Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 00:27:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525237.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_SRR10525237 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525237.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 00:27:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525237.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,889,064
Mapped reads	1,741,974 / 92.21%
Unmapped reads	147,090 / 7.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,655 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	72,650 / 3.85%
Duplication rate	3.02%
Clipped reads	1,744,025 / 92.32%

2.2. ACGT Content

Number/percentage of A's	24,733,280 / 24.47%
Number/percentage of C's	18,727,509 / 18.53%
Number/percentage of T's	32,785,518 / 32.43%
Number/percentage of G's	24,835,717 / 24.57%
Number/percentage of N's	1,962 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.307

2.4. Mapping Quality

Mean Mapping Quality	44.65

2.5. Mismatches and indels

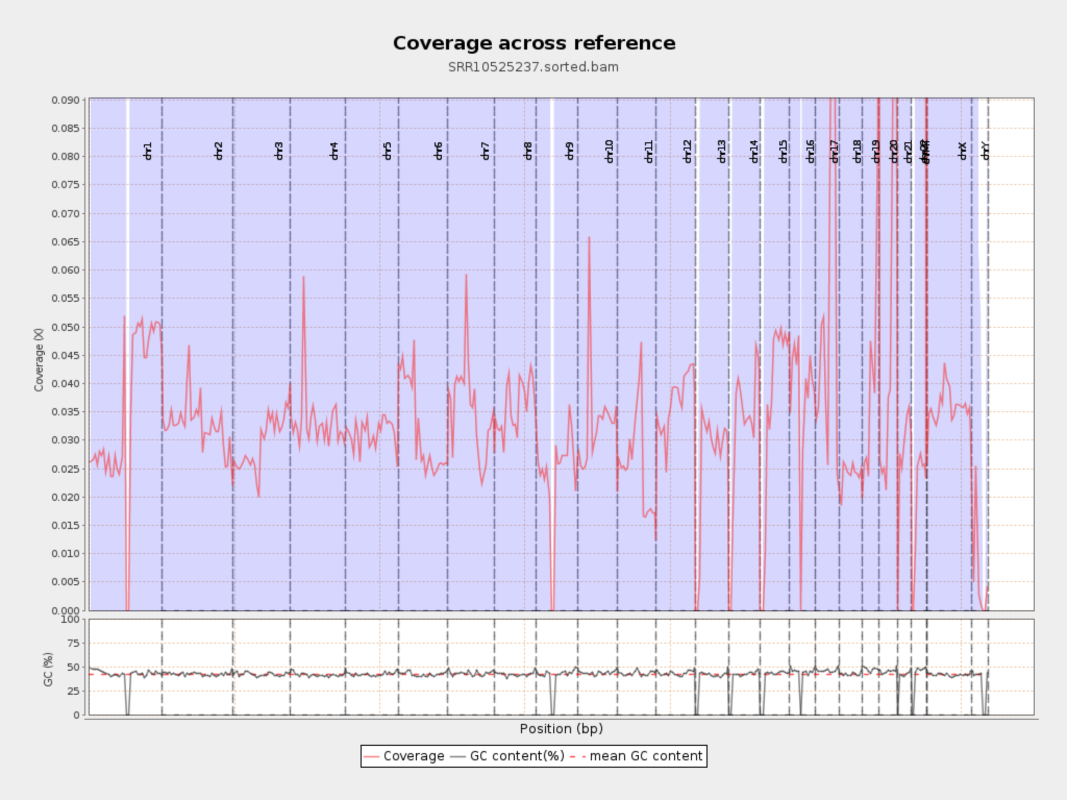
General error rate	0.52%
Mismatches	506,822
Insertions	8,324
Mapped reads with at least one insertion	0.48%
Deletions	19,590
Mapped reads with at least one deletion	1.12%
Homopolymer indels	41.1%

2.6. Chromosome stats

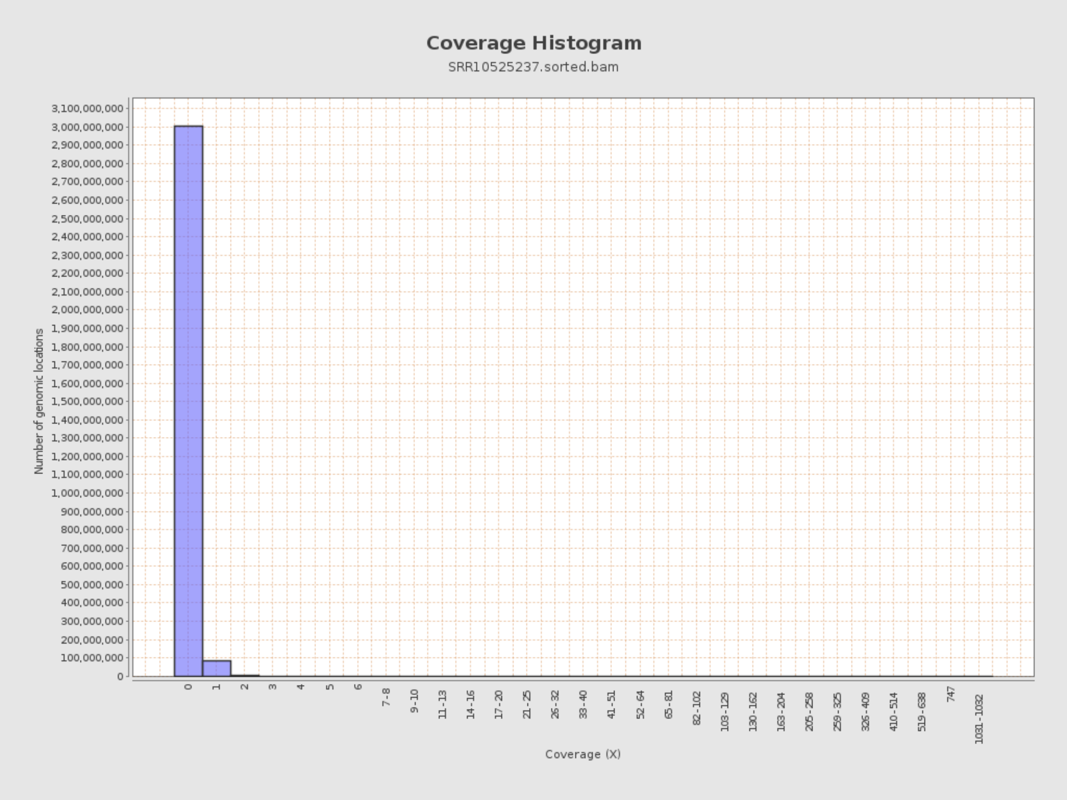
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8717219	0.035	0.4959
chr2	243199373	7999989	0.0329	0.461
chr3	198022430	5829651	0.0294	0.1927
chr4	191154276	6360822	0.0333	0.2402
chr5	180915260	5653472	0.0312	0.1935
chr6	171115067	5474161	0.032	0.231
chr7	159138663	5650616	0.0355	0.38

chr8	146364022	5278675	0.0361	0.4173
chr9	141213431	3333259	0.0236	0.2079
chr10	135534747	4473619	0.033	0.3257
chr11	135006516	3515982	0.026	0.2298
chr12	133851895	4945092	0.0369	0.2123
chr13	115169878	2993334	0.026	0.177
chr14	107349540	3346719	0.0312	0.1977
chr15	102531392	3641138	0.0355	0.2082
chr16	90354753	3389457	0.0375	0.2253
chr17	81195210	4318766	0.0532	0.2648
chr18	78077248	1871709	0.024	0.3532
chr19	59128983	2596890	0.0439	0.3795
chr20	63025520	3409405	0.0541	0.2674
chr21	48129895	1331152	0.0277	0.2249
chr22	51304566	937855	0.0183	0.1483
chrMT	16571	114605	6.916	4.8097
chrX	155270560	5562286	0.0358	0.2288
chrY	59373566	369574	0.0062	0.2636

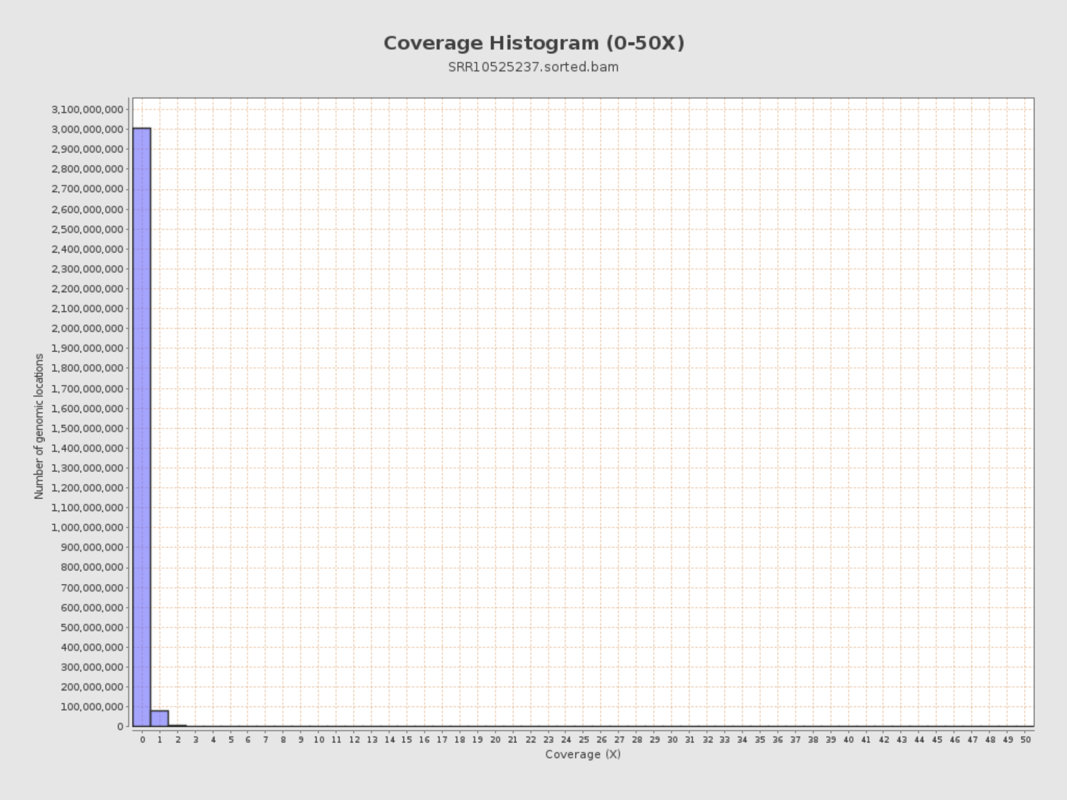
3. Results : Coverage across reference



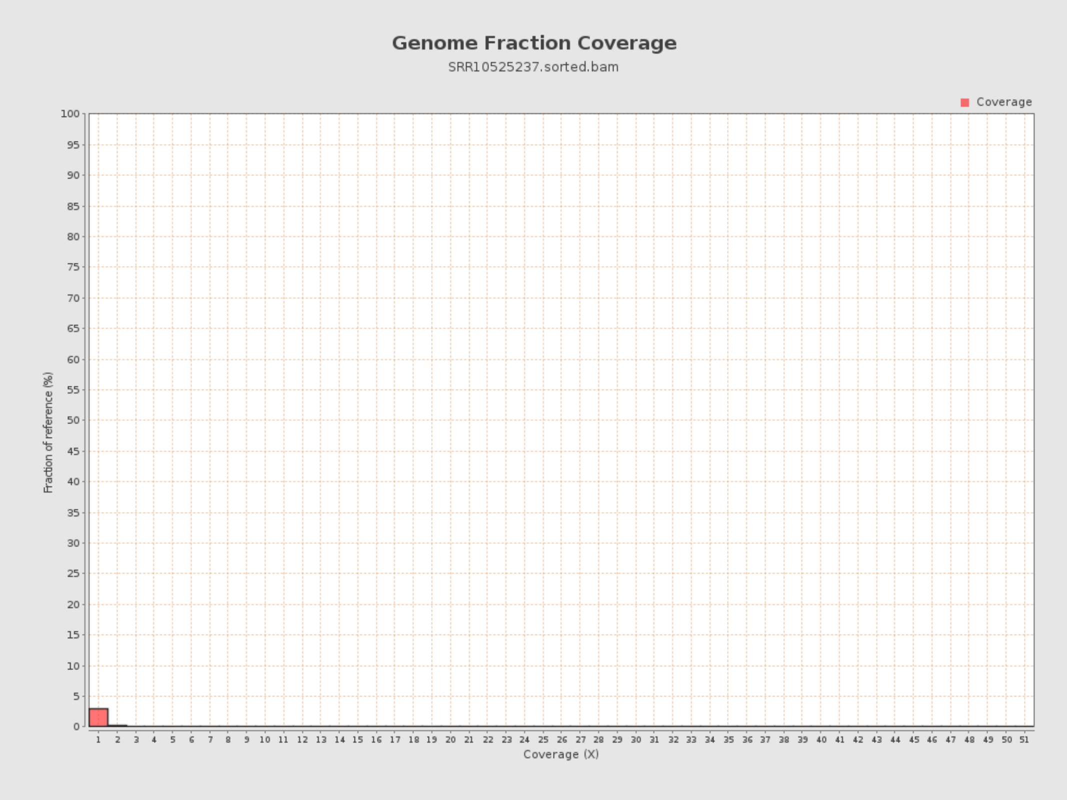
4. Results : Coverage Histogram



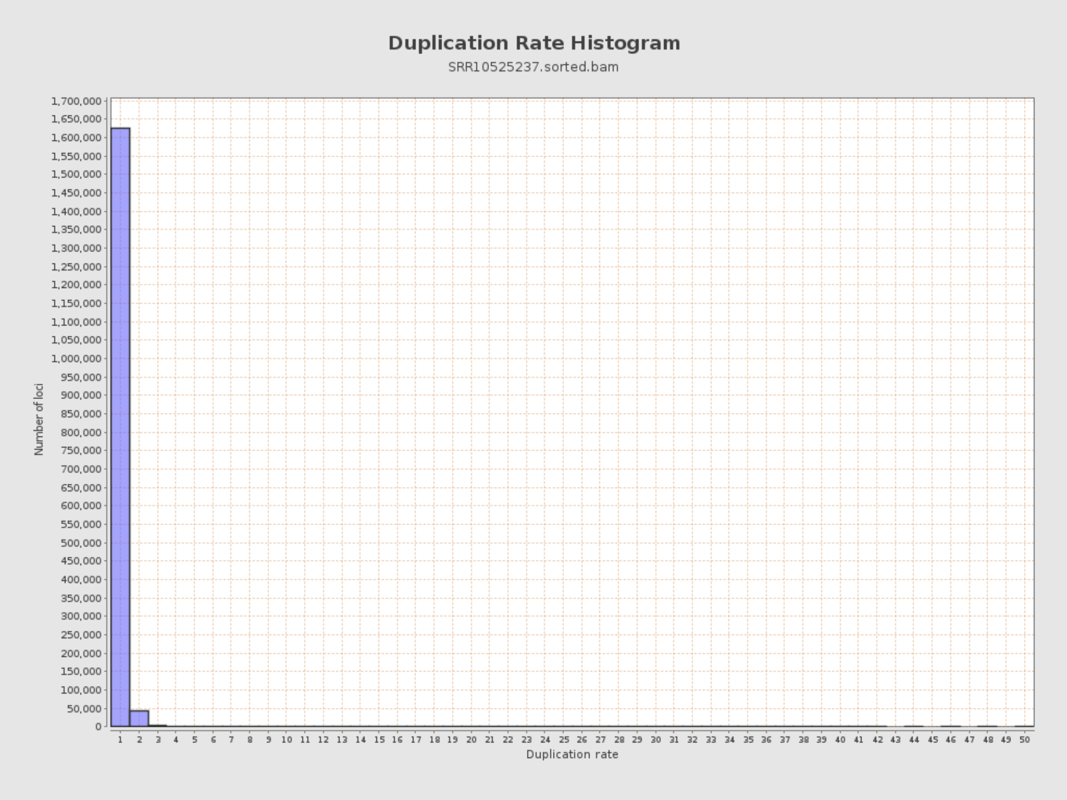
5. Results : Coverage Histogram (0-50X)



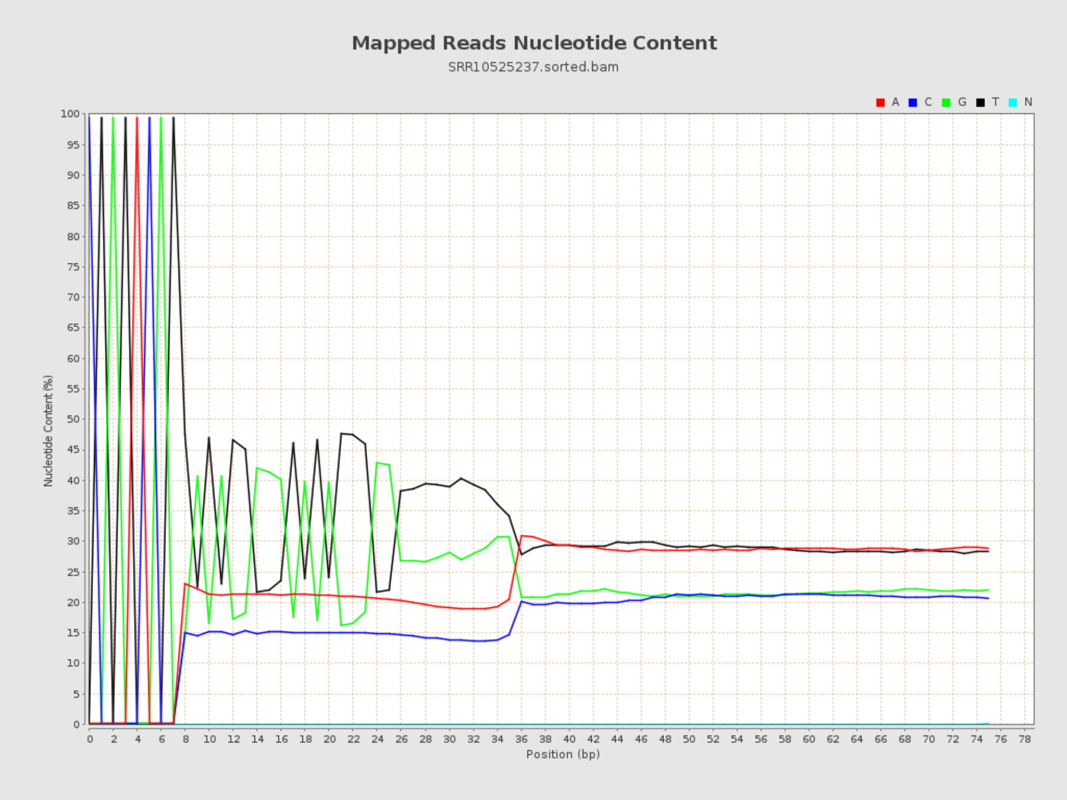
6. Results : Genome Fraction Coverage



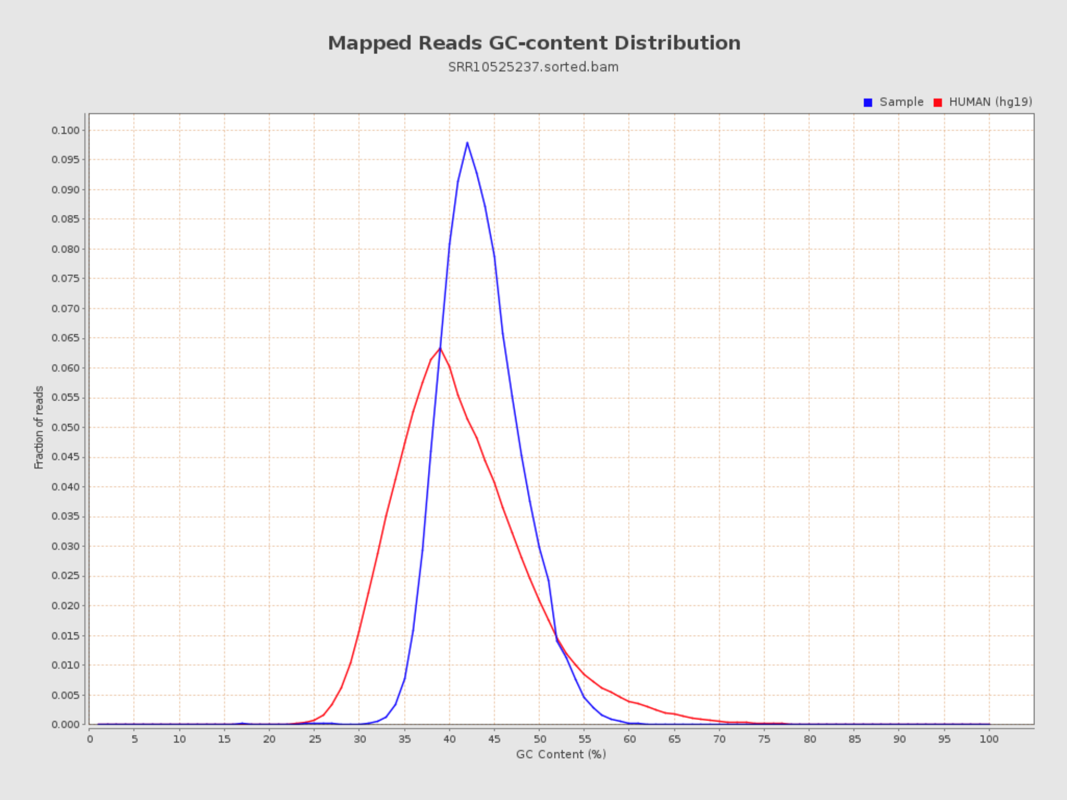
7. Results : Duplication Rate Histogram



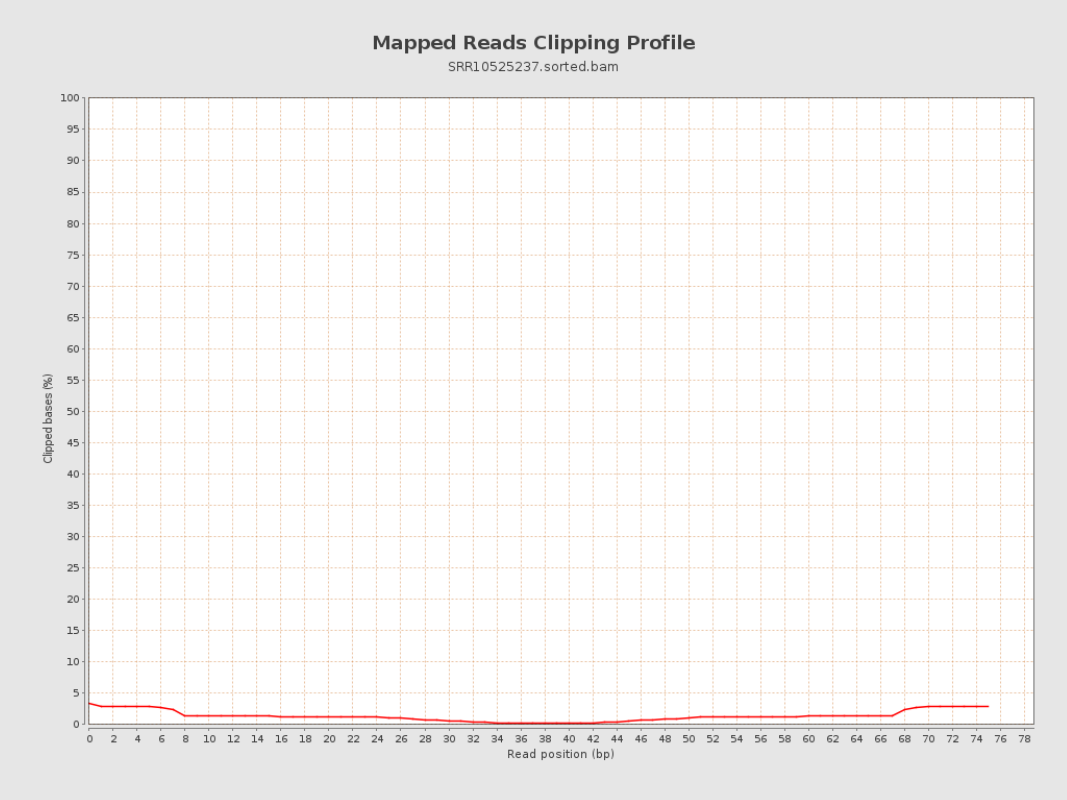
8. Results : Mapped Reads Nucleotide Content



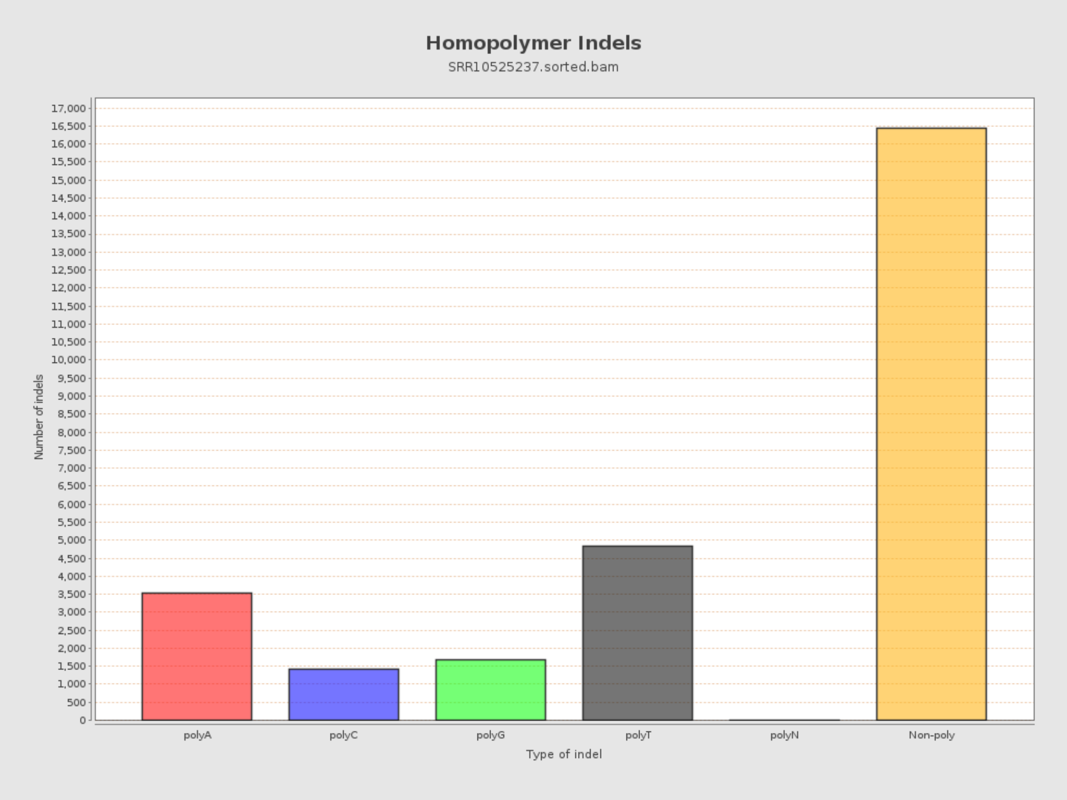
9. Results : Mapped Reads GC-content Distribution



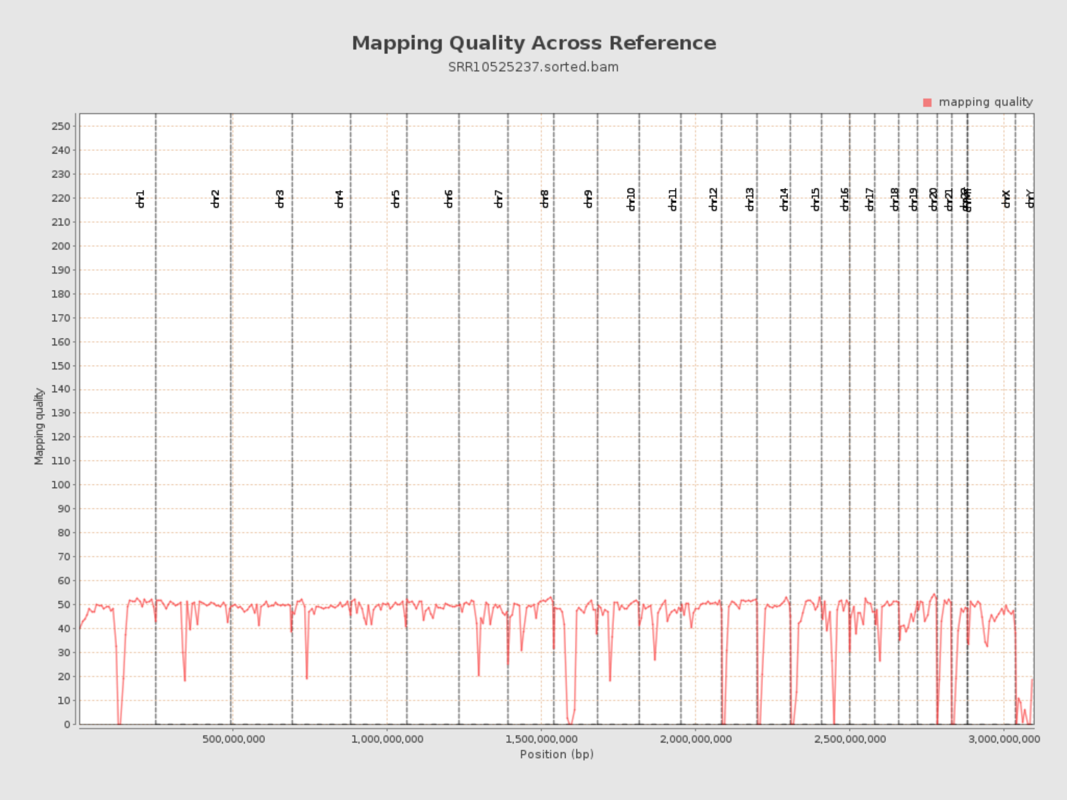
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram