Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:32:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237568.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_SRR6237568 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237568.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:32:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237568.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,452,206
Mapped reads	1,117,869 / 76.98%
Unmapped reads	334,337 / 23.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,951 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	91,289 / 6.29%
Duplication rate	6.89%
Clipped reads	697,131 / 48%

2.2. ACGT Content

Number/percentage of A's	18,638,693 / 26.82%
Number/percentage of C's	11,810,942 / 16.99%
Number/percentage of T's	22,981,814 / 33.07%
Number/percentage of G's	15,937,653 / 22.93%
Number/percentage of N's	135,262 / 0.19%
GC Percentage	39.92%

2.3. Coverage

Mean	0.0225

Standard Deviation	0.2347

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

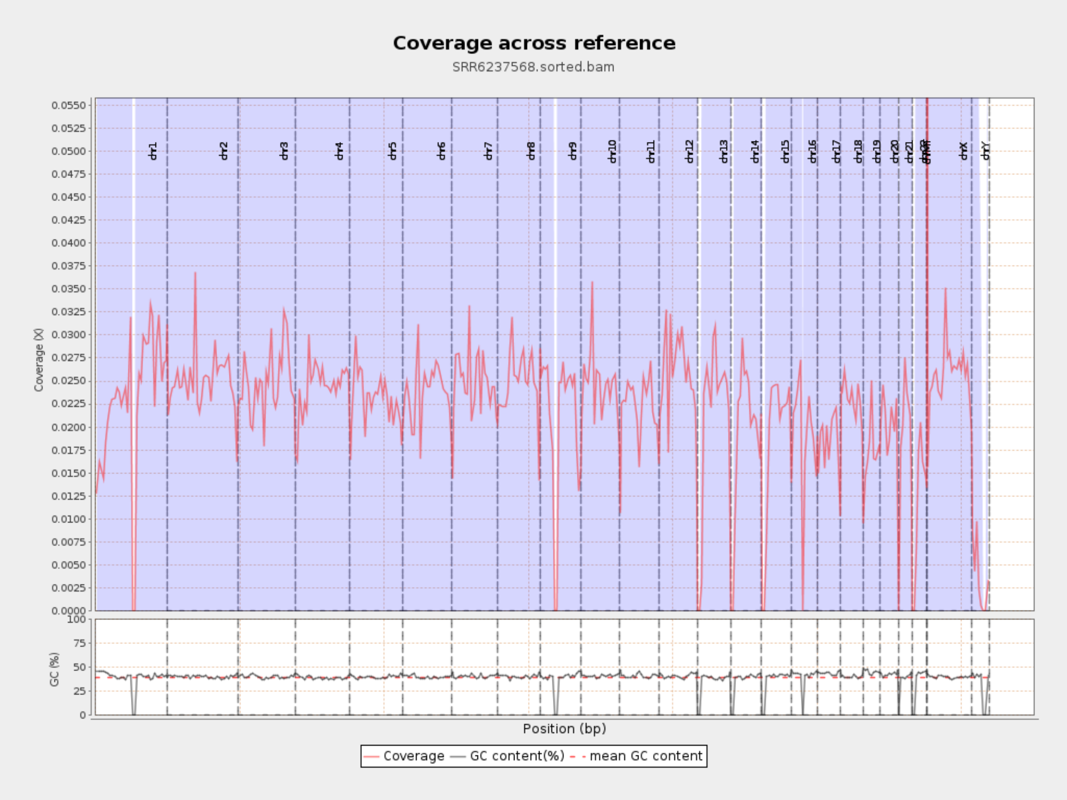
General error rate	1.04%
Mismatches	709,392
Insertions	5,826
Mapped reads with at least one insertion	0.52%
Deletions	27,764
Mapped reads with at least one deletion	2.45%
Homopolymer indels	49.41%

2.6. Chromosome stats

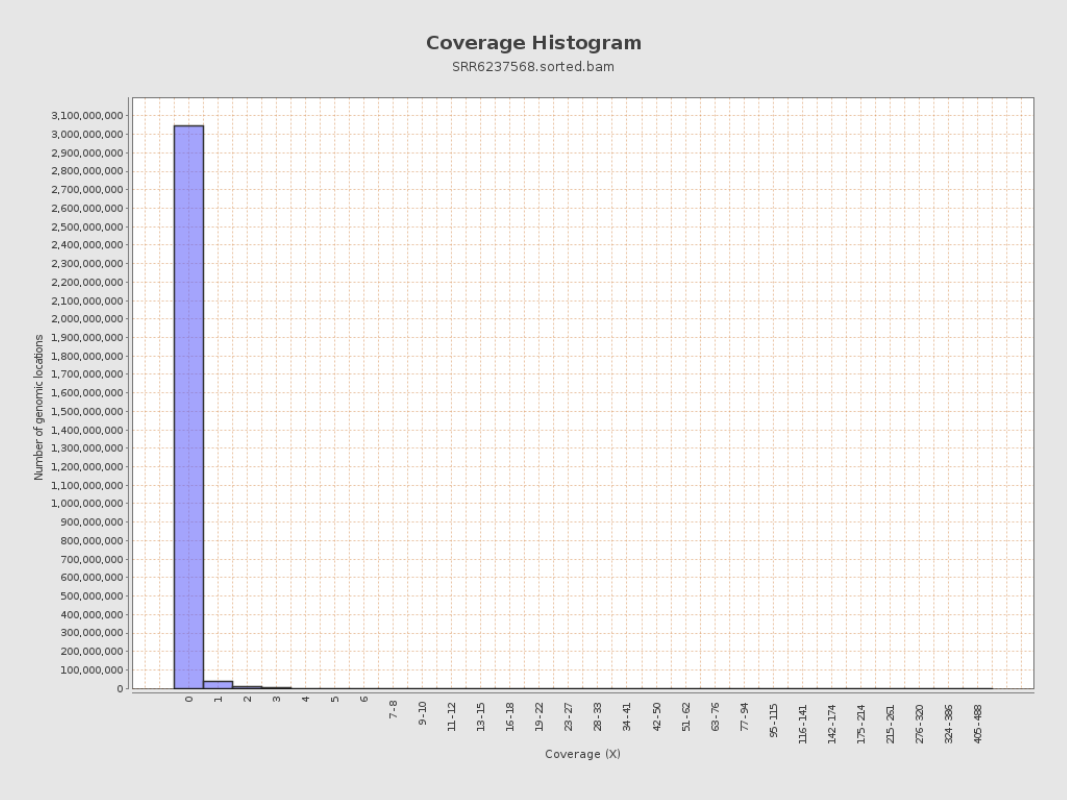
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5668850	0.0227	0.3045
chr2	243199373	6098239	0.0251	0.2599
chr3	198022430	4927566	0.0249	0.206
chr4	191154276	4654765	0.0244	0.2058
chr5	180915260	4220299	0.0233	0.1962
chr6	171115067	4082891	0.0239	0.2146
chr7	159138663	3951581	0.0248	0.2821

chr8	146364022	3656311	0.025	0.3536
chr9	141213431	2956940	0.0209	0.2268
chr10	135534747	3346005	0.0247	0.2338
chr11	135006516	3021718	0.0224	0.2276
chr12	133851895	3500783	0.0262	0.2119
chr13	115169878	2399848	0.0208	0.1901
chr14	107349540	2037489	0.019	0.1835
chr15	102531392	1904016	0.0186	0.1746
chr16	90354753	1693324	0.0187	0.1843
chr17	81195210	1492873	0.0184	0.1788
chr18	78077248	1807072	0.0231	0.3318
chr19	59128983	1030112	0.0174	0.2175
chr20	63025520	1290919	0.0205	0.191
chr21	48129895	932644	0.0194	0.1882
chr22	51304566	608854	0.0119	0.1388
chrMT	16571	50817	3.0666	2.9226
chrX	155270560	4014227	0.0259	0.2167
chrY	59373566	200075	0.0034	0.0801

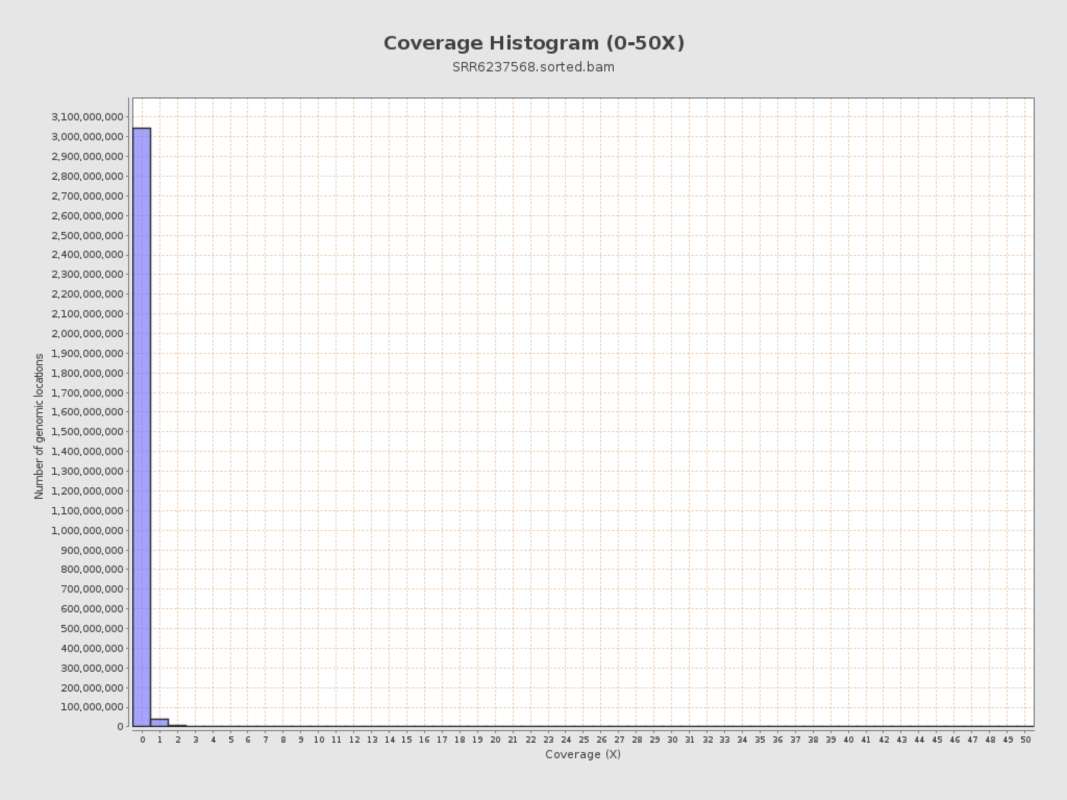
3. Results : Coverage across reference



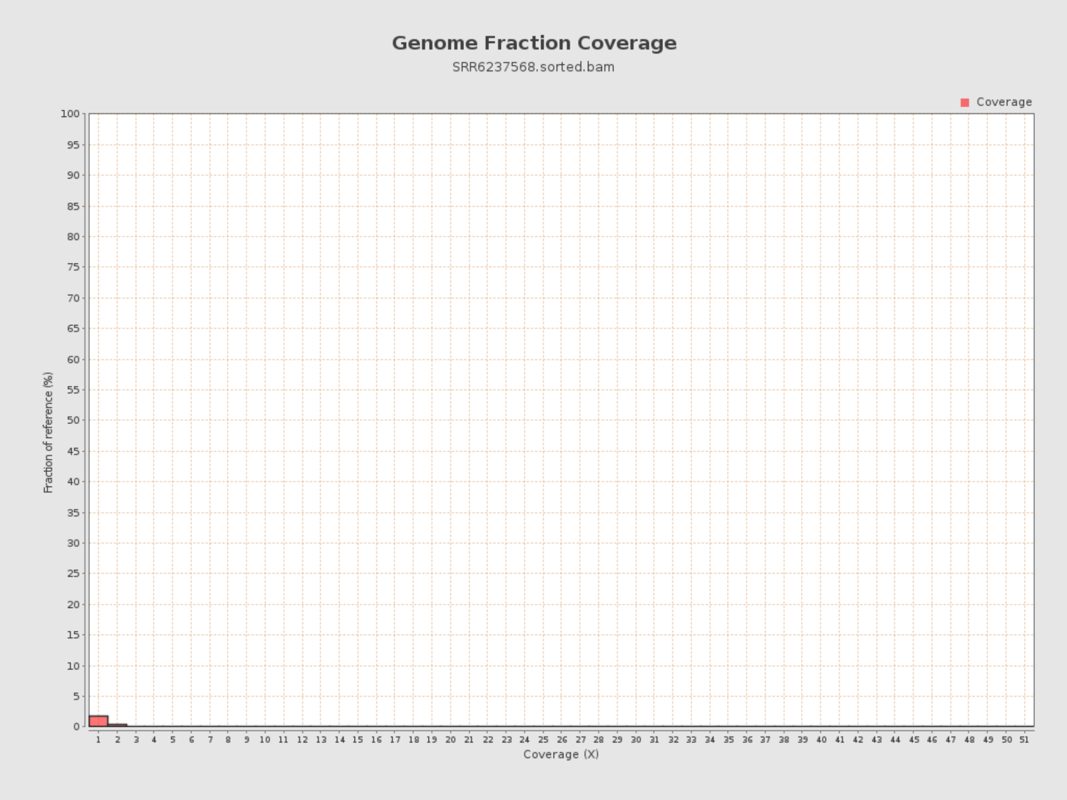
4. Results : Coverage Histogram



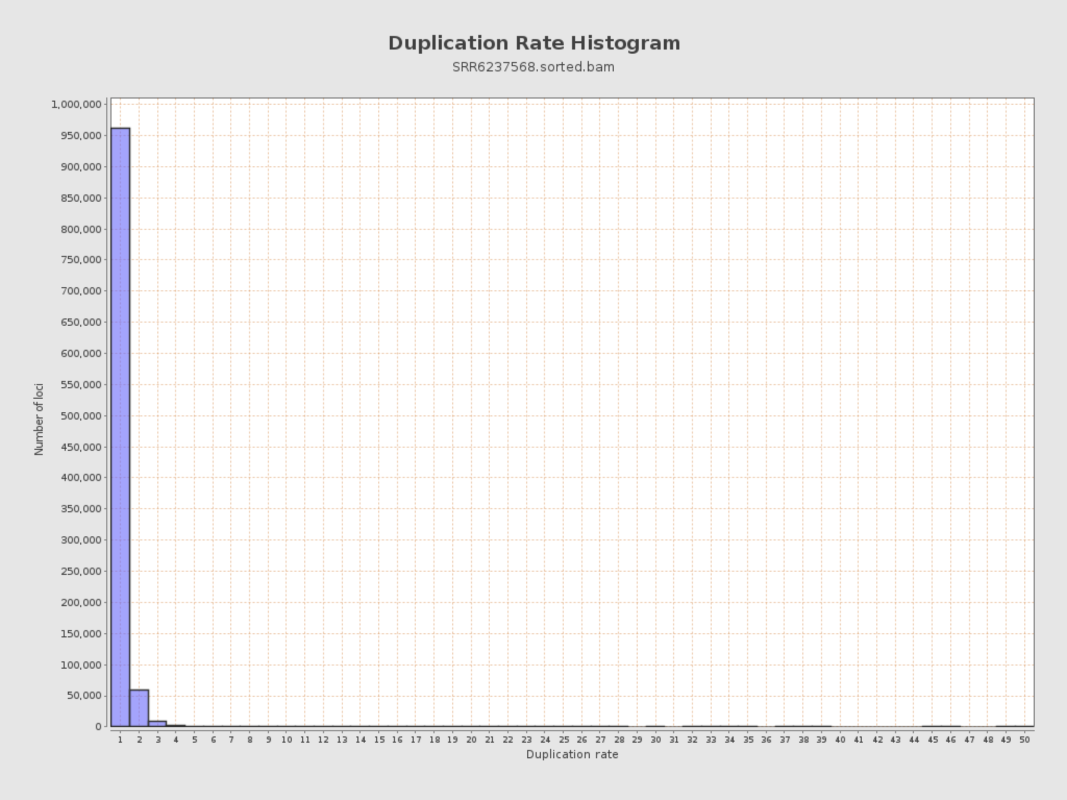
5. Results : Coverage Histogram (0-50X)



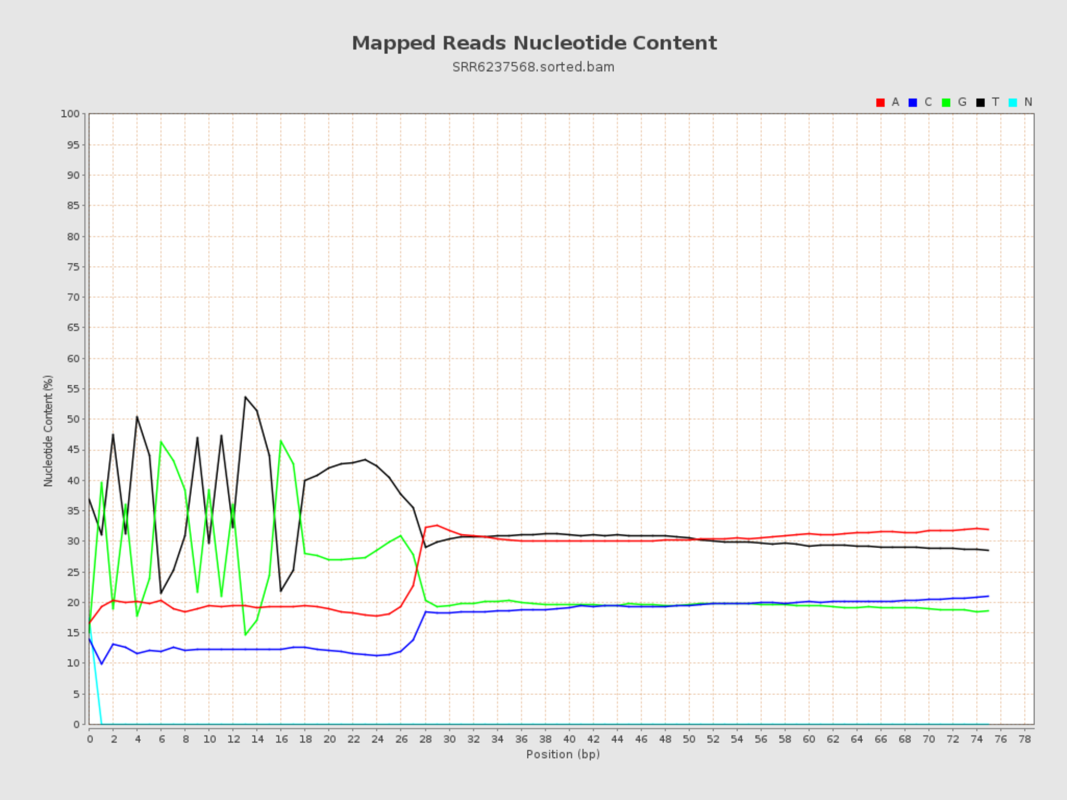
6. Results : Genome Fraction Coverage



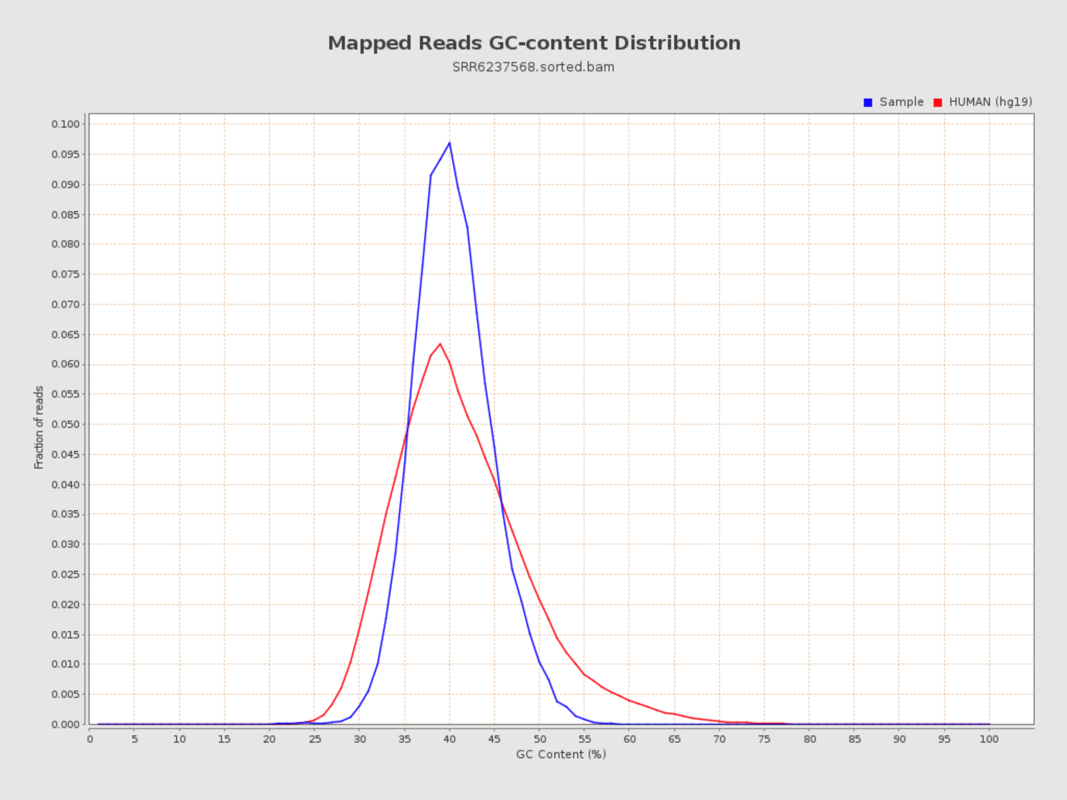
7. Results : Duplication Rate Histogram



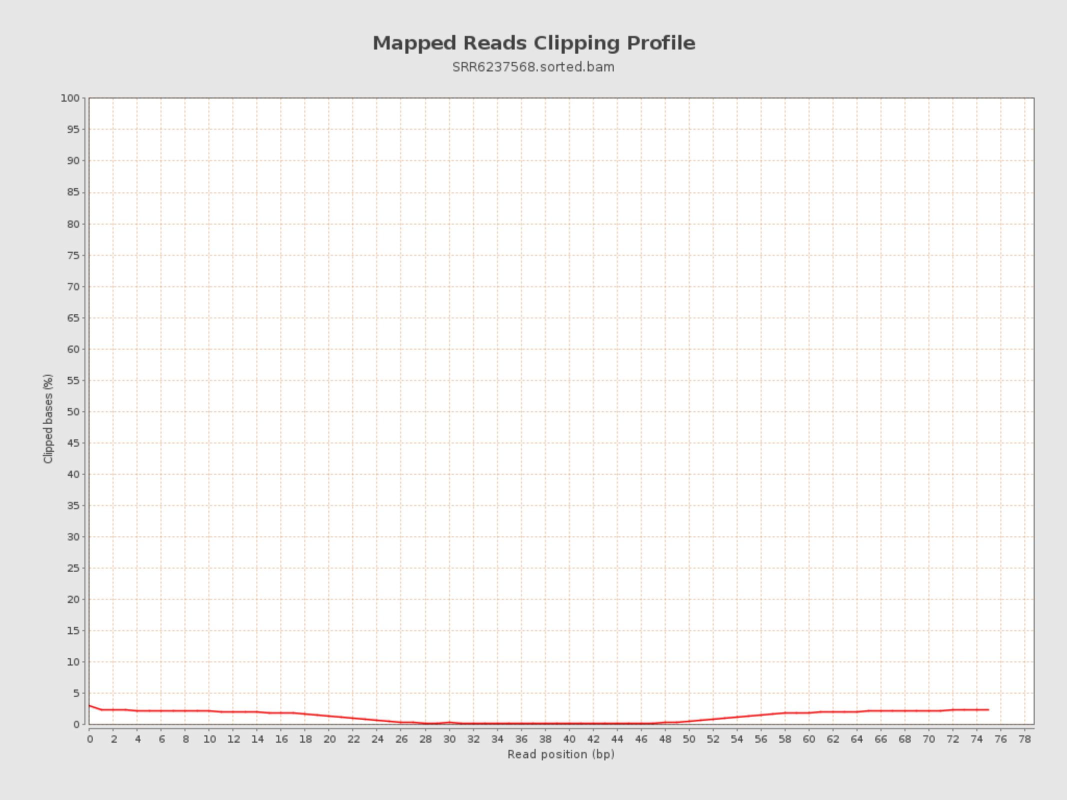
8. Results : Mapped Reads Nucleotide Content



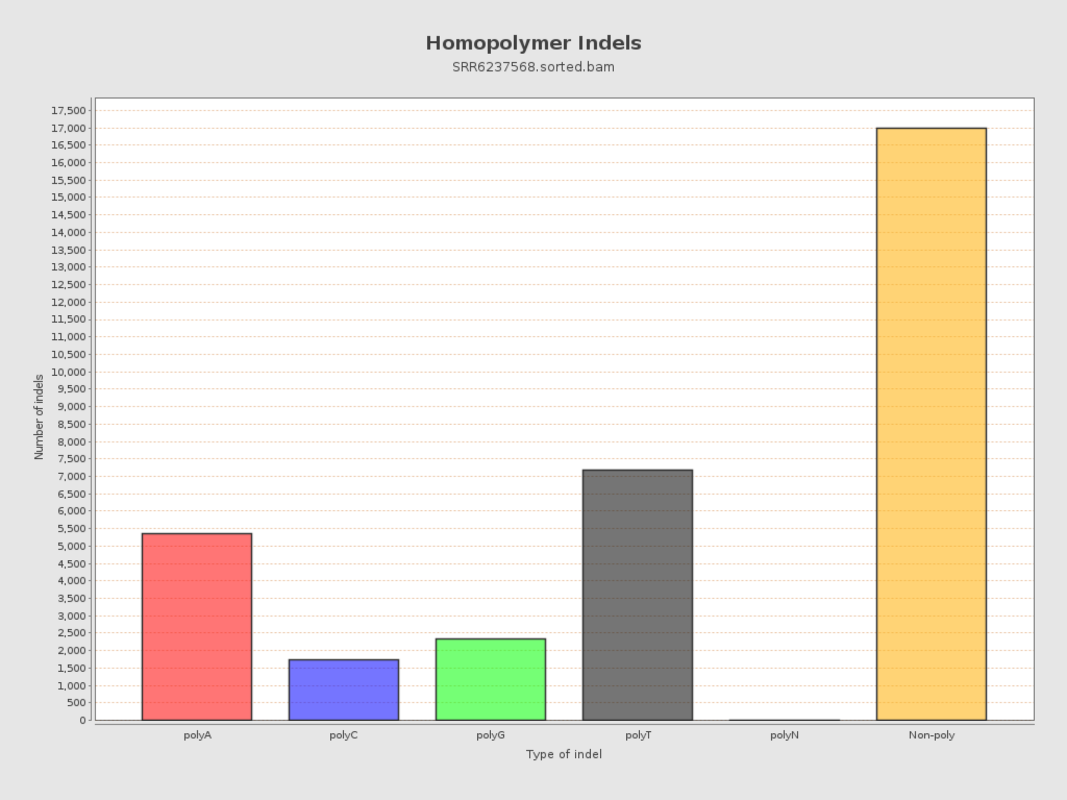
9. Results : Mapped Reads GC-content Distribution



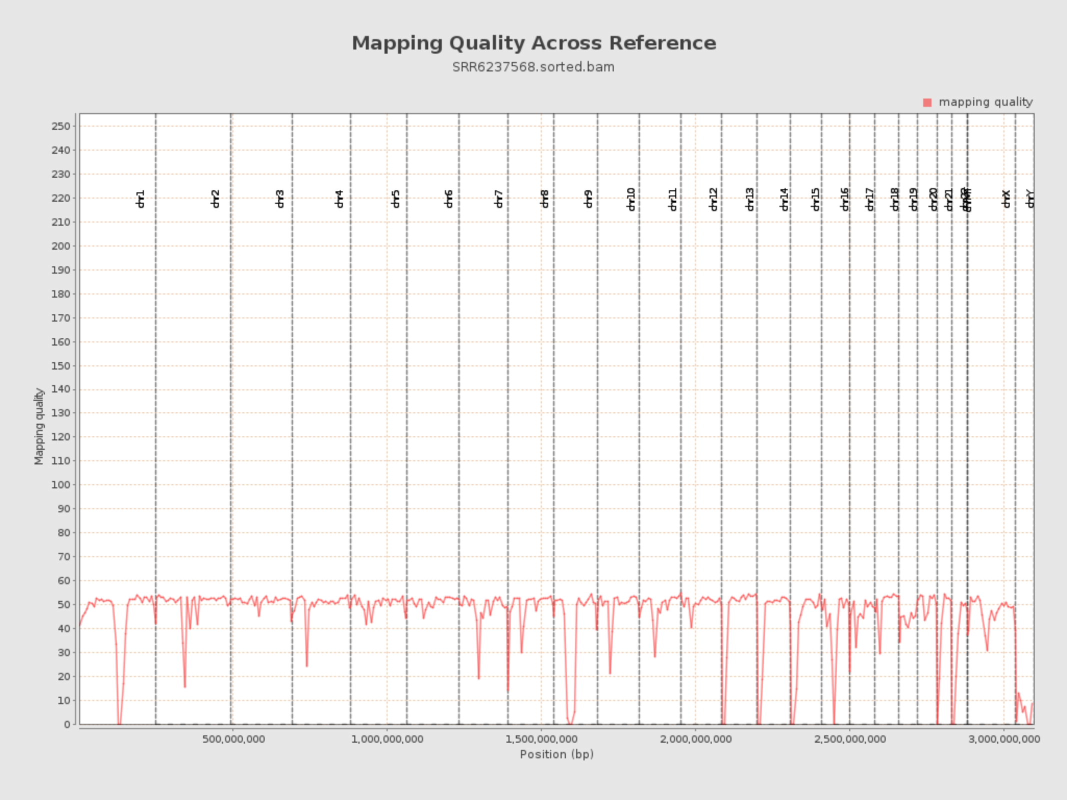
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram