Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:44:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238326.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_SRR6238326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238326.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:44:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,205,375
Mapped reads	2,001,939 / 90.78%
Unmapped reads	203,436 / 9.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,475 / 1.16%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	92,019 / 4.17%
Duplication rate	3.59%
Clipped reads	998,058 / 45.26%

2.2. ACGT Content

Number/percentage of A's	37,053,594 / 28.15%
Number/percentage of C's	24,553,746 / 18.66%
Number/percentage of T's	41,308,914 / 31.39%
Number/percentage of G's	28,653,536 / 21.77%
Number/percentage of N's	41,150 / 0.03%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0425

Standard Deviation	0.3924

2.4. Mapping Quality

Mean Mapping Quality	45.82

2.5. Mismatches and indels

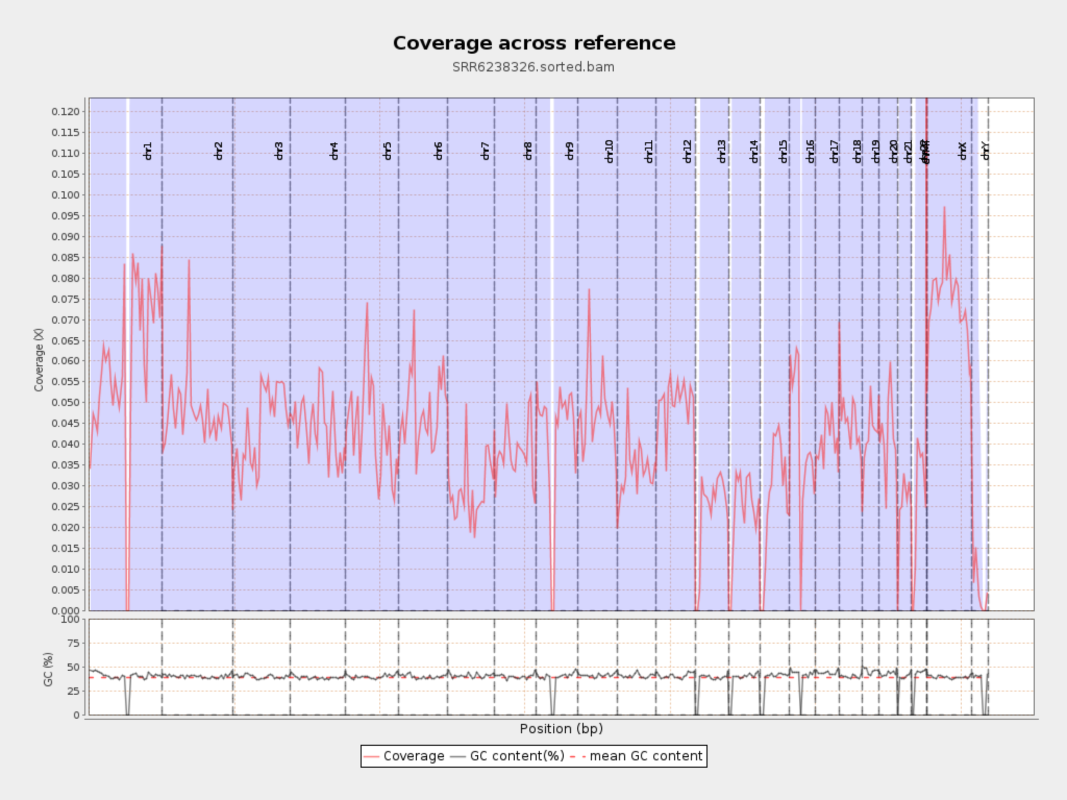
General error rate	0.84%
Mismatches	1,092,815
Insertions	9,613
Mapped reads with at least one insertion	0.48%
Deletions	38,036
Mapped reads with at least one deletion	1.88%
Homopolymer indels	46.06%

2.6. Chromosome stats

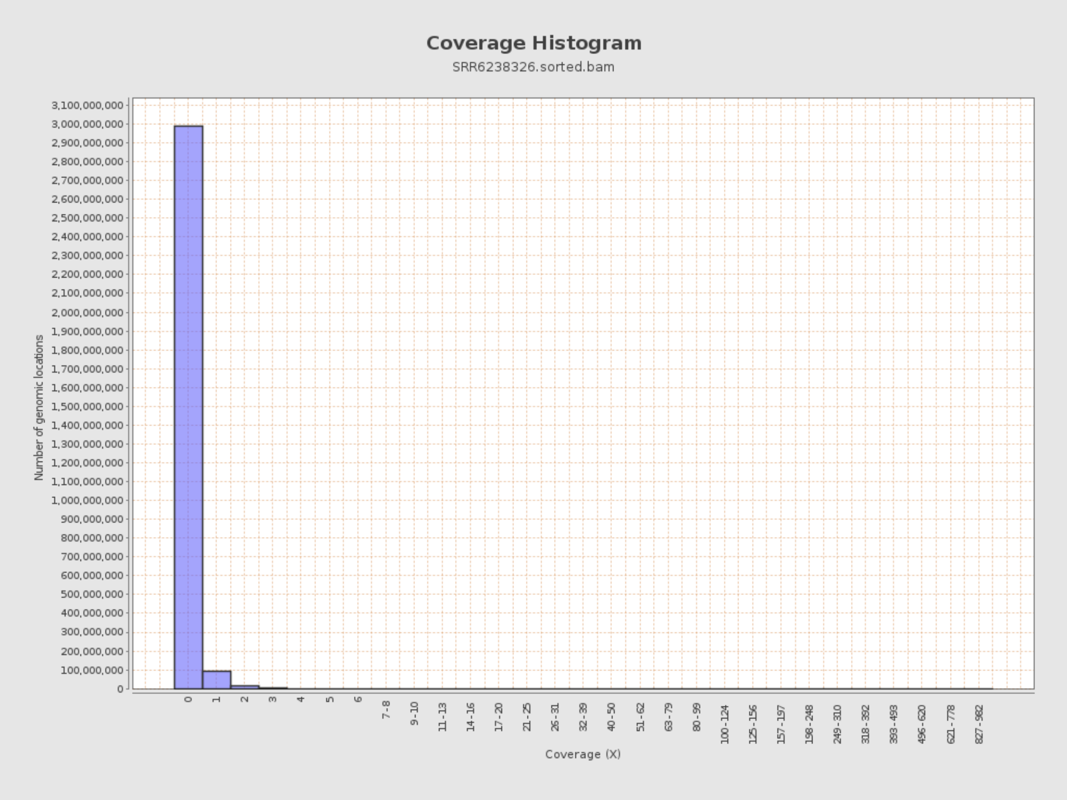
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14646037	0.0588	0.7711
chr2	243199373	11718417	0.0482	0.4395
chr3	198022430	8678557	0.0438	0.2426
chr4	191154276	8392267	0.0439	0.2599
chr5	180915260	7969961	0.0441	0.2455
chr6	171115067	8260160	0.0483	0.3378
chr7	159138663	4567329	0.0287	0.3437

chr8	146364022	5543748	0.0379	0.626
chr9	141213431	5845436	0.0414	0.3515
chr10	135534747	6561863	0.0484	0.3891
chr11	135006516	4584961	0.034	0.2784
chr12	133851895	6660029	0.0498	0.2665
chr13	115169878	2730829	0.0237	0.1781
chr14	107349540	2494274	0.0232	0.2211
chr15	102531392	2785533	0.0272	0.193
chr16	90354753	3702651	0.041	0.2589
chr17	81195210	3360002	0.0414	0.2509
chr18	78077248	3595032	0.046	0.5544
chr19	59128983	2516882	0.0426	0.5186
chr20	63025520	2650117	0.042	0.2467
chr21	48129895	1205500	0.025	0.2078
chr22	51304566	1264235	0.0246	0.1796
chrMT	16571	4576	0.2761	0.5964
chrX	155270560	11593865	0.0747	0.3565
chrY	59373566	344561	0.0058	0.1243

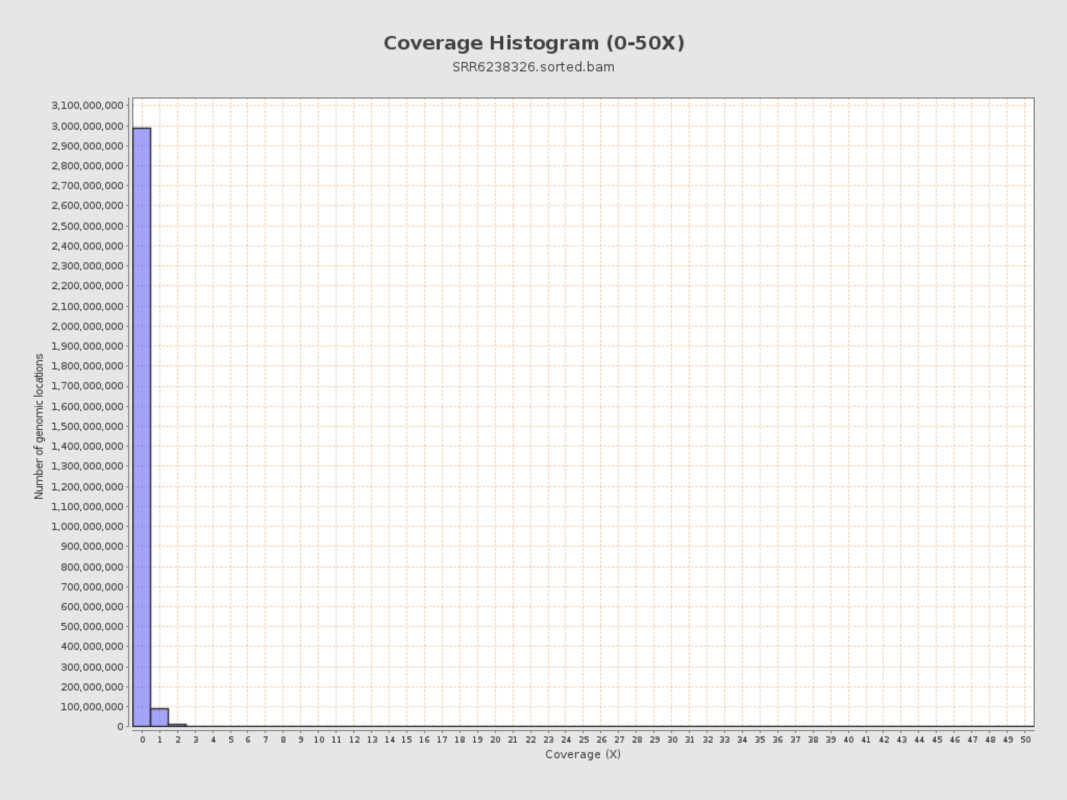
3. Results : Coverage across reference



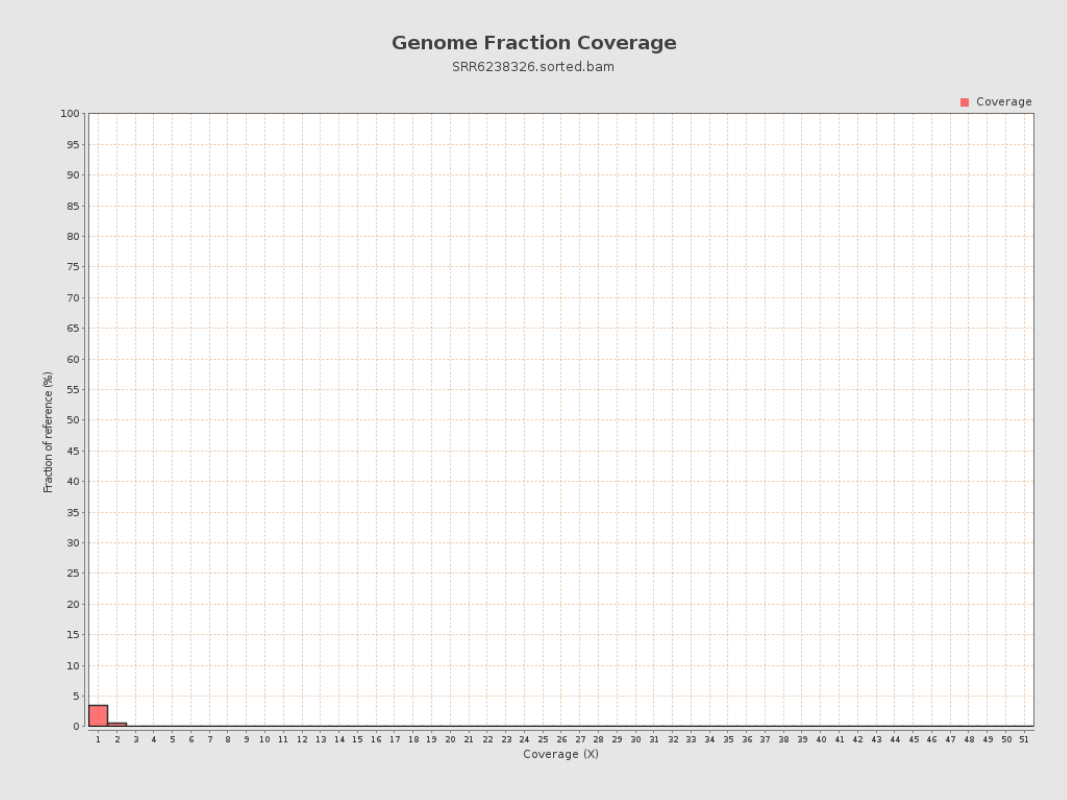
4. Results : Coverage Histogram



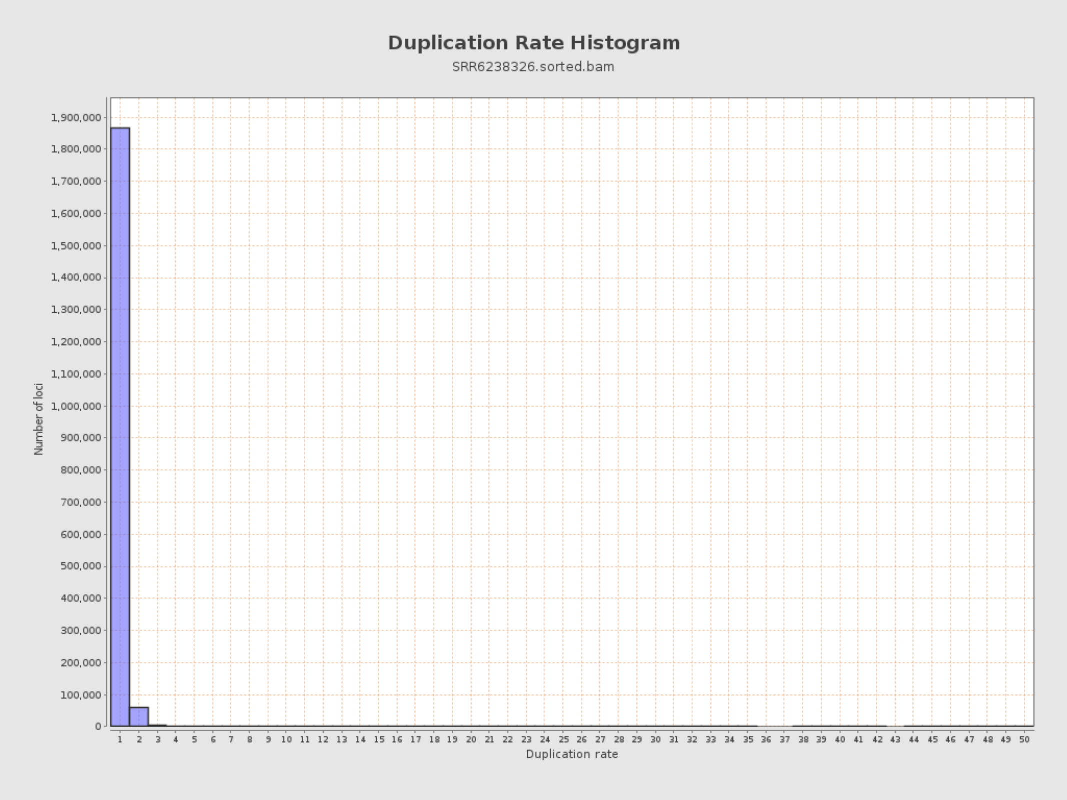
5. Results : Coverage Histogram (0-50X)



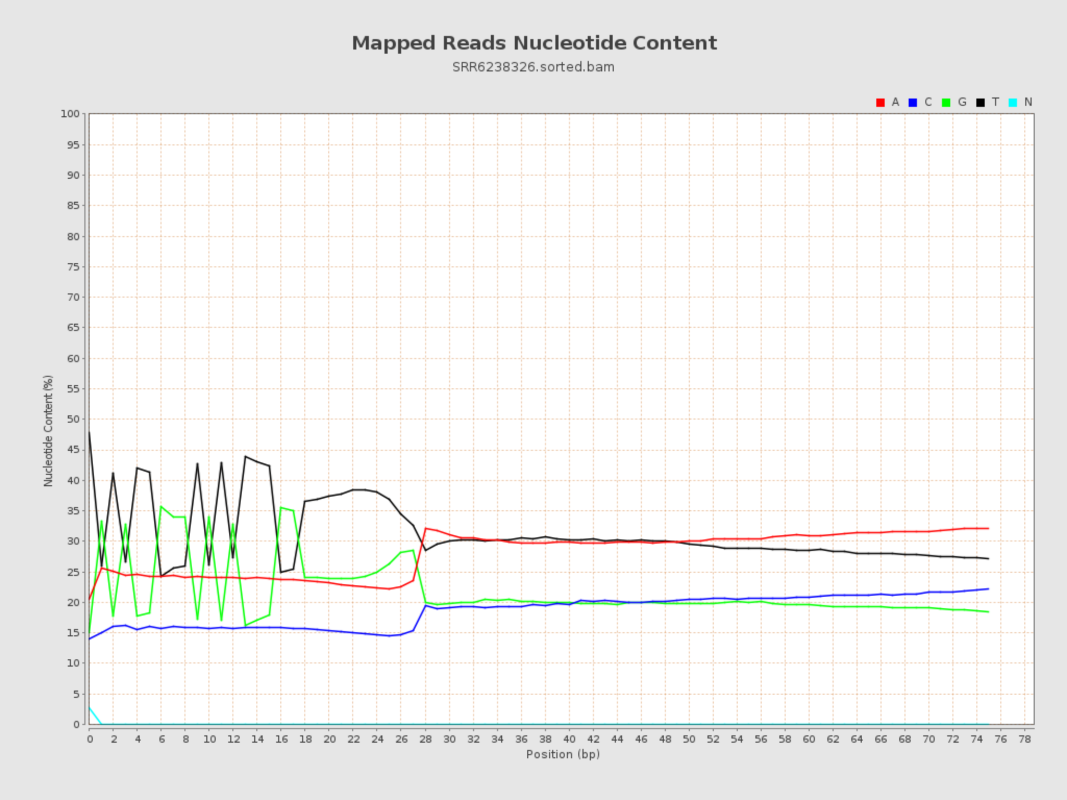
6. Results : Genome Fraction Coverage



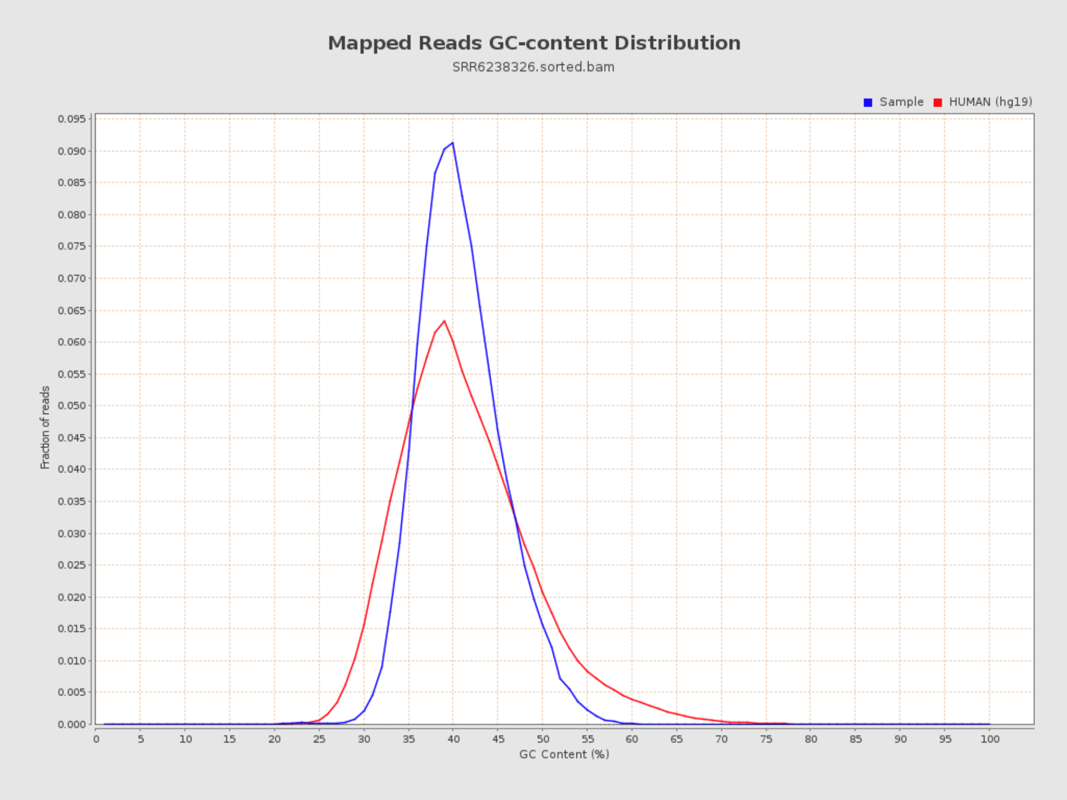
7. Results : Duplication Rate Histogram



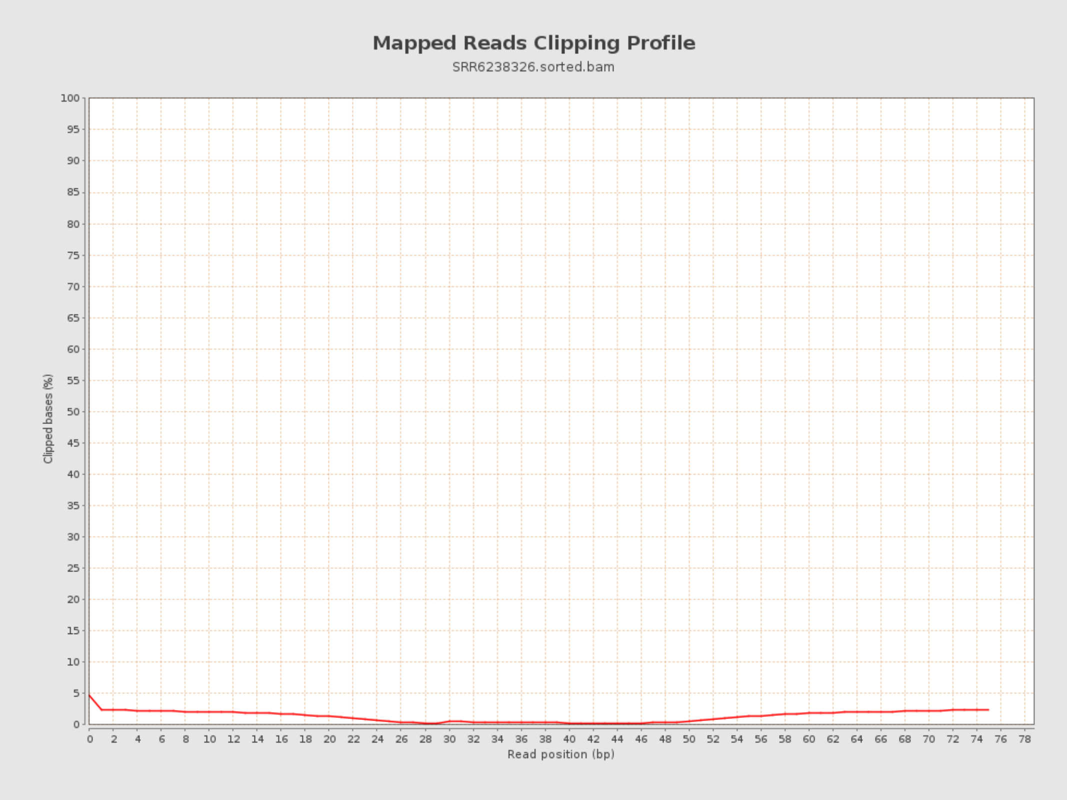
8. Results : Mapped Reads Nucleotide Content



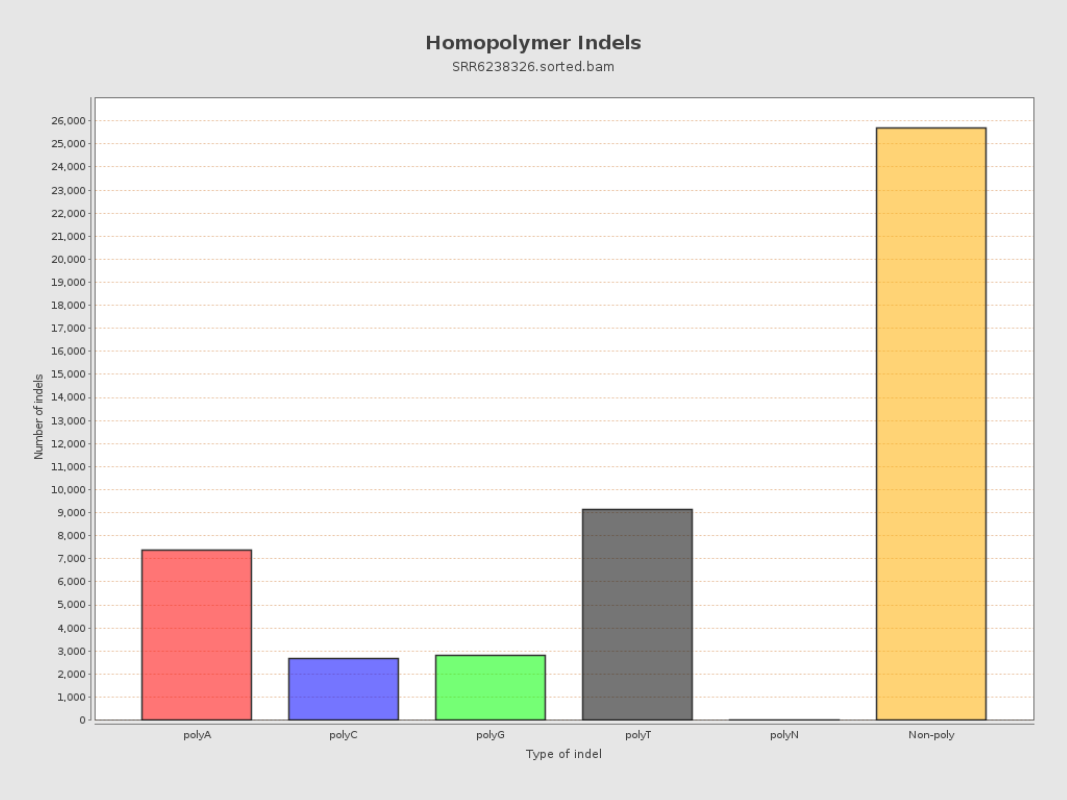
9. Results : Mapped Reads GC-content Distribution



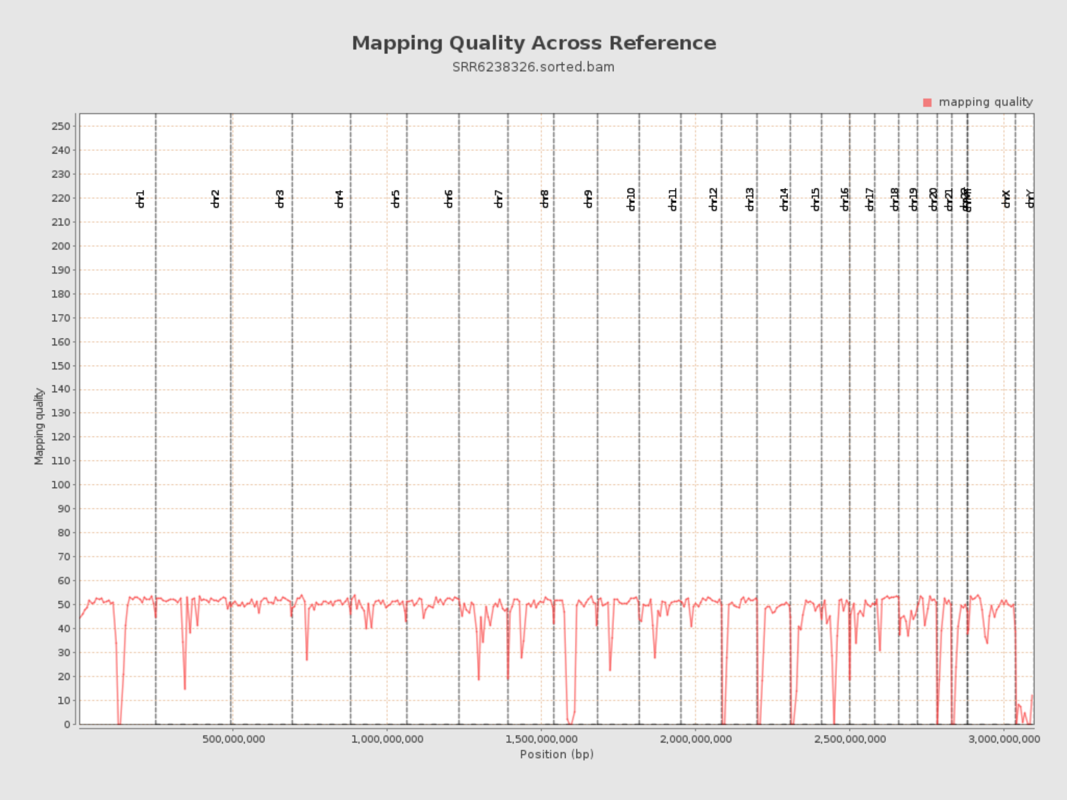
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram