

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:48:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231777.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_SRR6231777 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231777.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:48:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231777.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,845,113
Mapped reads	1,693,650 / 91.79%
Unmapped reads	151,463 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,550 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	84,828 / 4.6%
Duplication rate	2.14%
Clipped reads	830,117 / 44.99%

2.2. ACGT Content

Number/percentage of A's	32,440,516 / 28.97%
Number/percentage of C's	21,722,351 / 19.4%
Number/percentage of T's	31,765,916 / 28.37%
Number/percentage of G's	26,037,895 / 23.25%
Number/percentage of N's	8,204 / 0.01%
GC Percentage	42.65%

2.3. Coverage

Mean	0.0362

Standard Deviation	4.9693
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2.4. Mapping Quality

Mean Mapping Quality	43.24
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2.5. Mismatches and indels

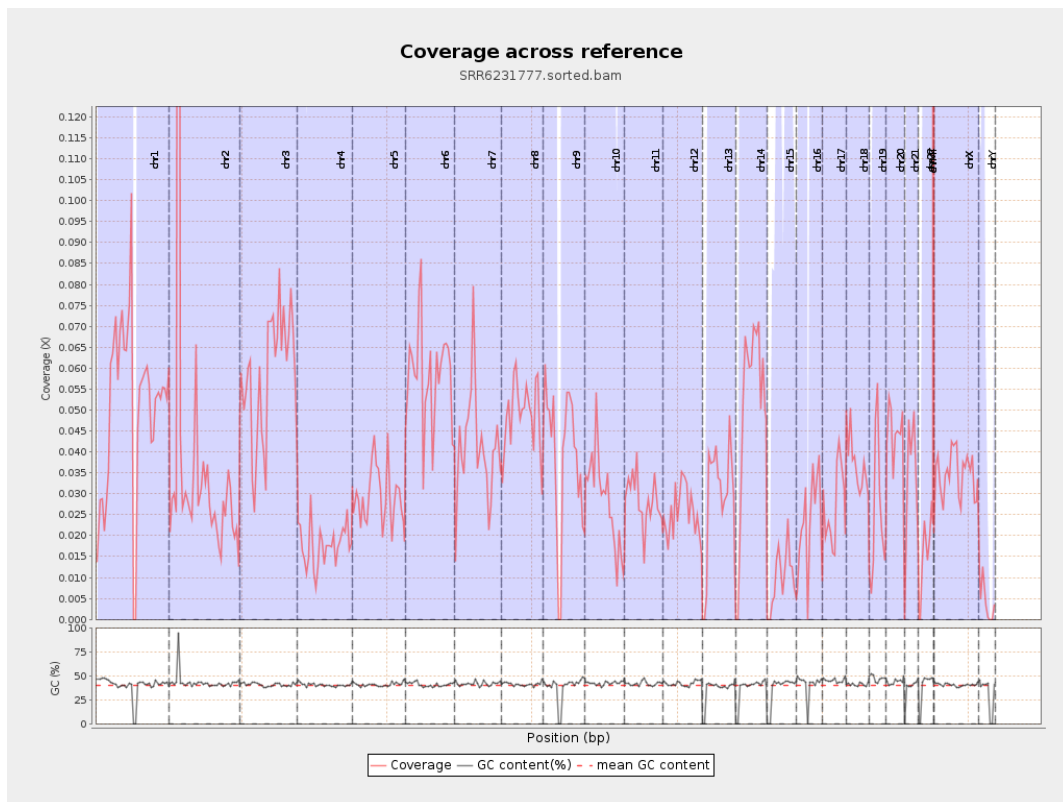
General error rate	0.65%
Mismatches	711,582
Insertions	8,115
Mapped reads with at least one insertion	0.47%
Deletions	25,653
Mapped reads with at least one deletion	1.5%
Homopolymer indels	44.98%

2.6. Chromosome stats

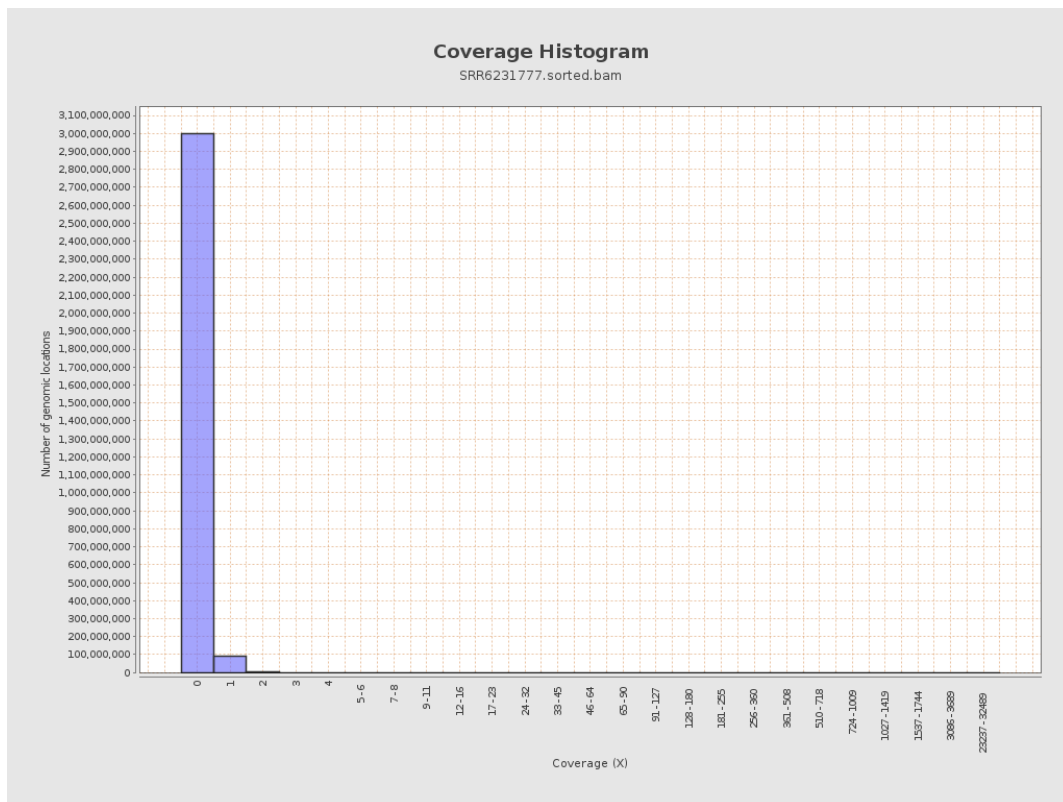
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12495903	0.0501	0.8456
chr2	243199373	9612590	0.0395	17.6828
chr3	198022430	11587718	0.0585	0.2612
chr4	191154276	3366820	0.0176	0.1529
chr5	180915260	5323713	0.0294	0.1851
chr6	171115067	9912131	0.0579	0.3155
chr7	159138663	6587433	0.0414	0.5282

chr8	146364022	7116559	0.0486	0.4329
chr9	141213431	5447605	0.0386	0.2921
chr10	135534747	3886485	0.0287	0.2821
chr11	135006516	3794498	0.0281	0.2543
chr12	133851895	3419694	0.0255	0.1742
chr13	115169878	3344243	0.029	0.1817
chr14	107349540	5444662	0.0507	0.2822
chr15	102531392	1034054	0.0101	0.11
chr16	90354753	2137393	0.0237	0.2002
chr17	81195210	2190386	0.027	0.197
chr18	78077248	2890920	0.037	0.5738
chr19	59128983	1543063	0.0261	0.4516
chr20	63025520	2797824	0.0444	0.2331
chr21	48129895	1592755	0.0331	0.2015
chr22	51304566	815476	0.0159	0.1342
chrMT	16571	89934	5.4272	3.8117
chrX	155270560	5338446	0.0344	0.2175
chrY	59373566	247529	0.0042	0.0923

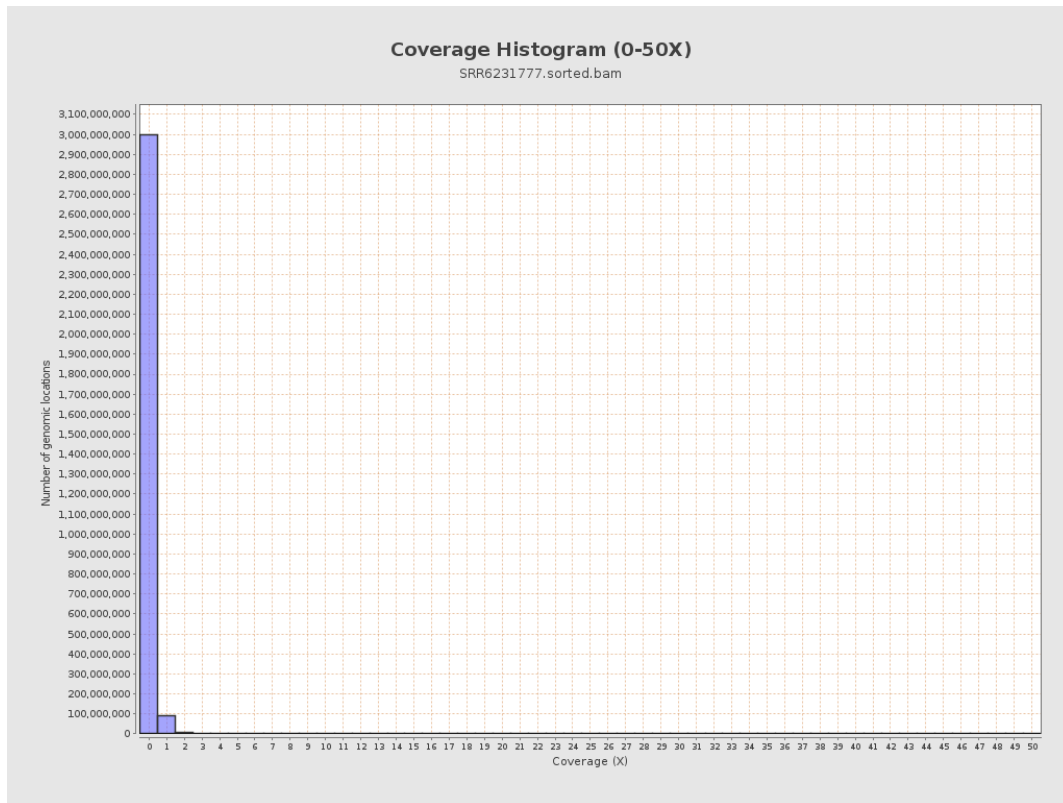
3. Results : Coverage across reference



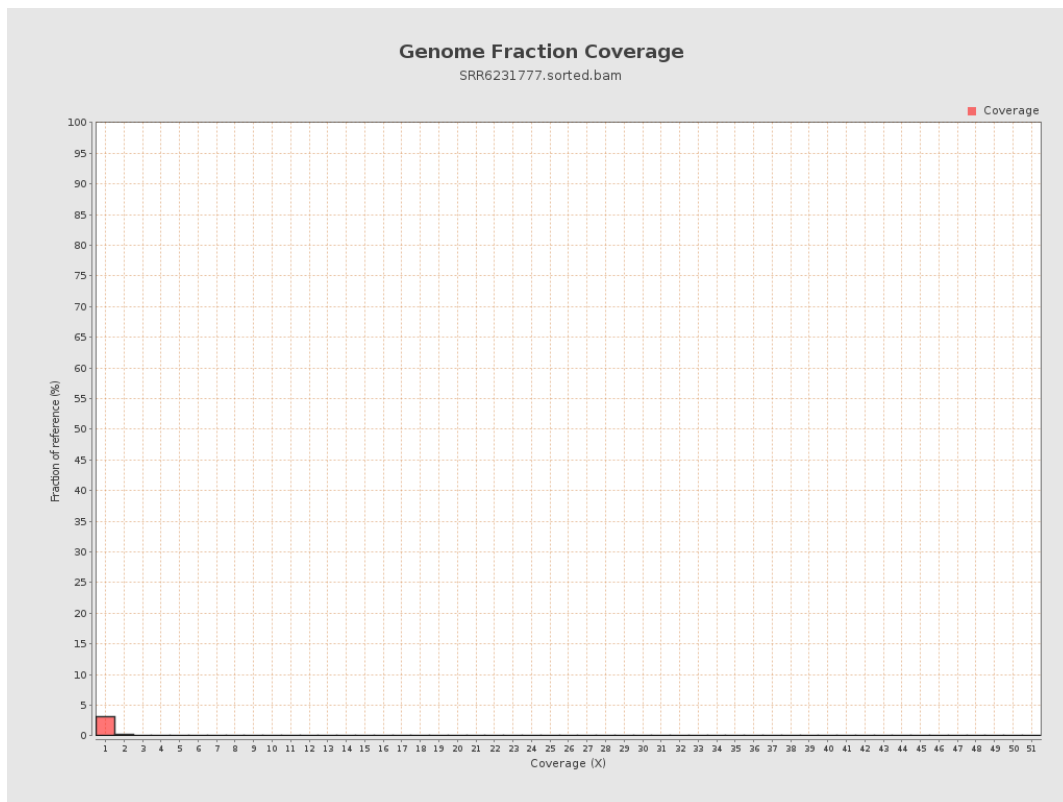
4. Results : Coverage Histogram



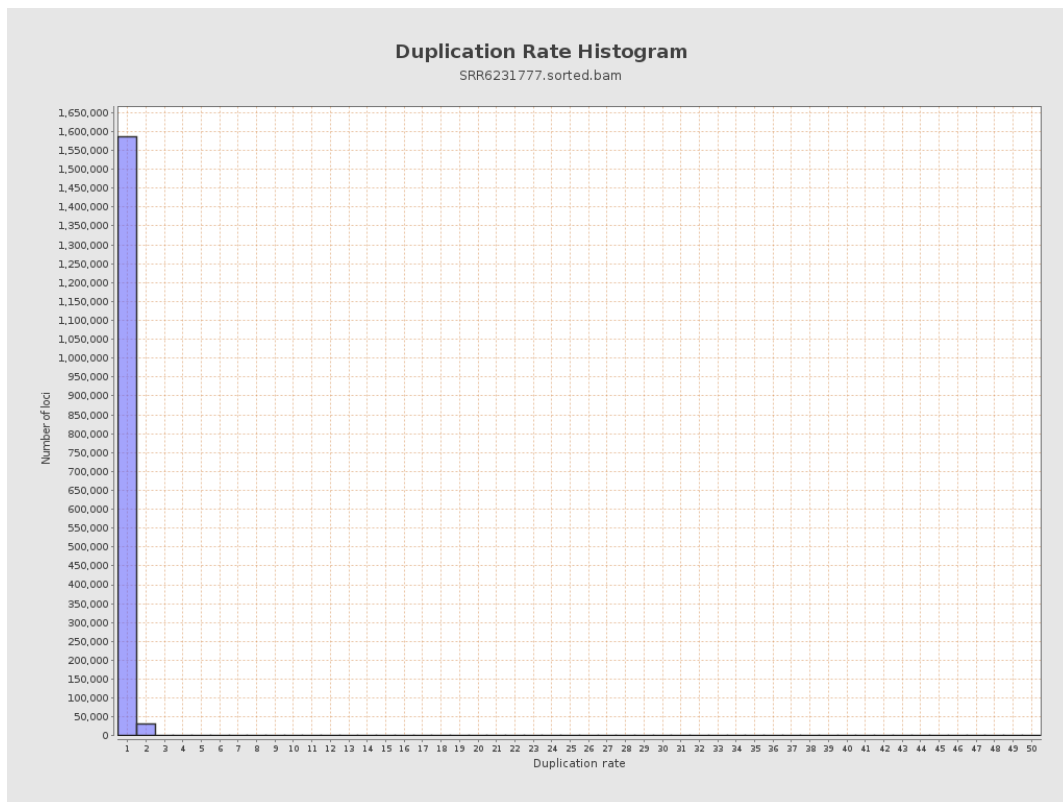
5. Results : Coverage Histogram (0-50X)



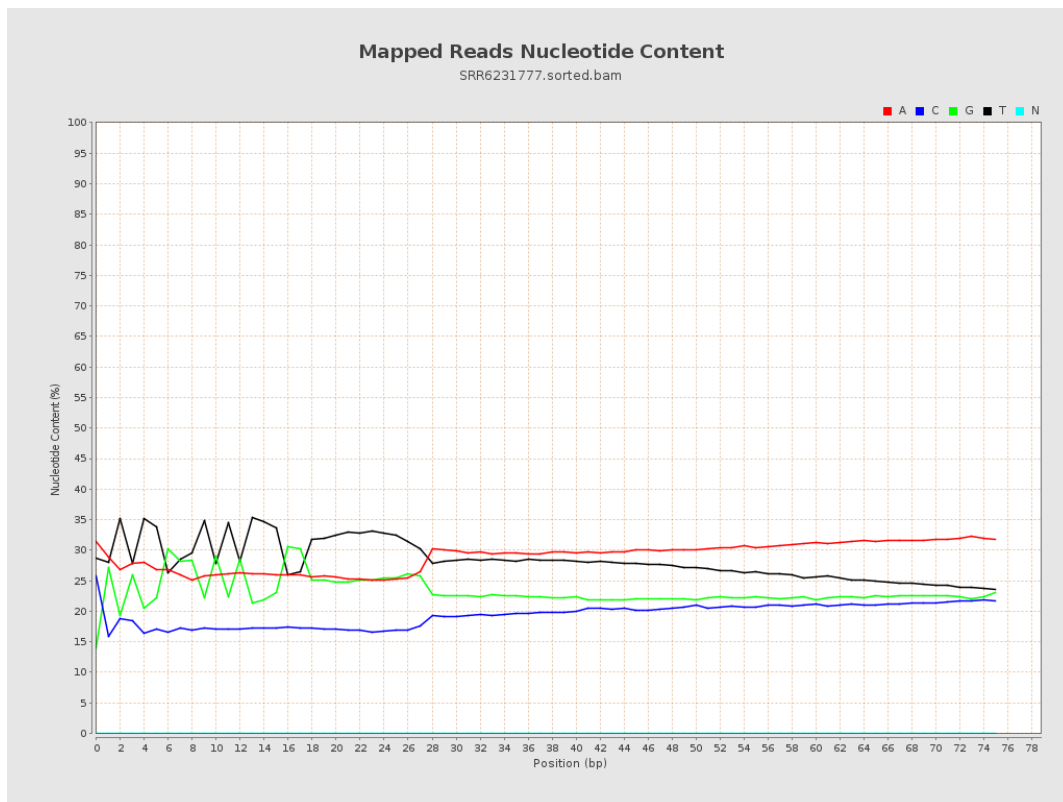
6. Results : Genome Fraction Coverage



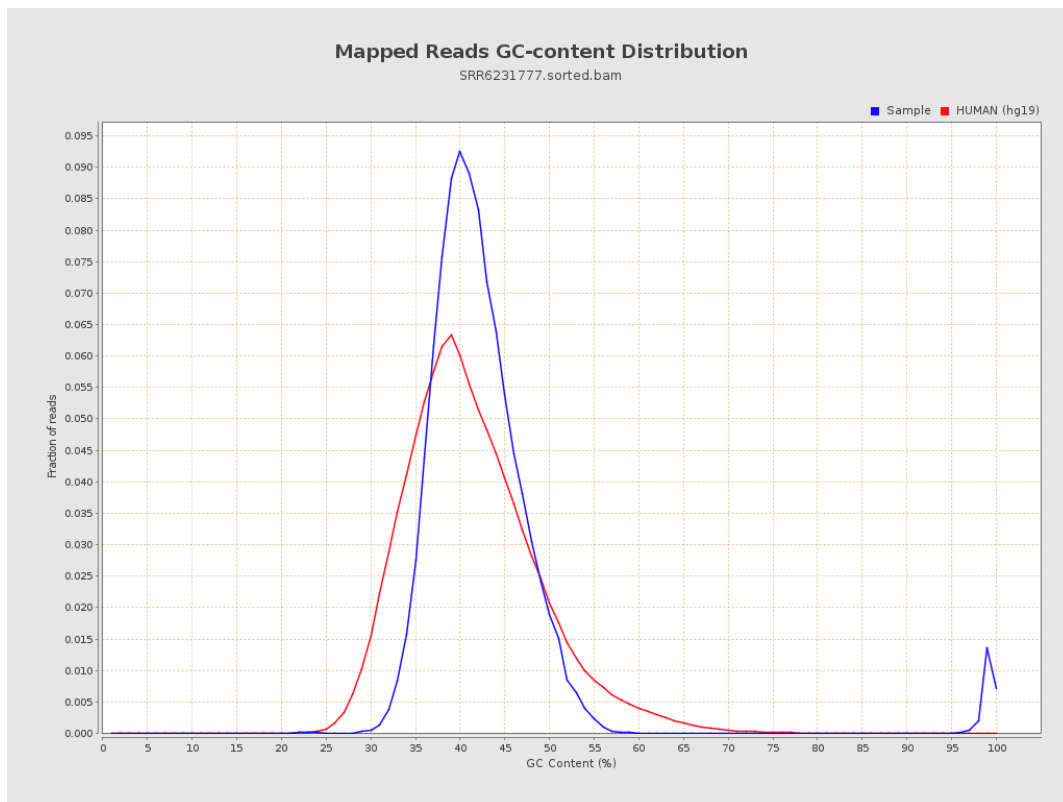
7. Results : Duplication Rate Histogram



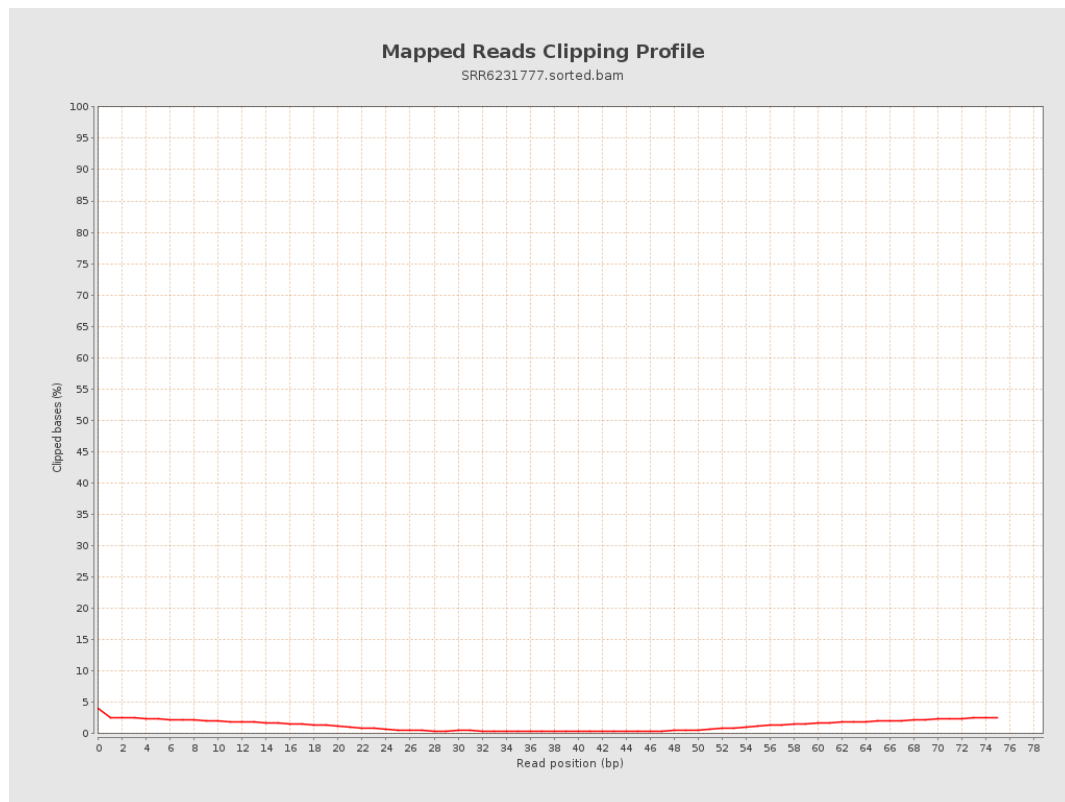
8. Results : Mapped Reads Nucleotide Content



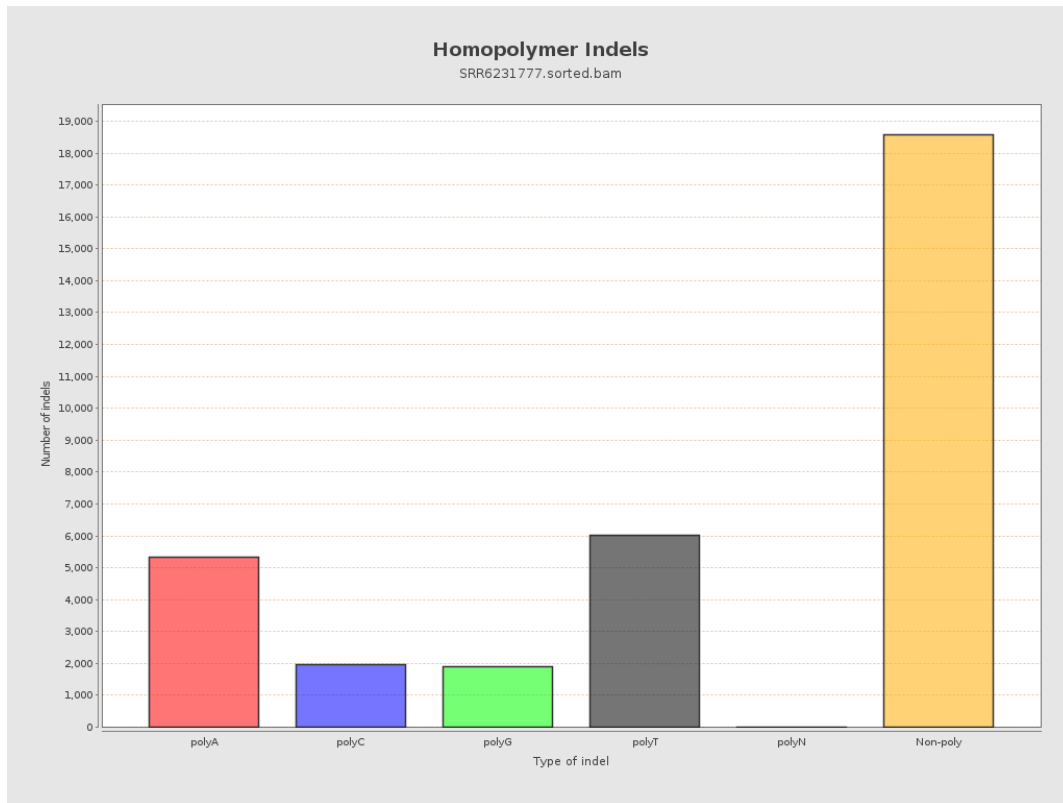
9. Results : Mapped Reads GC-content Distribution



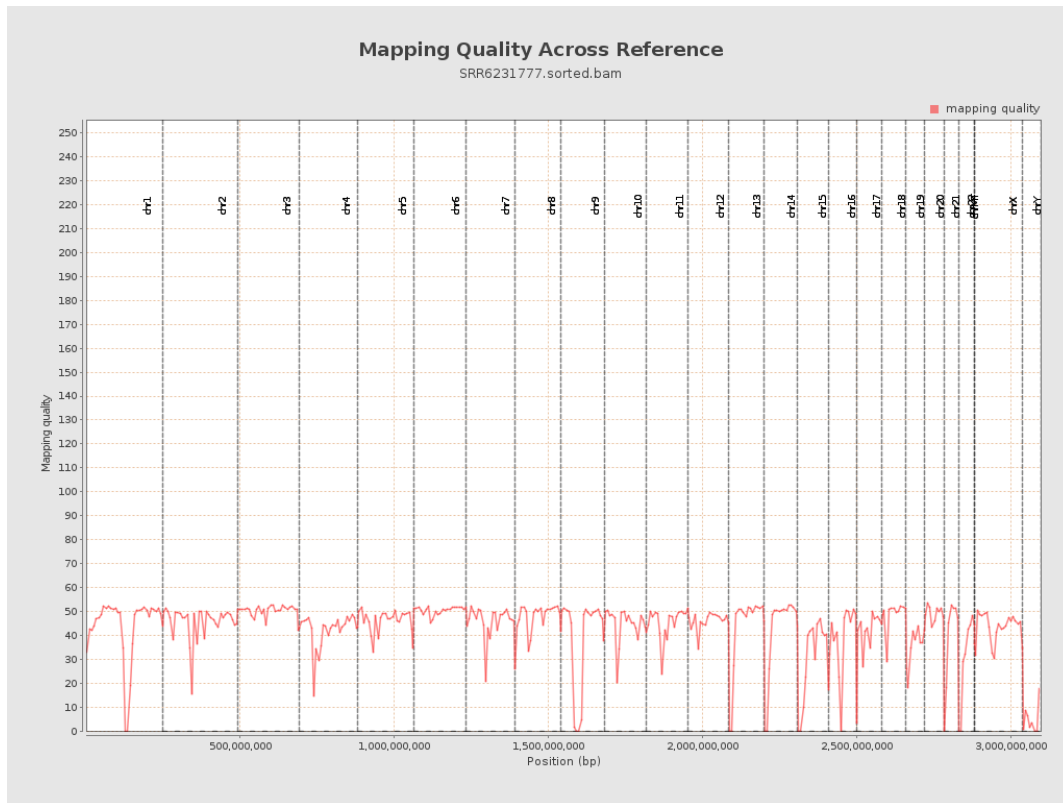
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

