Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 08:29:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237842.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_SRR6237842 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237842.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 08:29:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237842.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,687,651
Mapped reads	1,130,521 / 66.99%
Unmapped reads	557,130 / 33.01%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,740 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	93,921 / 5.57%
Duplication rate	7.01%
Clipped reads	707,900 / 41.95%

2.2. ACGT Content

Number/percentage of A's	18,656,774 / 26.71%
Number/percentage of C's	12,462,257 / 17.84%
Number/percentage of T's	22,828,641 / 32.68%
Number/percentage of G's	15,849,516 / 22.69%
Number/percentage of N's	58,174 / 0.08%
GC Percentage	40.53%

2.3. Coverage

Mean	0.0226

Standard Deviation	0.2518

2.4. Mapping Quality

Mean Mapping Quality	46.27

2.5. Mismatches and indels

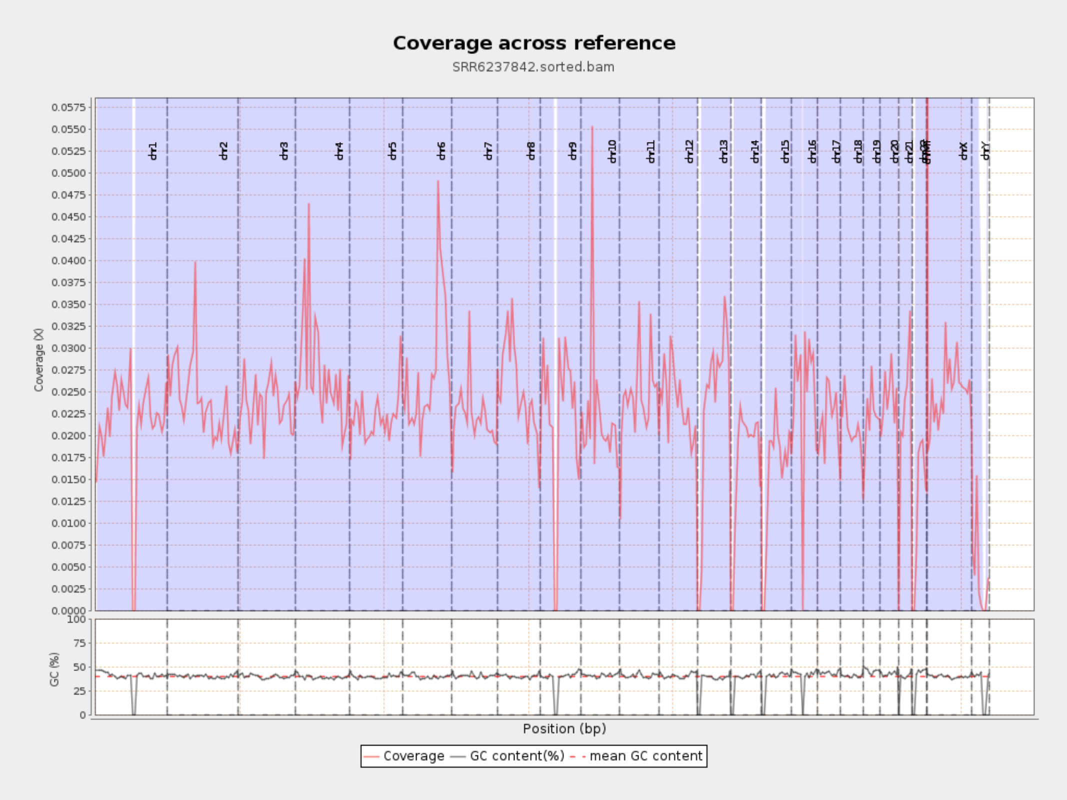
General error rate	0.85%
Mismatches	580,494
Insertions	5,771
Mapped reads with at least one insertion	0.51%
Deletions	16,563
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.93%

2.6. Chromosome stats

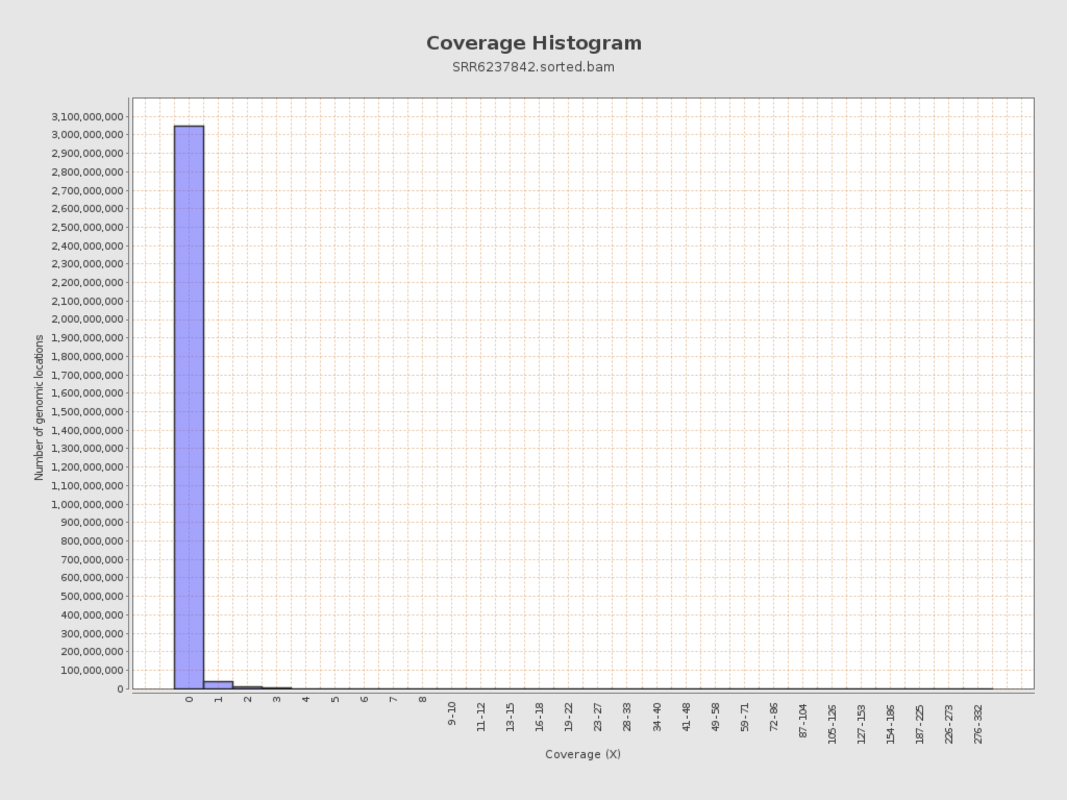
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5324647	0.0214	0.3187
chr2	243199373	5804291	0.0239	0.3087
chr3	198022430	4641469	0.0234	0.2055
chr4	191154276	5163344	0.027	0.2465
chr5	180915260	4019169	0.0222	0.198
chr6	171115067	4642305	0.0271	0.2398
chr7	159138663	3545166	0.0223	0.2511

chr8	146364022	3728549	0.0255	0.2983
chr9	141213431	3116197	0.0221	0.2557
chr10	135534747	3009509	0.0222	0.3202
chr11	135006516	3346345	0.0248	0.2369
chr12	133851895	3187437	0.0238	0.2079
chr13	115169878	2692043	0.0234	0.205
chr14	107349540	1825954	0.017	0.1889
chr15	102531392	1595318	0.0156	0.1631
chr16	90354753	2201990	0.0244	0.2414
chr17	81195210	1759714	0.0217	0.2017
chr18	78077248	1636206	0.021	0.3766
chr19	59128983	1308568	0.0221	0.2785
chr20	63025520	1511079	0.024	0.2128
chr21	48129895	1049397	0.0218	0.2241
chr22	51304566	625139	0.0122	0.1438
chrMT	16571	30777	1.8573	1.9132
chrX	155270560	3883747	0.025	0.2285
chrY	59373566	234847	0.004	0.1349

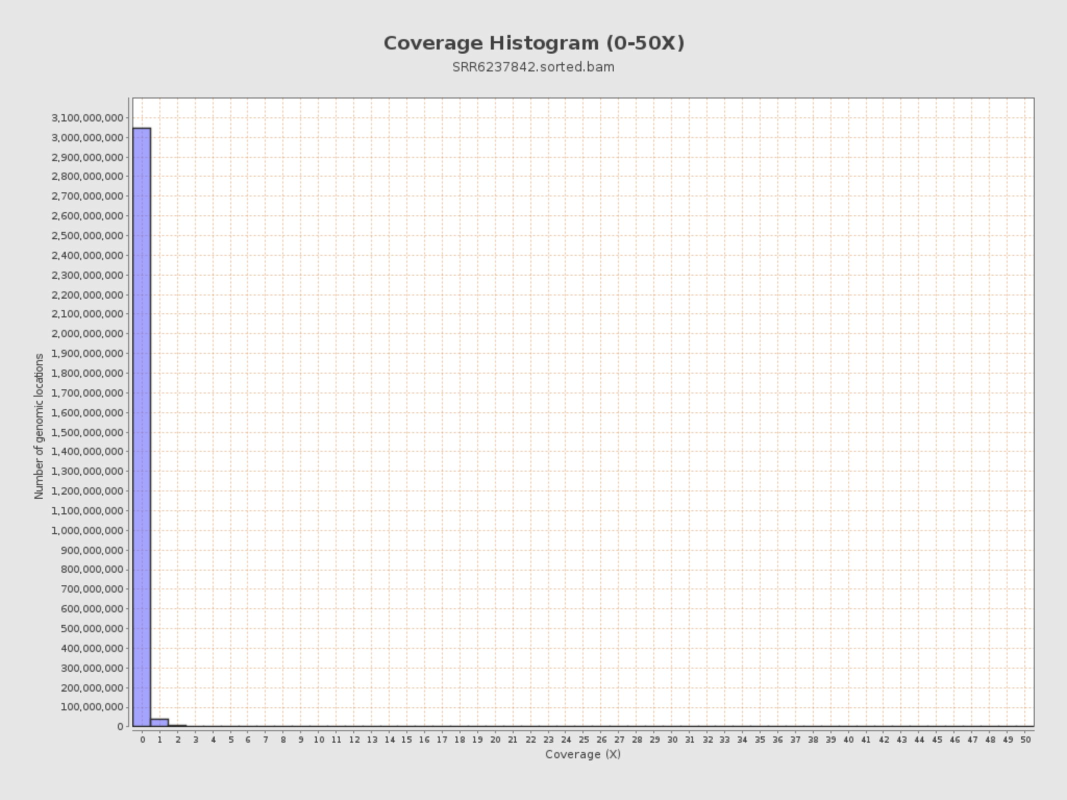
3. Results : Coverage across reference



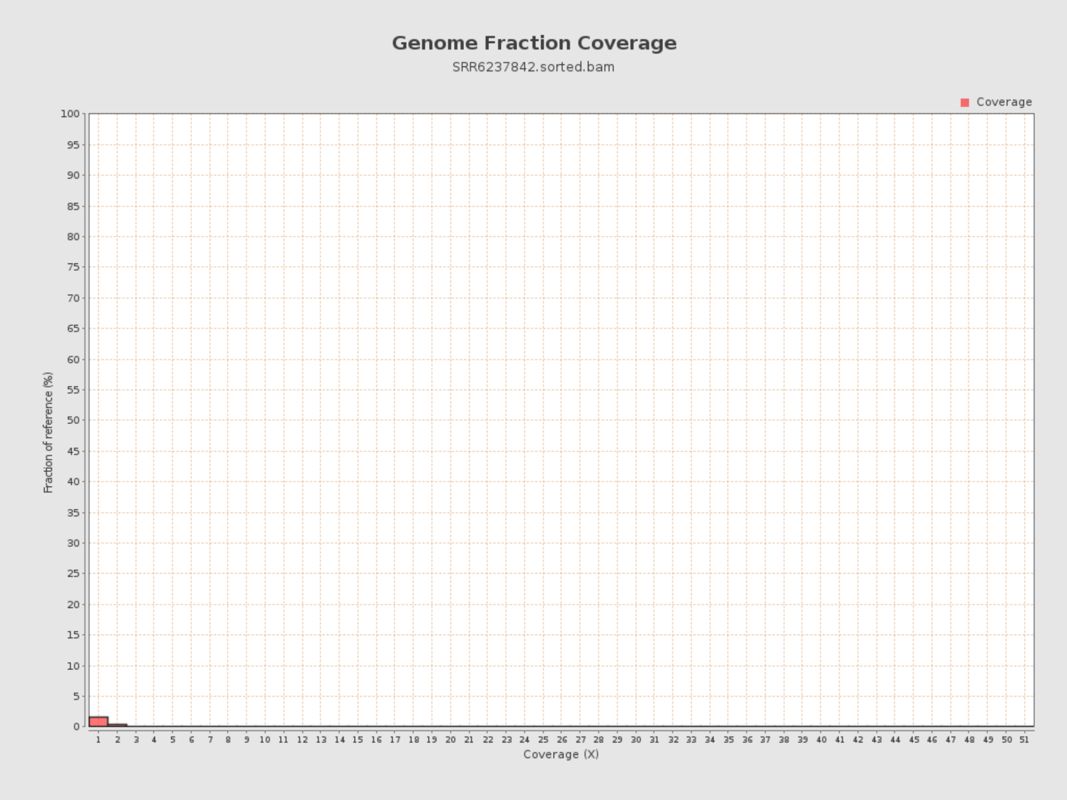
4. Results : Coverage Histogram



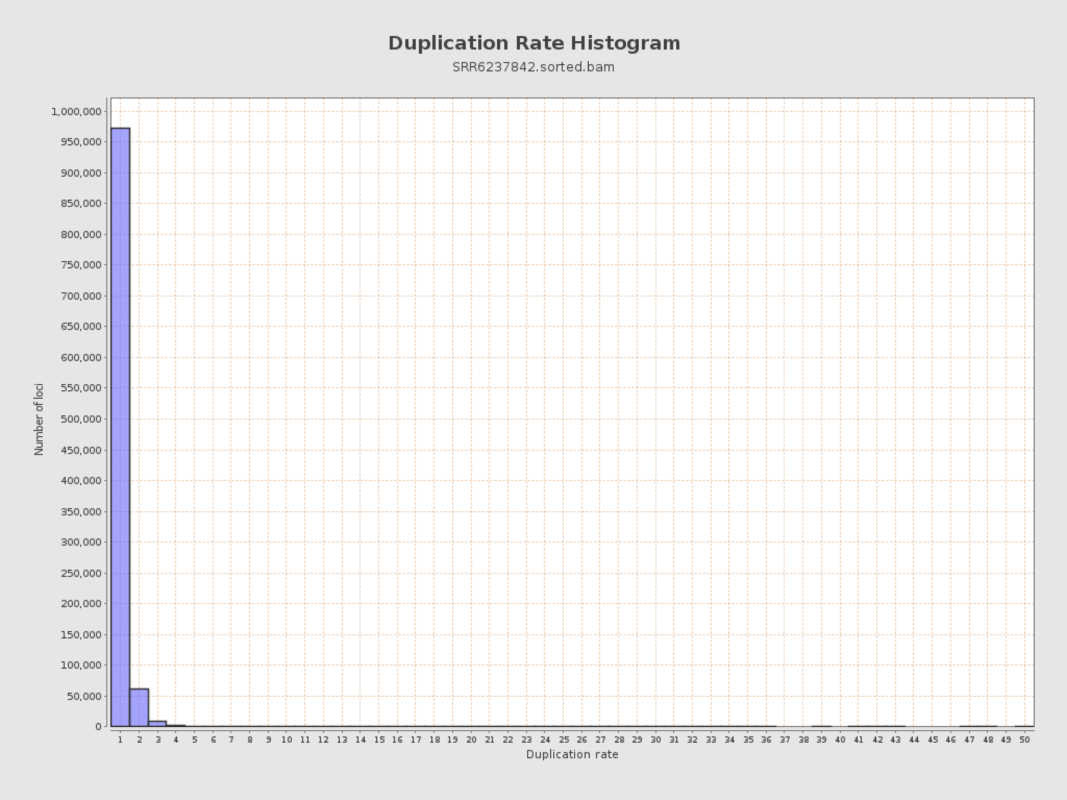
5. Results : Coverage Histogram (0-50X)



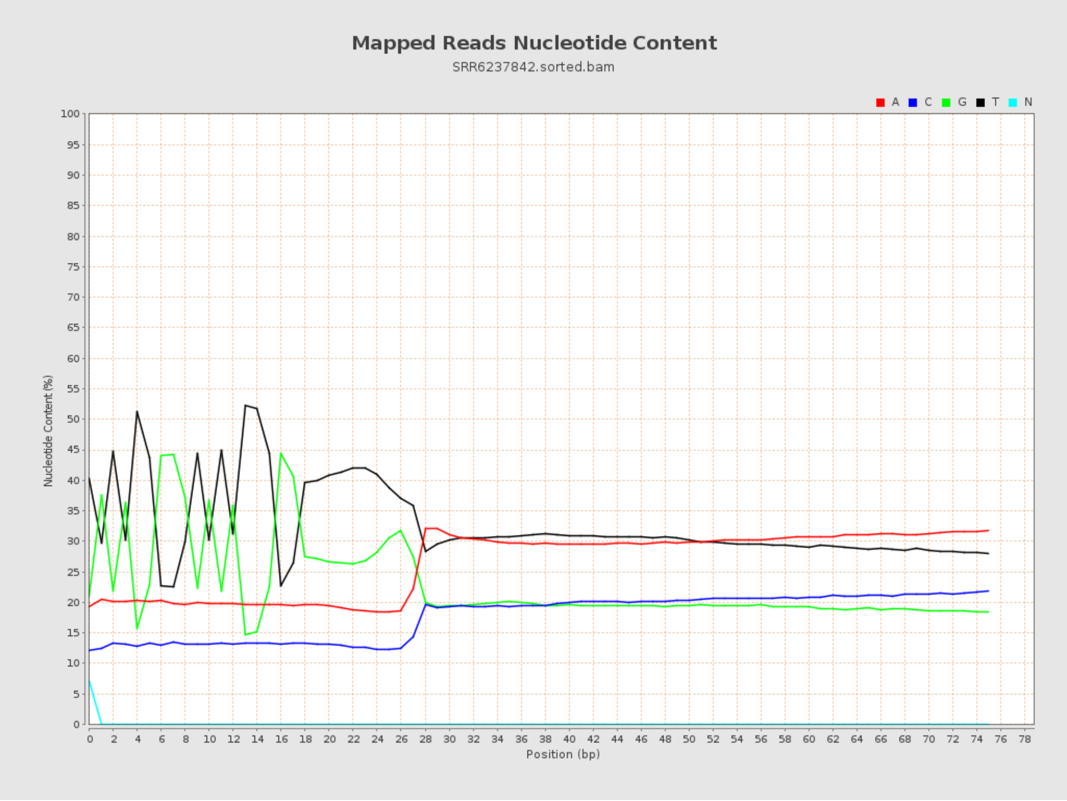
6. Results : Genome Fraction Coverage



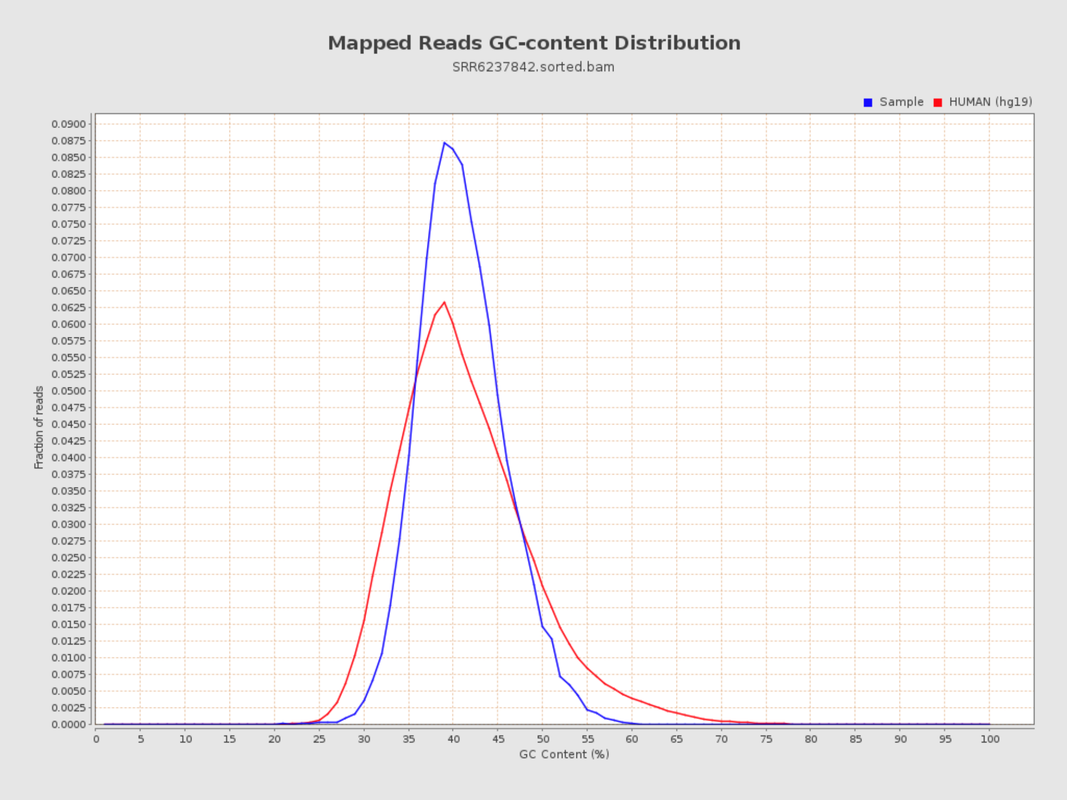
7. Results : Duplication Rate Histogram



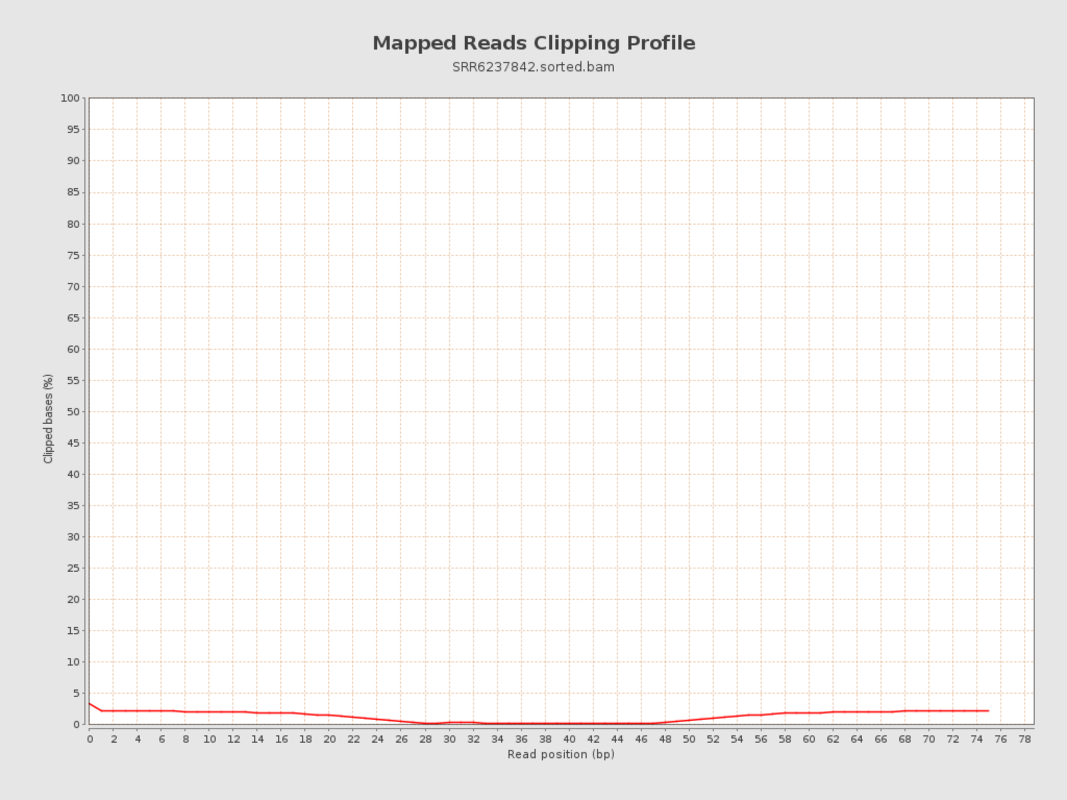
8. Results : Mapped Reads Nucleotide Content



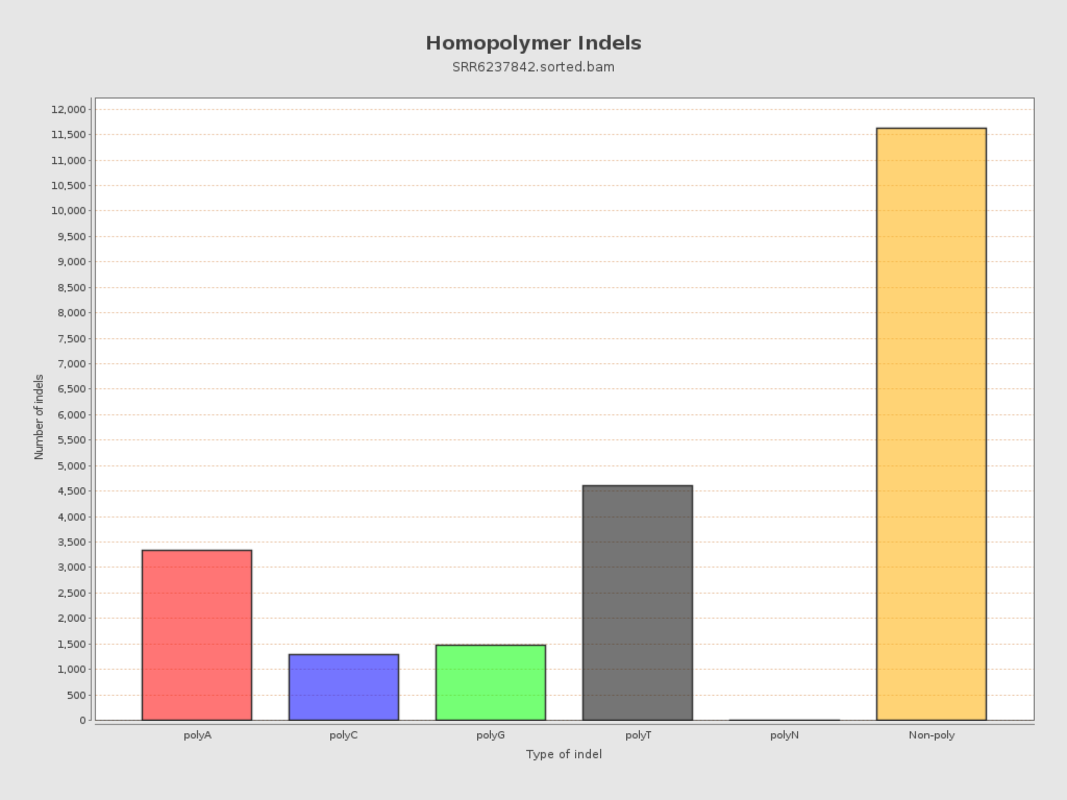
9. Results : Mapped Reads GC-content Distribution



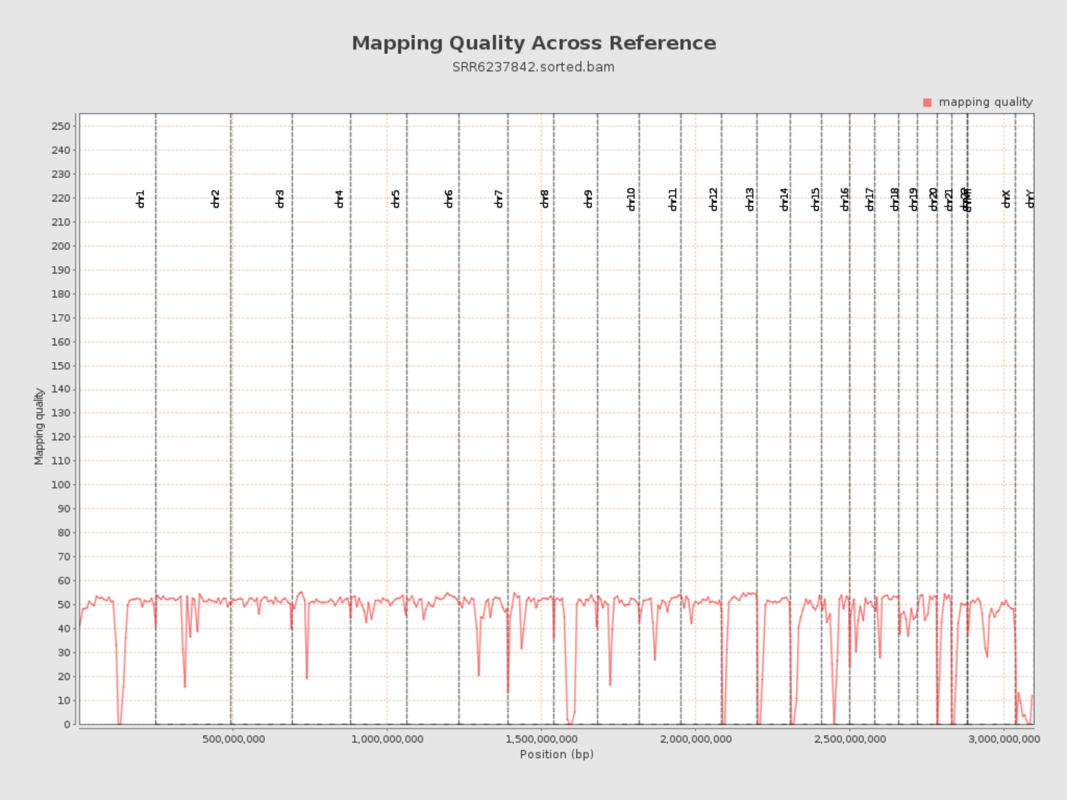
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram