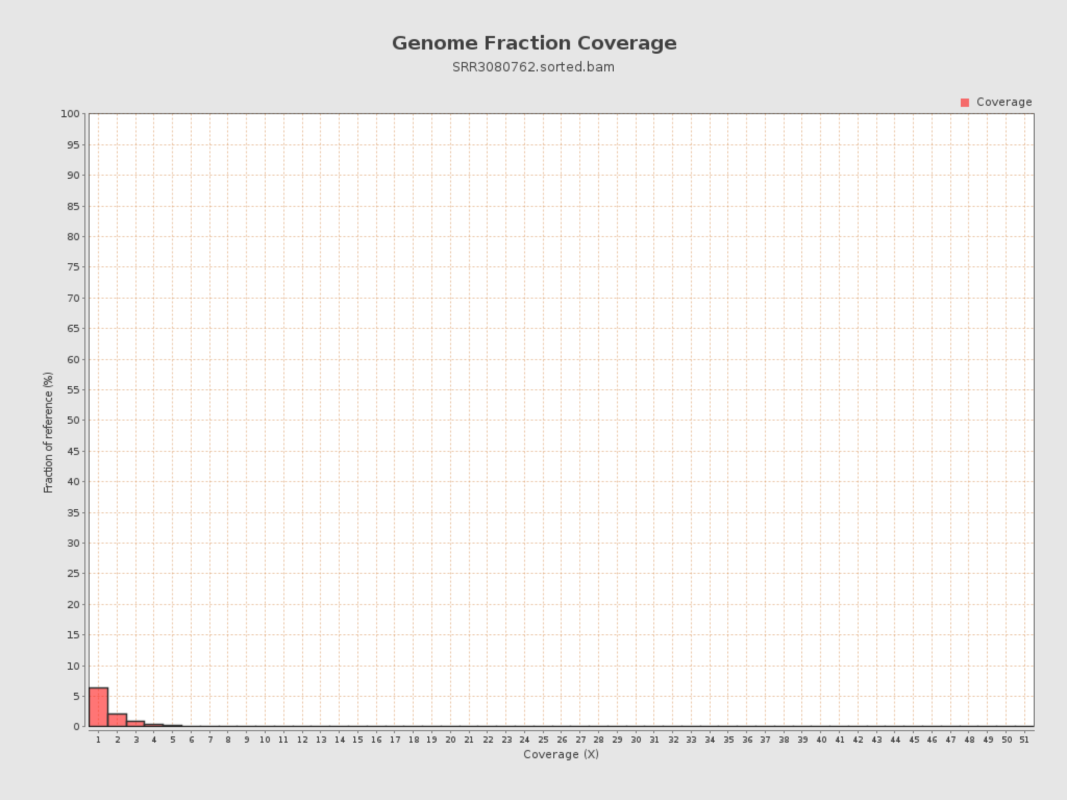
4. Results : Coverage Histogram



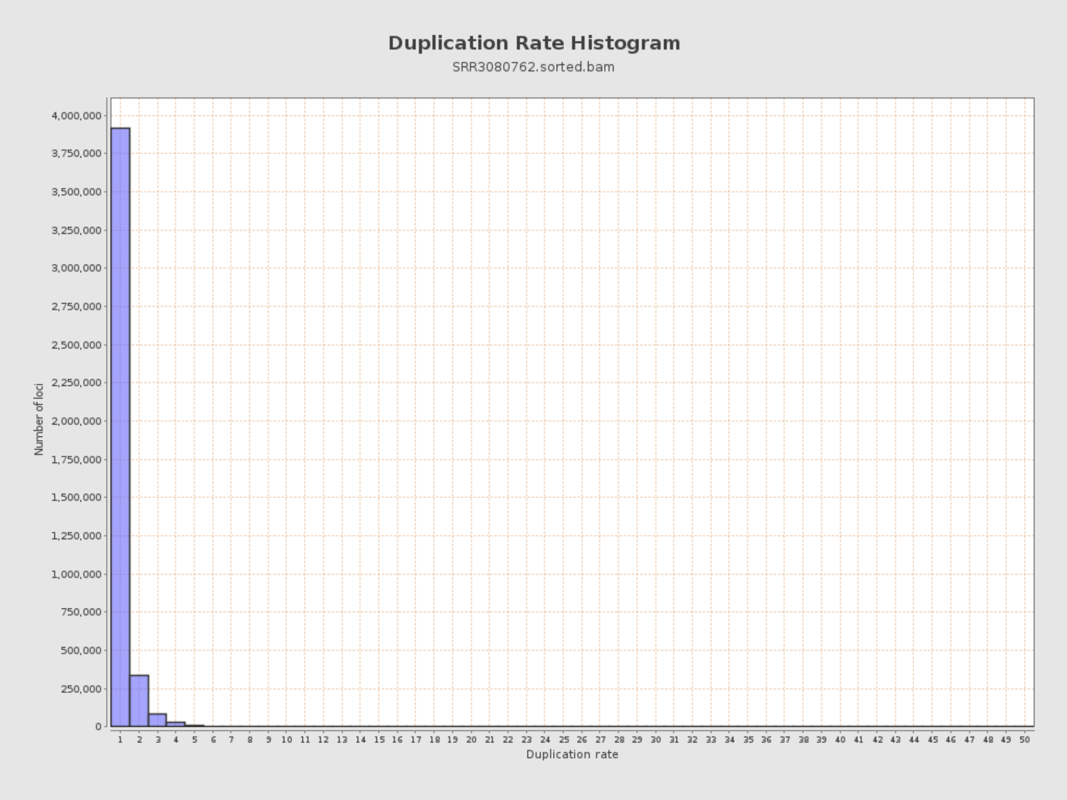
5. Results : Coverage Histogram (0-50X)



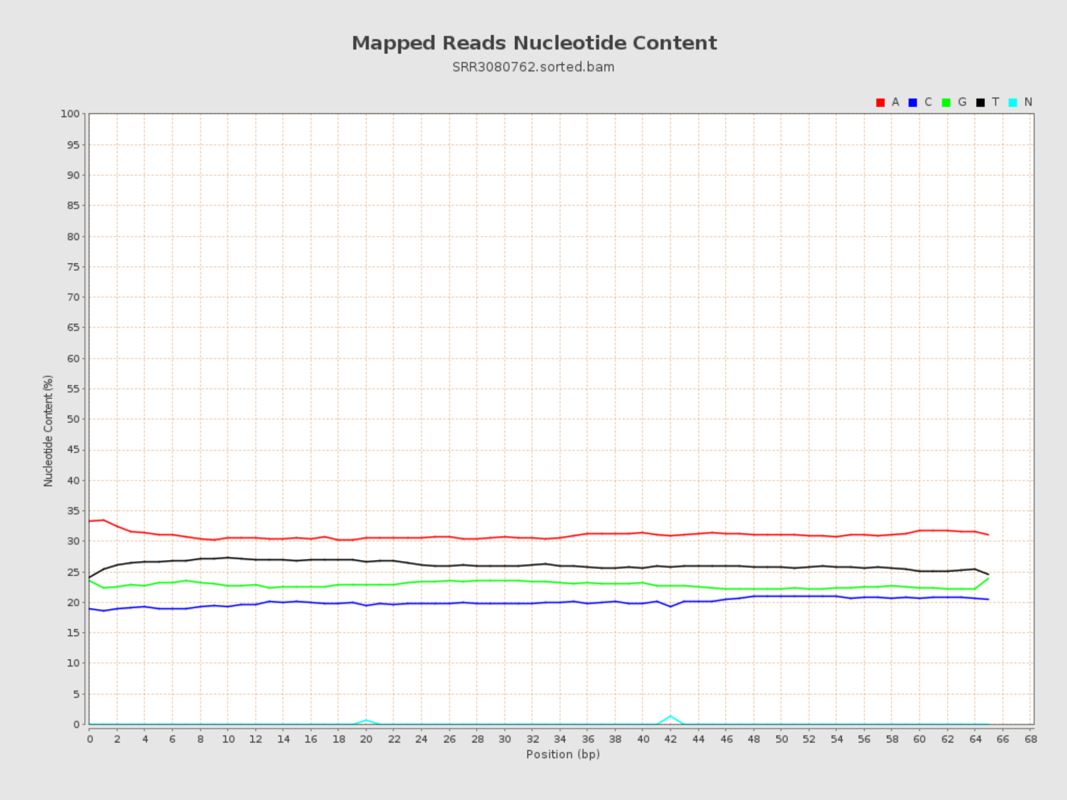
6. Results : Genome Fraction Coverage



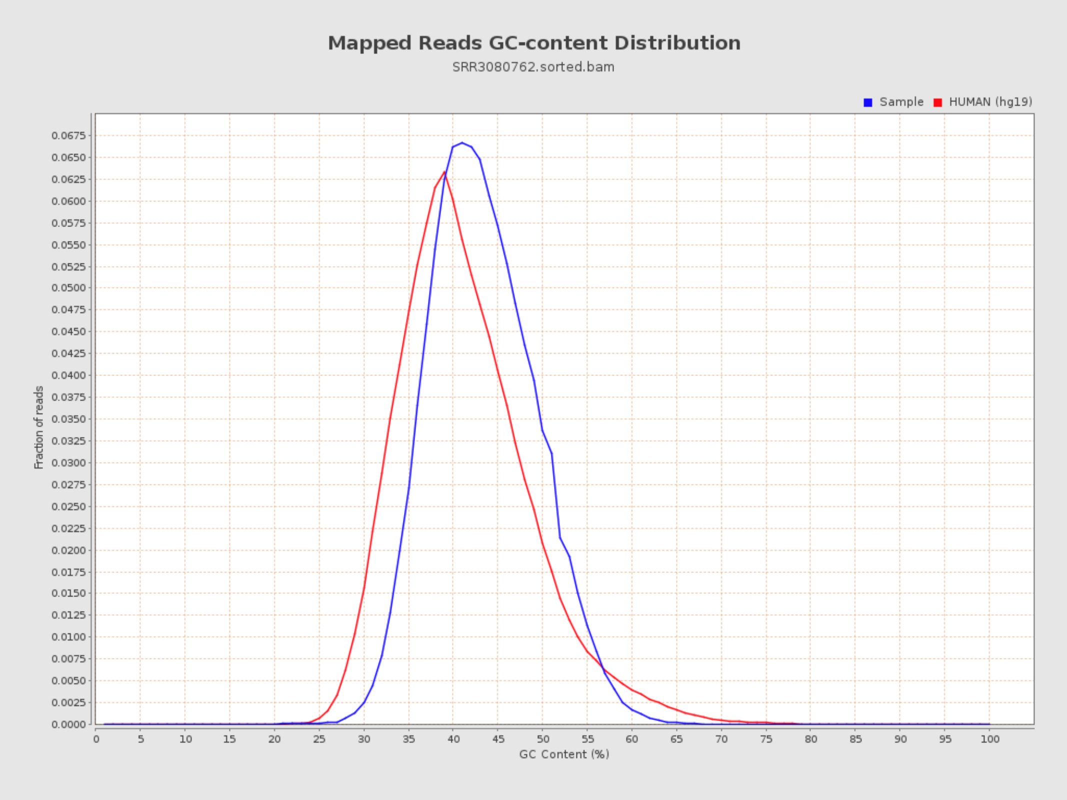
7. Results : Duplication Rate Histogram



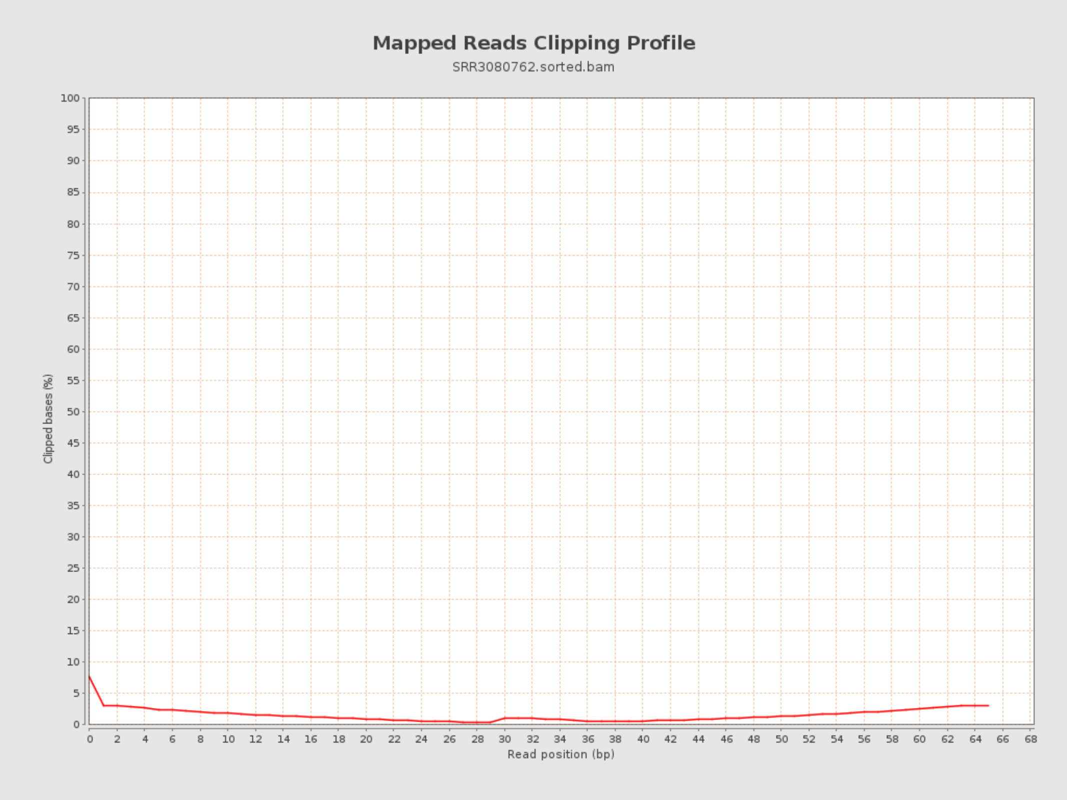
8. Results : Mapped Reads Nucleotide Content



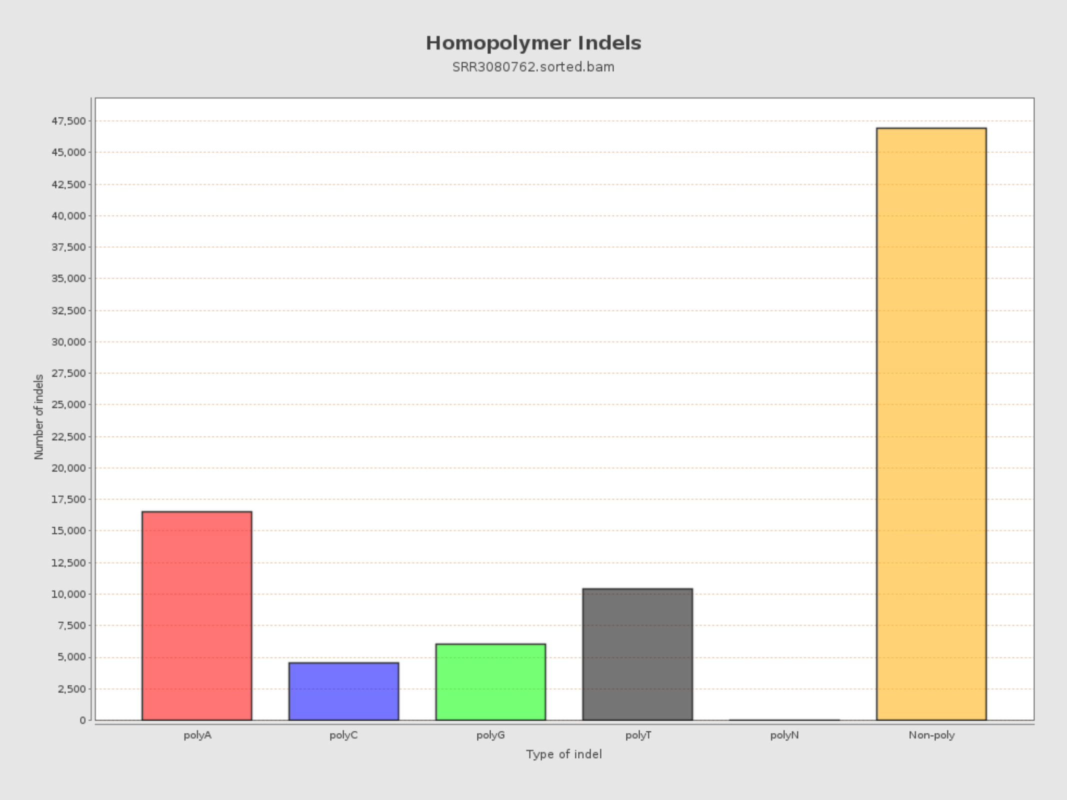
9. Results : Mapped Reads GC-content Distribution



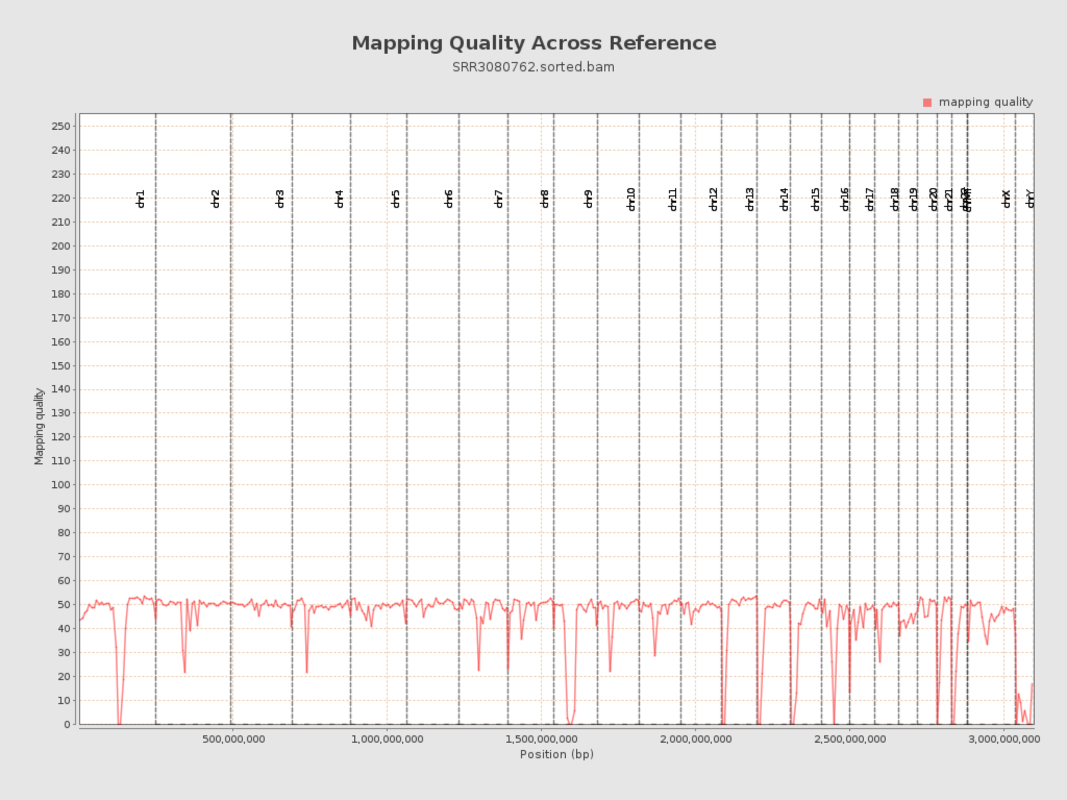
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram