Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 01:26:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238661.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_SRR6238661 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238661.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 01:26:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238661.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,931,813
Mapped reads	2,654,627 / 90.55%
Unmapped reads	277,186 / 9.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,591 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	938,626 / 32.02%
Duplication rate	21.4%
Clipped reads	1,732,880 / 59.11%

2.2. ACGT Content

Number/percentage of A's	39,594,370 / 24.27%
Number/percentage of C's	28,688,910 / 17.58%
Number/percentage of T's	54,900,985 / 33.65%
Number/percentage of G's	39,979,696 / 24.5%
Number/percentage of N's	7,906 / 0%
GC Percentage	42.08%

2.3. Coverage

Mean	0.0527

Standard Deviation	0.8183

2.4. Mapping Quality

Mean Mapping Quality	36.64

2.5. Mismatches and indels

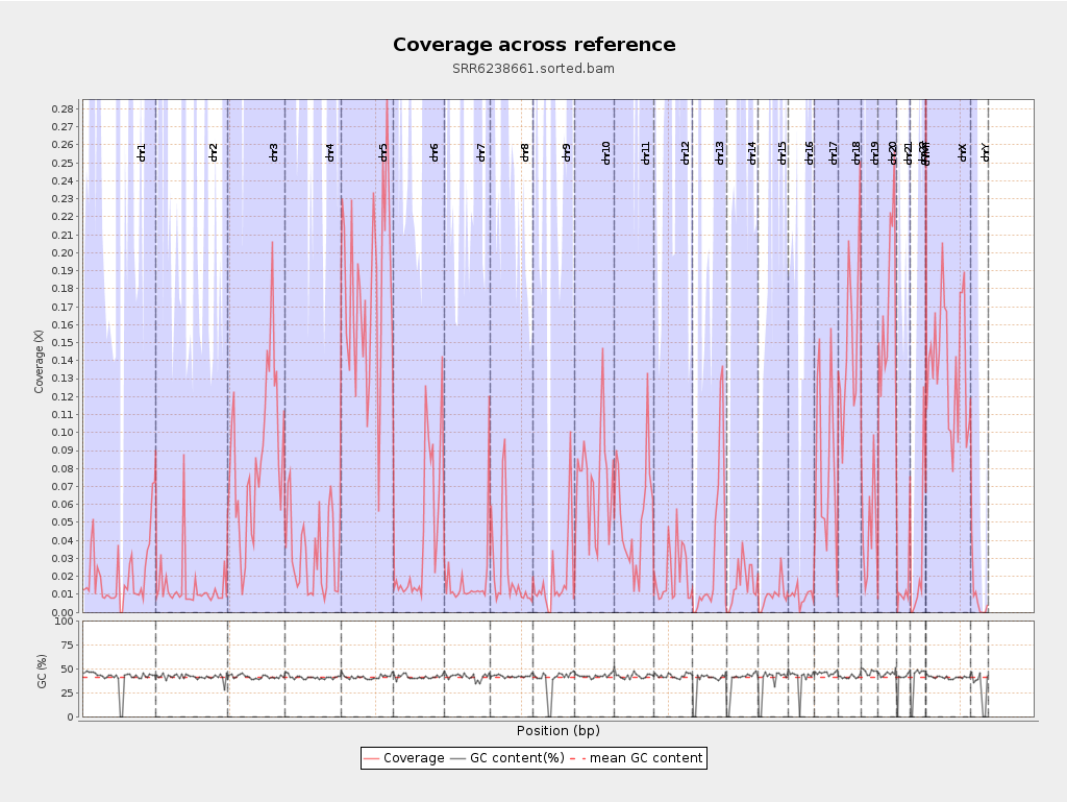
General error rate	0.57%
Mismatches	920,348
Insertions	10,152
Mapped reads with at least one insertion	0.38%
Deletions	41,589
Mapped reads with at least one deletion	1.55%
Homopolymer indels	41.7%

2.6. Chromosome stats

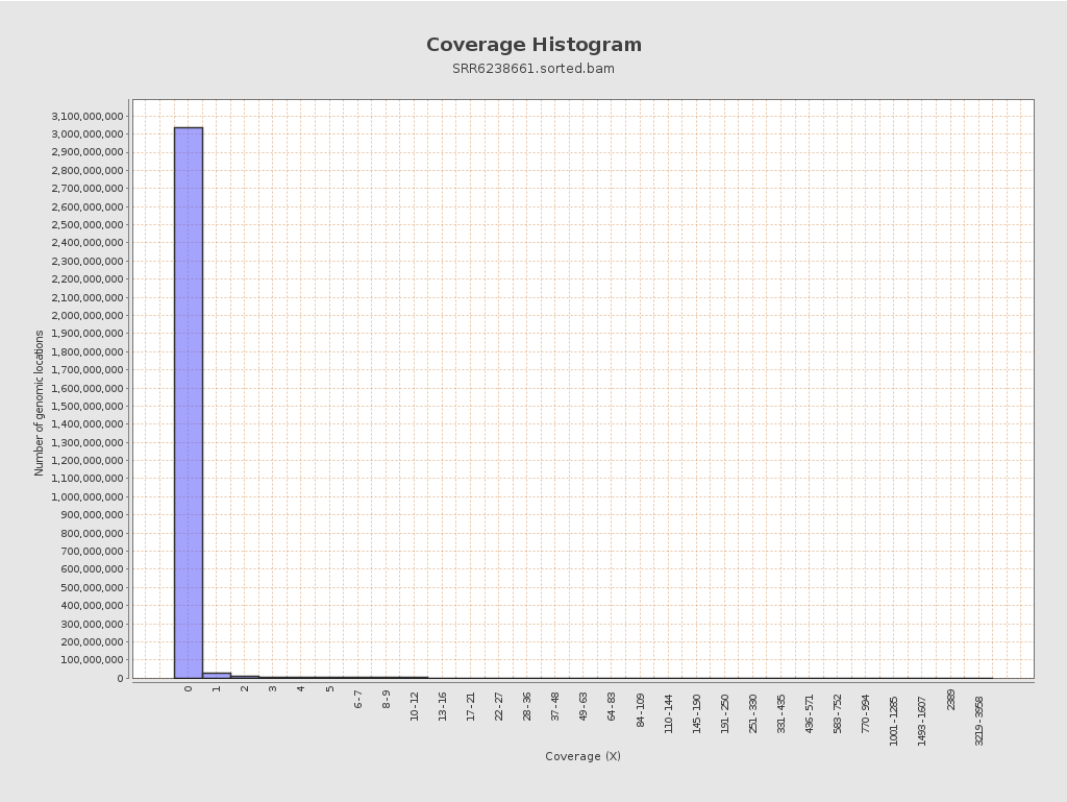
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	5281250	0.0212	0.6171
chr2	243199373	3344861	0.0138	1.8511
chr3	198022430	16822901	0.085	0.6879
chr4	191154276	6488184	0.0339	0.4165
chr5	180915260	31941522	0.1766	1.0156
chr6	171115067	7134080	0.0417	0.7311
chr7	159138663	2960436	0.0186	0.4057

chr8	146364022	3261883	0.0223	0.5828
chr9	141213431	2581138	0.0183	0.4878
chr10	135534747	9896665	0.073	0.6707
chr11	135006516	7162869	0.0531	0.539
chr12	133851895	2875210	0.0215	0.3286
chr13	115169878	3935687	0.0342	0.55
chr14	107349540	1734062	0.0162	0.2859
chr15	102531392	944456	0.0092	0.4021
chr16	90354753	806486	0.0089	0.2135
chr17	81195210	6795258	0.0837	0.7037
chr18	78077248	11450976	0.1467	1.4617
chr19	59128983	2617592	0.0443	0.6514
chr20	63025520	11009547	0.1747	1.05
chr21	48129895	736874	0.0153	0.2747
chr22	51304566	1430229	0.0279	0.402
chrMT	16571	5468	0.33	0.7915
chrX	155270560	21546611	0.1388	0.8961
chrY	59373566	476979	0.008	0.2943

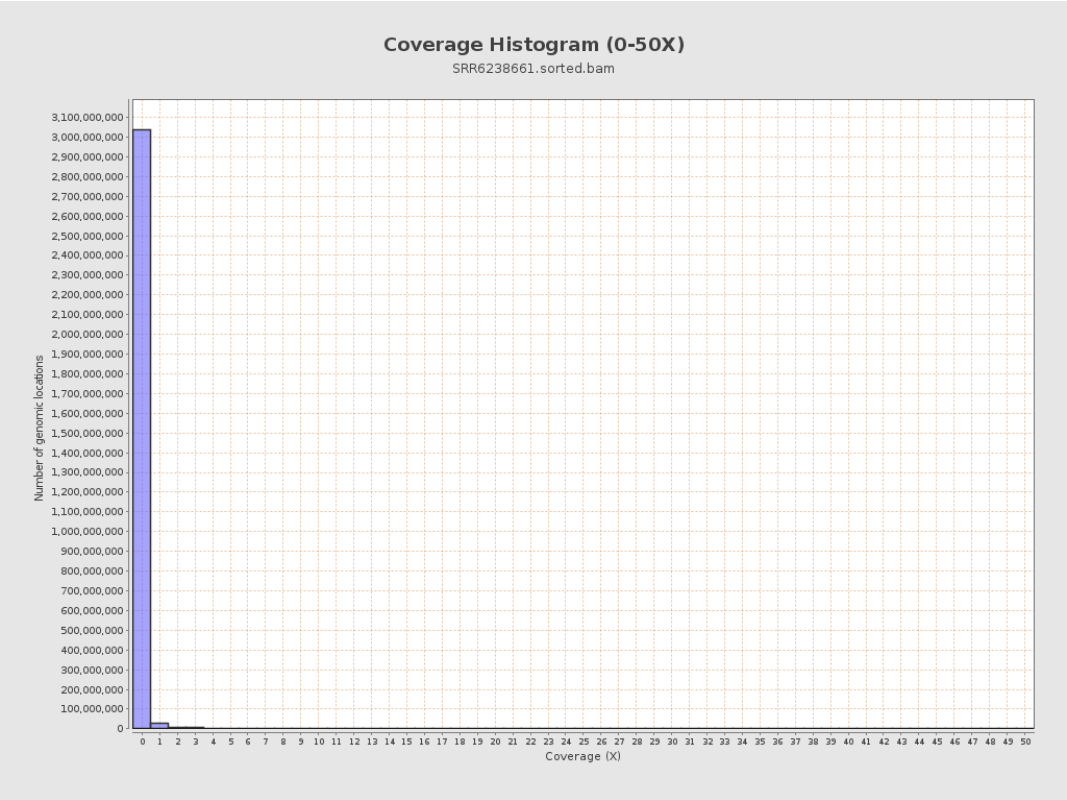
3. Results : Coverage across reference



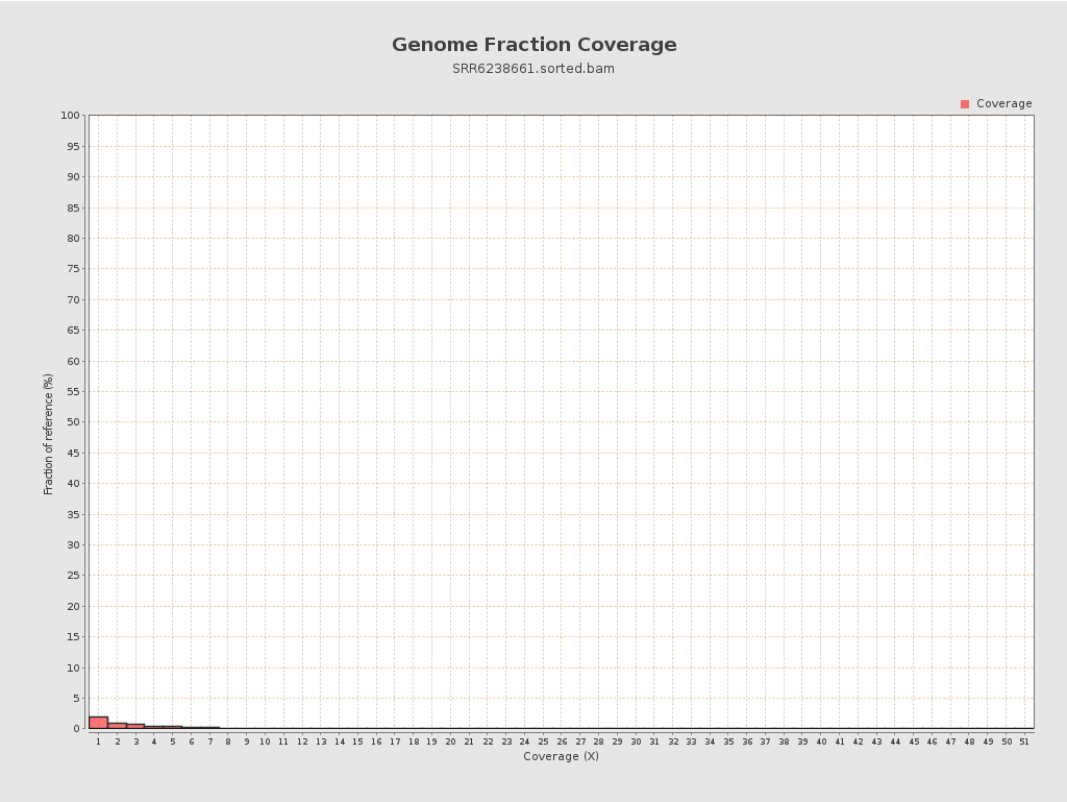
4. Results : Coverage Histogram



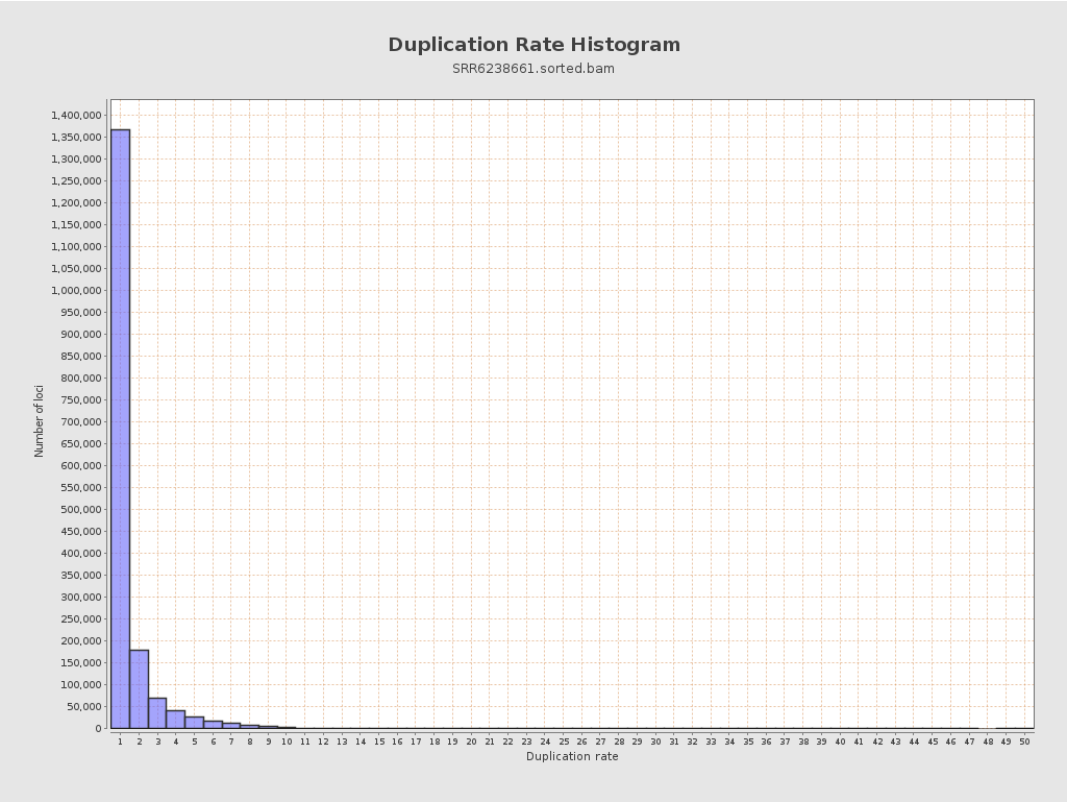
5. Results : Coverage Histogram (0-50X)



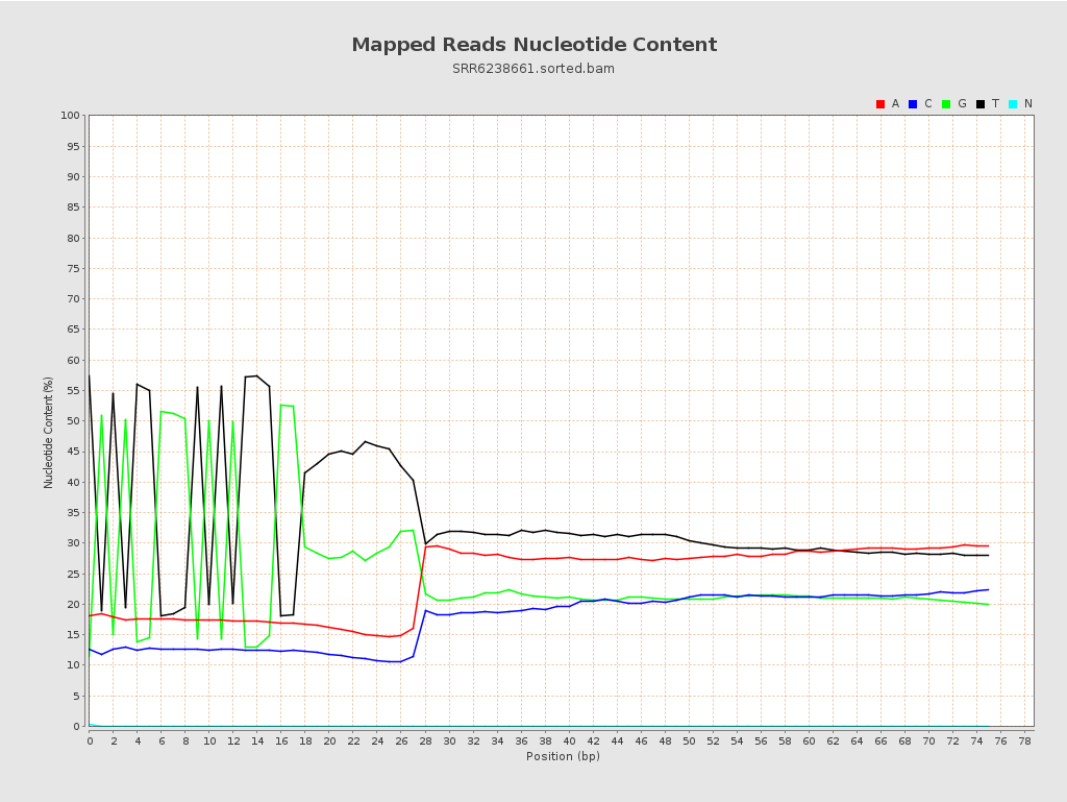
6. Results : Genome Fraction Coverage



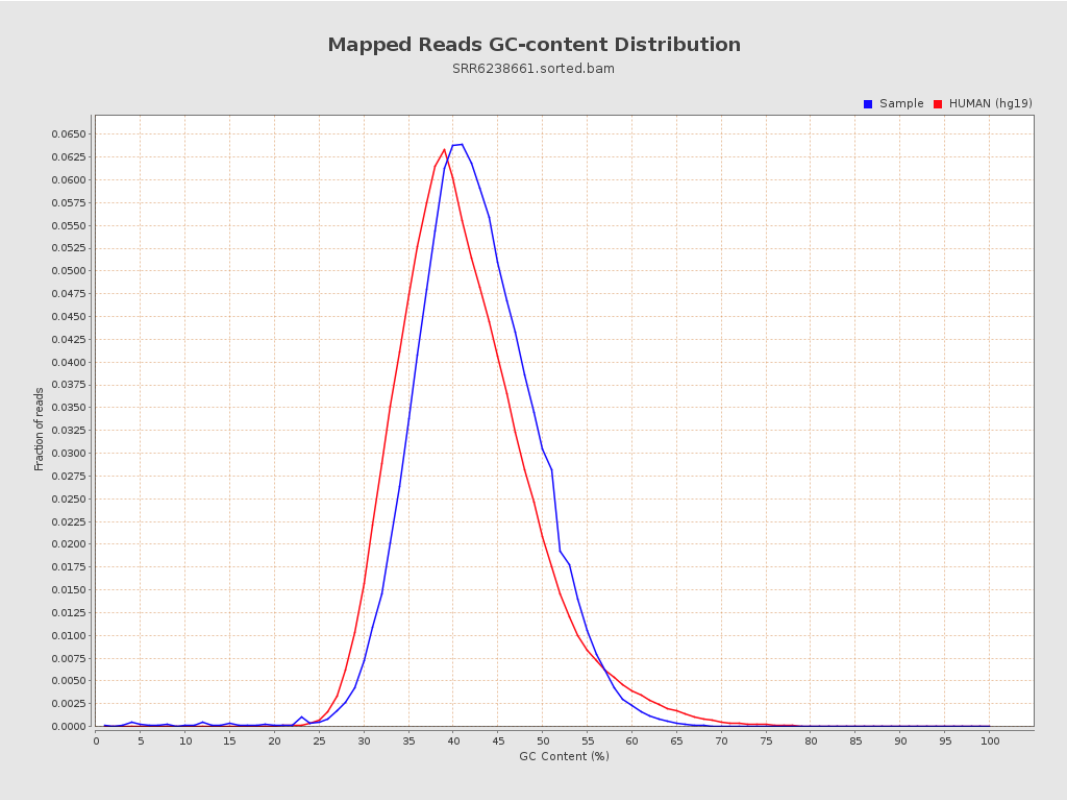
7. Results : Duplication Rate Histogram



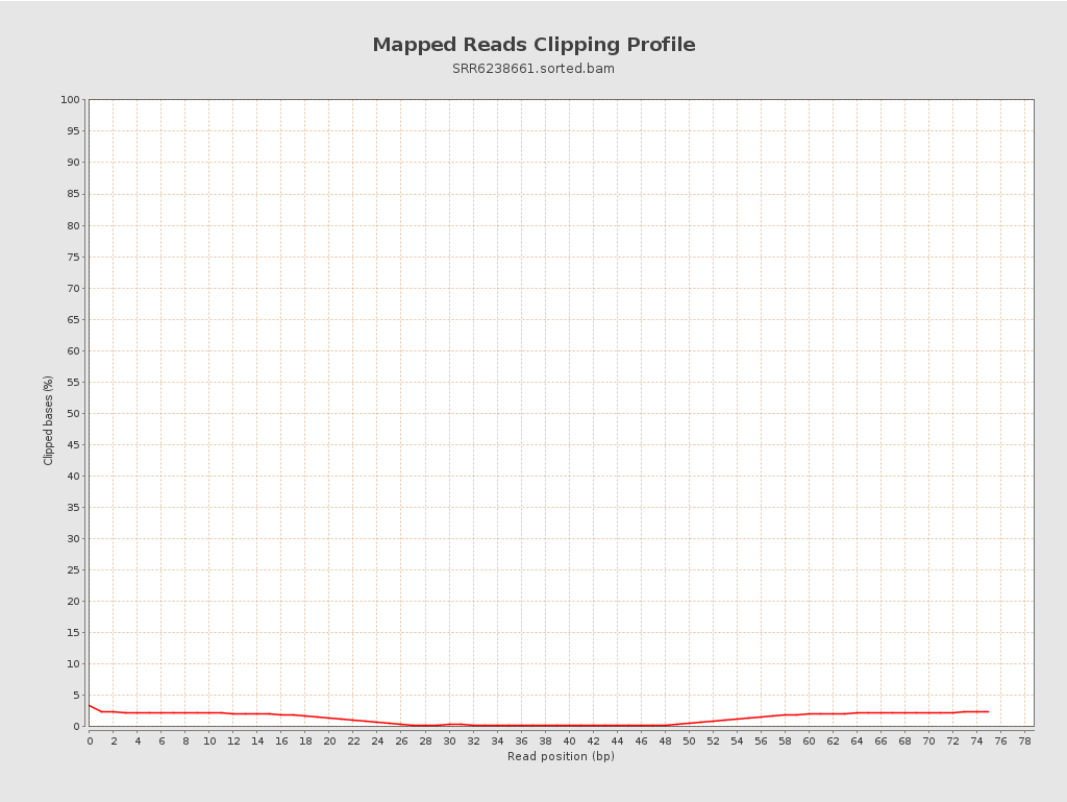
8. Results : Mapped Reads Nucleotide Content



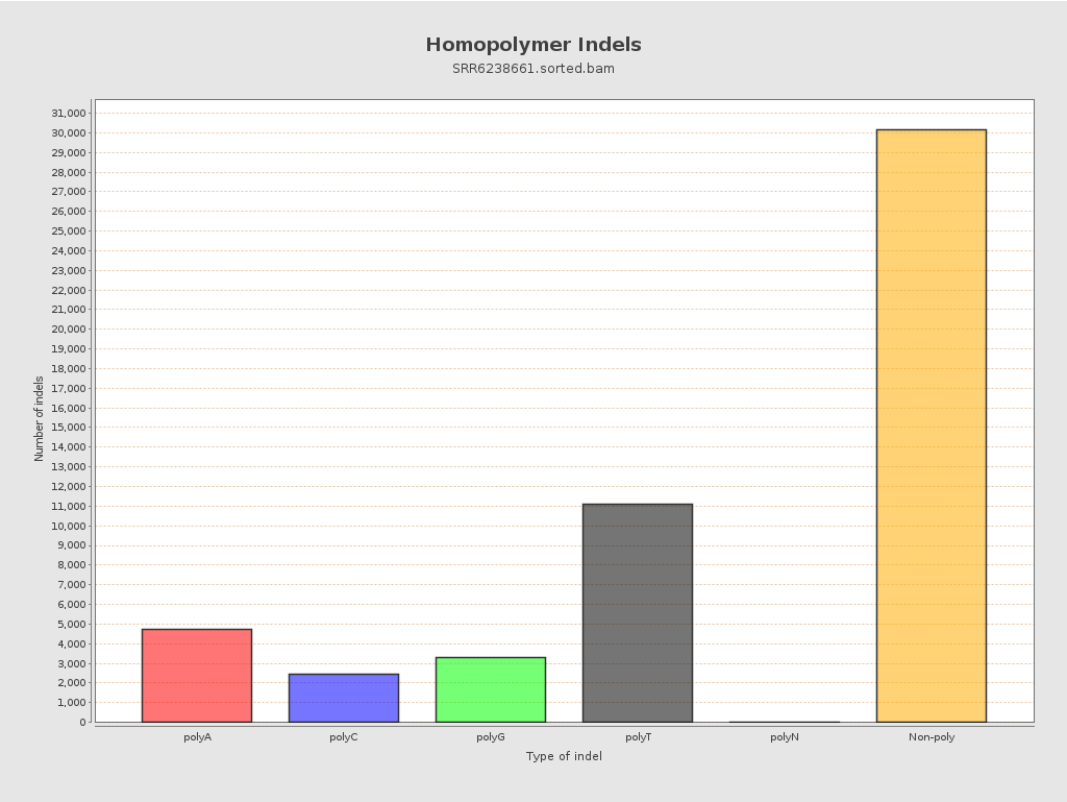
9. Results : Mapped Reads GC-content Distribution



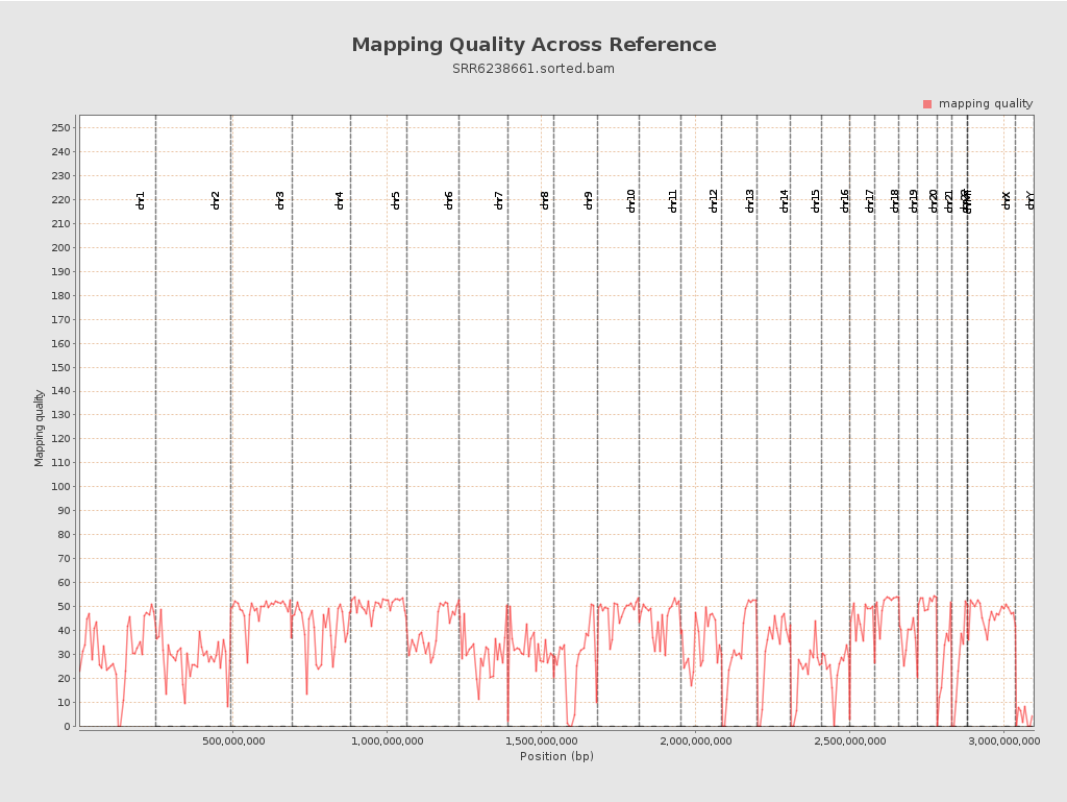
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram