Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:24:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238533.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_SRR6238533 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238533.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:24:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238533.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,013,783
Mapped reads	2,746,267 / 91.12%
Unmapped reads	267,516 / 8.88%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,801 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	201,947 / 6.7%
Duplication rate	5.55%
Clipped reads	1,748,229 / 58.01%

2.2. ACGT Content

Number/percentage of A's	41,085,149 / 24.29%
Number/percentage of C's	30,631,531 / 18.11%
Number/percentage of T's	55,234,417 / 32.66%
Number/percentage of G's	42,158,773 / 24.93%
Number/percentage of N's	11,599 / 0.01%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0547

Standard Deviation	0.678

2.4. Mapping Quality

Mean Mapping Quality	41.06

2.5. Mismatches and indels

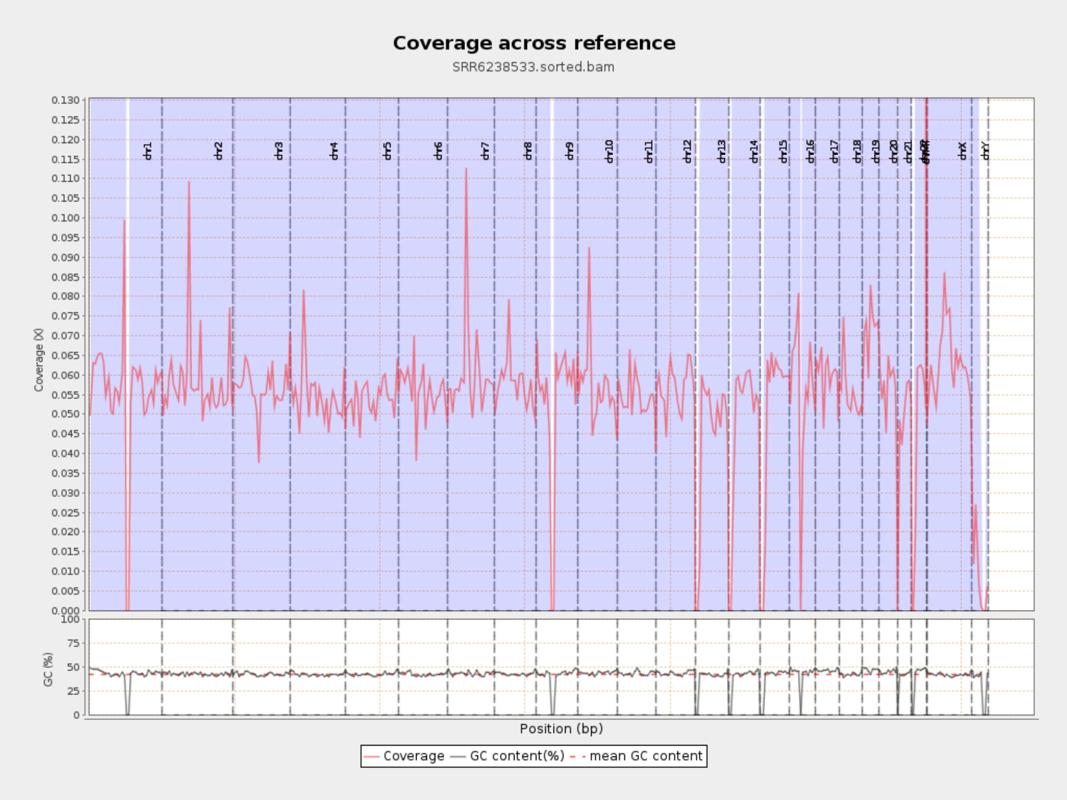
General error rate	0.59%
Mismatches	972,086
Insertions	13,210
Mapped reads with at least one insertion	0.48%
Deletions	44,294
Mapped reads with at least one deletion	1.6%
Homopolymer indels	41.34%

2.6. Chromosome stats

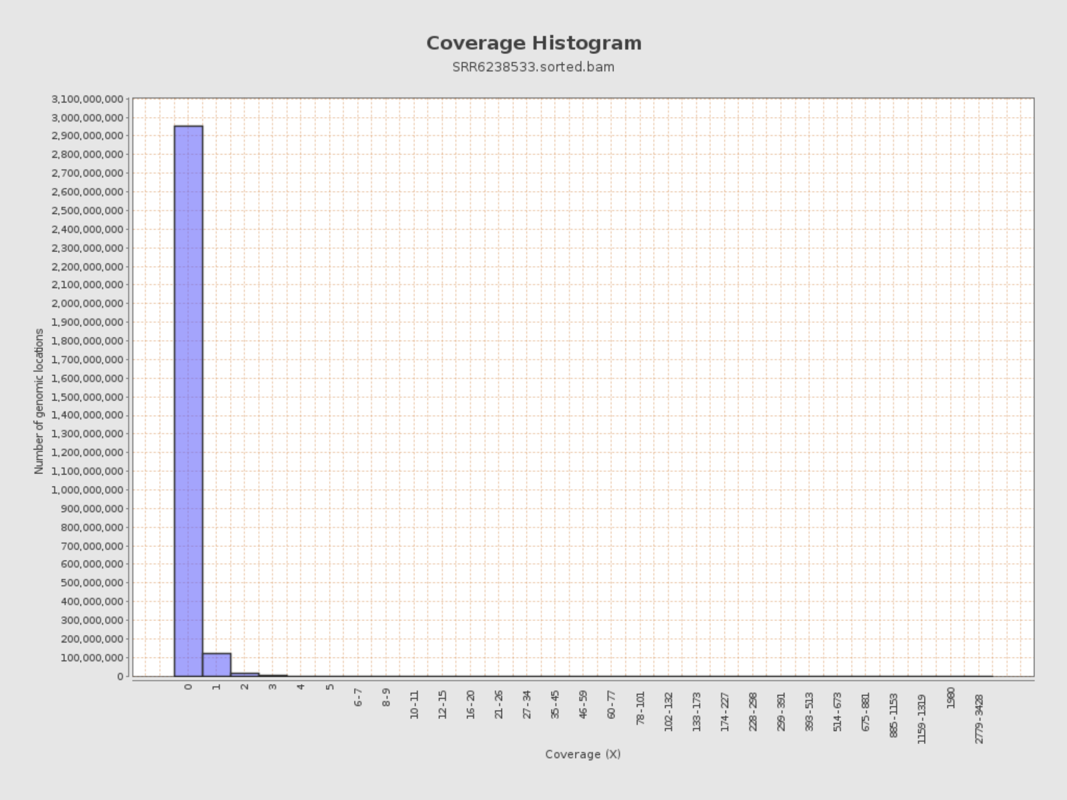
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13830369	0.0555	1.0639
chr2	243199373	14201560	0.0584	1.5433
chr3	198022430	11163898	0.0564	0.2913
chr4	191154276	10432971	0.0546	0.313
chr5	180915260	9771754	0.054	0.2856
chr6	171115067	9582325	0.056	0.5044
chr7	159138663	9619589	0.0604	0.8877

chr8	146364022	8466184	0.0578	0.4603
chr9	141213431	7392588	0.0524	0.4676
chr10	135534747	7724231	0.057	0.4675
chr11	135006516	7333665	0.0543	0.4301
chr12	133851895	7637286	0.0571	0.2967
chr13	115169878	5020205	0.0436	0.3515
chr14	107349540	5088323	0.0474	0.2916
chr15	102531392	5041016	0.0492	0.3765
chr16	90354753	5066338	0.0561	0.3605
chr17	81195210	4855419	0.0598	0.3182
chr18	78077248	4367288	0.0559	1.0718
chr19	59128983	4220613	0.0714	0.6951
chr20	63025520	3569657	0.0566	0.3099
chr21	48129895	2246897	0.0467	0.3085
chr22	51304566	2128338	0.0415	0.2365
chrMT	16571	73602	4.4416	3.6221
chrX	155270560	9819854	0.0632	0.3583
chrY	59373566	545030	0.0092	0.2508

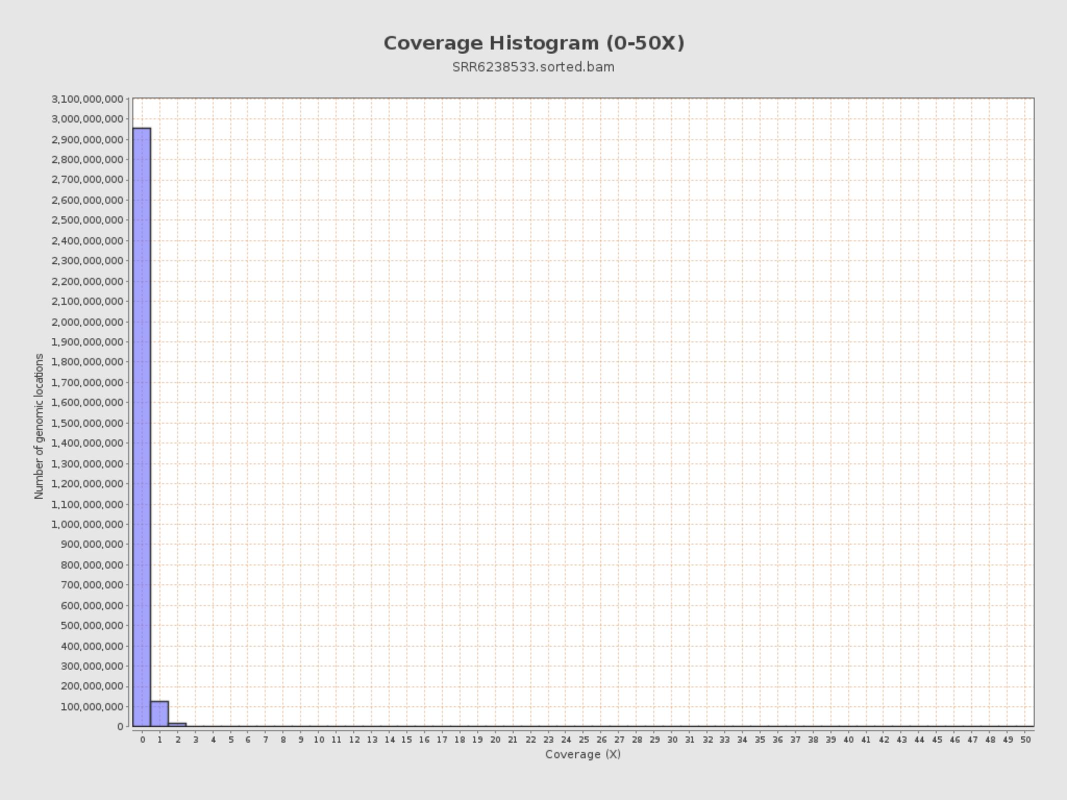
3. Results : Coverage across reference



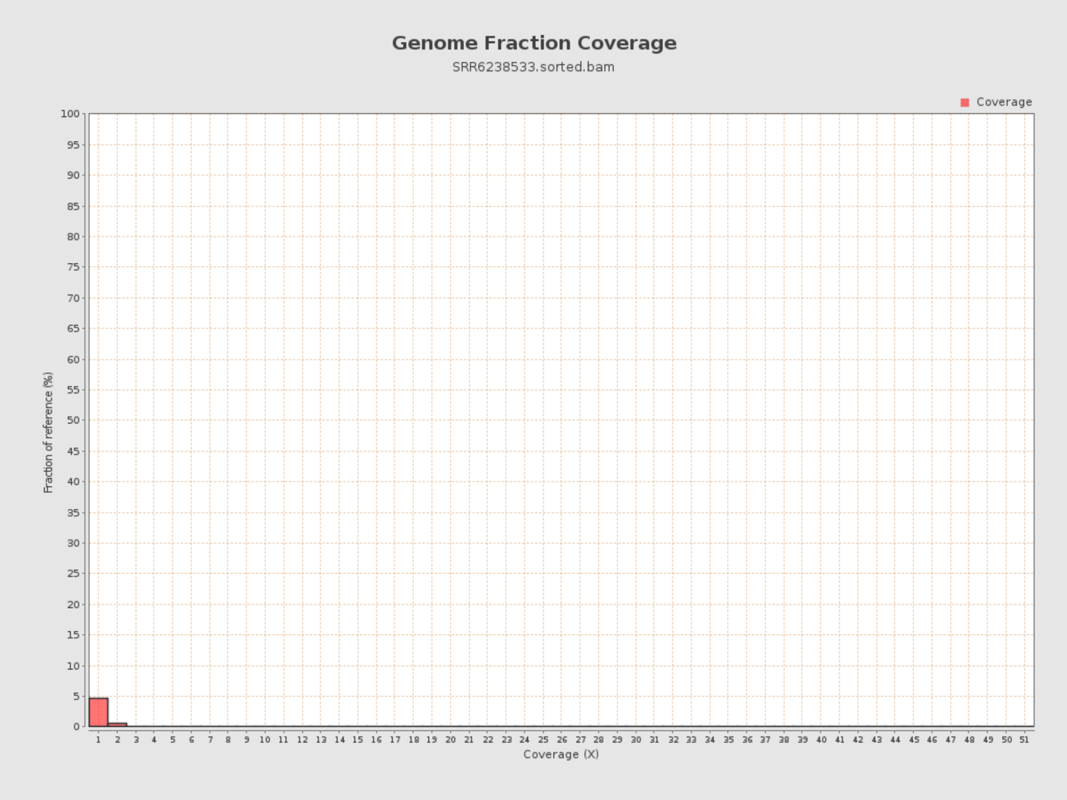
4. Results : Coverage Histogram



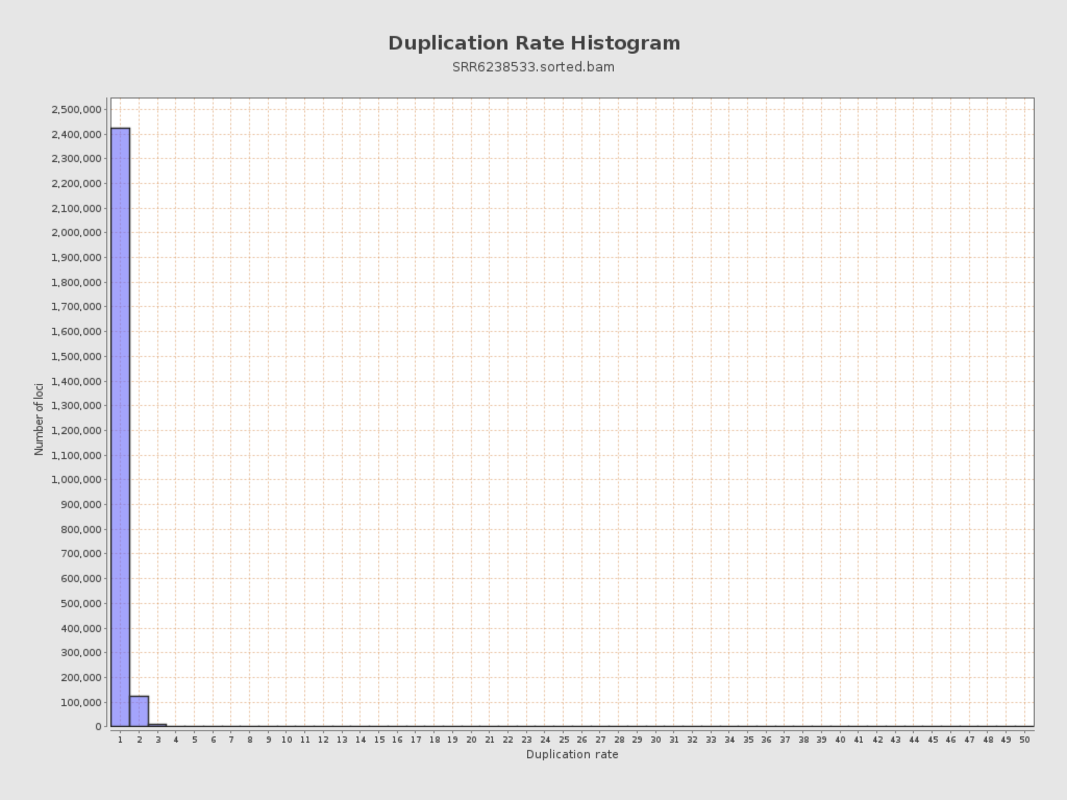
5. Results : Coverage Histogram (0-50X)



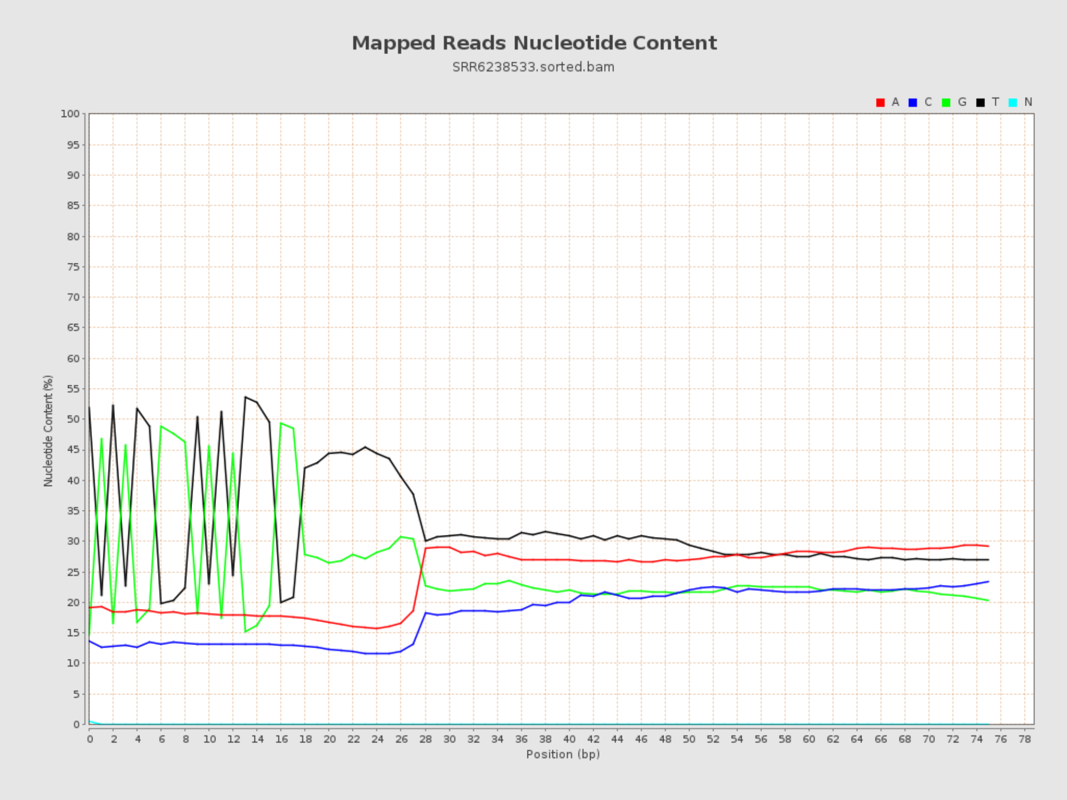
6. Results : Genome Fraction Coverage



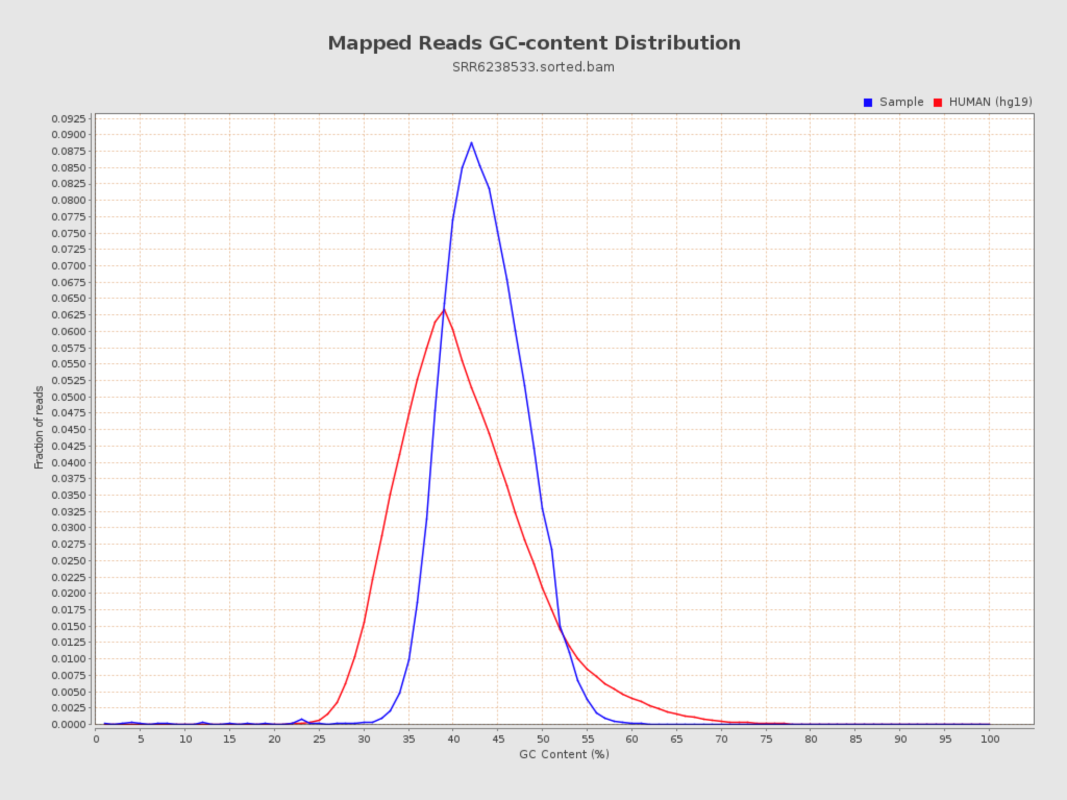
7. Results : Duplication Rate Histogram



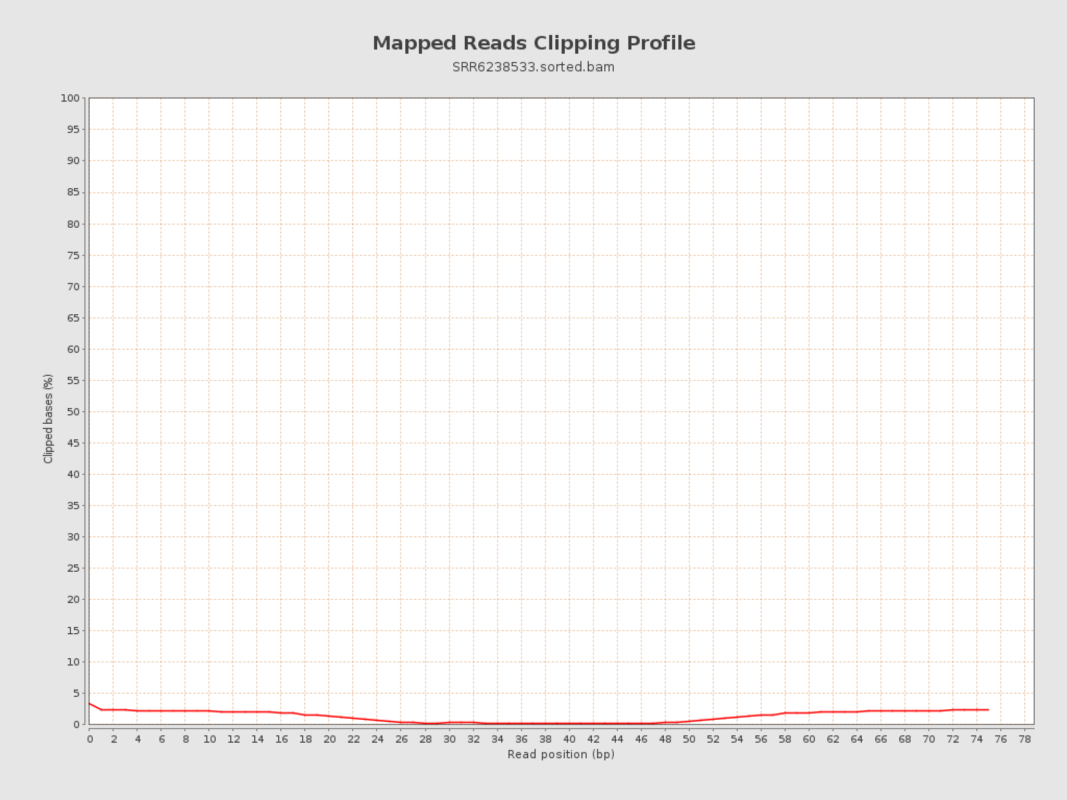
8. Results : Mapped Reads Nucleotide Content



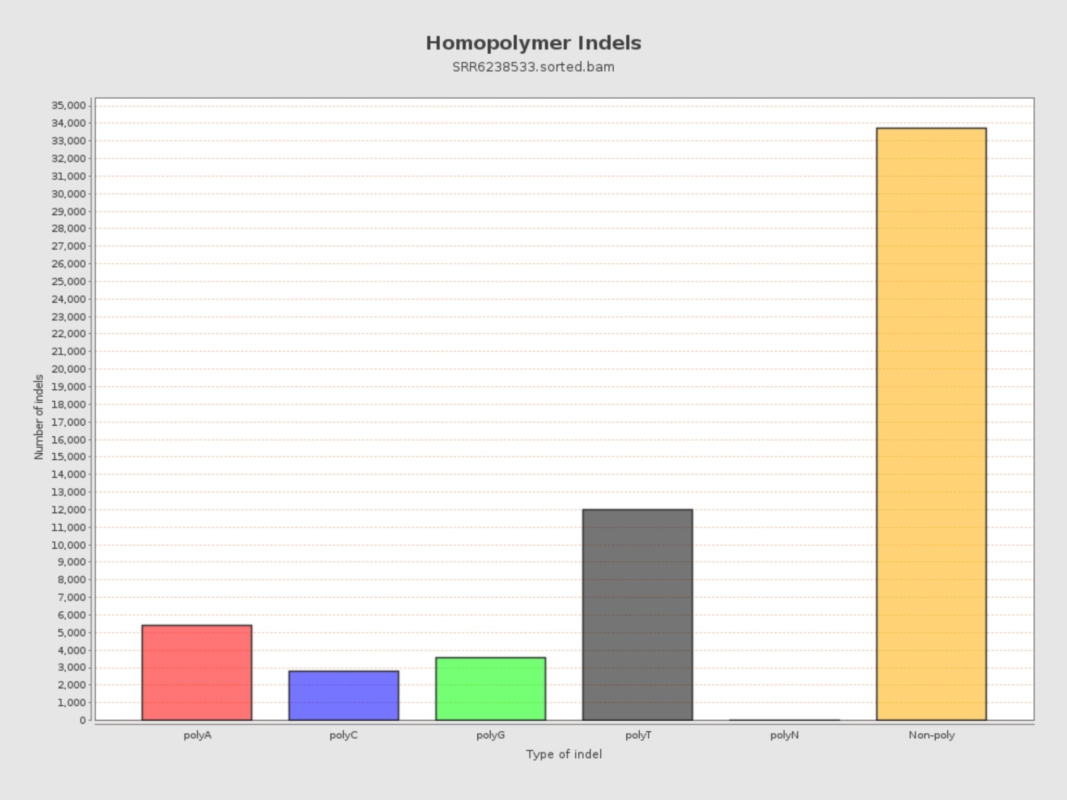
9. Results : Mapped Reads GC-content Distribution



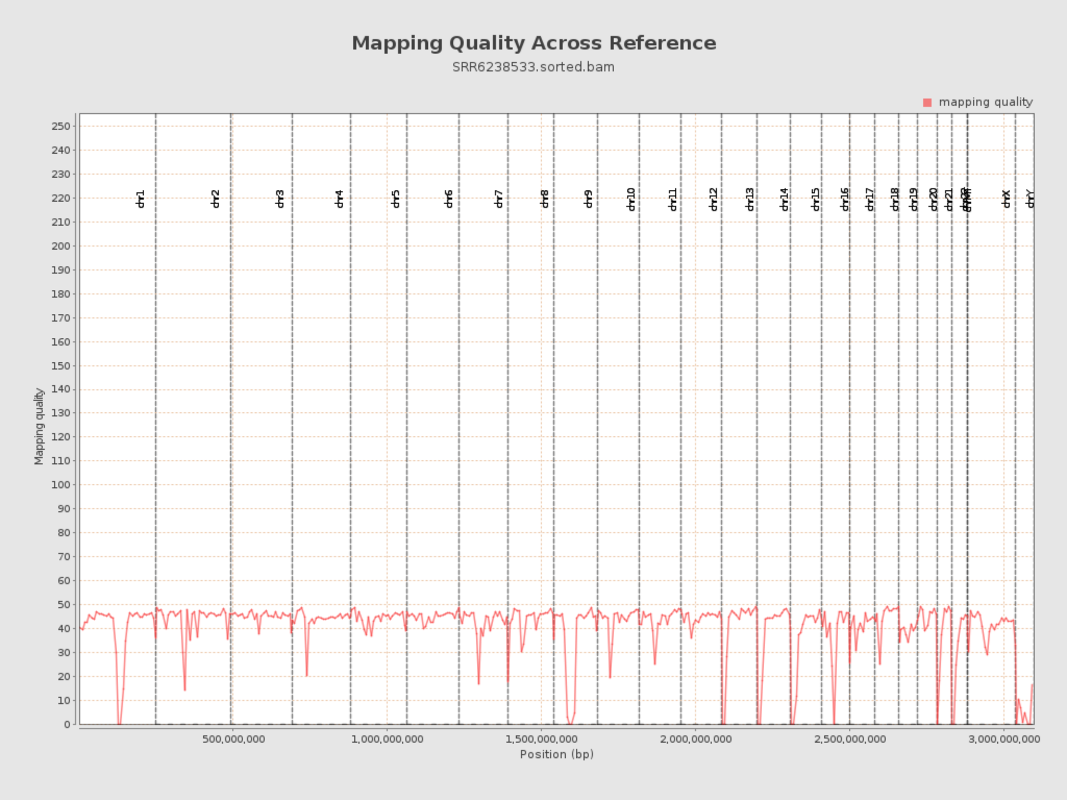
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram