

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 00:09:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237283.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_SRR6237283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237283.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 00:09:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,094,327
Mapped reads	1,841,261 / 87.92%
Unmapped reads	253,066 / 12.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,578 / 0.93%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	478,708 / 22.86%
Duplication rate	19.43%
Clipped reads	1,173,249 / 56.02%

2.2. ACGT Content

Number/percentage of A's	29,217,804 / 25.7%
Number/percentage of C's	19,005,439 / 16.72%
Number/percentage of T's	38,737,854 / 34.08%
Number/percentage of G's	26,700,287 / 23.49%
Number/percentage of N's	11,452 / 0.01%
GC Percentage	40.21%

2.3. Coverage

Mean	0.0367

Standard Deviation	0.5892
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2.4. Mapping Quality

Mean Mapping Quality	44.04
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2.5. Mismatches and indels

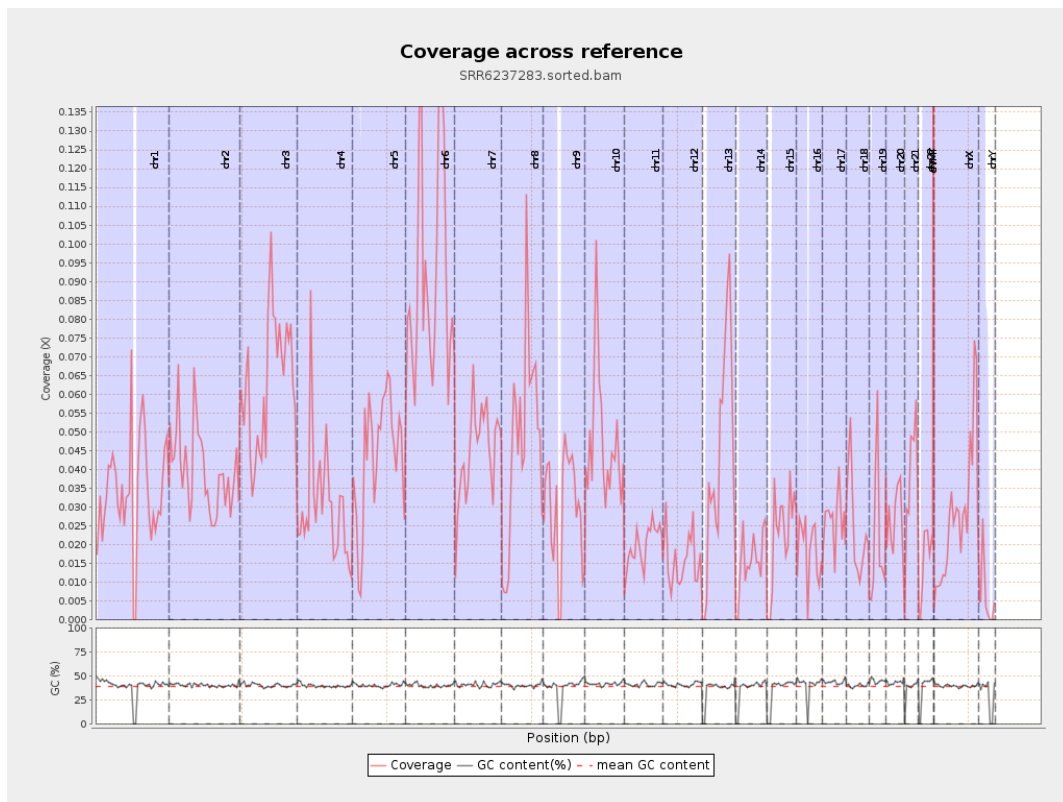
General error rate	0.66%
Mismatches	732,454
Insertions	8,770
Mapped reads with at least one insertion	0.47%
Deletions	38,956
Mapped reads with at least one deletion	2.09%
Homopolymer indels	41.73%

2.6. Chromosome stats

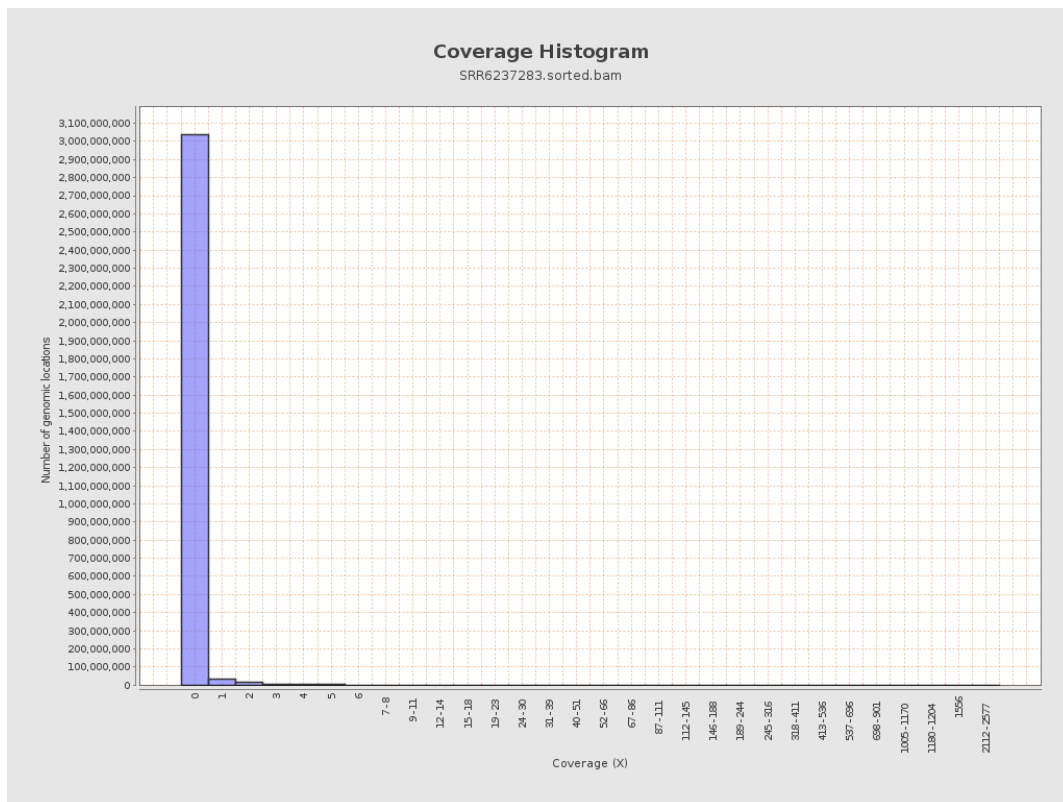
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8398466	0.0337	0.7408
chr2	243199373	9685782	0.0398	1.2319
chr3	198022430	12463450	0.0629	0.4364
chr4	191154276	5626161	0.0294	0.392
chr5	180915260	7852660	0.0434	0.3608
chr6	171115067	15575646	0.091	0.8502
chr7	159138663	7162615	0.045	0.4763

chr8	146364022	6782155	0.0463	0.7925
chr9	141213431	4271991	0.0303	0.3434
chr10	135534747	6380242	0.0471	0.5751
chr11	135006516	2666329	0.0197	0.2459
chr12	133851895	2139257	0.016	0.2241
chr13	115169878	4931604	0.0428	0.3949
chr14	107349540	1631788	0.0152	0.2189
chr15	102531392	2327108	0.0227	0.2839
chr16	90354753	1655432	0.0183	0.2539
chr17	81195210	2137559	0.0263	0.2949
chr18	78077248	1929012	0.0247	0.8894
chr19	59128983	1300686	0.022	0.4267
chr20	63025520	1636475	0.026	0.2892
chr21	48129895	1761677	0.0366	0.37
chr22	51304566	772020	0.015	0.2009
chrMT	16571	6207	0.3746	0.9009
chrX	155270560	4305111	0.0277	0.2897
chrY	59373566	340829	0.0057	0.296

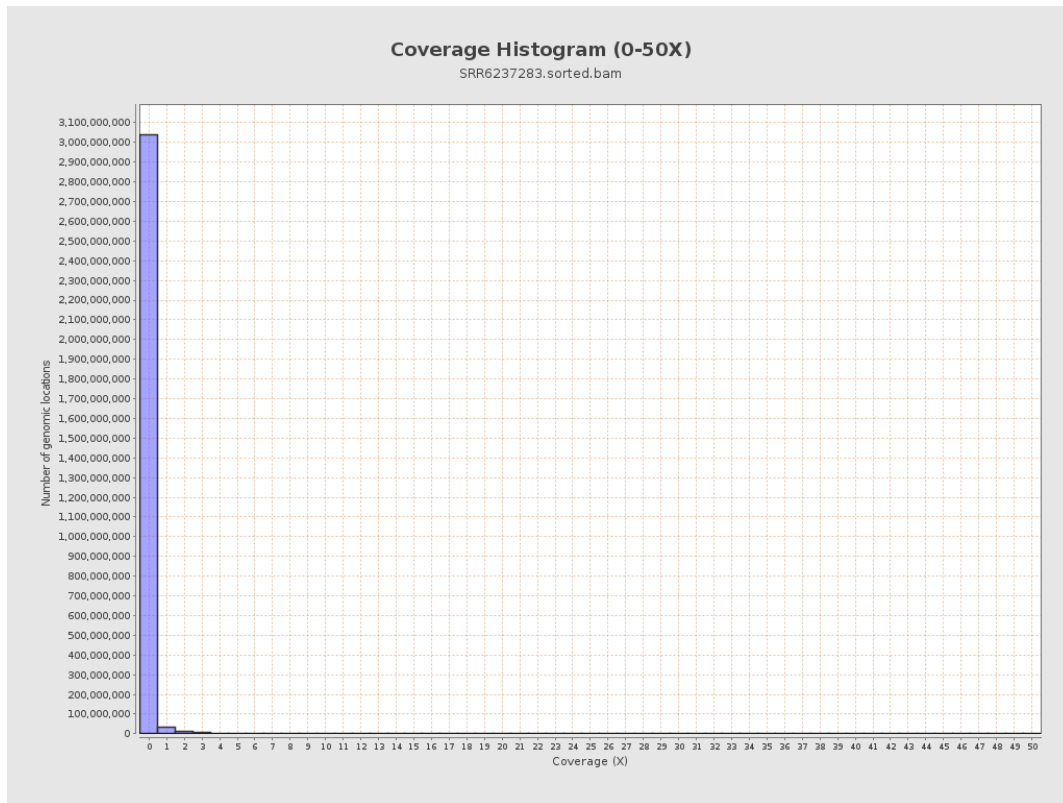
3. Results : Coverage across reference



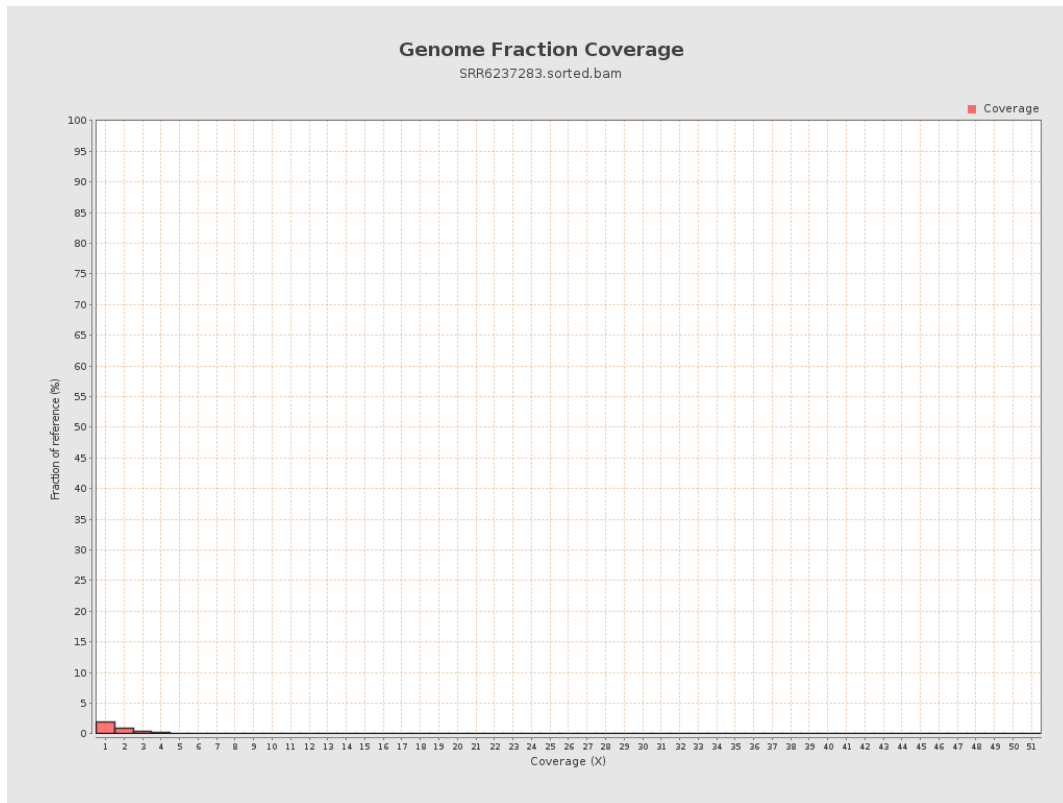
4. Results : Coverage Histogram



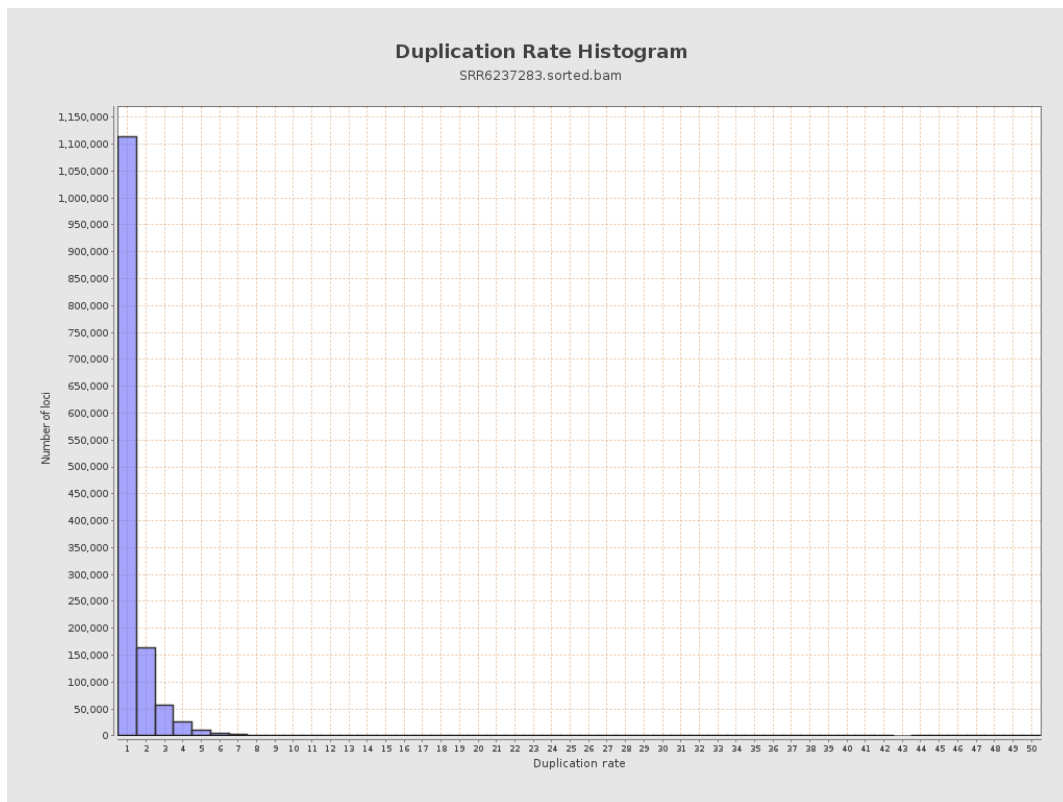
5. Results : Coverage Histogram (0-50X)



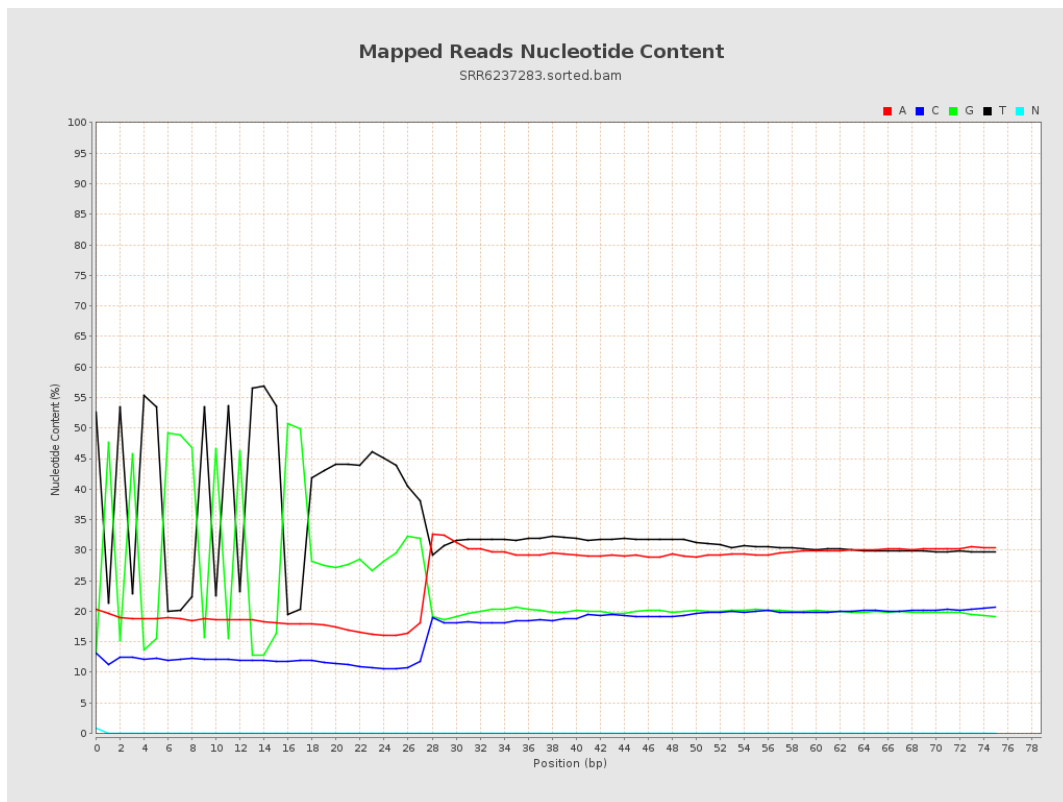
6. Results : Genome Fraction Coverage



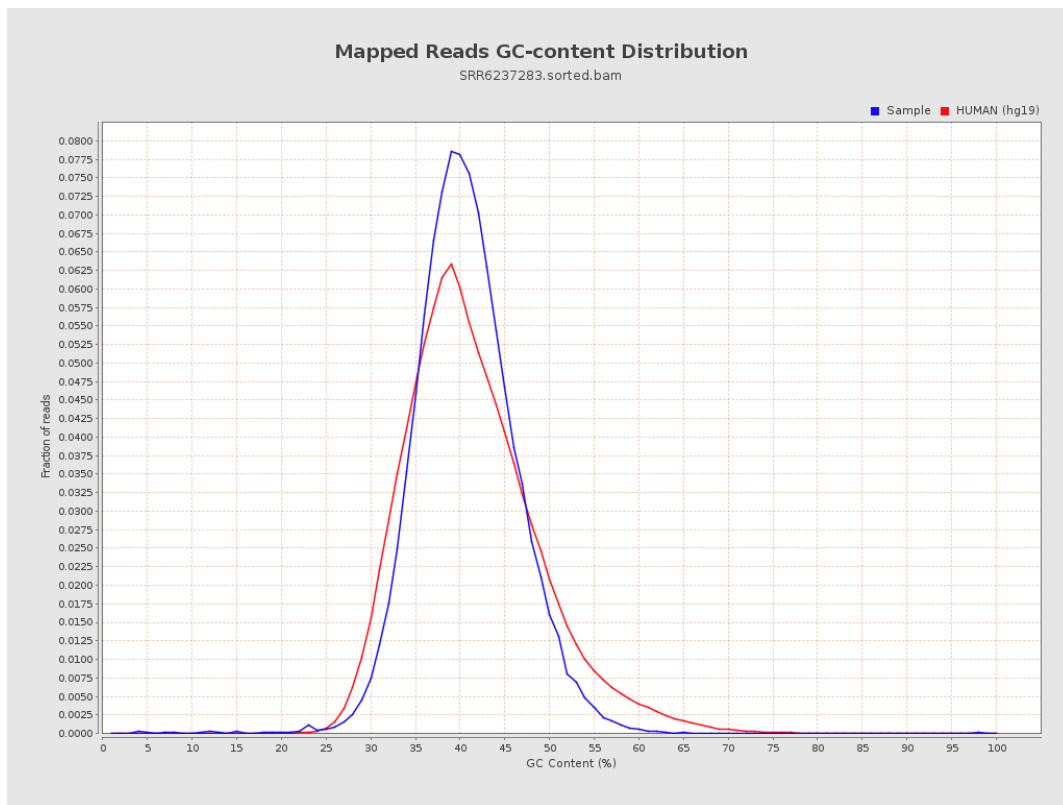
7. Results : Duplication Rate Histogram



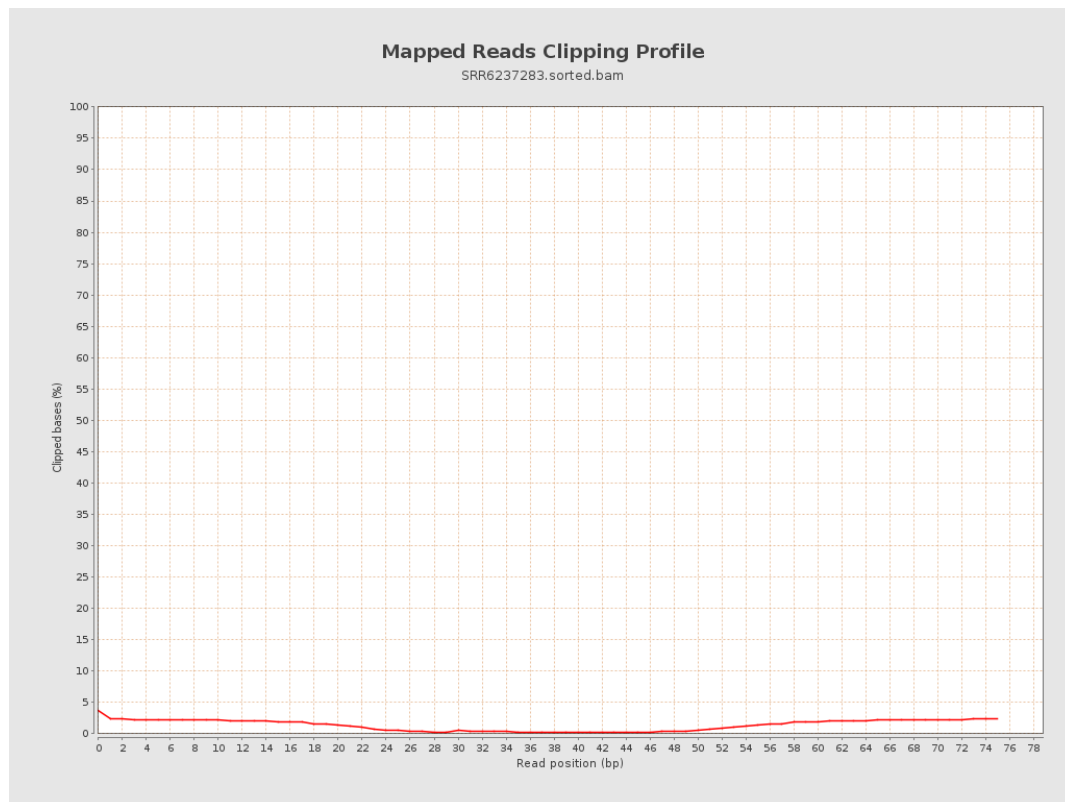
8. Results : Mapped Reads Nucleotide Content



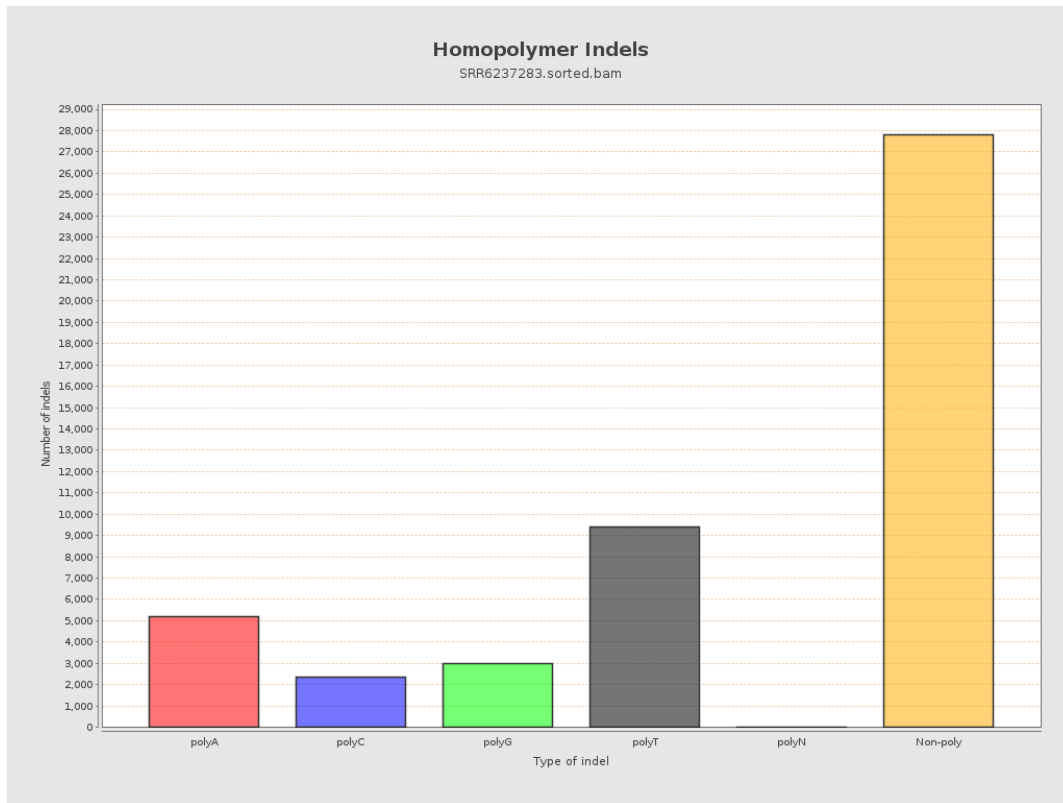
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

