Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:42:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237865.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_SRR6237865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237865.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:42:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,280,106
Mapped reads	2,046,086 / 89.74%
Unmapped reads	234,020 / 10.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,533 / 0.59%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	80,471 / 3.53%
Duplication rate	2.8%
Clipped reads	1,076,525 / 47.21%

2.2. ACGT Content

Number/percentage of A's	35,907,845 / 27.22%
Number/percentage of C's	23,957,868 / 18.16%
Number/percentage of T's	41,368,156 / 31.36%
Number/percentage of G's	30,559,446 / 23.17%
Number/percentage of N's	102,816 / 0.08%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0426

Standard Deviation	0.4348

2.4. Mapping Quality

Mean Mapping Quality	43.28

2.5. Mismatches and indels

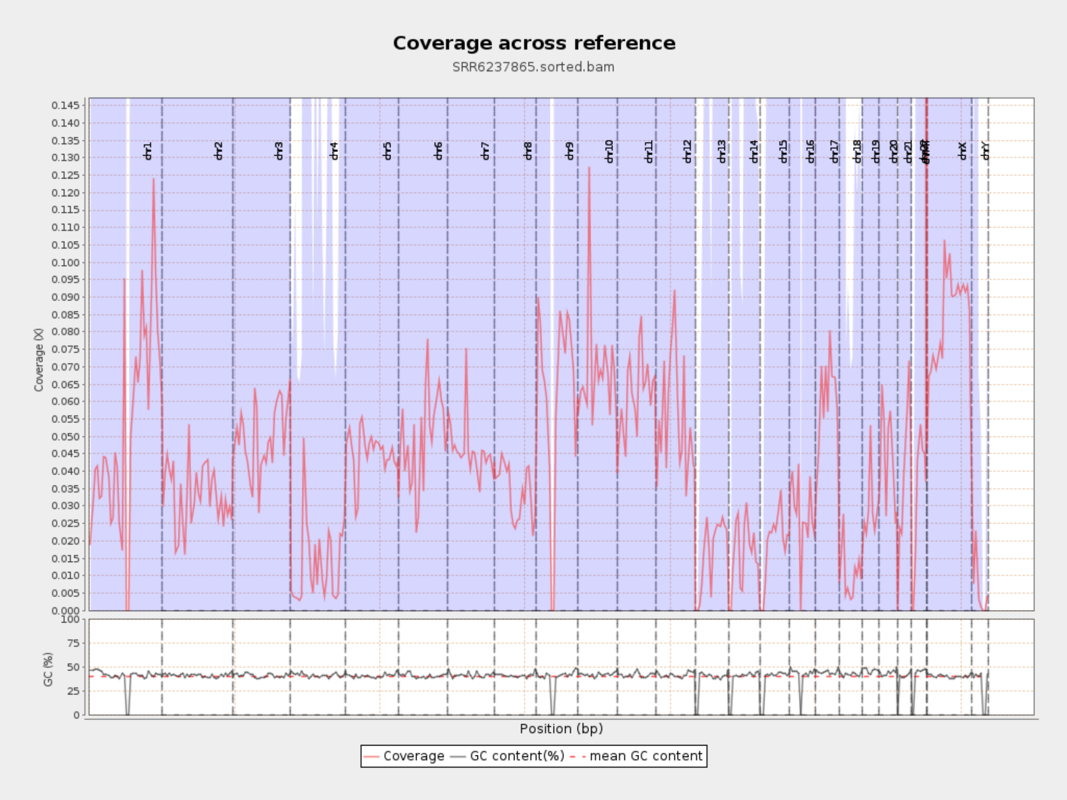
General error rate	0.74%
Mismatches	952,509
Insertions	10,923
Mapped reads with at least one insertion	0.53%
Deletions	32,142
Mapped reads with at least one deletion	1.55%
Homopolymer indels	47.78%

2.6. Chromosome stats

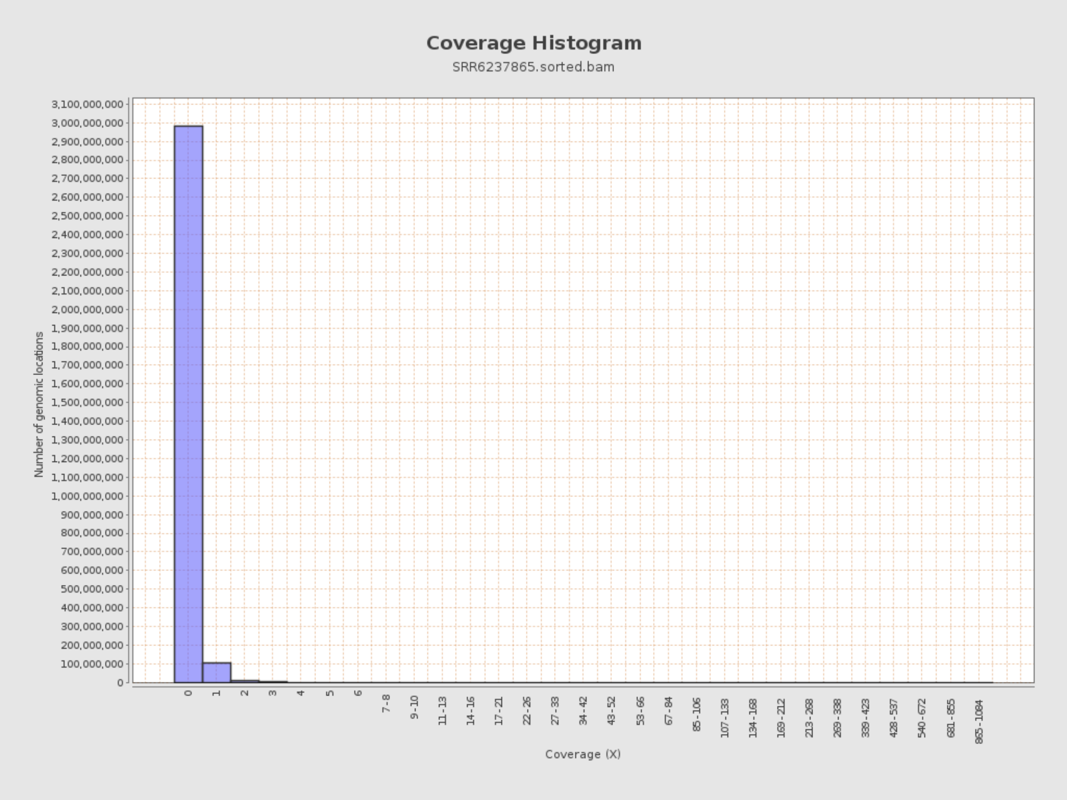
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13244574	0.0531	0.9429
chr2	243199373	8093826	0.0333	0.3341
chr3	198022430	9795053	0.0495	0.2579
chr4	191154276	2504251	0.0131	0.2128
chr5	180915260	8178109	0.0452	0.2373
chr6	171115067	8475256	0.0495	0.2997
chr7	159138663	7352376	0.0462	0.5039

chr8	146364022	4967803	0.0339	0.2621
chr9	141213431	8916394	0.0631	0.4573
chr10	135534747	9328760	0.0688	0.6372
chr11	135006516	8394943	0.0622	0.4214
chr12	133851895	7446454	0.0556	0.2723
chr13	115169878	1894161	0.0164	0.1398
chr14	107349540	1706130	0.0159	0.1988
chr15	102531392	1957598	0.0191	0.1511
chr16	90354753	2484299	0.0275	0.2591
chr17	81195210	4838926	0.0596	0.4539
chr18	78077248	844300	0.0108	0.6413
chr19	59128983	1738483	0.0294	0.6072
chr20	63025520	2781018	0.0441	0.245
chr21	48129895	1872167	0.0389	0.2915
chr22	51304566	1646109	0.0321	0.1968
chrMT	16571	68743	4.1484	3.1406
chrX	155270560	12993892	0.0837	0.3603
chrY	59373566	426738	0.0072	0.222

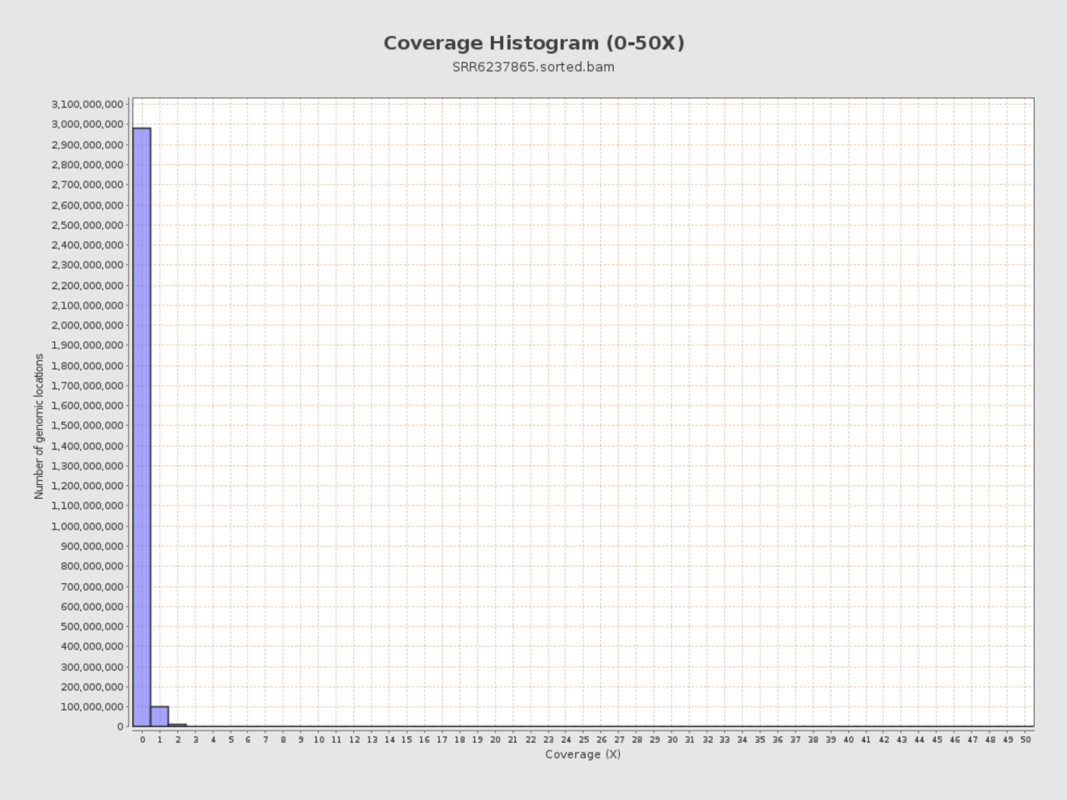
3. Results : Coverage across reference



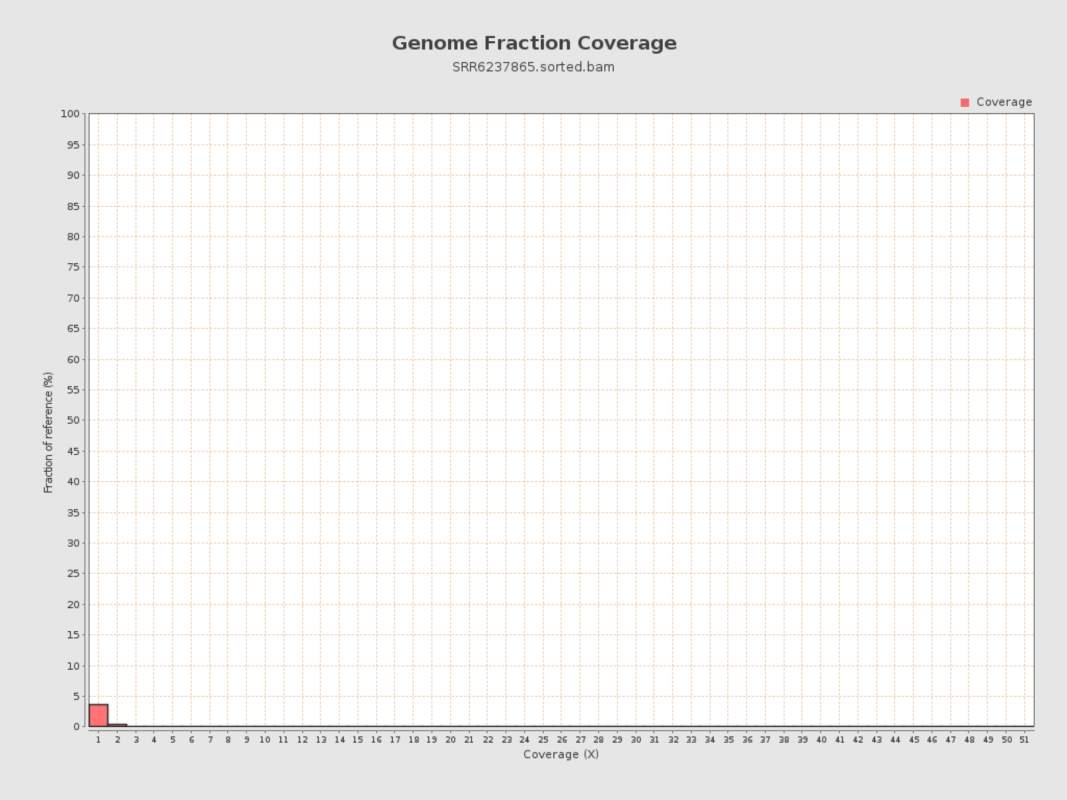
4. Results : Coverage Histogram



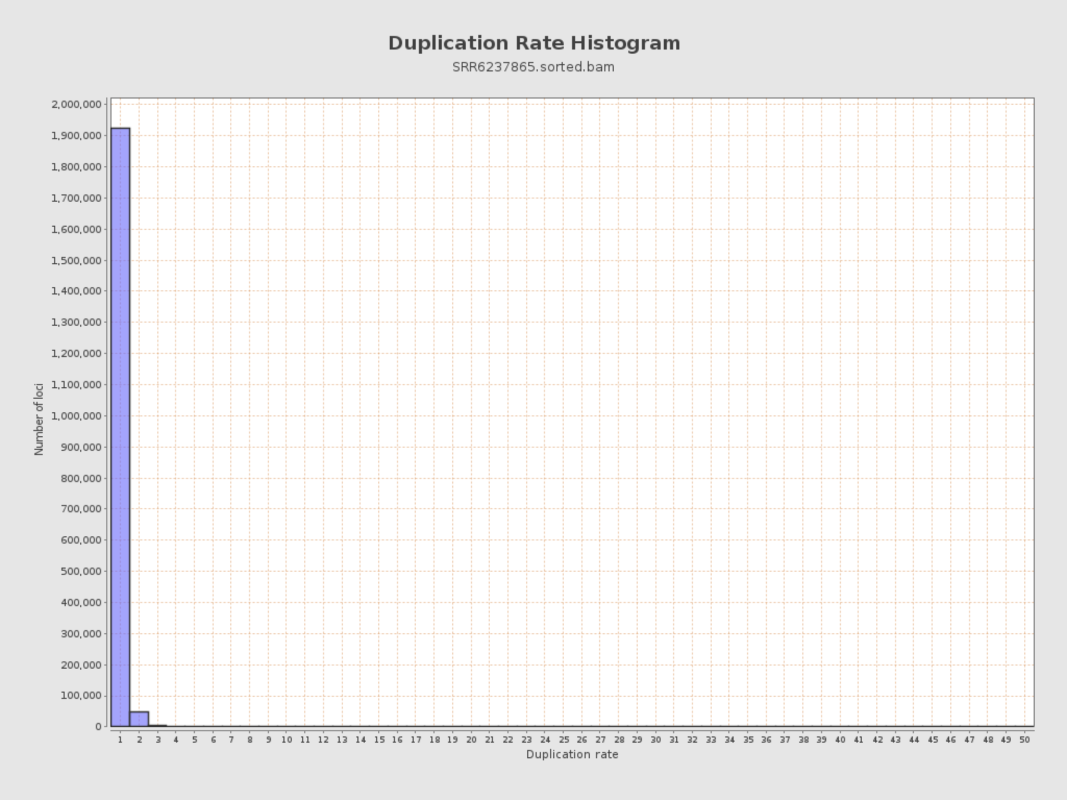
5. Results : Coverage Histogram (0-50X)



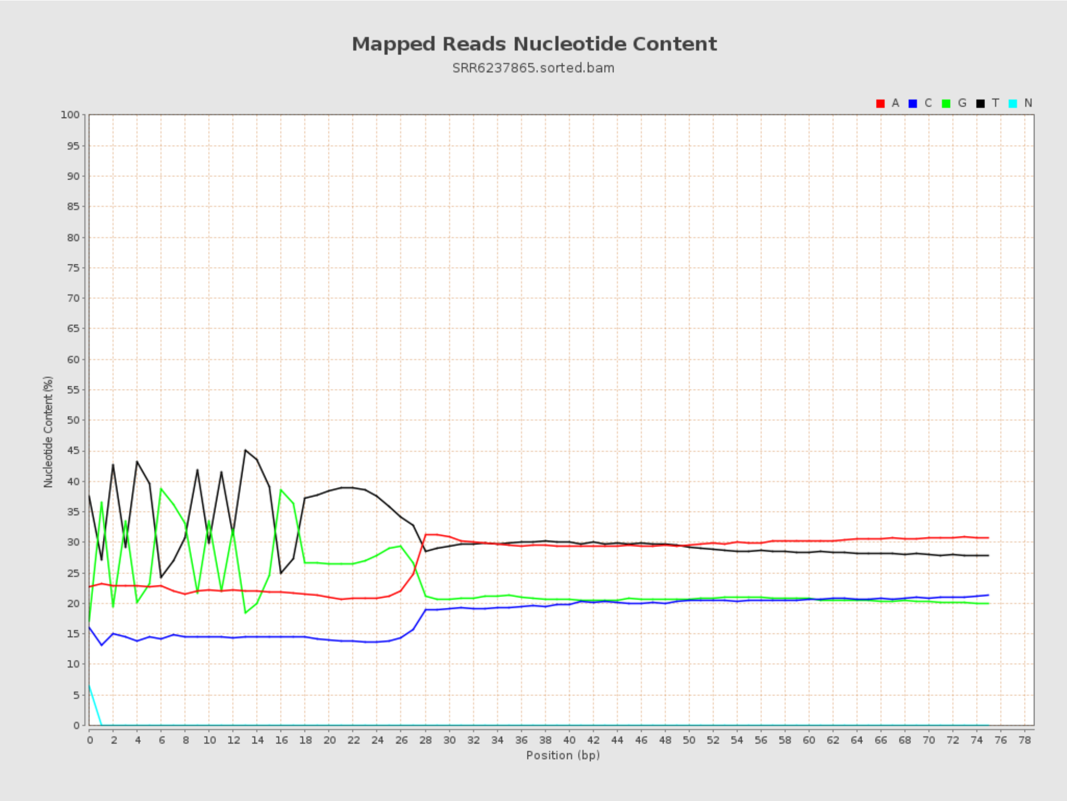
6. Results : Genome Fraction Coverage



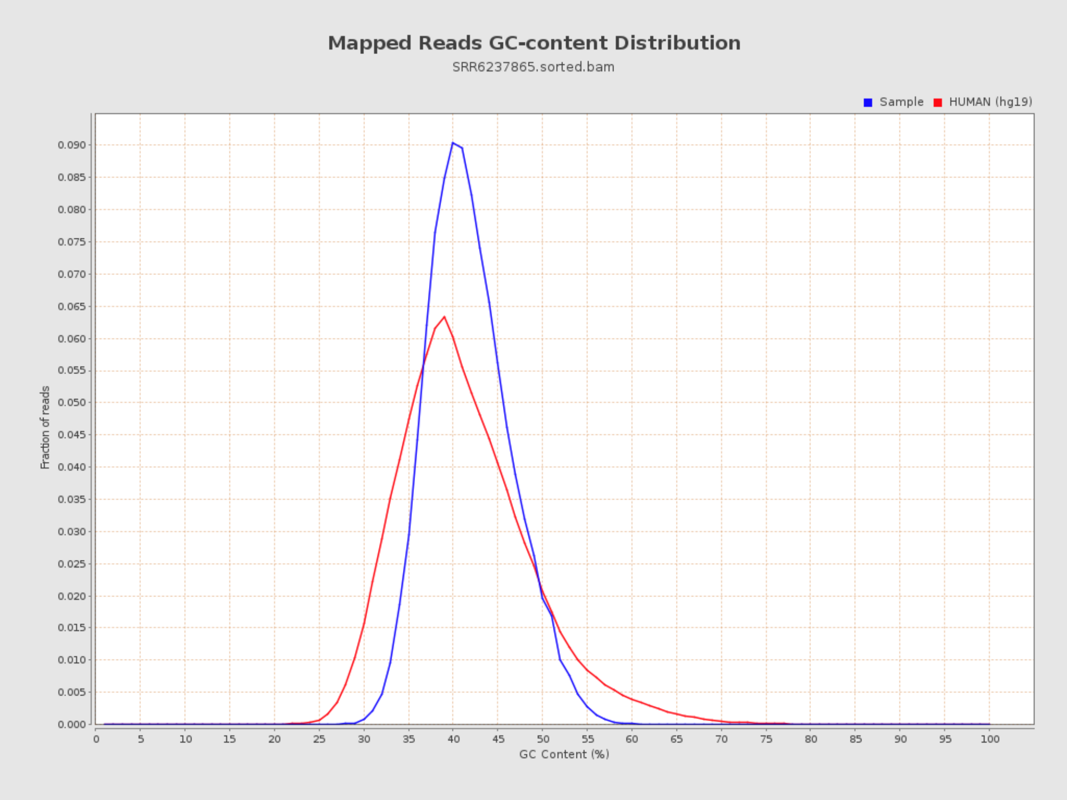
7. Results : Duplication Rate Histogram



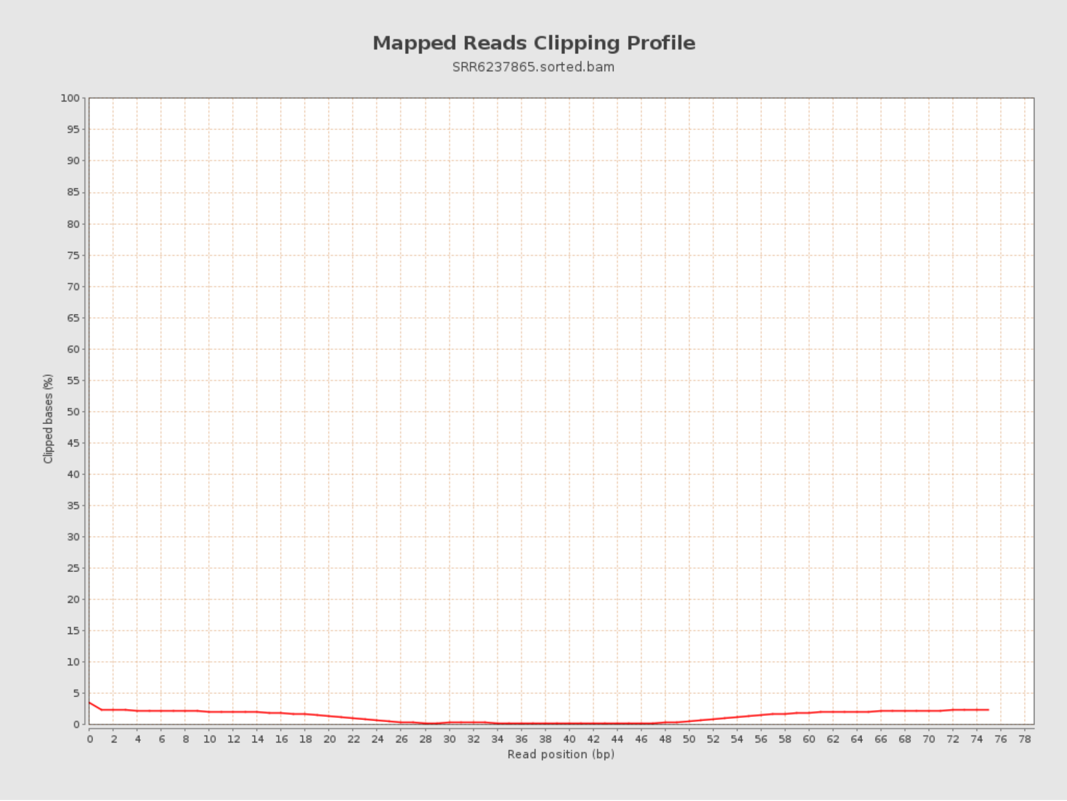
8. Results : Mapped Reads Nucleotide Content



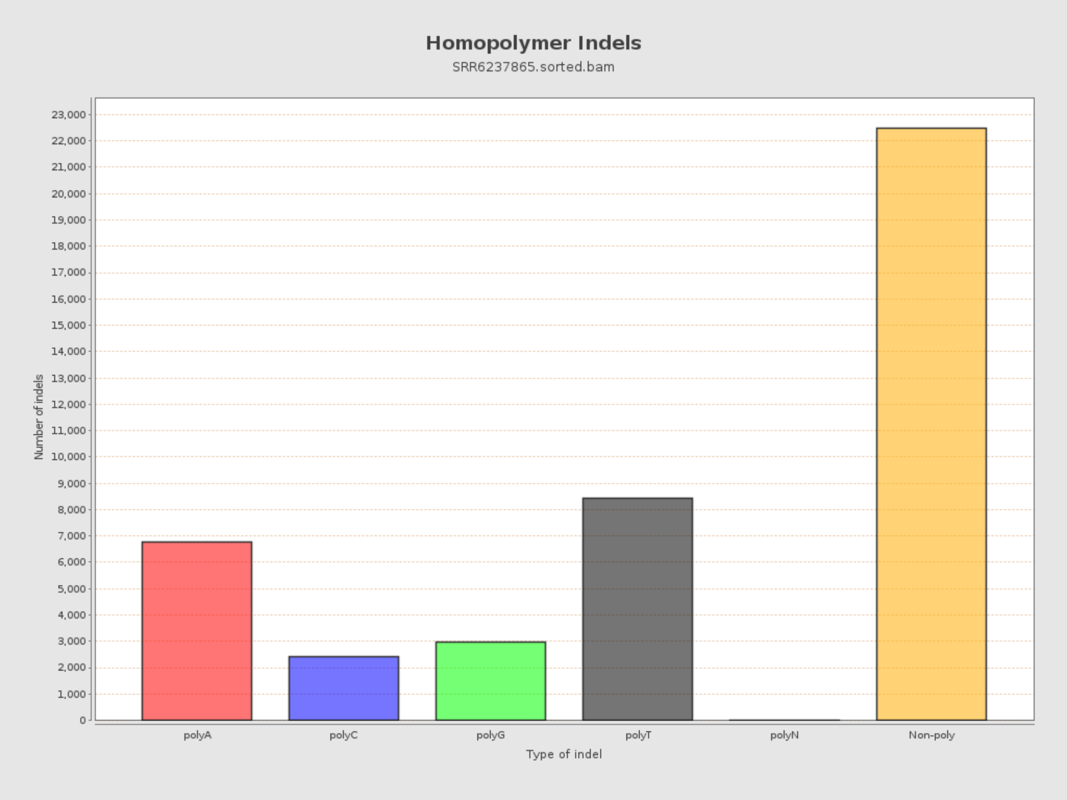
9. Results : Mapped Reads GC-content Distribution



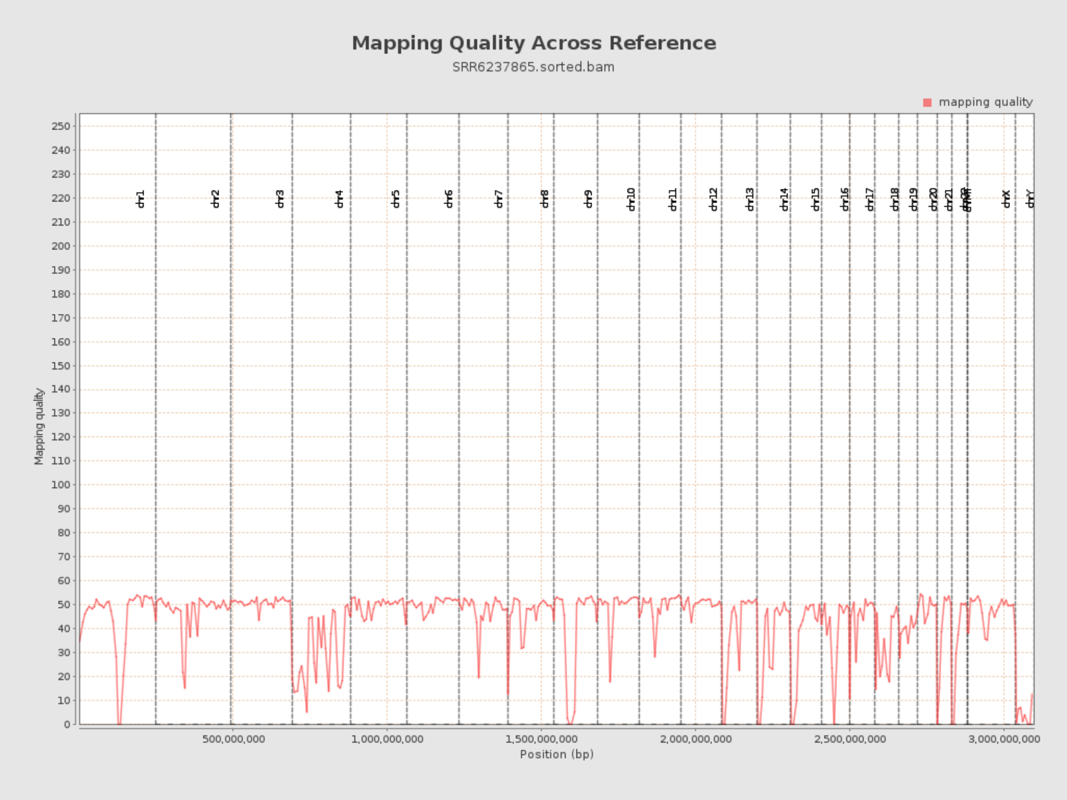
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram