Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:53:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237849.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_SRR6237849 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237849.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:53:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237849.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,525,116
Mapped reads	1,857,662 / 73.57%
Unmapped reads	667,454 / 26.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,172 / 0.36%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	193,957 / 7.68%
Duplication rate	8.45%
Clipped reads	1,197,847 / 47.44%

2.2. ACGT Content

Number/percentage of A's	29,793,683 / 26.19%
Number/percentage of C's	20,129,130 / 17.7%
Number/percentage of T's	36,492,031 / 32.08%
Number/percentage of G's	27,250,330 / 23.96%
Number/percentage of N's	84,802 / 0.07%
GC Percentage	41.65%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.345

2.4. Mapping Quality

Mean Mapping Quality	45.53

2.5. Mismatches and indels

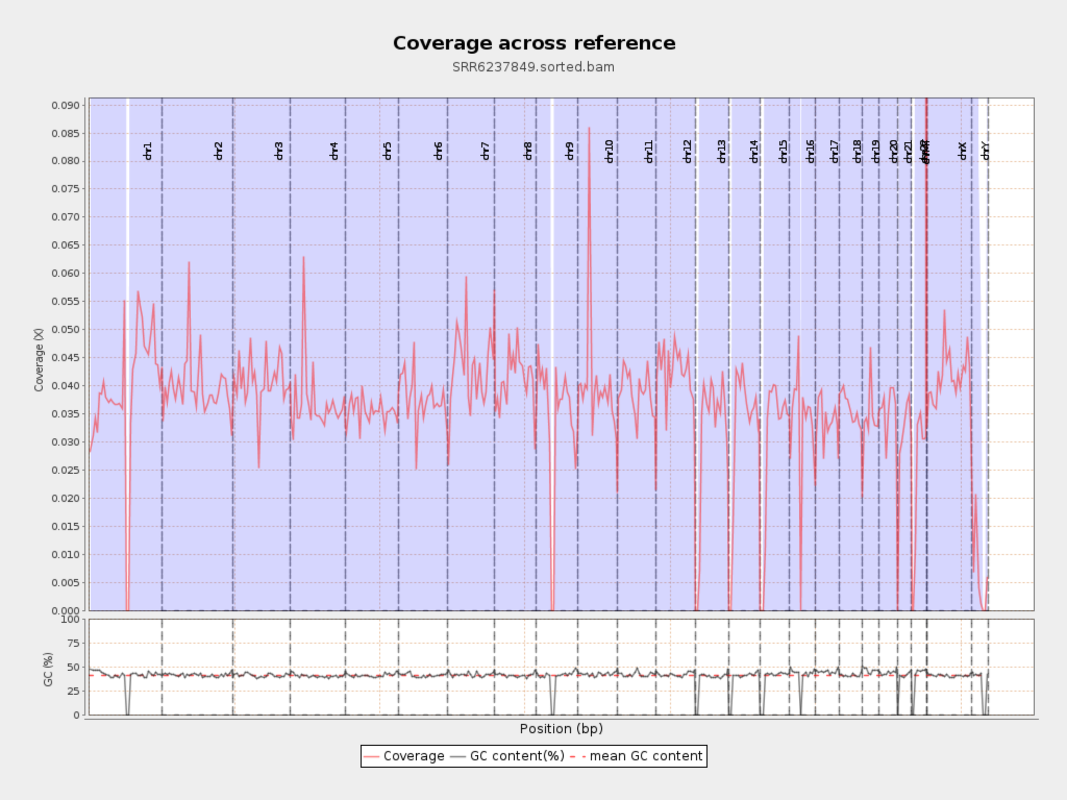
General error rate	0.87%
Mismatches	968,025
Insertions	9,323
Mapped reads with at least one insertion	0.5%
Deletions	39,905
Mapped reads with at least one deletion	2.12%
Homopolymer indels	47.95%

2.6. Chromosome stats

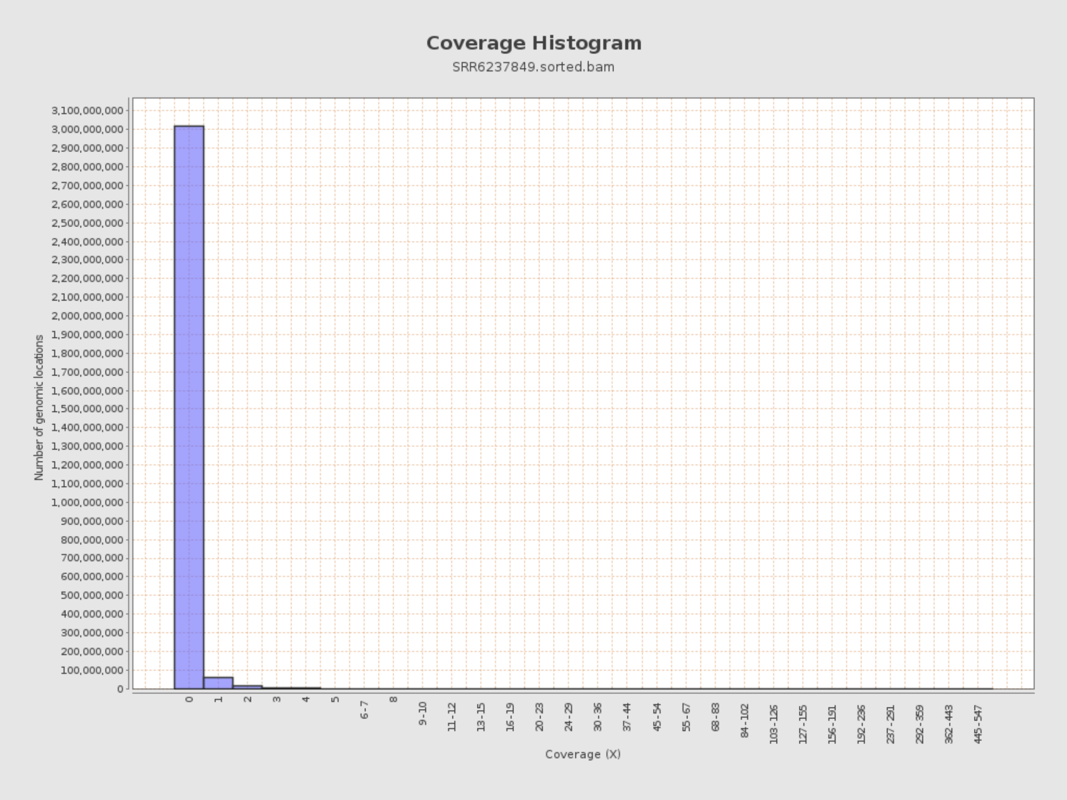
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9756491	0.0391	0.5094
chr2	243199373	9719408	0.04	0.4058
chr3	198022430	8050053	0.0407	0.2849
chr4	191154276	7060018	0.0369	0.2856
chr5	180915260	6424876	0.0355	0.2567
chr6	171115067	6465314	0.0378	0.3
chr7	159138663	6859648	0.0431	0.4337

chr8	146364022	6022045	0.0411	0.3441
chr9	141213431	4768355	0.0338	0.315
chr10	135534747	5506573	0.0406	0.4646
chr11	135006516	5195889	0.0385	0.3489
chr12	133851895	5716393	0.0427	0.2909
chr13	115169878	3542277	0.0308	0.2442
chr14	107349540	3409338	0.0318	0.2571
chr15	102531392	3046777	0.0297	0.2356
chr16	90354753	2981281	0.033	0.2834
chr17	81195210	2721953	0.0335	0.27
chr18	78077248	2812664	0.036	0.4804
chr19	59128983	2045253	0.0346	0.3994
chr20	63025520	2231677	0.0354	0.2672
chr21	48129895	1433951	0.0298	0.2562
chr22	51304566	1147704	0.0224	0.2027
chrMT	16571	56746	3.4244	3.1841
chrX	155270560	6459903	0.0416	0.3037
chrY	59373566	380176	0.0064	0.1619

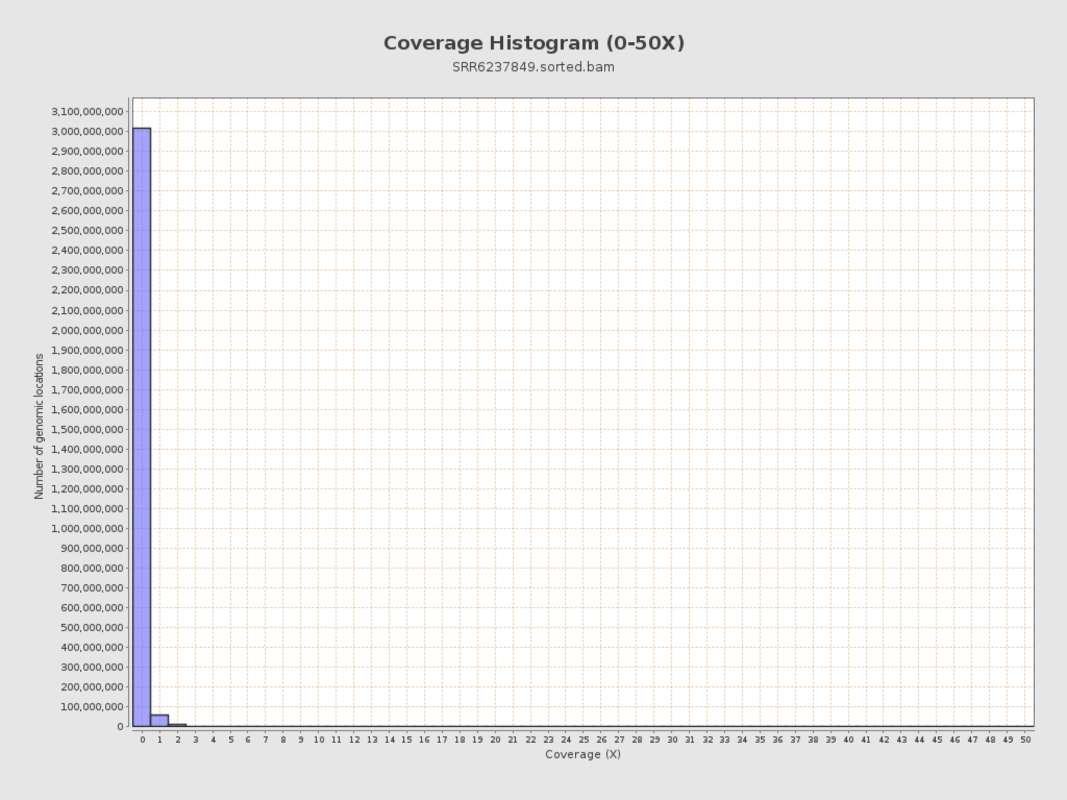
3. Results : Coverage across reference



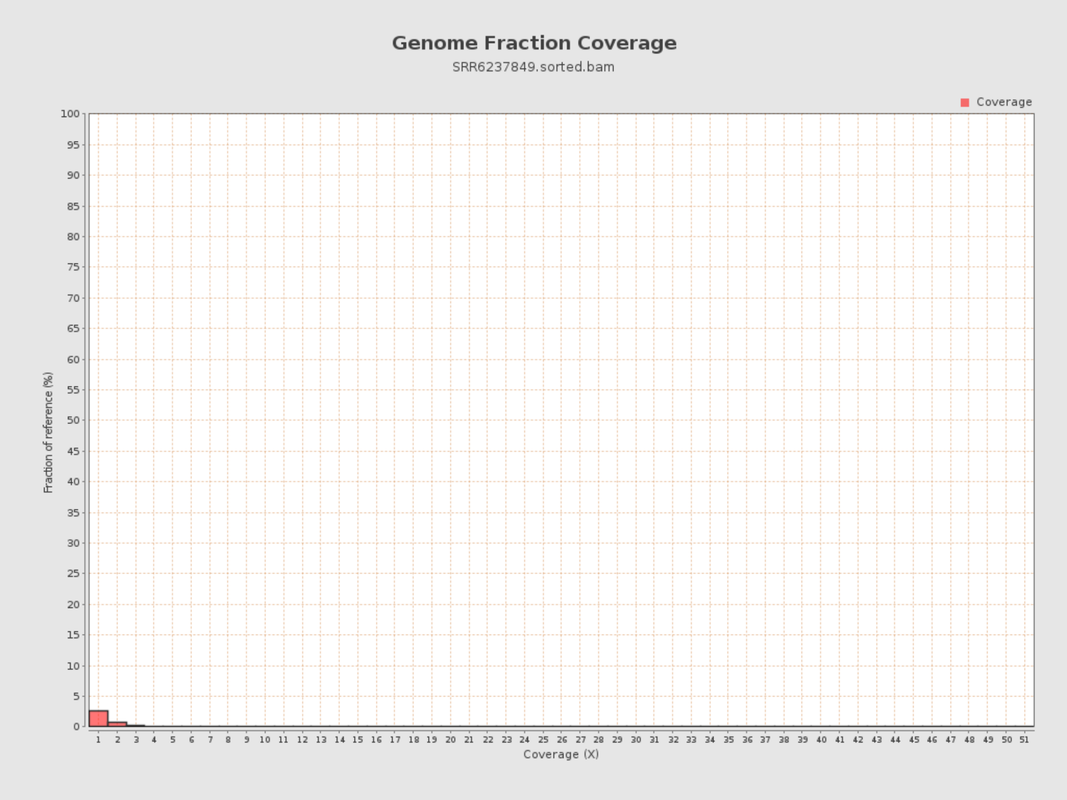
4. Results : Coverage Histogram



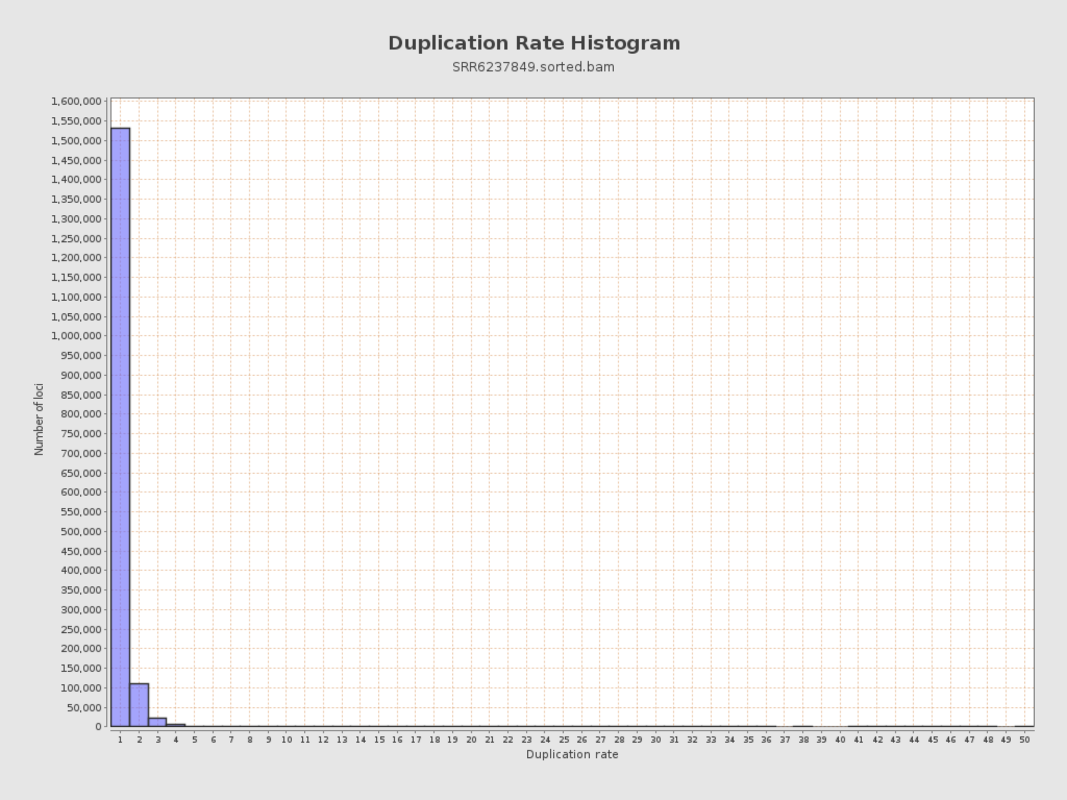
5. Results : Coverage Histogram (0-50X)



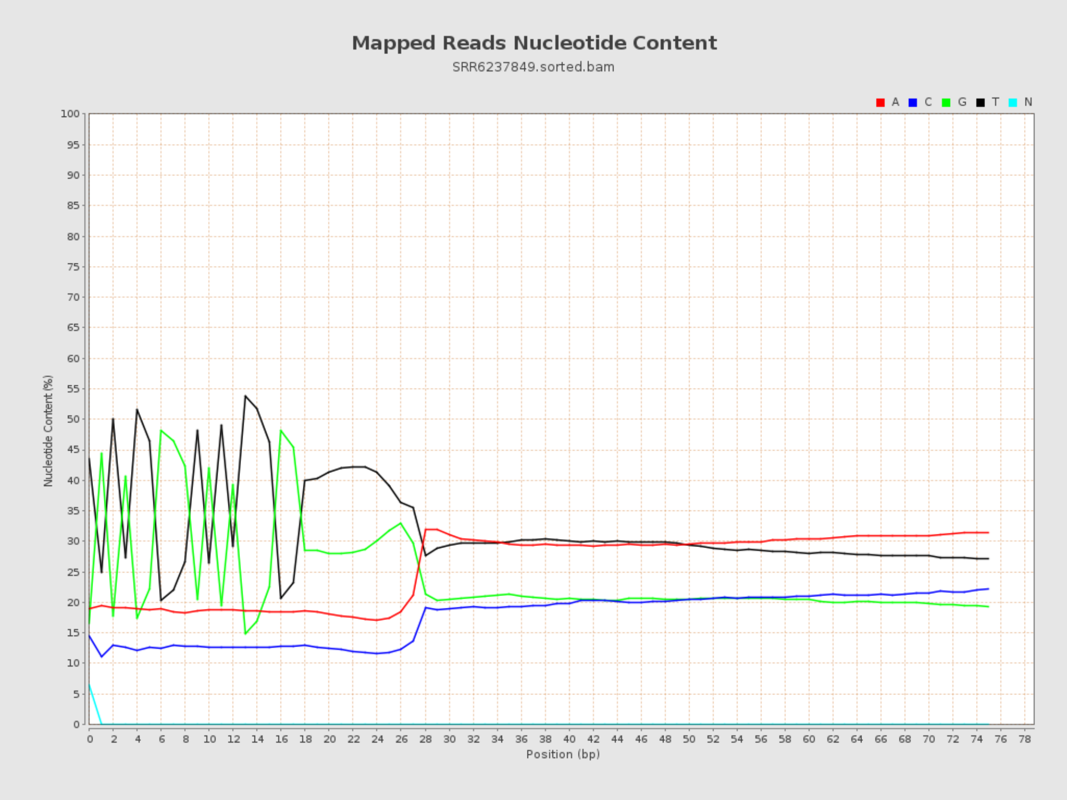
6. Results : Genome Fraction Coverage



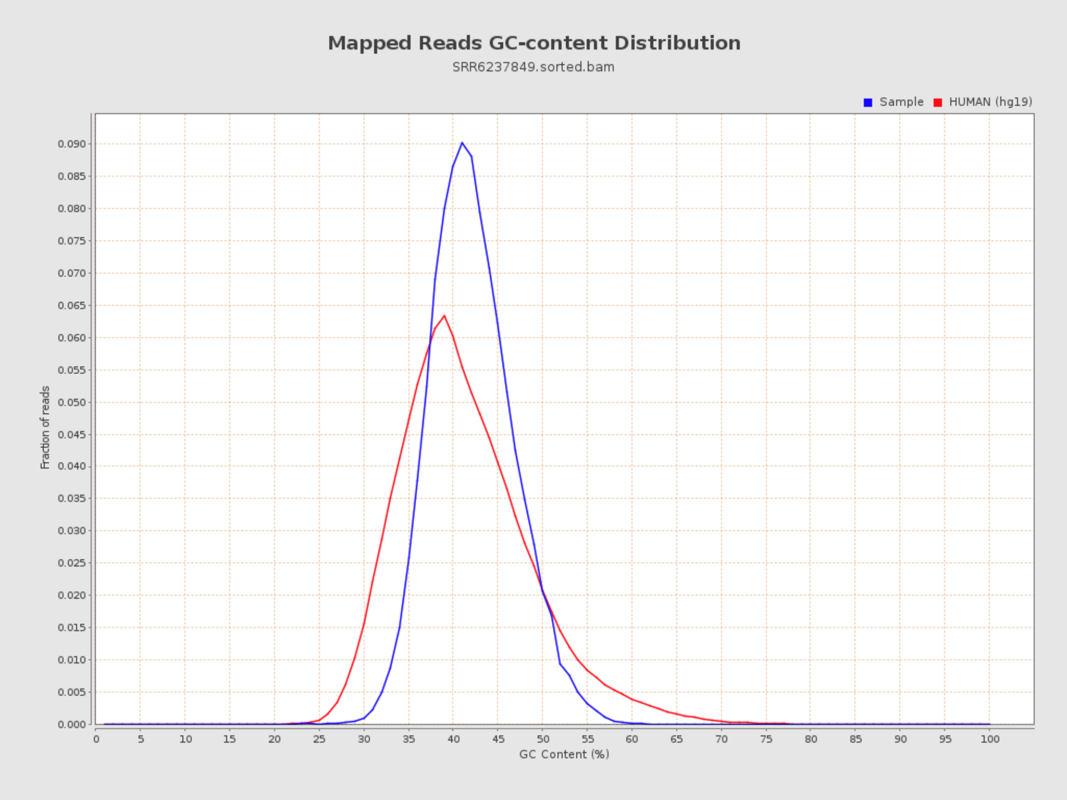
7. Results : Duplication Rate Histogram



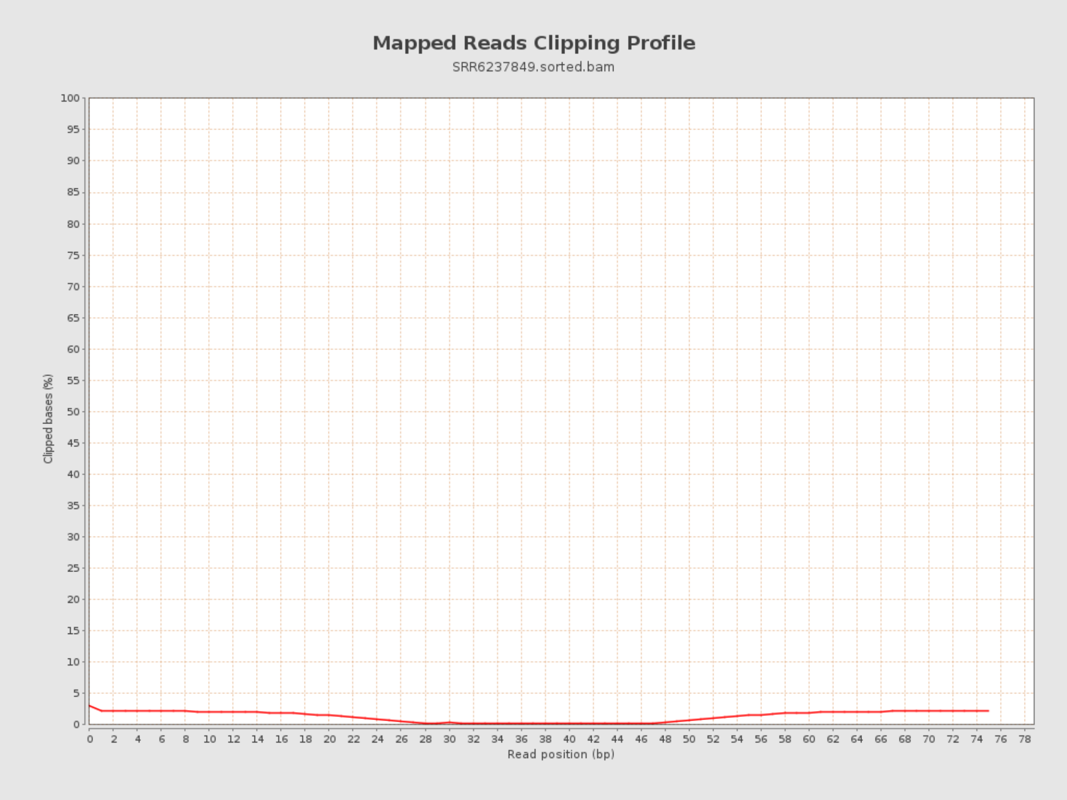
8. Results : Mapped Reads Nucleotide Content



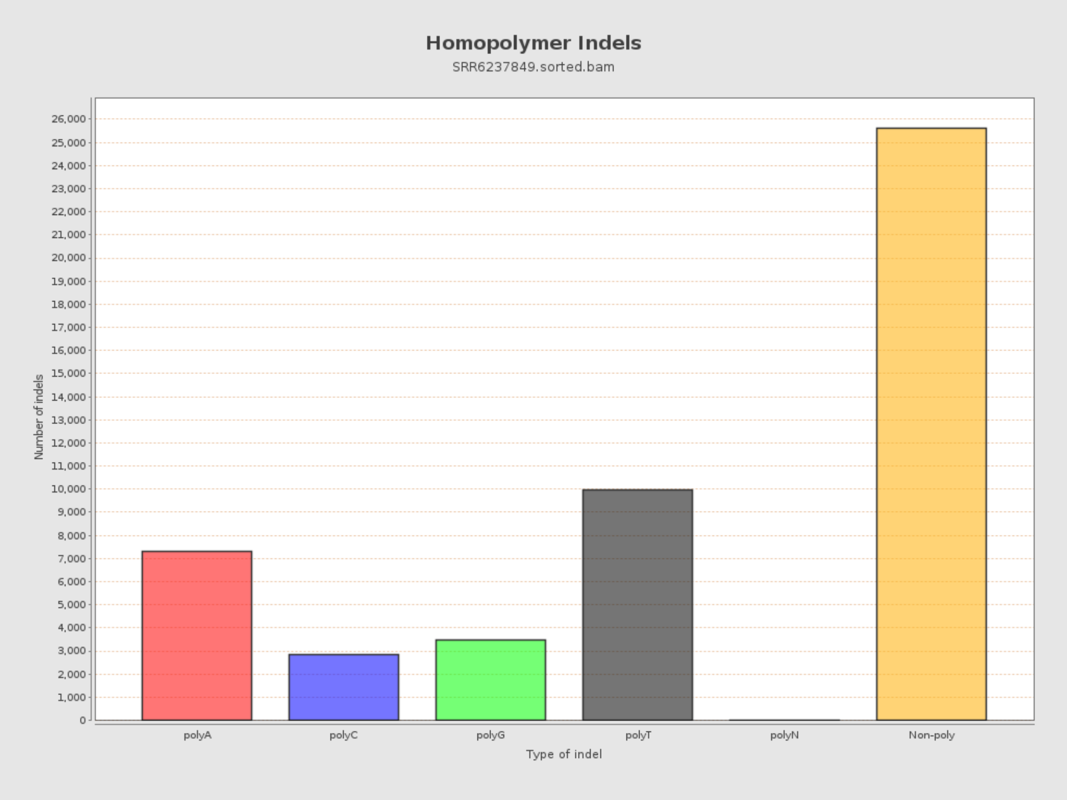
9. Results : Mapped Reads GC-content Distribution



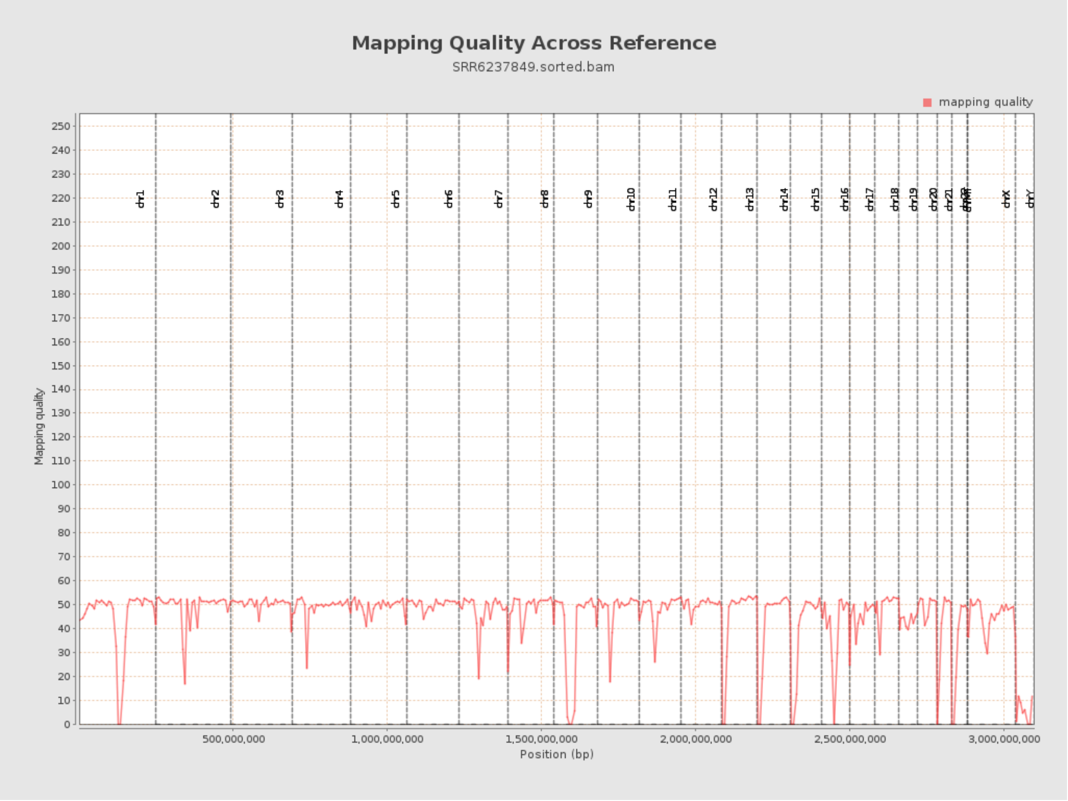
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram