Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:41:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013285.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_SRR6013285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013285.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:41:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,392,626
Mapped reads	3,097,675 / 91.31%
Unmapped reads	294,951 / 8.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,780 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	122,764 / 3.62%
Duplication rate	2.54%
Clipped reads	1,358,053 / 40.03%

2.2. ACGT Content

Number/percentage of A's	57,290,842 / 27.71%
Number/percentage of C's	38,106,493 / 18.43%
Number/percentage of T's	64,724,756 / 31.3%
Number/percentage of G's	46,647,705 / 22.56%
Number/percentage of N's	2,875 / 0%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0668

Standard Deviation	0.6501

2.4. Mapping Quality

Mean Mapping Quality	45.43

2.5. Mismatches and indels

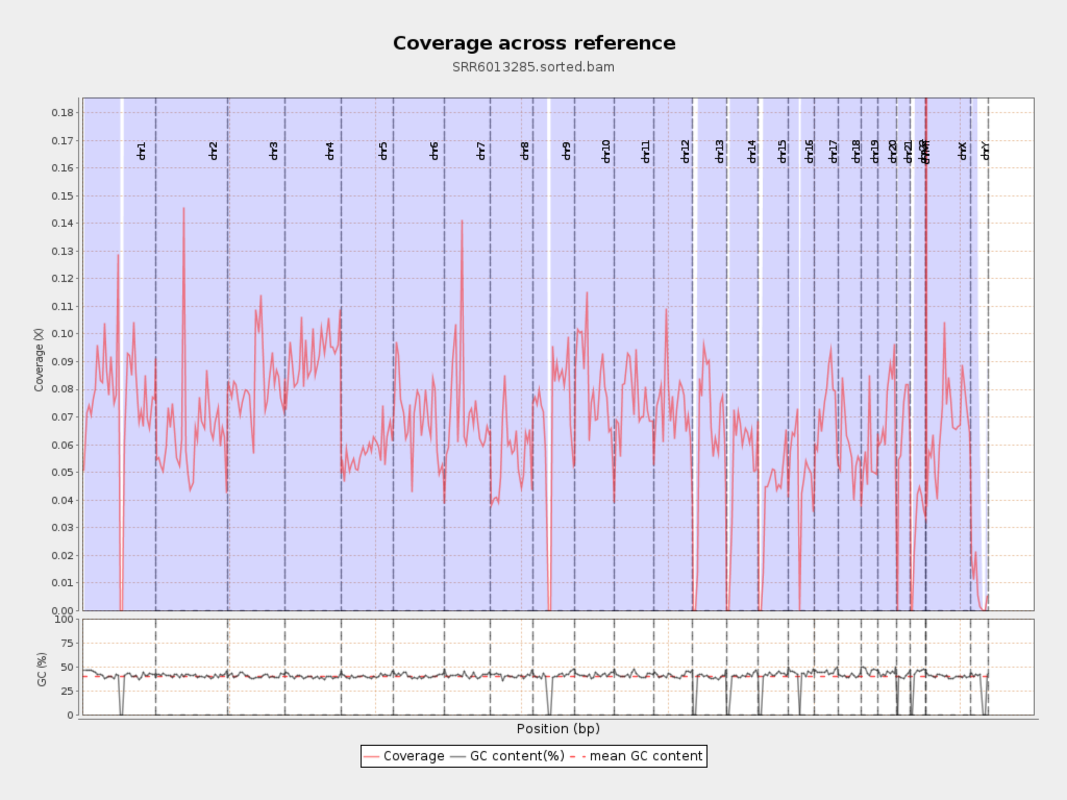
General error rate	0.71%
Mismatches	1,437,341
Insertions	14,651
Mapped reads with at least one insertion	0.47%
Deletions	46,451
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.69%

2.6. Chromosome stats

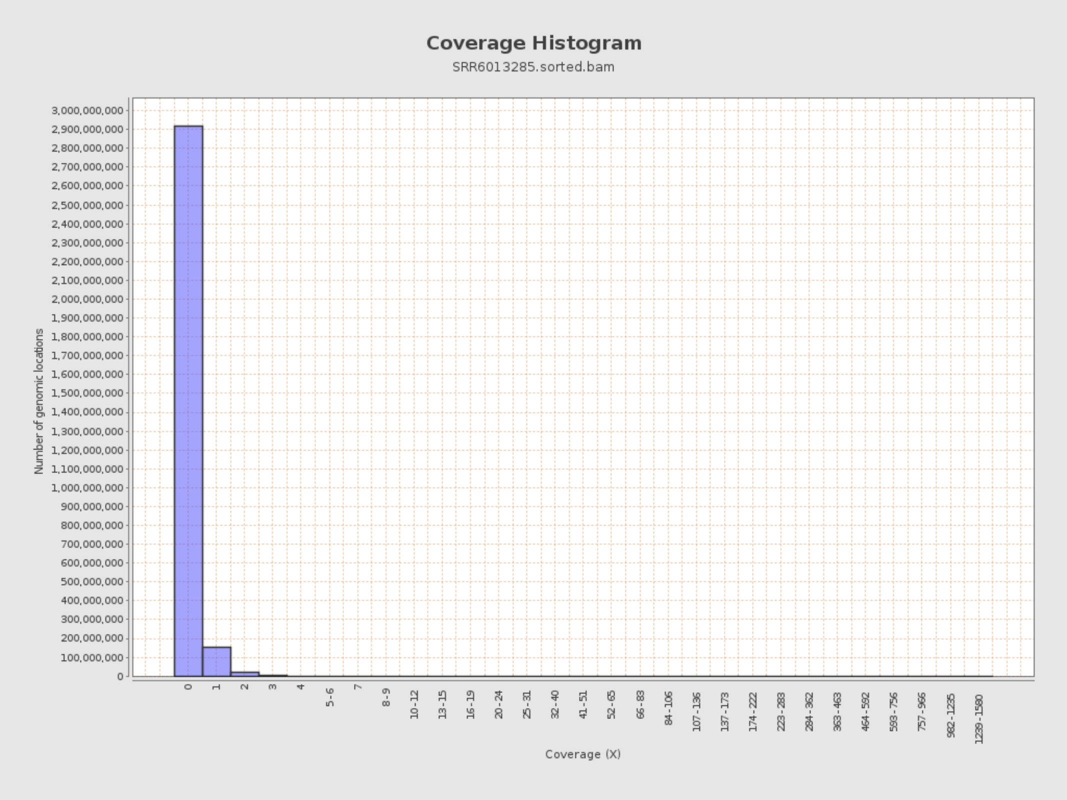
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18952826	0.076	1.3408
chr2	243199373	15781720	0.0649	0.7523
chr3	198022430	16241480	0.082	0.3246
chr4	191154276	17660042	0.0924	0.3791
chr5	180915260	10427036	0.0576	0.276
chr6	171115067	11974439	0.07	0.4062
chr7	159138663	11474366	0.0721	1.0086

chr8	146364022	8047182	0.055	0.7832
chr9	141213431	9884370	0.07	0.5935
chr10	135534747	11132921	0.0821	0.5435
chr11	135006516	10107951	0.0749	0.6249
chr12	133851895	9882330	0.0738	0.3276
chr13	115169878	7106831	0.0617	0.2793
chr14	107349540	5664740	0.0528	0.3137
chr15	102531392	4089434	0.0399	0.2749
chr16	90354753	4390108	0.0486	0.3063
chr17	81195210	6040077	0.0744	0.4066
chr18	78077248	4602366	0.0589	1.0909
chr19	59128983	3245066	0.0549	0.8361
chr20	63025520	4641758	0.0736	0.3403
chr21	48129895	3007732	0.0625	0.3186
chr22	51304566	1512260	0.0295	0.1881
chrMT	16571	32148	1.94	1.8553
chrX	155270560	10509324	0.0677	0.3933
chrY	59373566	443555	0.0075	0.155

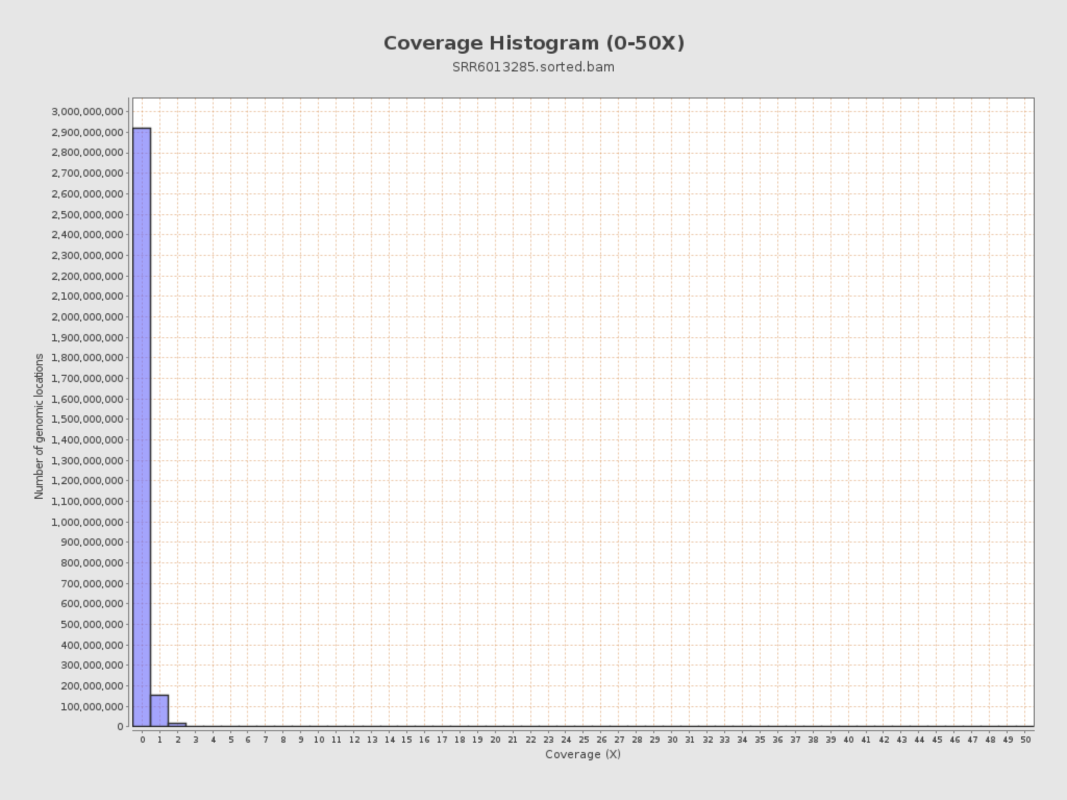
3. Results : Coverage across reference



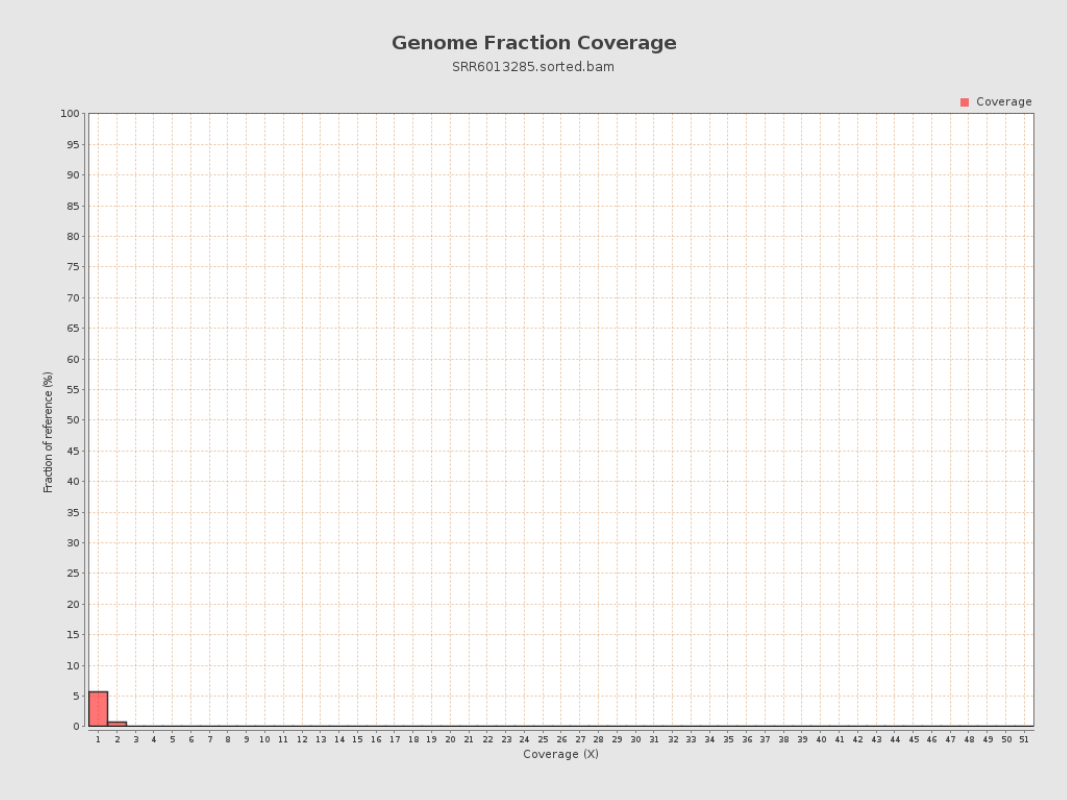
4. Results : Coverage Histogram



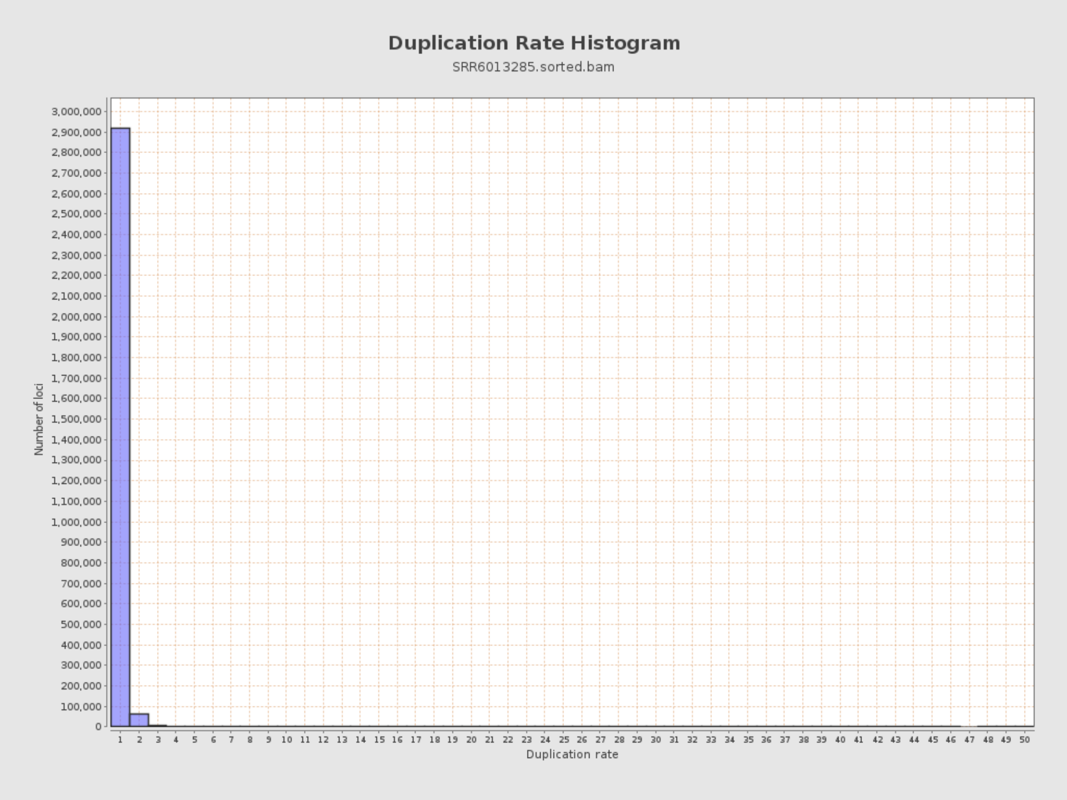
5. Results : Coverage Histogram (0-50X)



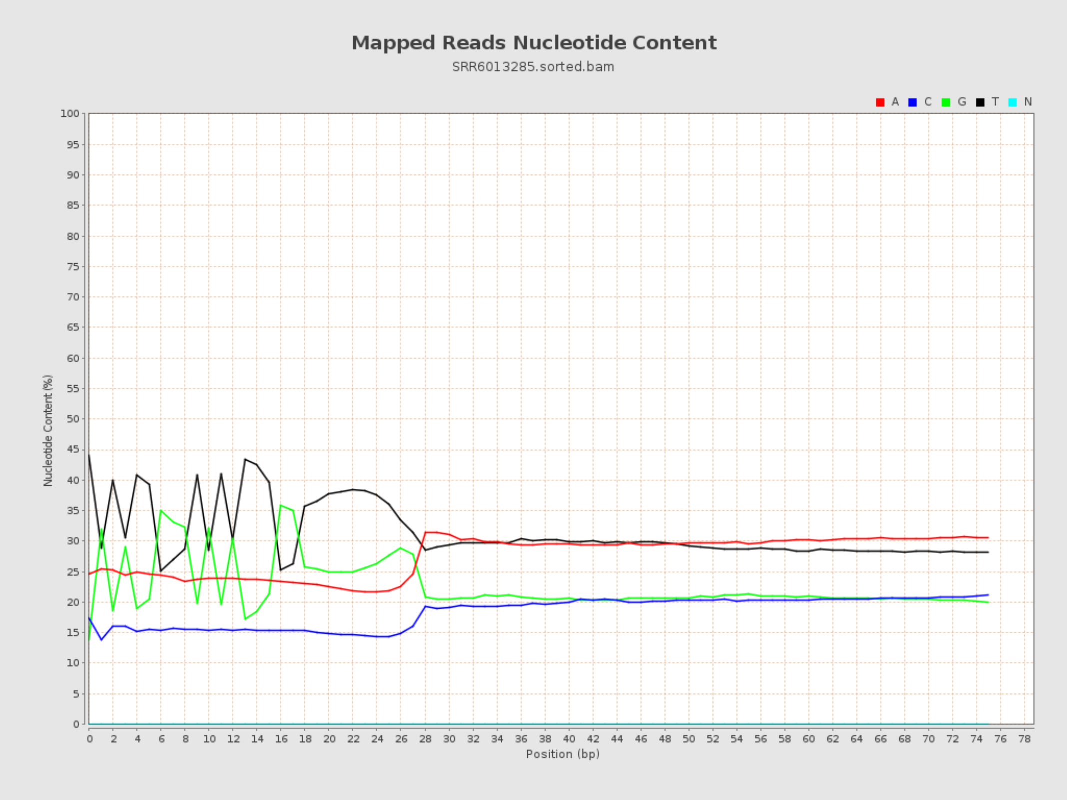
6. Results : Genome Fraction Coverage



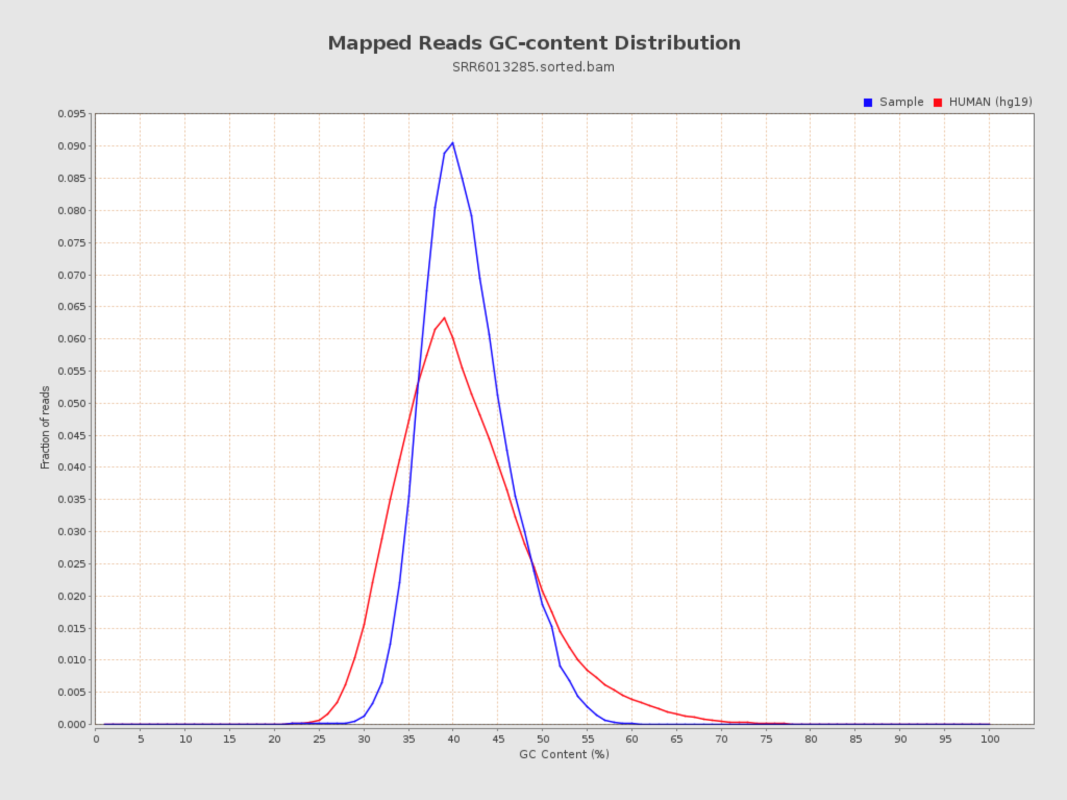
7. Results : Duplication Rate Histogram



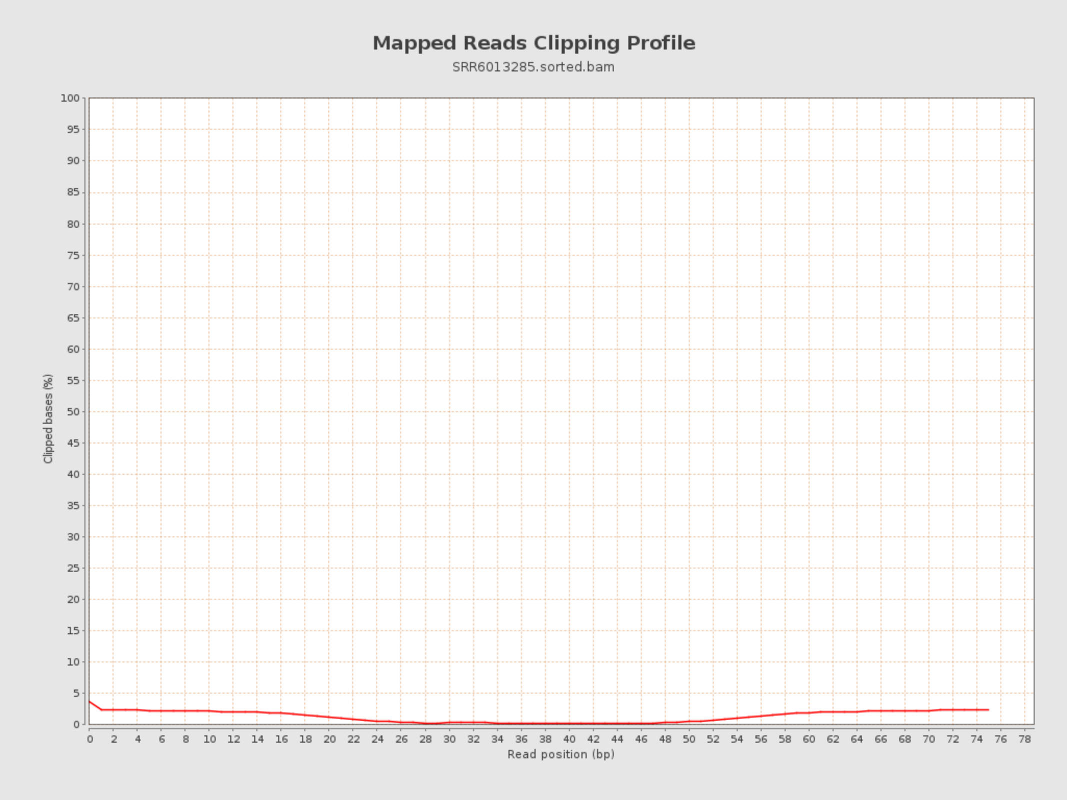
8. Results : Mapped Reads Nucleotide Content



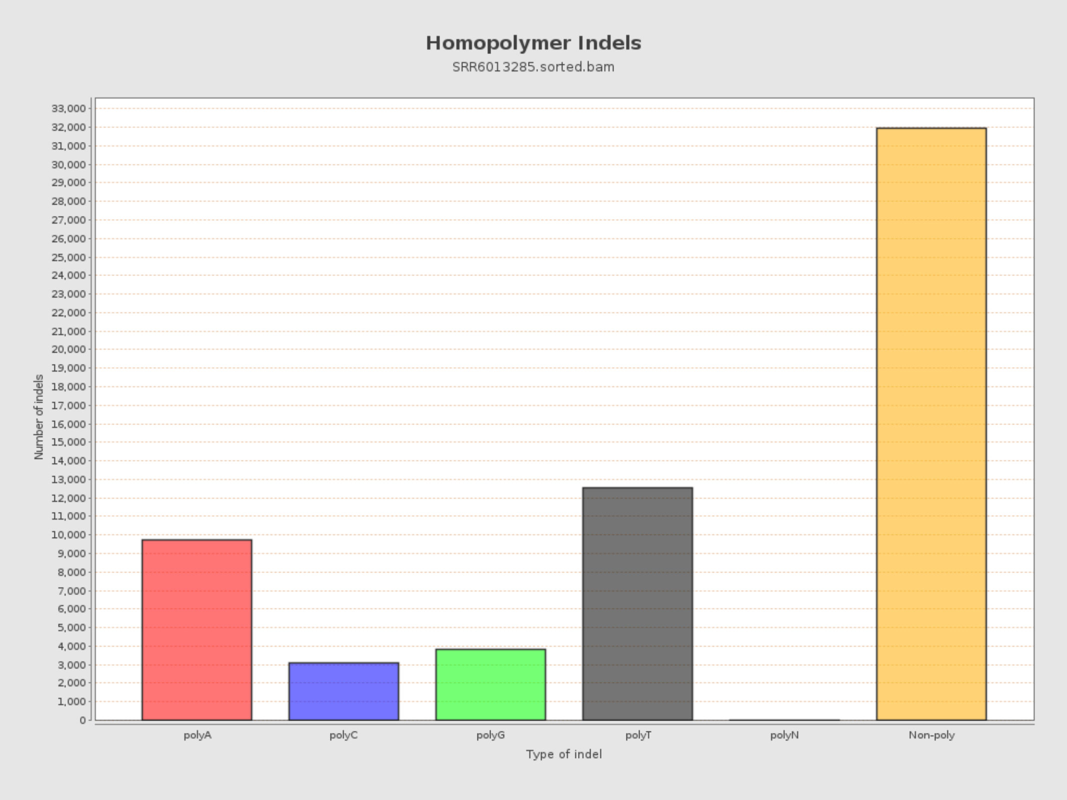
9. Results : Mapped Reads GC-content Distribution



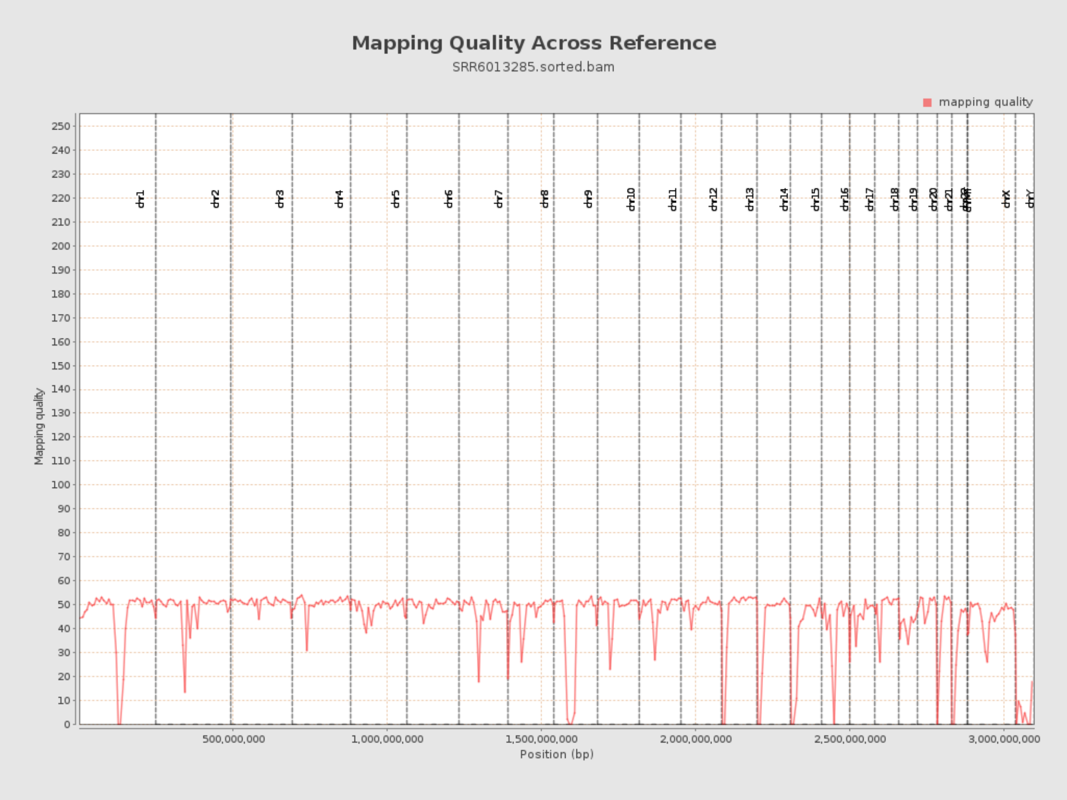
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram