Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:05:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068161.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_SRR6068161 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068161.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:05:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068161.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,129,638
Mapped reads	4,845,861 / 94.47%
Unmapped reads	283,777 / 5.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,429 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	453,977 / 8.85%
Duplication rate	6.9%
Clipped reads	2,543,756 / 49.59%

2.2. ACGT Content

Number/percentage of A's	81,289,445 / 25.95%
Number/percentage of C's	56,879,975 / 18.16%
Number/percentage of T's	101,279,579 / 32.34%
Number/percentage of G's	73,716,292 / 23.54%
Number/percentage of N's	35,420 / 0.01%
GC Percentage	41.7%

2.3. Coverage

Mean	0.1012

Standard Deviation	1.5134

2.4. Mapping Quality

Mean Mapping Quality	43.41

2.5. Mismatches and indels

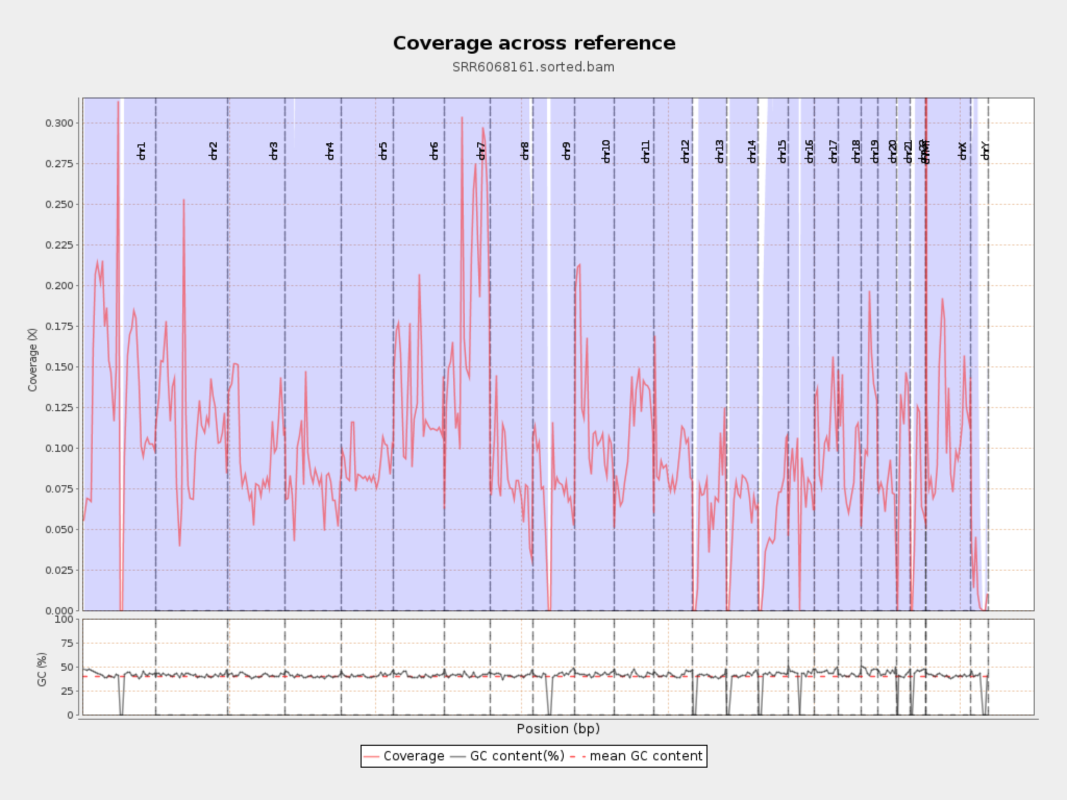
General error rate	0.6%
Mismatches	1,845,528
Insertions	20,662
Mapped reads with at least one insertion	0.42%
Deletions	76,467
Mapped reads with at least one deletion	1.56%
Homopolymer indels	44.45%

2.6. Chromosome stats

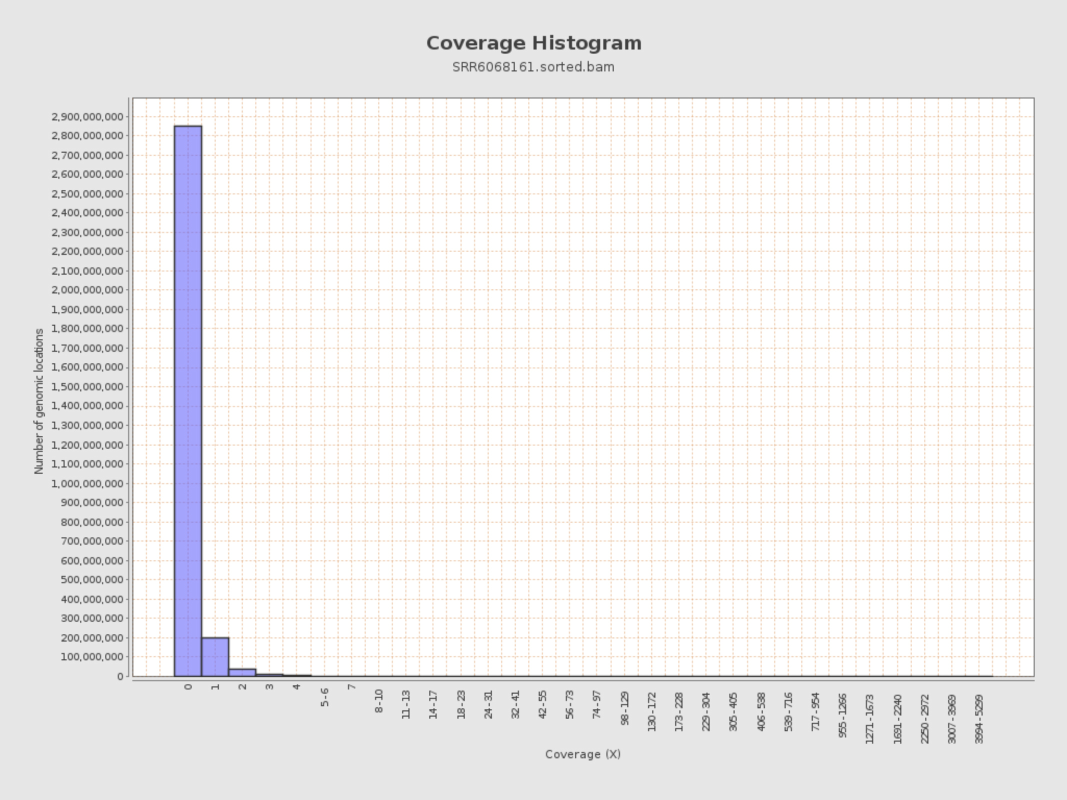
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	33574636	0.1347	4.0188
chr2	243199373	28708884	0.118	1.5919
chr3	198022430	19636905	0.0992	0.4003
chr4	191154276	15615869	0.0817	0.4288
chr5	180915260	16257141	0.0899	0.3926
chr6	171115067	22315662	0.1304	0.6592
chr7	159138663	30509915	0.1917	2.3932

chr8	146364022	11617219	0.0794	1.4309
chr9	141213431	10136319	0.0718	0.9275
chr10	135534747	16699230	0.1232	0.8406
chr11	135006516	14935350	0.1106	0.7311
chr12	133851895	12555185	0.0938	0.4597
chr13	115169878	7277699	0.0632	0.3511
chr14	107349540	6471637	0.0603	0.4782
chr15	102531392	5111474	0.0499	0.3833
chr16	90354753	6684656	0.074	0.4497
chr17	81195210	9205692	0.1134	0.5045
chr18	78077248	7490817	0.0959	1.7191
chr19	59128983	7254998	0.1227	2.3451
chr20	63025520	4650211	0.0738	0.4315
chr21	48129895	4999874	0.1039	0.4389
chr22	51304566	3263965	0.0636	0.3039
chrMT	16571	143806	8.6782	5.5399
chrX	155270560	17377415	0.1119	0.6177
chrY	59373566	838461	0.0141	0.4407

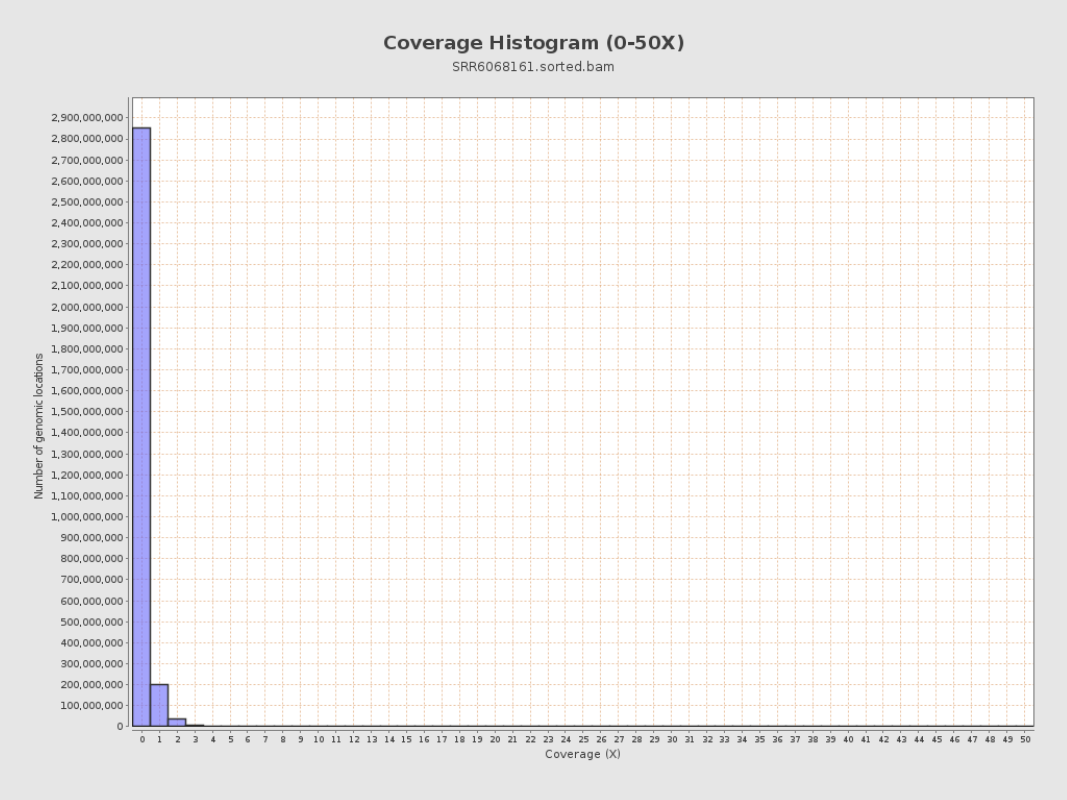
3. Results : Coverage across reference



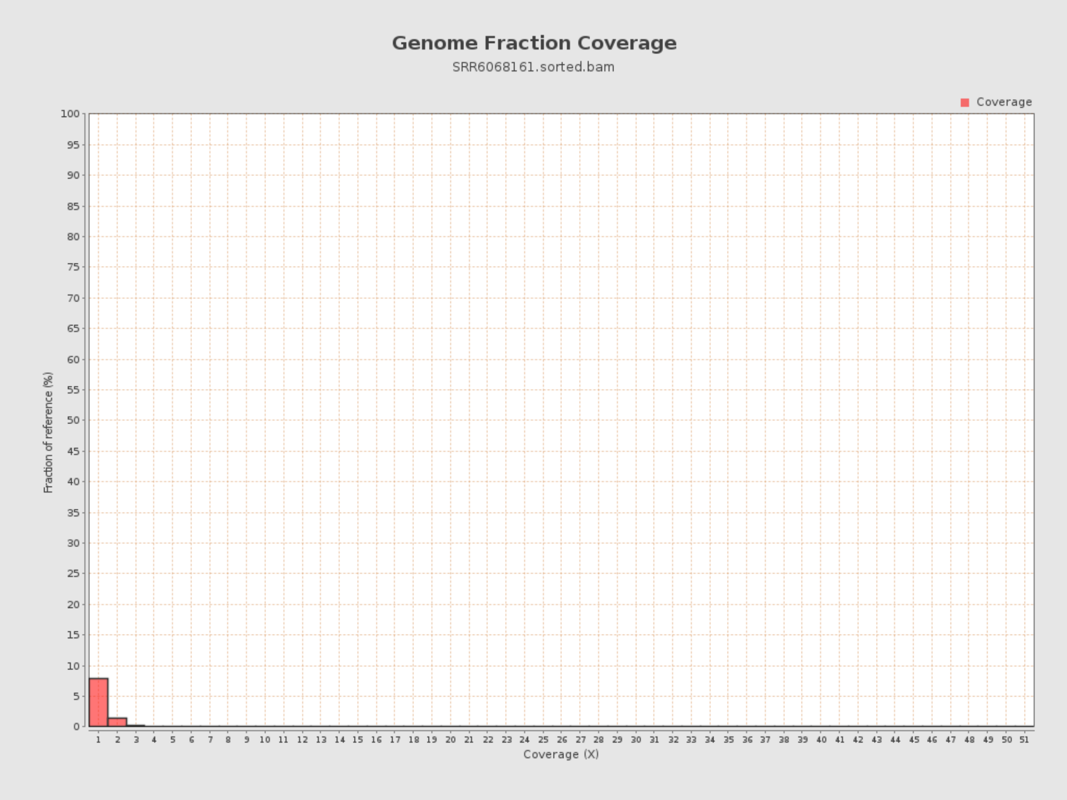
4. Results : Coverage Histogram



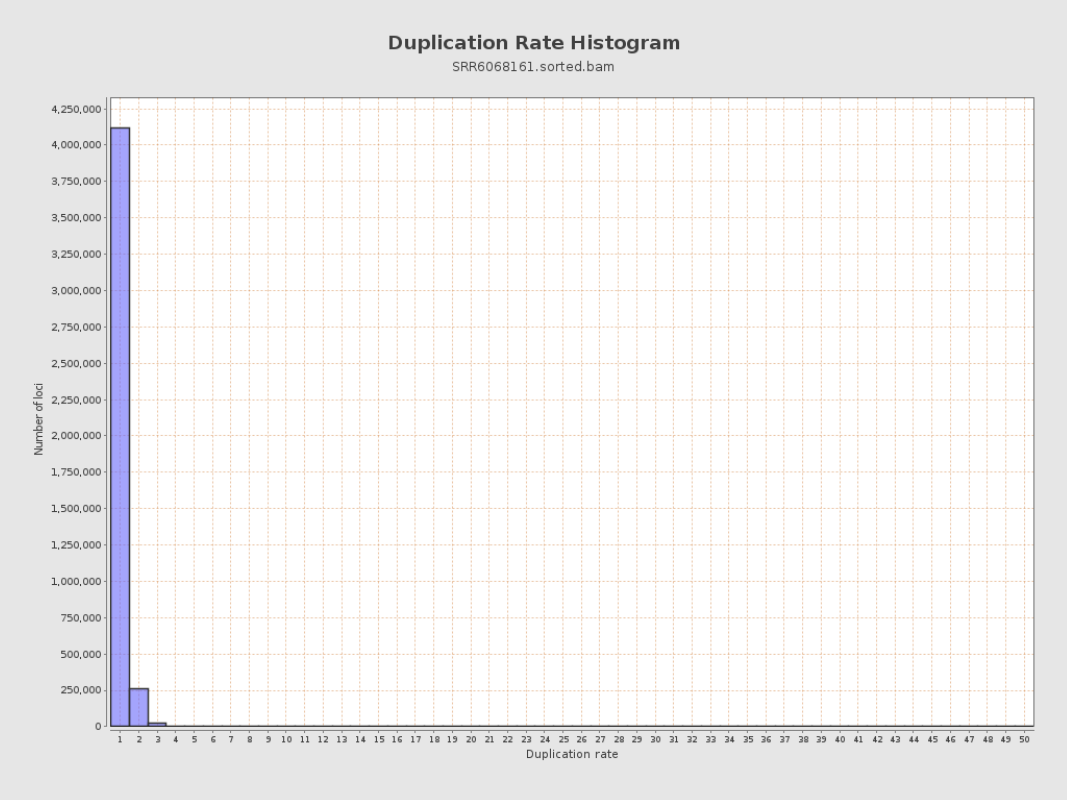
5. Results : Coverage Histogram (0-50X)



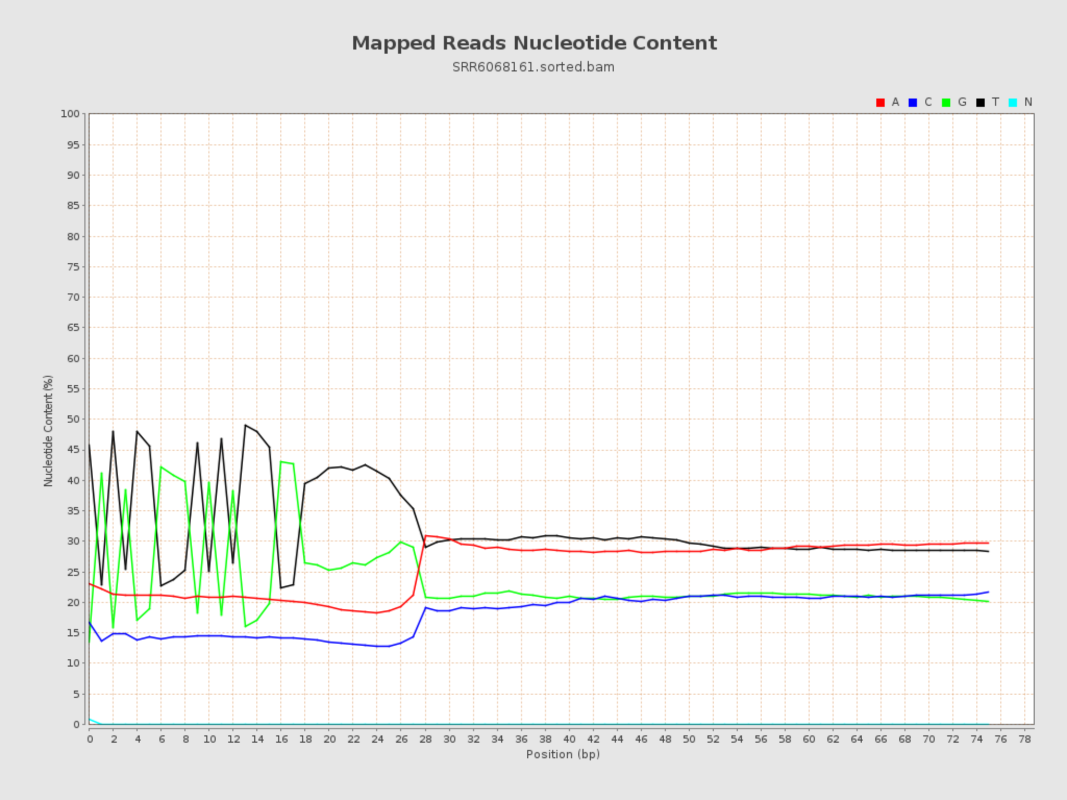
6. Results : Genome Fraction Coverage



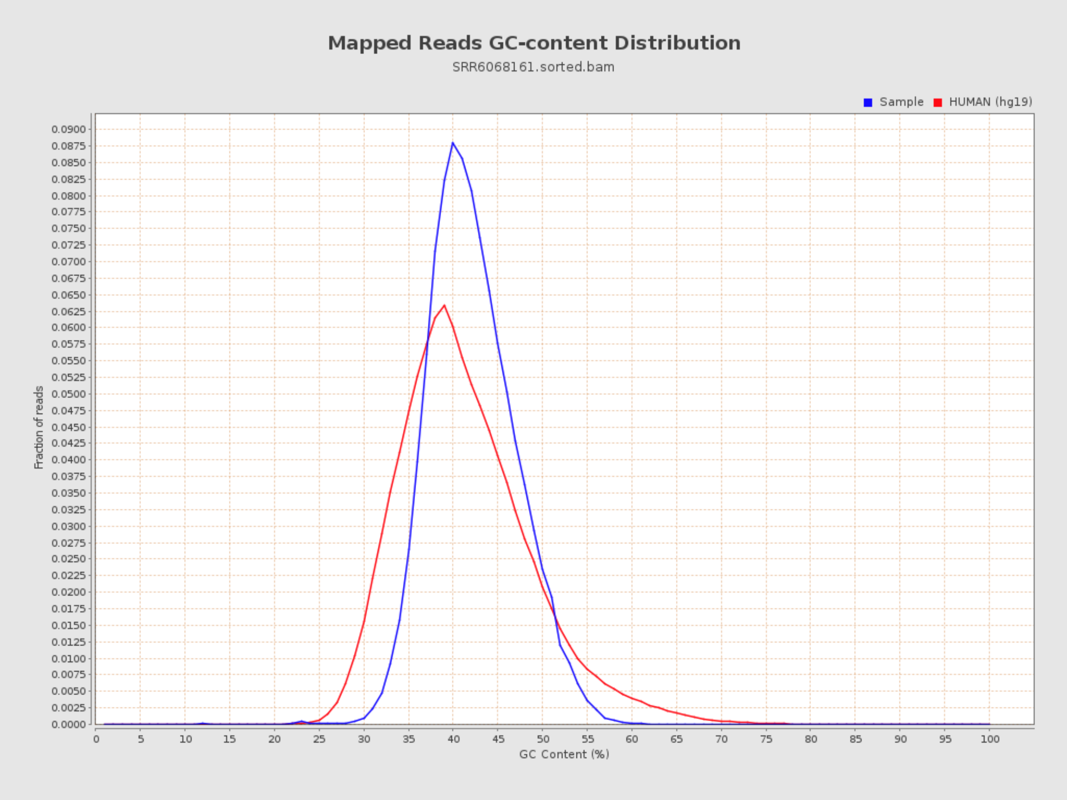
7. Results : Duplication Rate Histogram



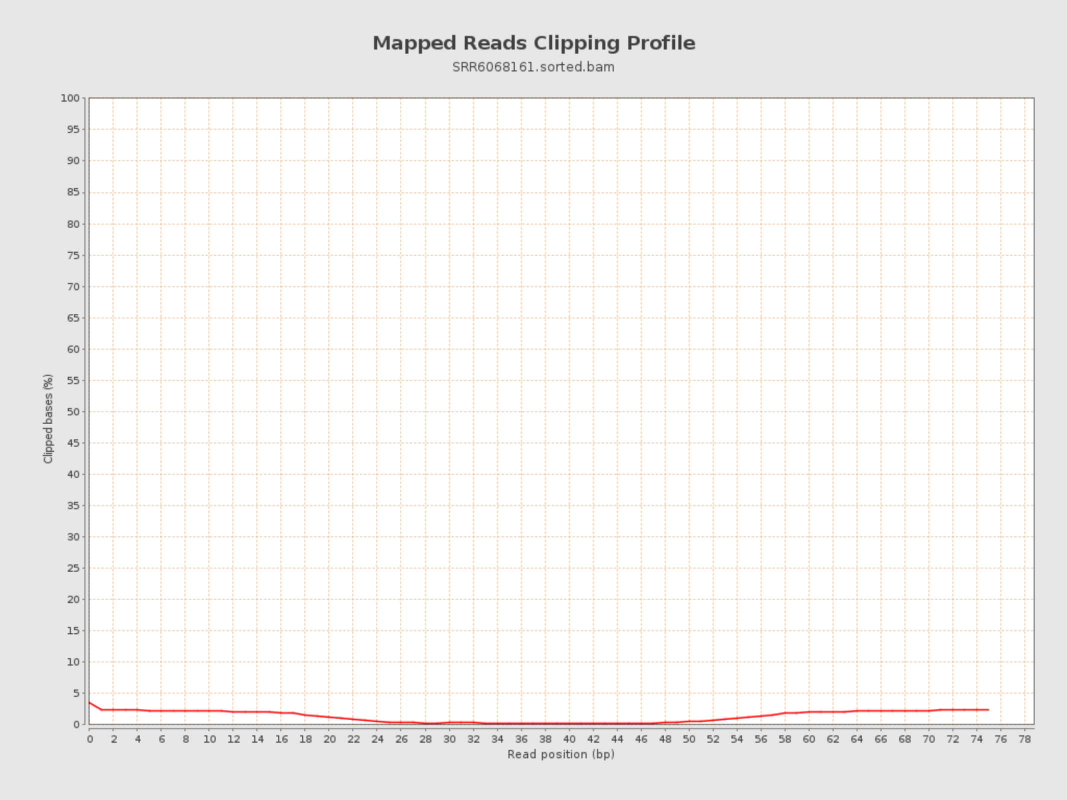
8. Results : Mapped Reads Nucleotide Content



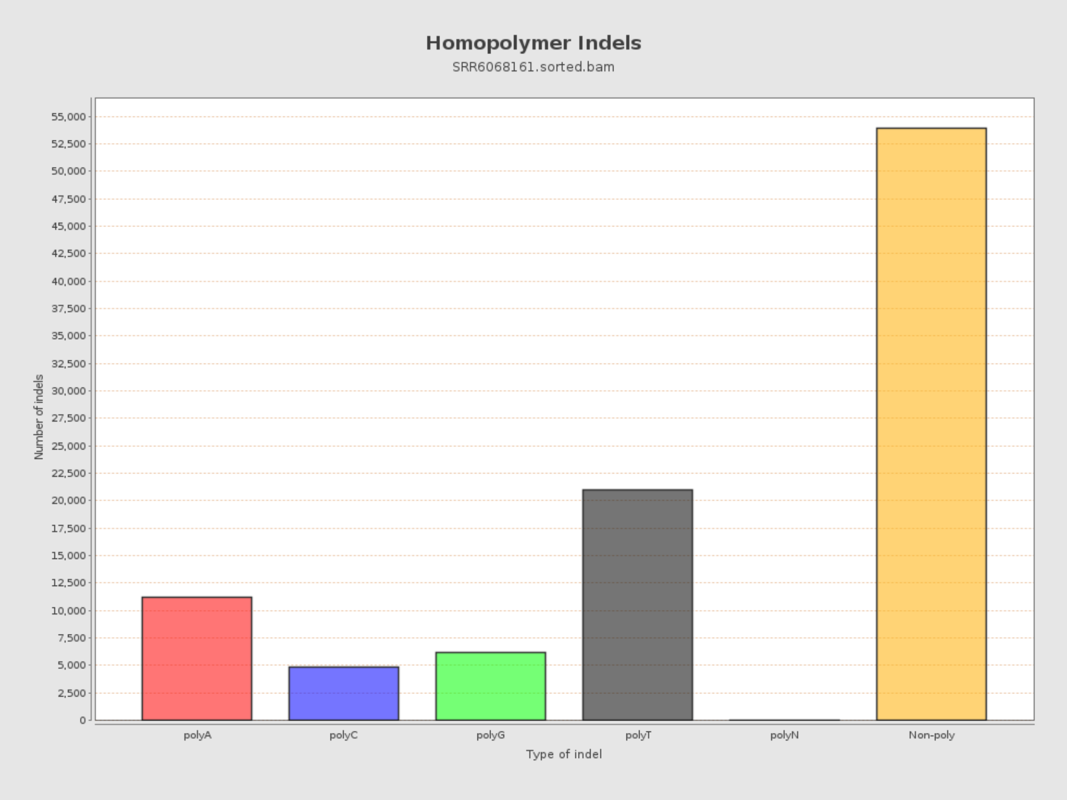
9. Results : Mapped Reads GC-content Distribution



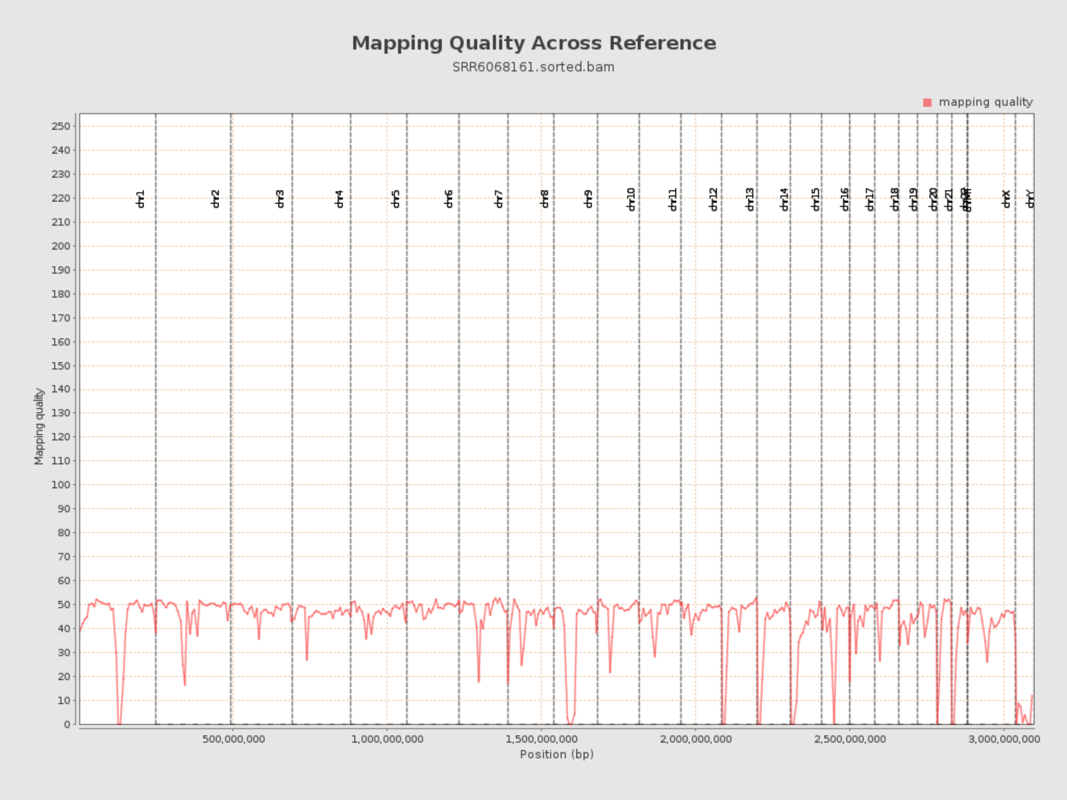
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram