Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:44:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013203.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_SRR6013203 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013203.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:44:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013203.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,168,558
Mapped reads	3,598,109 / 86.32%
Unmapped reads	570,449 / 13.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,640 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	254,988 / 6.12%
Duplication rate	5.64%
Clipped reads	1,961,835 / 47.06%

2.2. ACGT Content

Number/percentage of A's	66,081,376 / 28.56%
Number/percentage of C's	43,282,151 / 18.71%
Number/percentage of T's	71,957,978 / 31.1%
Number/percentage of G's	50,054,894 / 21.63%
Number/percentage of N's	1,995 / 0%
GC Percentage	40.34%

2.3. Coverage

Mean	0.0748

Standard Deviation	0.5696

2.4. Mapping Quality

Mean Mapping Quality	45.68

2.5. Mismatches and indels

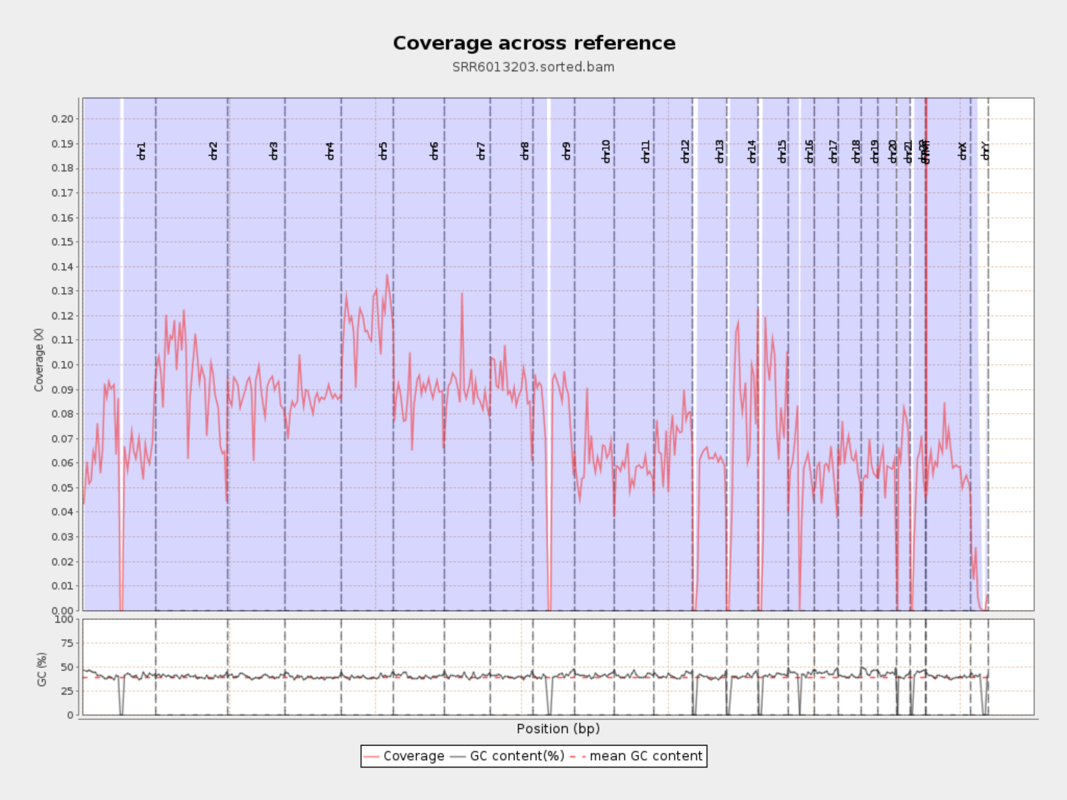
General error rate	0.74%
Mismatches	1,681,453
Insertions	17,178
Mapped reads with at least one insertion	0.47%
Deletions	58,664
Mapped reads with at least one deletion	1.61%
Homopolymer indels	45.11%

2.6. Chromosome stats

Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16083405	0.0645	0.7691
chr2	243199373	23070446	0.0949	0.9086
chr3	198022430	17546149	0.0886	0.3875
chr4	191154276	16479196	0.0862	0.4039
chr5	180915260	21241113	0.1174	0.4538
chr6	171115067	15005258	0.0877	0.4835
chr7	159138663	14325805	0.09	0.9032

chr8	146364022	13312536	0.091	0.7969
chr9	141213431	10892259	0.0771	0.511
chr10	135534747	8326295	0.0614	0.4732
chr11	135006516	7698725	0.057	0.3734
chr12	133851895	9467507	0.0707	0.3564
chr13	115169878	5977904	0.0519	0.305
chr14	107349540	8019315	0.0747	0.3883
chr15	102531392	7579492	0.0739	0.357
chr16	90354753	4768970	0.0528	0.3507
chr17	81195210	4491481	0.0553	0.3097
chr18	78077248	4953269	0.0634	0.9596
chr19	59128983	3349414	0.0566	0.6047
chr20	63025520	3594366	0.057	0.3174
chr21	48129895	3058975	0.0636	0.3621
chr22	51304566	2256854	0.044	0.2697
chrMT	16571	60286	3.638	3.1833
chrX	155270560	9400114	0.0605	0.3568
chrY	59373566	518446	0.0087	0.1845

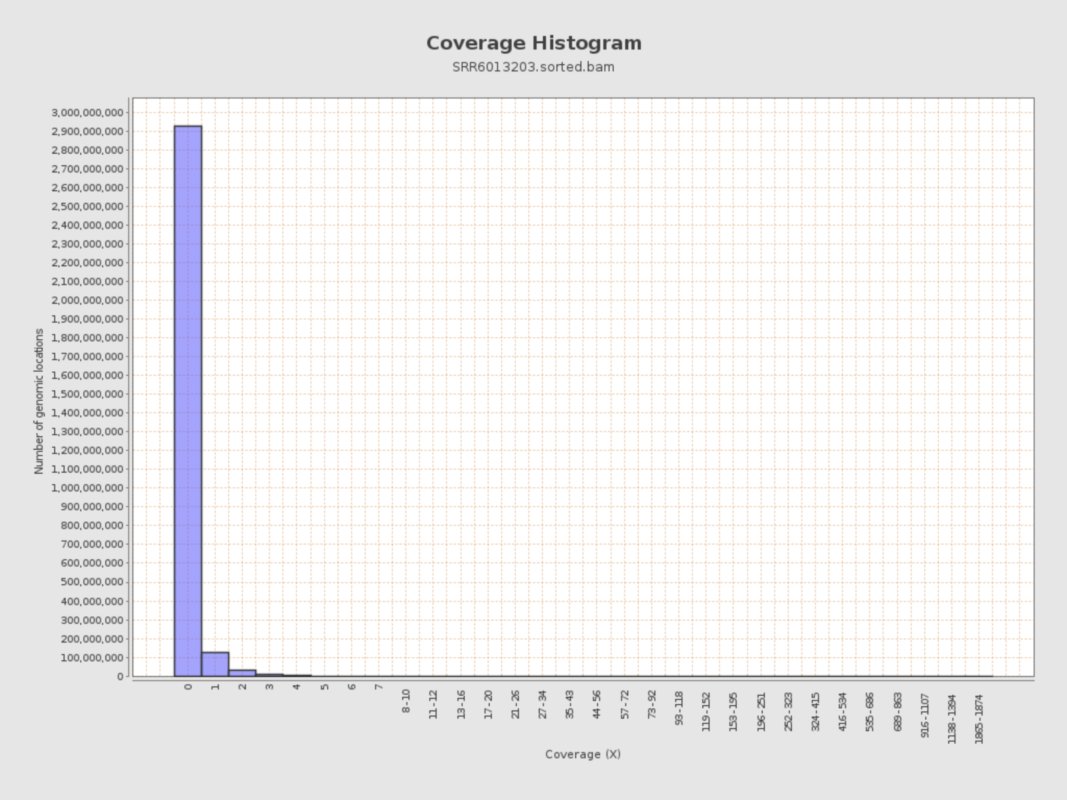
3. Results : Coverage across reference



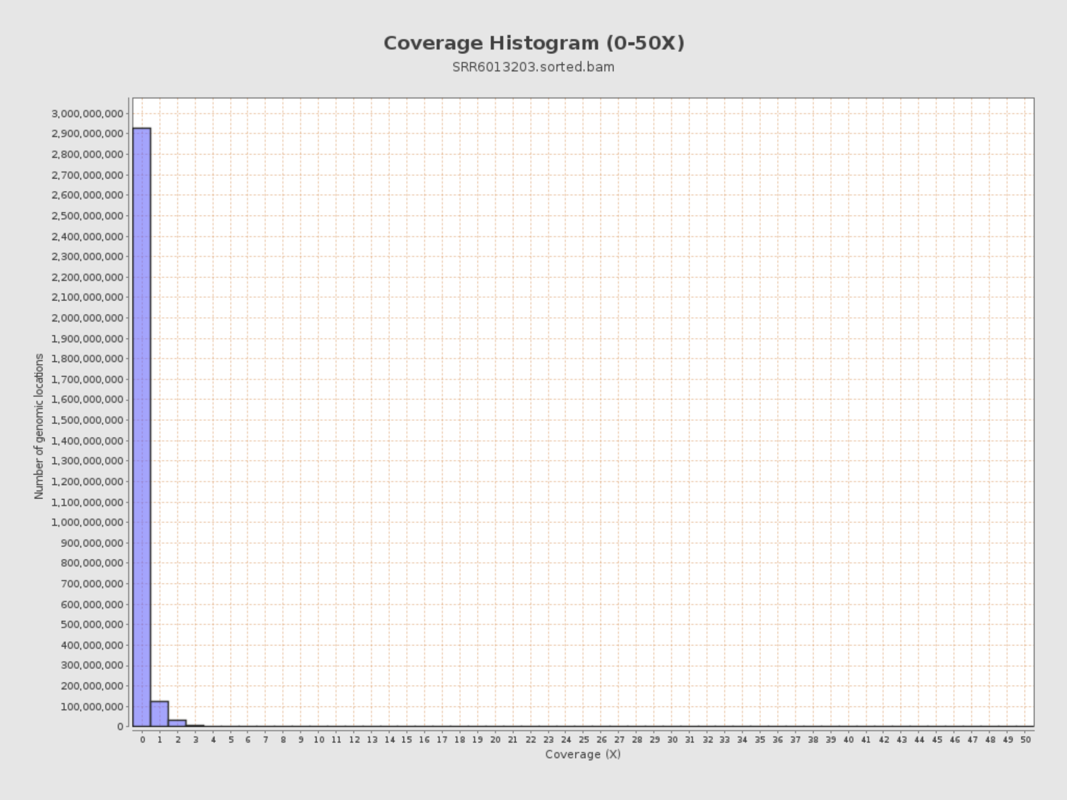
Coverage across reference

SRR6013203.sorted.bam

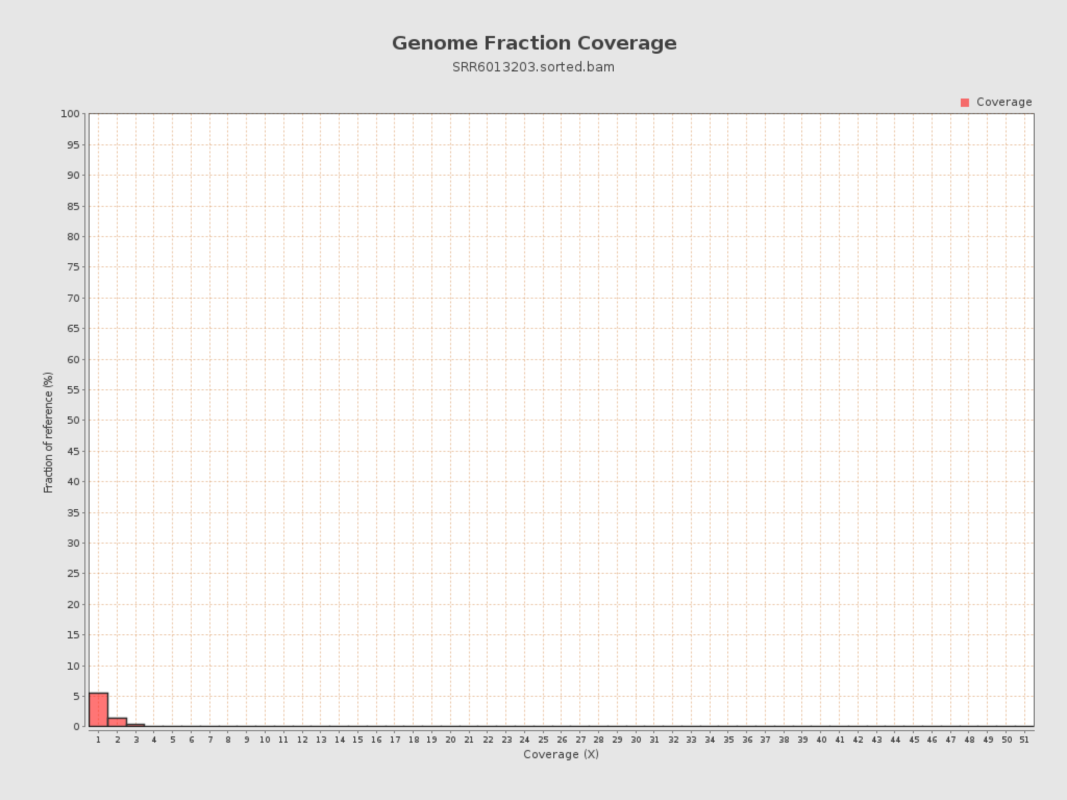
4. Results : Coverage Histogram



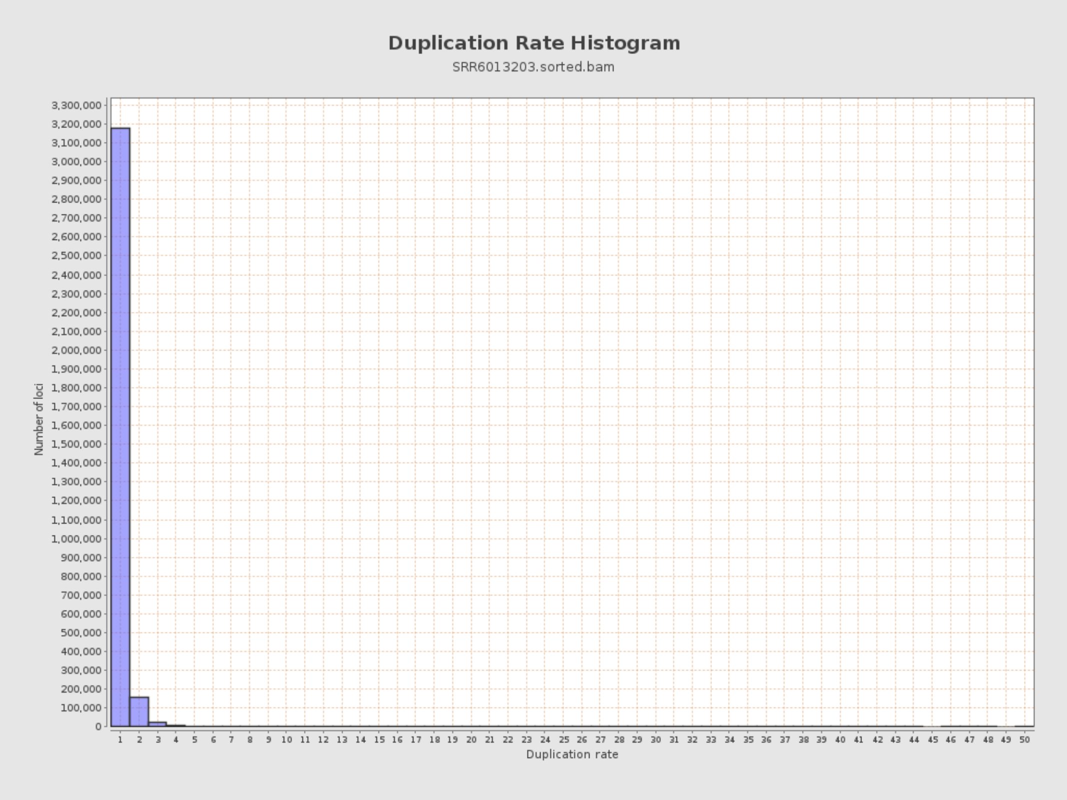
5. Results : Coverage Histogram (0-50X)



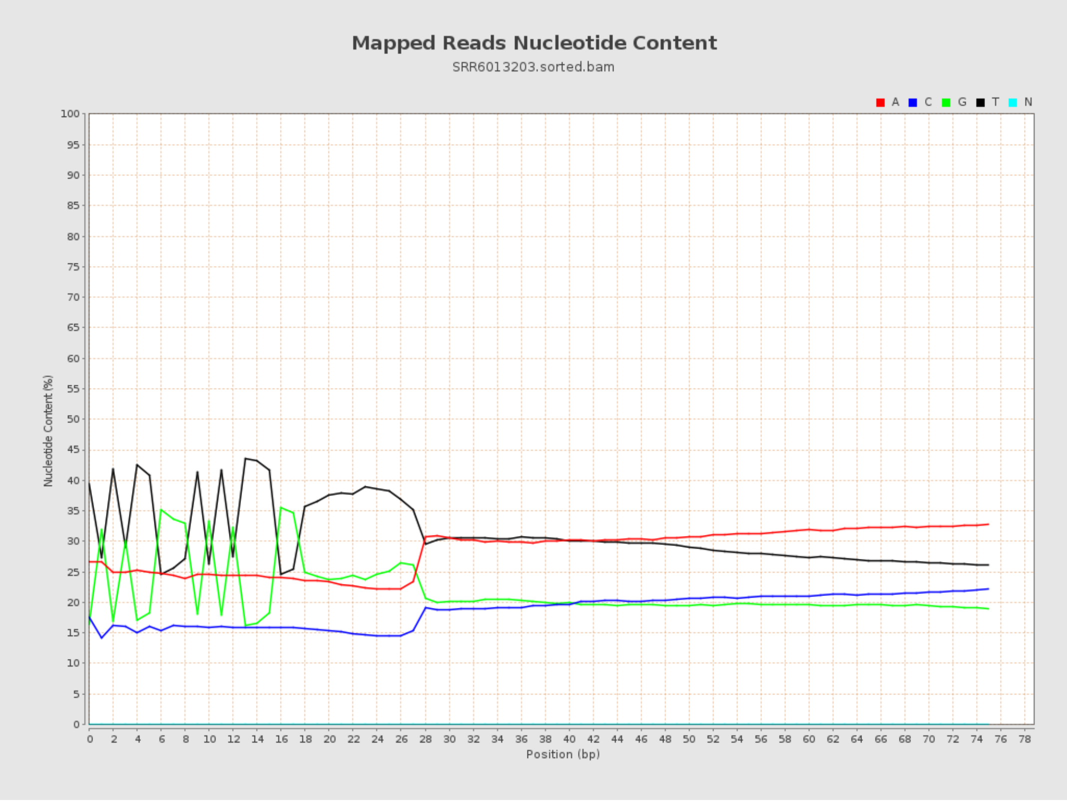
6. Results : Genome Fraction Coverage



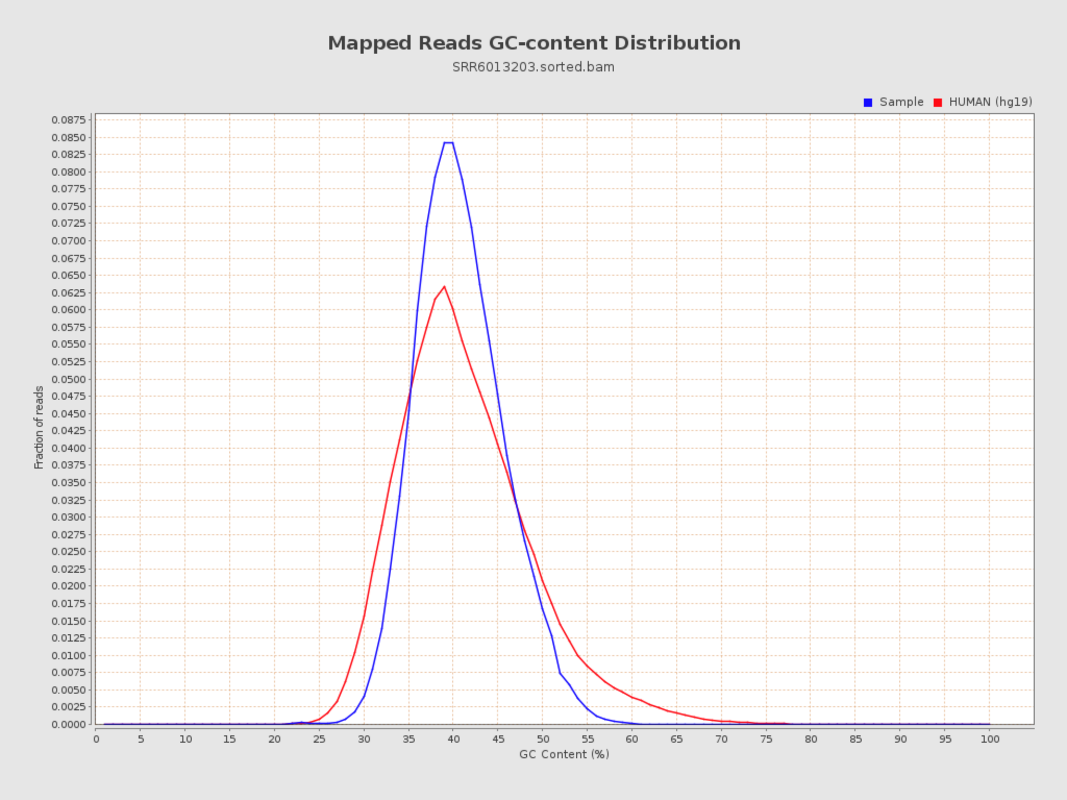
7. Results : Duplication Rate Histogram



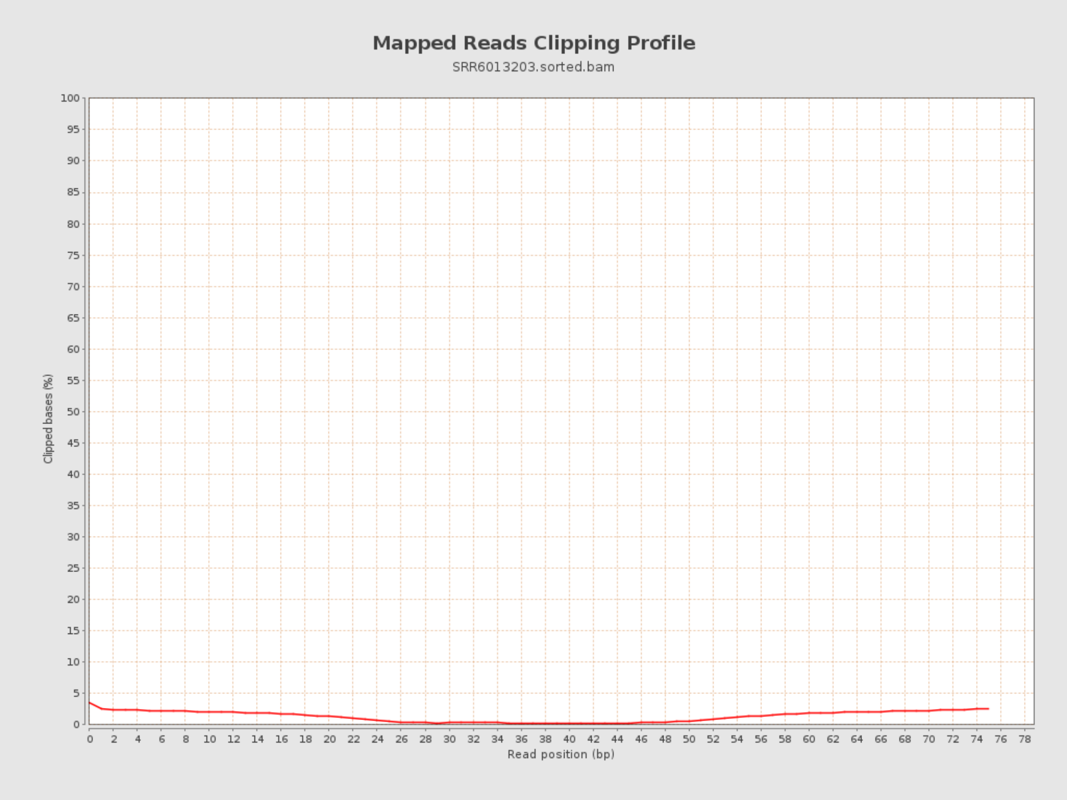
8. Results : Mapped Reads Nucleotide Content



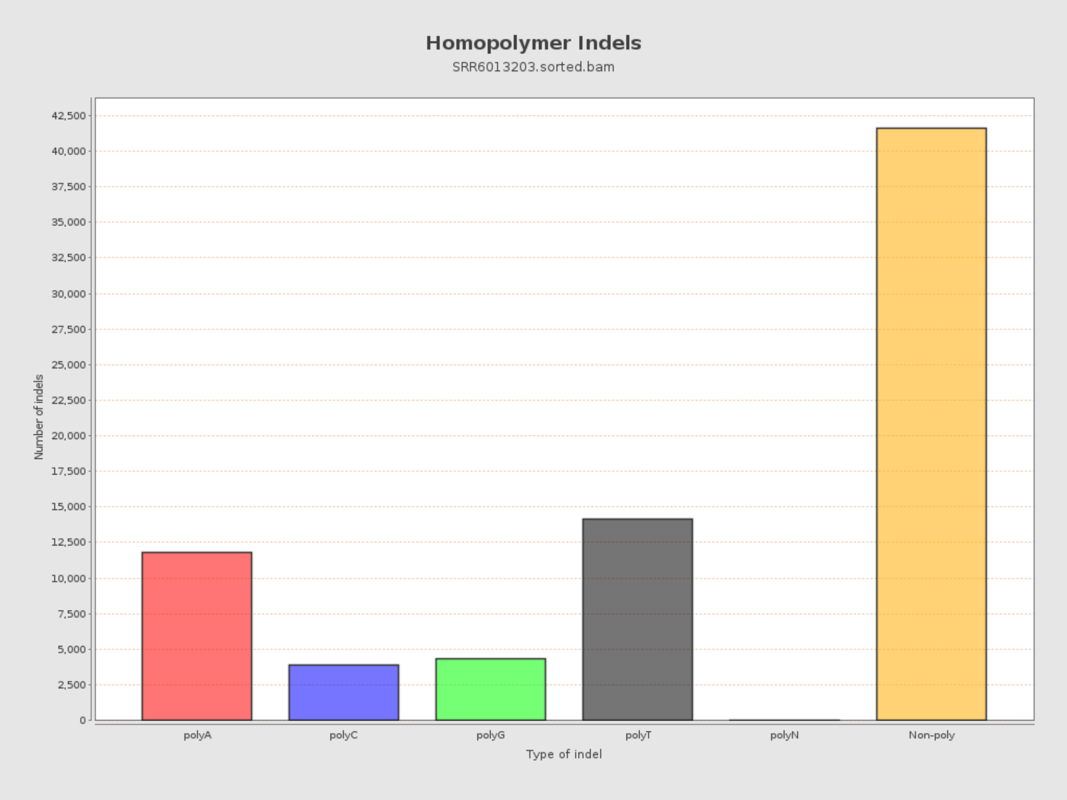
9. Results : Mapped Reads GC-content Distribution



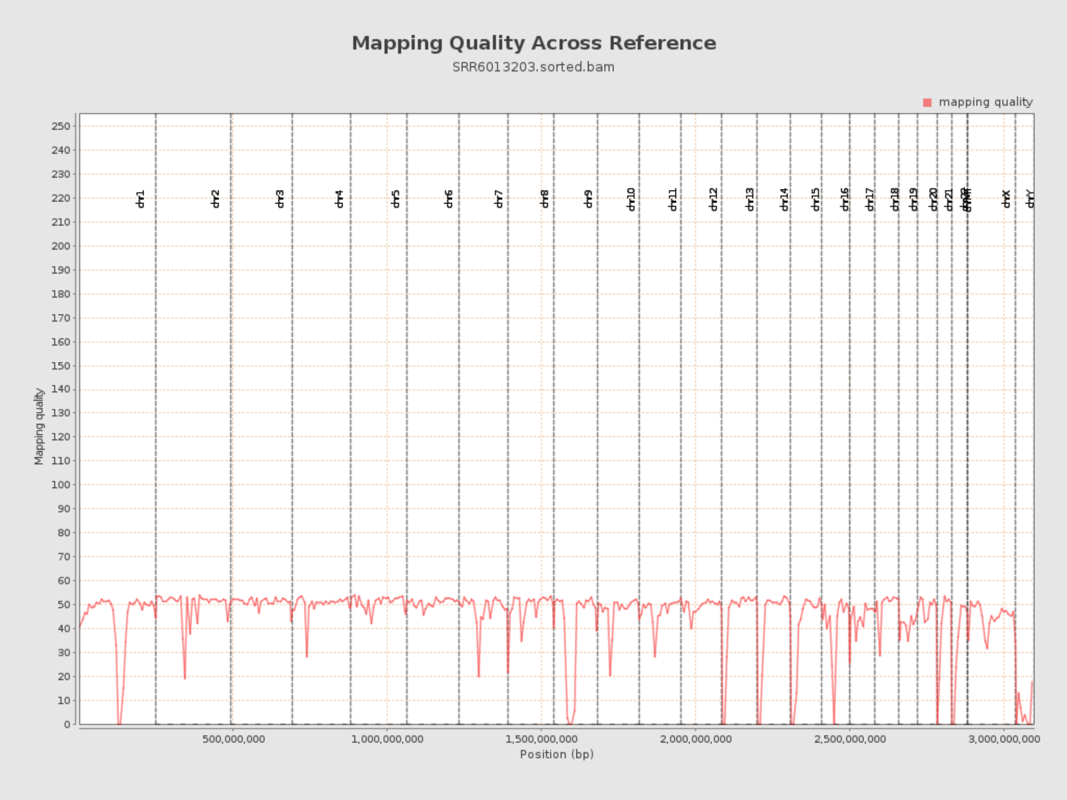
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram