Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:34:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013200.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_SRR6013200 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013200.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:34:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013200.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,697,985
Mapped reads	1,272,816 / 74.96%
Unmapped reads	425,169 / 25.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,140 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	93,462 / 5.5%
Duplication rate	5.86%
Clipped reads	643,402 / 37.89%

2.2. ACGT Content

Number/percentage of A's	22,381,261 / 27.04%
Number/percentage of C's	14,907,473 / 18.01%
Number/percentage of T's	26,763,639 / 32.34%
Number/percentage of G's	18,704,824 / 22.6%
Number/percentage of N's	1,166 / 0%
GC Percentage	40.61%

2.3. Coverage

Mean	0.0267

Standard Deviation	0.3185

2.4. Mapping Quality

Mean Mapping Quality	45.29

2.5. Mismatches and indels

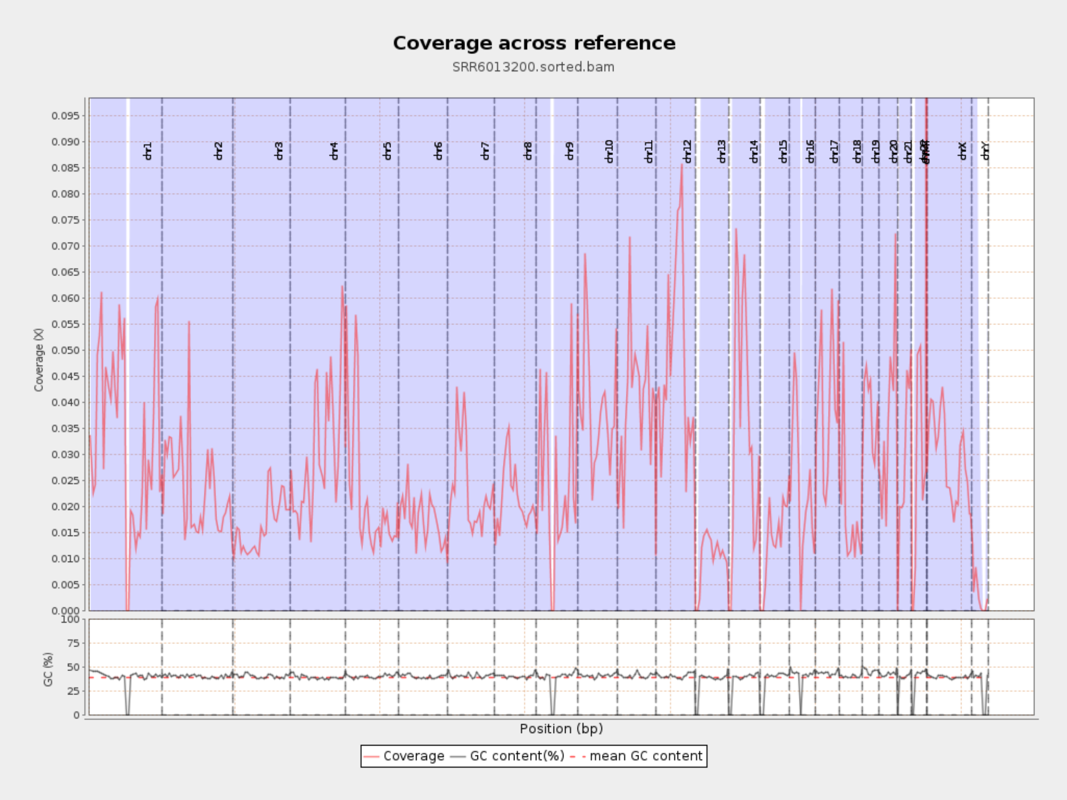
General error rate	0.79%
Mismatches	643,911
Insertions	5,855
Mapped reads with at least one insertion	0.46%
Deletions	23,177
Mapped reads with at least one deletion	1.8%
Homopolymer indels	46.73%

2.6. Chromosome stats

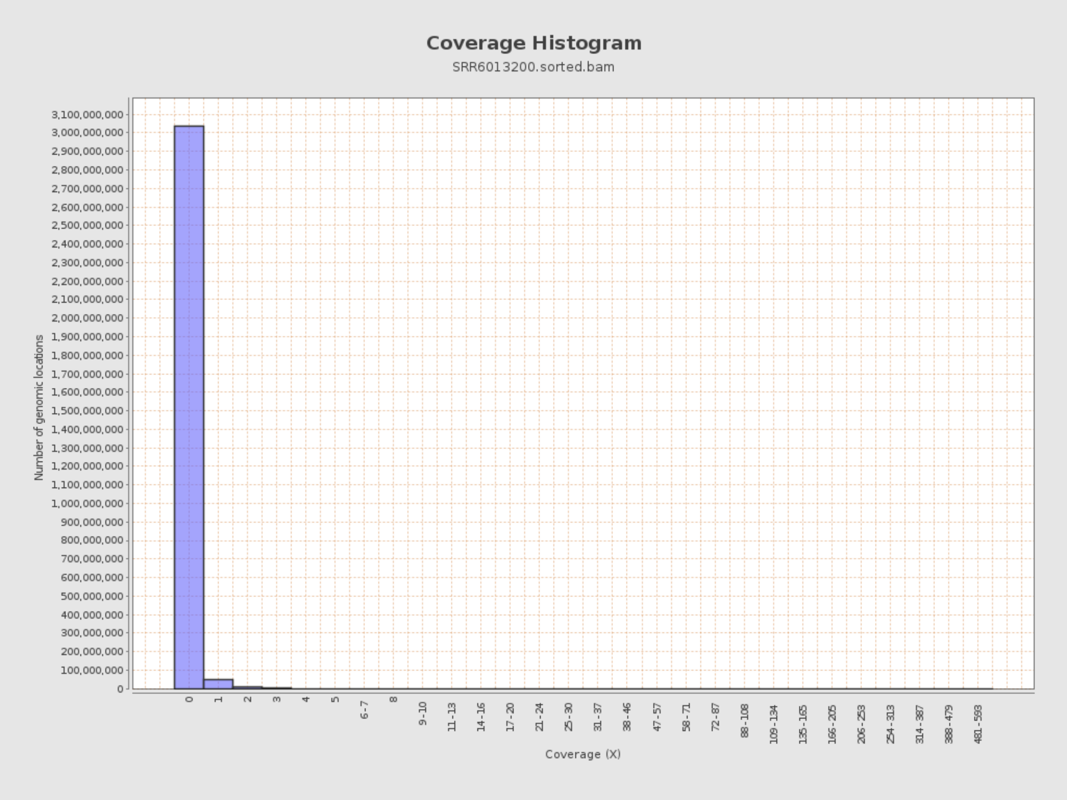
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8406455	0.0337	0.5344
chr2	243199373	5724699	0.0235	0.4339
chr3	198022430	3207611	0.0162	0.1632
chr4	191154276	5911359	0.0309	0.2302
chr5	180915260	4021373	0.0222	0.1963
chr6	171115067	2970697	0.0174	0.1889
chr7	159138663	3739526	0.0235	0.3078

chr8	146364022	3136663	0.0214	0.3092
chr9	141213431	3336830	0.0236	0.3377
chr10	135534747	5271139	0.0389	0.3236
chr11	135006516	5393858	0.04	0.3437
chr12	133851895	6548736	0.0489	0.2888
chr13	115169878	1155239	0.01	0.1308
chr14	107349540	3748245	0.0349	0.2506
chr15	102531392	1389583	0.0136	0.1512
chr16	90354753	2152124	0.0238	0.215
chr17	81195210	3205284	0.0395	0.2564
chr18	78077248	1440049	0.0184	0.6551
chr19	59128983	2271312	0.0384	0.3823
chr20	63025520	2337234	0.0371	0.2502
chr21	48129895	1401504	0.0291	0.2218
chr22	51304566	1252525	0.0244	0.201
chrMT	16571	13642	0.8232	1.3428
chrX	155270560	4567907	0.0294	0.257
chrY	59373566	194153	0.0033	0.0781

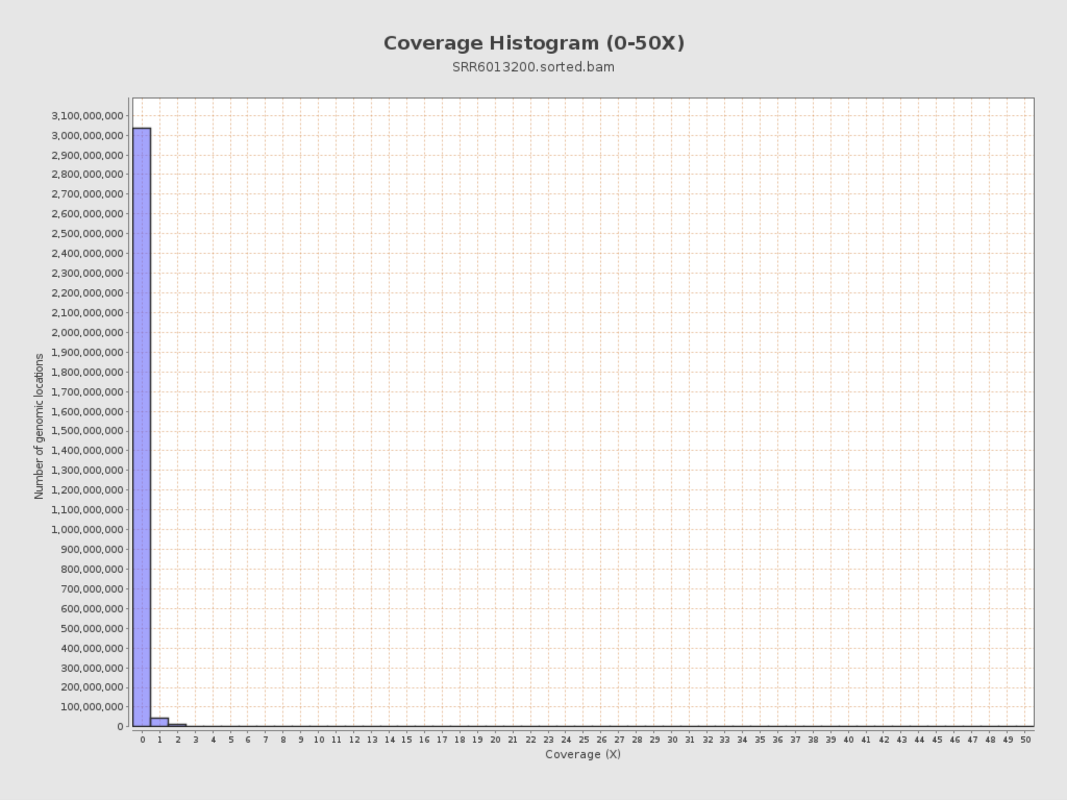
3. Results : Coverage across reference



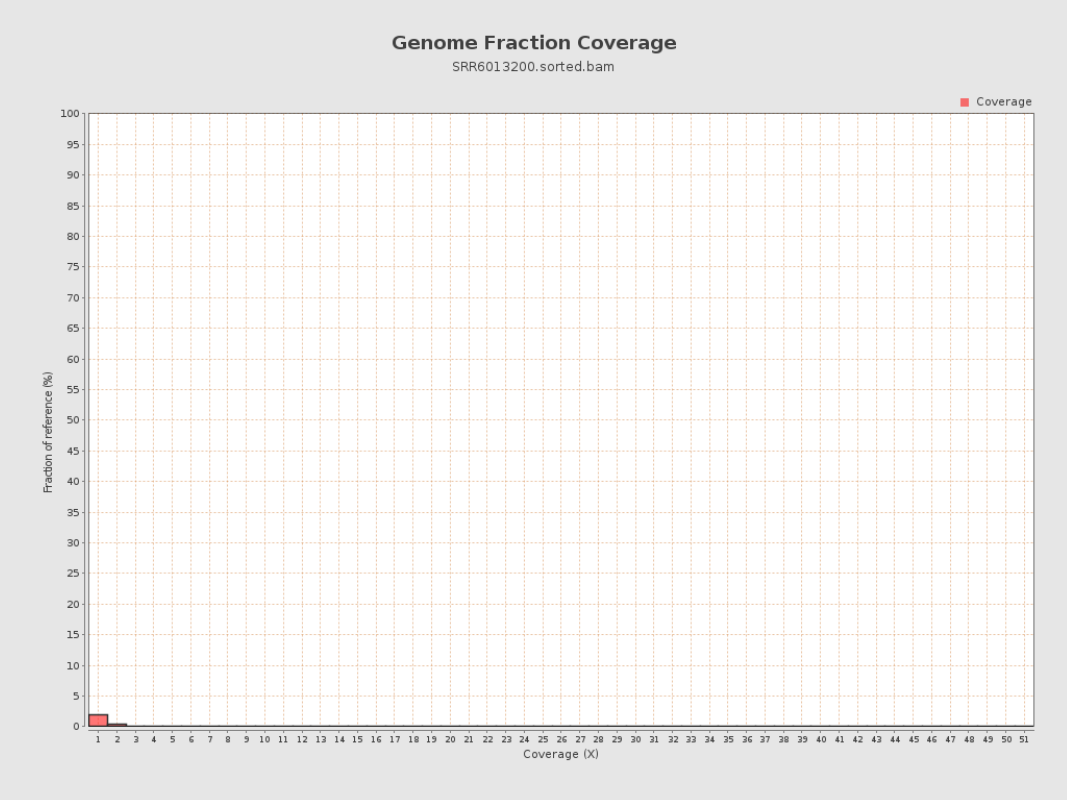
4. Results : Coverage Histogram



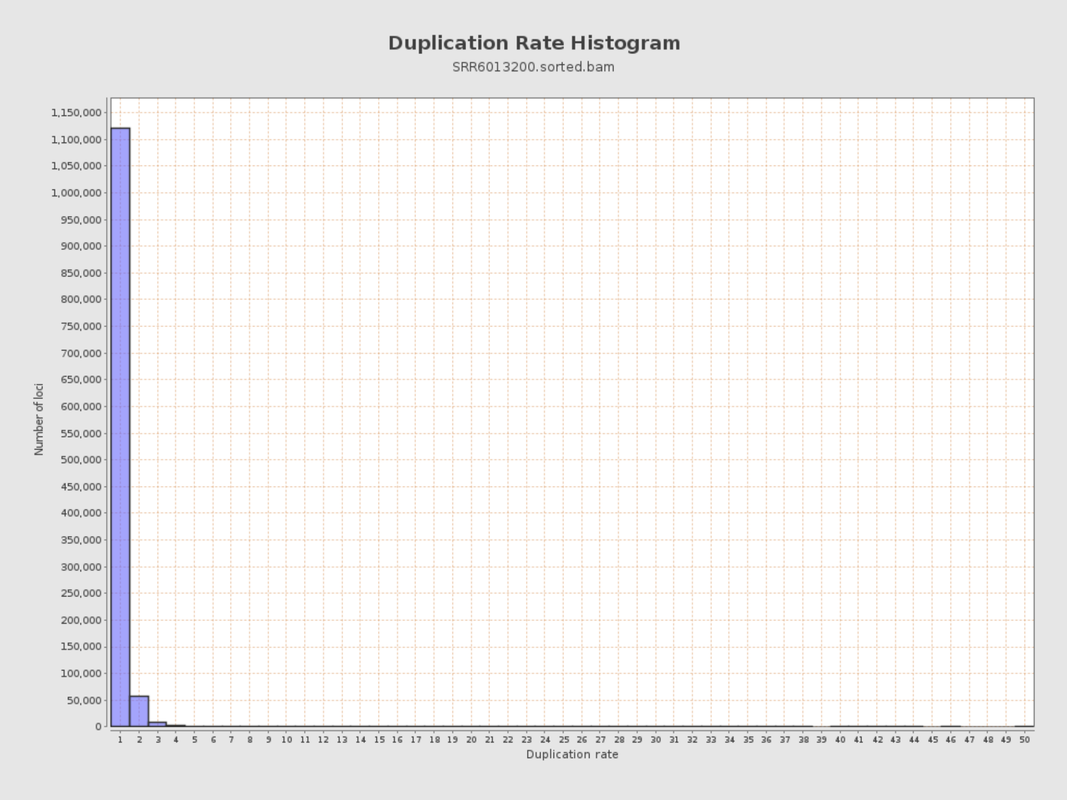
5. Results : Coverage Histogram (0-50X)



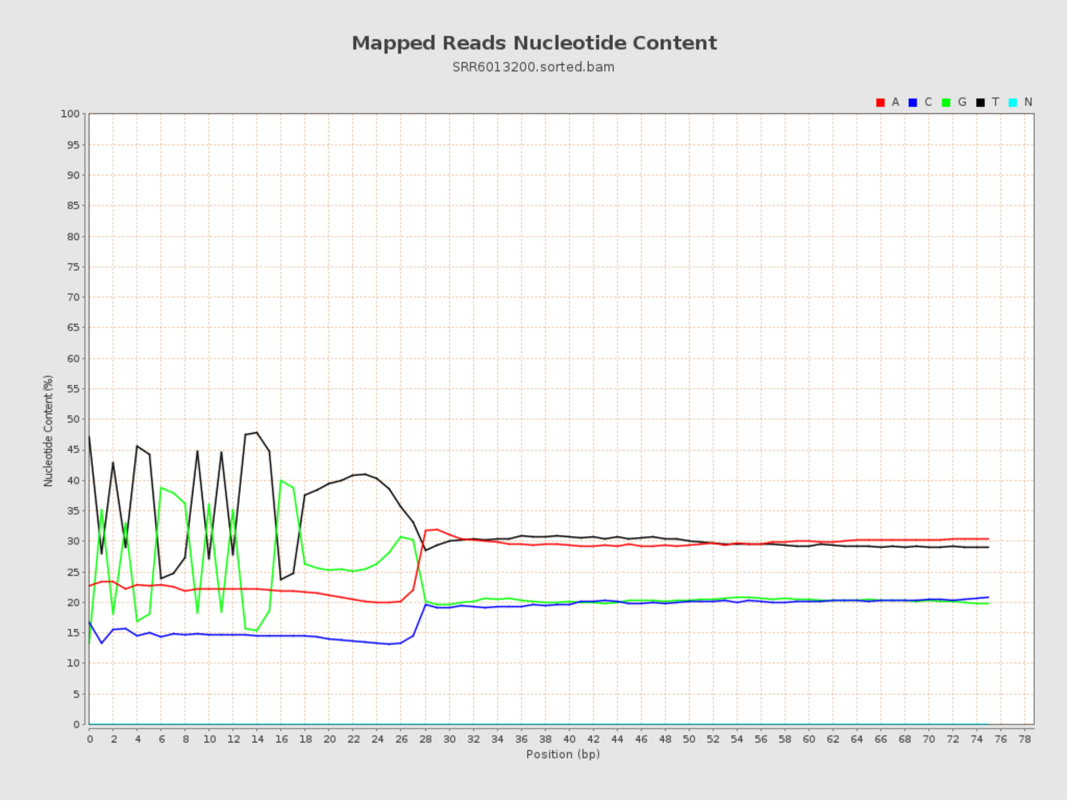
6. Results : Genome Fraction Coverage



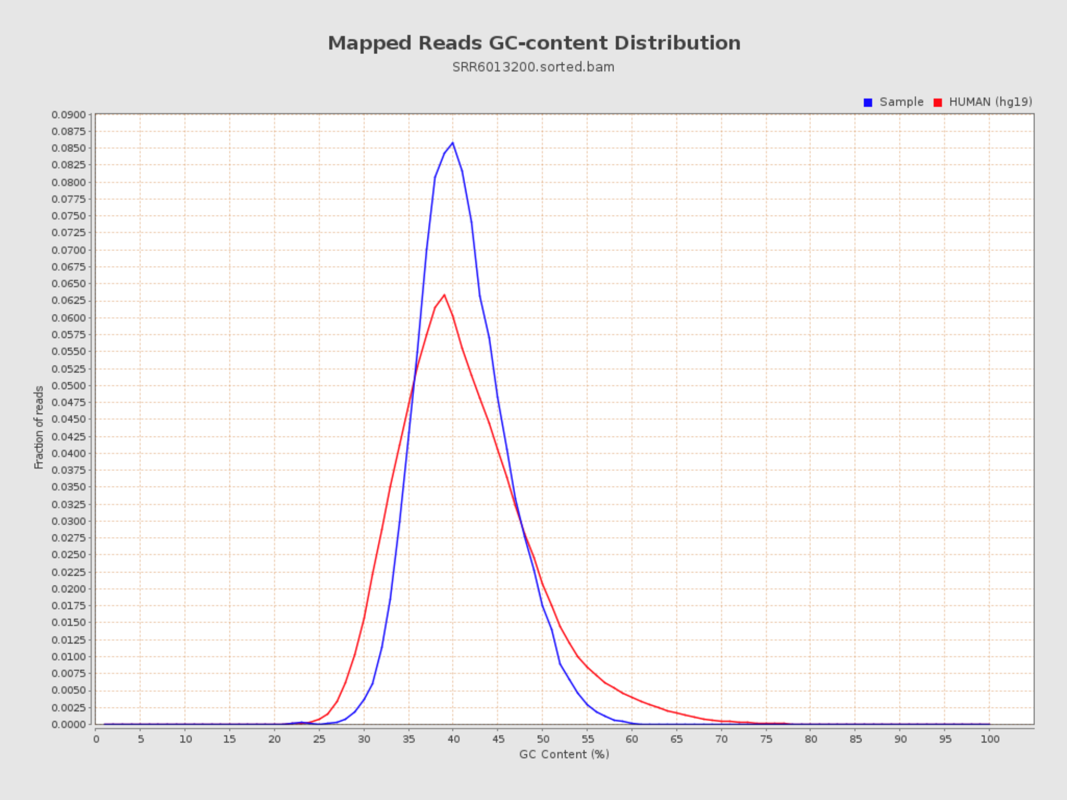
7. Results : Duplication Rate Histogram



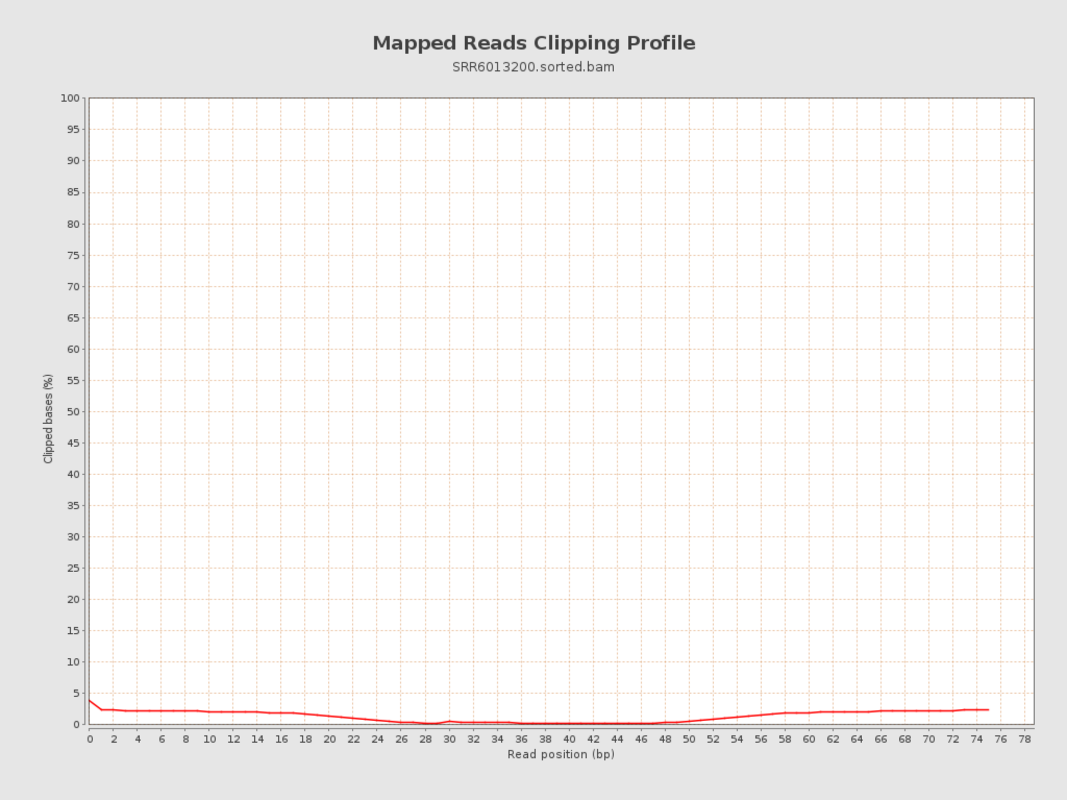
8. Results : Mapped Reads Nucleotide Content



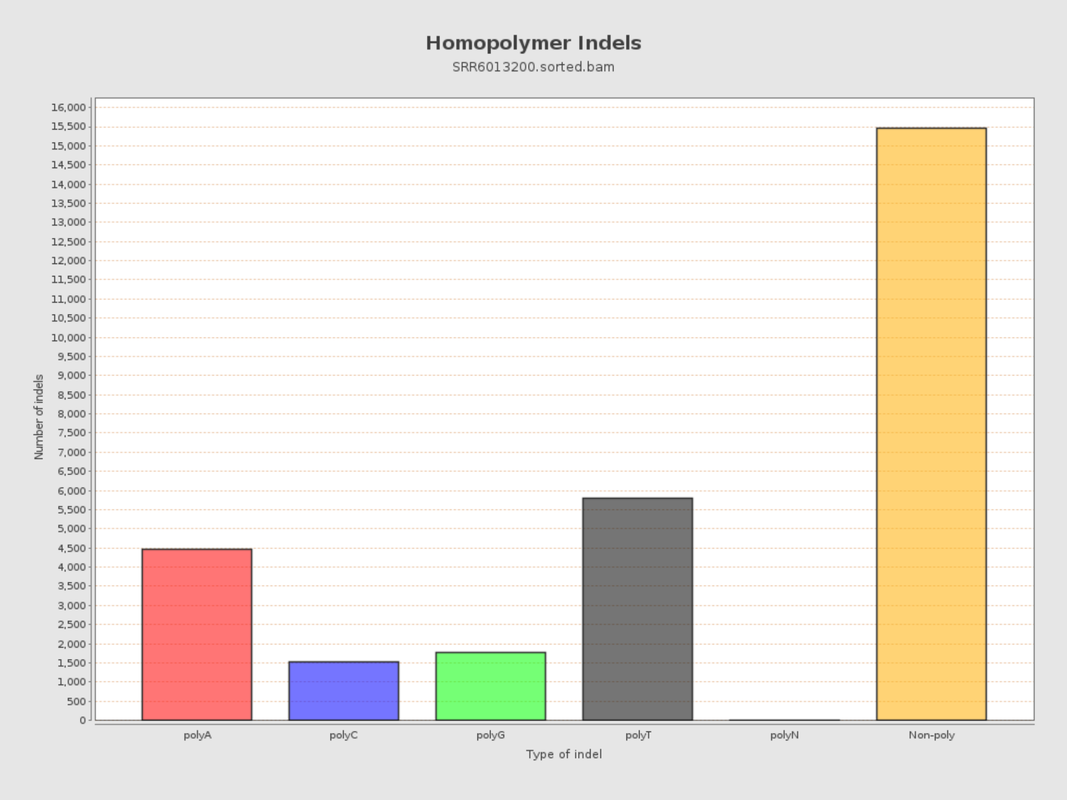
9. Results : Mapped Reads GC-content Distribution



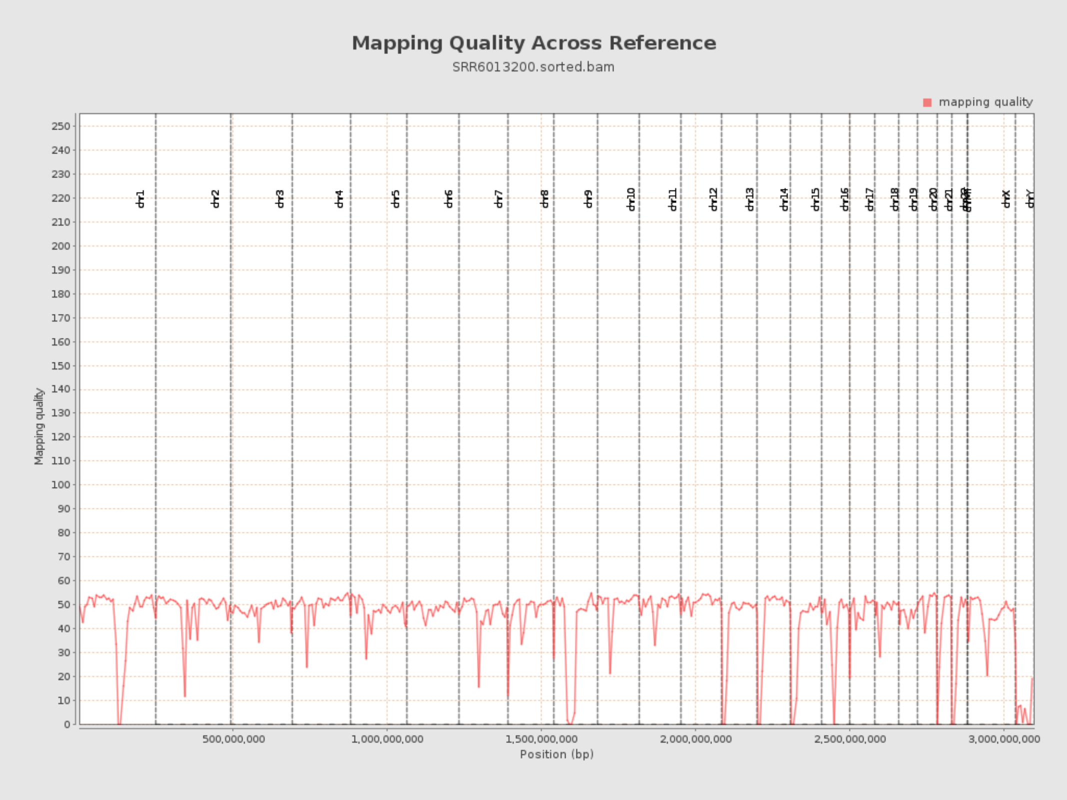
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram