Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:10:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237334.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_SRR6237334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237334.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:10:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,495,173
Mapped reads	4,095,359 / 91.11%
Unmapped reads	399,814 / 8.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	41,409 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	1,158,300 / 25.77%
Duplication rate	21.11%
Clipped reads	2,725,694 / 60.64%

2.2. ACGT Content

Number/percentage of A's	64,777,802 / 25.92%
Number/percentage of C's	42,452,769 / 16.99%
Number/percentage of T's	84,358,412 / 33.76%
Number/percentage of G's	58,284,027 / 23.32%
Number/percentage of N's	26,779 / 0.01%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0808

Standard Deviation	1.2275

2.4. Mapping Quality

Mean Mapping Quality	39.97

2.5. Mismatches and indels

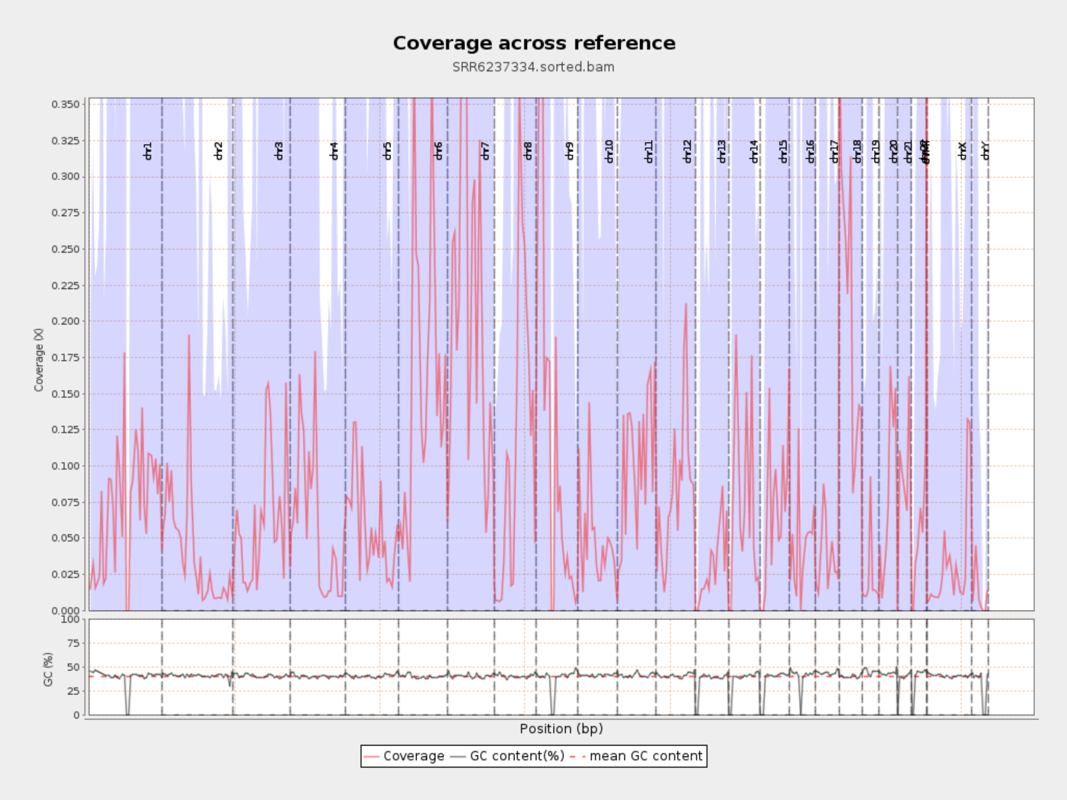
General error rate	0.67%
Mismatches	1,638,548
Insertions	16,859
Mapped reads with at least one insertion	0.41%
Deletions	86,036
Mapped reads with at least one deletion	2.07%
Homopolymer indels	41.63%

2.6. Chromosome stats

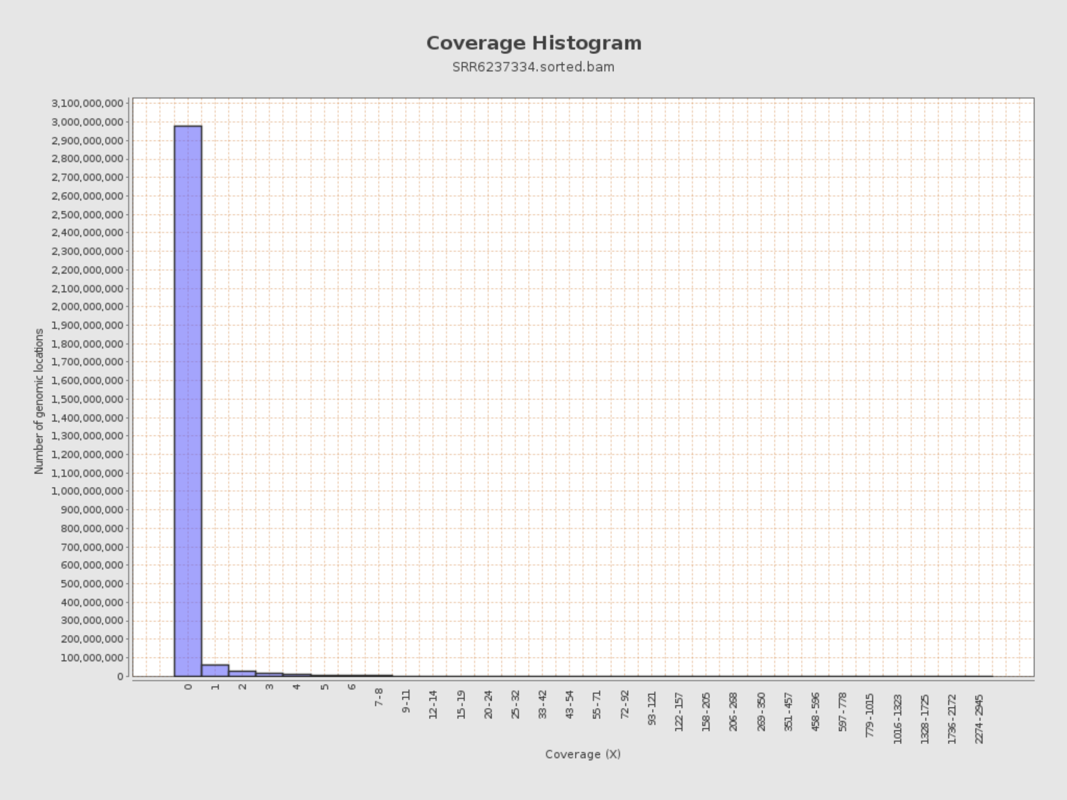
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17823777	0.0715	1.2648
chr2	243199373	9990314	0.0411	1.6654
chr3	198022430	12398232	0.0626	0.4571
chr4	191154276	11739648	0.0614	0.5221
chr5	180915260	10488106	0.058	0.4513
chr6	171115067	27111851	0.1584	1.3531
chr7	159138663	33576825	0.211	3.2061

chr8	146364022	16668706	0.1139	1.275
chr9	141213431	17414360	0.1233	1.0849
chr10	135534747	6632730	0.0489	0.8471
chr11	135006516	13822623	0.1024	0.8647
chr12	133851895	11384597	0.0851	0.5981
chr13	115169878	3642886	0.0316	0.4059
chr14	107349540	7936915	0.0739	0.5519
chr15	102531392	6959037	0.0679	0.5099
chr16	90354753	4168531	0.0461	0.5433
chr17	81195210	3060253	0.0377	0.5067
chr18	78077248	16201897	0.2075	2.5233
chr19	59128983	1353490	0.0229	1.5692
chr20	63025520	5176306	0.0821	0.5379
chr21	48129895	4305596	0.0895	0.5949
chr22	51304566	2471859	0.0482	0.3775
chrMT	16571	10700	0.6457	1.5126
chrX	155270560	5034133	0.0324	0.4668
chrY	59373566	675628	0.0114	0.3758

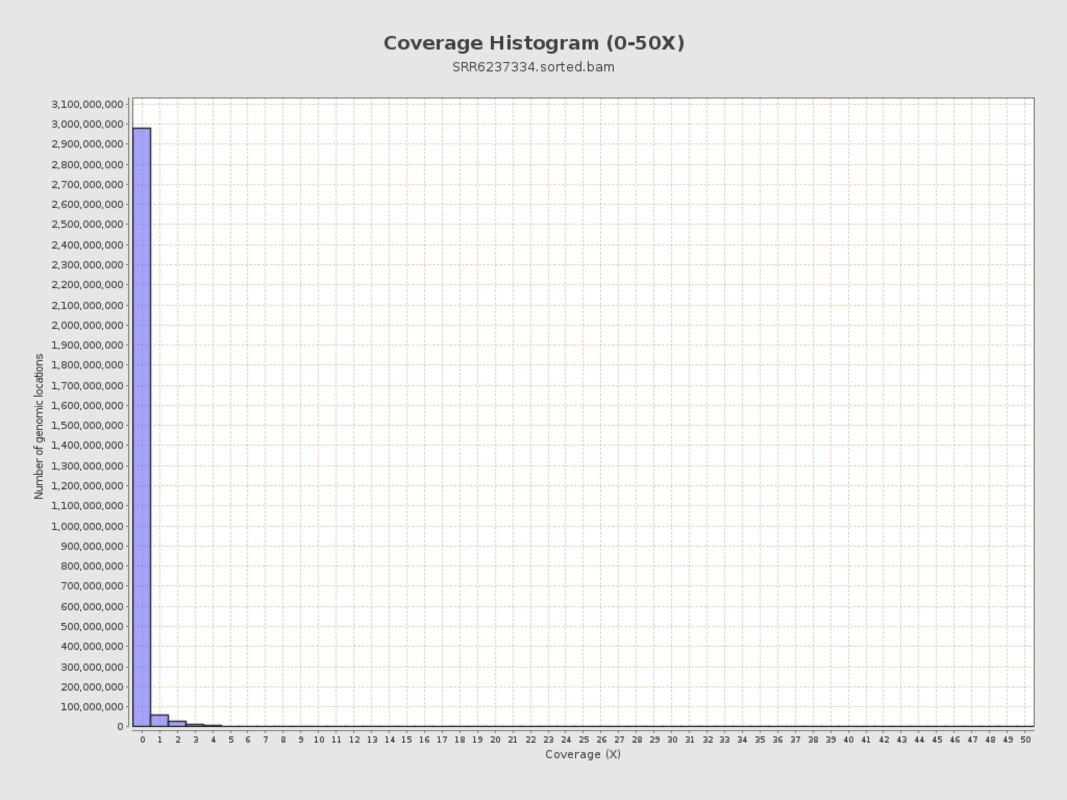
3. Results : Coverage across reference



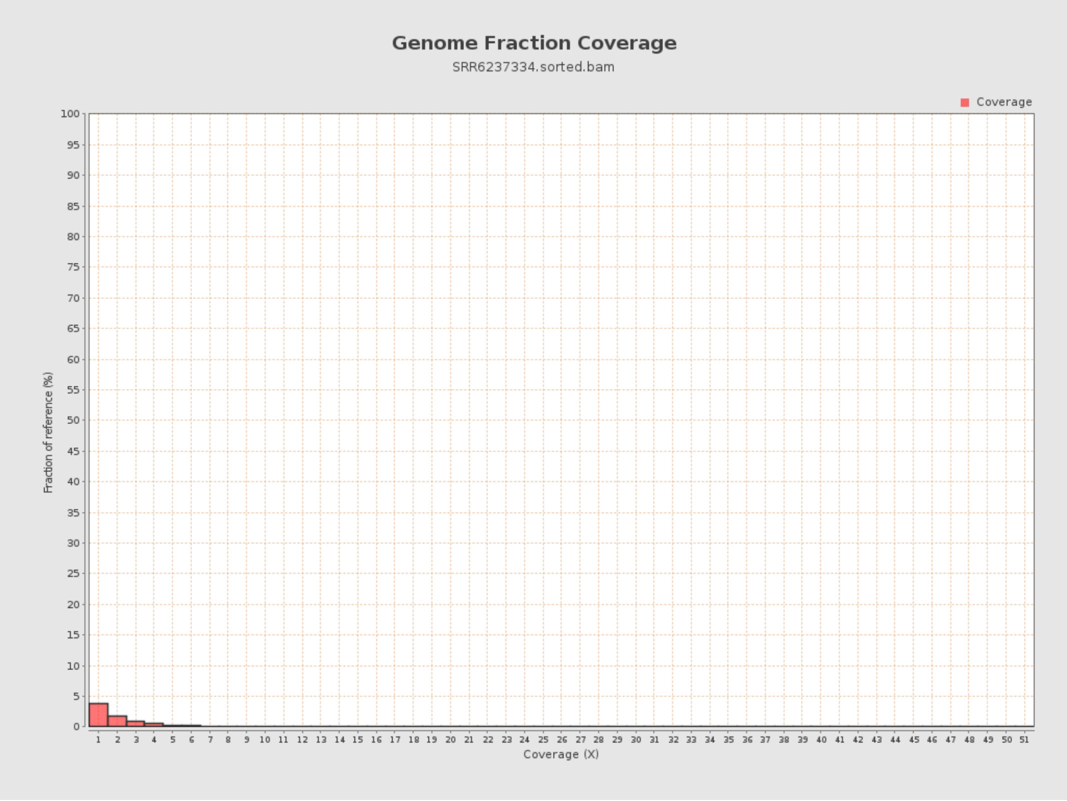
4. Results : Coverage Histogram



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



6. Results : Genome Fraction Coverage



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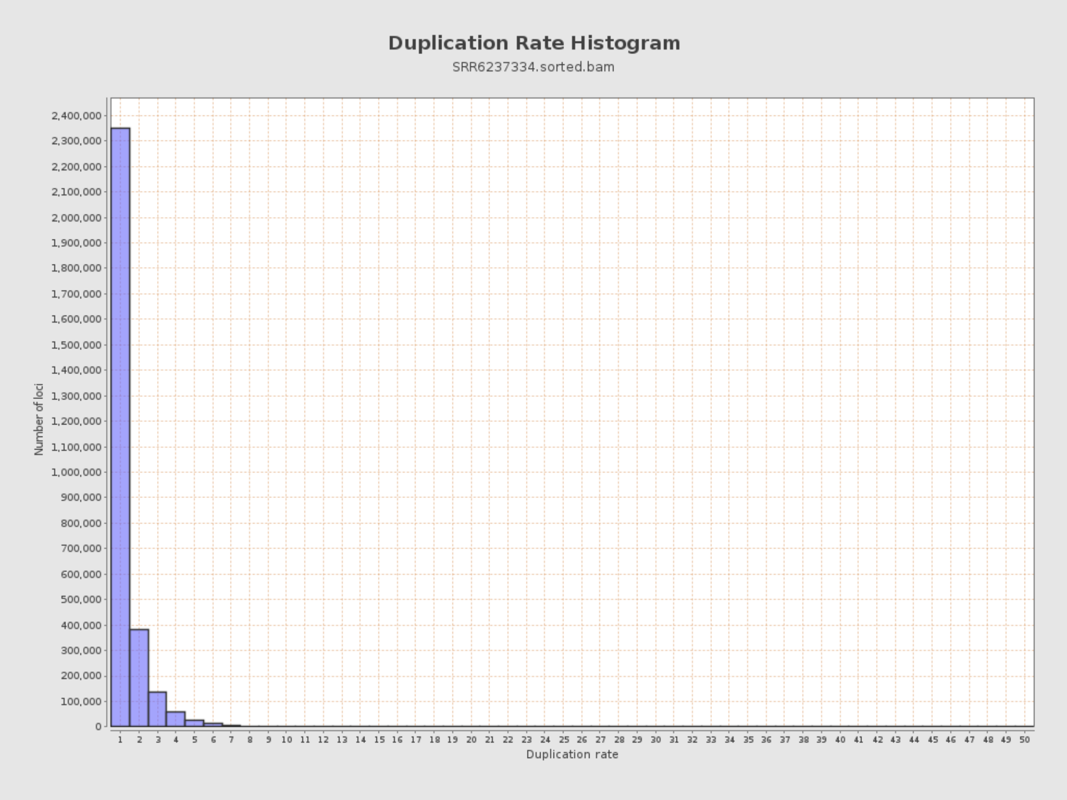
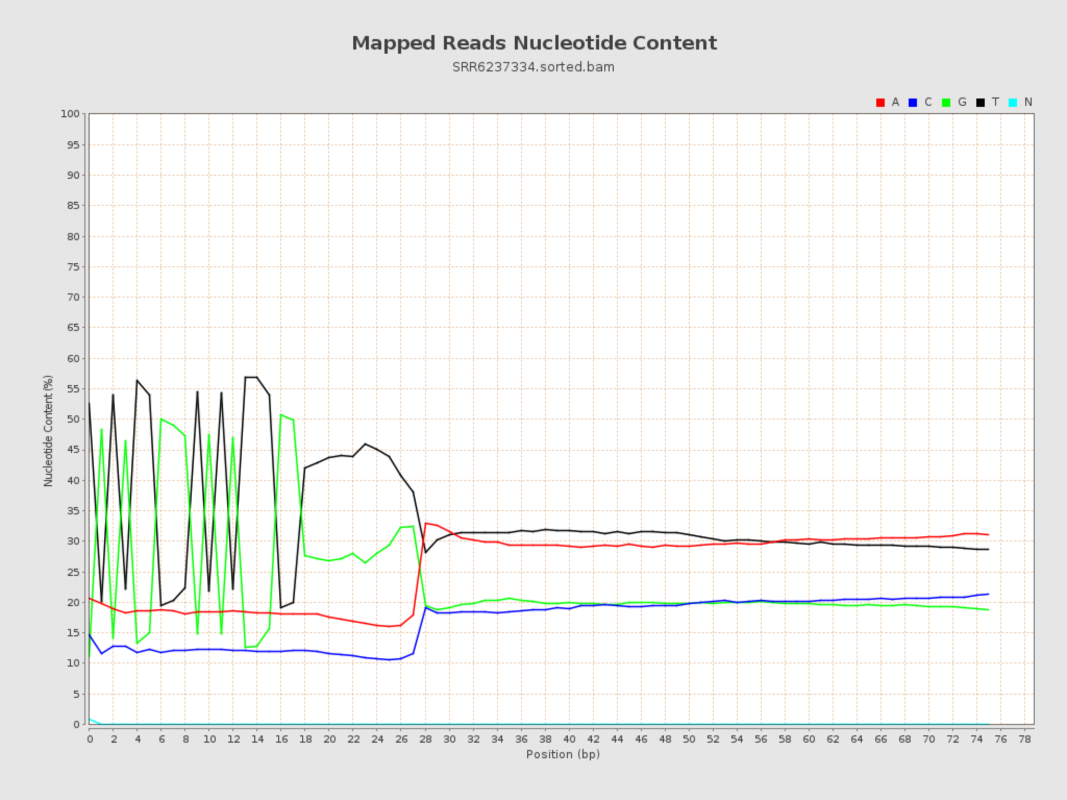
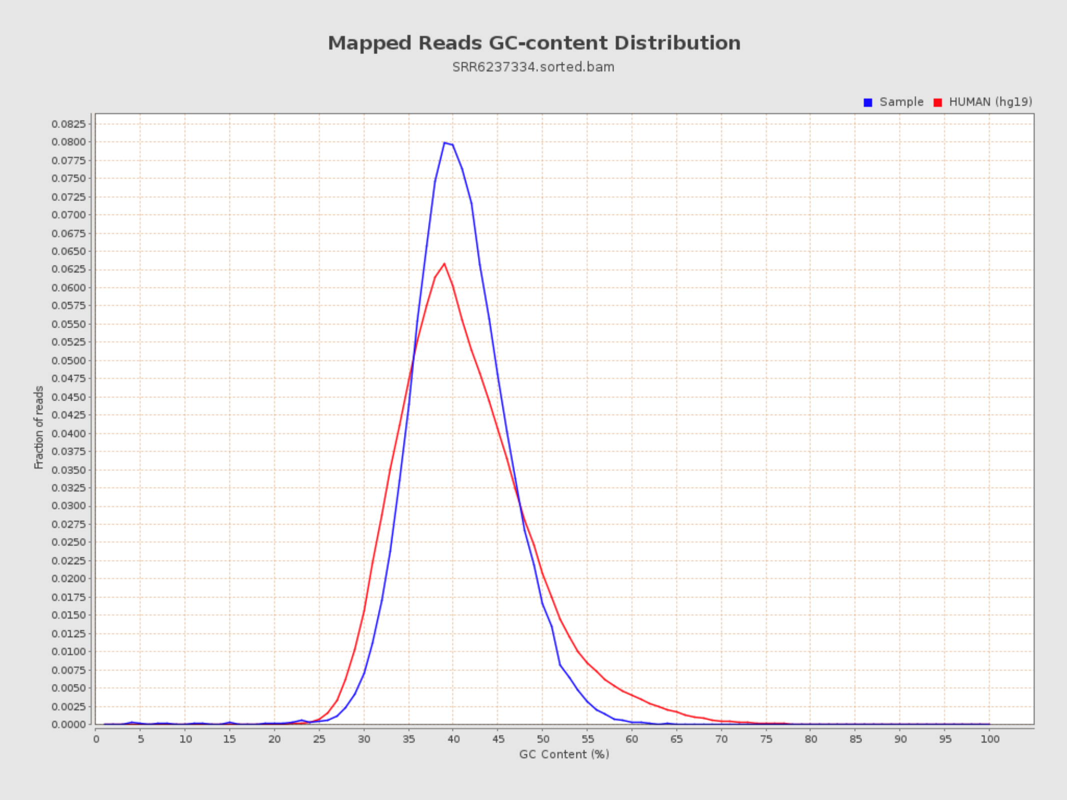
7. Results : Duplication Rate Histogram



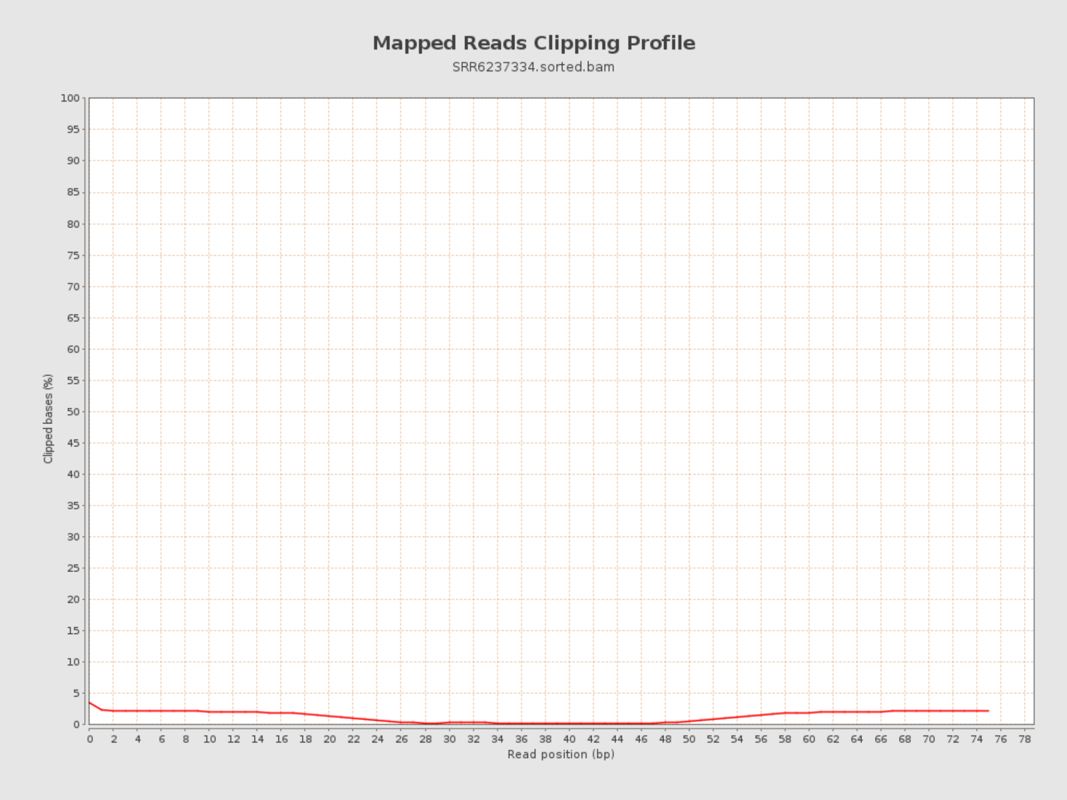
8. Results : Mapped Reads Nucleotide Content



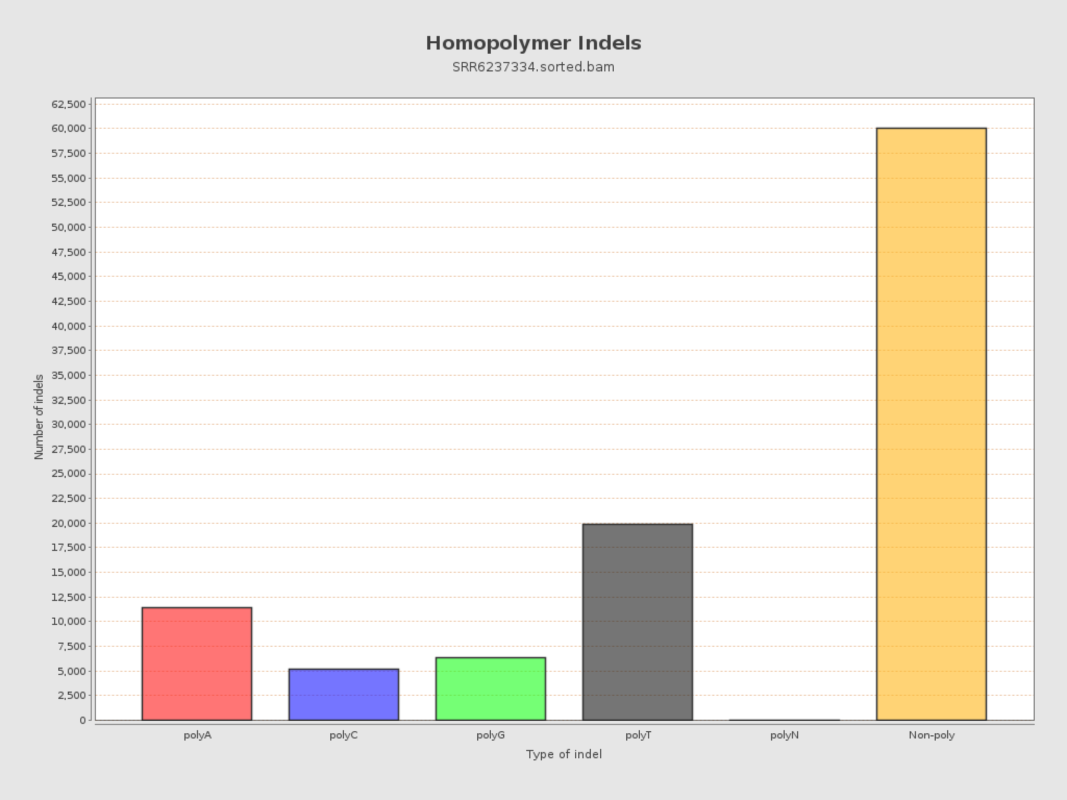
9. Results : Mapped Reads GC-content Distribution



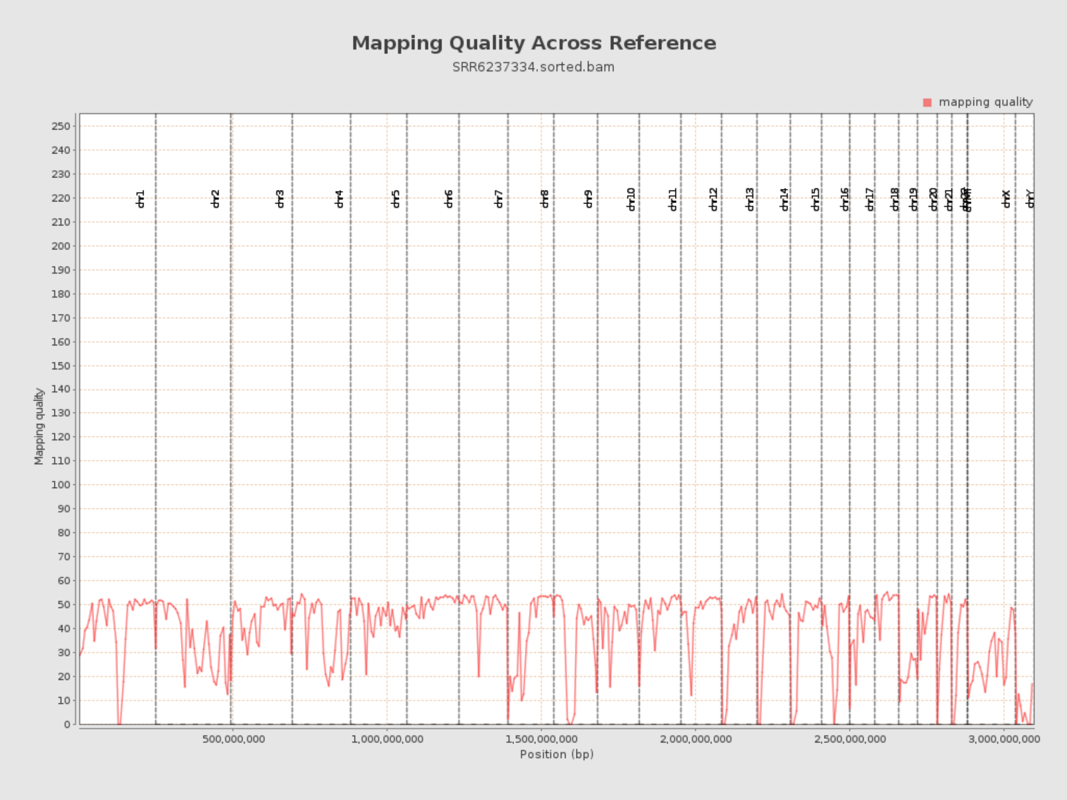
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram