Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 17:21:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013235.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_SRR6013235 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013235.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 17:21:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013235.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,858,666
Mapped reads	1,661,617 / 89.4%
Unmapped reads	197,049 / 10.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,607 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	124,152 / 6.68%
Duplication rate	5.88%
Clipped reads	684,540 / 36.83%

2.2. ACGT Content

Number/percentage of A's	31,700,996 / 28.2%
Number/percentage of C's	20,630,604 / 18.35%
Number/percentage of T's	35,971,678 / 32%
Number/percentage of G's	24,079,133 / 21.42%
Number/percentage of N's	25,084 / 0.02%
GC Percentage	39.77%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.3996

2.4. Mapping Quality

Mean Mapping Quality	47.04

2.5. Mismatches and indels

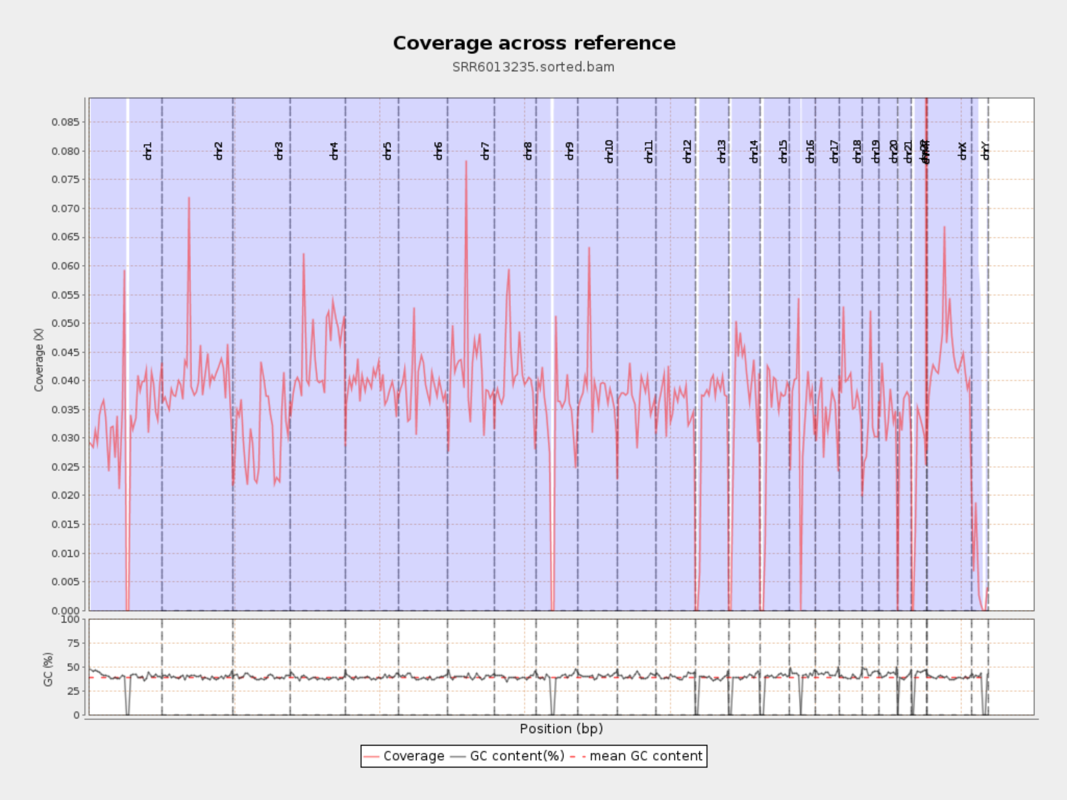
General error rate	0.81%
Mismatches	890,465
Insertions	8,711
Mapped reads with at least one insertion	0.52%
Deletions	24,972
Mapped reads with at least one deletion	1.49%
Homopolymer indels	47.45%

2.6. Chromosome stats

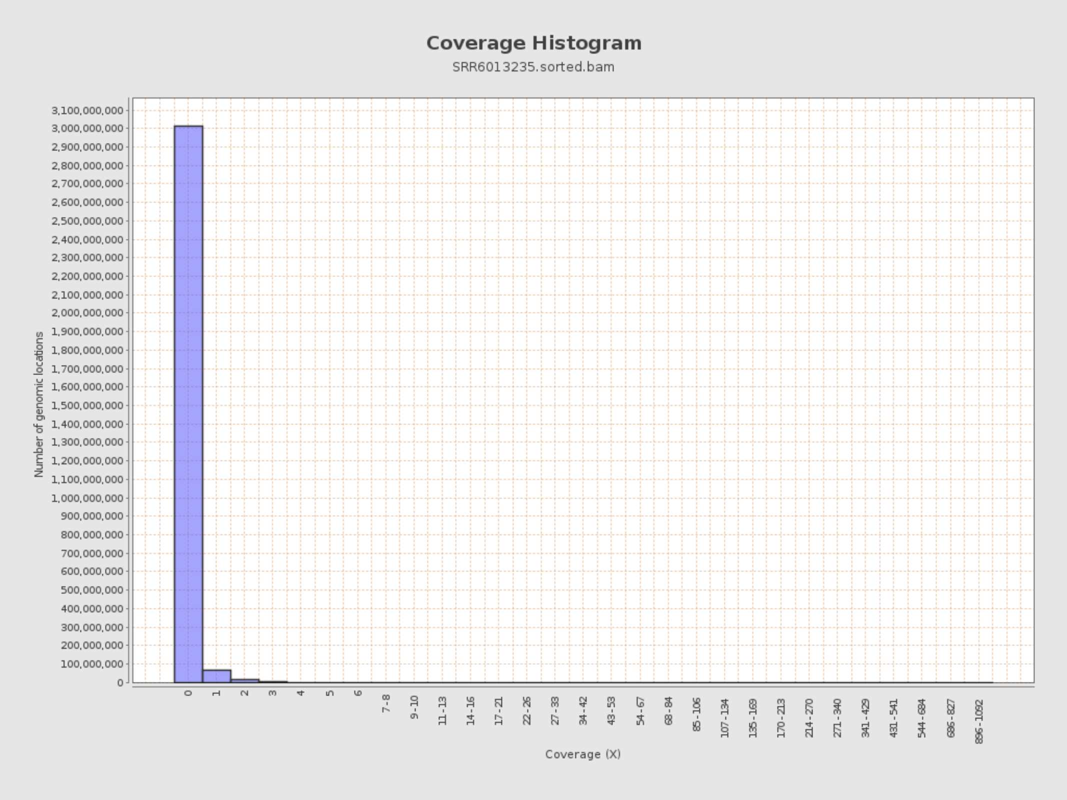
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8129623	0.0326	0.6442
chr2	243199373	9893095	0.0407	0.4313
chr3	198022430	6065523	0.0306	0.2233
chr4	191154276	8570349	0.0448	0.2953
chr5	180915260	7082311	0.0391	0.254
chr6	171115067	6692458	0.0391	0.2848
chr7	159138663	6747514	0.0424	0.6075

chr8	146364022	6030801	0.0412	0.6987
chr9	141213431	4578445	0.0324	0.3553
chr10	135534747	5257430	0.0388	0.3592
chr11	135006516	4986531	0.0369	0.3039
chr12	133851895	4813986	0.036	0.2478
chr13	115169878	3694413	0.0321	0.2284
chr14	107349540	3785295	0.0353	0.252
chr15	102531392	3207833	0.0313	0.2236
chr16	90354753	3100690	0.0343	0.2694
chr17	81195210	2704490	0.0333	0.2583
chr18	78077248	3065734	0.0393	0.7071
chr19	59128983	1917886	0.0324	0.4701
chr20	63025520	2189661	0.0347	0.2433
chr21	48129895	1525530	0.0317	0.2469
chr22	51304566	1167206	0.0228	0.1871
chrMT	16571	125259	7.5589	5.3049
chrX	155270560	6792437	0.0437	0.2991
chrY	59373566	326574	0.0055	0.1578

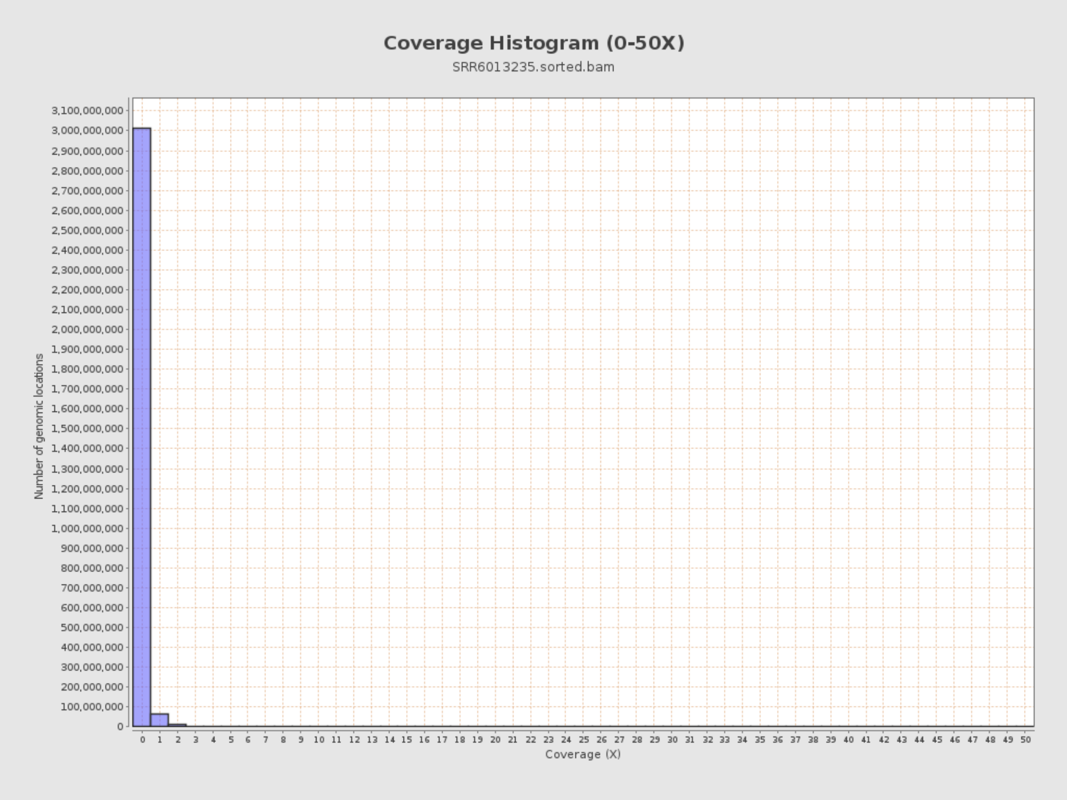
3. Results : Coverage across reference



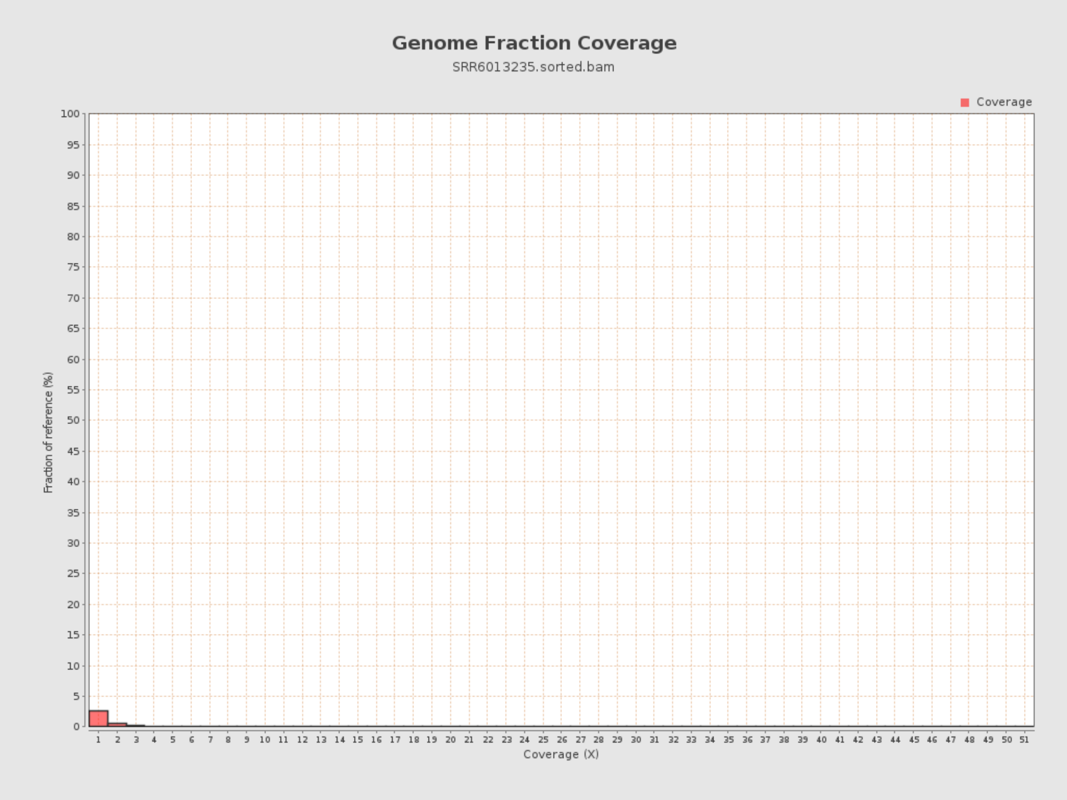
4. Results : Coverage Histogram



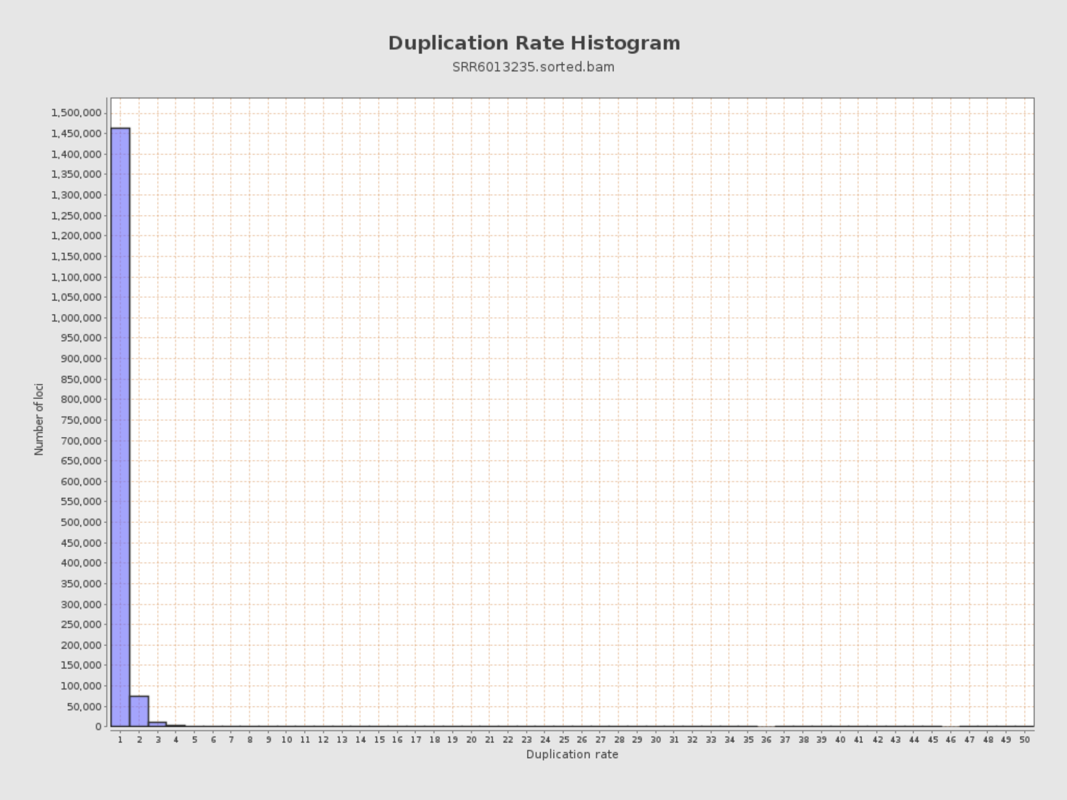
5. Results : Coverage Histogram (0-50X)



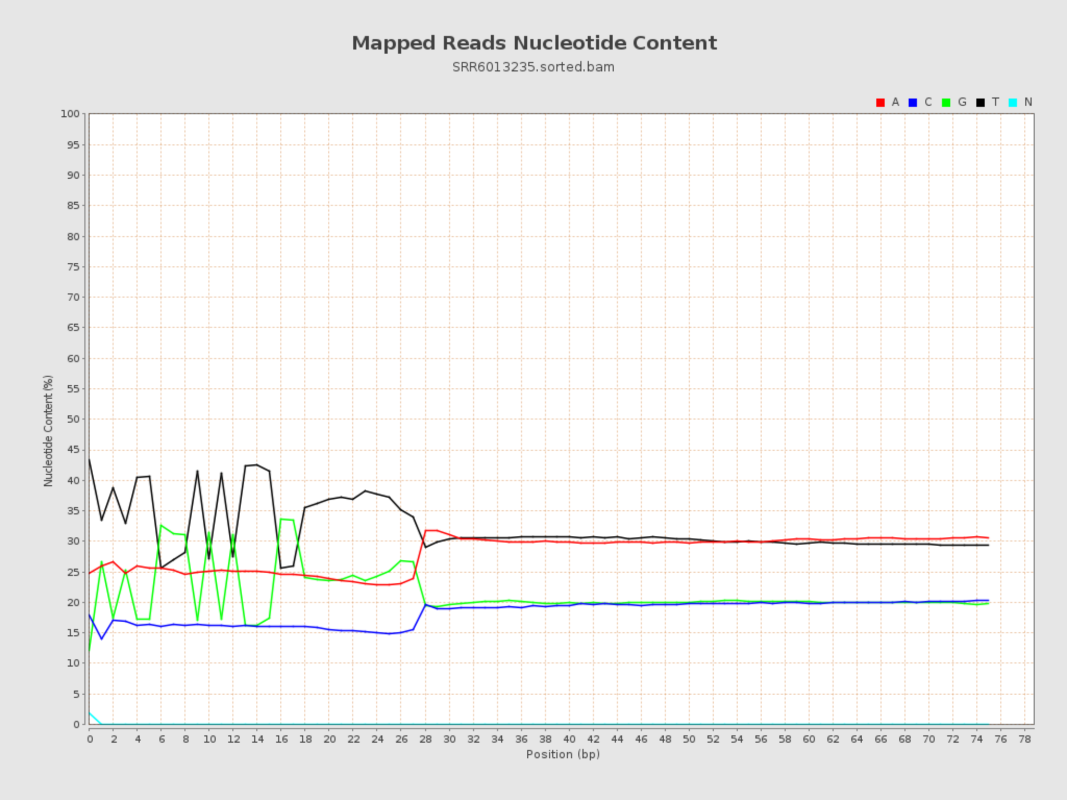
6. Results : Genome Fraction Coverage



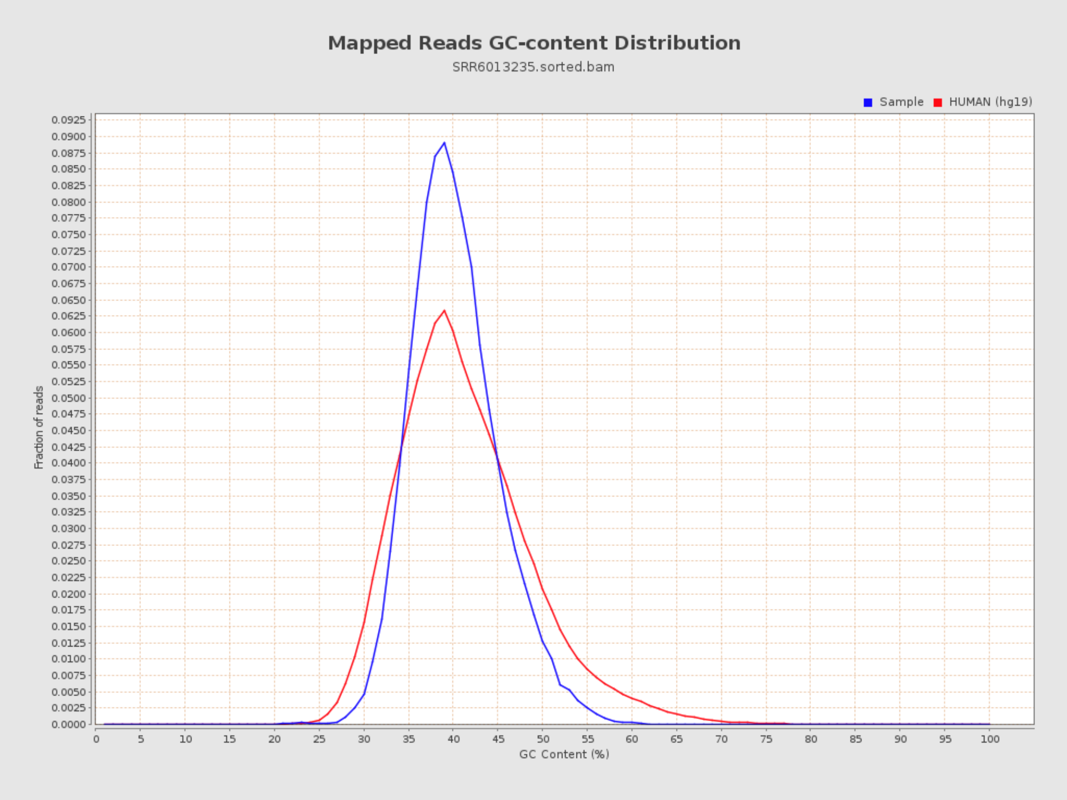
7. Results : Duplication Rate Histogram



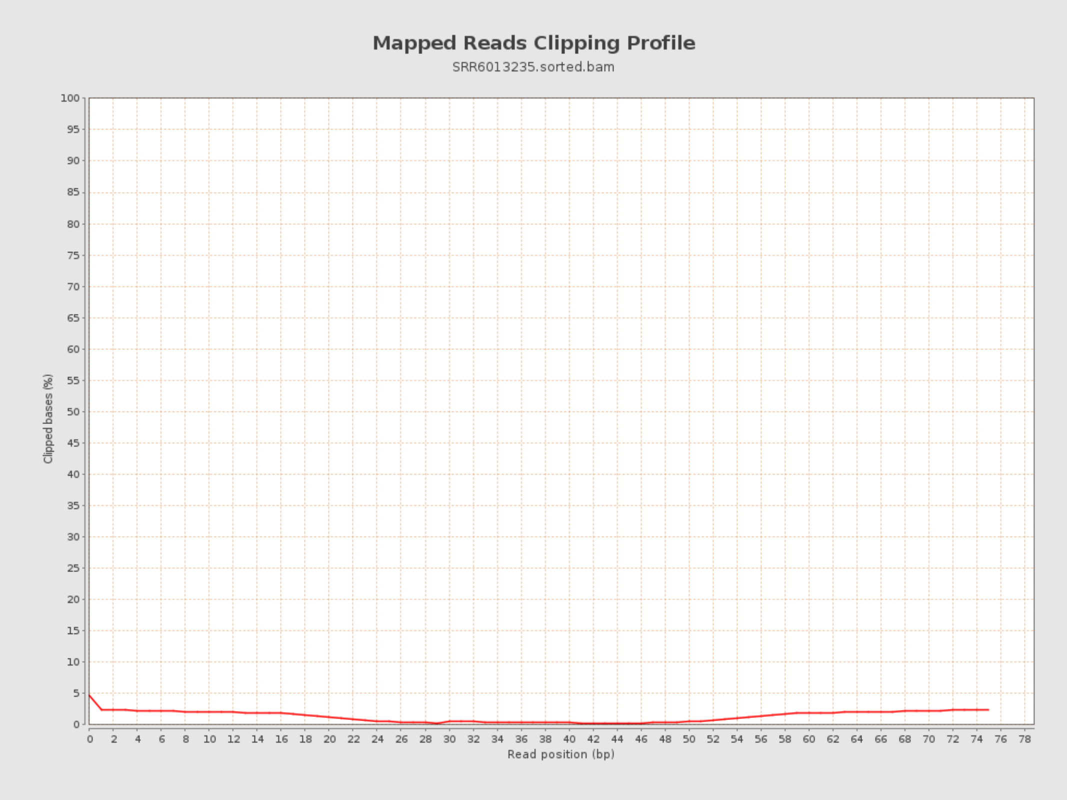
8. Results : Mapped Reads Nucleotide Content



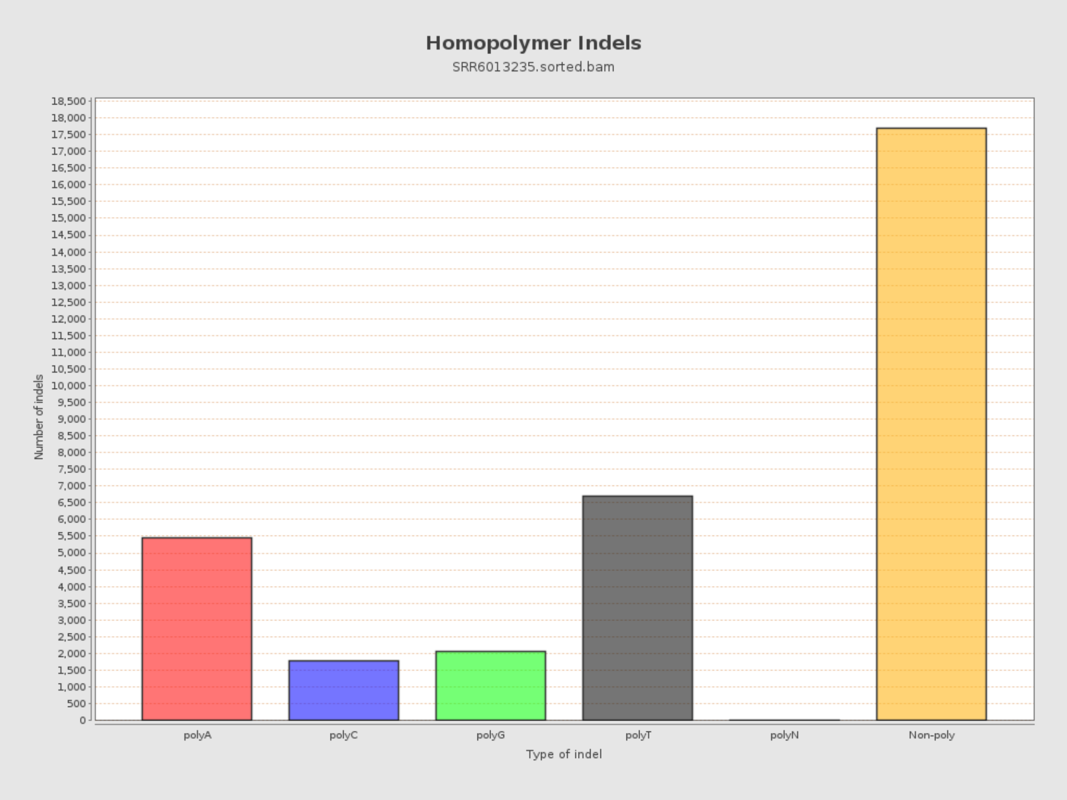
9. Results : Mapped Reads GC-content Distribution



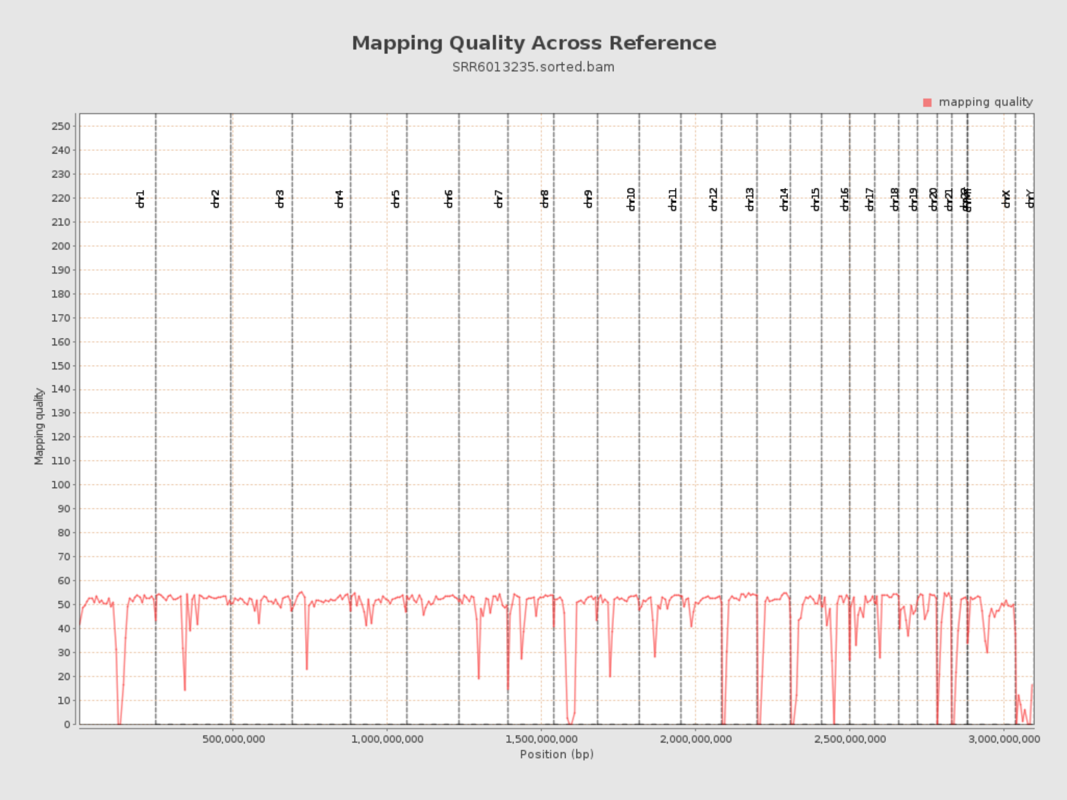
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram