Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:58:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013291.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_SRR6013291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013291.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:58:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,505,137
Mapped reads	2,241,431 / 89.47%
Unmapped reads	263,706 / 10.53%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,564 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	103,790 / 4.14%
Duplication rate	3.51%
Clipped reads	959,485 / 38.3%

2.2. ACGT Content

Number/percentage of A's	42,119,944 / 28.09%
Number/percentage of C's	27,186,116 / 18.13%
Number/percentage of T's	48,050,460 / 32.05%
Number/percentage of G's	32,565,888 / 21.72%
Number/percentage of N's	2,268 / 0%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0485

Standard Deviation	0.4367

2.4. Mapping Quality

Mean Mapping Quality	46.33

2.5. Mismatches and indels

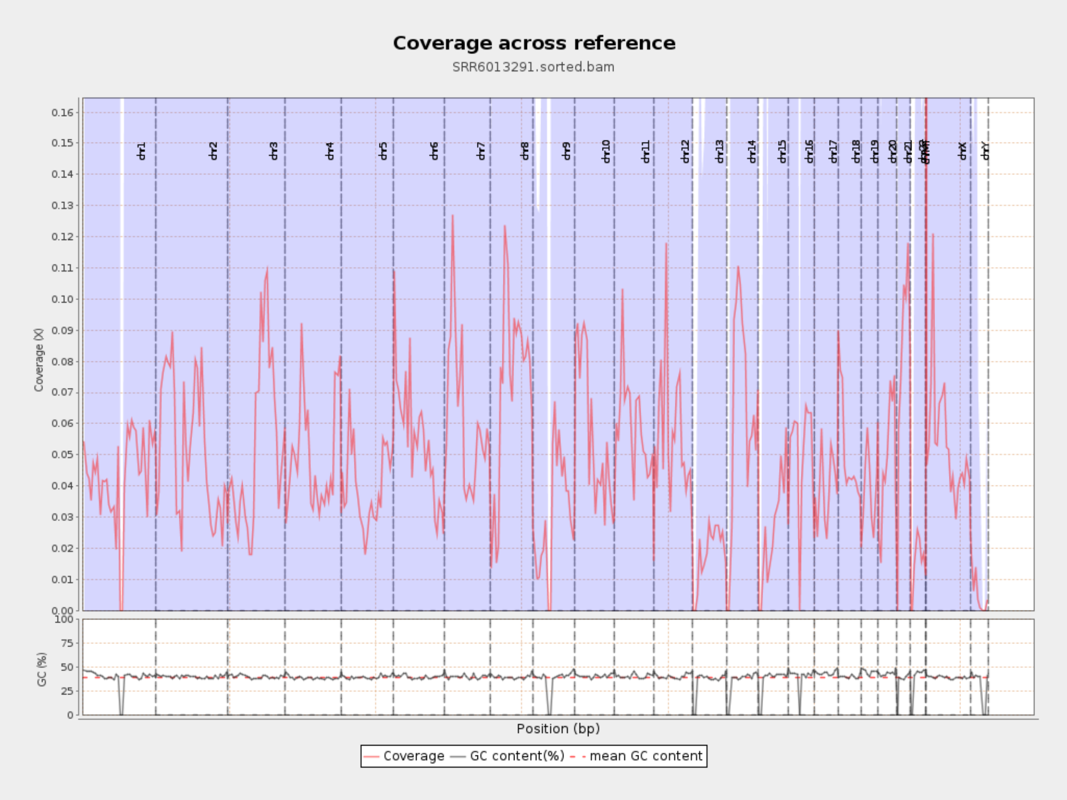
General error rate	0.75%
Mismatches	1,102,881
Insertions	10,589
Mapped reads with at least one insertion	0.47%
Deletions	41,358
Mapped reads with at least one deletion	1.82%
Homopolymer indels	47.08%

2.6. Chromosome stats

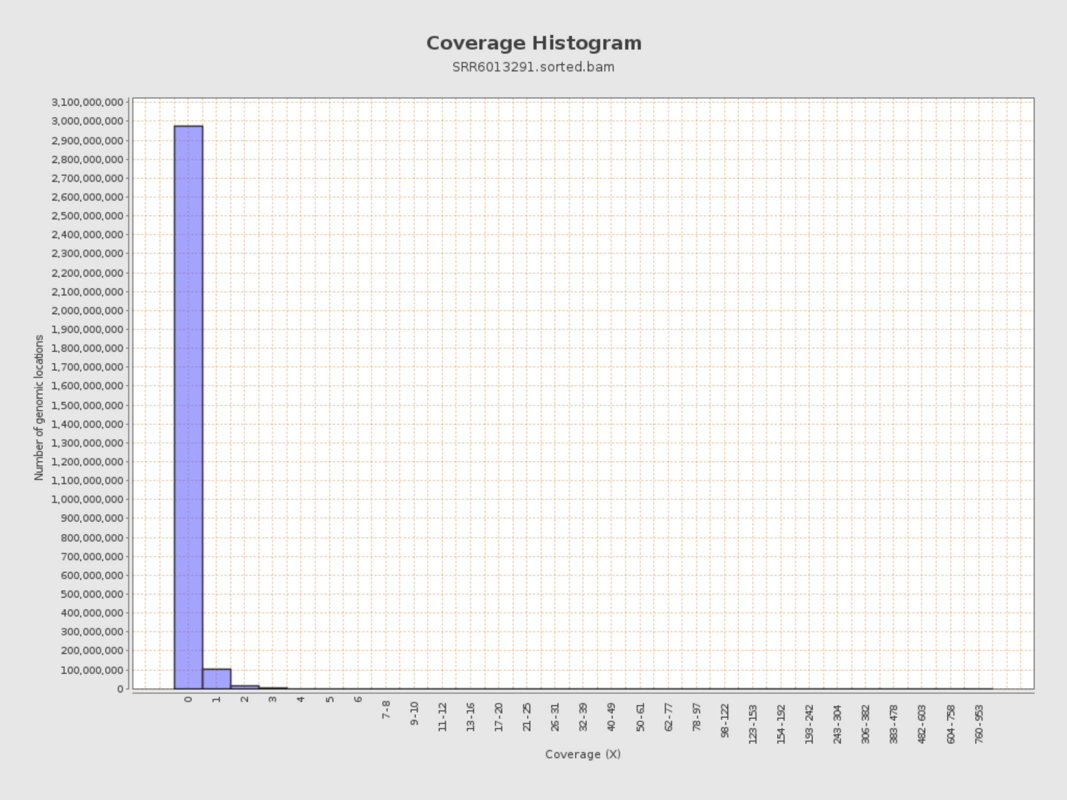
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10697262	0.0429	0.7082
chr2	243199373	12667729	0.0521	0.5171
chr3	198022430	10453050	0.0528	0.2698
chr4	191154276	9485736	0.0496	0.2789
chr5	180915260	7292714	0.0403	0.241
chr6	171115067	9431048	0.0551	0.4221
chr7	159138663	9734143	0.0612	0.6413

chr8	146364022	10574132	0.0722	0.6658
chr9	141213431	4336277	0.0307	0.3727
chr10	135534747	7788210	0.0575	0.4163
chr11	135006516	7949974	0.0589	0.4529
chr12	133851895	7514535	0.0561	0.2847
chr13	115169878	2124091	0.0184	0.1589
chr14	107349540	6841320	0.0637	0.3095
chr15	102531392	2669961	0.026	0.2019
chr16	90354753	4469624	0.0495	0.2762
chr17	81195210	3184165	0.0392	0.283
chr18	78077248	3945996	0.0505	0.7414
chr19	59128983	2351420	0.0398	0.5003
chr20	63025520	3091150	0.049	0.2746
chr21	48129895	3939148	0.0818	0.3546
chr22	51304566	780632	0.0152	0.1391
chrMT	16571	33818	2.0408	2.0365
chrX	155270560	8332753	0.0537	0.3237
chrY	59373566	307058	0.0052	0.1161

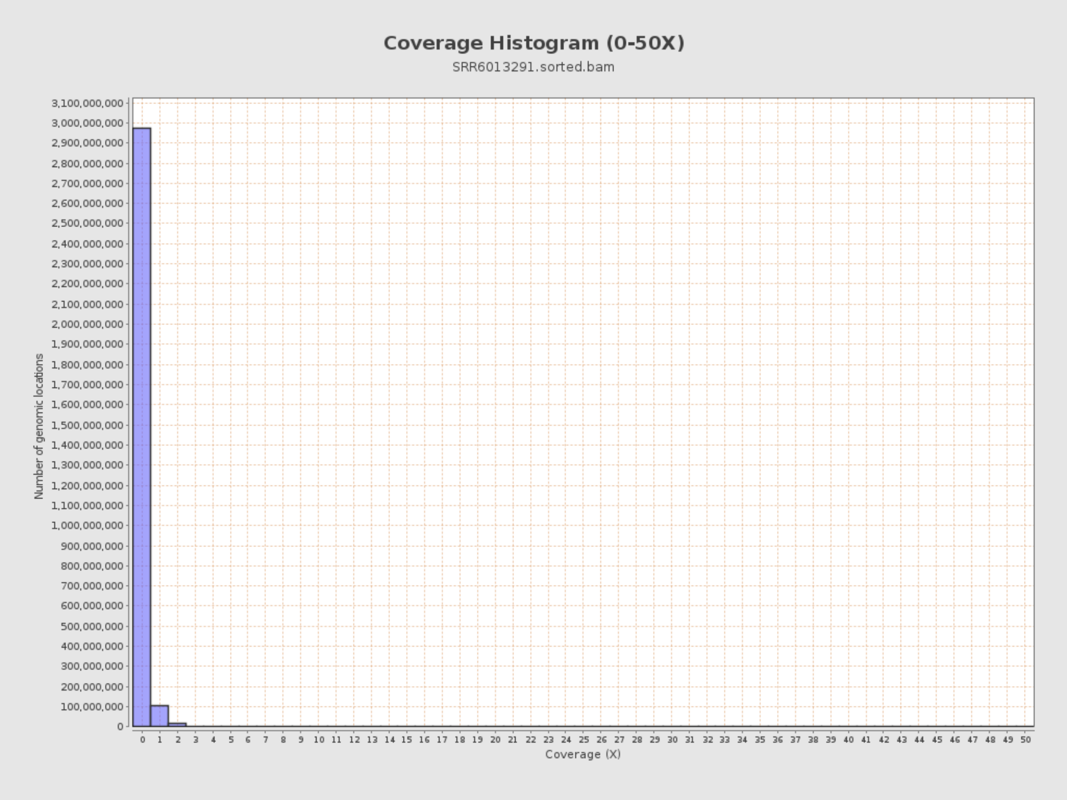
3. Results : Coverage across reference



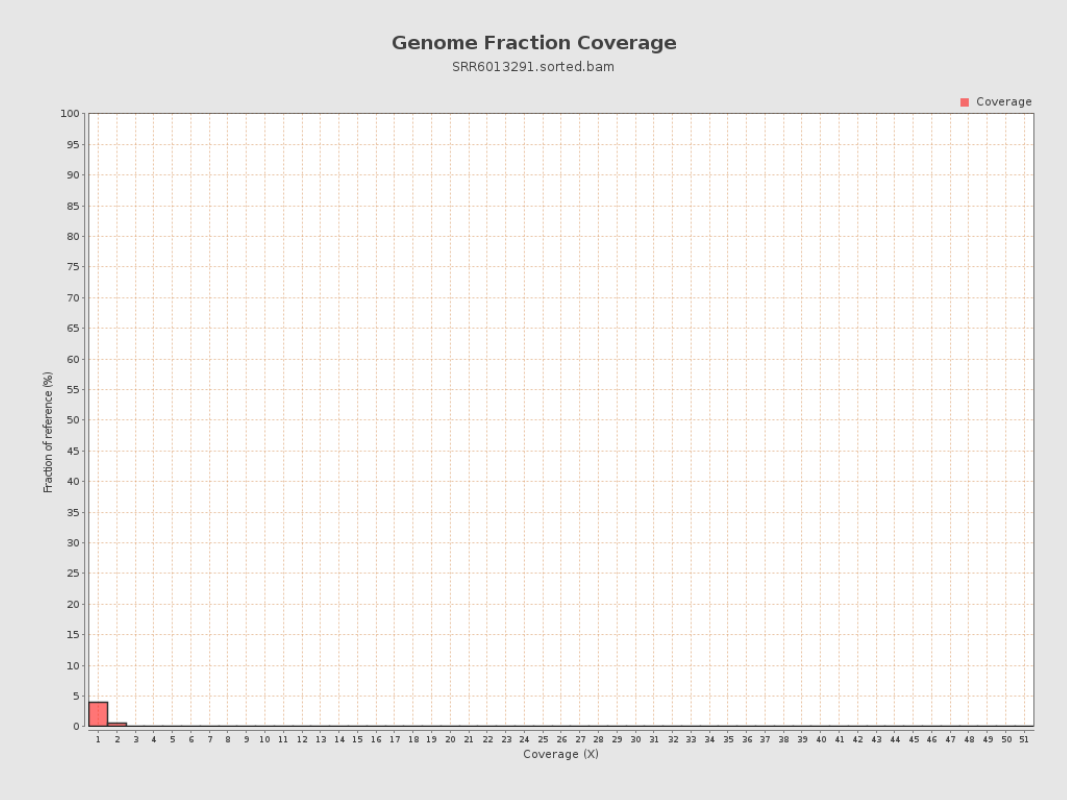
4. Results : Coverage Histogram



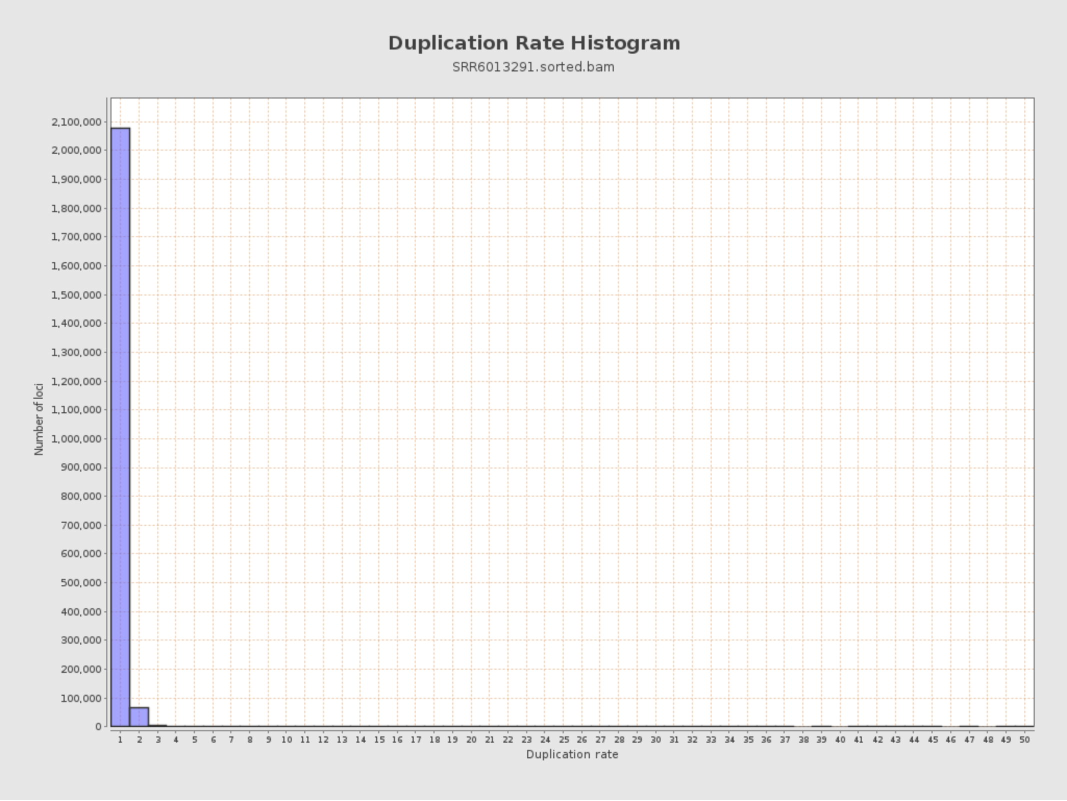
5. Results : Coverage Histogram (0-50X)



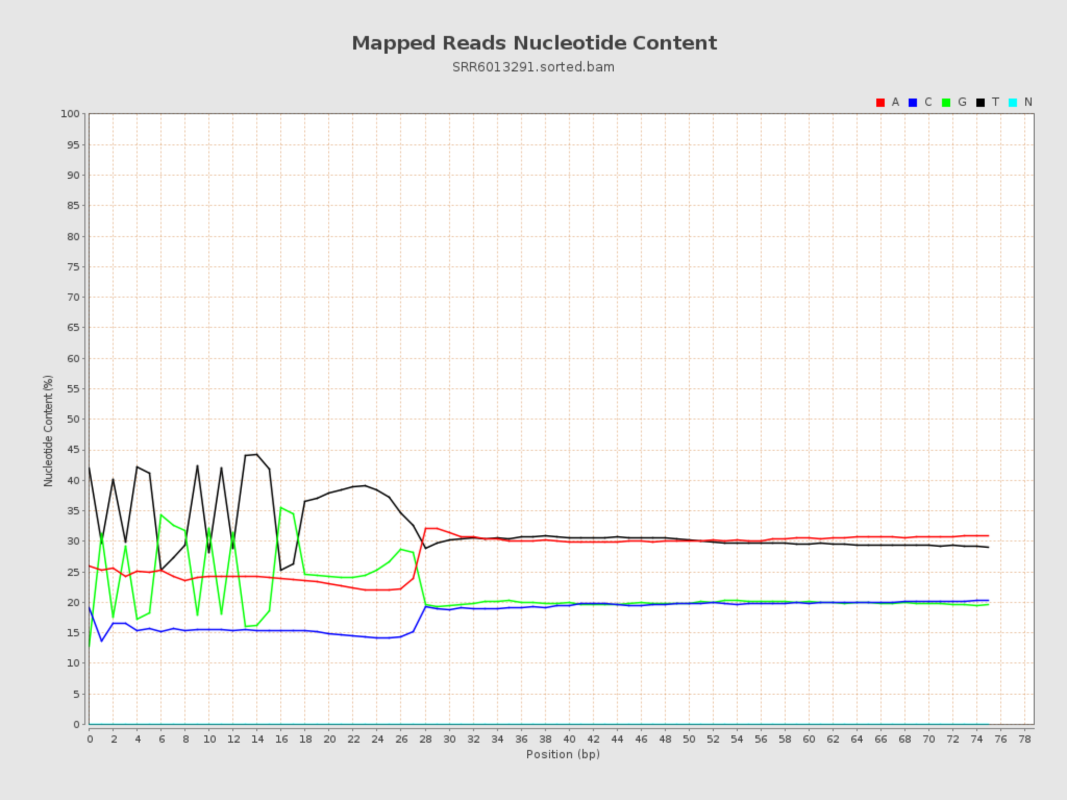
6. Results : Genome Fraction Coverage



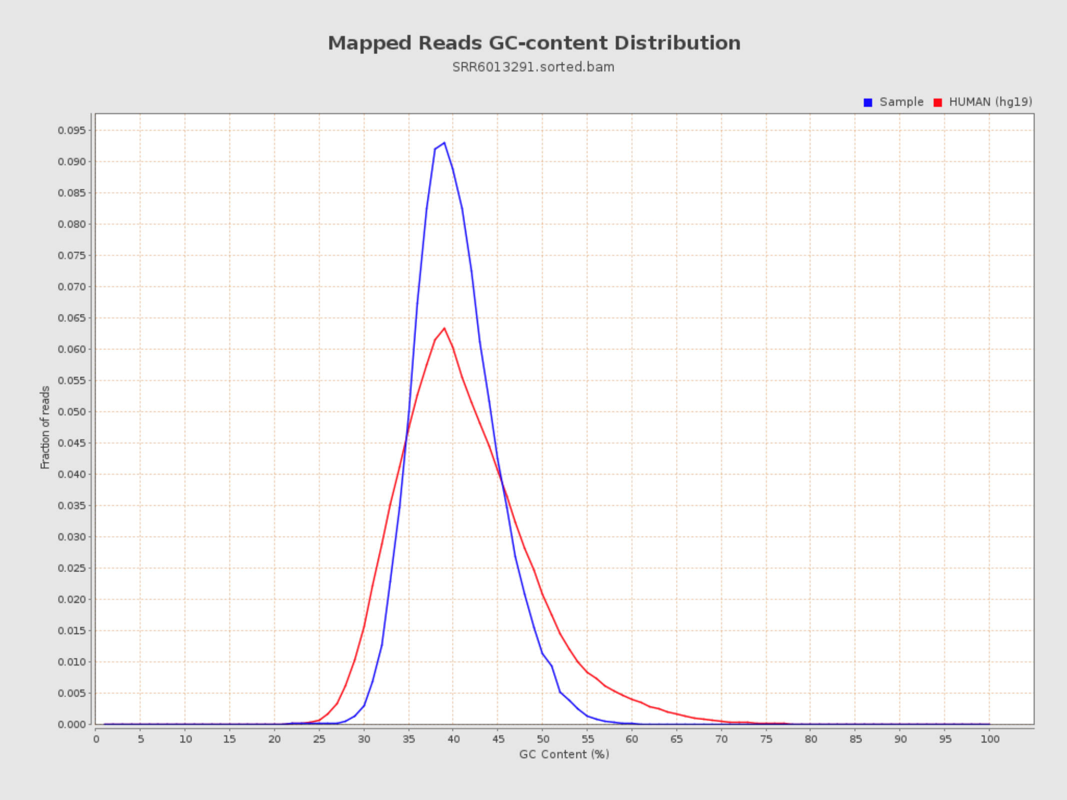
7. Results : Duplication Rate Histogram



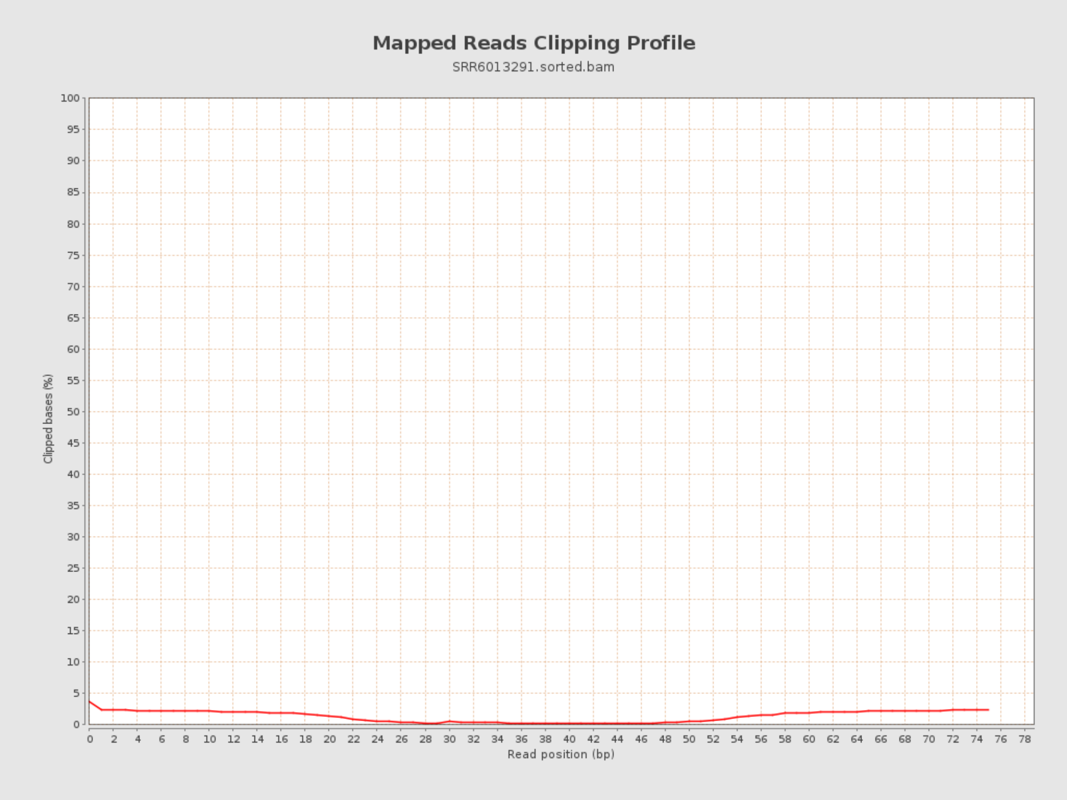
8. Results : Mapped Reads Nucleotide Content



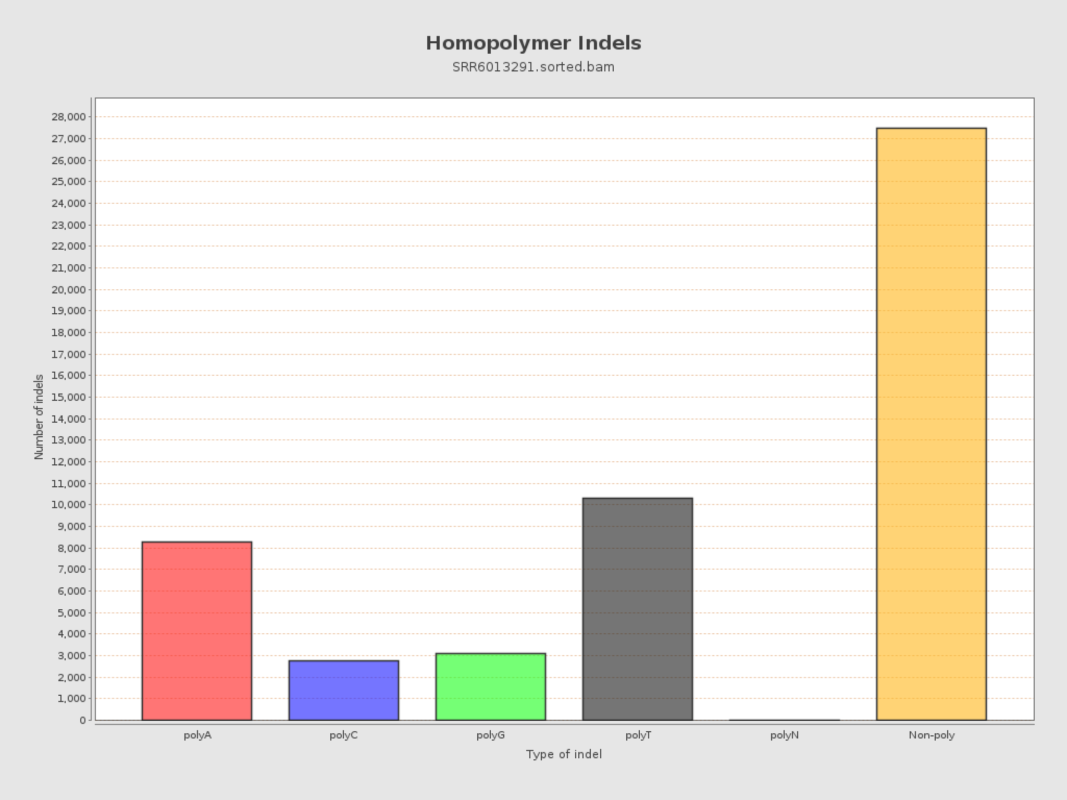
9. Results : Mapped Reads GC-content Distribution



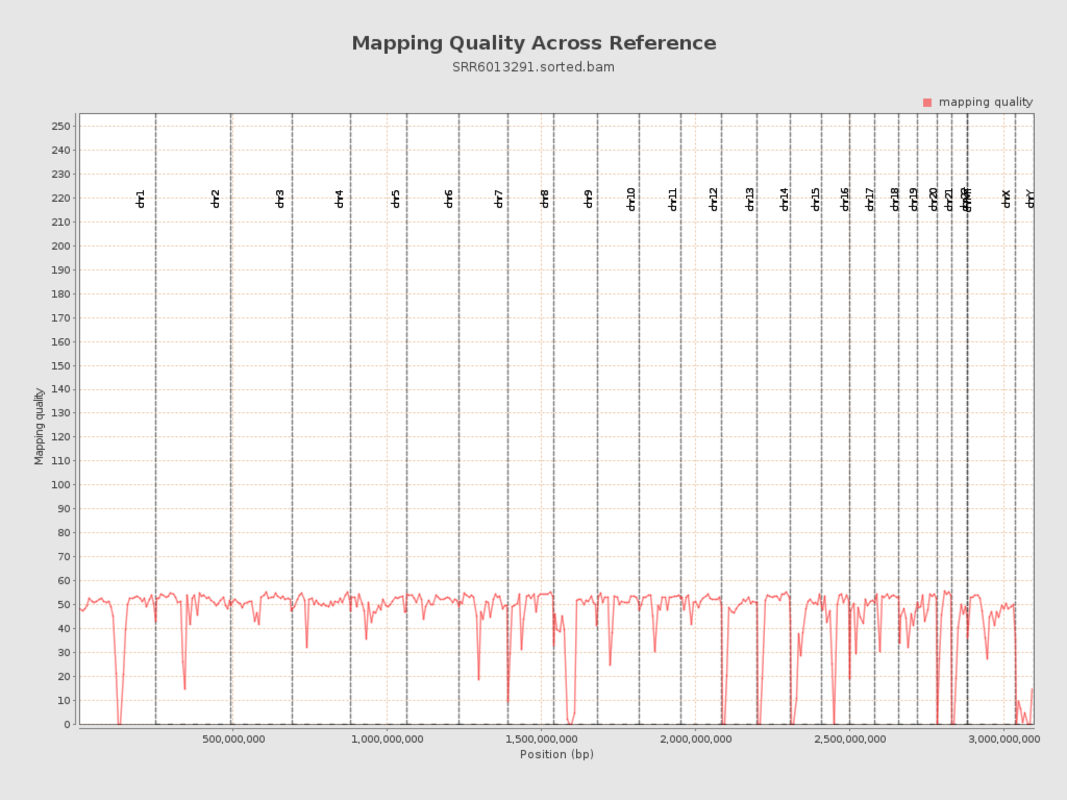
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram