Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 18:33:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013263.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_SRR6013263 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013263.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 18:33:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013263.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,089,100
Mapped reads	1,845,587 / 88.34%
Unmapped reads	243,513 / 11.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,366 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	124,361 / 5.95%
Duplication rate	5.28%
Clipped reads	772,911 / 37%

2.2. ACGT Content

Number/percentage of A's	35,152,881 / 28.23%
Number/percentage of C's	22,602,157 / 18.15%
Number/percentage of T's	40,254,926 / 32.33%
Number/percentage of G's	26,488,720 / 21.27%
Number/percentage of N's	26,591 / 0.02%
GC Percentage	39.42%

2.3. Coverage

Mean	0.0402

Standard Deviation	0.4066

2.4. Mapping Quality

Mean Mapping Quality	42.72

2.5. Mismatches and indels

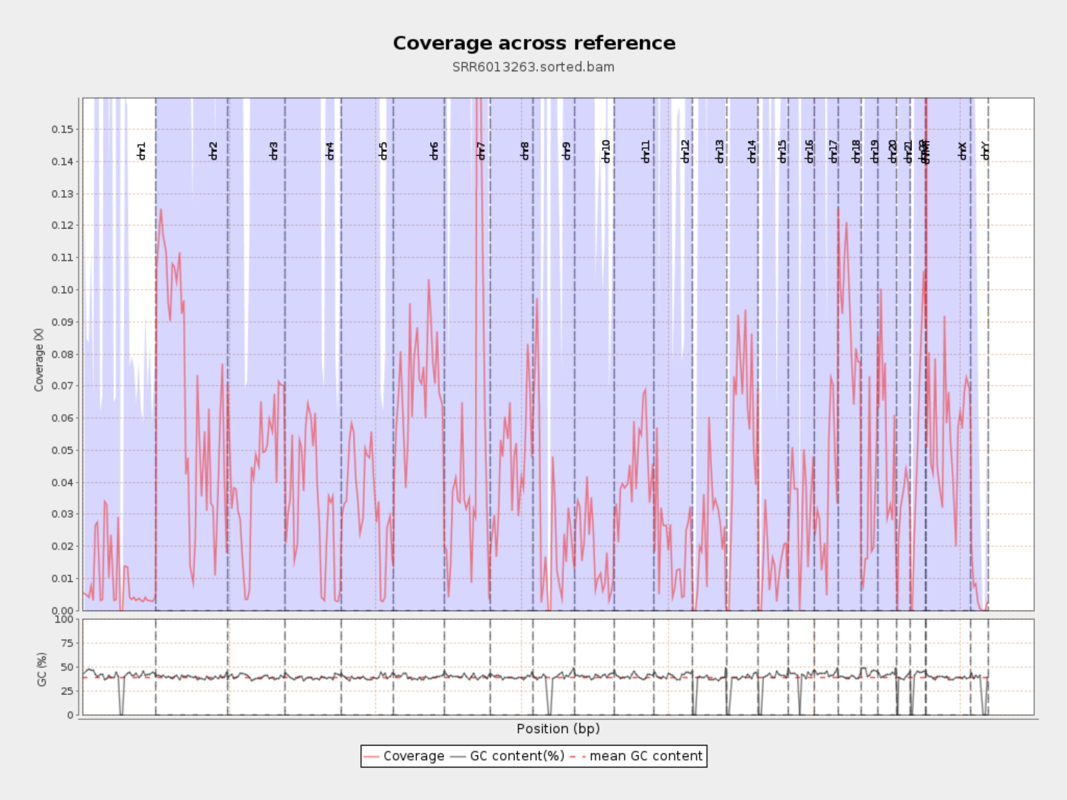
General error rate	0.84%
Mismatches	1,029,880
Insertions	9,169
Mapped reads with at least one insertion	0.49%
Deletions	31,582
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.24%

2.6. Chromosome stats

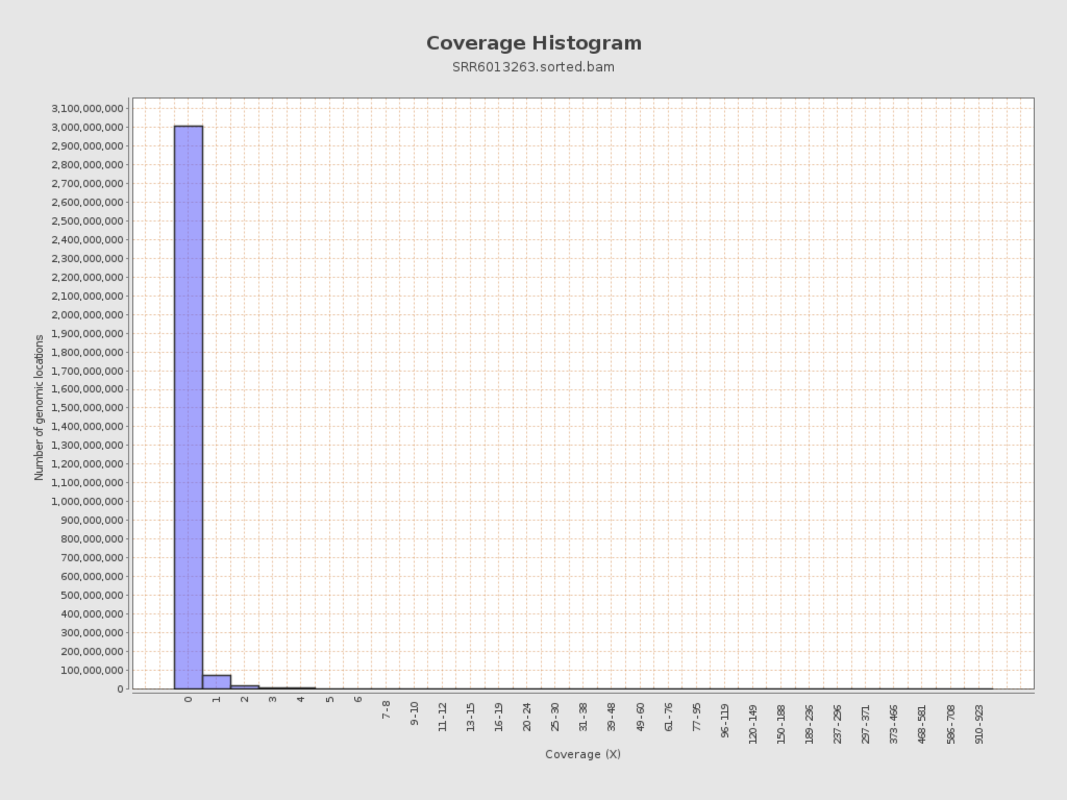
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2263163	0.0091	0.4786
chr2	243199373	16362524	0.0673	0.6716
chr3	198022430	8722845	0.044	0.2694
chr4	191154276	6353494	0.0332	0.238
chr5	180915260	6089078	0.0337	0.2385
chr6	171115067	12113178	0.0708	0.4451
chr7	159138663	8412466	0.0529	0.5286

chr8	146364022	6738854	0.046	0.5145
chr9	141213431	3830736	0.0271	0.4145
chr10	135534747	2525630	0.0186	0.3162
chr11	135006516	6000882	0.0444	0.3624
chr12	133851895	2654114	0.0198	0.1862
chr13	115169878	2817770	0.0245	0.2033
chr14	107349540	6267771	0.0584	0.3252
chr15	102531392	1419292	0.0138	0.1505
chr16	90354753	2991655	0.0331	0.2686
chr17	81195210	2970864	0.0366	0.2525
chr18	78077248	7245739	0.0928	0.8572
chr19	59128983	1805444	0.0305	0.4175
chr20	63025520	3475947	0.0552	0.3093
chr21	48129895	1521436	0.0316	0.232
chr22	51304566	2796177	0.0545	0.3032
chrMT	16571	123353	7.4439	6.0046
chrX	155270560	8804203	0.0567	0.3368
chrY	59373566	271806	0.0046	0.098

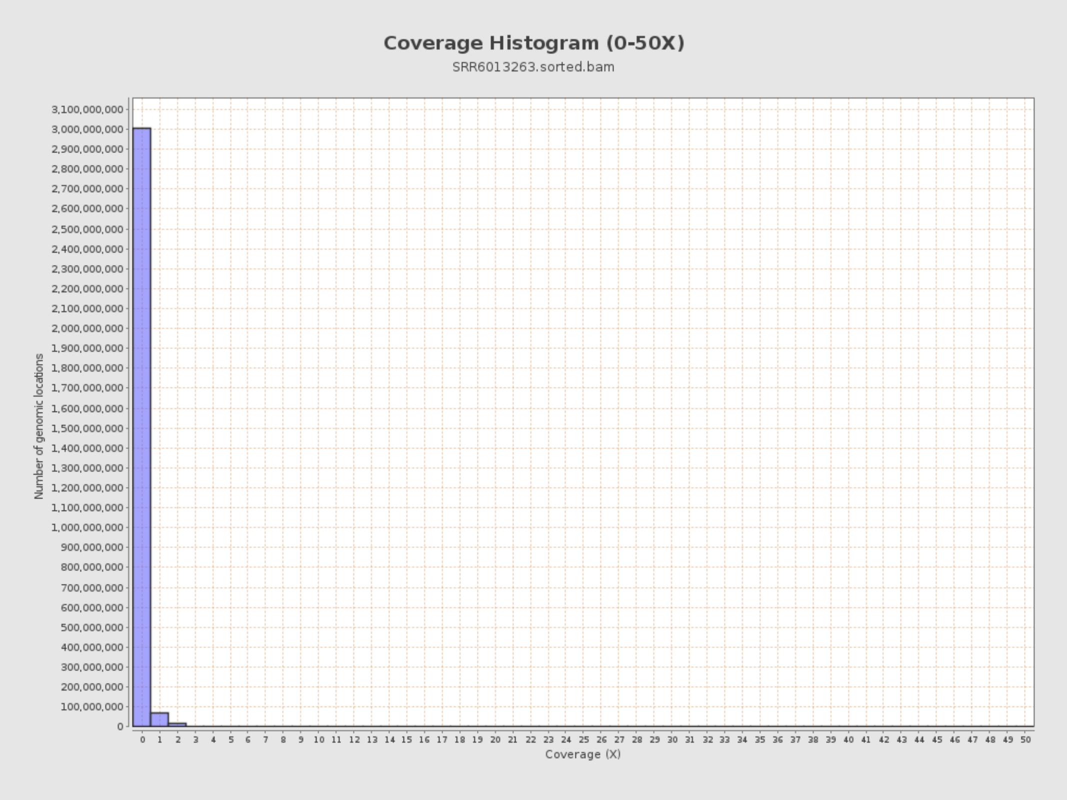
3. Results : Coverage across reference



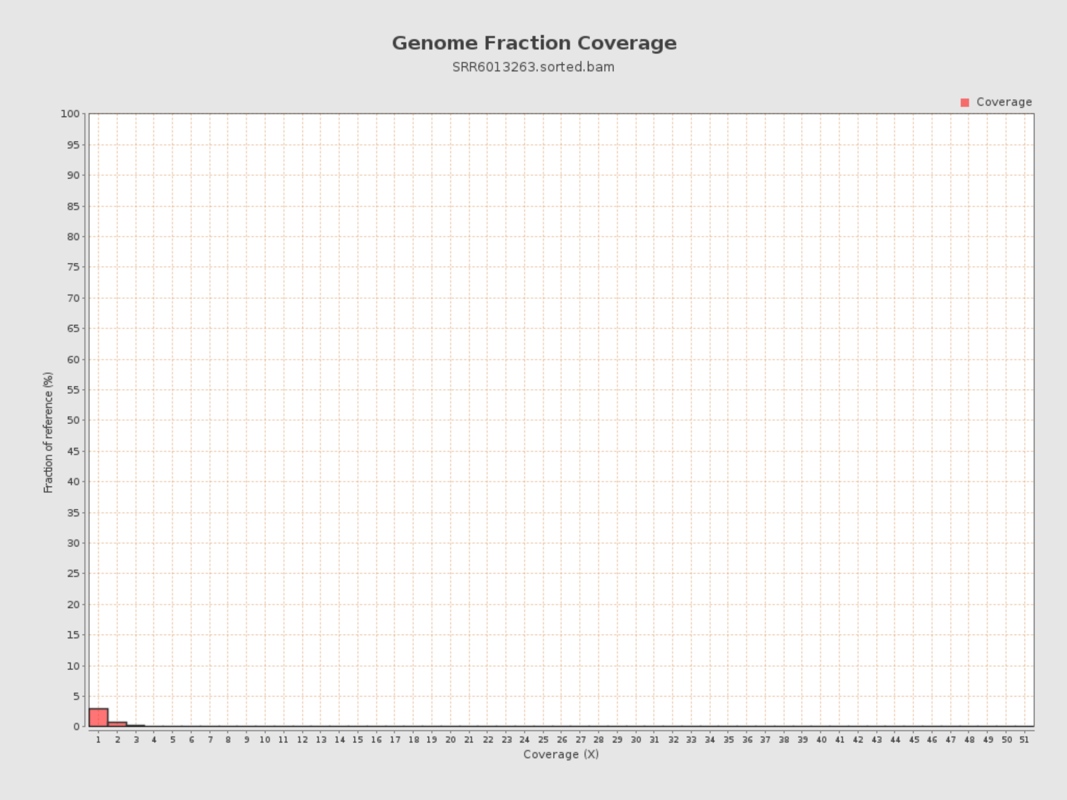
4. Results : Coverage Histogram



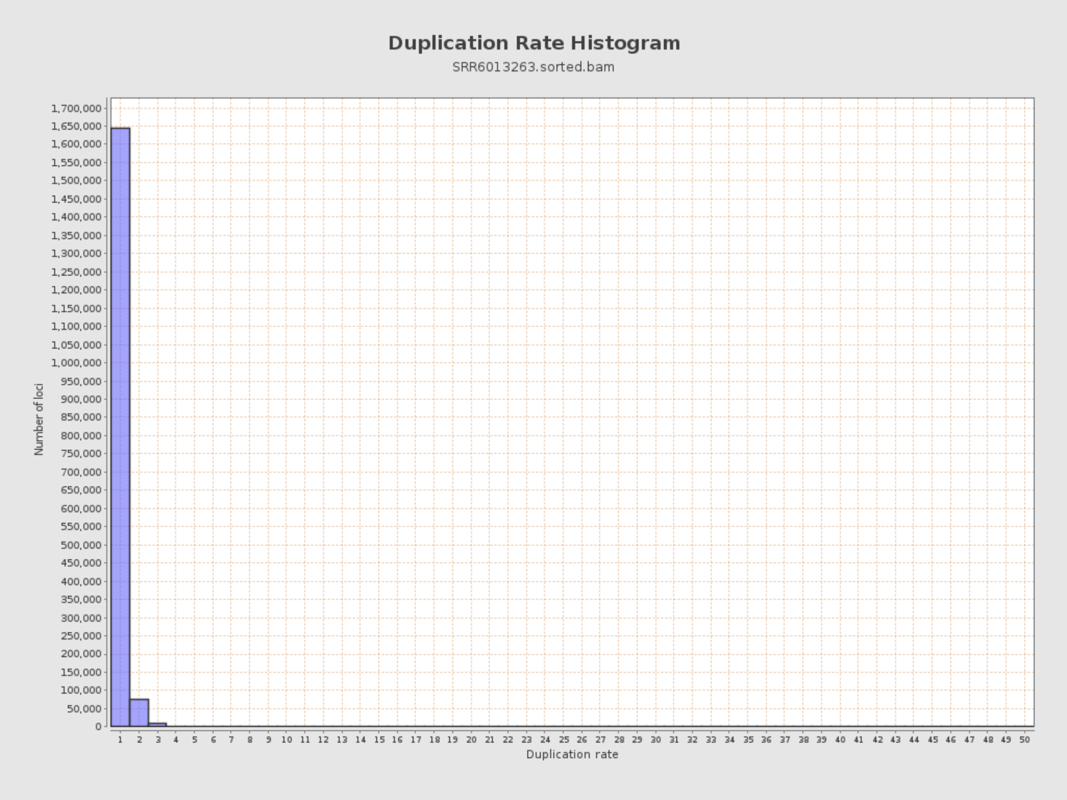
5. Results : Coverage Histogram (0-50X)



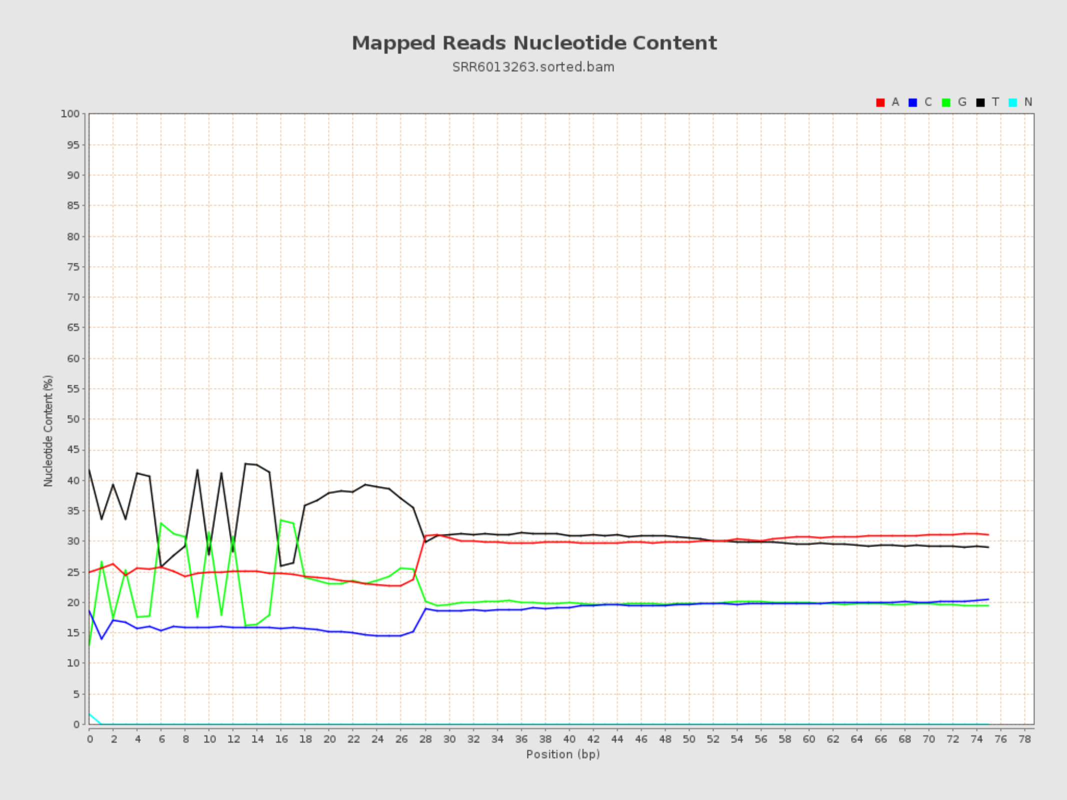
6. Results : Genome Fraction Coverage



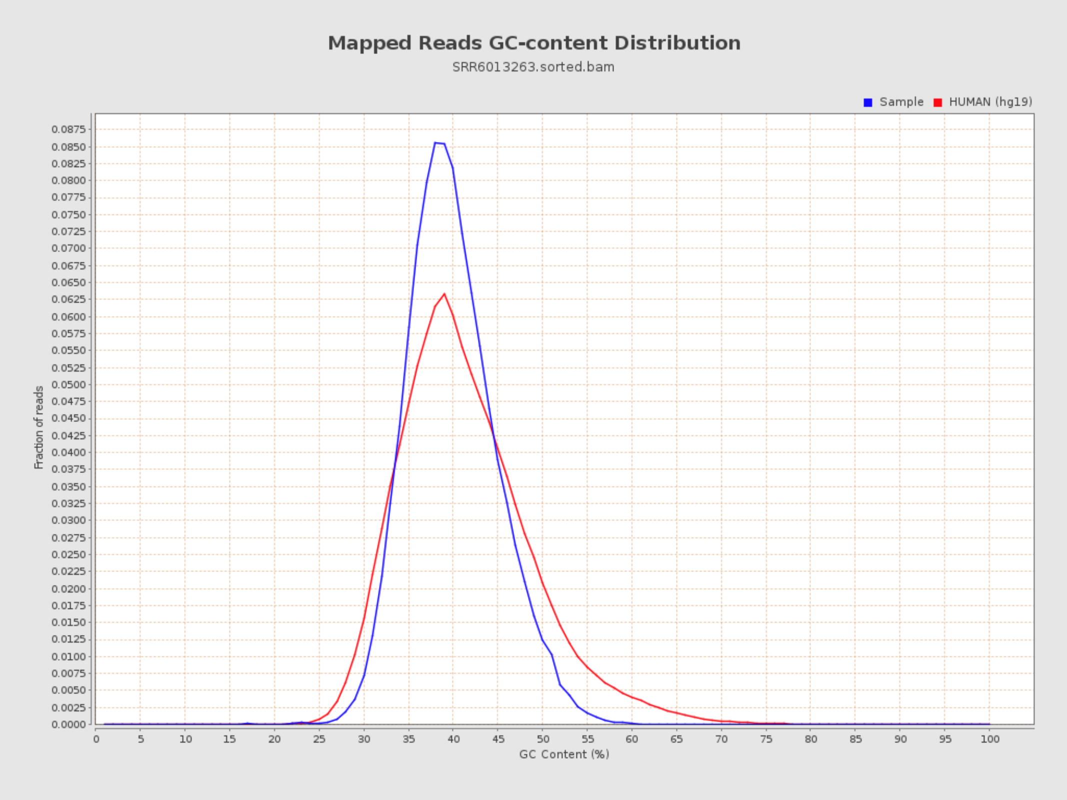
7. Results : Duplication Rate Histogram



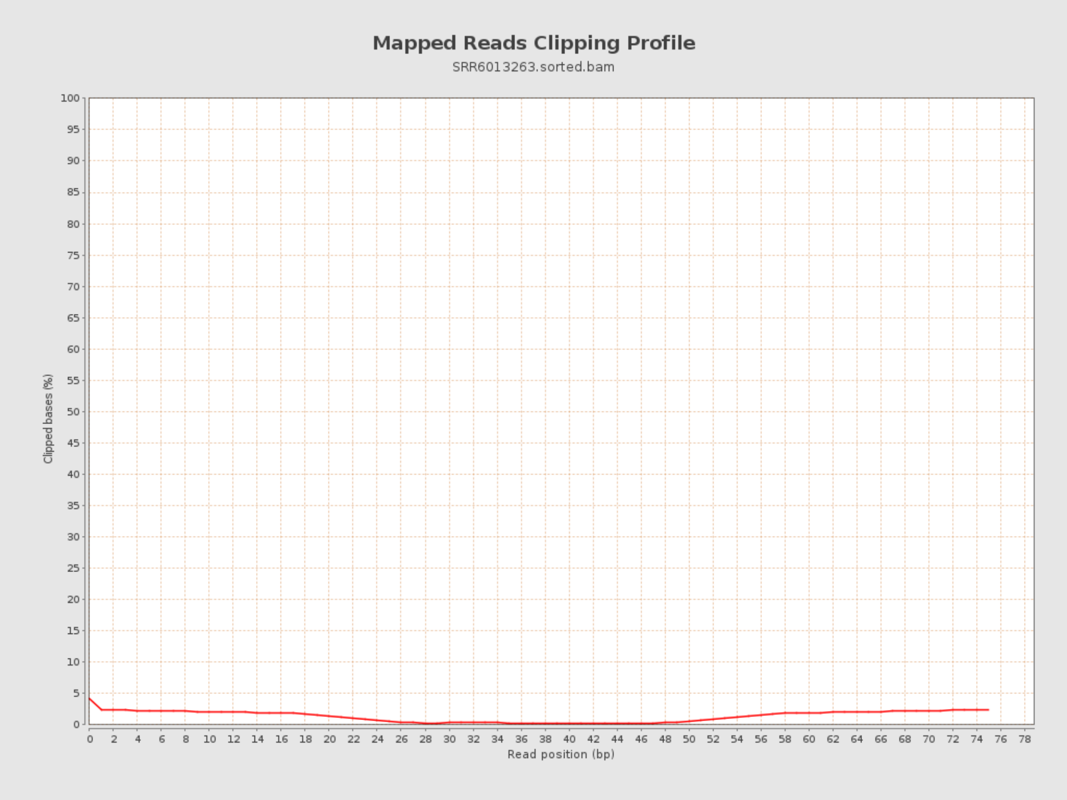
8. Results : Mapped Reads Nucleotide Content



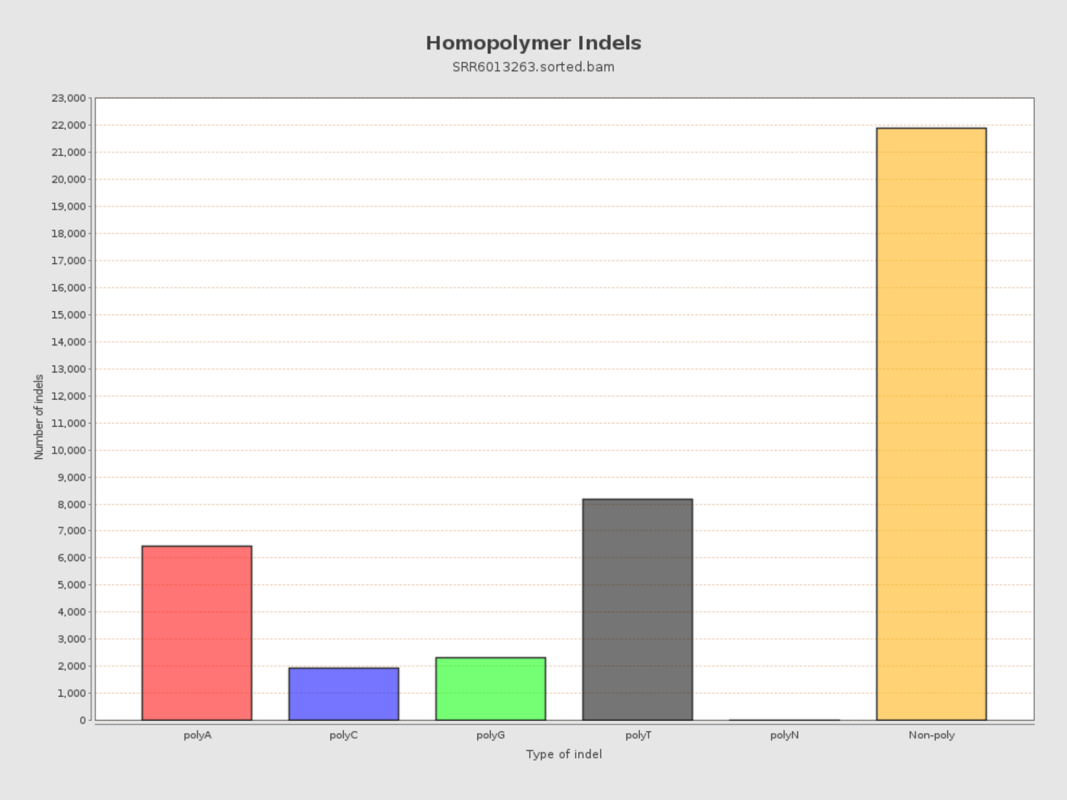
9. Results : Mapped Reads GC-content Distribution



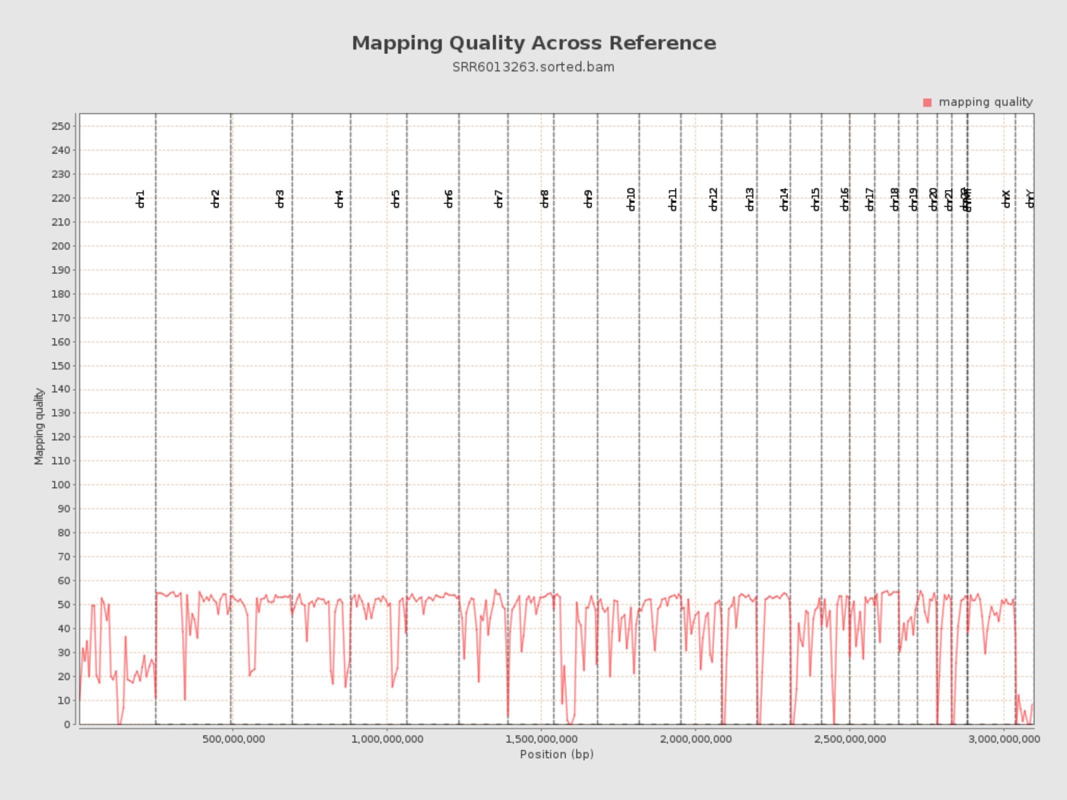
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram