Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:01:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237852.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_SRR6237852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237852.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:01:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,659,744
Mapped reads	1,252,025 / 75.43%
Unmapped reads	407,719 / 24.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,675 / 0.28%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	102,114 / 6.15%
Duplication rate	5.93%
Clipped reads	819,647 / 49.38%

2.2. ACGT Content

Number/percentage of A's	20,106,795 / 26.07%
Number/percentage of C's	13,289,269 / 17.23%
Number/percentage of T's	24,902,644 / 32.29%
Number/percentage of G's	18,770,614 / 24.34%
Number/percentage of N's	64,028 / 0.08%
GC Percentage	41.56%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2672

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

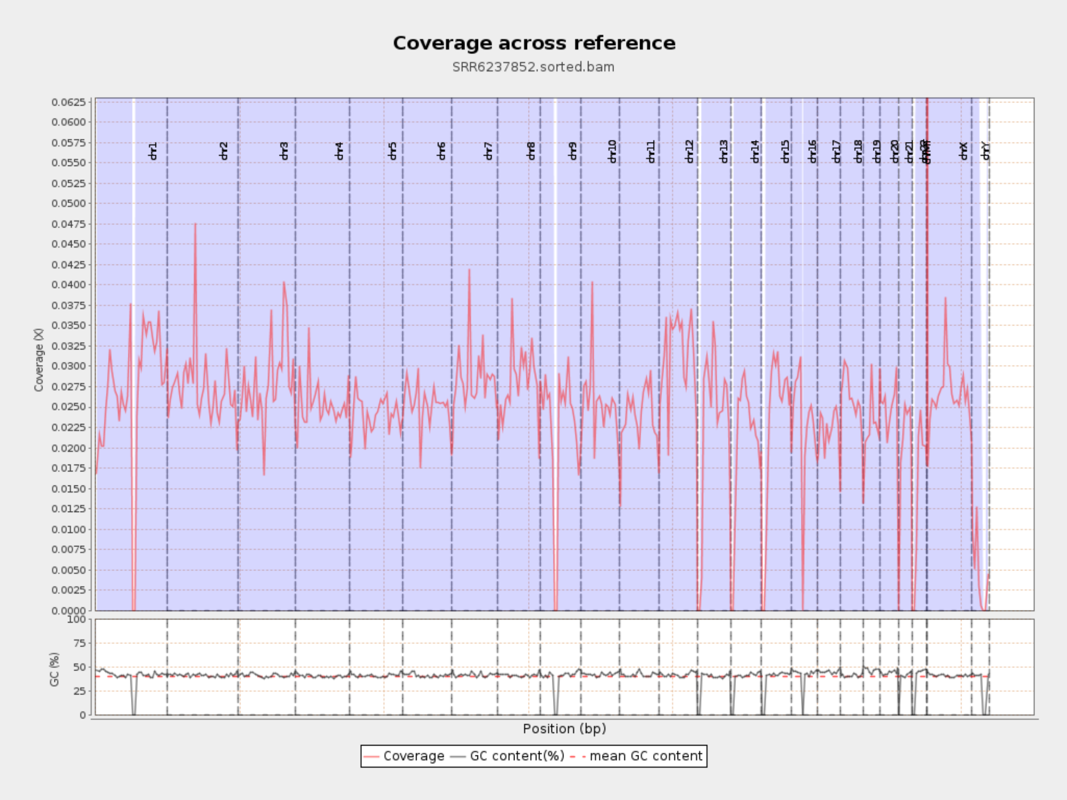
General error rate	1.06%
Mismatches	805,021
Insertions	7,052
Mapped reads with at least one insertion	0.56%
Deletions	35,169
Mapped reads with at least one deletion	2.77%
Homopolymer indels	49.28%

2.6. Chromosome stats

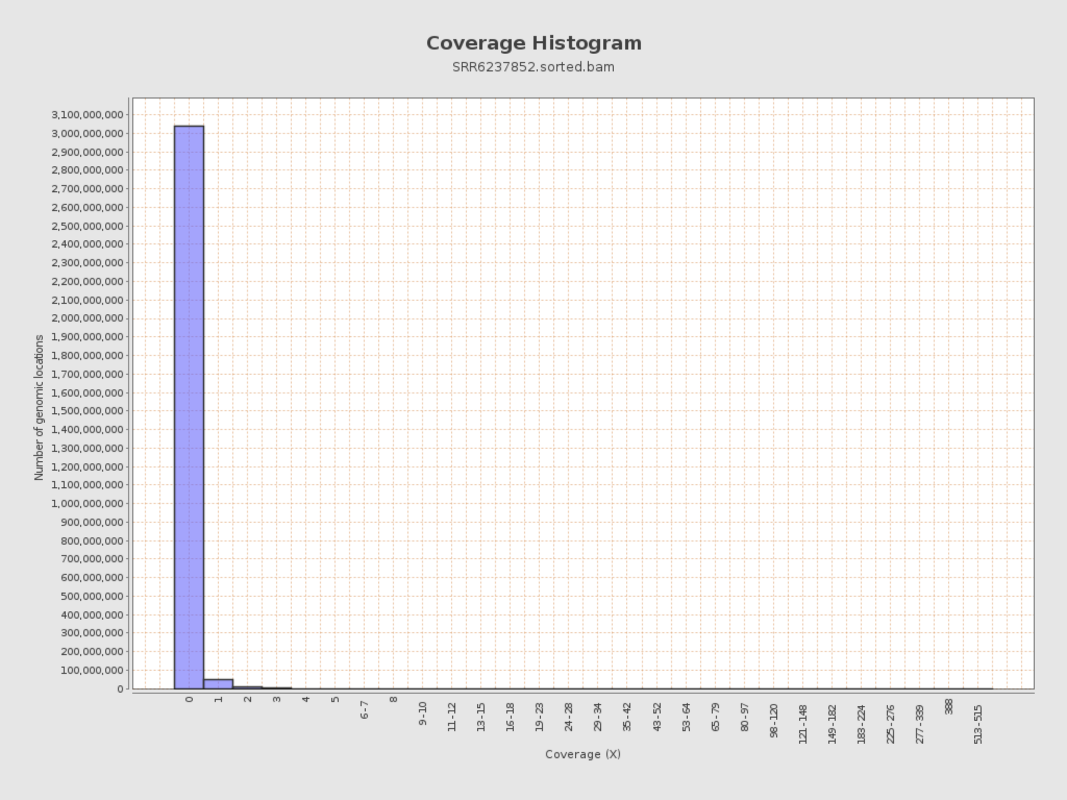
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6688223	0.0268	0.3136
chr2	243199373	6665476	0.0274	0.3623
chr3	198022430	5520327	0.0279	0.2366
chr4	191154276	4813208	0.0252	0.2162
chr5	180915260	4377534	0.0242	0.205
chr6	171115067	4320247	0.0252	0.2351
chr7	159138663	4544510	0.0286	0.374

chr8	146364022	4100400	0.028	0.2789
chr9	141213431	3153433	0.0223	0.255
chr10	135534747	3439914	0.0254	0.253
chr11	135006516	3246357	0.024	0.2781
chr12	133851895	4210323	0.0315	0.2489
chr13	115169878	2634119	0.0229	0.2149
chr14	107349540	2172547	0.0202	0.1968
chr15	102531392	2333685	0.0228	0.2068
chr16	90354753	2013485	0.0223	0.2204
chr17	81195210	1791885	0.0221	0.212
chr18	78077248	2056087	0.0263	0.4536
chr19	59128983	1351137	0.0229	0.2501
chr20	63025520	1560930	0.0248	0.2147
chr21	48129895	980468	0.0204	0.2032
chr22	51304566	764323	0.0149	0.1617
chrMT	16571	49744	3.0019	3.1746
chrX	155270560	4151003	0.0267	0.2322
chrY	59373566	250060	0.0042	0.1036

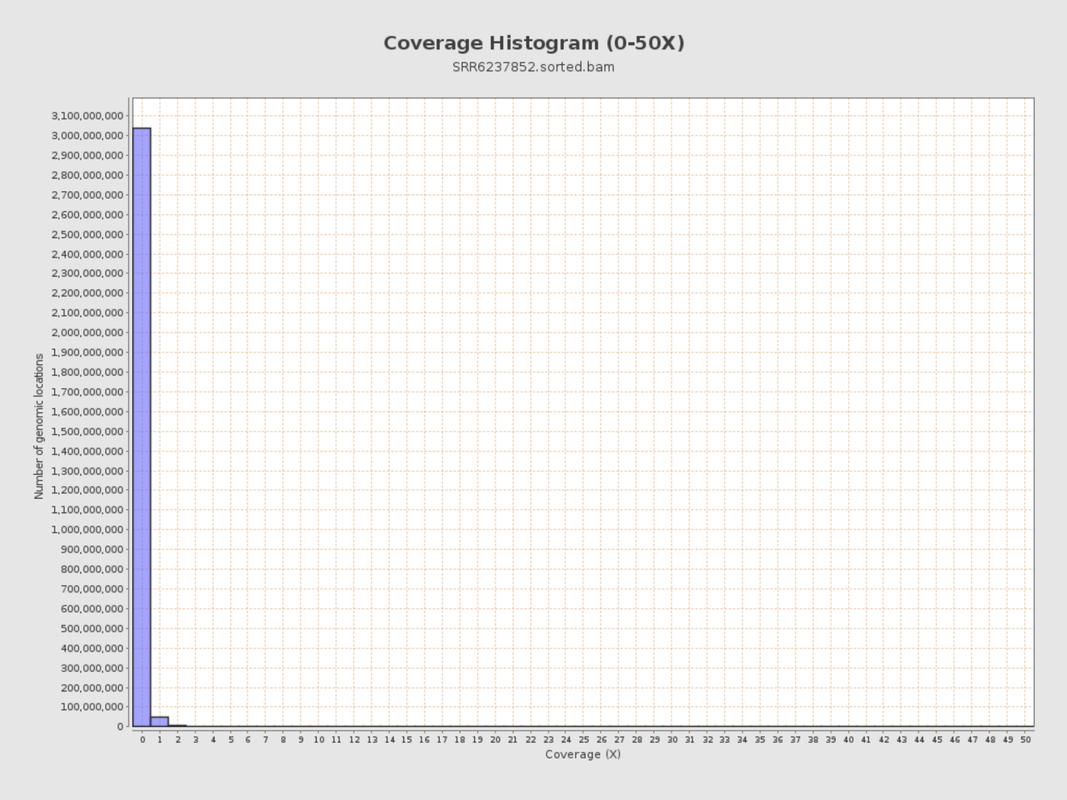
3. Results : Coverage across reference



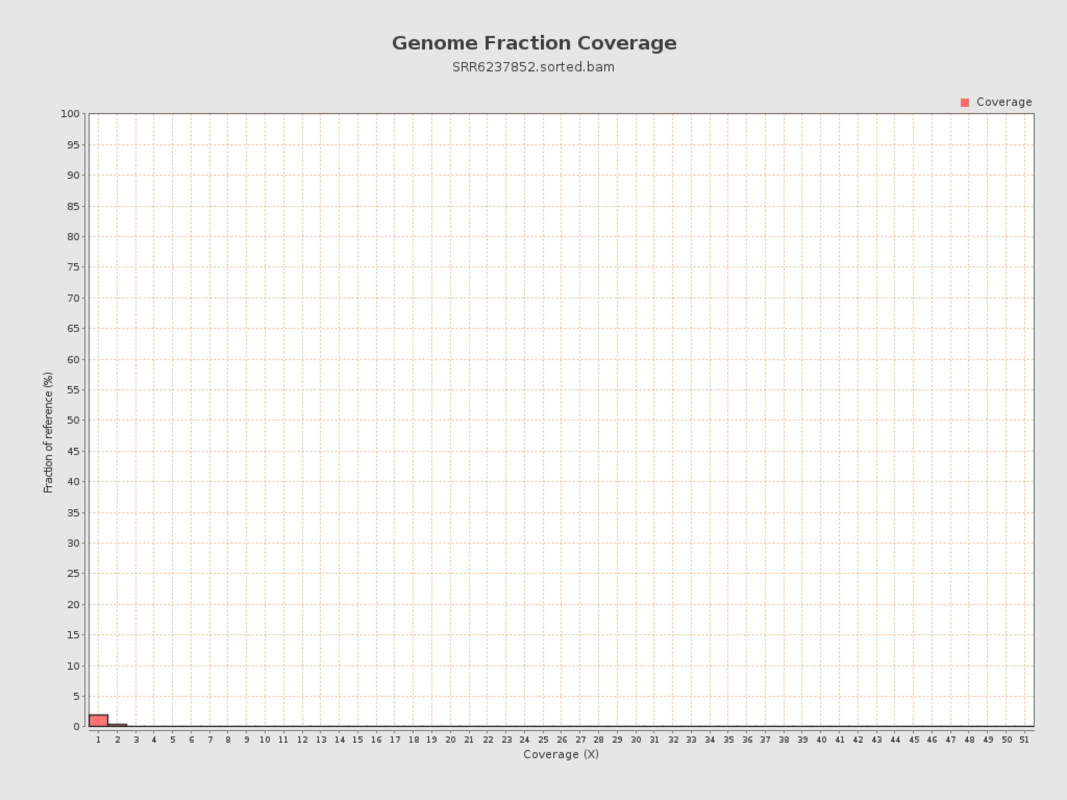
4. Results : Coverage Histogram



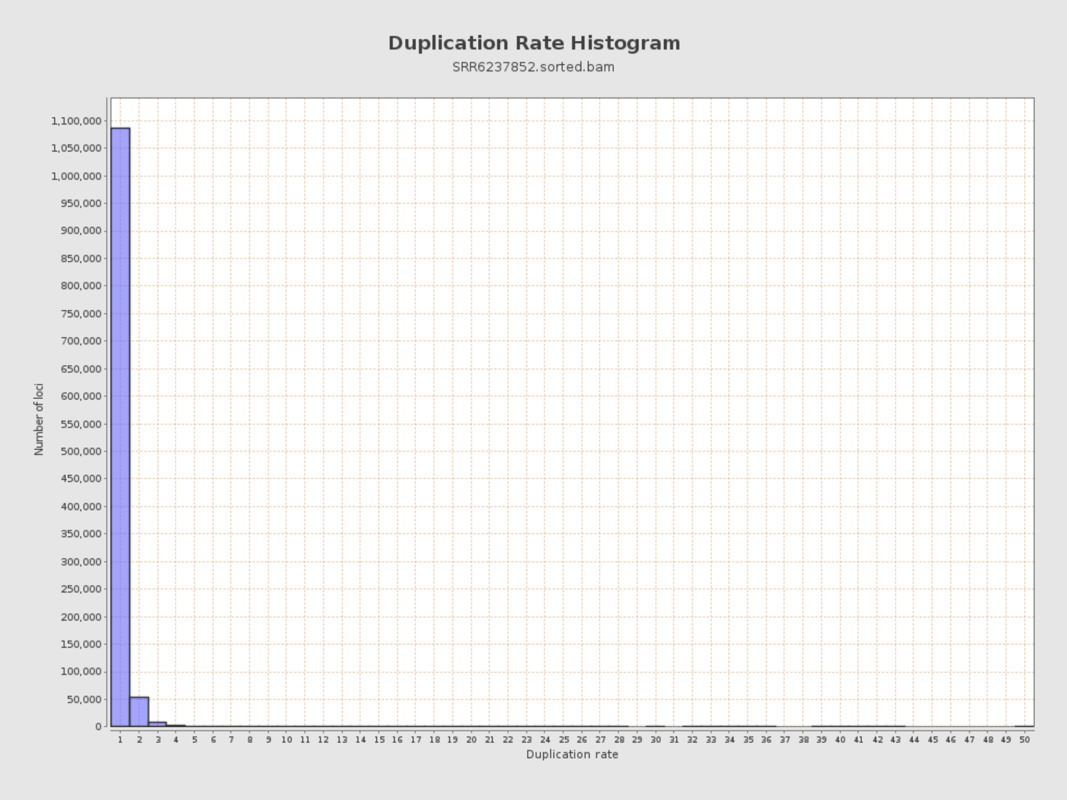
5. Results : Coverage Histogram (0-50X)



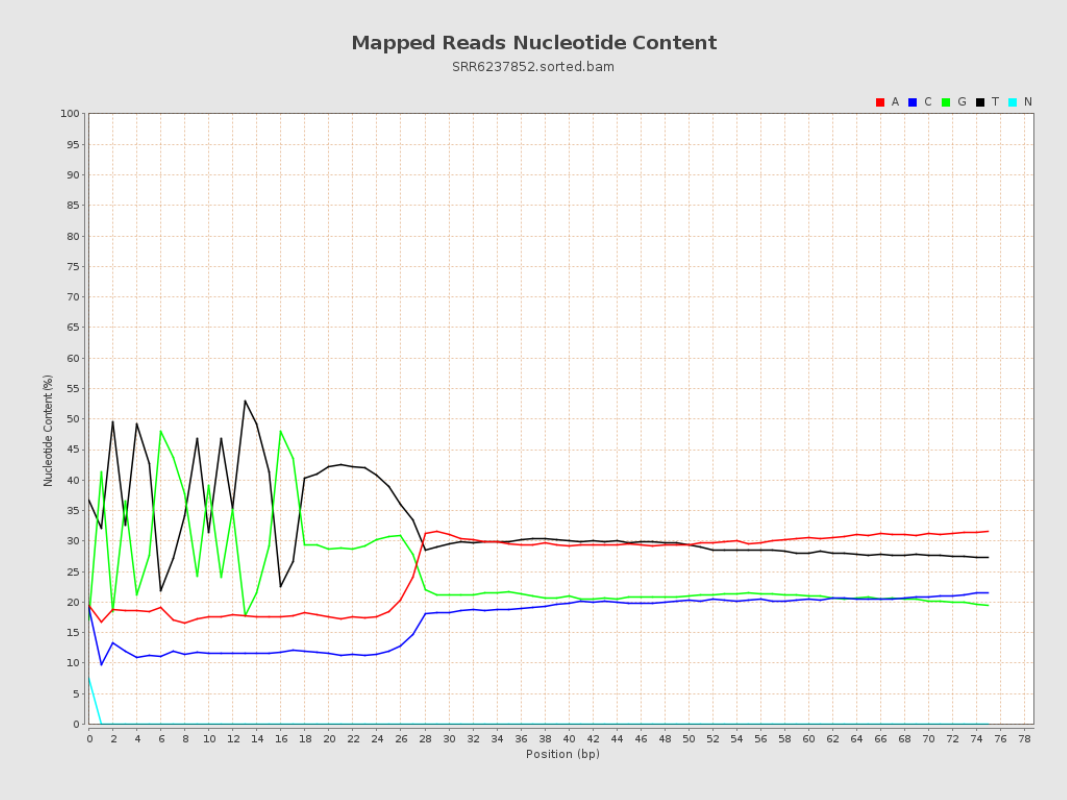
6. Results : Genome Fraction Coverage



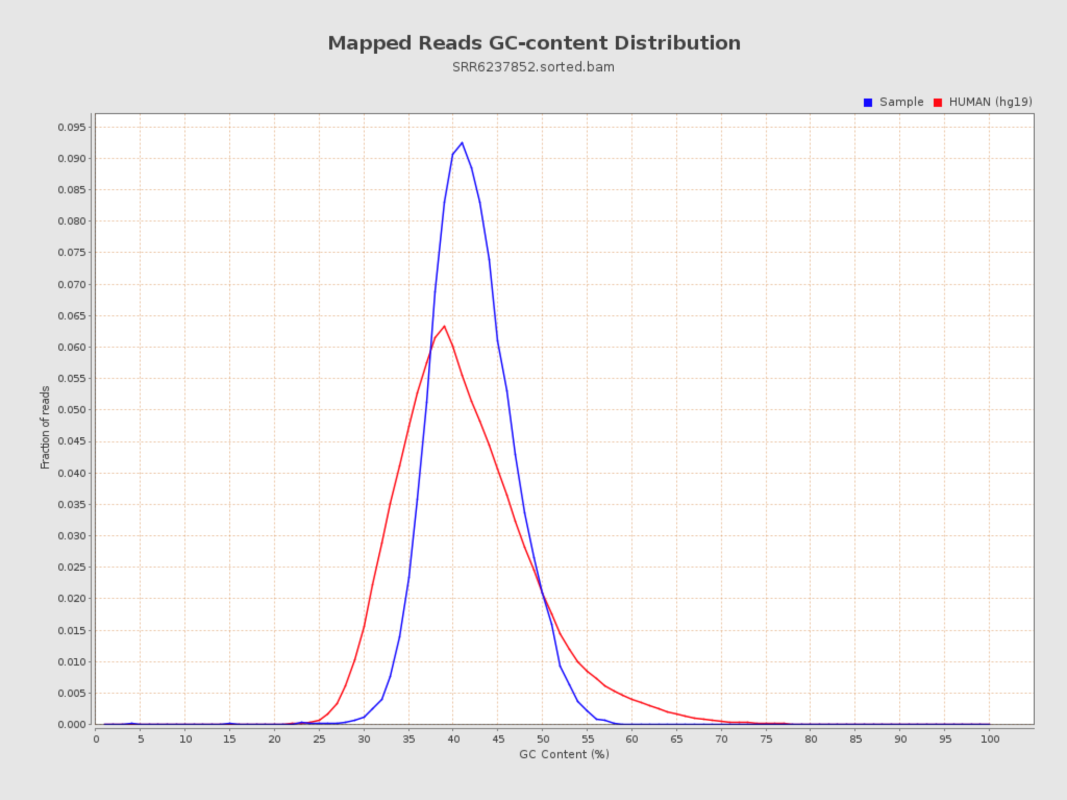
7. Results : Duplication Rate Histogram



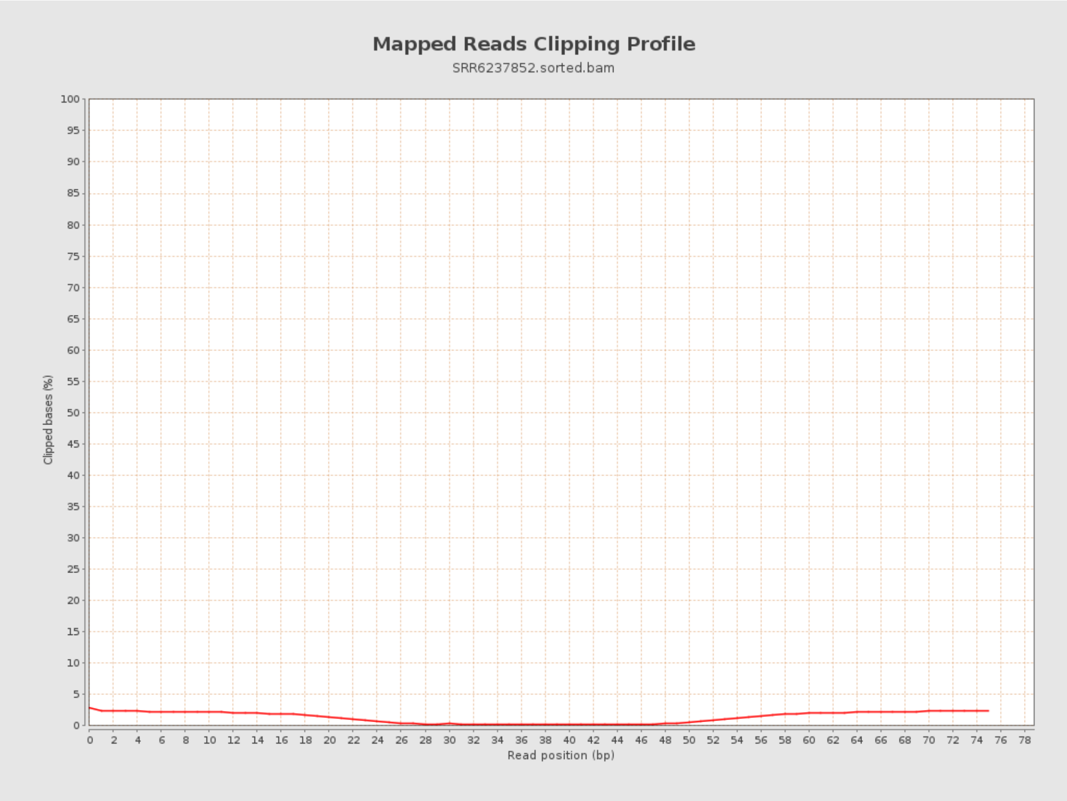
8. Results : Mapped Reads Nucleotide Content



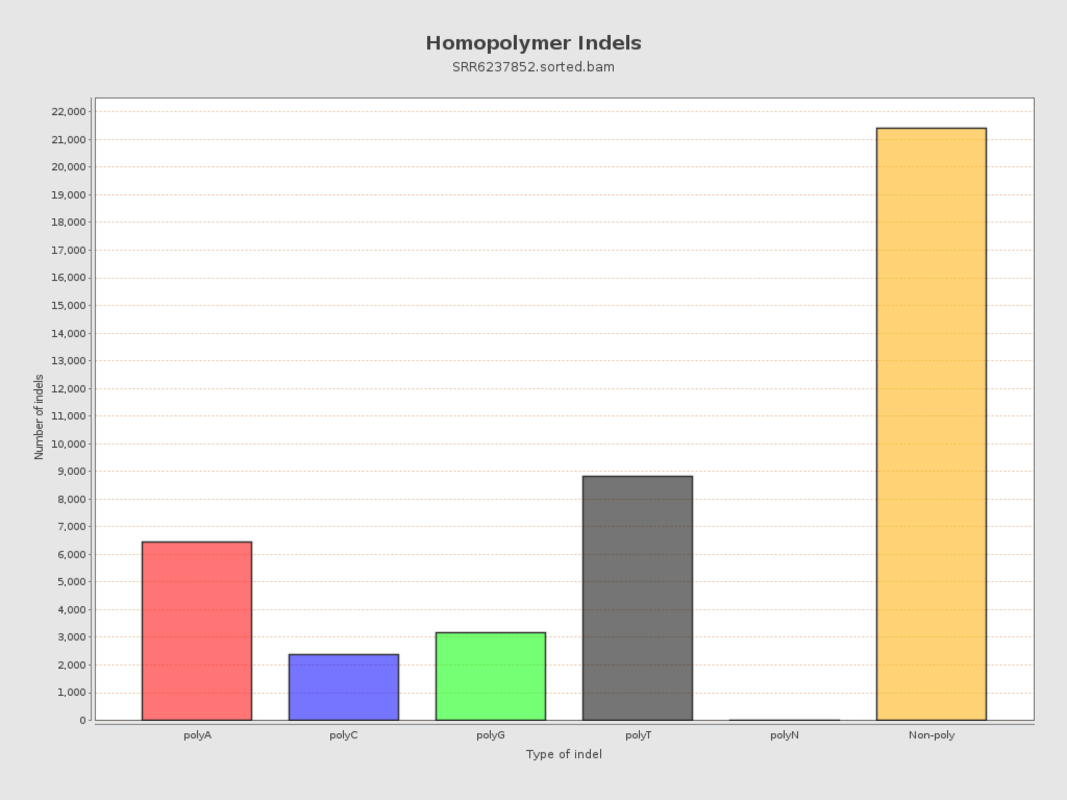
9. Results : Mapped Reads GC-content Distribution



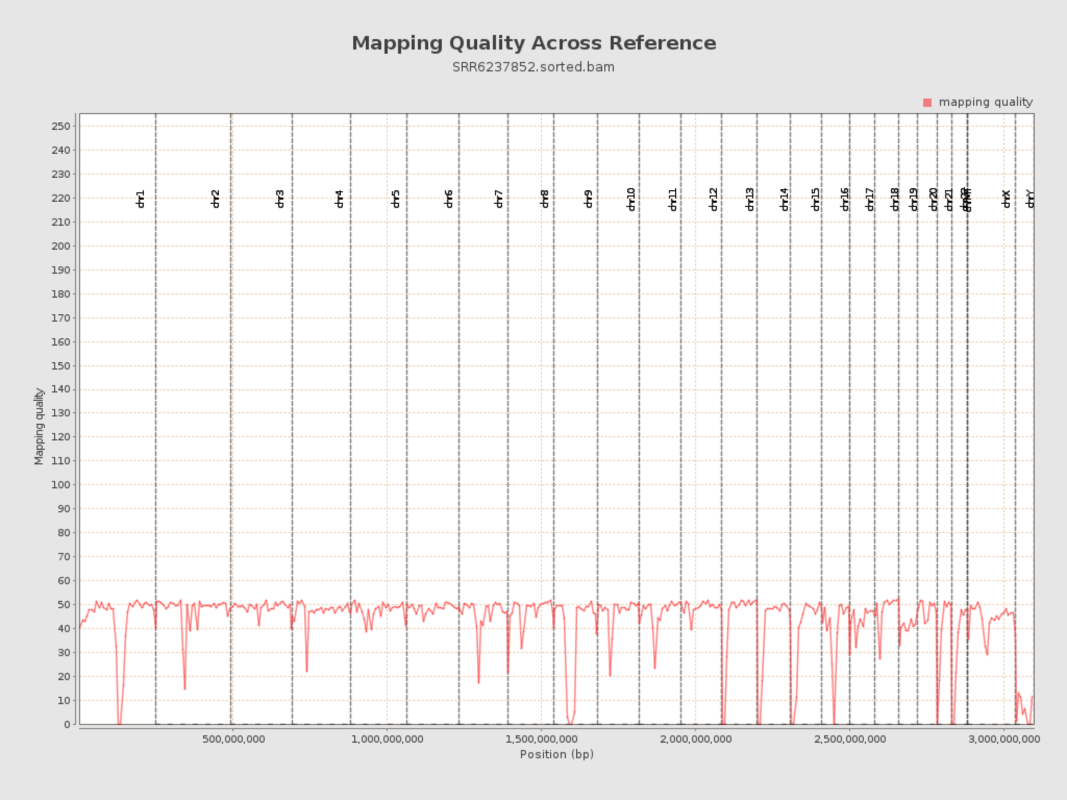
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram