Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:15:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013193.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_SRR6013193 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013193.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:15:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013193.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,749,502
Mapped reads	1,474,896 / 84.3%
Unmapped reads	274,606 / 15.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,521 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	102,880 / 5.88%
Duplication rate	5.6%
Clipped reads	770,642 / 44.05%

2.2. ACGT Content

Number/percentage of A's	25,690,693 / 26.92%
Number/percentage of C's	17,322,992 / 18.15%
Number/percentage of T's	30,702,233 / 32.17%
Number/percentage of G's	21,712,736 / 22.75%
Number/percentage of N's	1,223 / 0%
GC Percentage	40.91%

2.3. Coverage

Mean	0.0308

Standard Deviation	0.3265

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

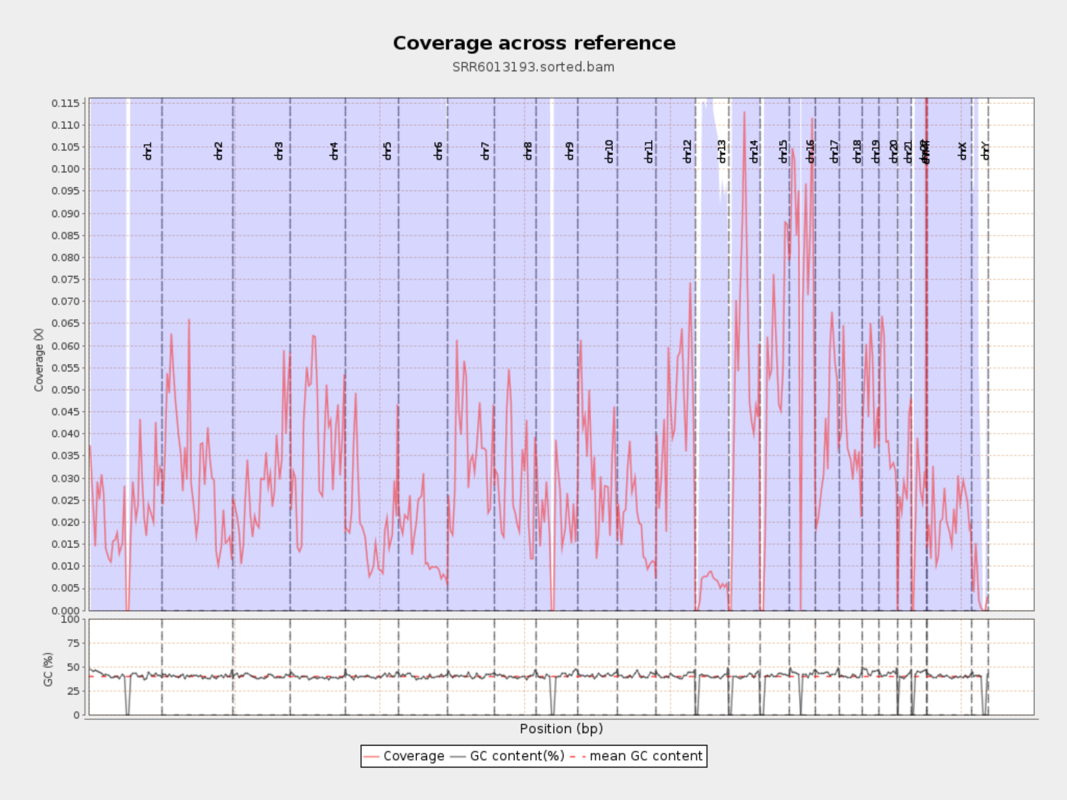
General error rate	0.81%
Mismatches	759,313
Insertions	7,024
Mapped reads with at least one insertion	0.47%
Deletions	28,473
Mapped reads with at least one deletion	1.91%
Homopolymer indels	45.68%

2.6. Chromosome stats

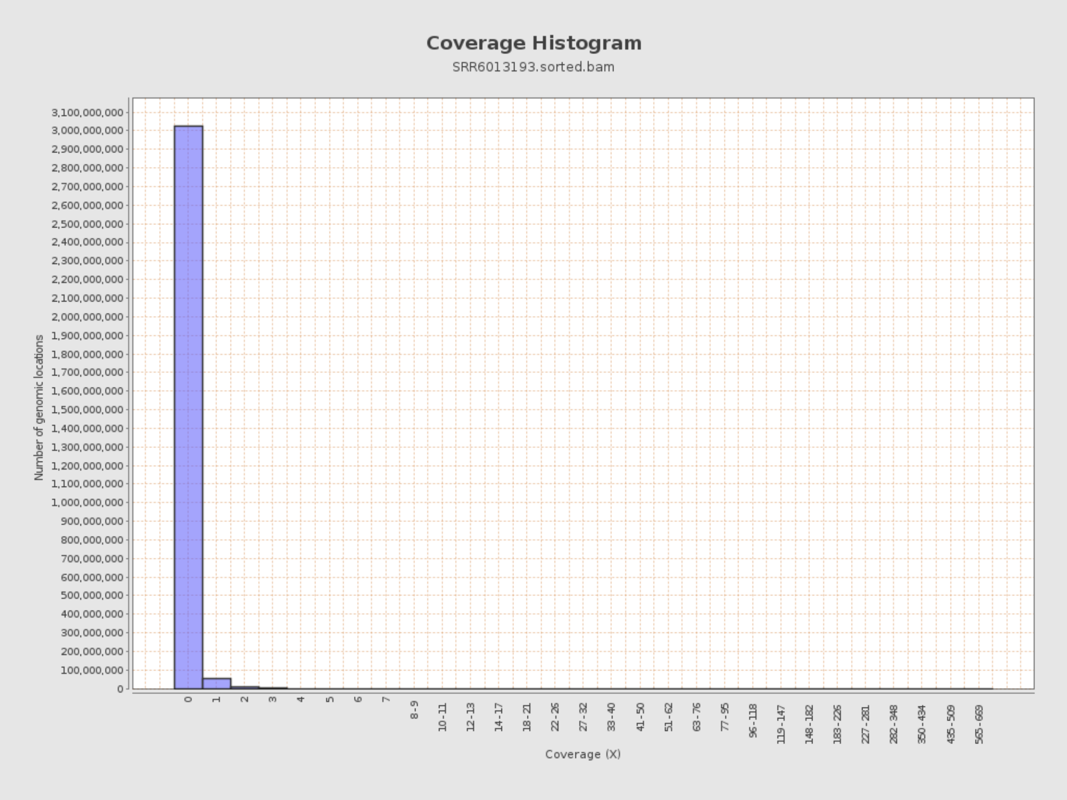
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5473234	0.022	0.4358
chr2	243199373	7754505	0.0319	0.4281
chr3	198022430	5639514	0.0285	0.2106
chr4	191154276	7429132	0.0389	0.2532
chr5	180915260	3483805	0.0193	0.1777
chr6	171115067	2697384	0.0158	0.1822
chr7	159138663	5770081	0.0363	0.4092

chr8	146364022	4190205	0.0286	0.4608
chr9	141213431	2867470	0.0203	0.348
chr10	135534747	4552692	0.0336	0.2988
chr11	135006516	2685598	0.0199	0.2359
chr12	133851895	6080018	0.0454	0.2728
chr13	115169878	671755	0.0058	0.0946
chr14	107349540	5700801	0.0531	0.2994
chr15	102531392	5250339	0.0512	0.2854
chr16	90354753	7196785	0.0797	0.3706
chr17	81195210	3312564	0.0408	0.259
chr18	78077248	2994773	0.0384	0.6337
chr19	59128983	2982801	0.0504	0.522
chr20	63025520	2732449	0.0434	0.2661
chr21	48129895	1377831	0.0286	0.2273
chr22	51304566	1143391	0.0223	0.185
chrMT	16571	12391	0.7478	1.1293
chrX	155270560	3251152	0.0209	0.2032
chrY	59373566	228880	0.0039	0.1416

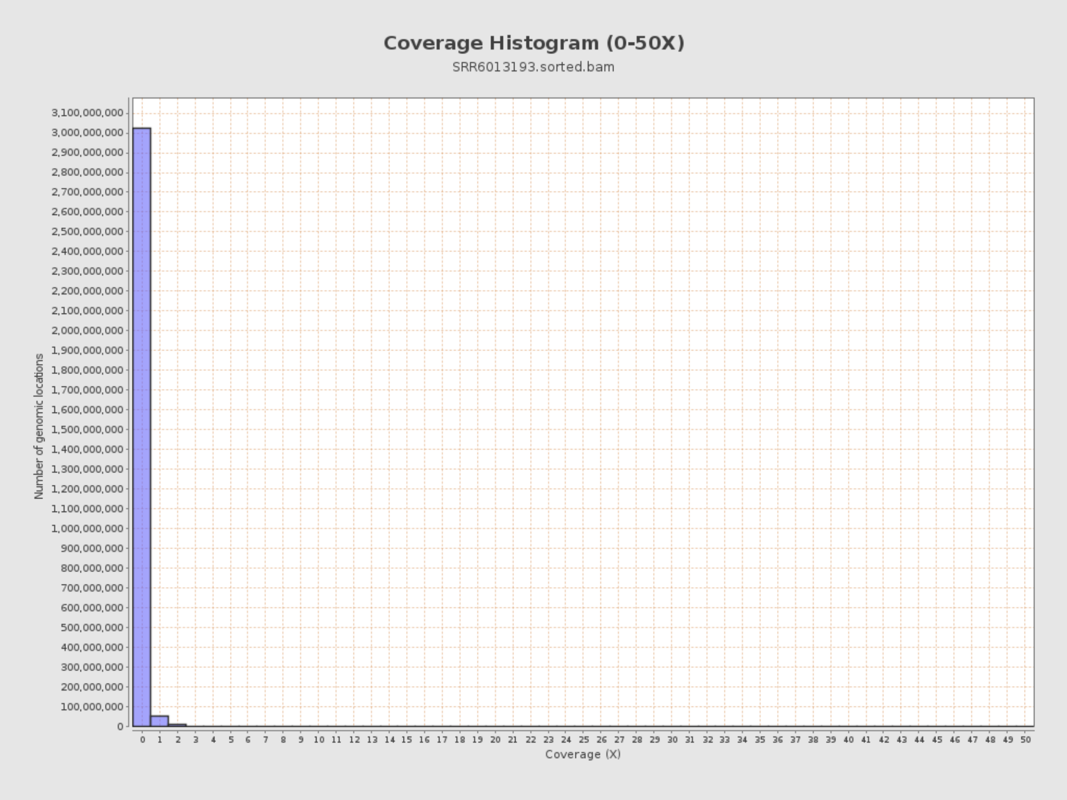
3. Results : Coverage across reference



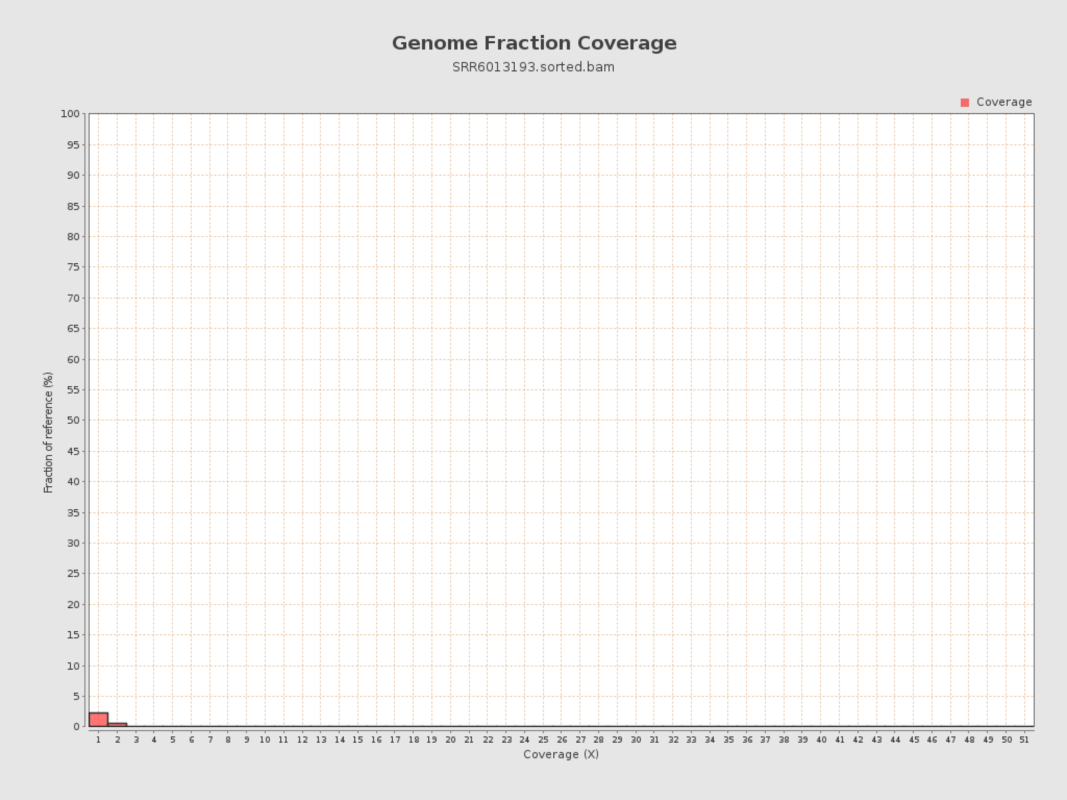
4. Results : Coverage Histogram



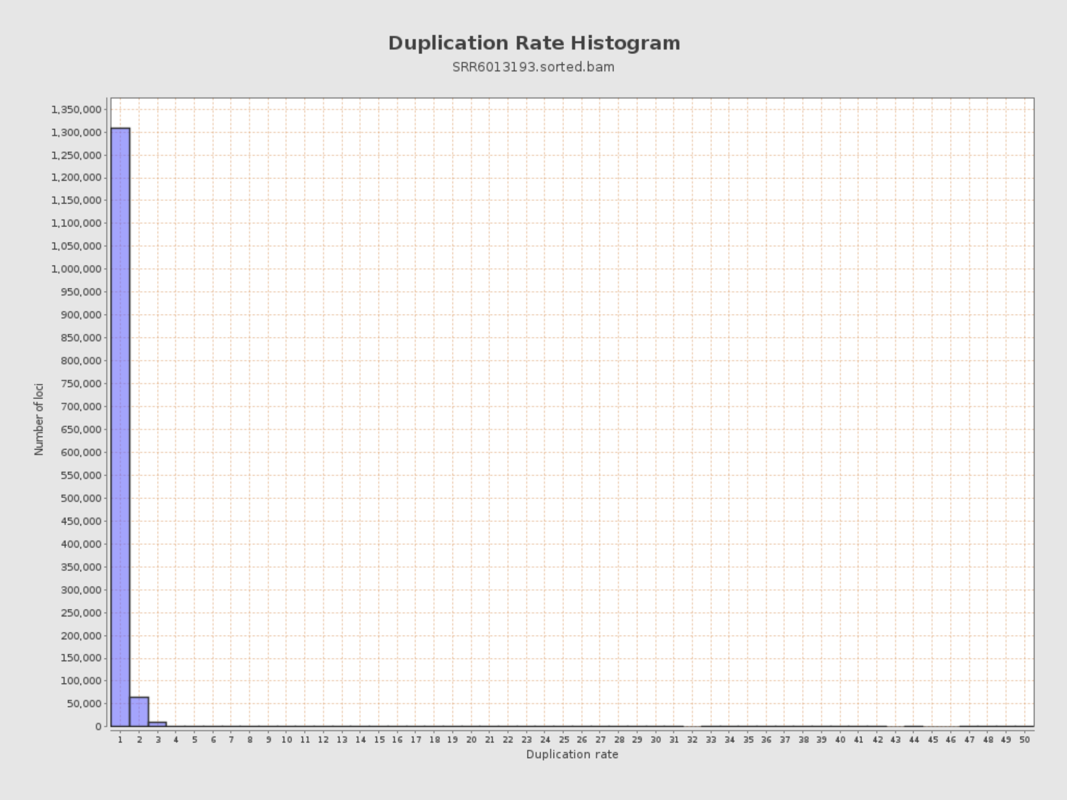
5. Results : Coverage Histogram (0-50X)



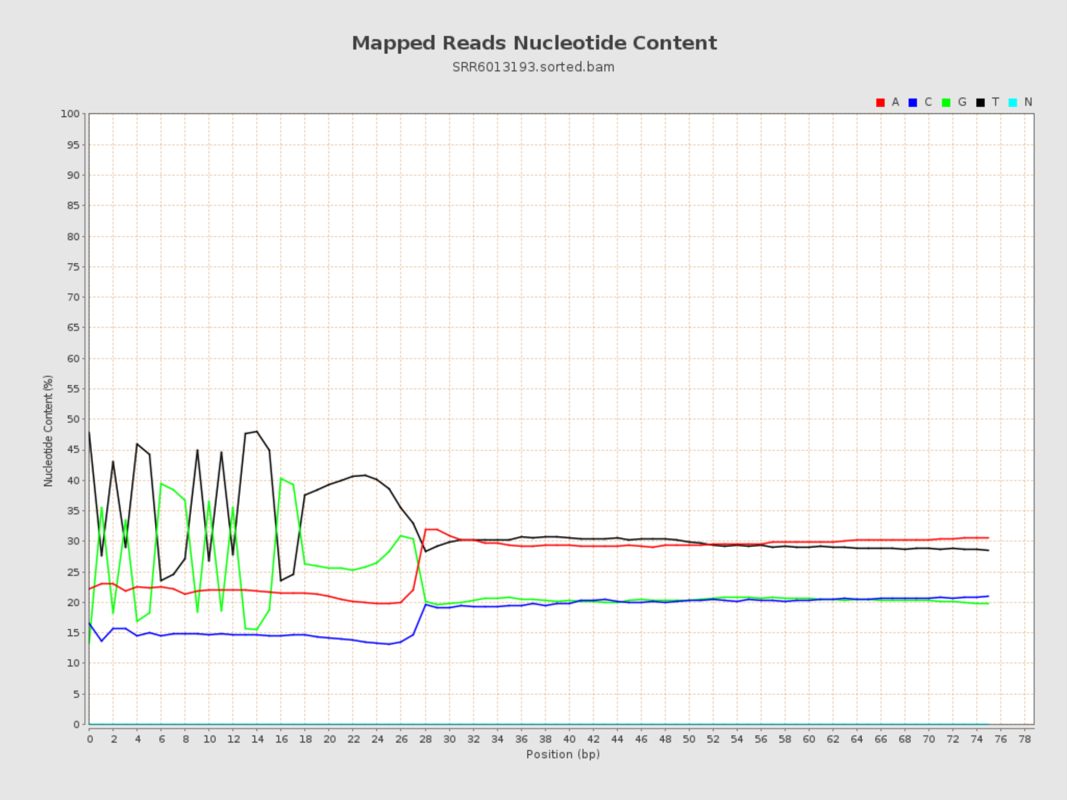
6. Results : Genome Fraction Coverage



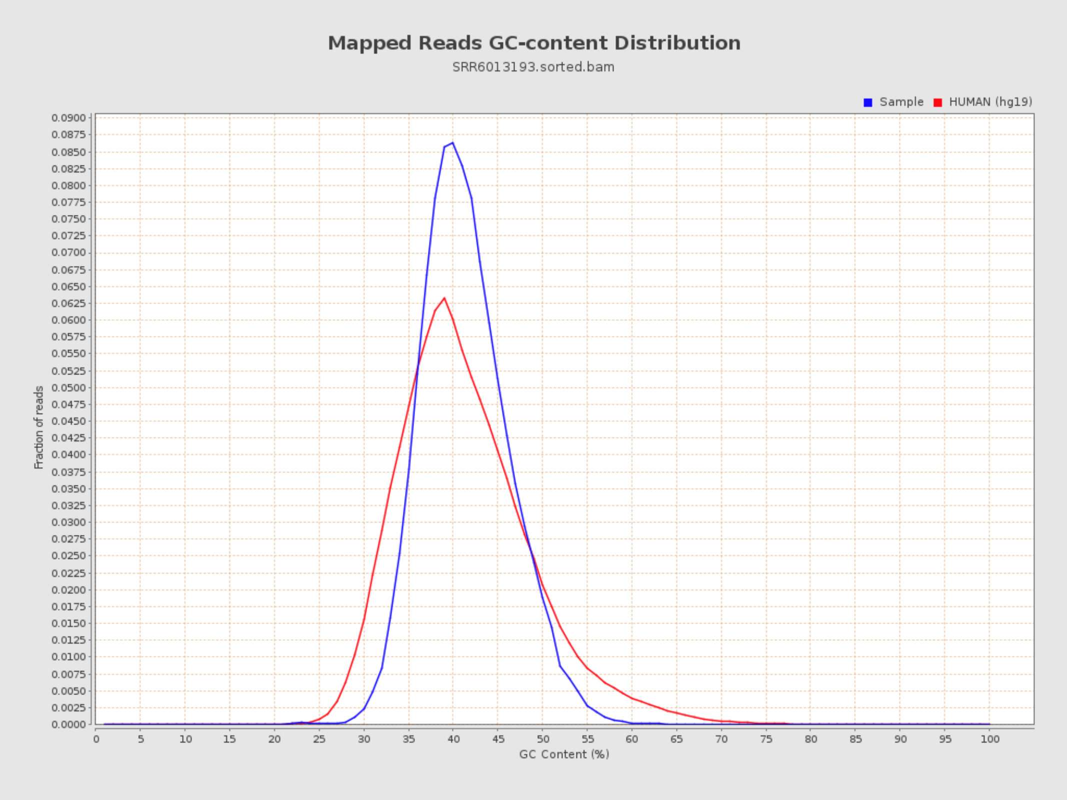
7. Results : Duplication Rate Histogram



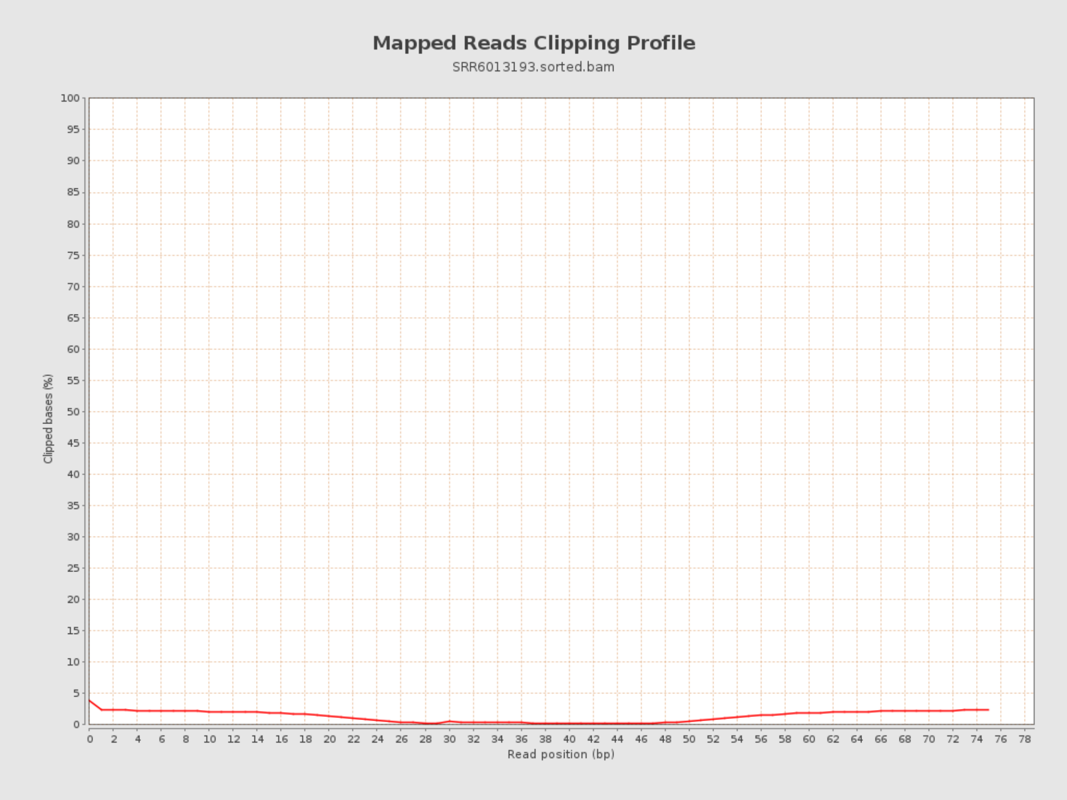
8. Results : Mapped Reads Nucleotide Content



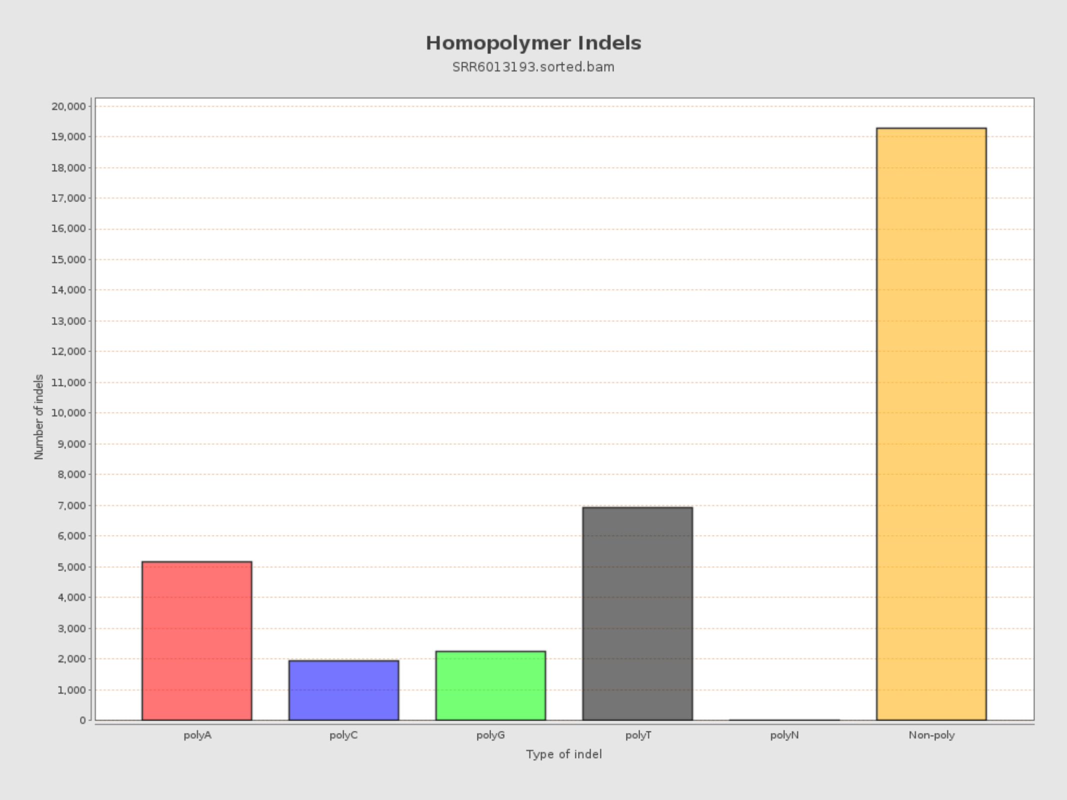
9. Results : Mapped Reads GC-content Distribution



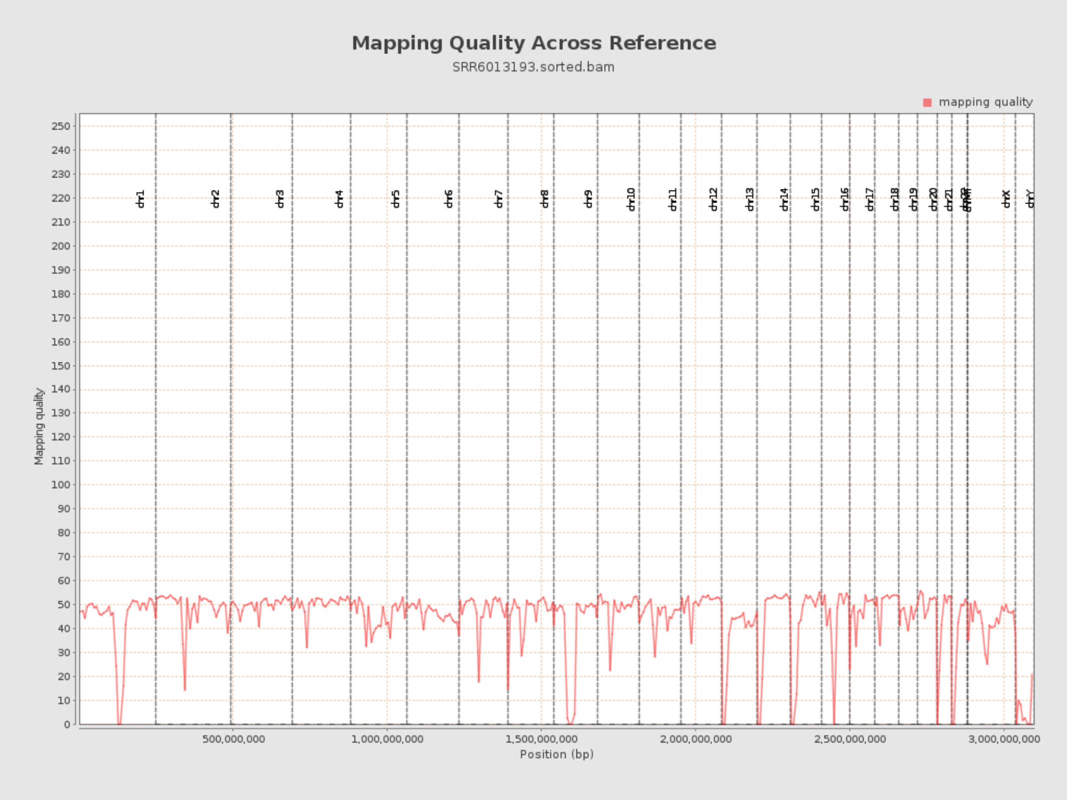
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram