Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 02:43:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237327.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_SRR6237327 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237327.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 02:43:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237327.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,211,933
Mapped reads	2,761,559 / 85.98%
Unmapped reads	450,374 / 14.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,027 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,066,840 / 33.21%
Duplication rate	22.24%
Clipped reads	1,908,158 / 59.41%

2.2. ACGT Content

Number/percentage of A's	42,716,534 / 25.46%
Number/percentage of C's	29,763,419 / 17.74%
Number/percentage of T's	55,131,625 / 32.86%
Number/percentage of G's	40,133,038 / 23.92%
Number/percentage of N's	17,315 / 0.01%
GC Percentage	41.66%

2.3. Coverage

Mean	0.0542

Standard Deviation	0.7917

2.4. Mapping Quality

Mean Mapping Quality	43.45

2.5. Mismatches and indels

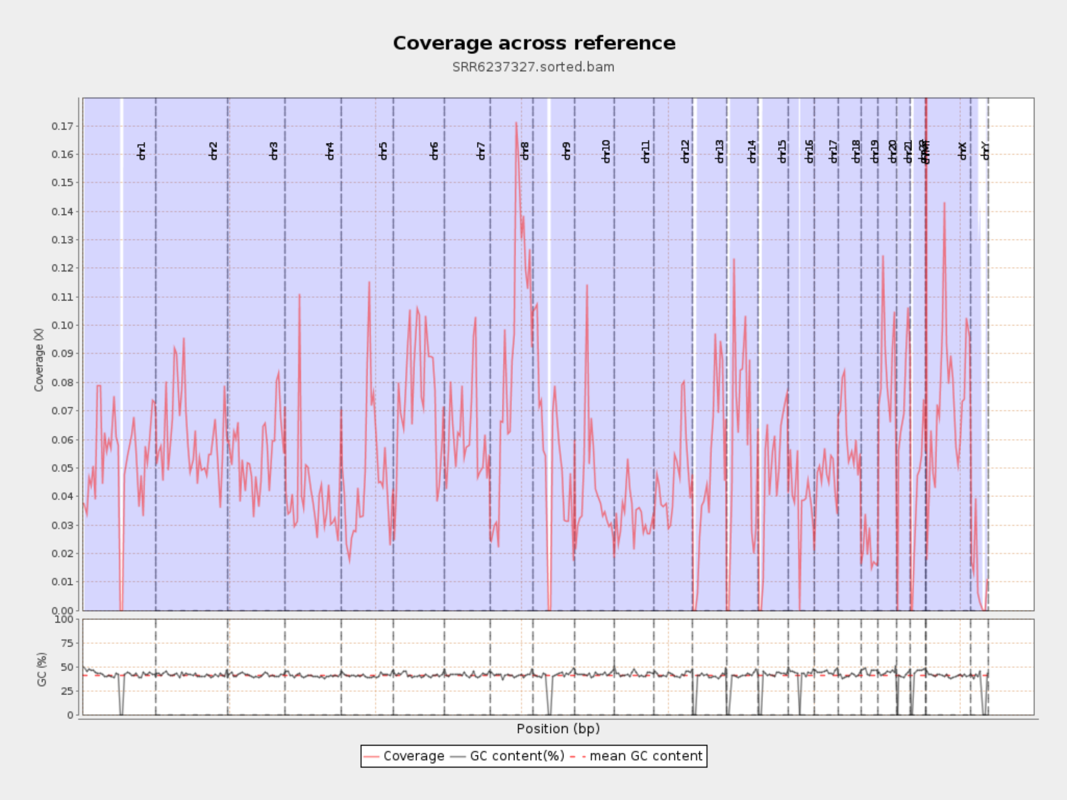
General error rate	0.66%
Mismatches	1,086,011
Insertions	12,310
Mapped reads with at least one insertion	0.44%
Deletions	47,877
Mapped reads with at least one deletion	1.72%
Homopolymer indels	43.73%

2.6. Chromosome stats

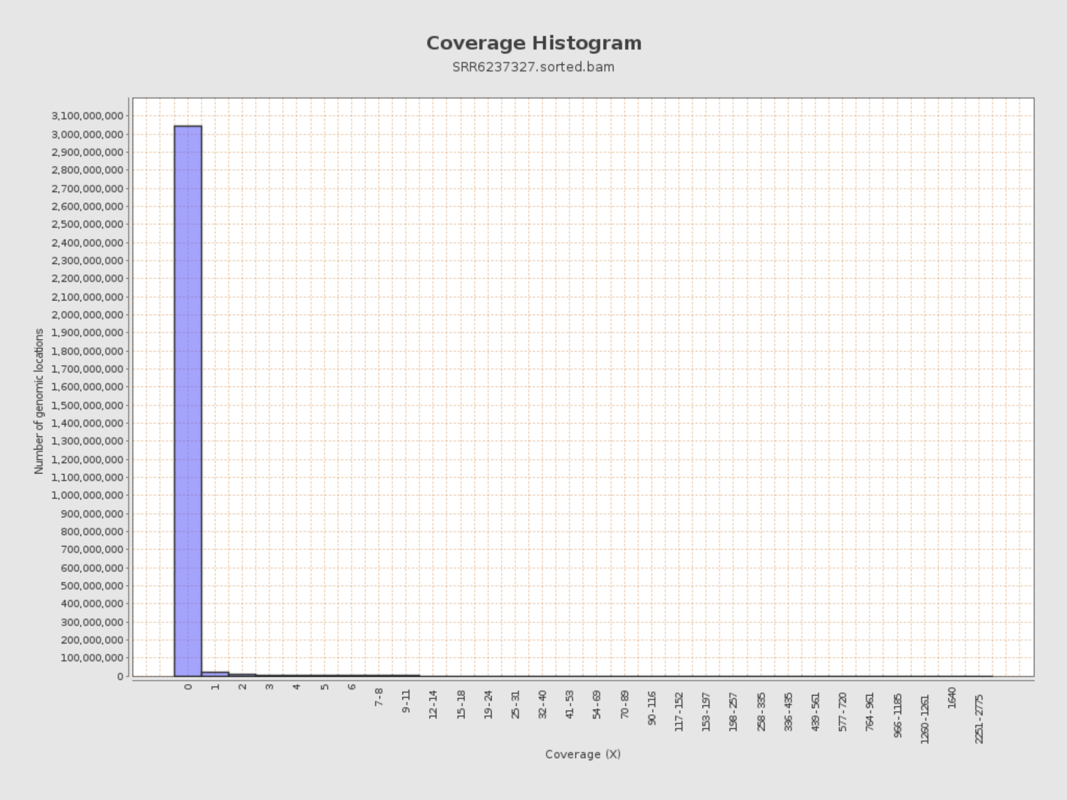
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12974527	0.0521	0.6845
chr2	243199373	14769476	0.0607	1.4803
chr3	198022430	10967298	0.0554	0.5953
chr4	191154276	7631208	0.0399	0.5851
chr5	180915260	8479206	0.0469	0.5627
chr6	171115067	12975335	0.0758	0.8535
chr7	159138663	9881531	0.0621	0.8202

chr8	146364022	13068870	0.0893	0.9289
chr9	141213431	7532598	0.0533	0.6441
chr10	135534747	5838136	0.0431	0.7477
chr11	135006516	4427026	0.0328	0.5373
chr12	133851895	6287289	0.047	0.571
chr13	115169878	5590922	0.0485	0.6418
chr14	107349540	6256402	0.0583	0.6057
chr15	102531392	4785725	0.0467	0.5662
chr16	90354753	3454725	0.0382	0.5159
chr17	81195210	3790945	0.0467	0.5786
chr18	78077248	4877389	0.0625	1.484
chr19	59128983	1255638	0.0212	0.4957
chr20	63025520	5550001	0.0881	0.7535
chr21	48129895	3414495	0.0709	0.7012
chr22	51304566	2009082	0.0392	0.5099
chrMT	16571	23666	1.4282	3.3432
chrX	155270560	11354844	0.0731	0.7338
chrY	59373566	647688	0.0109	0.3726

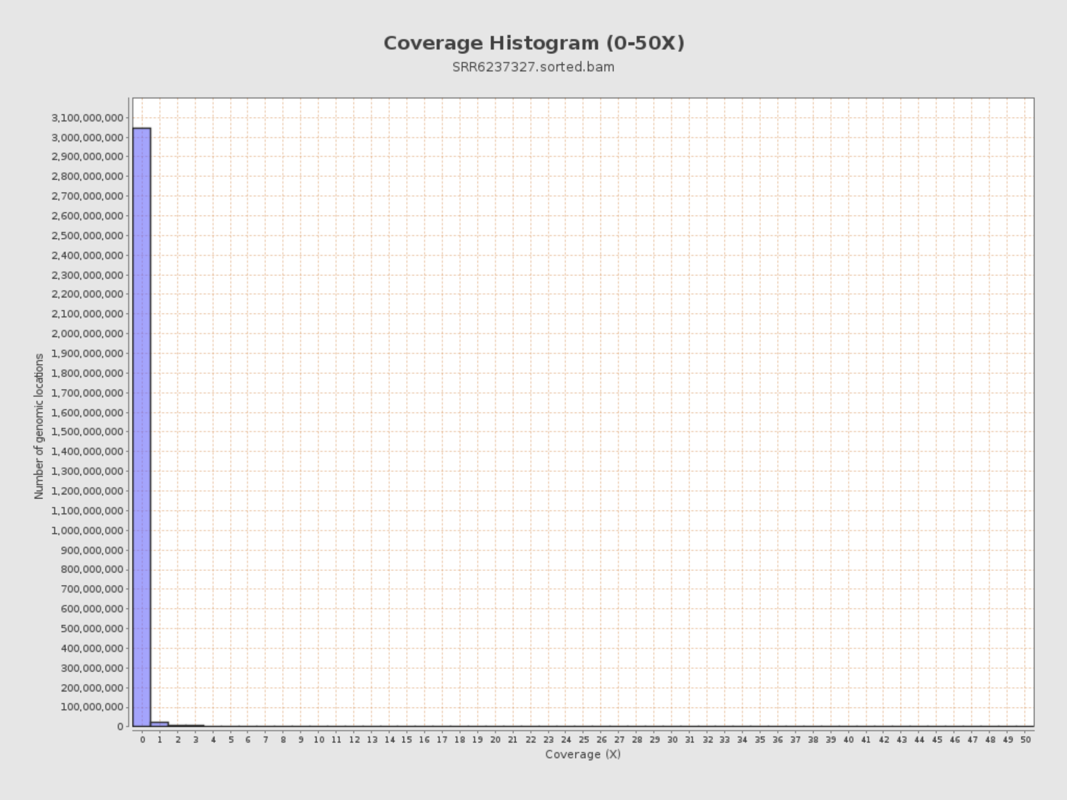
3. Results : Coverage across reference



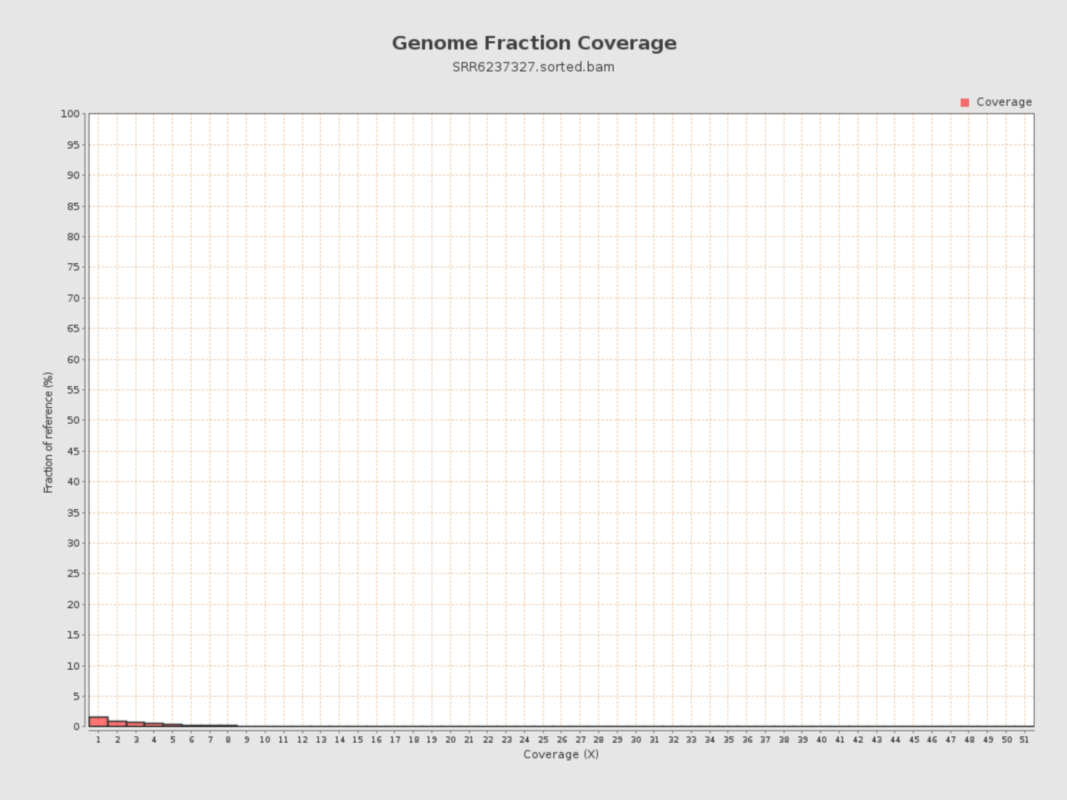
4. Results : Coverage Histogram



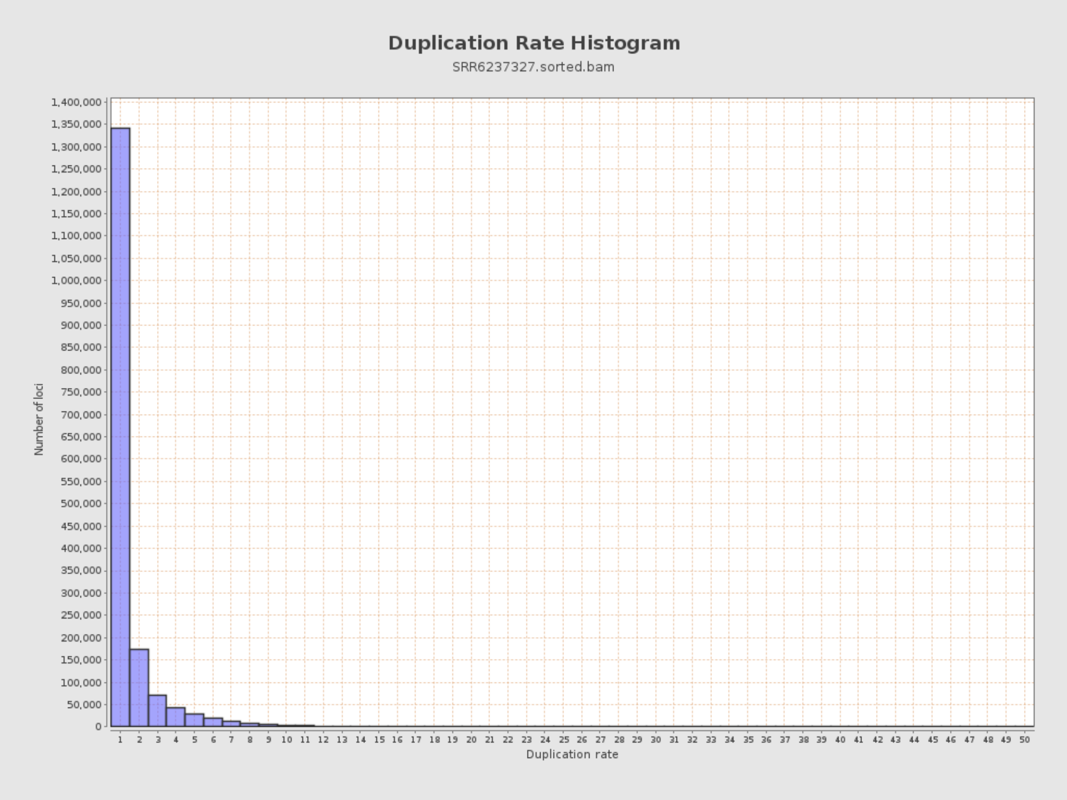
5. Results : Coverage Histogram (0-50X)



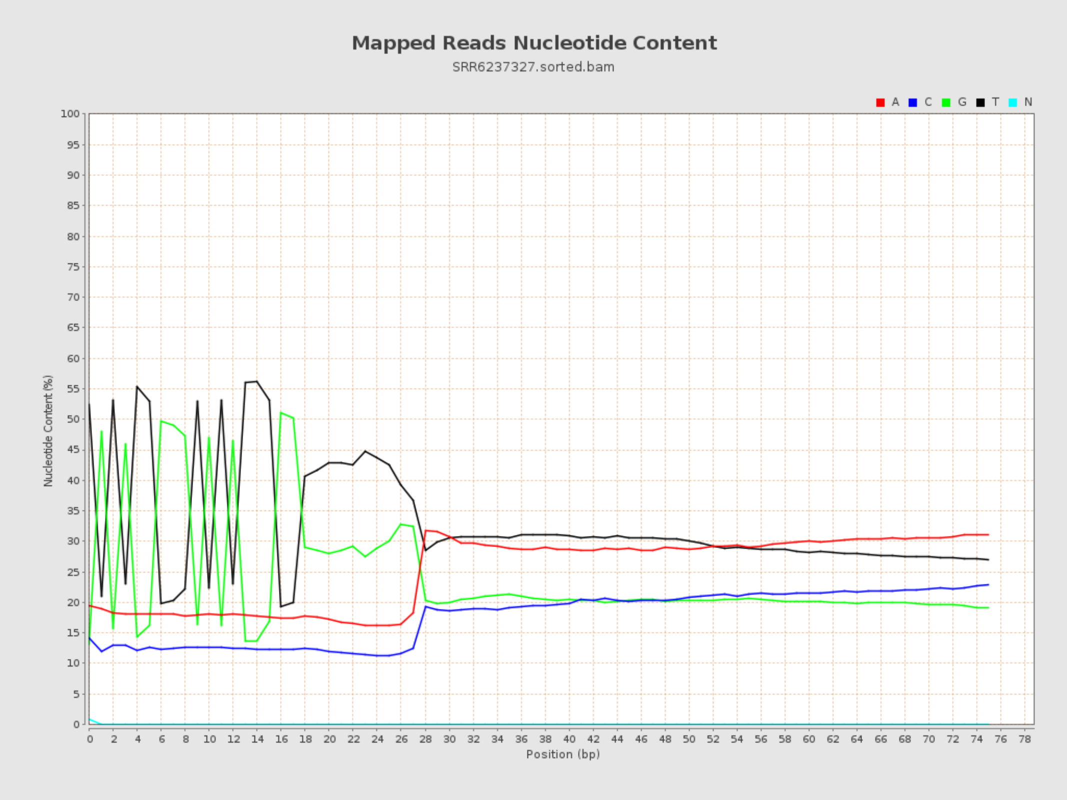
6. Results : Genome Fraction Coverage



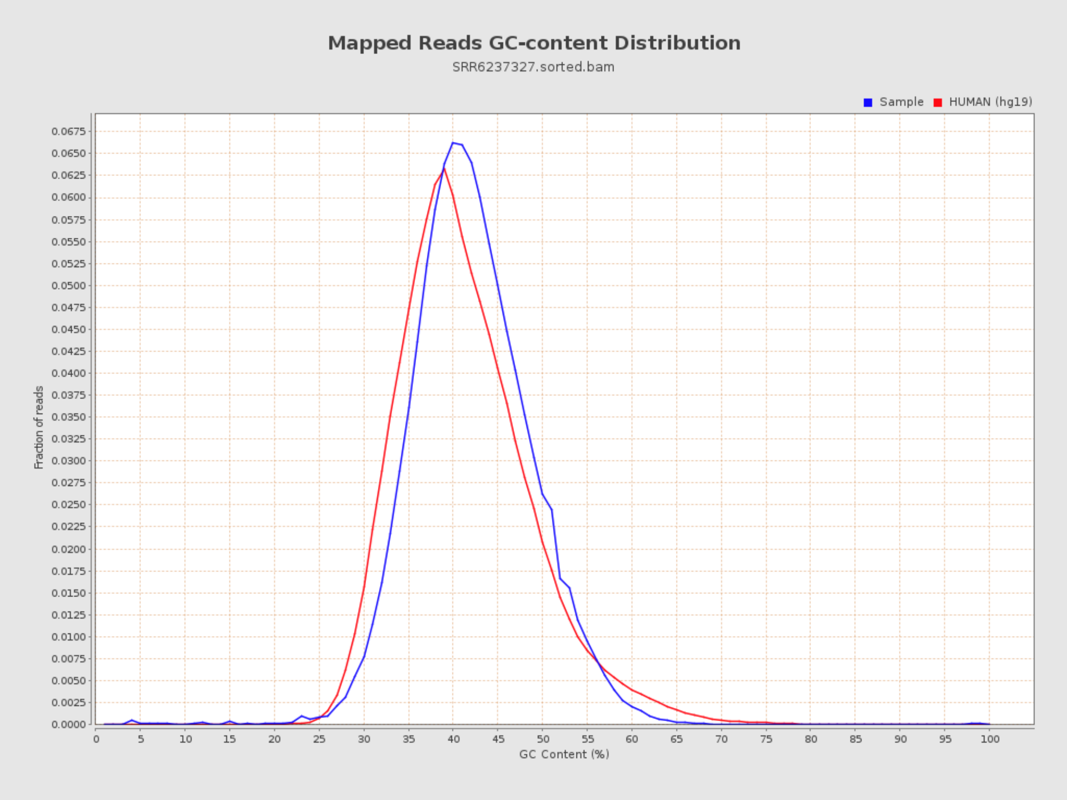
7. Results : Duplication Rate Histogram



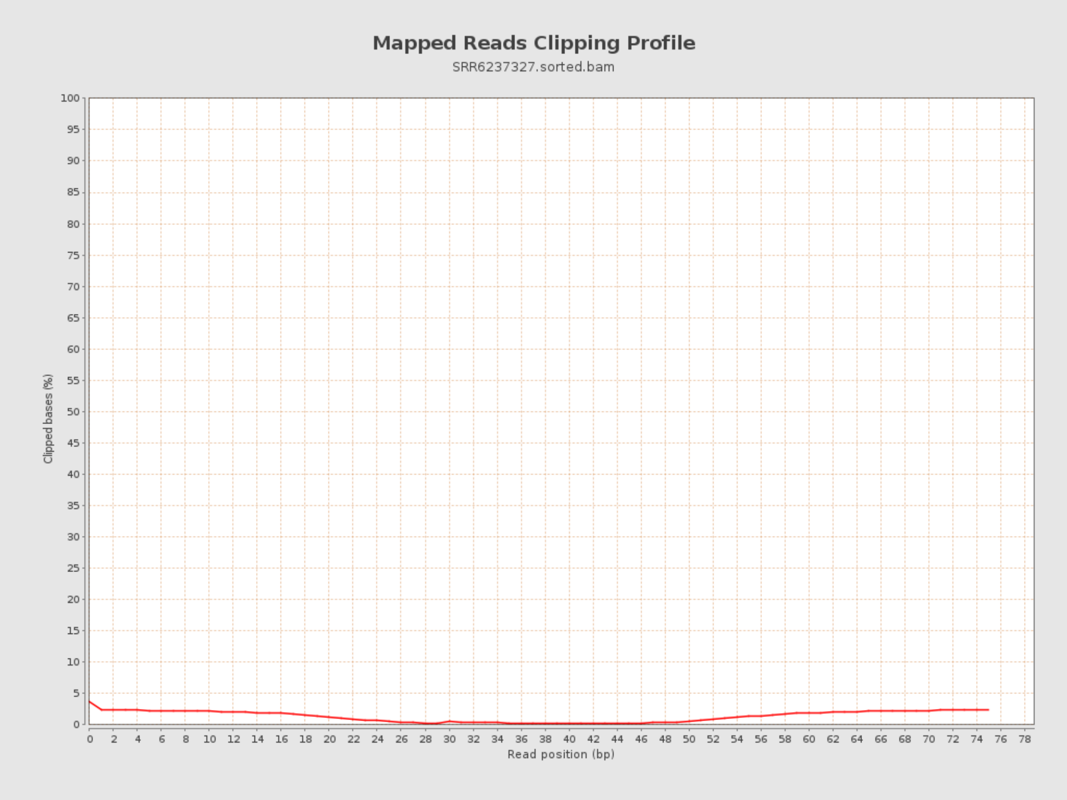
8. Results : Mapped Reads Nucleotide Content



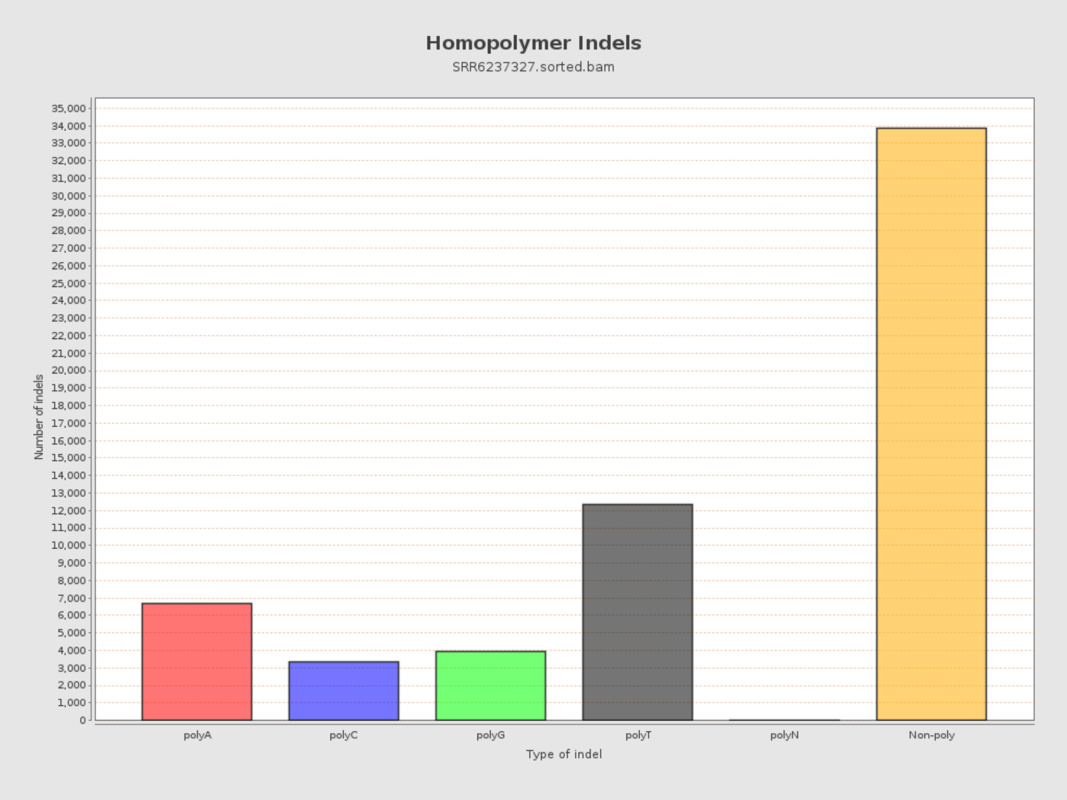
9. Results : Mapped Reads GC-content Distribution



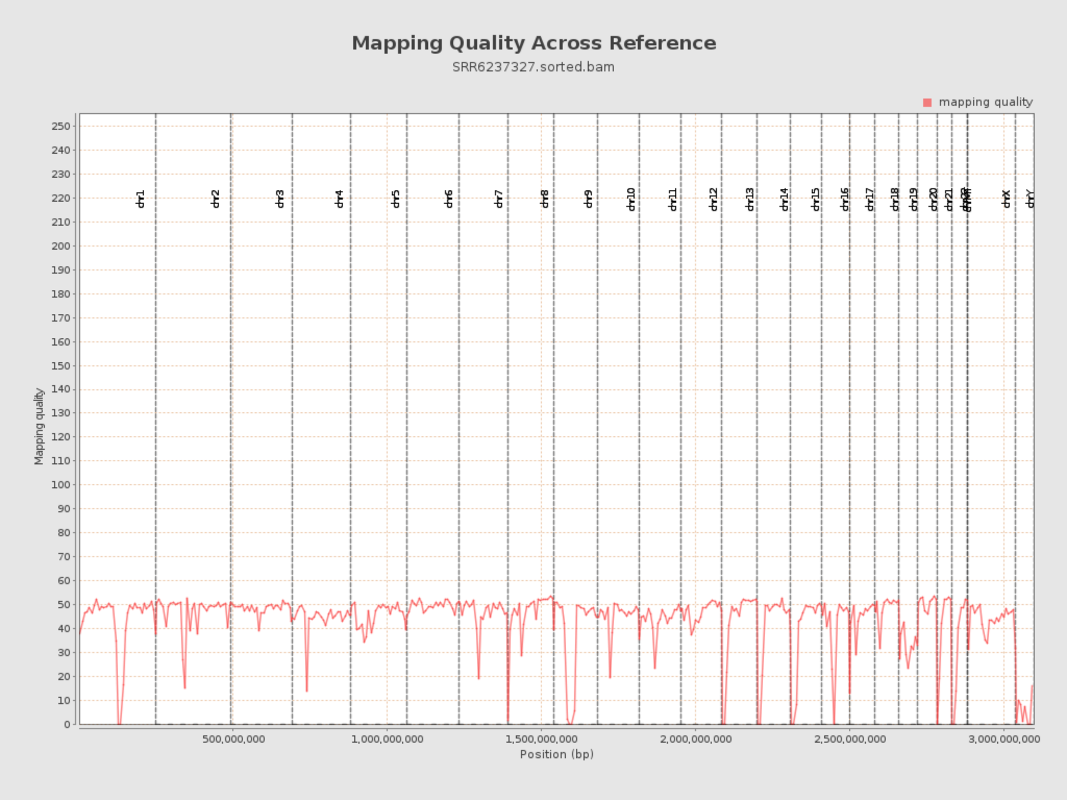
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram