Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 06:45:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237808.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_SRR6237808 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237808.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 06:45:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237808.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,132,557
Mapped reads	1,901,199 / 60.69%
Unmapped reads	1,231,358 / 39.31%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,128 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	138,852 / 4.43%
Duplication rate	6.08%
Clipped reads	1,099,633 / 35.1%

2.2. ACGT Content

Number/percentage of A's	32,307,395 / 27%
Number/percentage of C's	23,670,280 / 19.79%
Number/percentage of T's	35,970,339 / 30.07%
Number/percentage of G's	27,585,797 / 23.06%
Number/percentage of N's	102,677 / 0.09%
GC Percentage	42.84%

2.3. Coverage

Mean	0.0387

Standard Deviation	0.3475

2.4. Mapping Quality

Mean Mapping Quality	45.95

2.5. Mismatches and indels

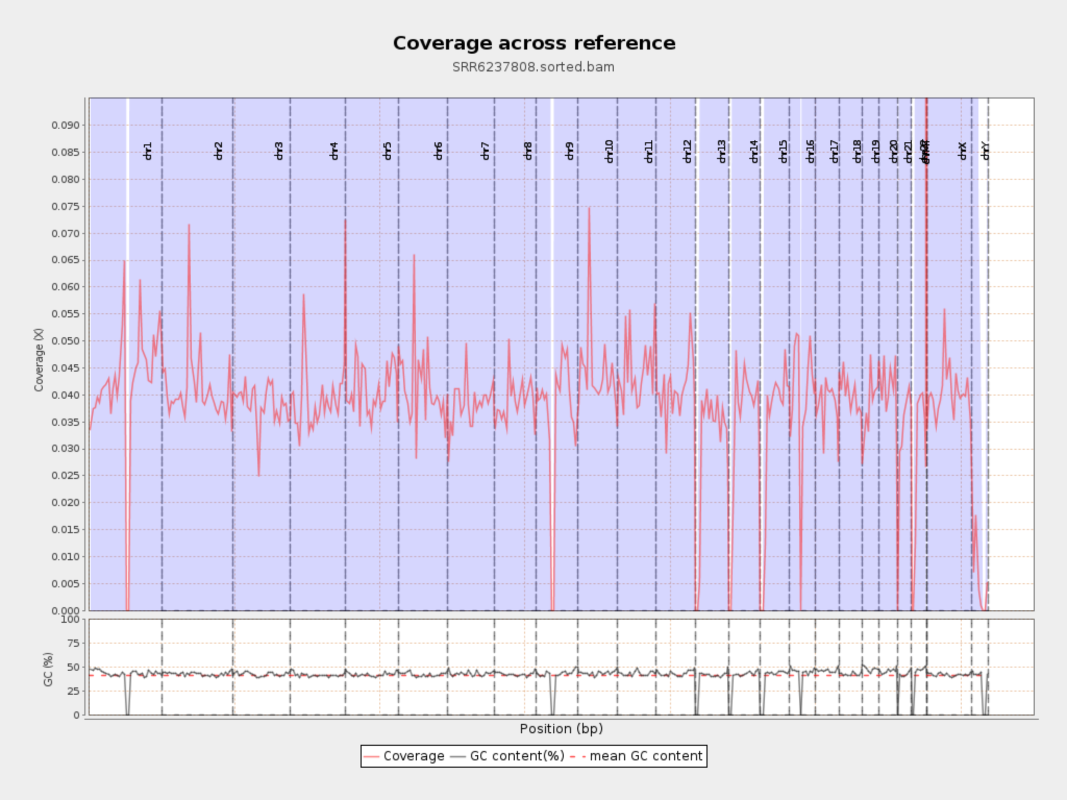
General error rate	0.8%
Mismatches	945,192
Insertions	8,832
Mapped reads with at least one insertion	0.46%
Deletions	28,562
Mapped reads with at least one deletion	1.49%
Homopolymer indels	46.66%

2.6. Chromosome stats

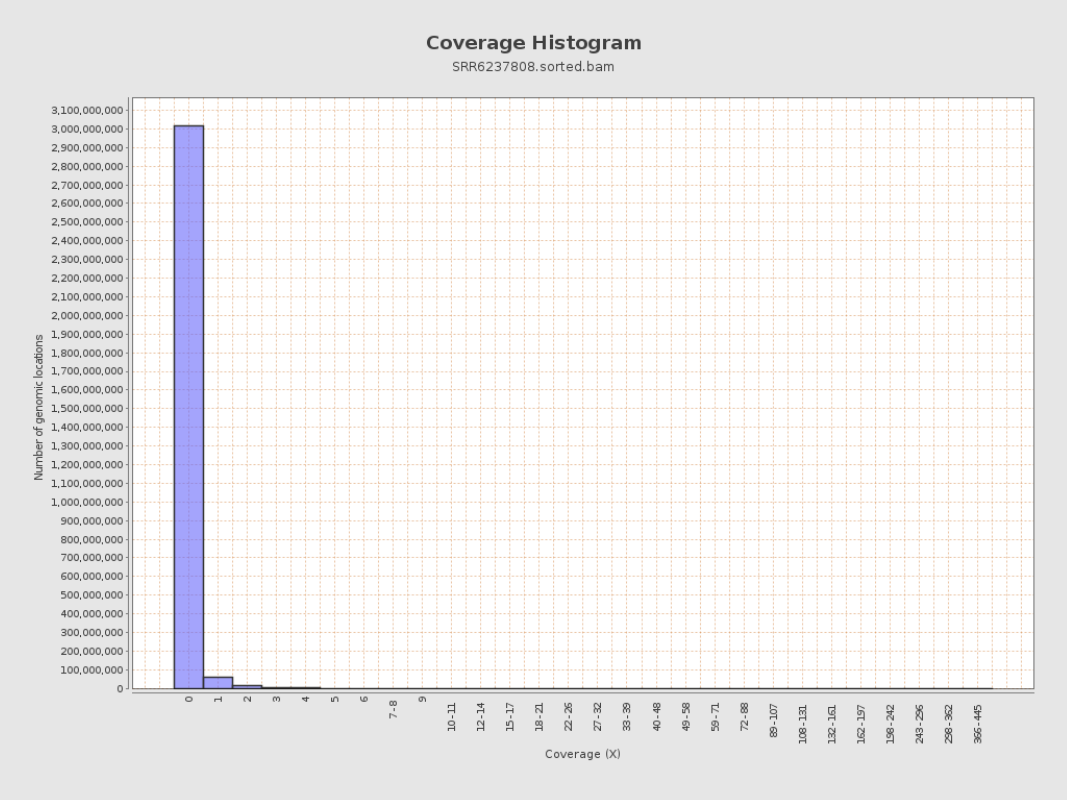
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10468285	0.042	0.5046
chr2	243199373	10022555	0.0412	0.3963
chr3	198022430	7608374	0.0384	0.2747
chr4	191154276	7420333	0.0388	0.2898
chr5	180915260	7430014	0.0411	0.2858
chr6	171115067	7086915	0.0414	0.3184
chr7	159138663	6125288	0.0385	0.3487

chr8	146364022	5703225	0.039	0.3153
chr9	141213431	5057441	0.0358	0.3319
chr10	135534747	6036976	0.0445	0.3727
chr11	135006516	5994356	0.0444	0.3677
chr12	133851895	5504015	0.0411	0.2857
chr13	115169878	3493680	0.0303	0.2419
chr14	107349540	3677968	0.0343	0.2755
chr15	102531392	3359561	0.0328	0.2538
chr16	90354753	3574583	0.0396	0.3037
chr17	81195210	3088518	0.038	0.2974
chr18	78077248	3143874	0.0403	0.5336
chr19	59128983	2266100	0.0383	0.378
chr20	63025520	2638945	0.0419	0.2975
chr21	48129895	1558664	0.0324	0.2715
chr22	51304566	1341870	0.0262	0.2288
chrMT	16571	432417	26.0948	17.0476
chrX	155270560	6288349	0.0405	0.3056
chrY	59373566	360938	0.0061	0.1515

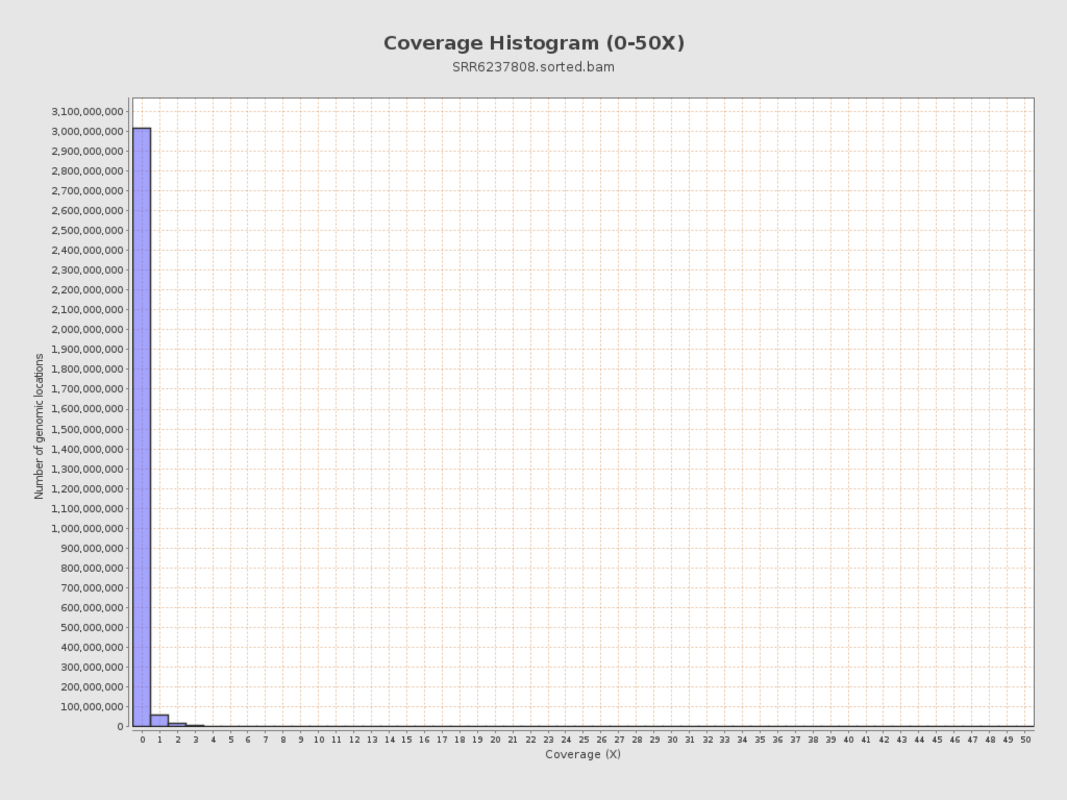
3. Results : Coverage across reference



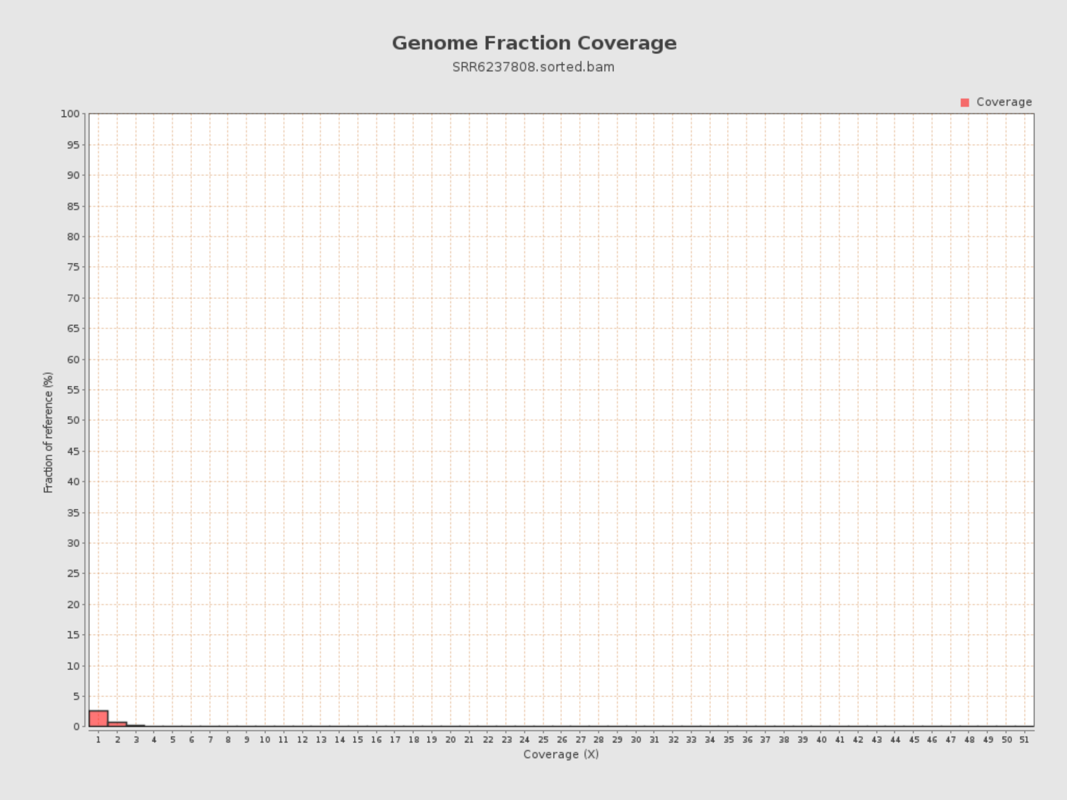
4. Results : Coverage Histogram



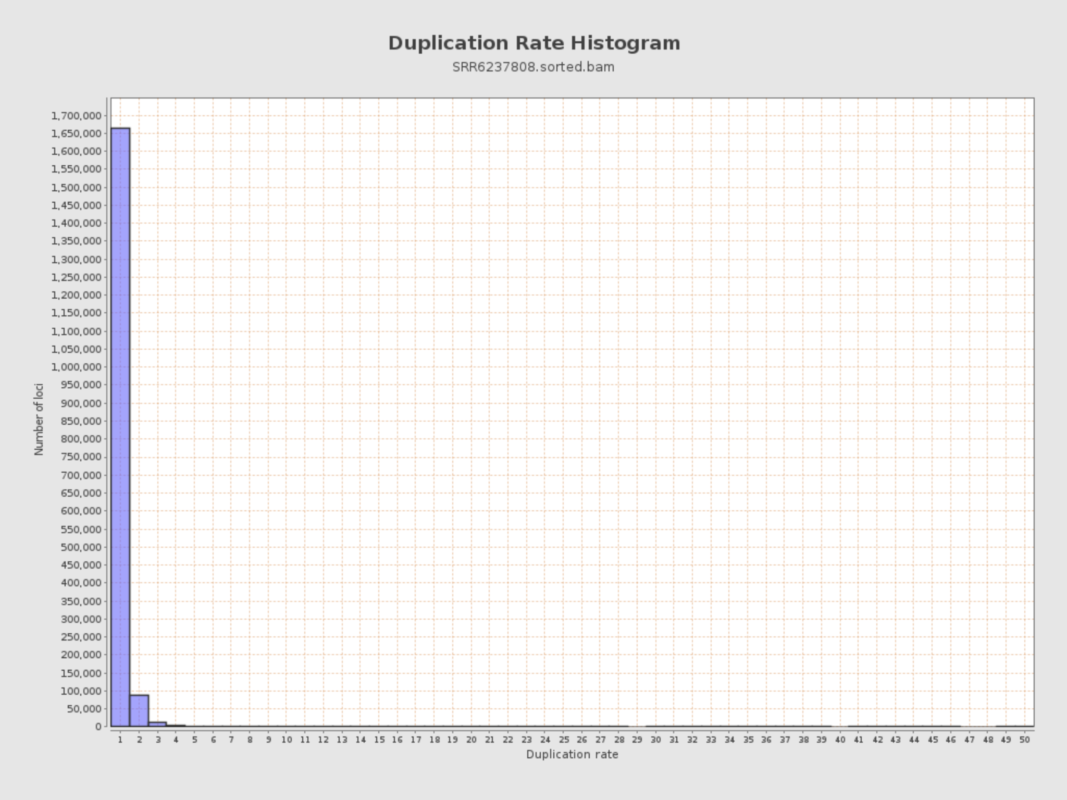
5. Results : Coverage Histogram (0-50X)



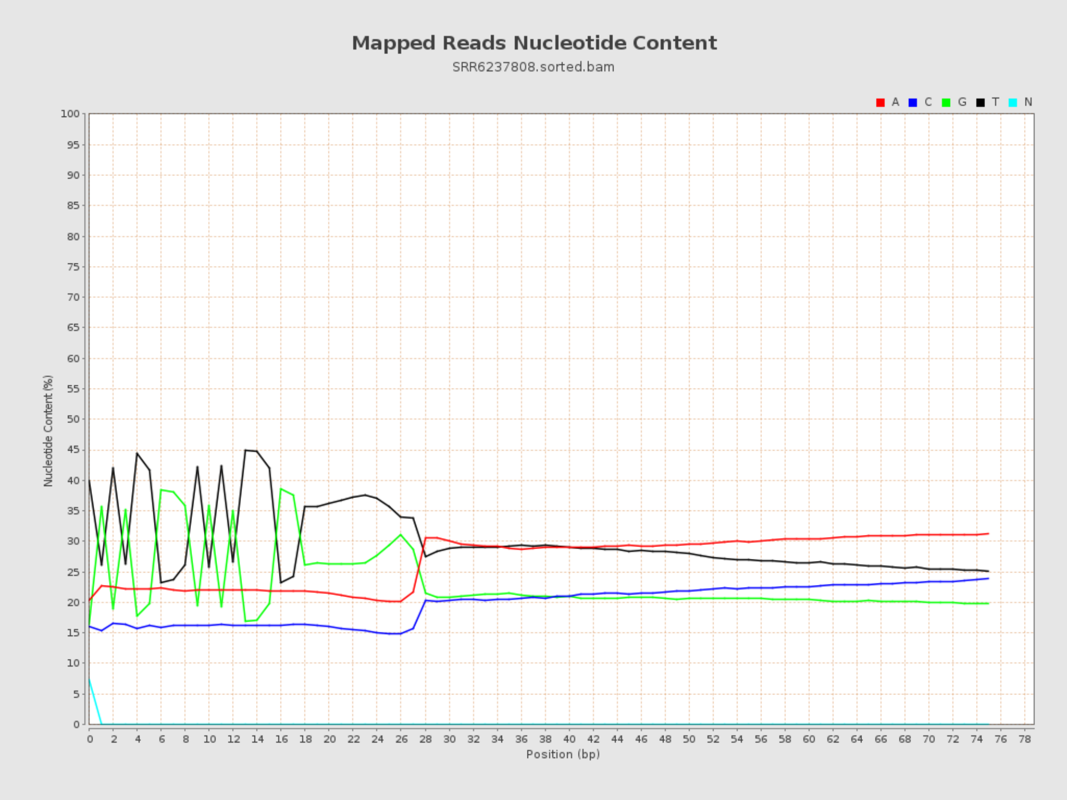
6. Results : Genome Fraction Coverage



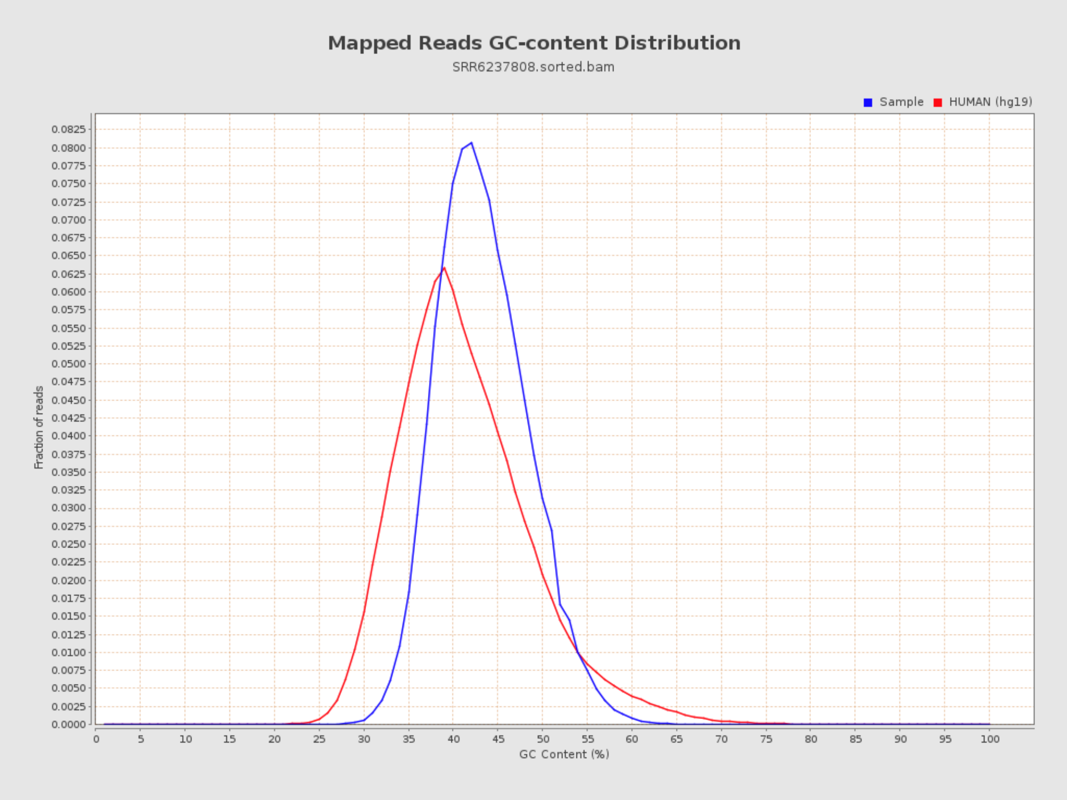
7. Results : Duplication Rate Histogram



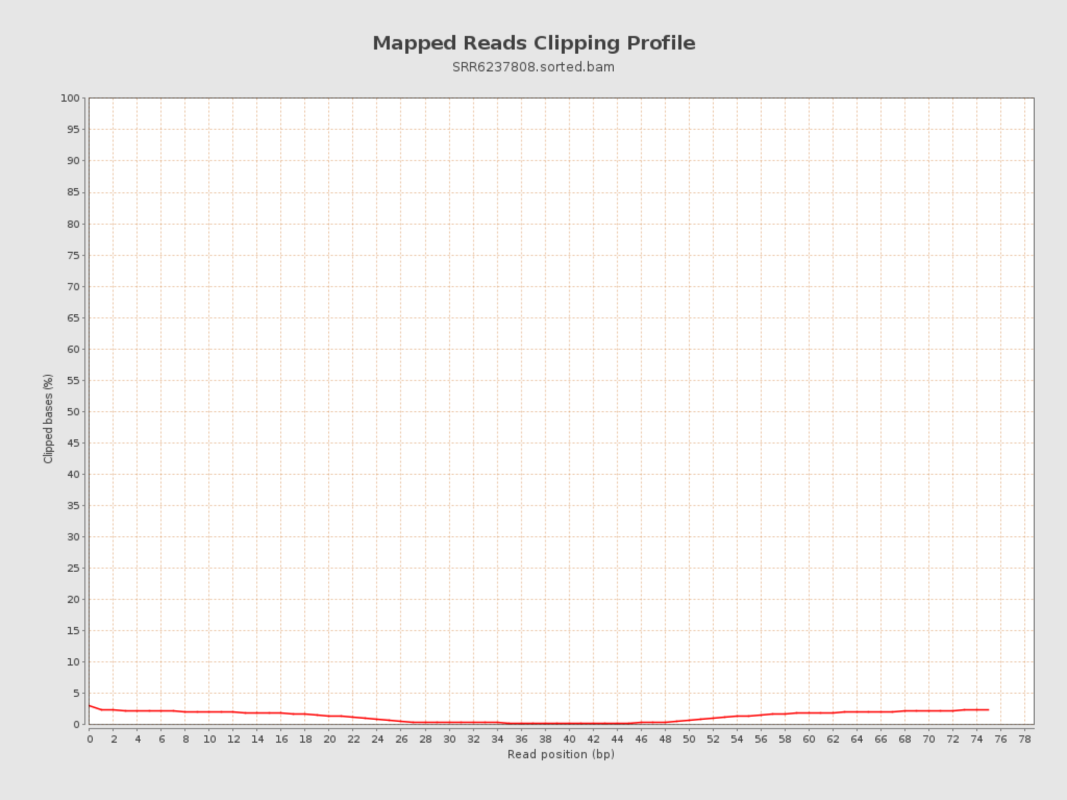
8. Results : Mapped Reads Nucleotide Content



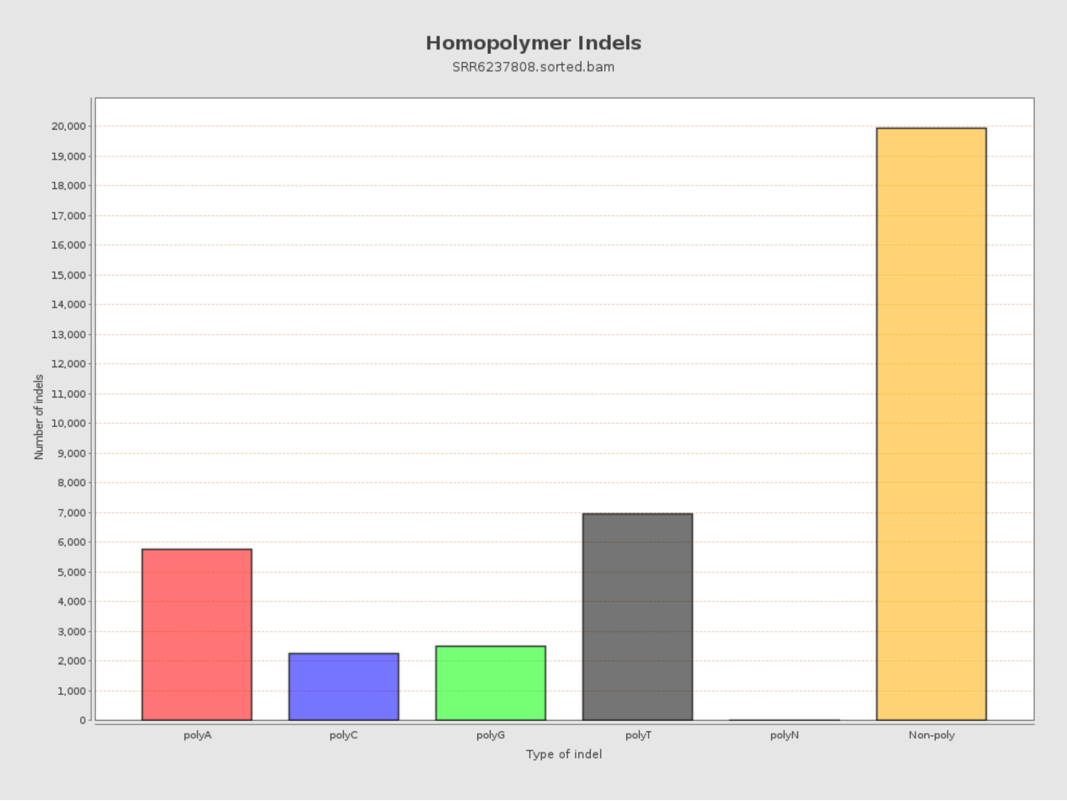
9. Results : Mapped Reads GC-content Distribution



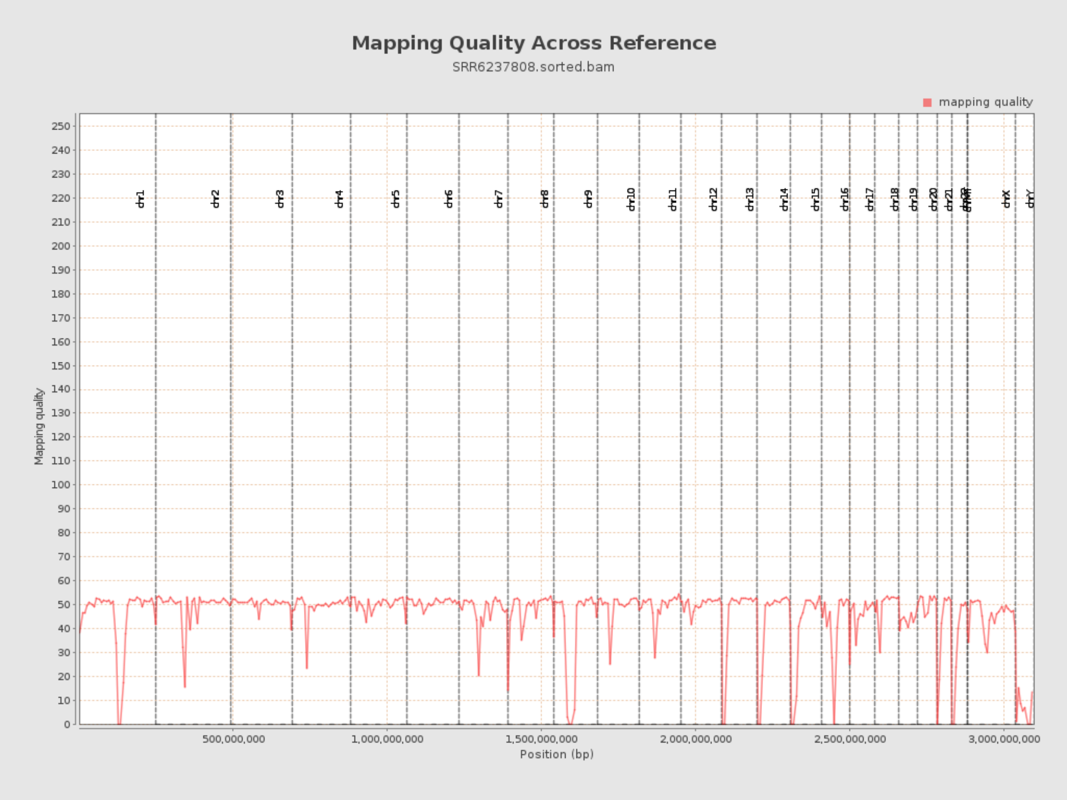
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram