Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:51:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003997.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_SRR6003997 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003997.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:51:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003997.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,718,076
Mapped reads	2,987,642 / 80.35%
Unmapped reads	730,434 / 19.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,413 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	145,305 / 3.91%
Duplication rate	3.35%
Clipped reads	1,398,732 / 37.62%

2.2. ACGT Content

Number/percentage of A's	54,925,772 / 27.65%
Number/percentage of C's	36,216,735 / 18.23%
Number/percentage of T's	63,056,800 / 31.74%
Number/percentage of G's	44,430,337 / 22.37%
Number/percentage of N's	20,899 / 0.01%
GC Percentage	40.6%

2.3. Coverage

Mean	0.0642

Standard Deviation	0.6557

2.4. Mapping Quality

Mean Mapping Quality	43.54

2.5. Mismatches and indels

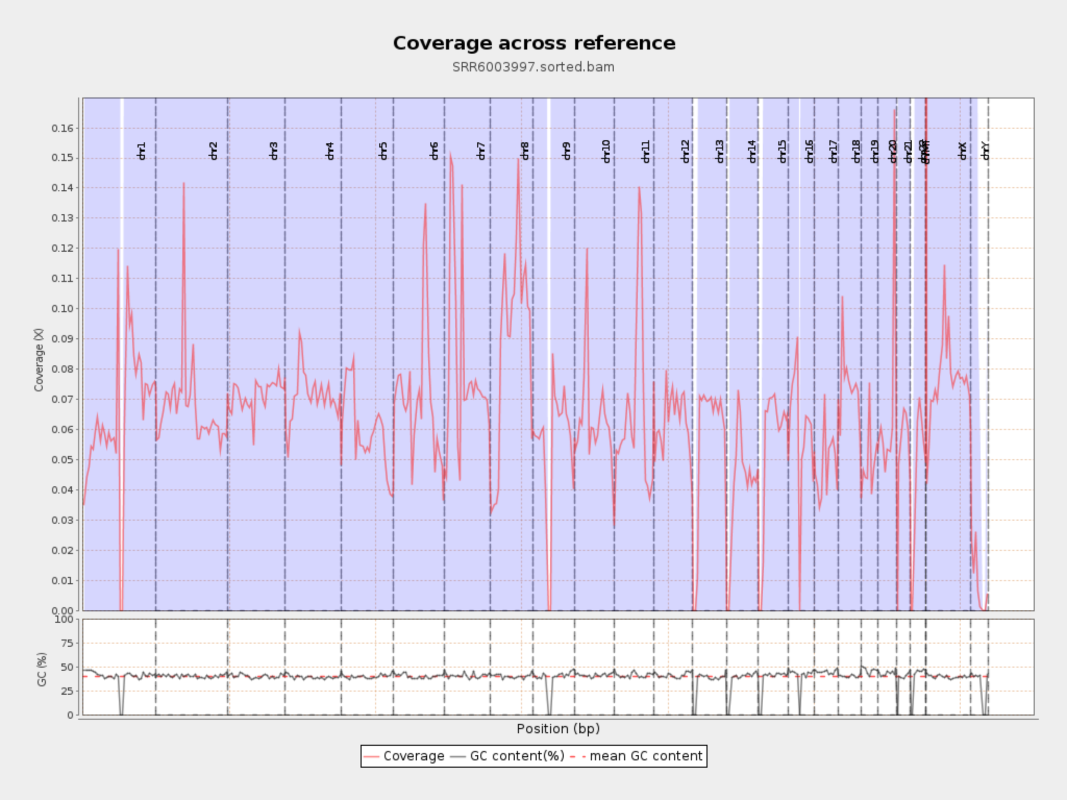
General error rate	1.03%
Mismatches	2,018,105
Insertions	18,936
Mapped reads with at least one insertion	0.63%
Deletions	54,582
Mapped reads with at least one deletion	1.81%
Homopolymer indels	46.54%

2.6. Chromosome stats

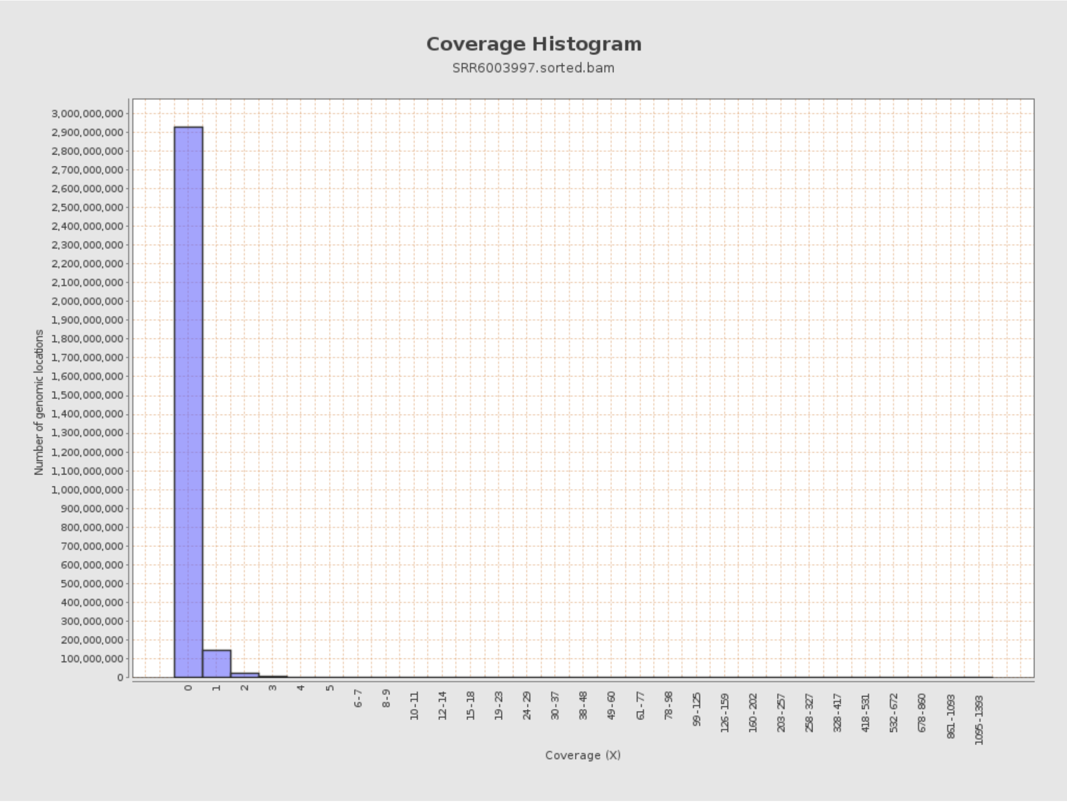
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16123484	0.0647	1.2048
chr2	243199373	16358572	0.0673	0.771
chr3	198022430	14166480	0.0715	0.3141
chr4	191154276	13630322	0.0713	0.3338
chr5	180915260	10799000	0.0597	0.2891
chr6	171115067	12087533	0.0706	0.3956
chr7	159138663	12673636	0.0796	1.0106

chr8	146364022	13147961	0.0898	0.9343
chr9	141213431	7760984	0.055	0.666
chr10	135534747	8652901	0.0638	0.5897
chr11	135006516	8846915	0.0655	0.5026
chr12	133851895	8392593	0.0627	0.3103
chr13	115169878	6490359	0.0564	0.2723
chr14	107349540	4468850	0.0416	0.3601
chr15	102531392	5418185	0.0528	0.2737
chr16	90354753	5288334	0.0585	0.4041
chr17	81195210	3915499	0.0482	0.2967
chr18	78077248	5860061	0.0751	1.4014
chr19	59128983	2928189	0.0495	0.861
chr20	63025520	4460551	0.0708	0.3423
chr21	48129895	2511651	0.0522	0.3295
chr22	51304566	2220837	0.0433	0.2368
chrMT	16571	122353	7.3836	5.1968
chrX	155270560	11898102	0.0766	0.4102
chrY	59373566	519067	0.0087	0.1889

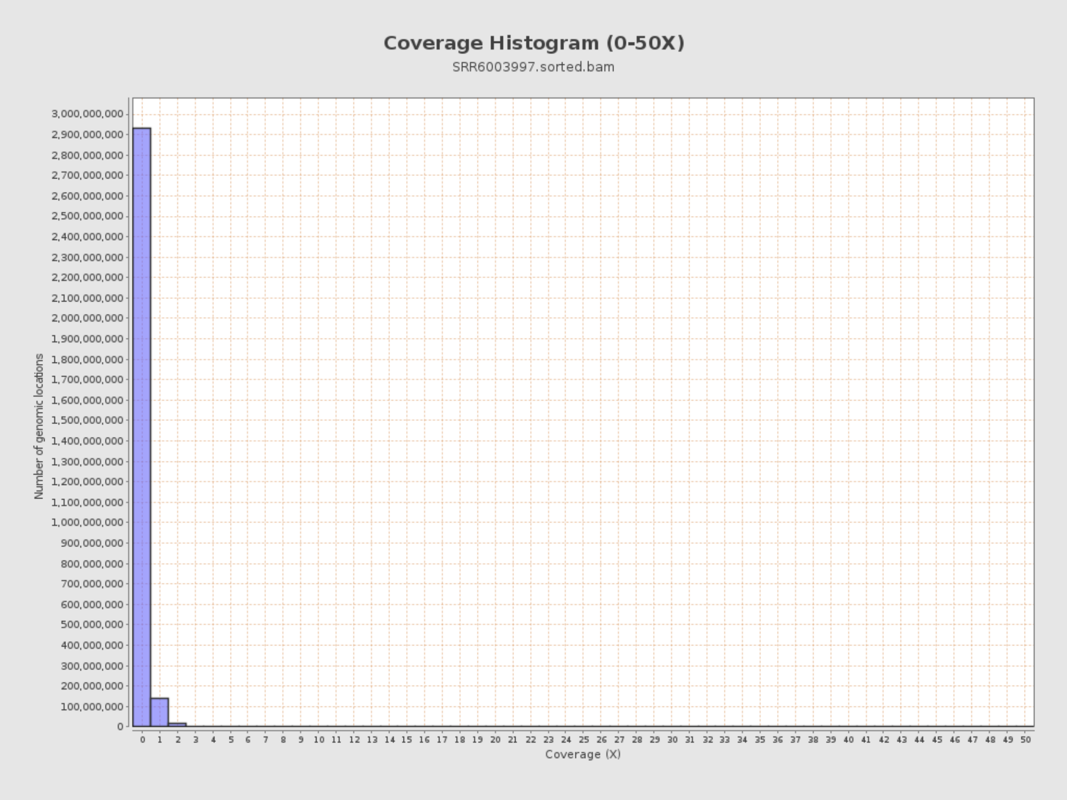
3. Results : Coverage across reference



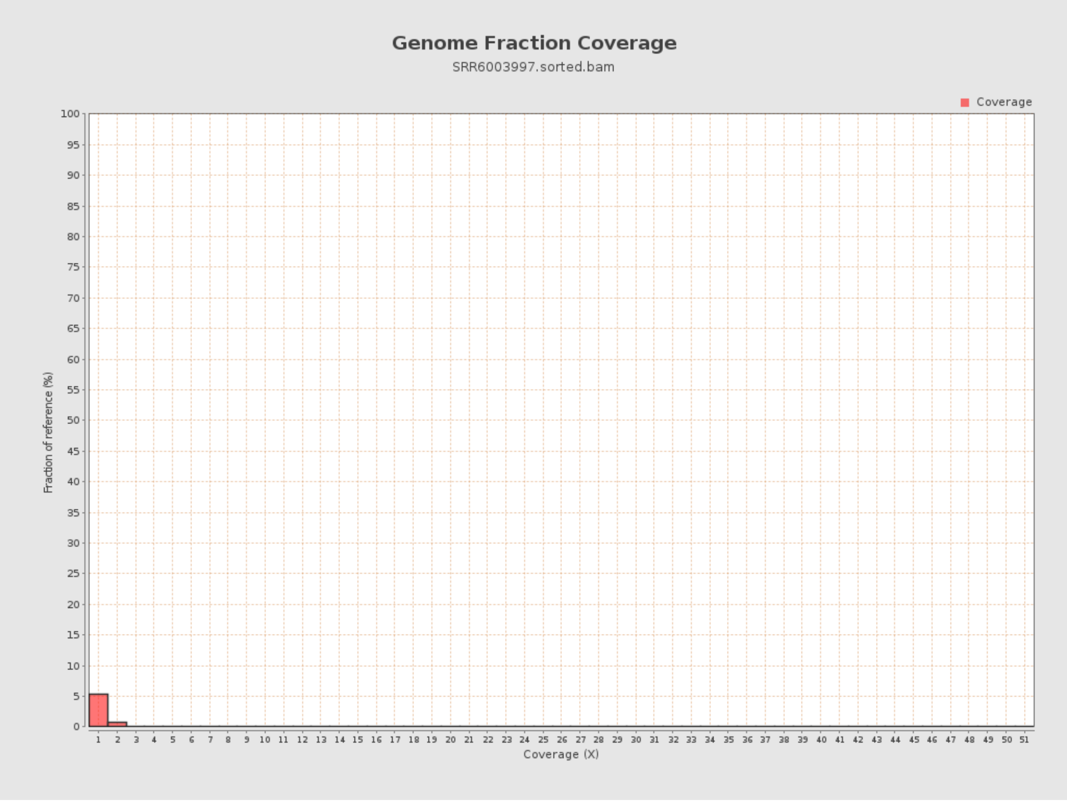
4. Results : Coverage Histogram



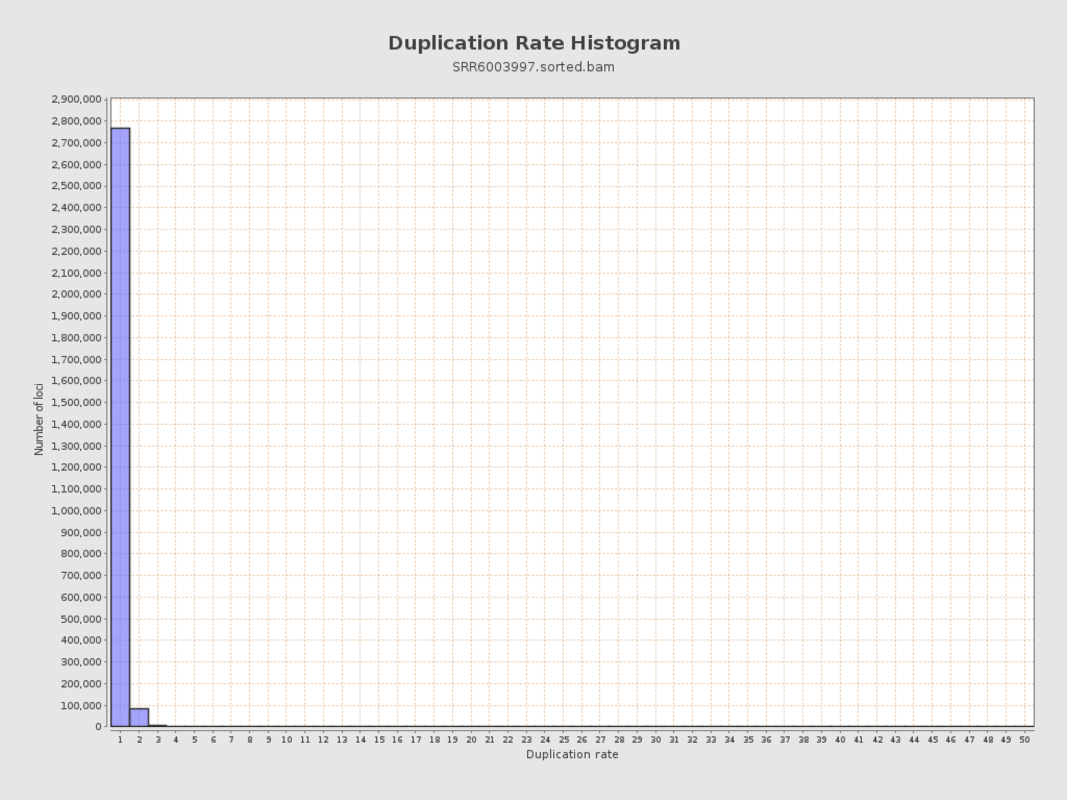
5. Results : Coverage Histogram (0-50X)



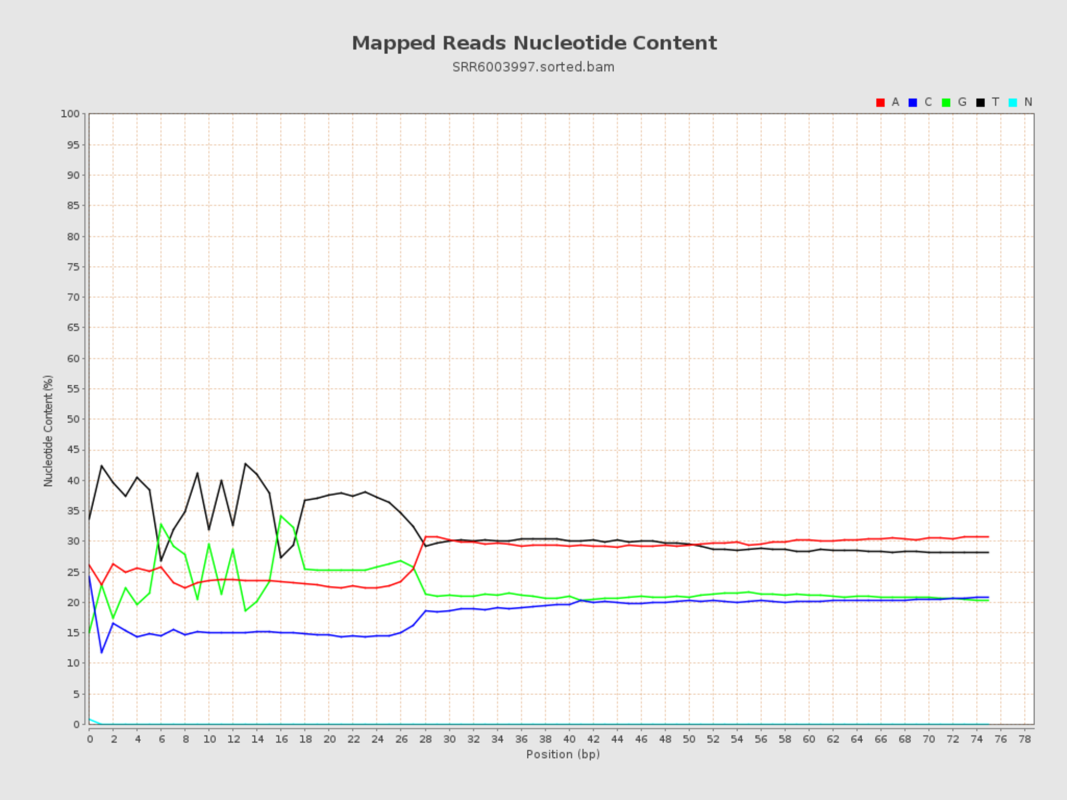
6. Results : Genome Fraction Coverage



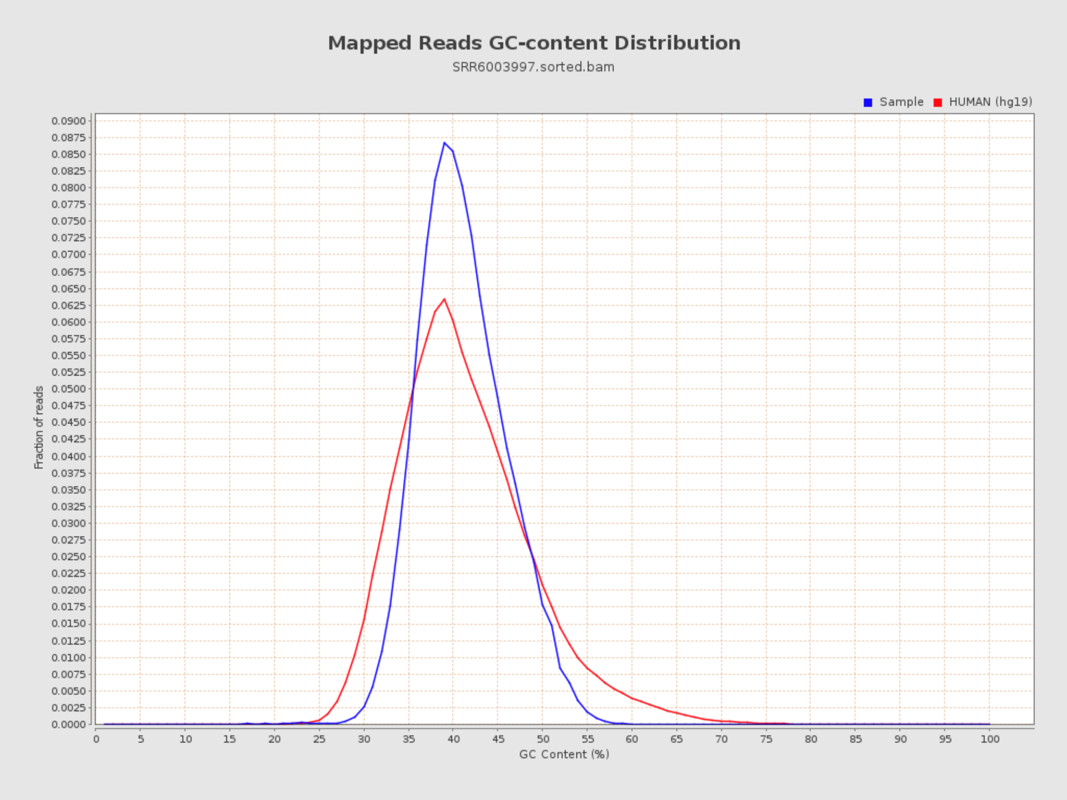
7. Results : Duplication Rate Histogram



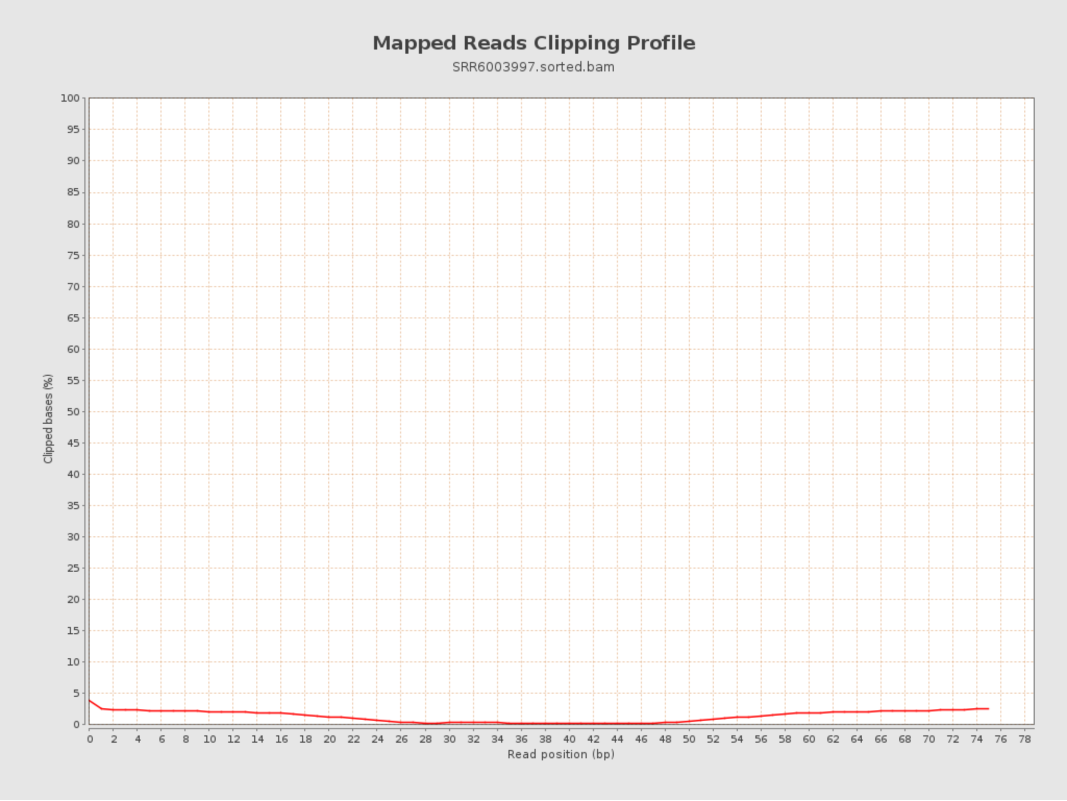
8. Results : Mapped Reads Nucleotide Content



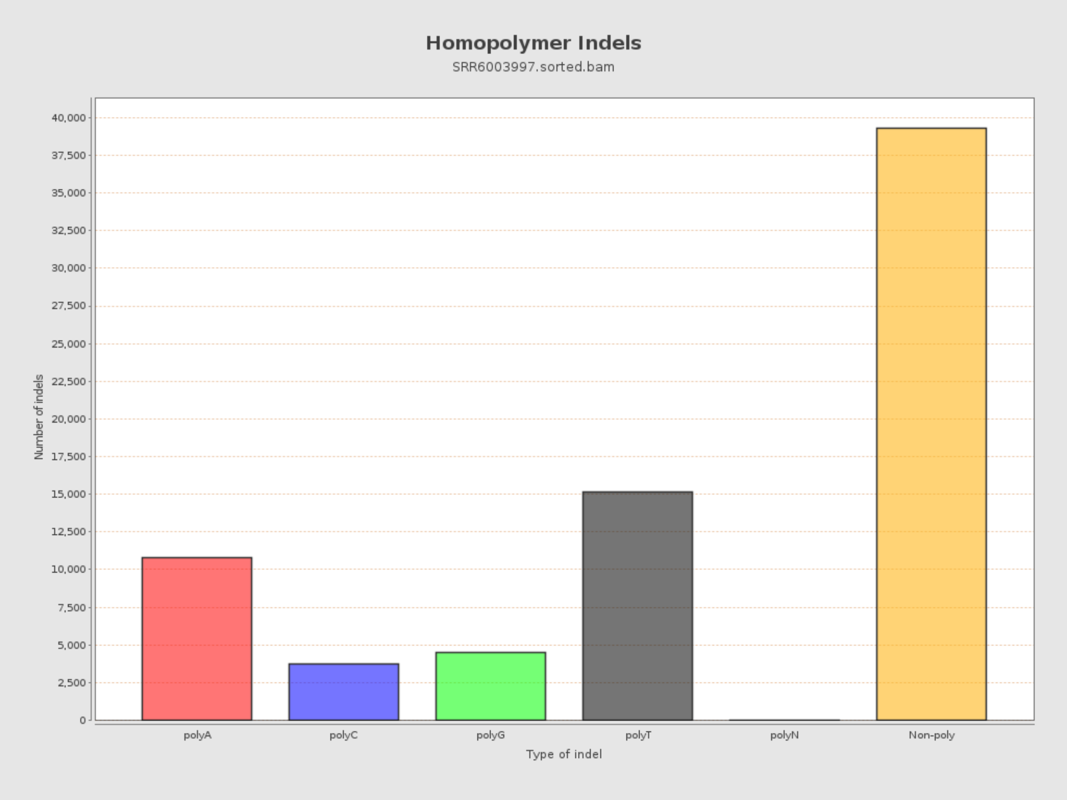
9. Results : Mapped Reads GC-content Distribution



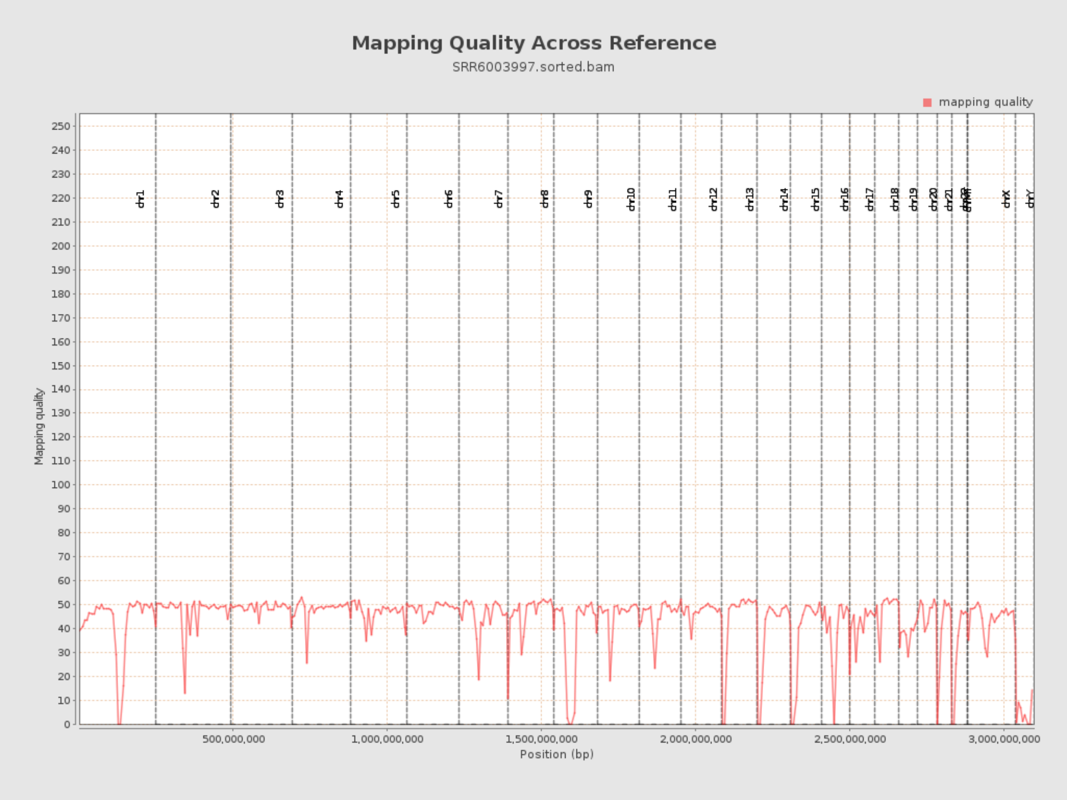
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram