

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 18:05:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6230337.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_SRR6230337 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6230337.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 18:05:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6230337.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,686,307
Mapped reads	2,202,868 / 82%
Unmapped reads	483,439 / 18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,501 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	109,643 / 4.08%
Duplication rate	3.6%
Clipped reads	1,248,675 / 46.48%

2.2. ACGT Content

Number/percentage of A's	37,280,985 / 26.44%
Number/percentage of C's	23,761,838 / 16.85%
Number/percentage of T's	47,109,192 / 33.41%
Number/percentage of G's	32,604,759 / 23.12%
Number/percentage of N's	259,621 / 0.18%
GC Percentage	39.97%

2.3. Coverage

Mean	0.0456

Standard Deviation	0.4864
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2.4. Mapping Quality

Mean Mapping Quality	46.15
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2.5. Mismatches and indels

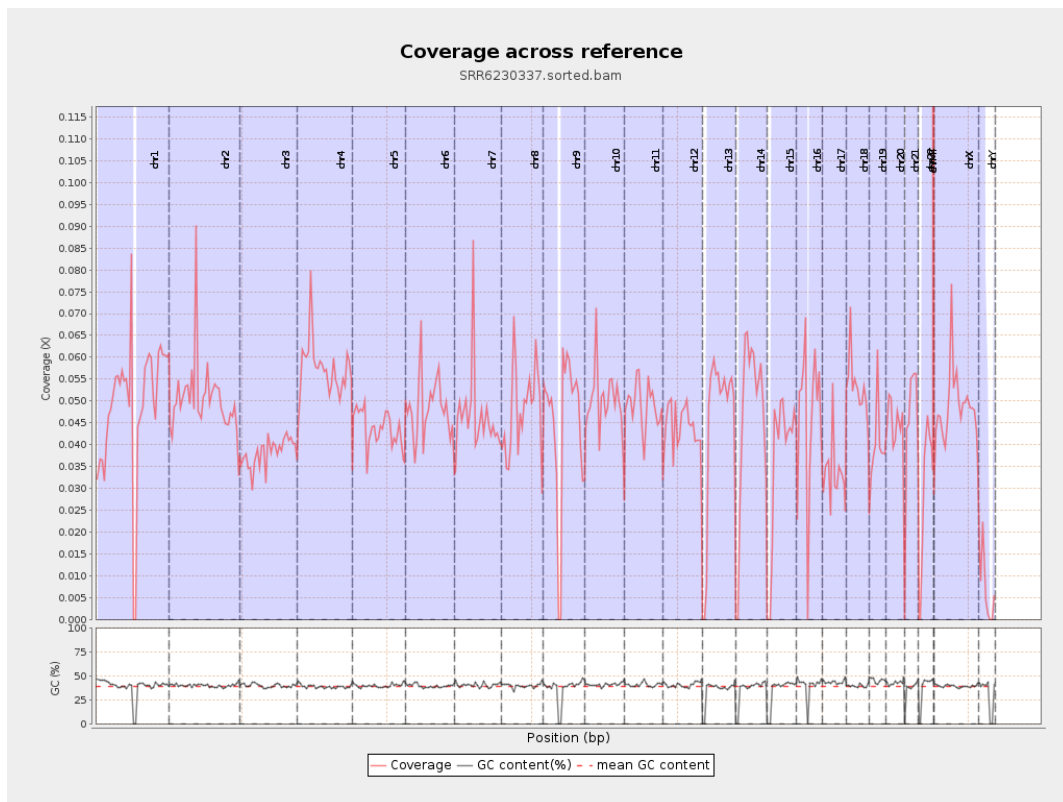
General error rate	0.97%
Mismatches	1,338,224
Insertions	13,147
Mapped reads with at least one insertion	0.59%
Deletions	40,776
Mapped reads with at least one deletion	1.83%
Homopolymer indels	49%

2.6. Chromosome stats

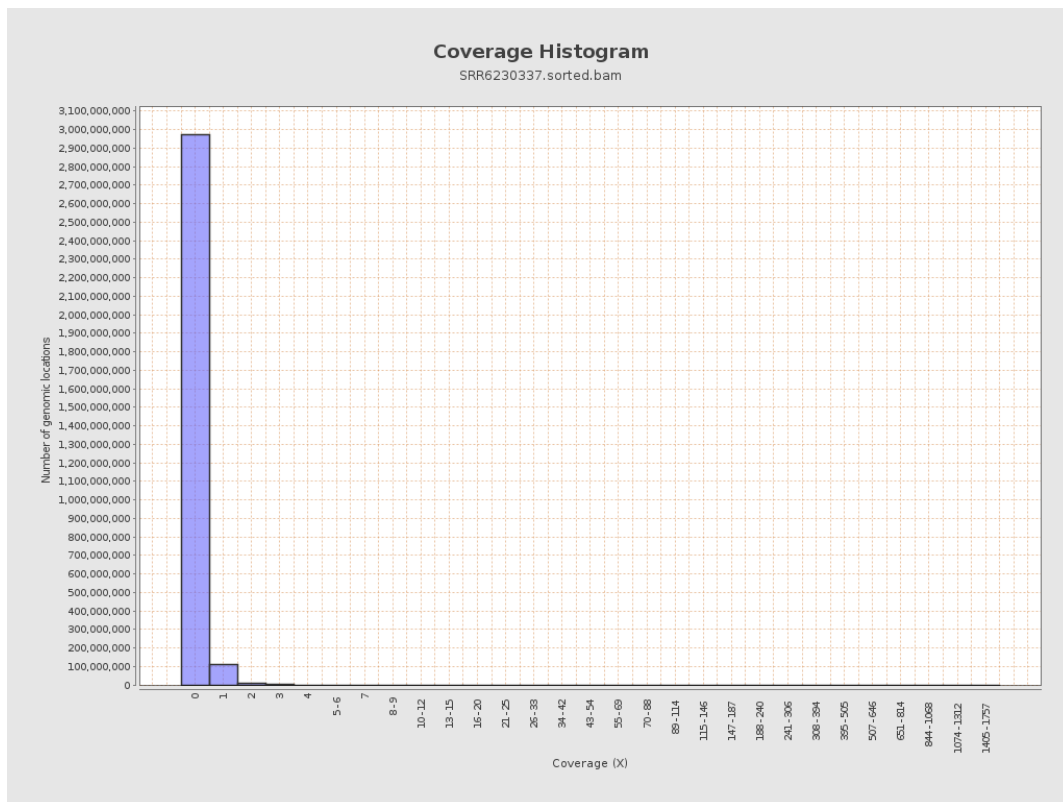
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12213247	0.049	0.7919
chr2	243199373	12295113	0.0506	0.514
chr3	198022430	7554645	0.0382	0.2177
chr4	191154276	10984105	0.0575	0.3114
chr5	180915260	7893222	0.0436	0.2375
chr6	171115067	8294209	0.0485	0.3383
chr7	159138663	7434095	0.0467	0.6036

chr8	146364022	6968605	0.0476	1.0813
chr9	141213431	6311845	0.0447	0.4942
chr10	135534747	6803489	0.0502	0.3637
chr11	135006516	6547672	0.0485	0.4809
chr12	133851895	5875870	0.0439	0.2426
chr13	115169878	5137221	0.0446	0.2355
chr14	107349540	5022574	0.0468	0.2652
chr15	102531392	3762661	0.0367	0.2158
chr16	90354753	4220557	0.0467	0.2771
chr17	81195210	2707944	0.0334	0.2754
chr18	78077248	4173817	0.0535	0.8717
chr19	59128983	2380723	0.0403	0.4993
chr20	63025520	2821807	0.0448	0.2581
chr21	48129895	2162754	0.0449	0.2659
chr22	51304566	1482214	0.0289	0.187
chrMT	16571	128540	7.7569	4.9849
chrX	155270560	7508337	0.0484	0.3109
chrY	59373566	396644	0.0067	0.159

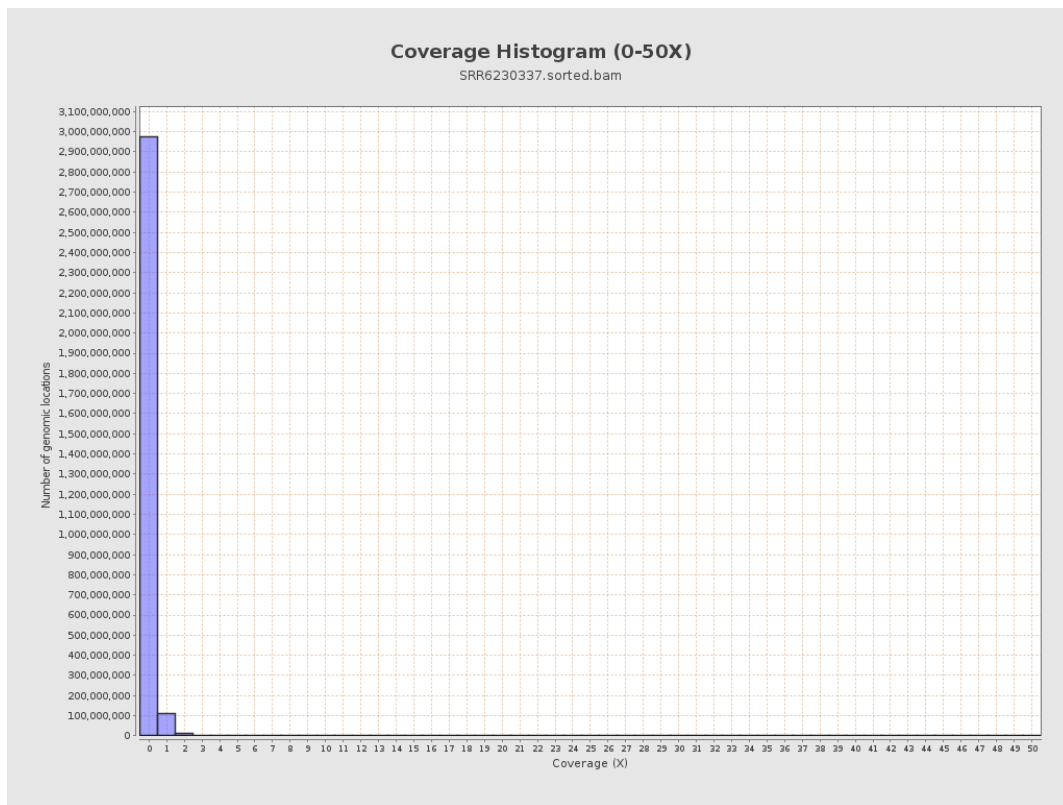
3. Results : Coverage across reference



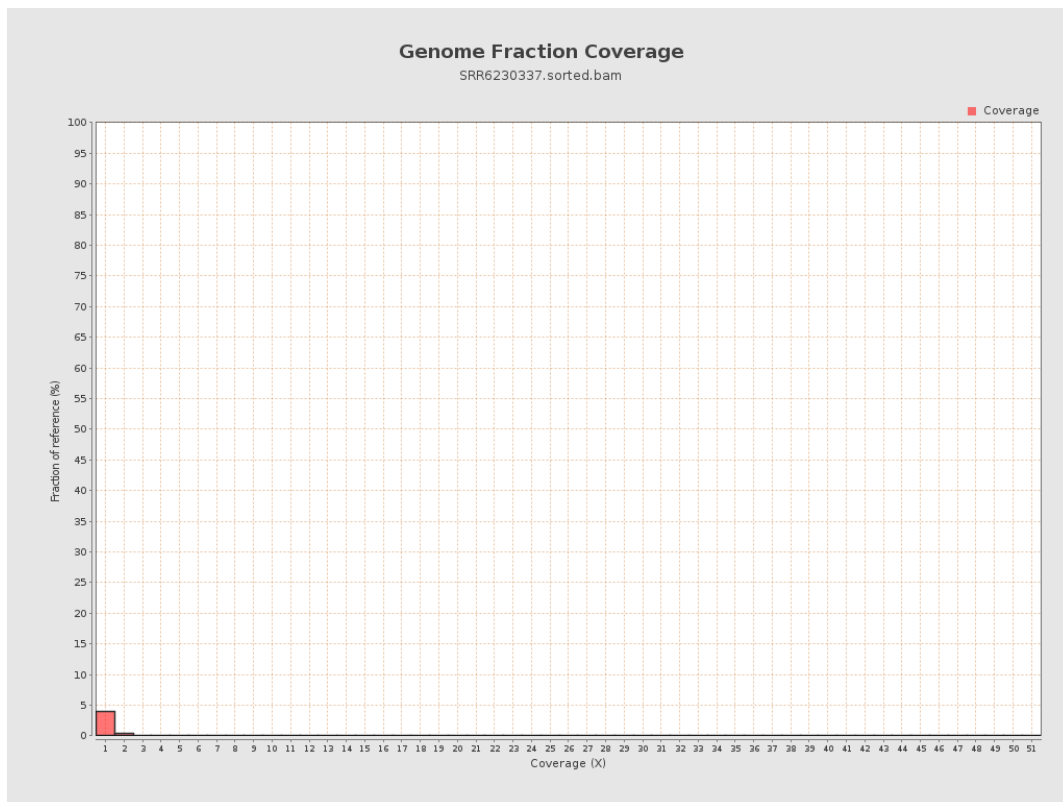
4. Results : Coverage Histogram



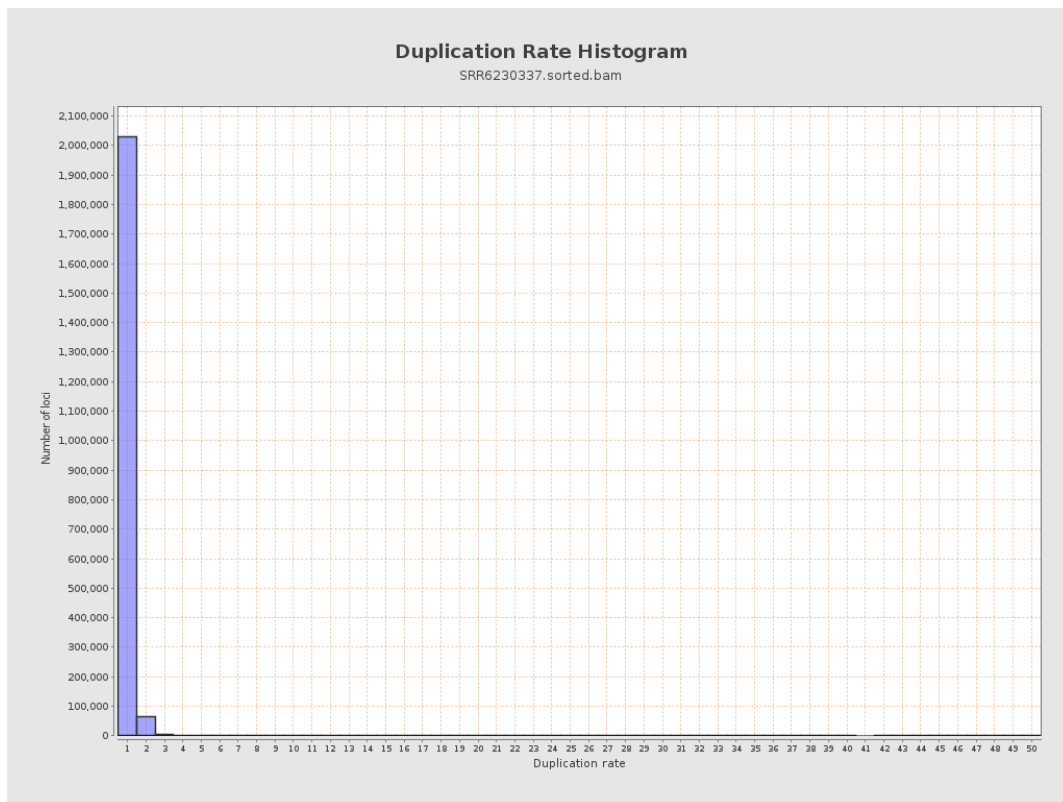
5. Results : Coverage Histogram (0-50X)



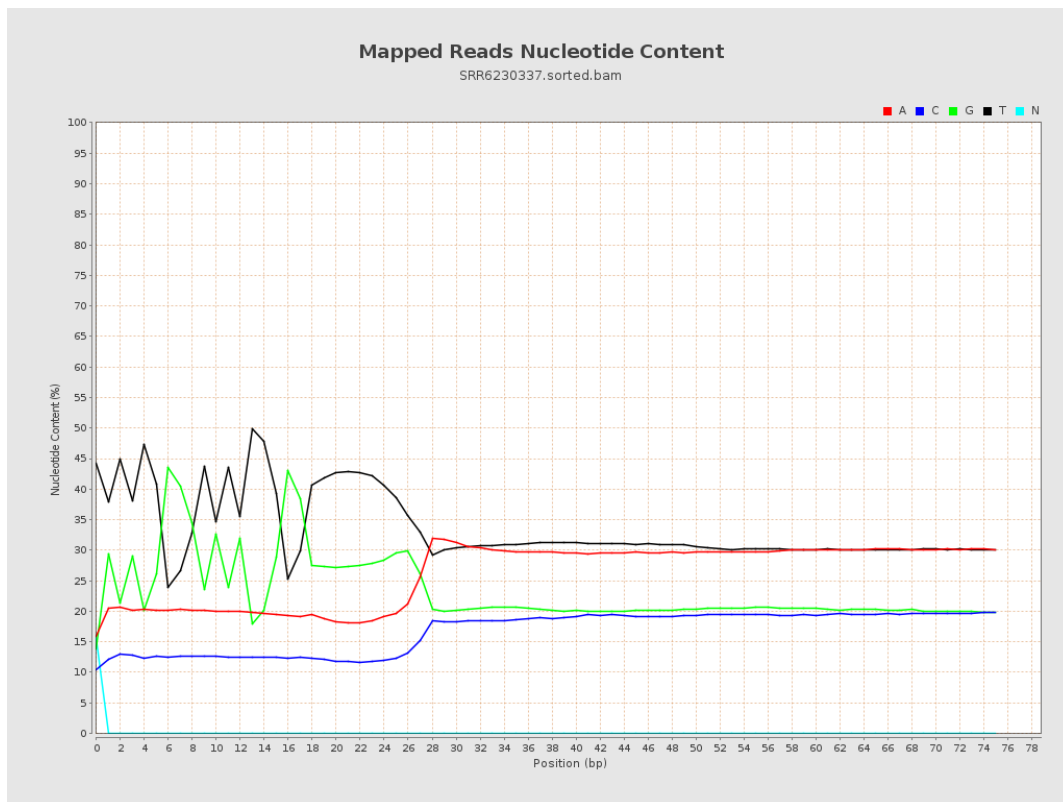
6. Results : Genome Fraction Coverage



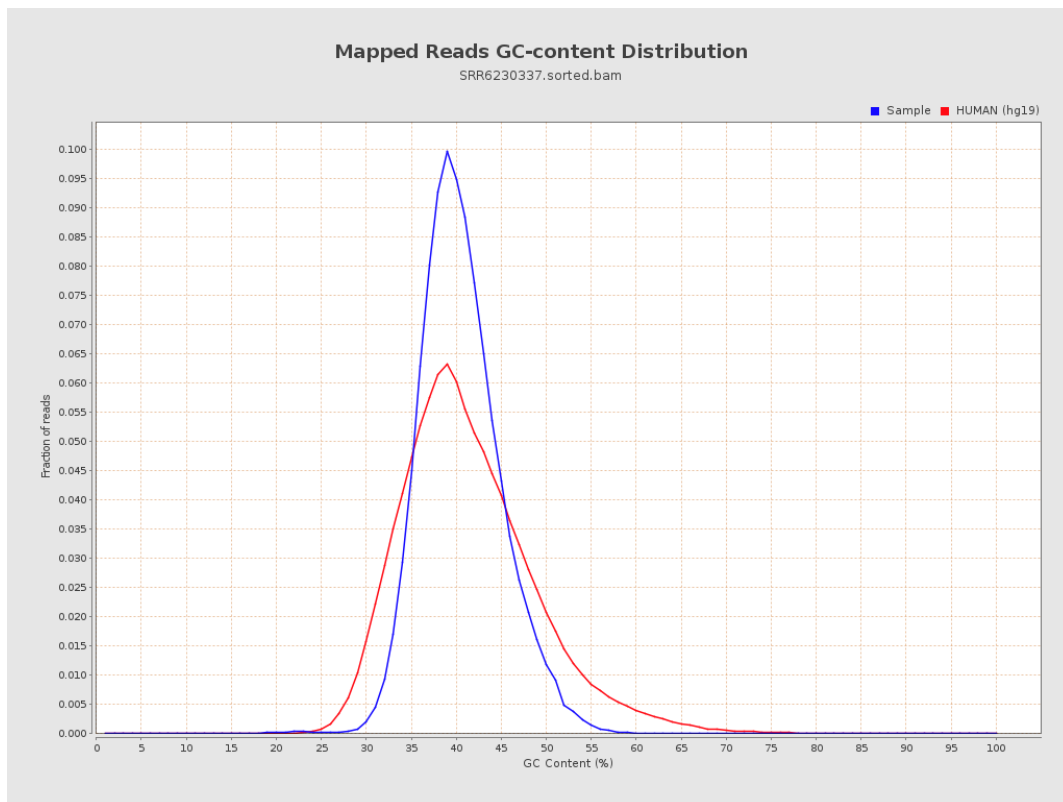
7. Results : Duplication Rate Histogram



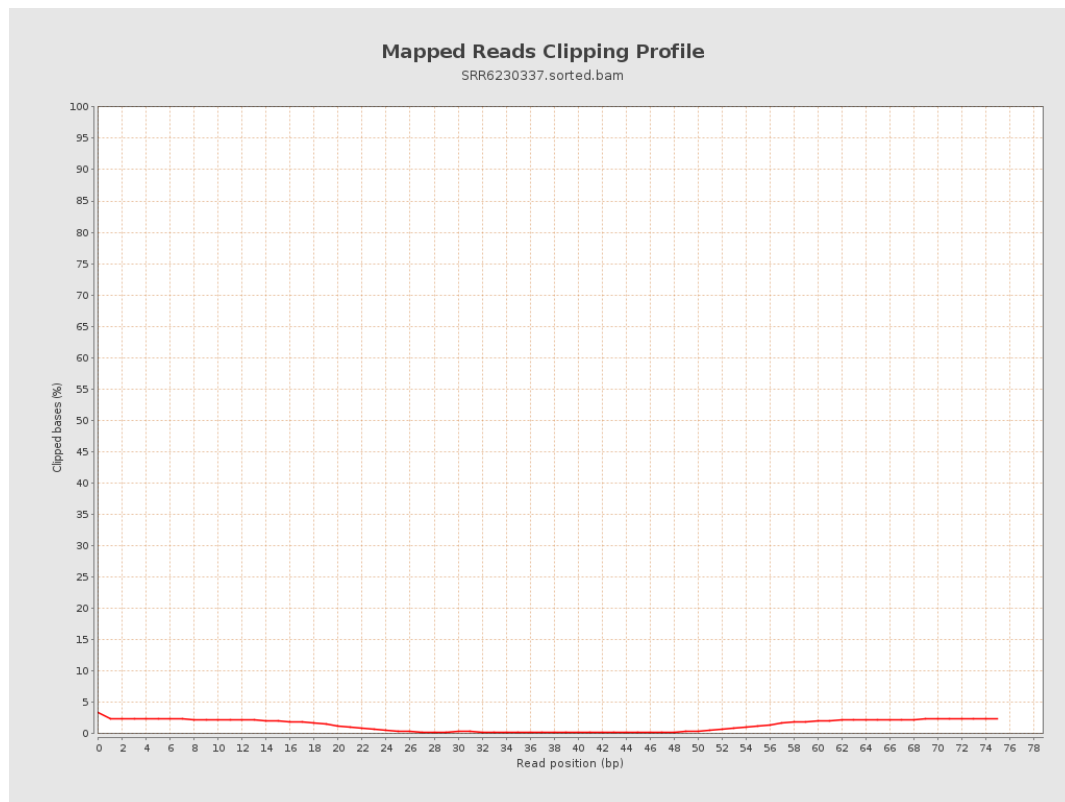
8. Results : Mapped Reads Nucleotide Content



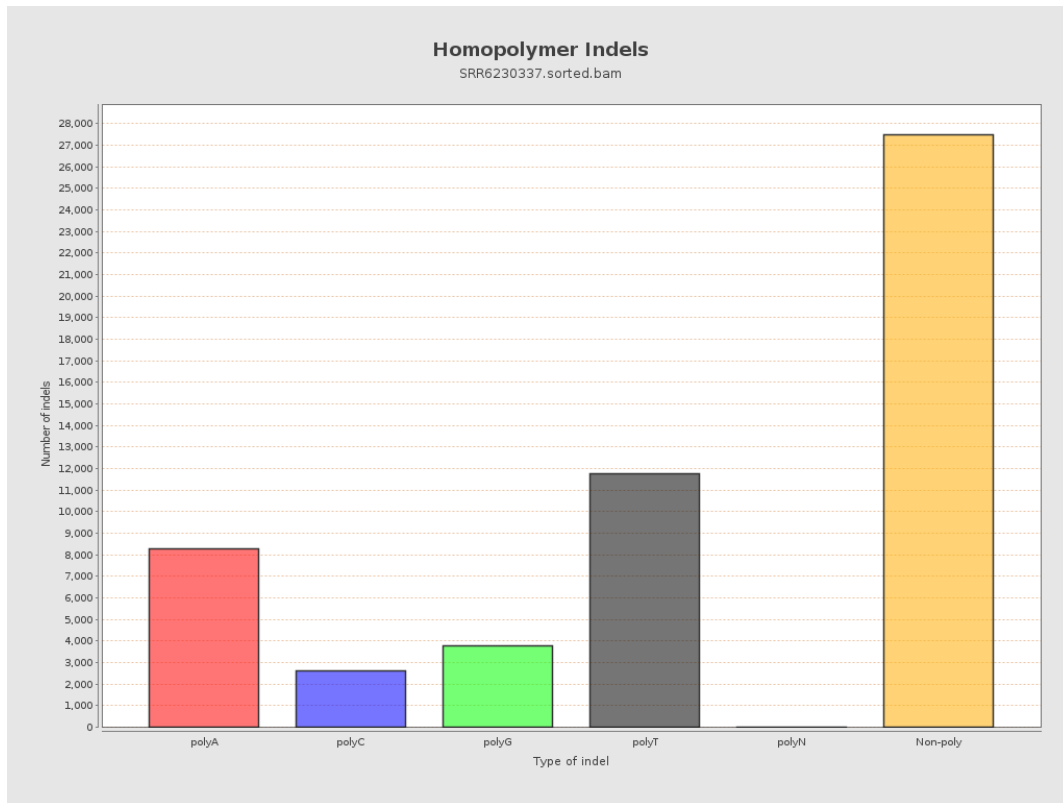
9. Results : Mapped Reads GC-content Distribution



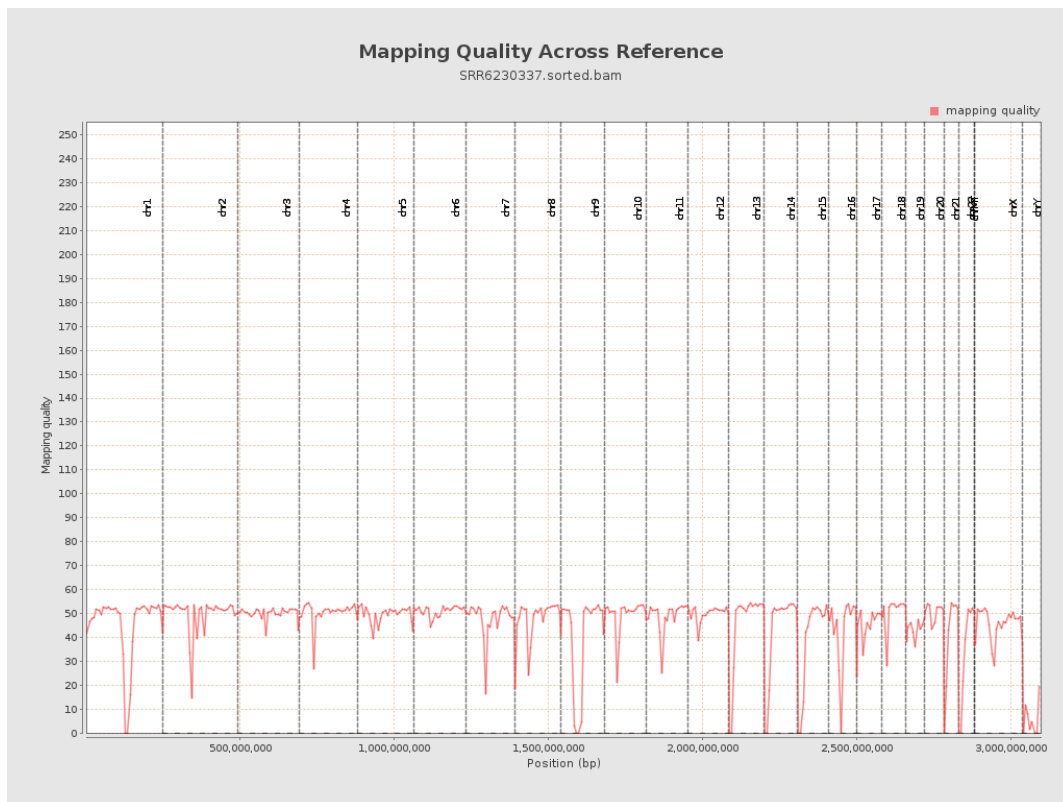
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

