Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 23:28:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004063.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_SRR6004063 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004063.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 23:28:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004063.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,139,374
Mapped reads	1,455,972 / 68.06%
Unmapped reads	683,402 / 31.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,270 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	250,004 / 11.69%
Duplication rate	11.9%
Clipped reads	792,967 / 37.07%

2.2. ACGT Content

Number/percentage of A's	25,814,203 / 27.66%
Number/percentage of C's	17,032,000 / 18.25%
Number/percentage of T's	29,833,854 / 31.96%
Number/percentage of G's	20,597,613 / 22.07%
Number/percentage of N's	62,776 / 0.07%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.4369

2.4. Mapping Quality

Mean Mapping Quality	43.36

2.5. Mismatches and indels

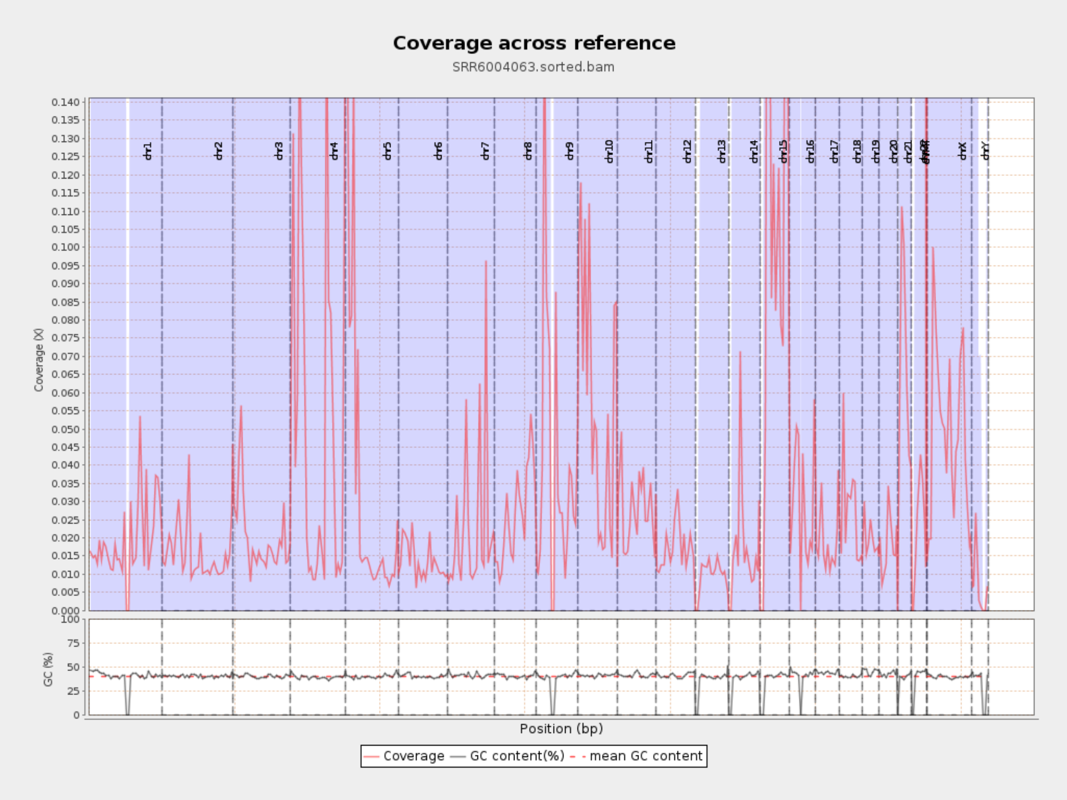
General error rate	0.96%
Mismatches	879,682
Insertions	8,210
Mapped reads with at least one insertion	0.56%
Deletions	26,700
Mapped reads with at least one deletion	1.81%
Homopolymer indels	44.79%

2.6. Chromosome stats

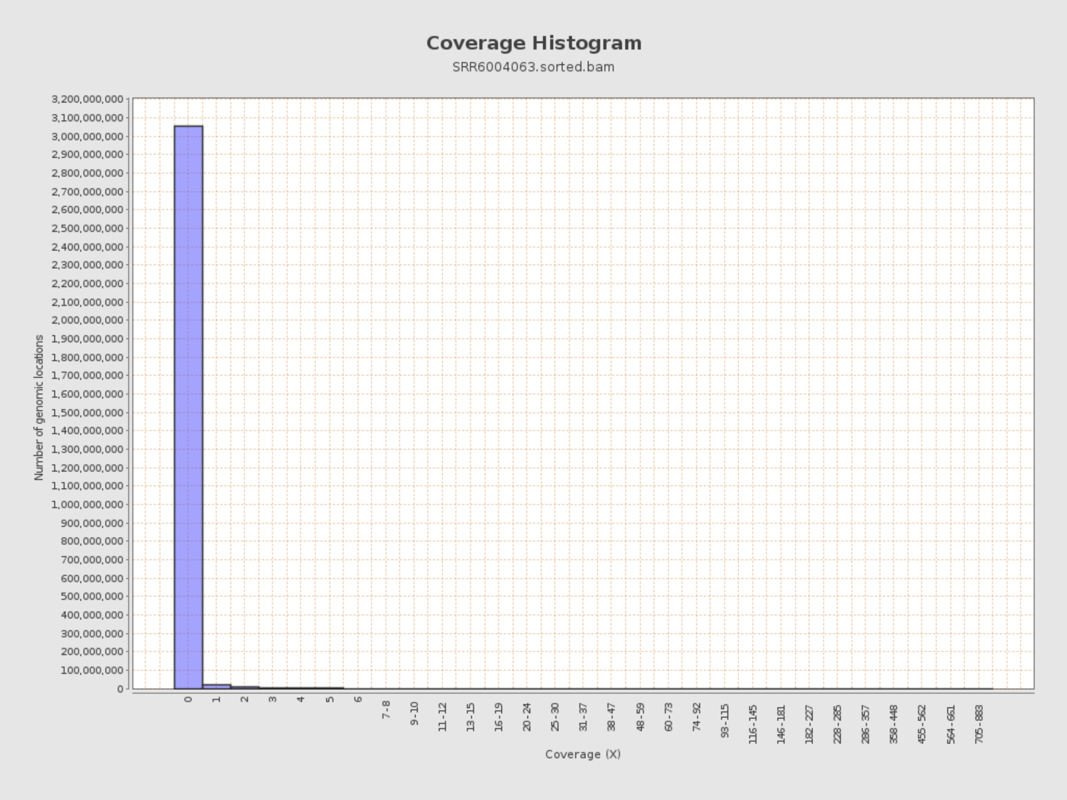
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4890852	0.0196	0.3198
chr2	243199373	3798307	0.0156	0.4073
chr3	198022430	4103903	0.0207	0.2776
chr4	191154276	10172592	0.0532	0.5327
chr5	180915260	6396609	0.0354	0.3654
chr6	171115067	2325147	0.0136	0.2357
chr7	159138663	3714310	0.0233	0.3555

chr8	146364022	3904818	0.0267	0.4021
chr9	141213431	5675255	0.0402	0.594
chr10	135534747	7686997	0.0567	0.6256
chr11	135006516	3680559	0.0273	0.3781
chr12	133851895	2294635	0.0171	0.2708
chr13	115169878	1116270	0.0097	0.1811
chr14	107349540	1828012	0.017	0.3503
chr15	102531392	11186772	0.1091	0.7362
chr16	90354753	2675168	0.0296	0.4469
chr17	81195210	1490960	0.0184	0.2587
chr18	78077248	2151542	0.0276	1.0265
chr19	59128983	1172768	0.0198	0.3431
chr20	63025520	1123861	0.0178	0.2814
chr21	48129895	3084477	0.0641	0.5367
chr22	51304566	1133489	0.0221	0.2739
chrMT	16571	42078	2.5393	3.1943
chrX	155270560	7360751	0.0474	0.4582
chrY	59373566	376440	0.0063	0.2628

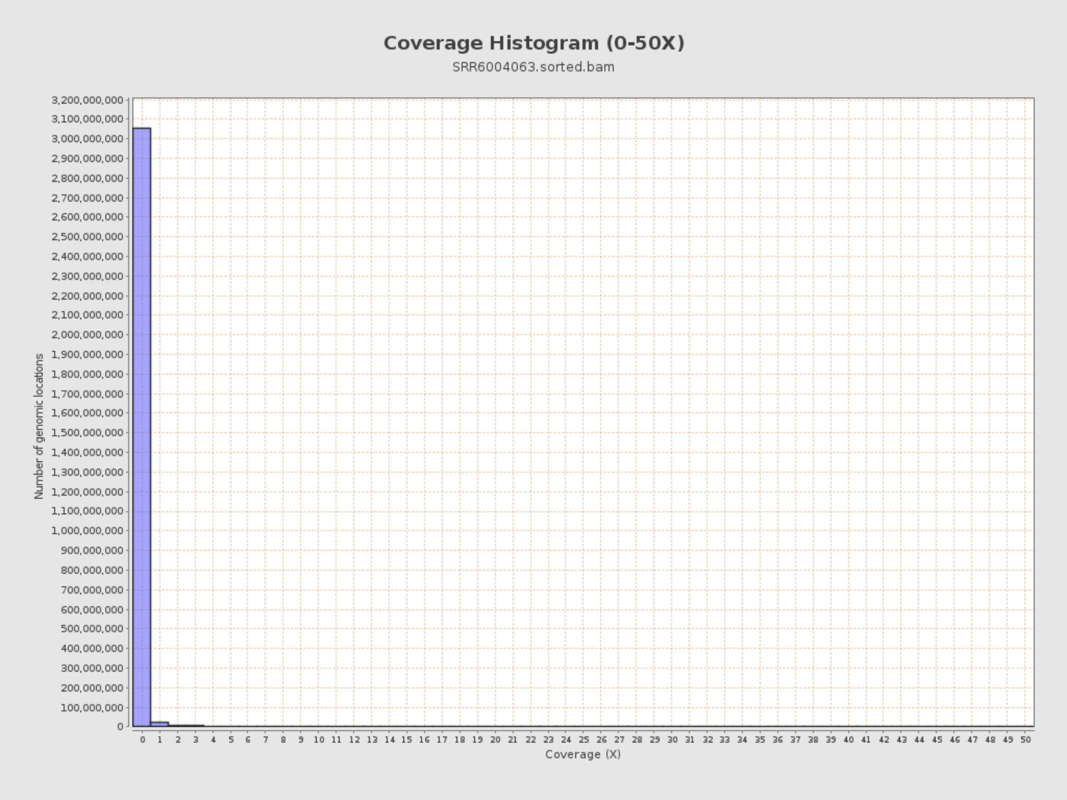
3. Results : Coverage across reference



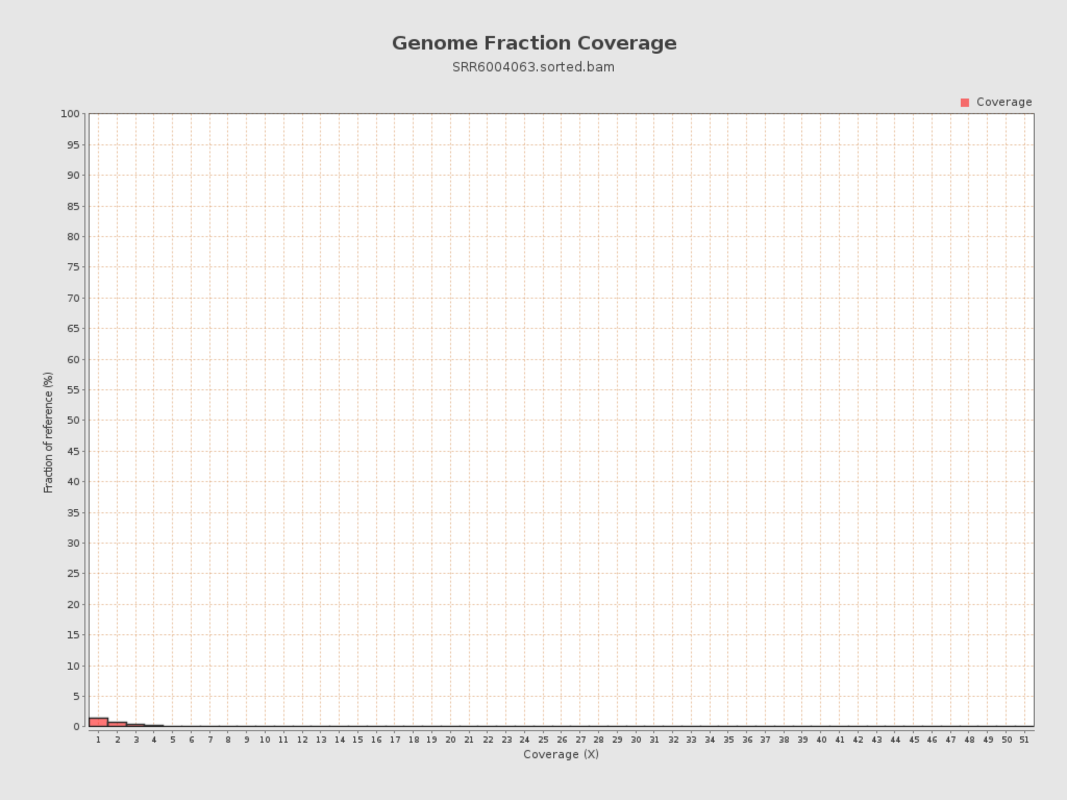
4. Results : Coverage Histogram



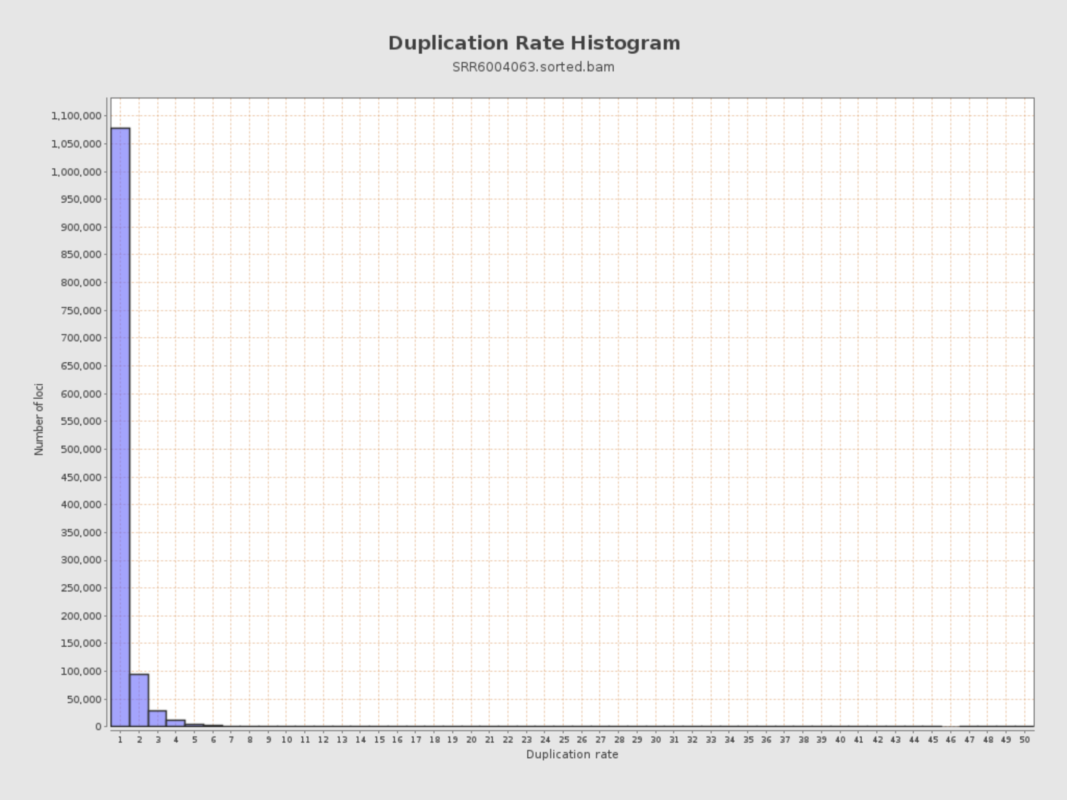
5. Results : Coverage Histogram (0-50X)



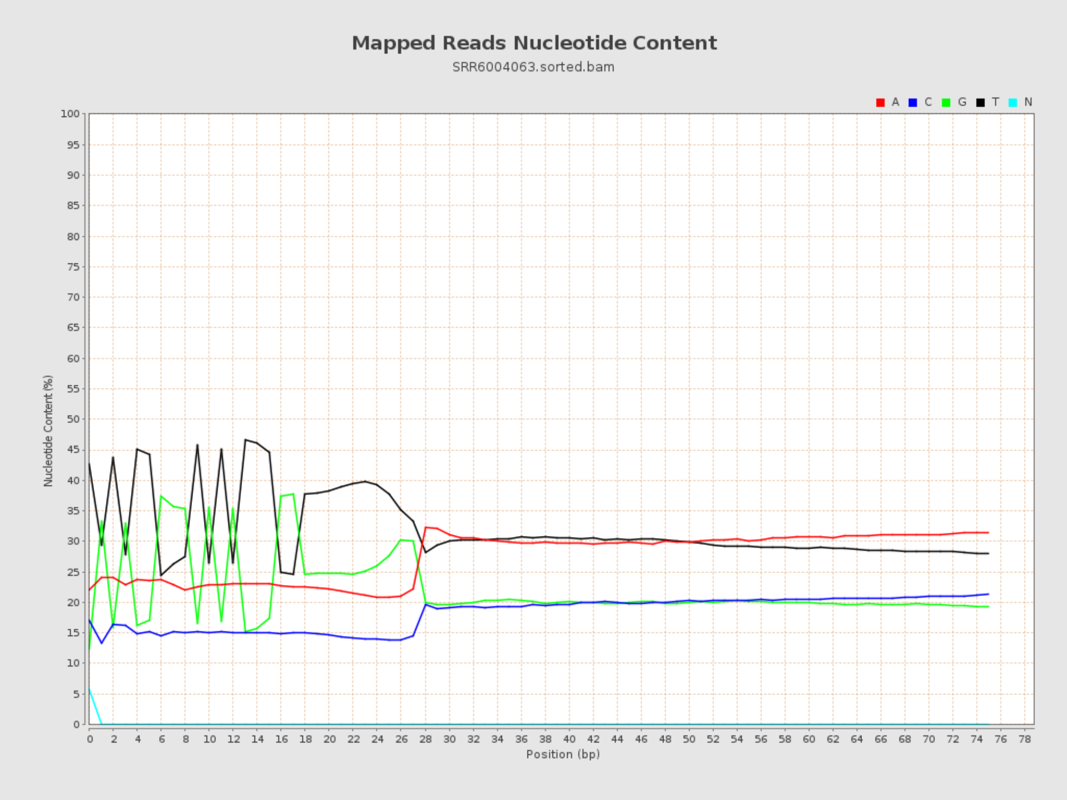
6. Results : Genome Fraction Coverage



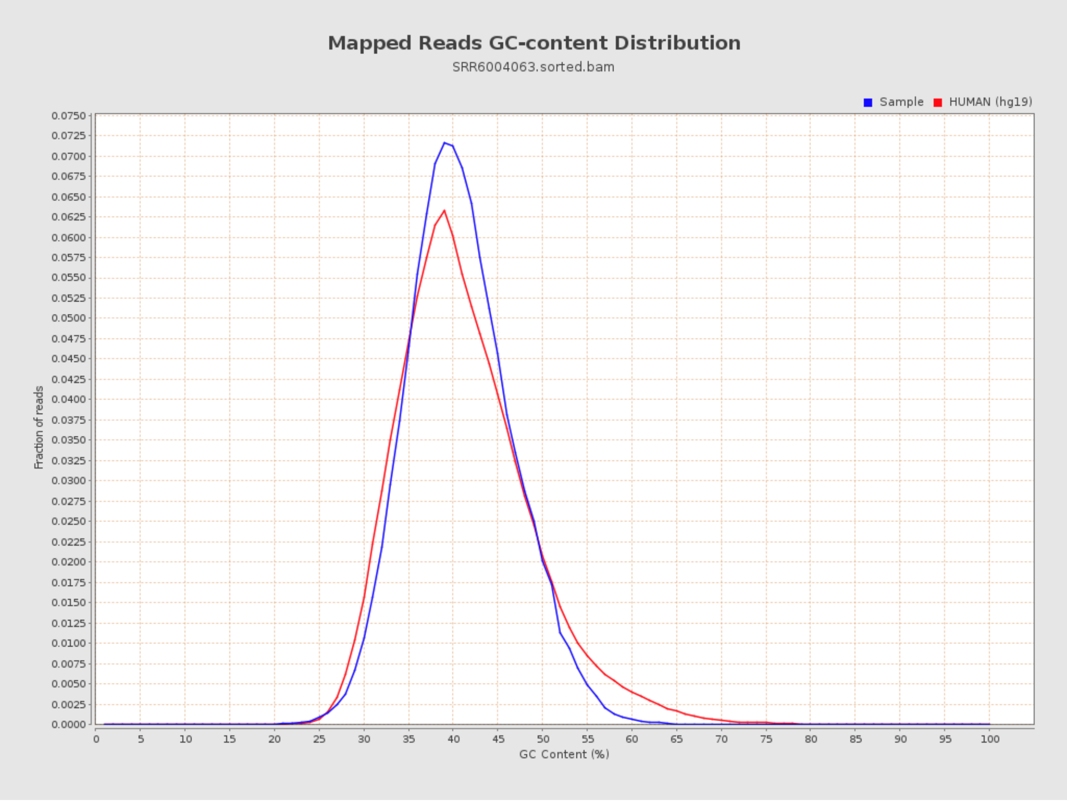
7. Results : Duplication Rate Histogram



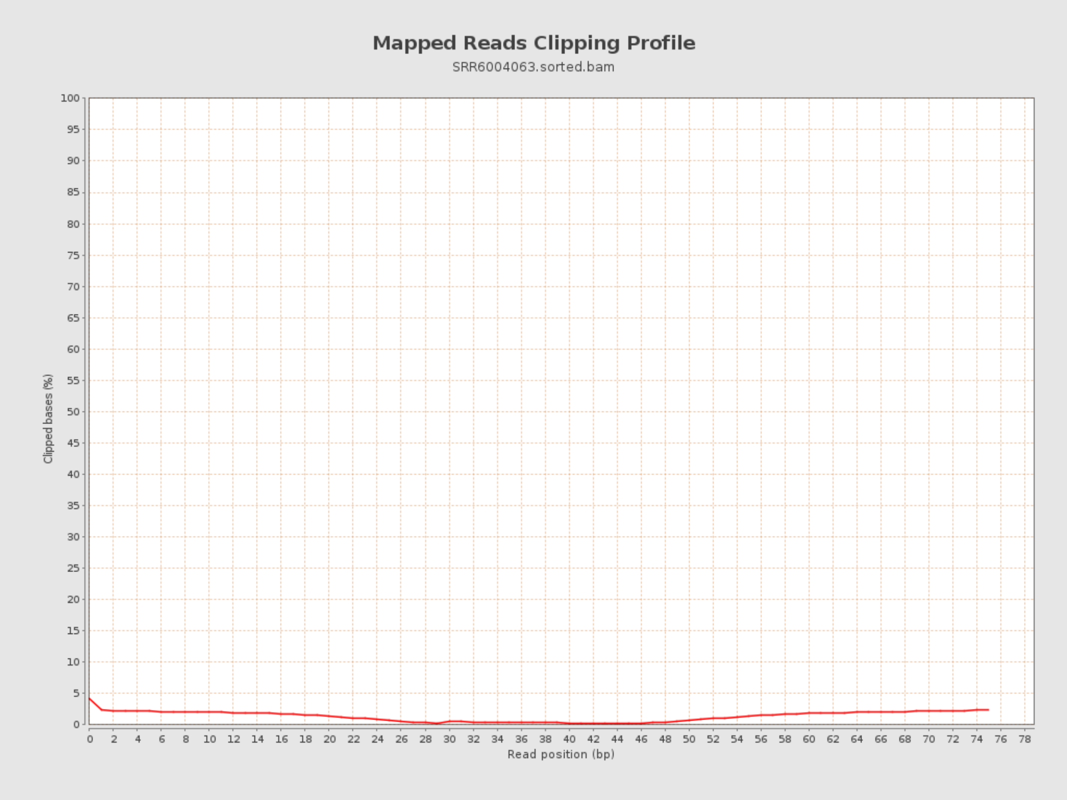
8. Results : Mapped Reads Nucleotide Content



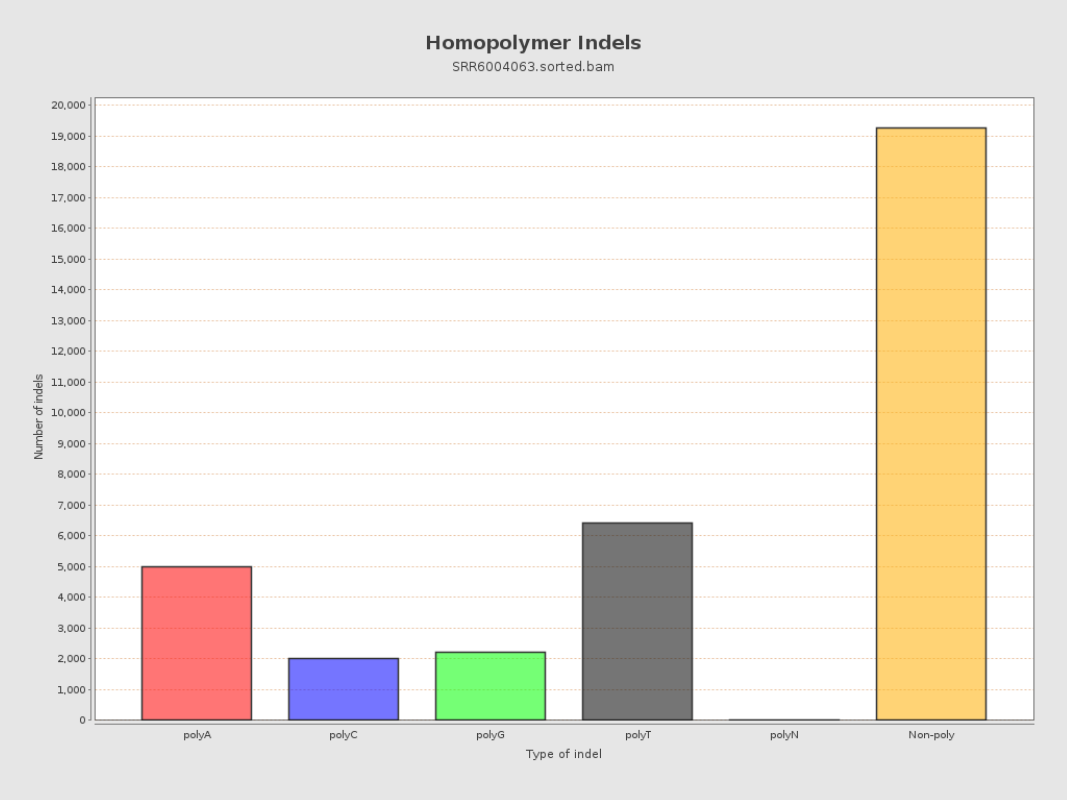
9. Results : Mapped Reads GC-content Distribution



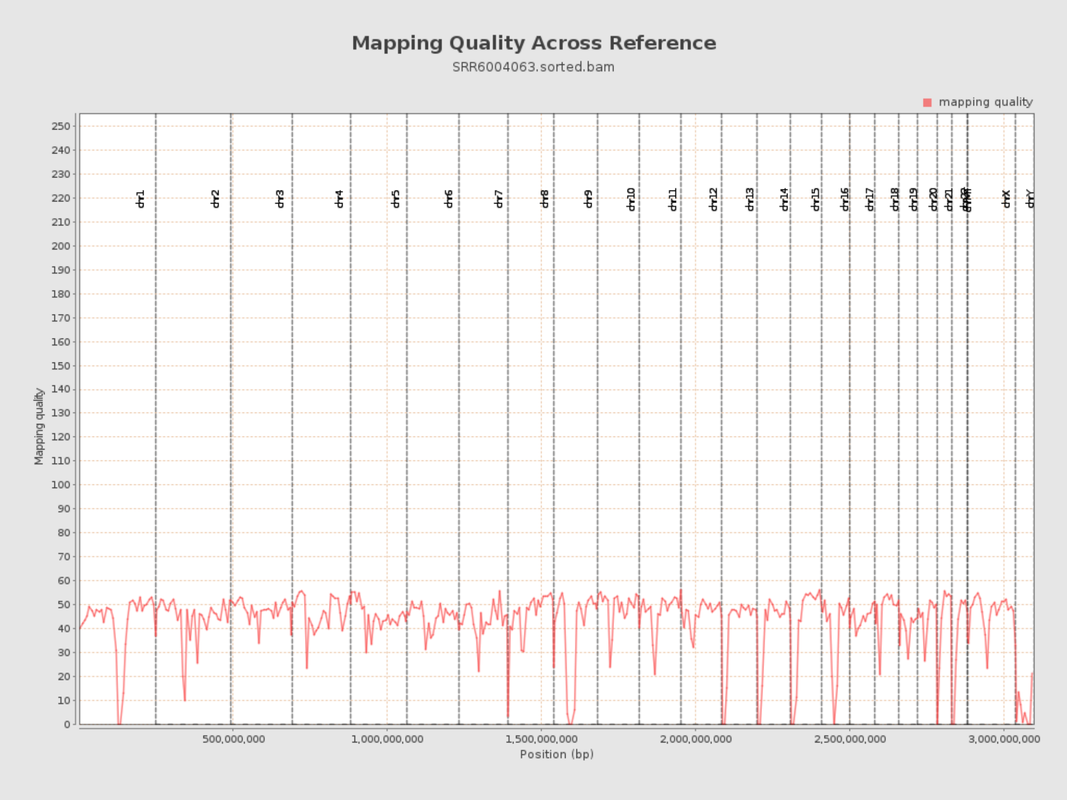
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram