Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:04:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237853.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_SRR6237853 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237853.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:04:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237853.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,296,973
Mapped reads	1,784,201 / 77.68%
Unmapped reads	512,772 / 22.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,992 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	151,227 / 6.58%
Duplication rate	5.85%
Clipped reads	1,238,127 / 53.9%

2.2. ACGT Content

Number/percentage of A's	29,303,664 / 27.01%
Number/percentage of C's	19,466,117 / 17.94%
Number/percentage of T's	33,551,889 / 30.93%
Number/percentage of G's	26,081,497 / 24.04%
Number/percentage of N's	89,321 / 0.08%
GC Percentage	41.98%

2.3. Coverage

Mean	0.0351

Standard Deviation	0.3457

2.4. Mapping Quality

Mean Mapping Quality	42.59

2.5. Mismatches and indels

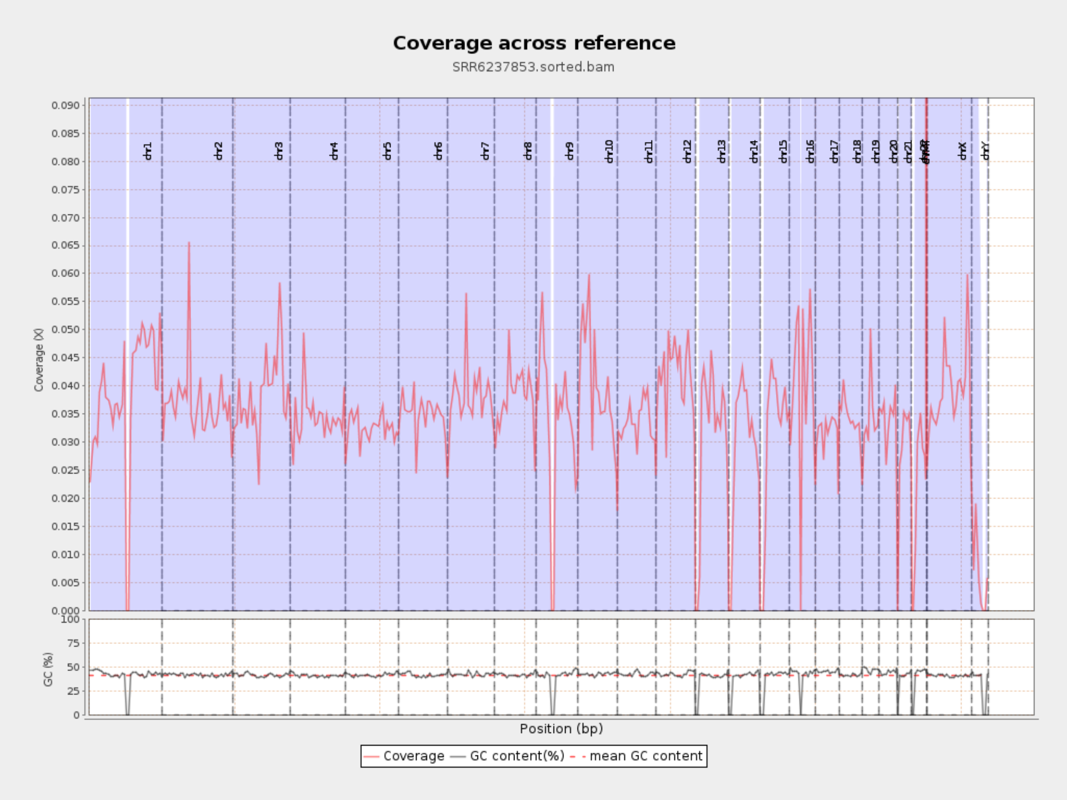
General error rate	1.05%
Mismatches	1,125,601
Insertions	10,483
Mapped reads with at least one insertion	0.58%
Deletions	46,932
Mapped reads with at least one deletion	2.59%
Homopolymer indels	48.21%

2.6. Chromosome stats

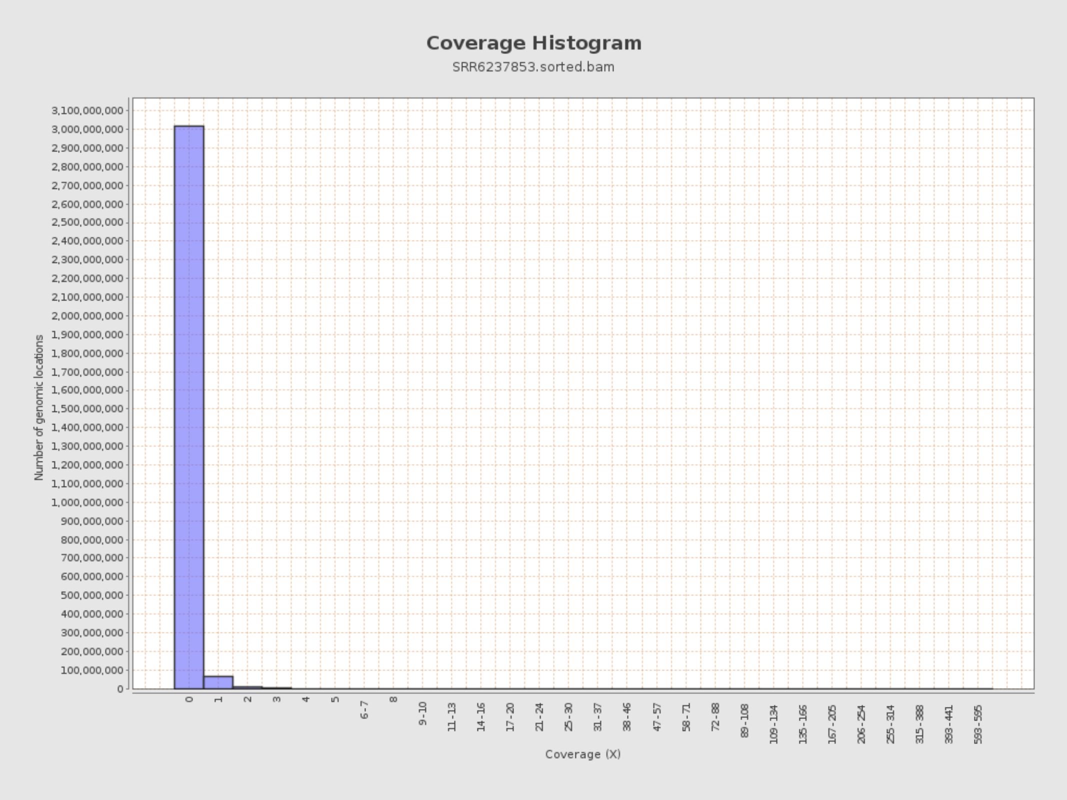
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9557638	0.0383	0.4197
chr2	243199373	9006552	0.037	0.4576
chr3	198022430	7591342	0.0383	0.2897
chr4	191154276	6547852	0.0343	0.2746
chr5	180915260	5899691	0.0326	0.2555
chr6	171115067	5977349	0.0349	0.2974
chr7	159138663	6125420	0.0385	0.4924

chr8	146364022	5541725	0.0379	0.3557
chr9	141213431	4742120	0.0336	0.3408
chr10	135534747	5516966	0.0407	0.3603
chr11	135006516	4506891	0.0334	0.3644
chr12	133851895	5641409	0.0421	0.3098
chr13	115169878	3552403	0.0308	0.2653
chr14	107349540	3146656	0.0293	0.2855
chr15	102531392	3156660	0.0308	0.2633
chr16	90354753	3621620	0.0401	0.3193
chr17	81195210	2562590	0.0316	0.2657
chr18	78077248	2694941	0.0345	0.5411
chr19	59128983	2040177	0.0345	0.3465
chr20	63025520	2144286	0.034	0.2782
chr21	48129895	1362240	0.0283	0.2591
chr22	51304566	1070694	0.0209	0.2043
chrMT	16571	60109	3.6274	4.2909
chrX	155270560	6125977	0.0395	0.3033
chrY	59373566	374330	0.0063	0.1505

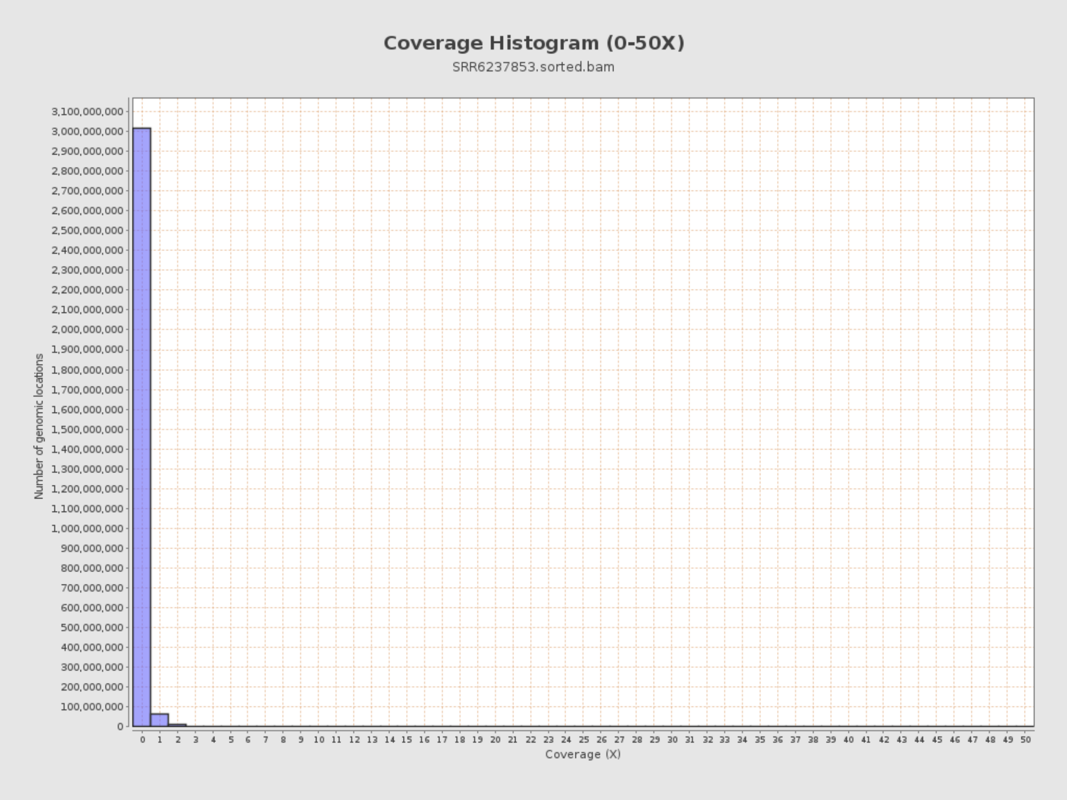
3. Results : Coverage across reference



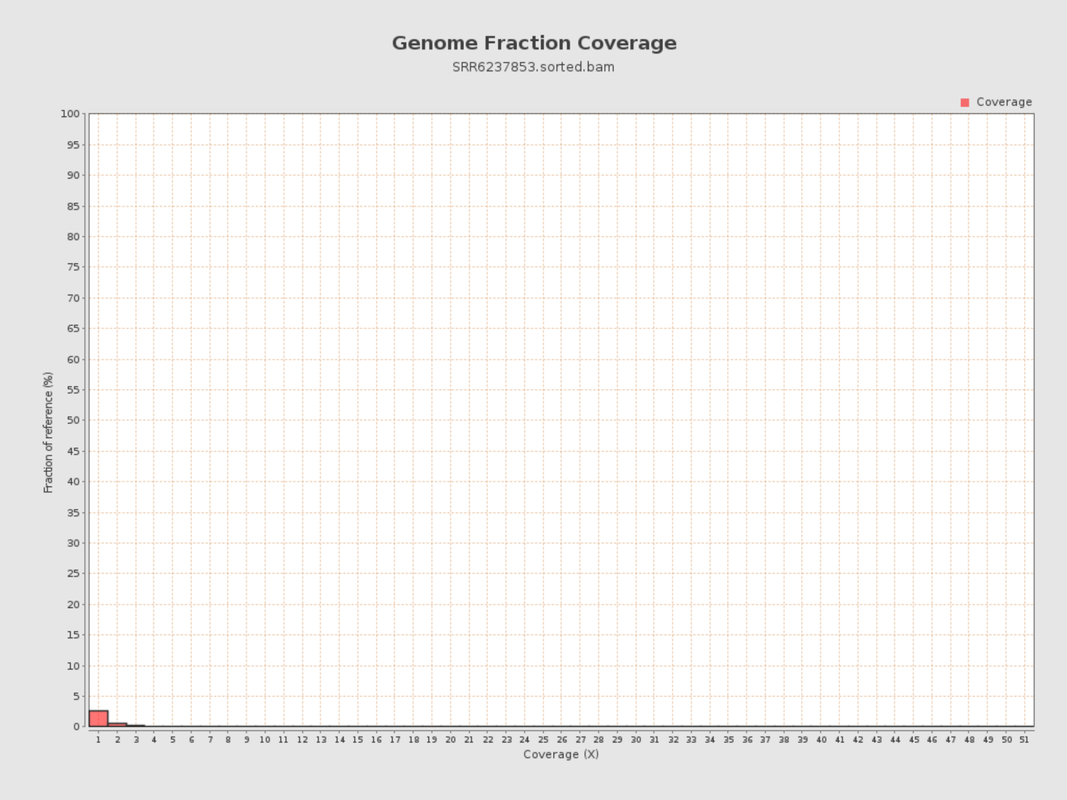
4. Results : Coverage Histogram



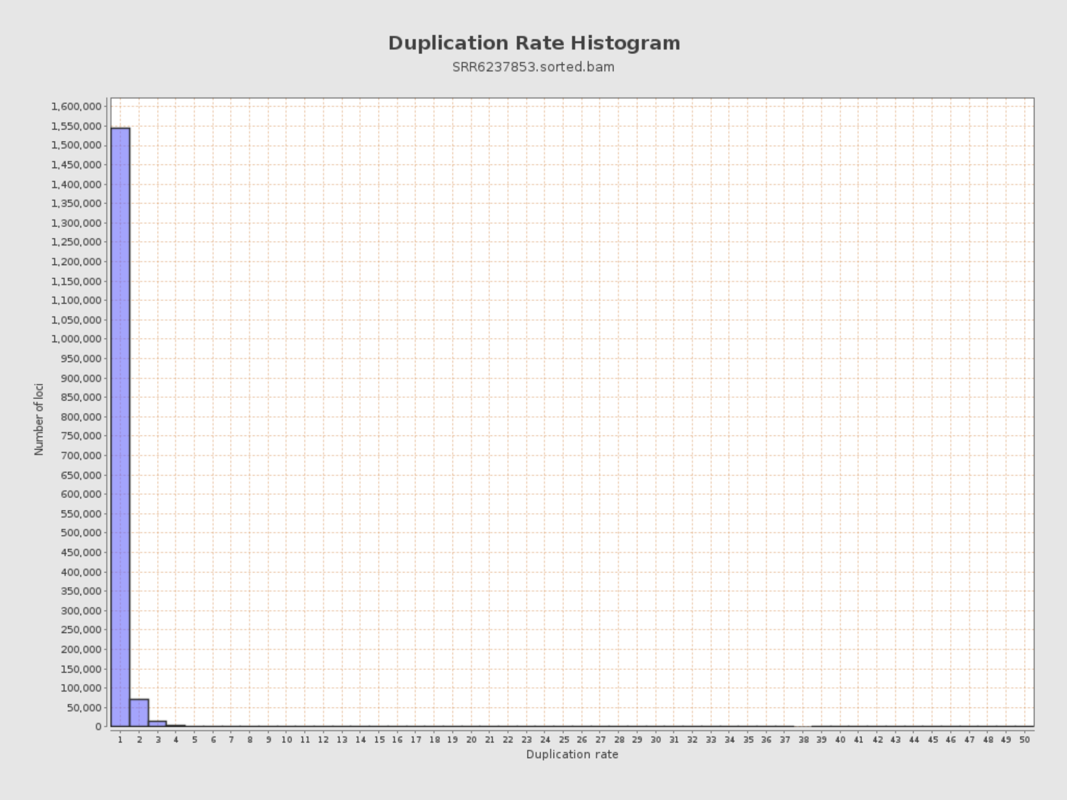
5. Results : Coverage Histogram (0-50X)



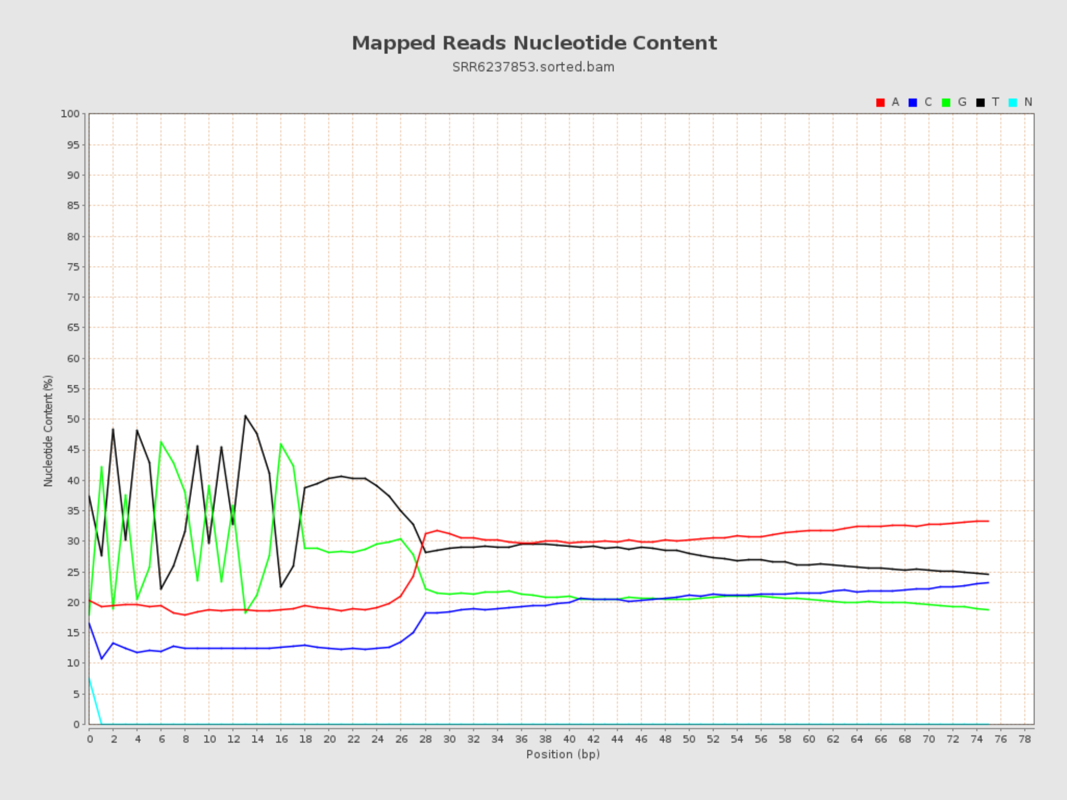
6. Results : Genome Fraction Coverage



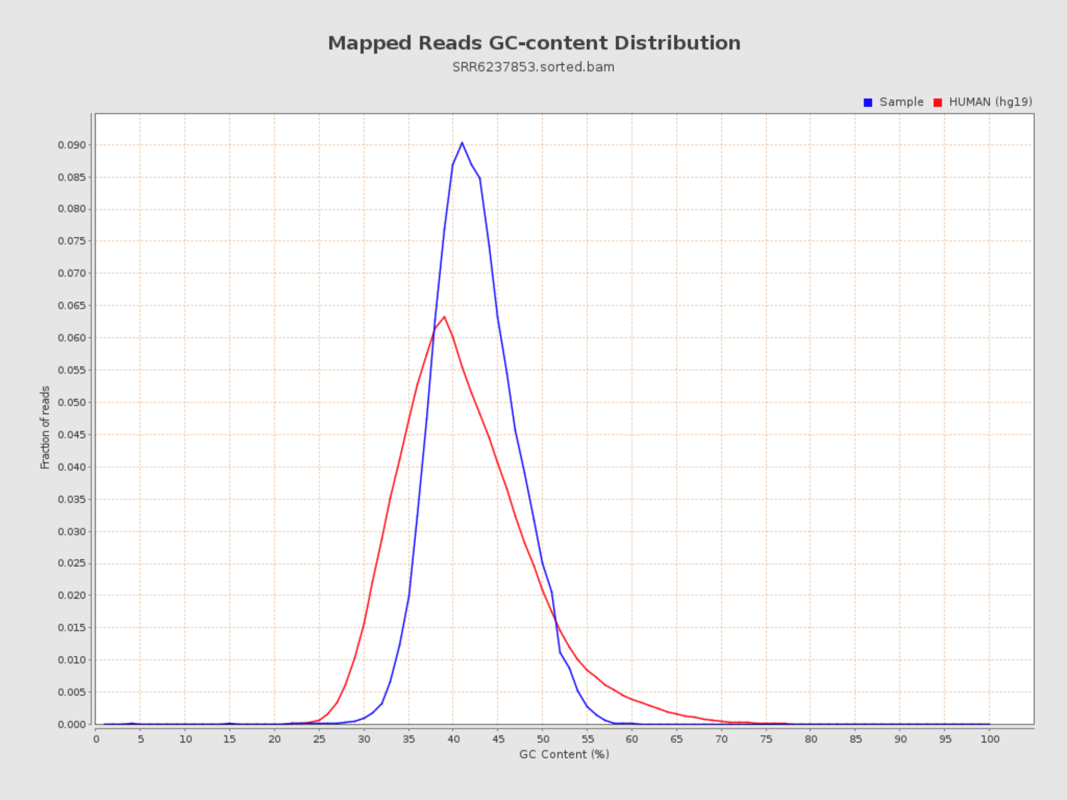
7. Results : Duplication Rate Histogram



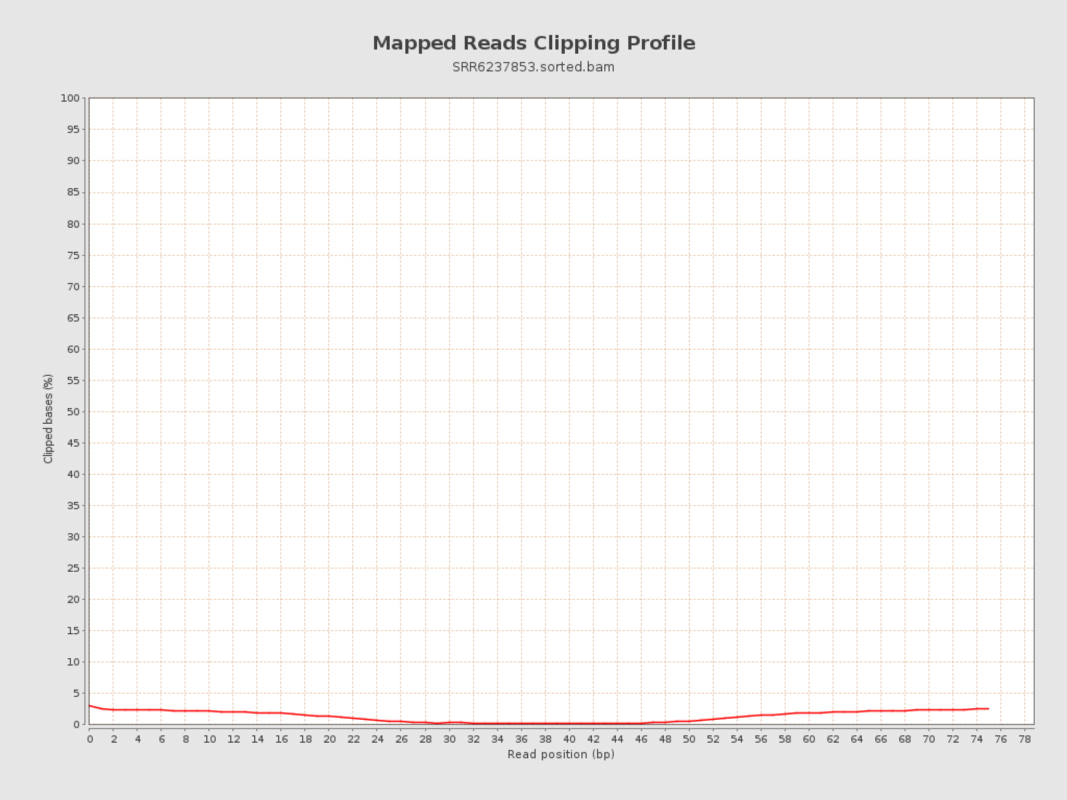
8. Results : Mapped Reads Nucleotide Content



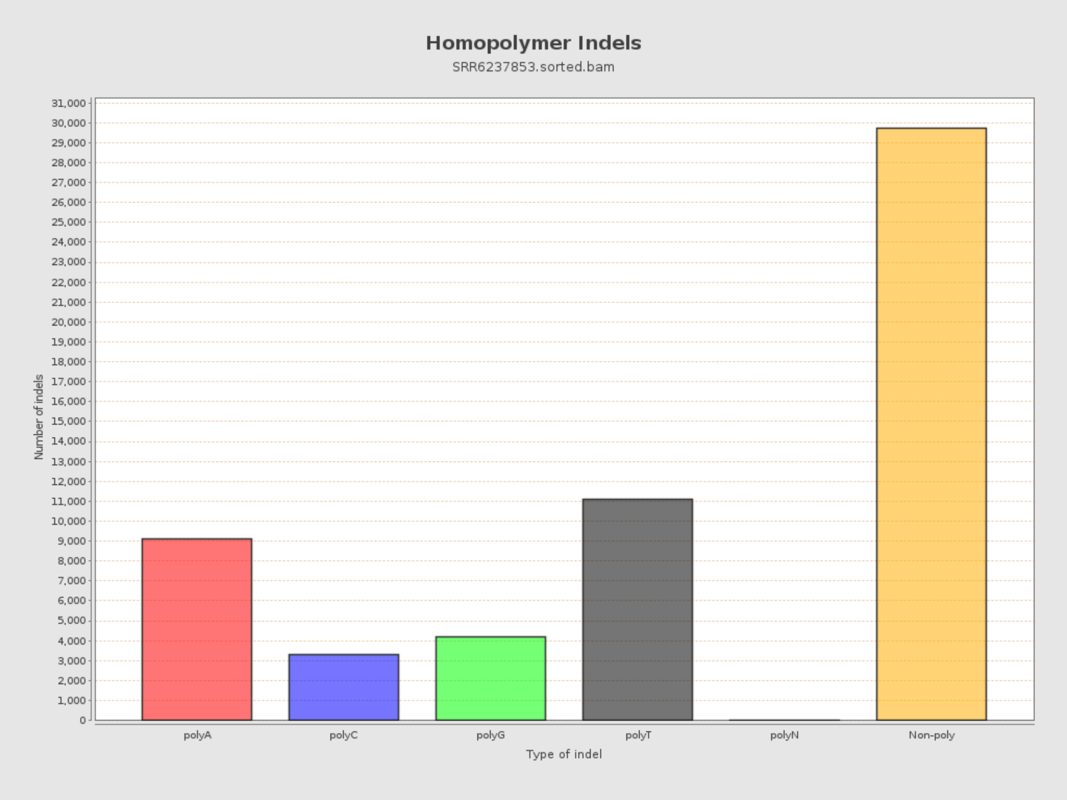
9. Results : Mapped Reads GC-content Distribution



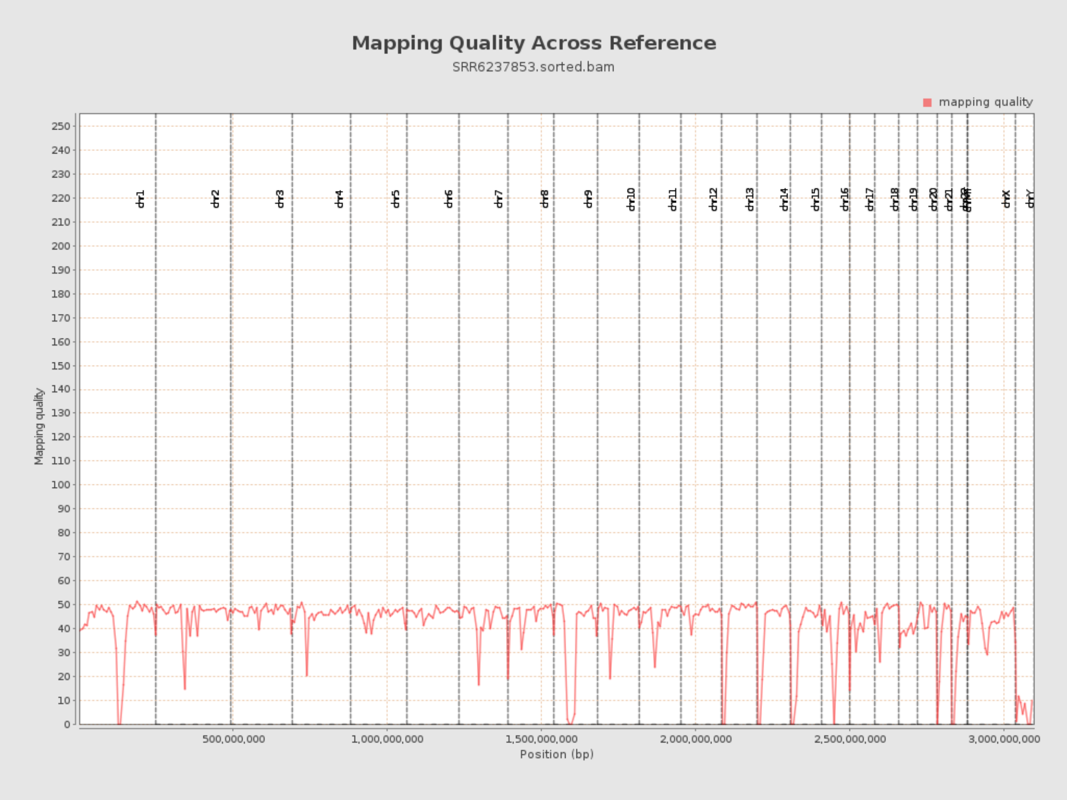
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram