Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 00:28:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063529.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_SRR6063529 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063529.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 00:28:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063529.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,286,568
Mapped reads	4,037,294 / 94.18%
Unmapped reads	249,274 / 5.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,357 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	602,322 / 14.05%
Duplication rate	12.07%
Clipped reads	2,188,058 / 51.04%

2.2. ACGT Content

Number/percentage of A's	66,517,084 / 25.74%
Number/percentage of C's	46,795,848 / 18.11%
Number/percentage of T's	83,924,508 / 32.47%
Number/percentage of G's	61,182,555 / 23.67%
Number/percentage of N's	29,371 / 0.01%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0835

Standard Deviation	0.9763

2.4. Mapping Quality

Mean Mapping Quality	45.67

2.5. Mismatches and indels

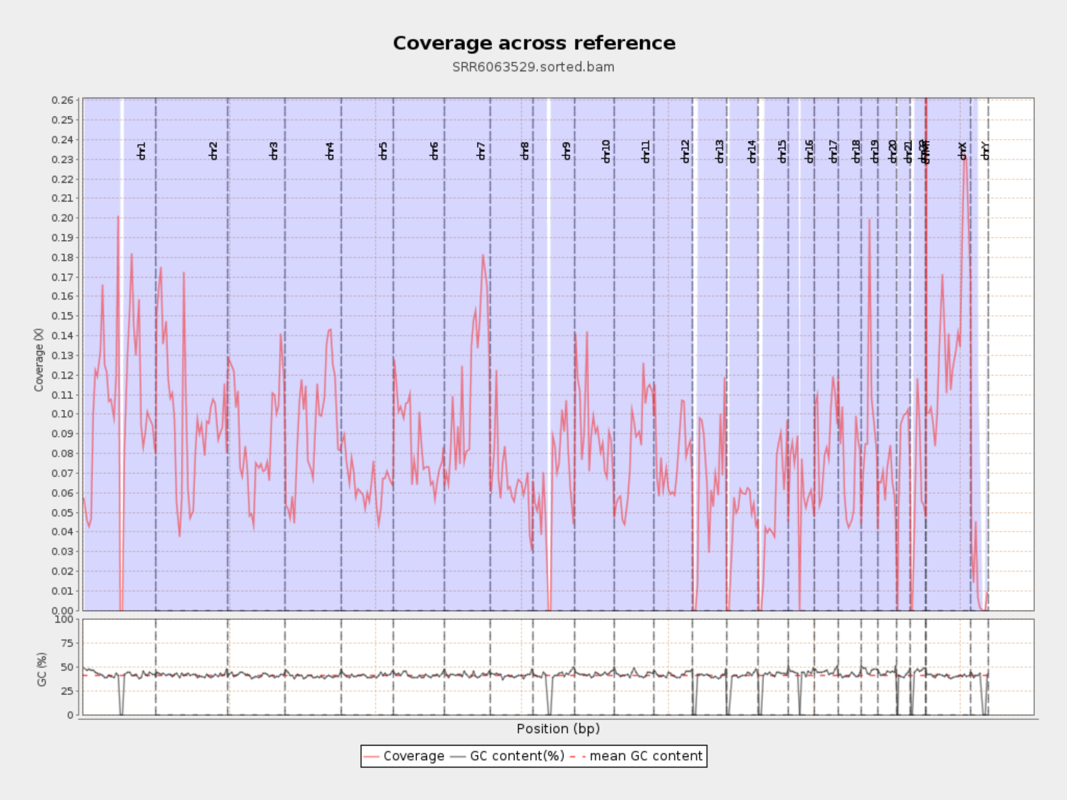
General error rate	0.55%
Mismatches	1,387,994
Insertions	16,598
Mapped reads with at least one insertion	0.41%
Deletions	57,428
Mapped reads with at least one deletion	1.41%
Homopolymer indels	44.42%

2.6. Chromosome stats

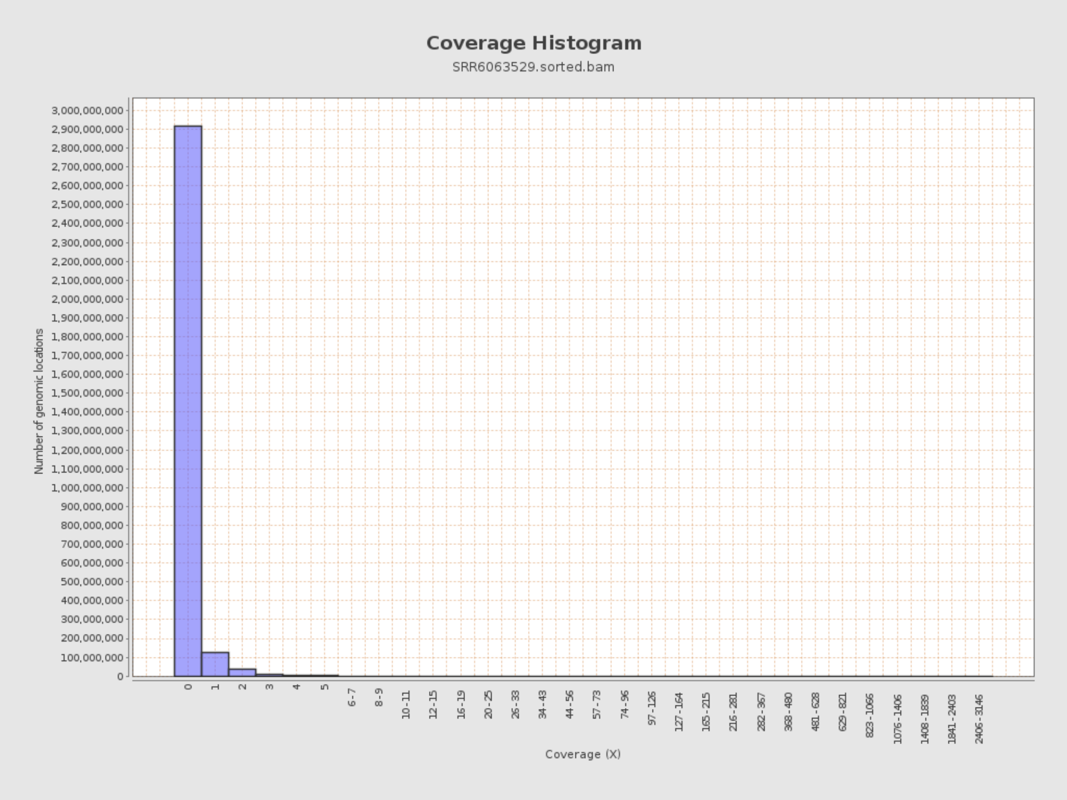
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25974574	0.1042	2.3297
chr2	243199373	24423657	0.1004	1.5242
chr3	198022430	17682868	0.0893	0.4095
chr4	191154276	18000579	0.0942	0.4739
chr5	180915260	11796585	0.0652	0.3587
chr6	171115067	14505547	0.0848	0.5601
chr7	159138663	18015397	0.1132	0.8925

chr8	146364022	9628627	0.0658	0.8832
chr9	141213431	8837205	0.0626	0.7041
chr10	135534747	12627914	0.0932	0.6561
chr11	135006516	11203487	0.083	0.5538
chr12	133851895	10306138	0.077	0.4423
chr13	115169878	7312013	0.0635	0.3849
chr14	107349540	5025988	0.0468	0.4161
chr15	102531392	5020412	0.049	0.3347
chr16	90354753	5553766	0.0615	0.3946
chr17	81195210	7315216	0.0901	0.4599
chr18	78077248	5619323	0.072	1.2993
chr19	59128983	5827280	0.0986	1.3442
chr20	63025520	4185701	0.0664	0.4073
chr21	48129895	3842786	0.0798	0.4367
chr22	51304566	2910901	0.0567	0.3204
chrMT	16571	536085	32.3508	18.1446
chrX	155270560	21633184	0.1393	0.627
chrY	59373566	764430	0.0129	0.5069

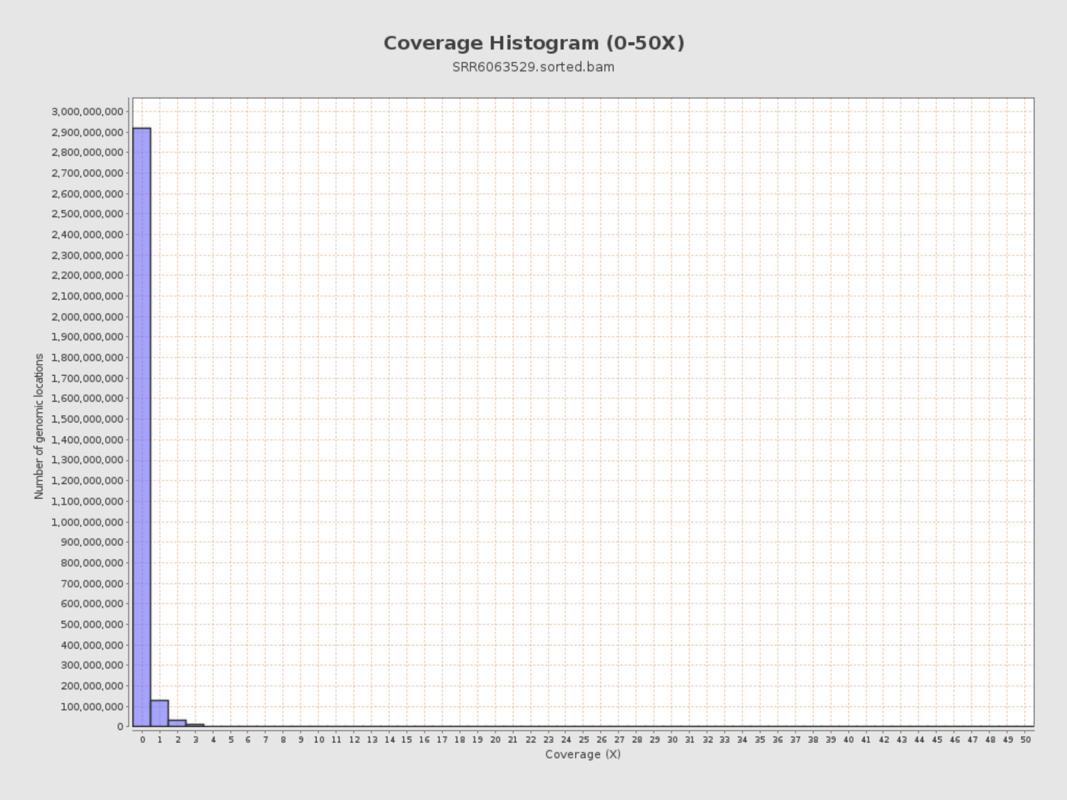
3. Results : Coverage across reference



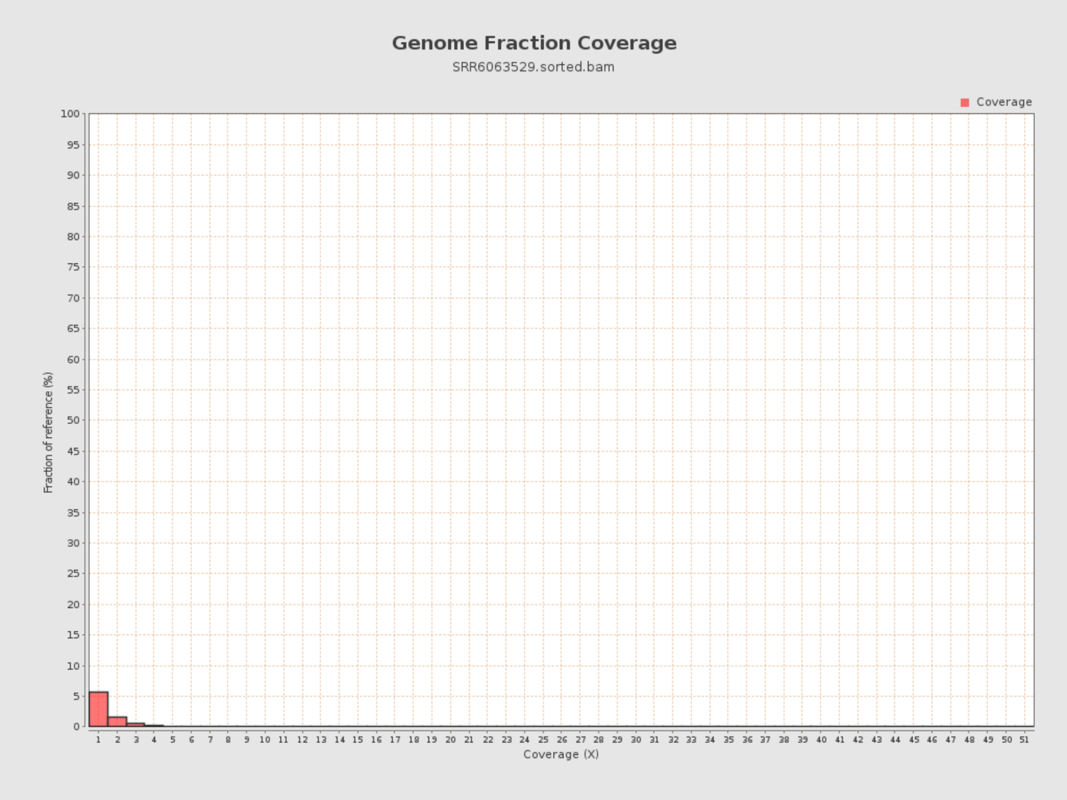
4. Results : Coverage Histogram



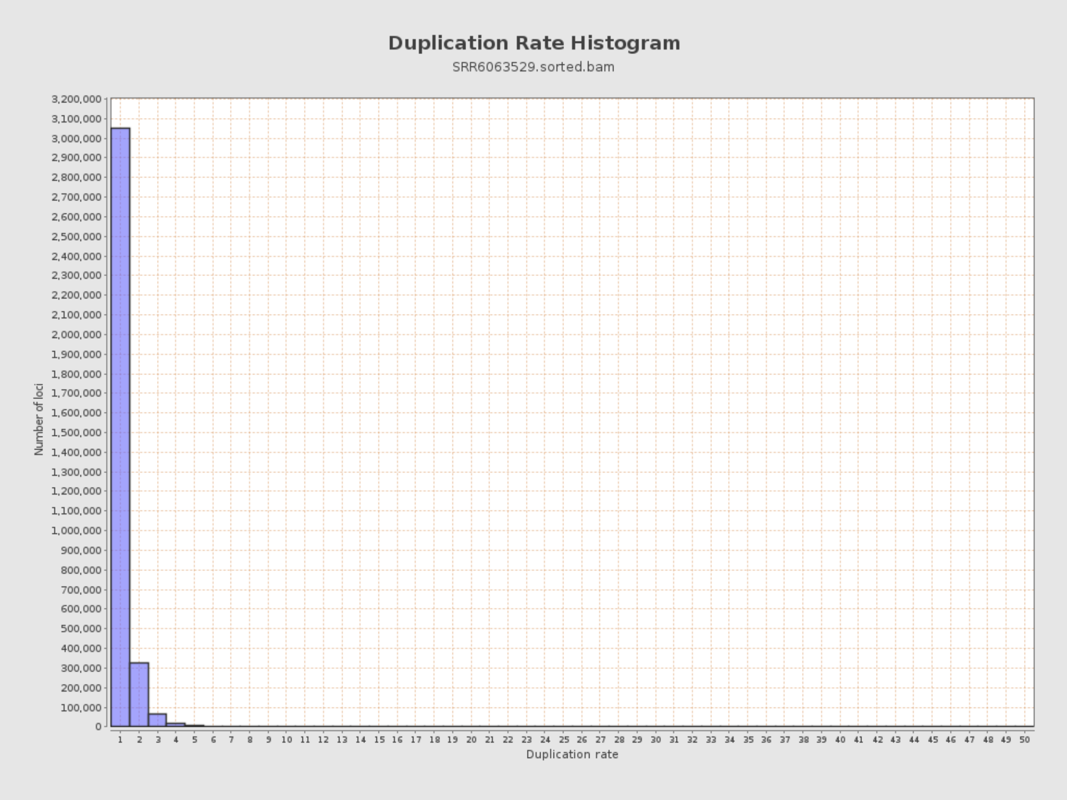
5. Results : Coverage Histogram (0-50X)



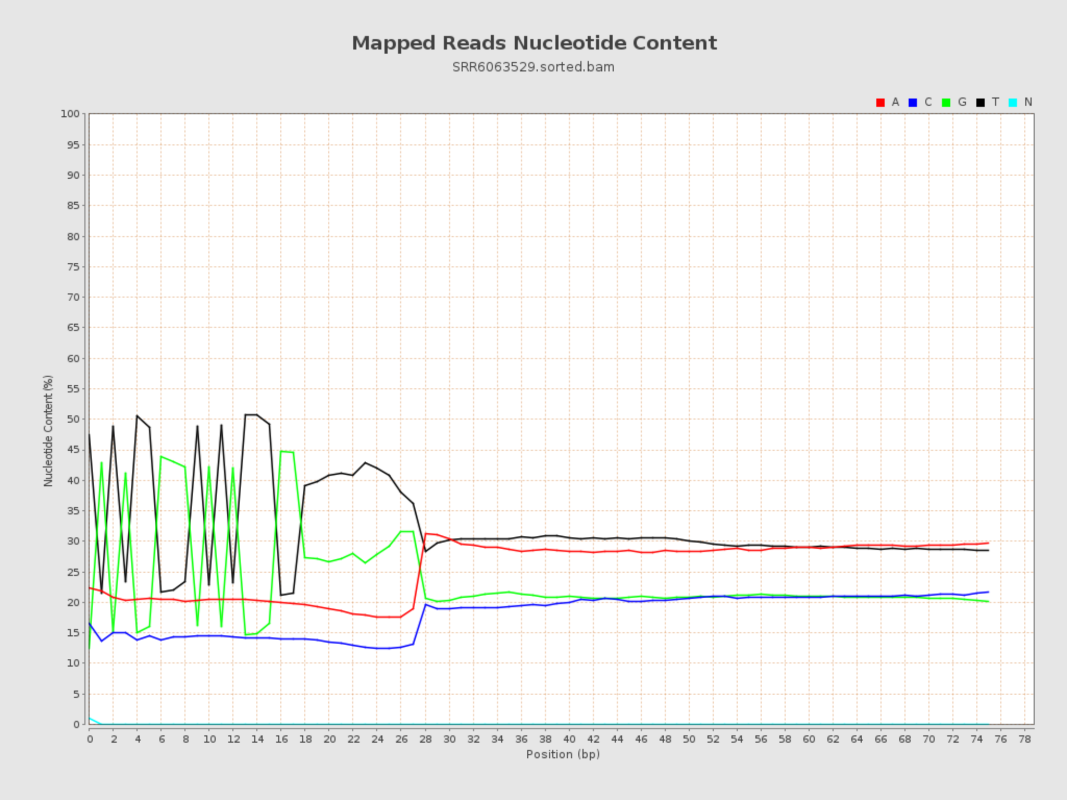
6. Results : Genome Fraction Coverage



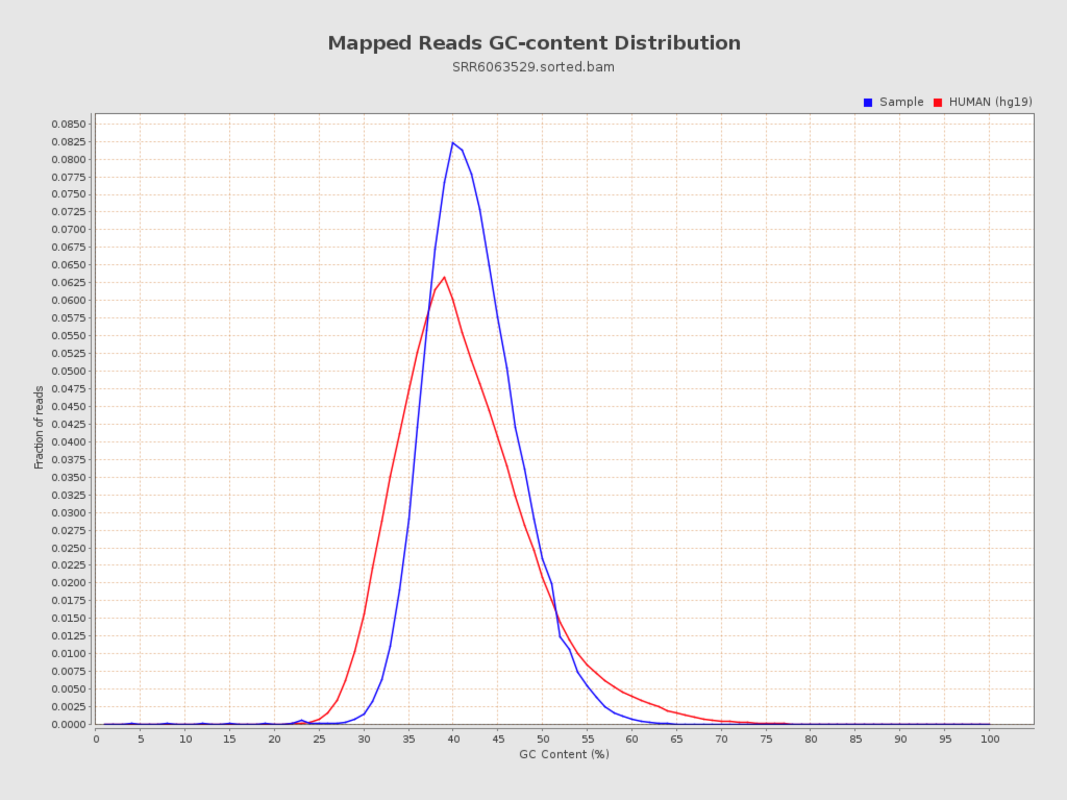
7. Results : Duplication Rate Histogram



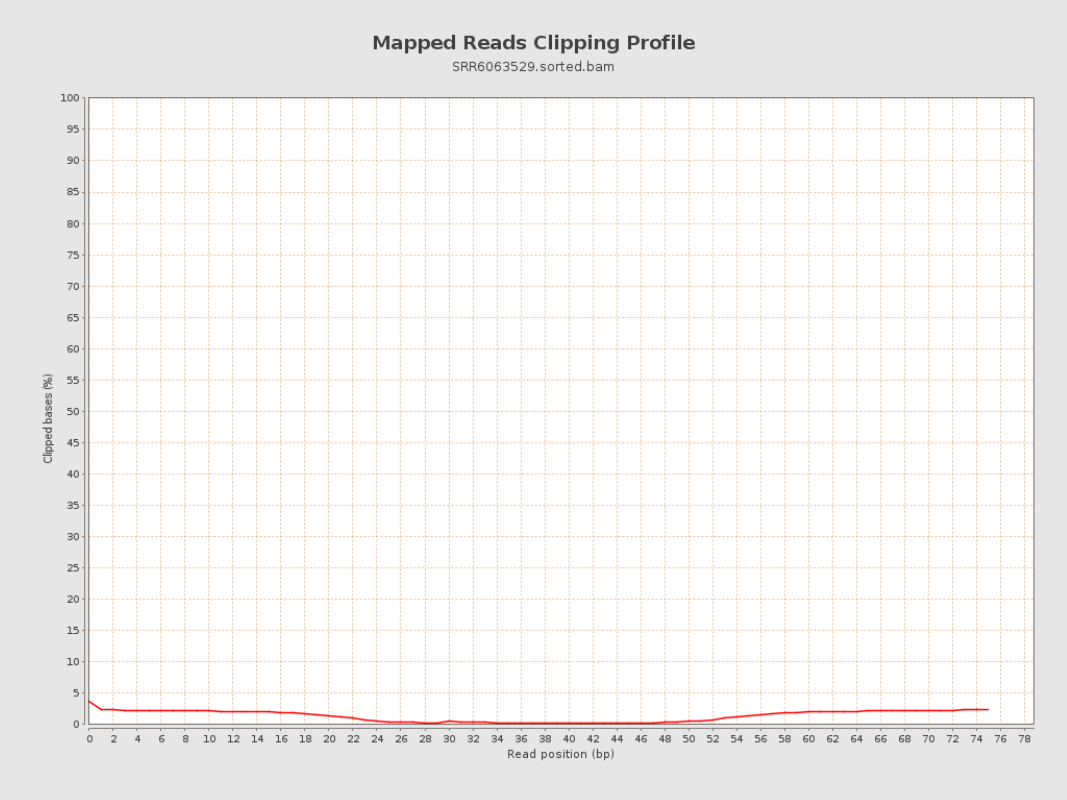
8. Results : Mapped Reads Nucleotide Content



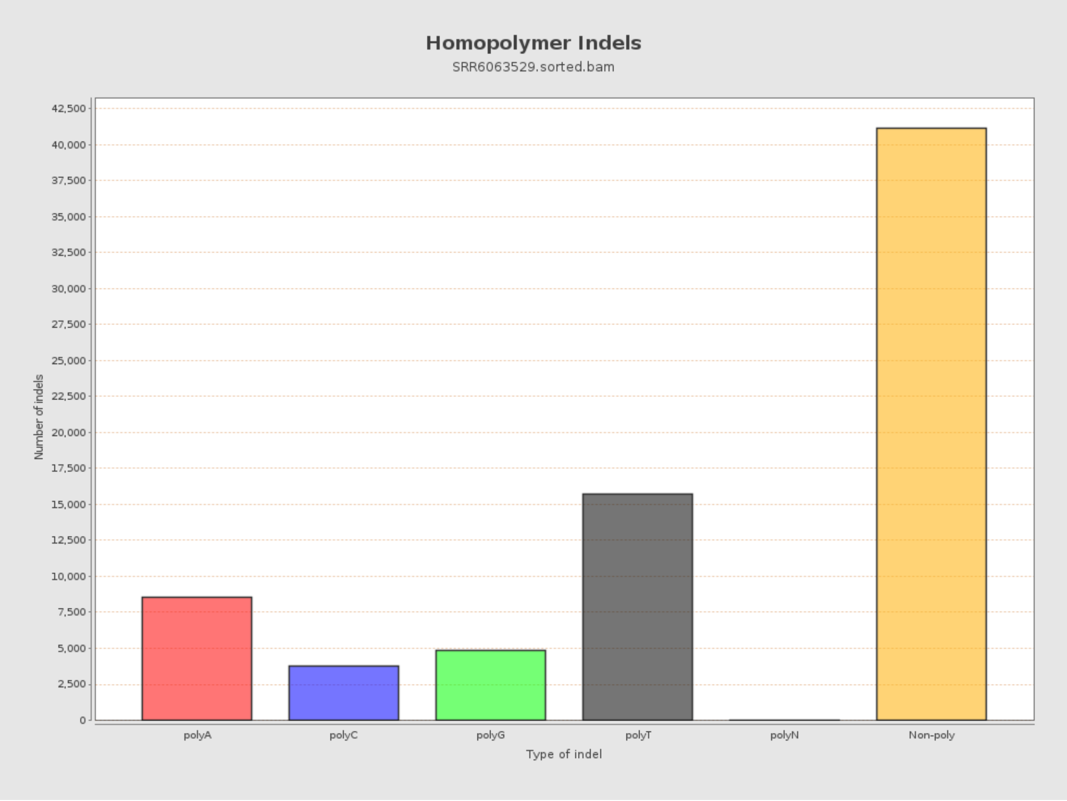
9. Results : Mapped Reads GC-content Distribution



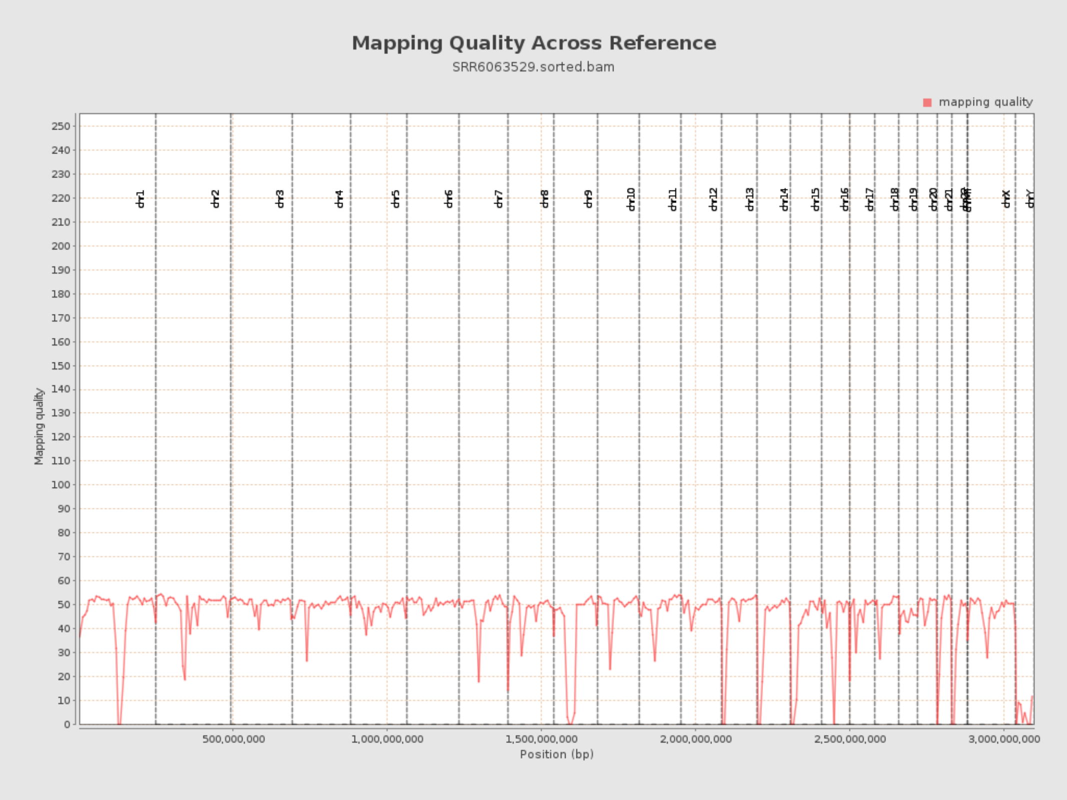
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram