Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:39:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237845.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_SRR6237845 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237845.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:39:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237845.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,255,593
Mapped reads	1,399,953 / 62.07%
Unmapped reads	855,640 / 37.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,041 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	159,905 / 7.09%
Duplication rate	9.14%
Clipped reads	950,023 / 42.12%

2.2. ACGT Content

Number/percentage of A's	23,085,754 / 27.3%
Number/percentage of C's	16,872,580 / 19.95%
Number/percentage of T's	25,248,776 / 29.86%
Number/percentage of G's	19,284,703 / 22.8%
Number/percentage of N's	74,091 / 0.09%
GC Percentage	42.76%

2.3. Coverage

Mean	0.0273

Standard Deviation	0.2988

2.4. Mapping Quality

Mean Mapping Quality	44.16

2.5. Mismatches and indels

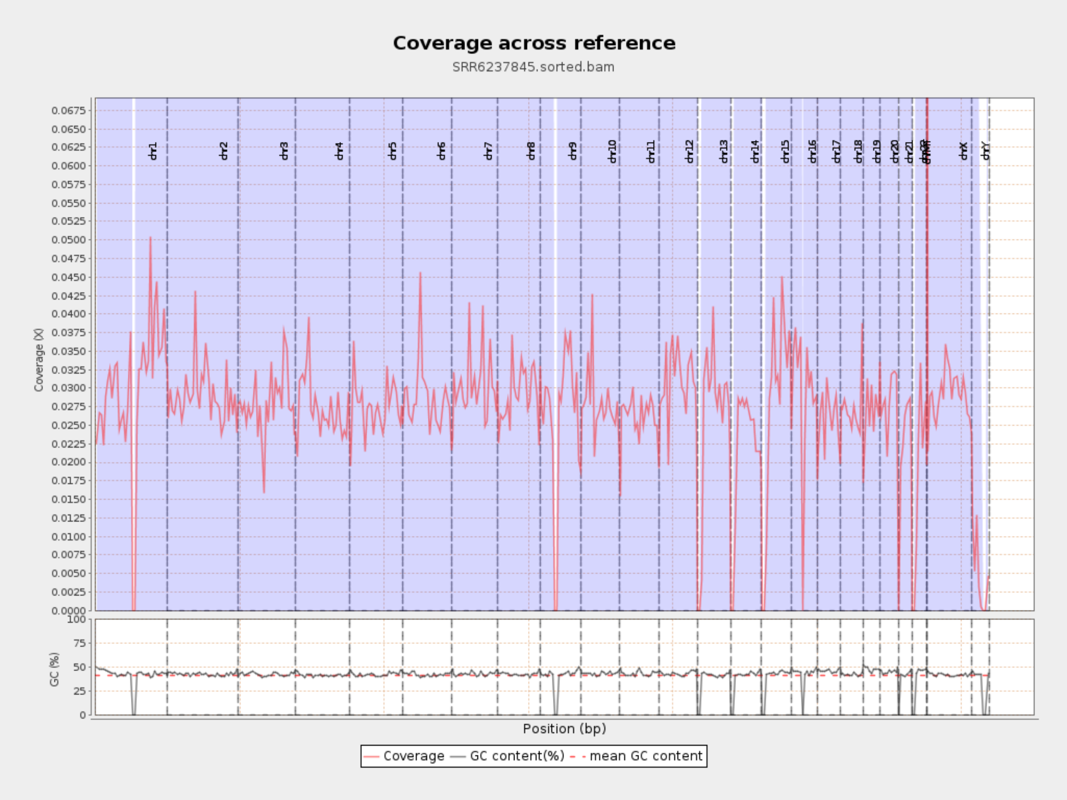
General error rate	0.99%
Mismatches	825,516
Insertions	6,577
Mapped reads with at least one insertion	0.47%
Deletions	31,731
Mapped reads with at least one deletion	2.24%
Homopolymer indels	46.97%

2.6. Chromosome stats

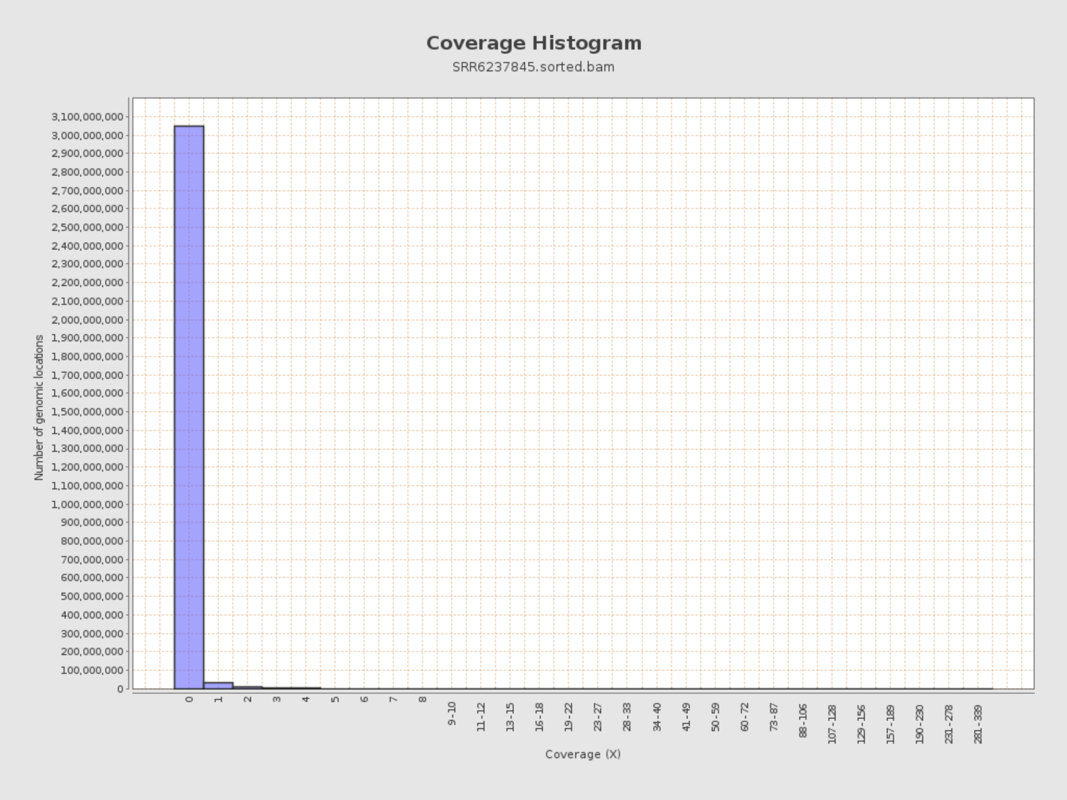
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7433676	0.0298	0.3809
chr2	243199373	7071445	0.0291	0.3342
chr3	198022430	5508727	0.0278	0.2658
chr4	191154276	5212256	0.0273	0.2718
chr5	180915260	4999127	0.0276	0.2639
chr6	171115067	4919638	0.0288	0.2853
chr7	159138663	4842339	0.0304	0.3779

chr8	146364022	4246704	0.029	0.2996
chr9	141213431	3714901	0.0263	0.2906
chr10	135534747	3799927	0.028	0.3014
chr11	135006516	3571312	0.0265	0.2975
chr12	133851895	4158255	0.0311	0.2867
chr13	115169878	2942480	0.0255	0.2618
chr14	107349540	2298512	0.0214	0.2364
chr15	102531392	2842512	0.0277	0.2742
chr16	90354753	2607636	0.0289	0.289
chr17	81195210	2111340	0.026	0.2673
chr18	78077248	2103842	0.0269	0.3793
chr19	59128983	1592929	0.0269	0.3075
chr20	63025520	1758573	0.0279	0.2746
chr21	48129895	1070914	0.0223	0.2457
chr22	51304566	933603	0.0182	0.2161
chrMT	16571	79065	4.7713	4.6673
chrX	155270560	4527314	0.0292	0.2786
chrY	59373566	269838	0.0045	0.1146

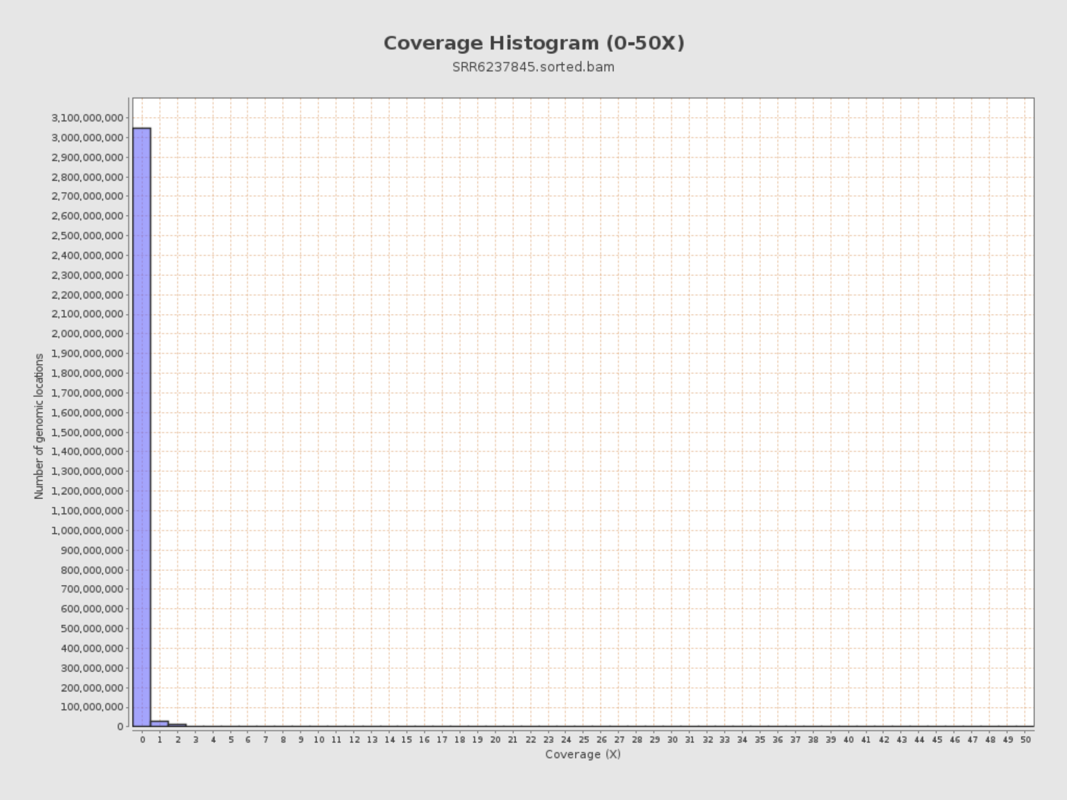
3. Results : Coverage across reference



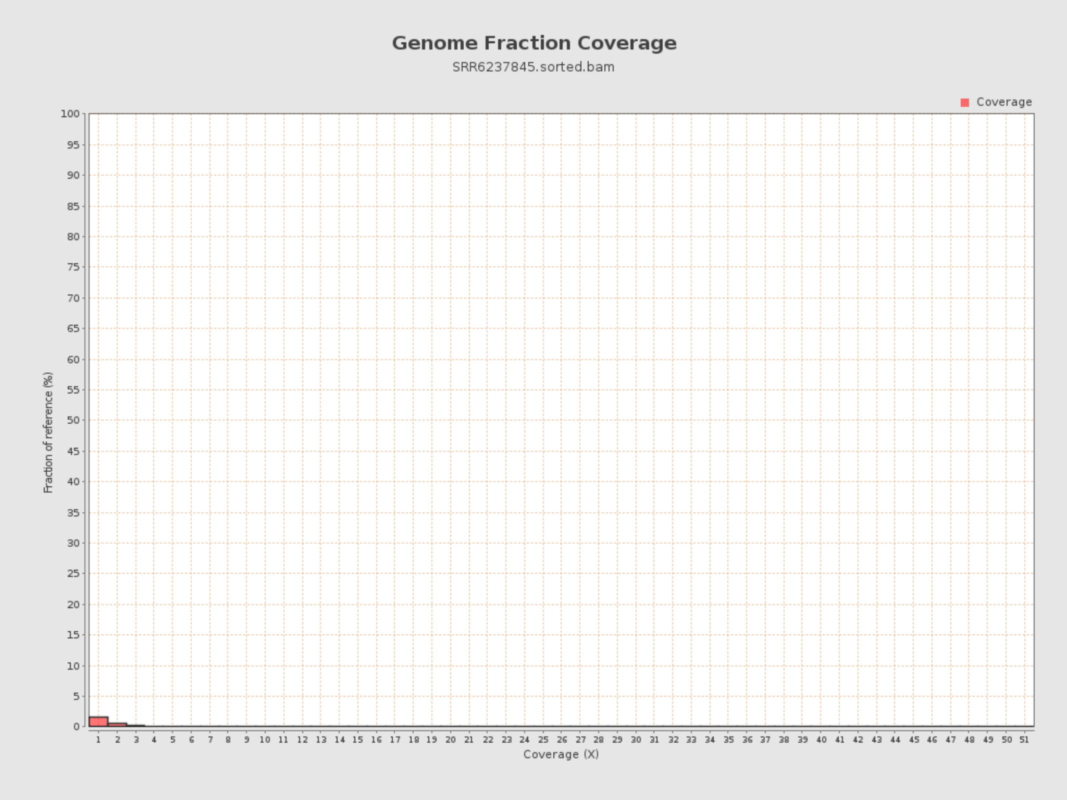
4. Results : Coverage Histogram



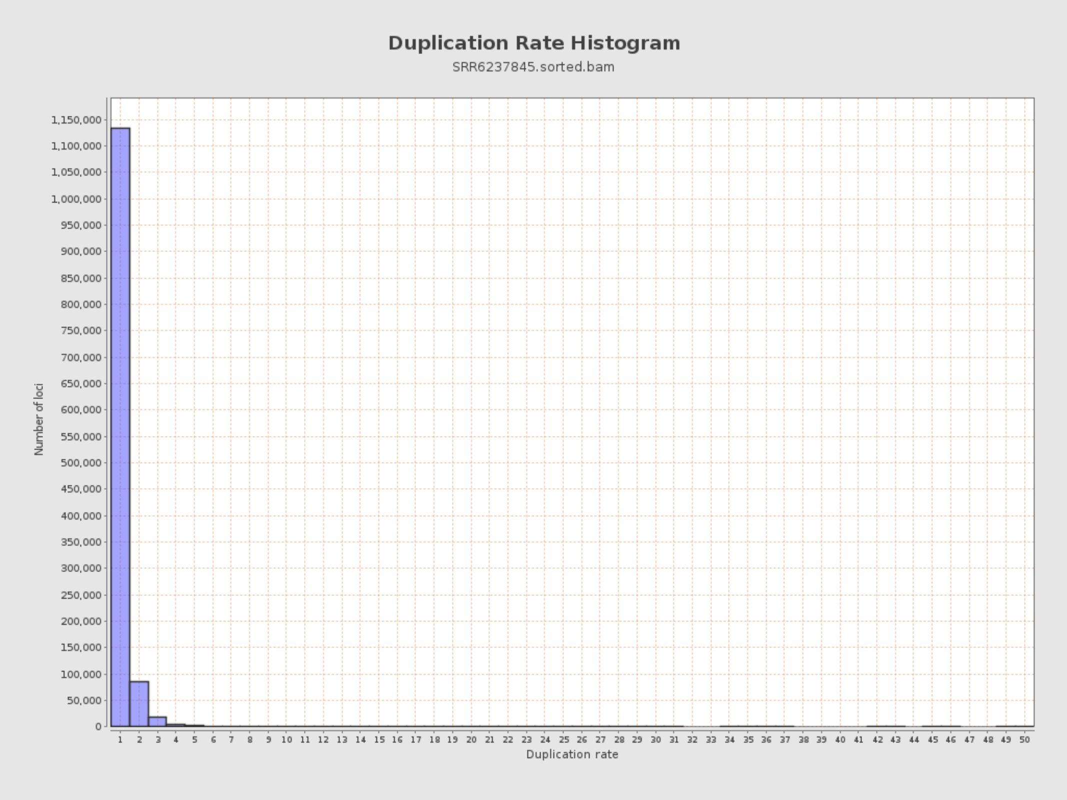
5. Results : Coverage Histogram (0-50X)



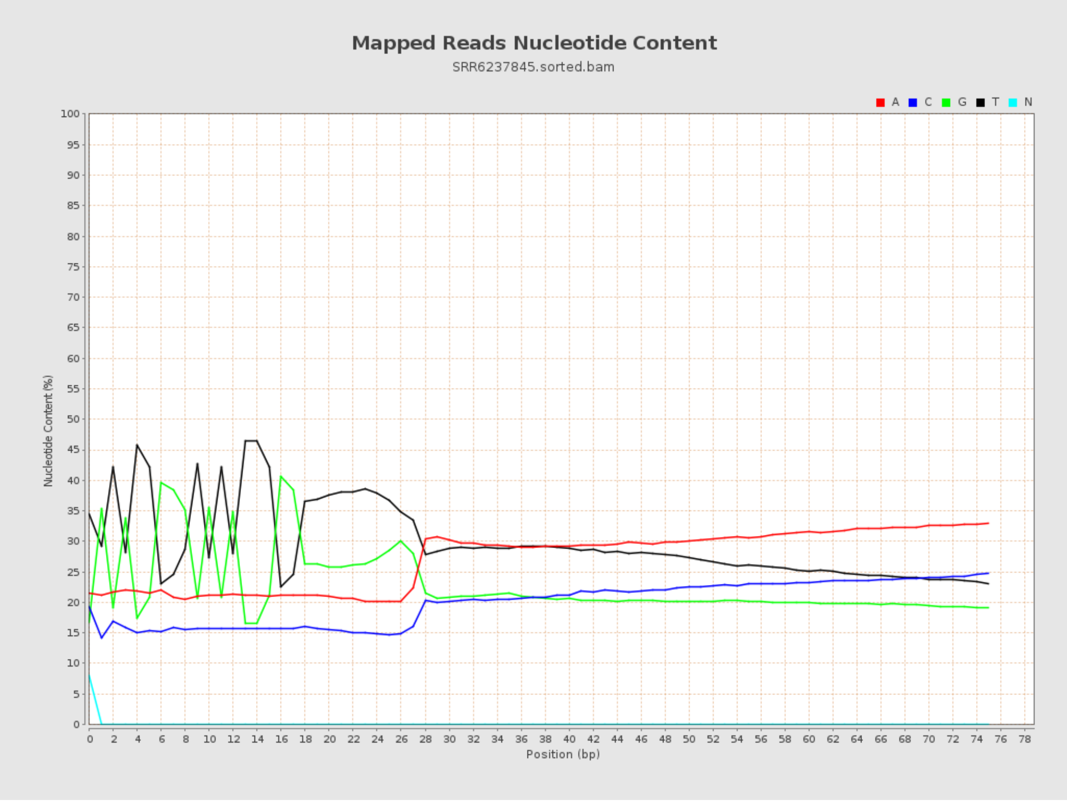
6. Results : Genome Fraction Coverage



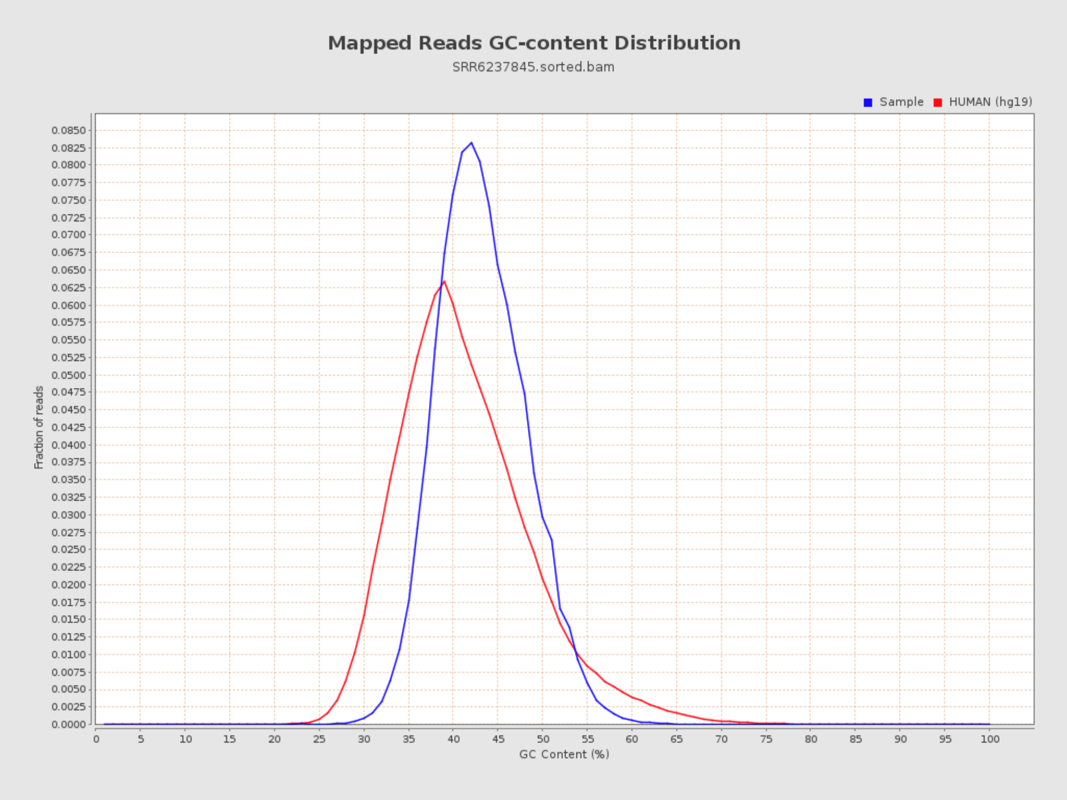
7. Results : Duplication Rate Histogram



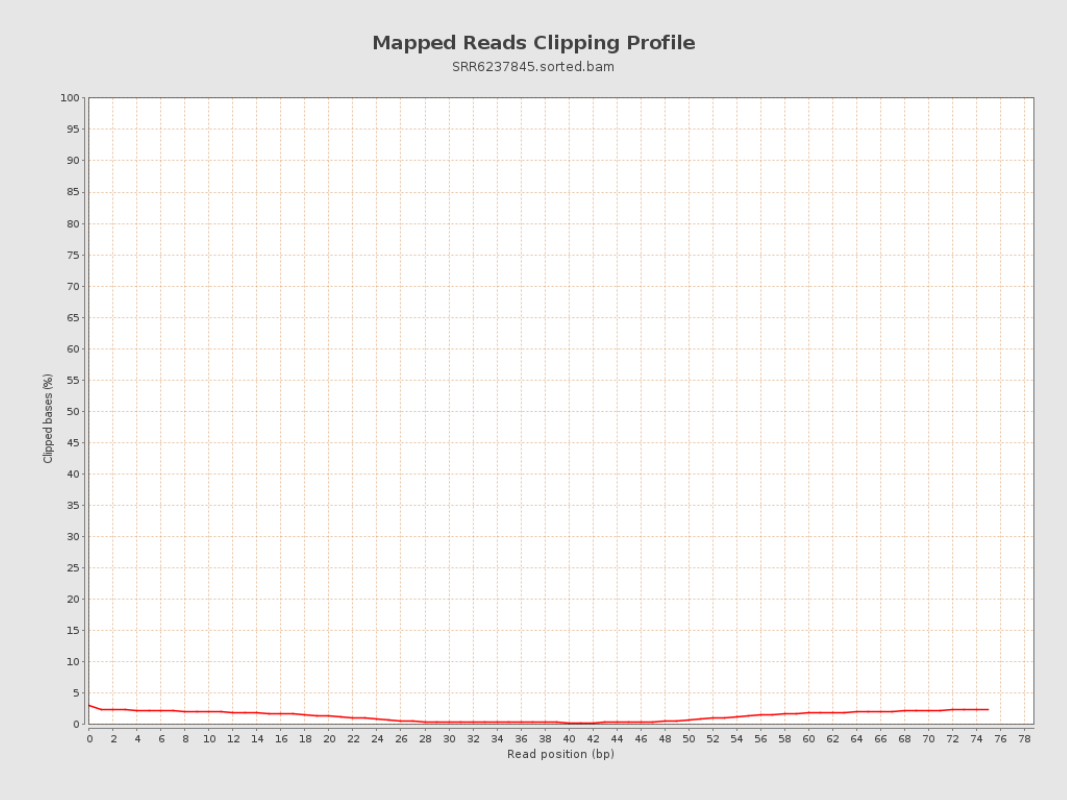
8. Results : Mapped Reads Nucleotide Content



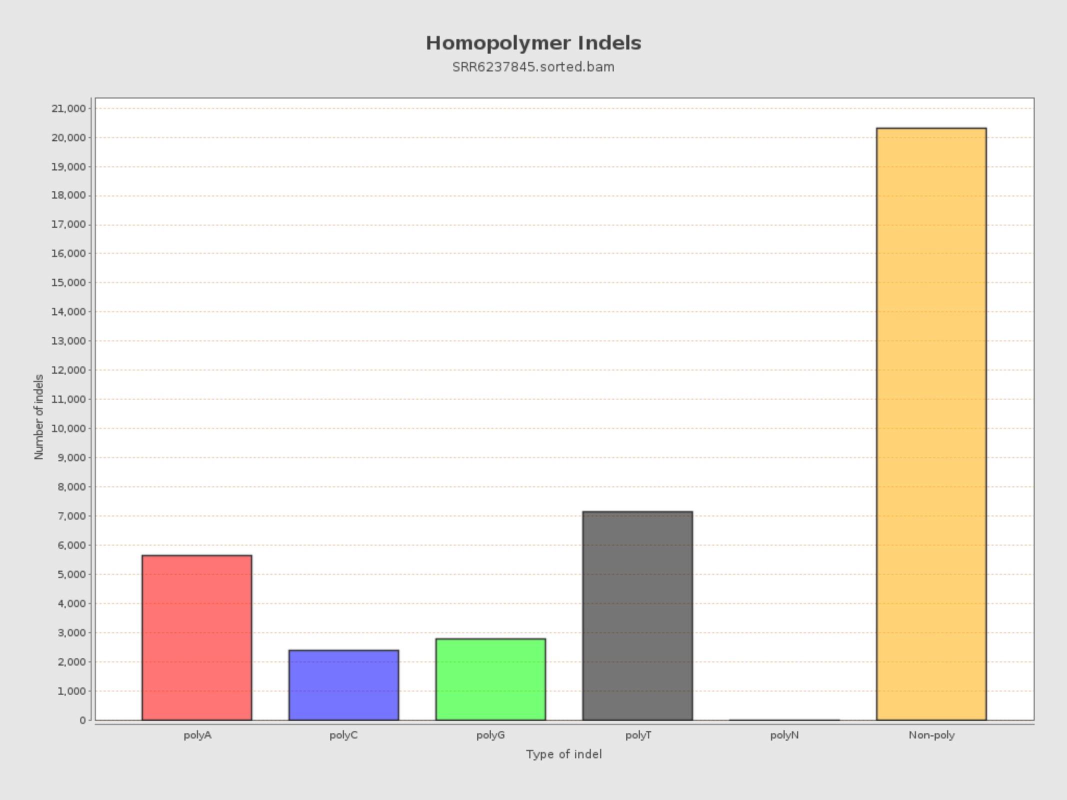
9. Results : Mapped Reads GC-content Distribution



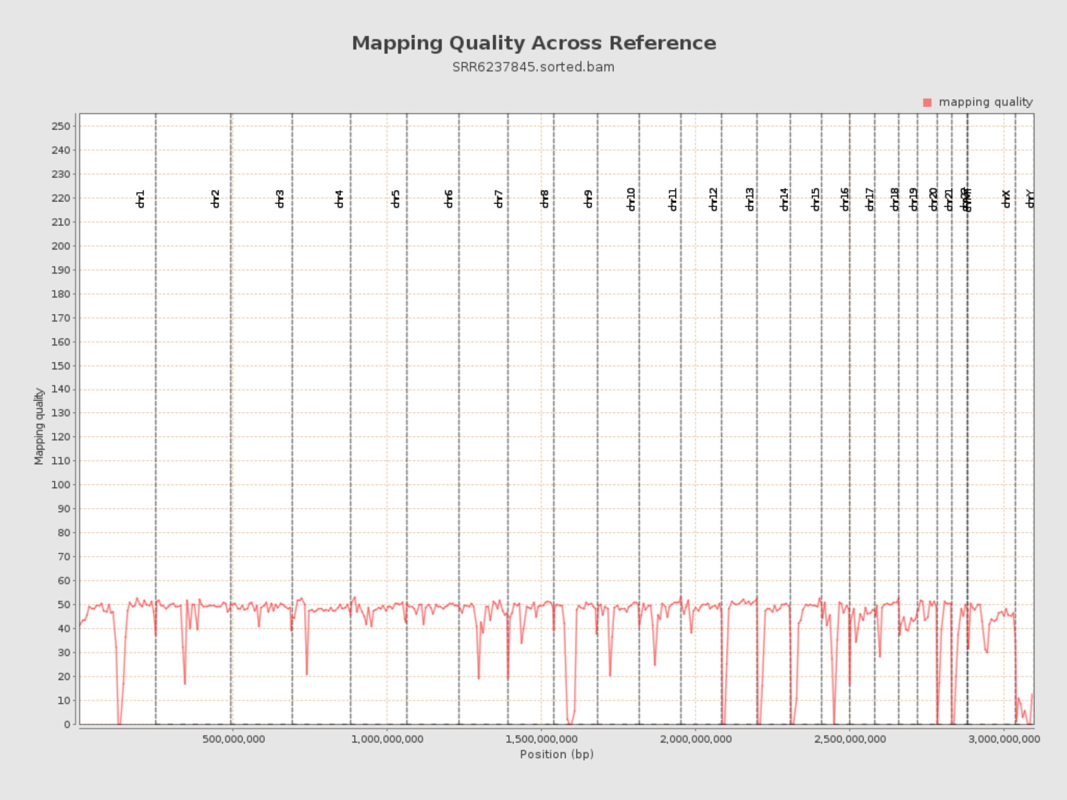
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram