Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 23:35:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013366.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_SRR6013366 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013366.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 23:35:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013366.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,161,507
Mapped reads	1,937,184 / 89.62%
Unmapped reads	224,323 / 10.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,688 / 0.45%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	100,898 / 4.67%
Duplication rate	3.49%
Clipped reads	774,807 / 35.85%

2.2. ACGT Content

Number/percentage of A's	37,802,288 / 28.83%
Number/percentage of C's	23,891,687 / 18.22%
Number/percentage of T's	41,617,712 / 31.74%
Number/percentage of G's	27,771,325 / 21.18%
Number/percentage of N's	28,038 / 0.02%
GC Percentage	39.4%

2.3. Coverage

Mean	0.0424

Standard Deviation	0.5417

2.4. Mapping Quality

Mean Mapping Quality	46.22

2.5. Mismatches and indels

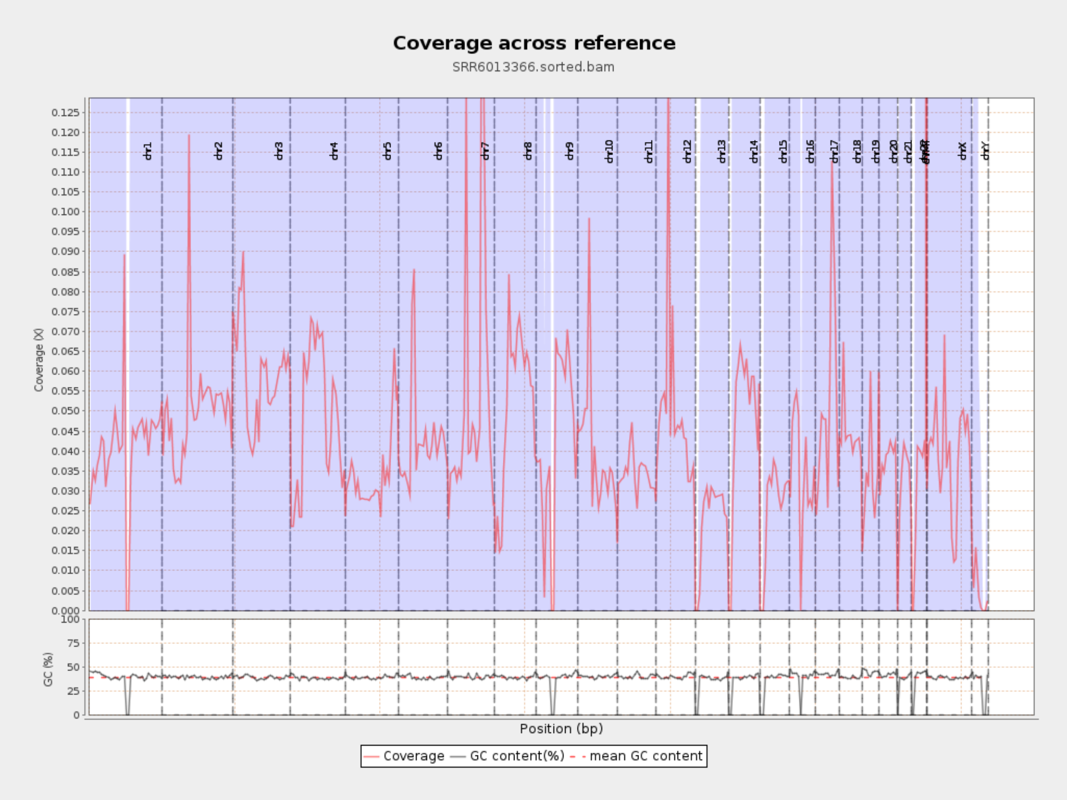
General error rate	0.83%
Mismatches	1,074,606
Insertions	10,315
Mapped reads with at least one insertion	0.53%
Deletions	33,723
Mapped reads with at least one deletion	1.72%
Homopolymer indels	46.19%

2.6. Chromosome stats

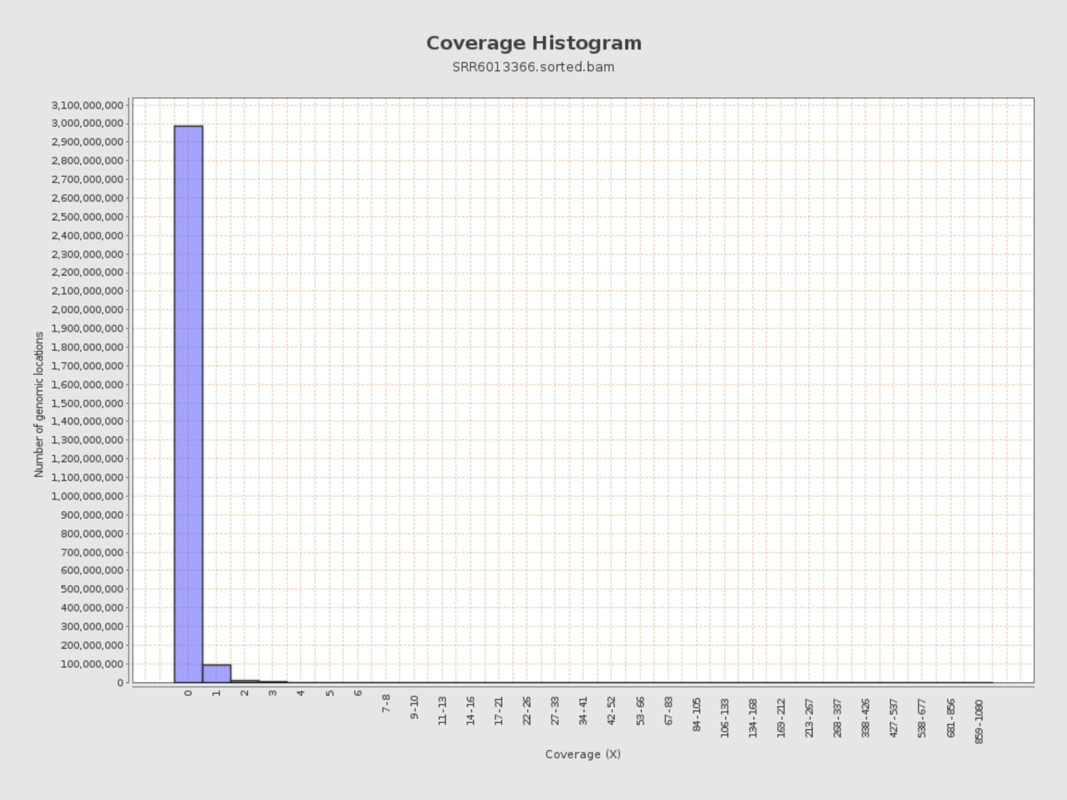
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10171908	0.0408	0.9361
chr2	243199373	12216510	0.0502	0.5877
chr3	198022430	11808000	0.0596	0.278
chr4	191154276	9178759	0.048	0.2871
chr5	180915260	6242140	0.0345	0.2156
chr6	171115067	7354676	0.043	0.3565
chr7	159138663	8973423	0.0564	1.1944

chr8	146364022	7555726	0.0516	0.5638
chr9	141213431	5972439	0.0423	0.4945
chr10	135534747	5431625	0.0401	0.6326
chr11	135006516	4619223	0.0342	0.3582
chr12	133851895	6782981	0.0507	0.2731
chr13	115169878	2602559	0.0226	0.1698
chr14	107349540	5155746	0.048	0.2826
chr15	102531392	2625849	0.0256	0.1838
chr16	90354753	3154162	0.0349	0.2717
chr17	81195210	4143418	0.051	0.3035
chr18	78077248	3495840	0.0448	0.9771
chr19	59128983	2007536	0.034	0.7066
chr20	63025520	2356306	0.0374	0.2355
chr21	48129895	1498750	0.0311	0.2347
chr22	51304566	1454294	0.0283	0.1881
chrMT	16571	59191	3.572	2.7041
chrX	155270560	6043431	0.0389	0.2704
chrY	59373566	265307	0.0045	0.16

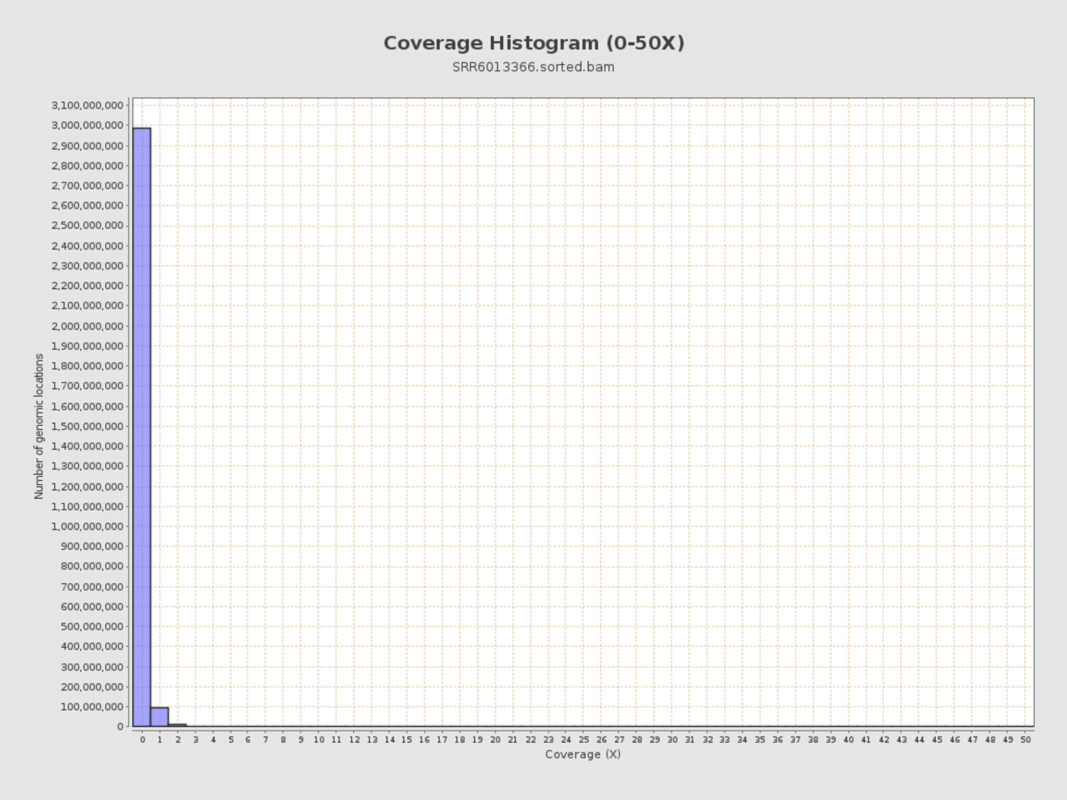
3. Results : Coverage across reference



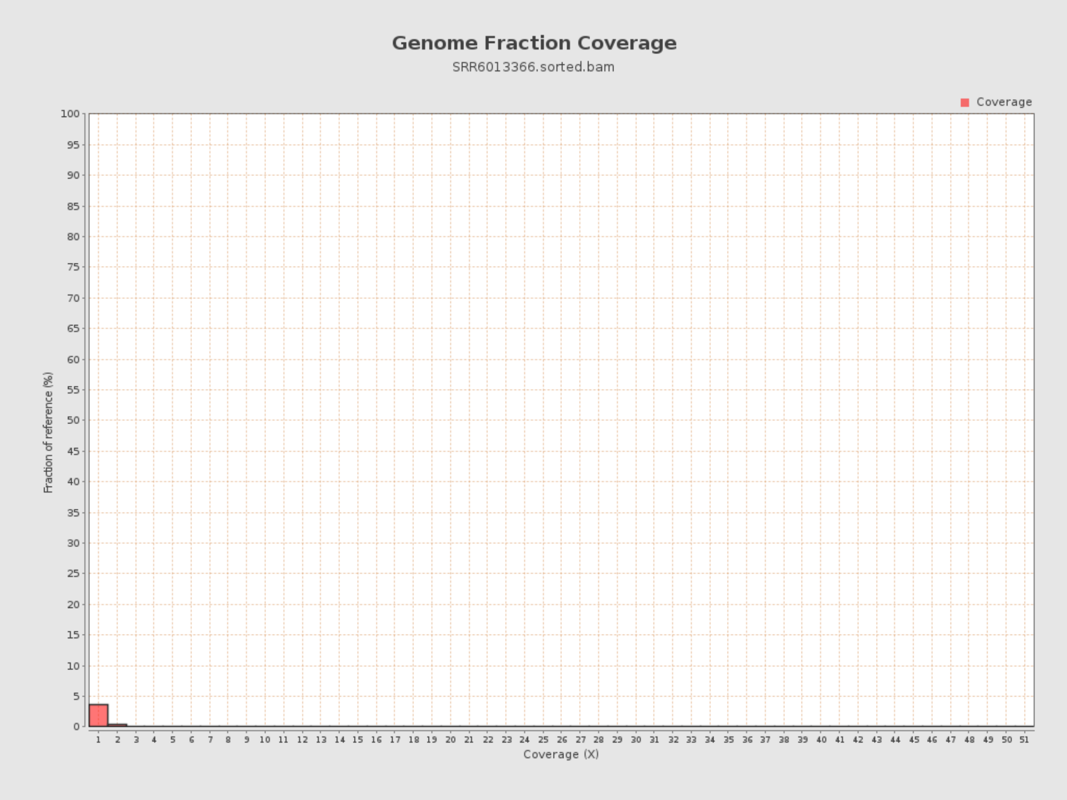
4. Results : Coverage Histogram



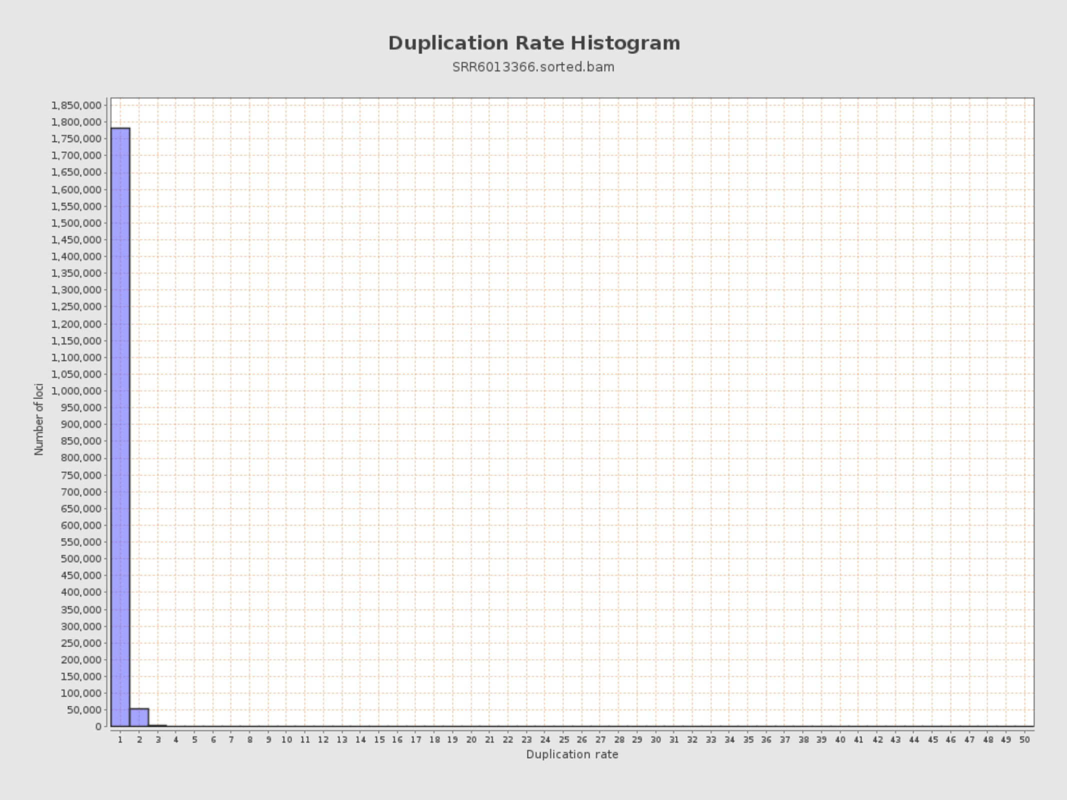
5. Results : Coverage Histogram (0-50X)



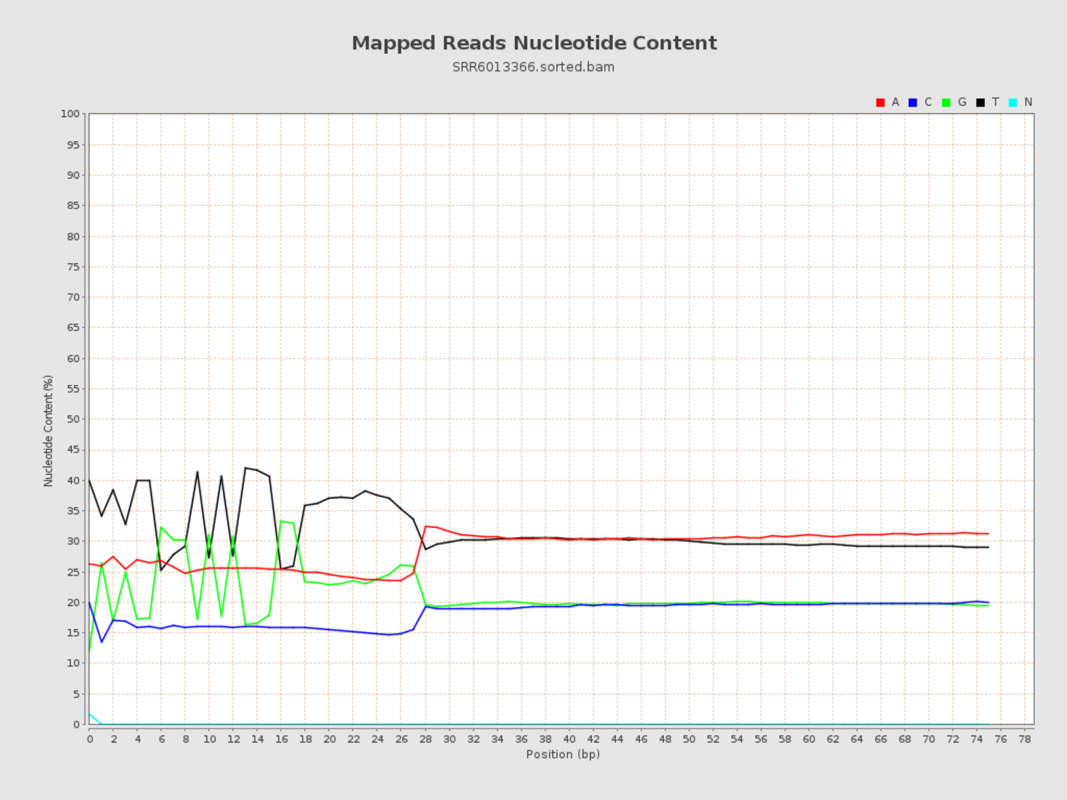
6. Results : Genome Fraction Coverage



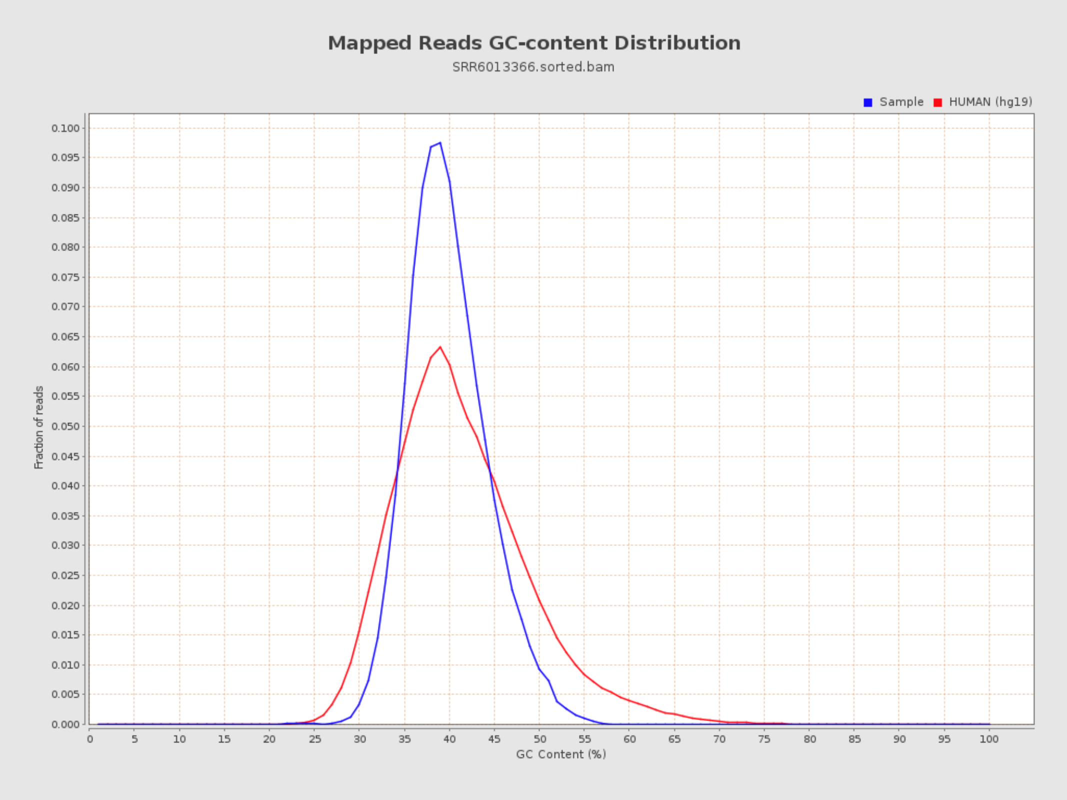
7. Results : Duplication Rate Histogram



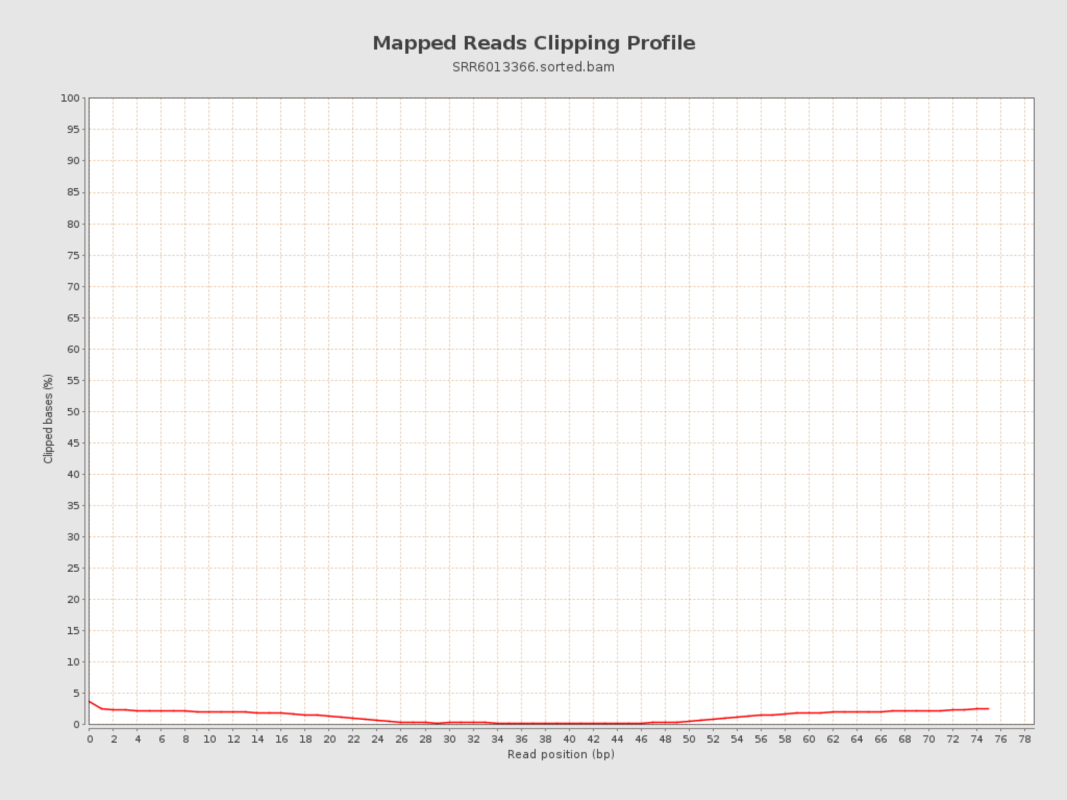
8. Results : Mapped Reads Nucleotide Content



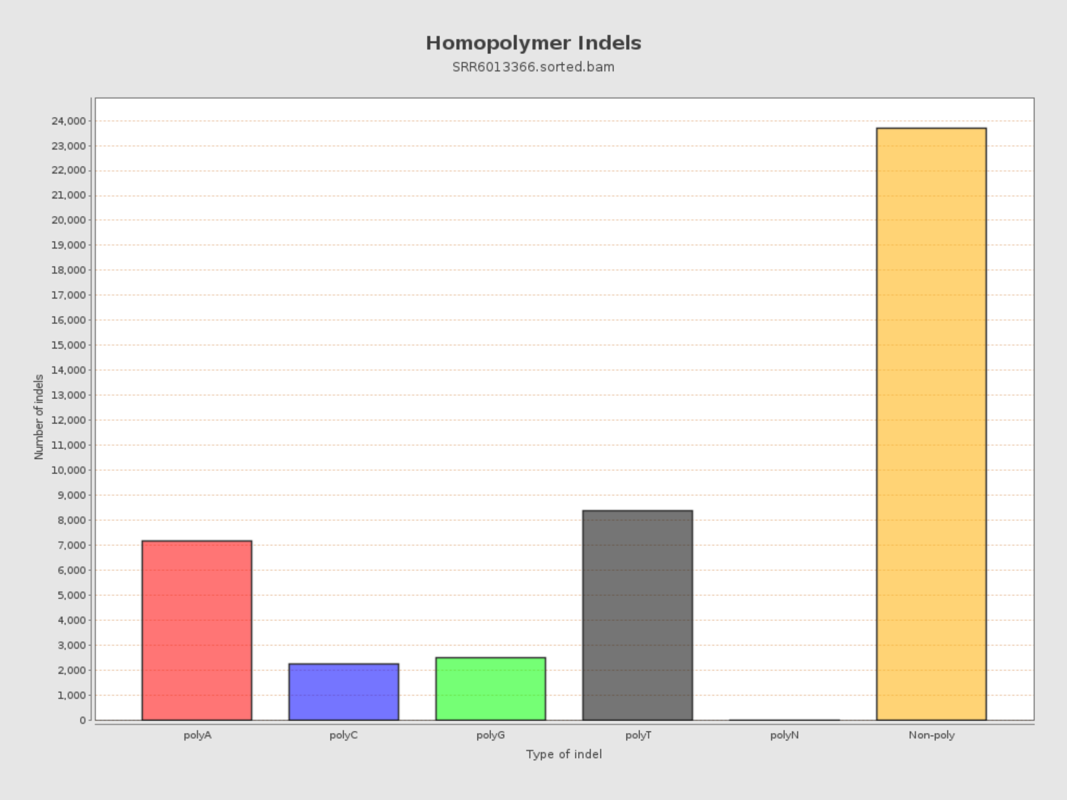
9. Results : Mapped Reads GC-content Distribution



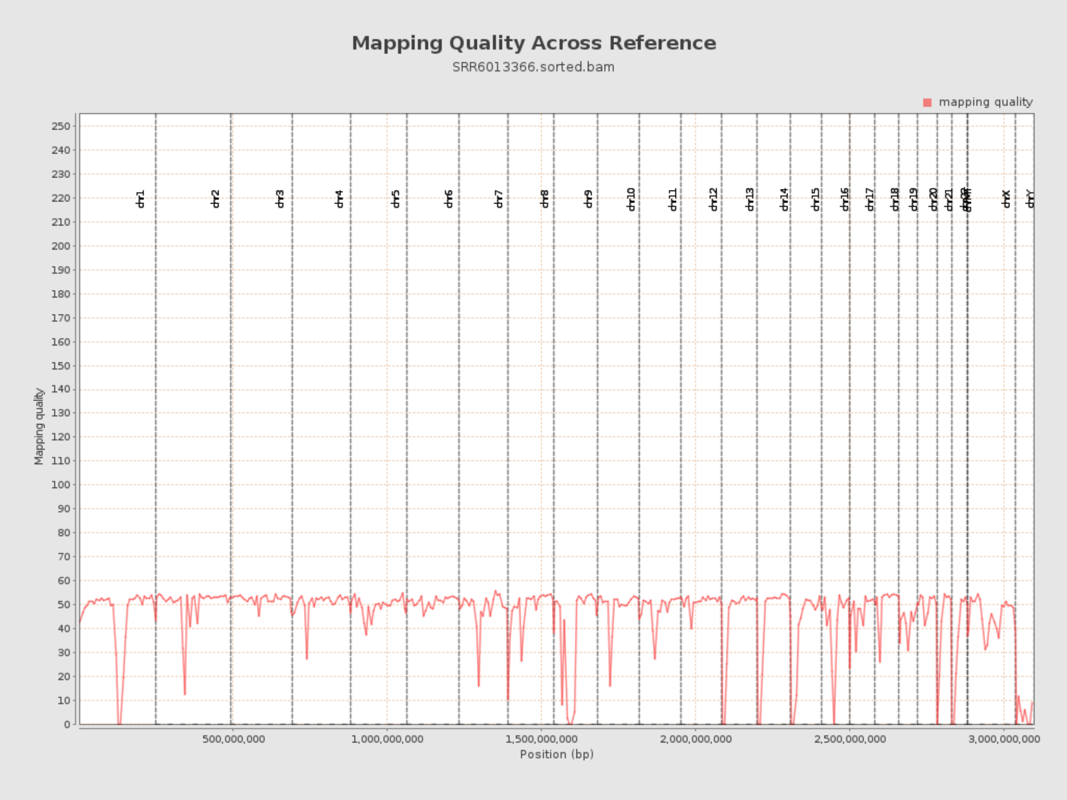
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram