Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 19:14:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238514.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_SRR6238514 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238514.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 19:14:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238514.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,619,470
Mapped reads	2,351,505 / 89.77%
Unmapped reads	267,965 / 10.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,017 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	828,219 / 31.62%
Duplication rate	22.84%
Clipped reads	1,546,437 / 59.04%

2.2. ACGT Content

Number/percentage of A's	34,236,315 / 23.85%
Number/percentage of C's	25,184,071 / 17.55%
Number/percentage of T's	48,549,902 / 33.83%
Number/percentage of G's	35,545,887 / 24.77%
Number/percentage of N's	9,251 / 0.01%
GC Percentage	42.31%

2.3. Coverage

Mean	0.0464

Standard Deviation	0.8148

2.4. Mapping Quality

Mean Mapping Quality	41.54

2.5. Mismatches and indels

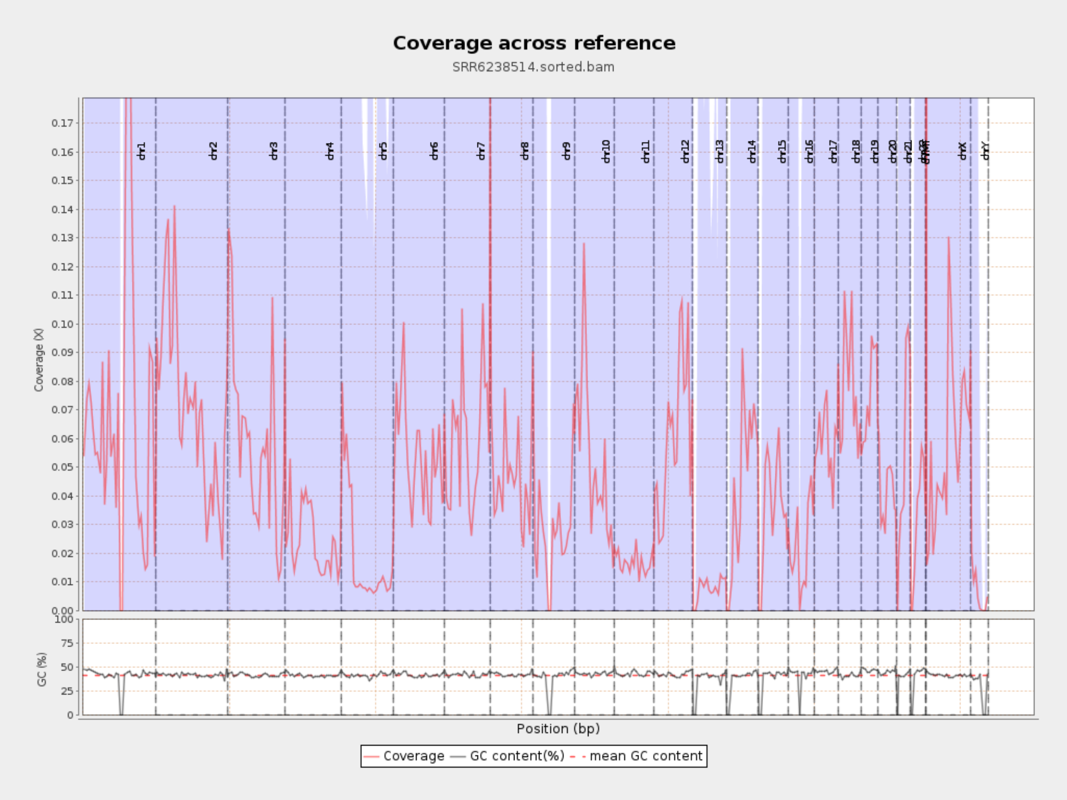
General error rate	0.56%
Mismatches	786,339
Insertions	9,107
Mapped reads with at least one insertion	0.39%
Deletions	36,827
Mapped reads with at least one deletion	1.55%
Homopolymer indels	41.45%

2.6. Chromosome stats

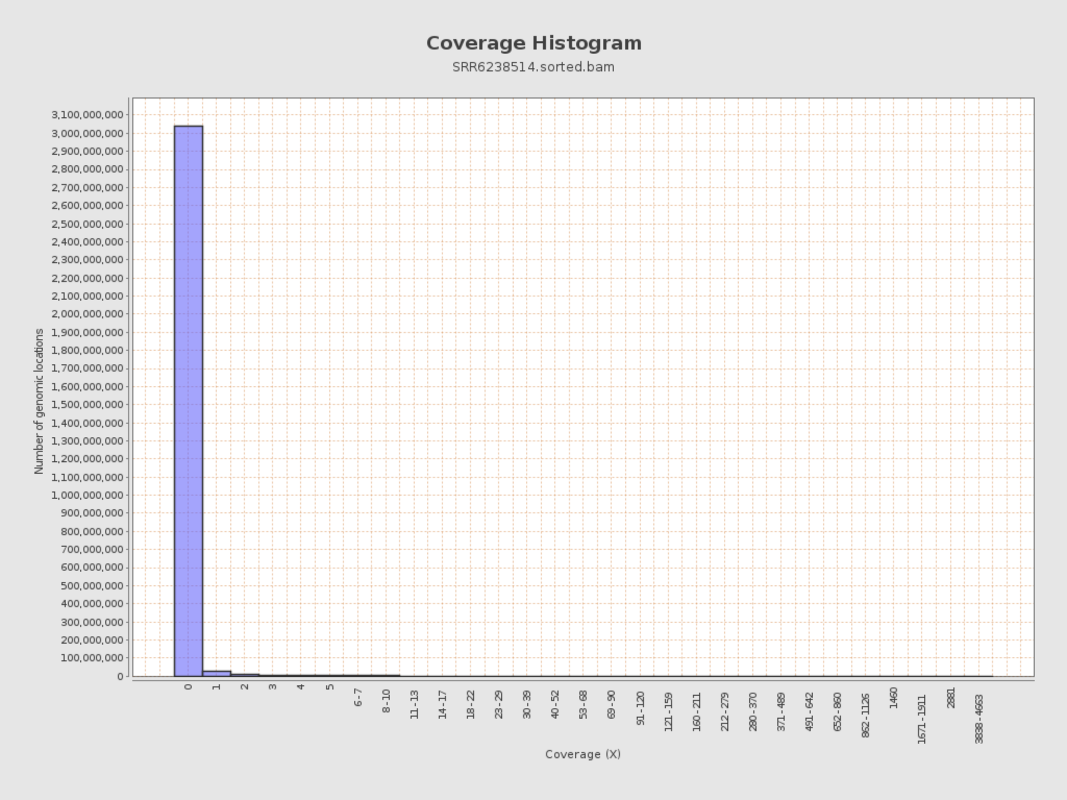
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16854141	0.0676	0.6979
chr2	243199373	17298528	0.0711	2.0866
chr3	198022430	11666901	0.0589	0.5469
chr4	191154276	4661715	0.0244	0.3323
chr5	180915260	3463184	0.0191	0.3032
chr6	171115067	9173720	0.0536	0.8064
chr7	159138663	9332925	0.0586	0.9454

chr8	146364022	6734208	0.046	0.5348
chr9	141213431	3830132	0.0271	0.3905
chr10	135534747	7213674	0.0532	0.5367
chr11	135006516	2246204	0.0166	0.2742
chr12	133851895	8231657	0.0615	0.565
chr13	115169878	892458	0.0077	0.3982
chr14	107349540	4757489	0.0443	0.4769
chr15	102531392	3670939	0.0358	0.5484
chr16	90354753	1930270	0.0214	0.3483
chr17	81195210	4745266	0.0584	0.5454
chr18	78077248	6058426	0.0776	1.3558
chr19	59128983	4424081	0.0748	0.6772
chr20	63025520	2571097	0.0408	0.4476
chr21	48129895	2635533	0.0548	0.5374
chr22	51304566	1650631	0.0322	0.3979
chrMT	16571	191642	11.5649	10.9705
chrX	155270560	8982933	0.0579	0.5362
chrY	59373566	369854	0.0062	0.2948

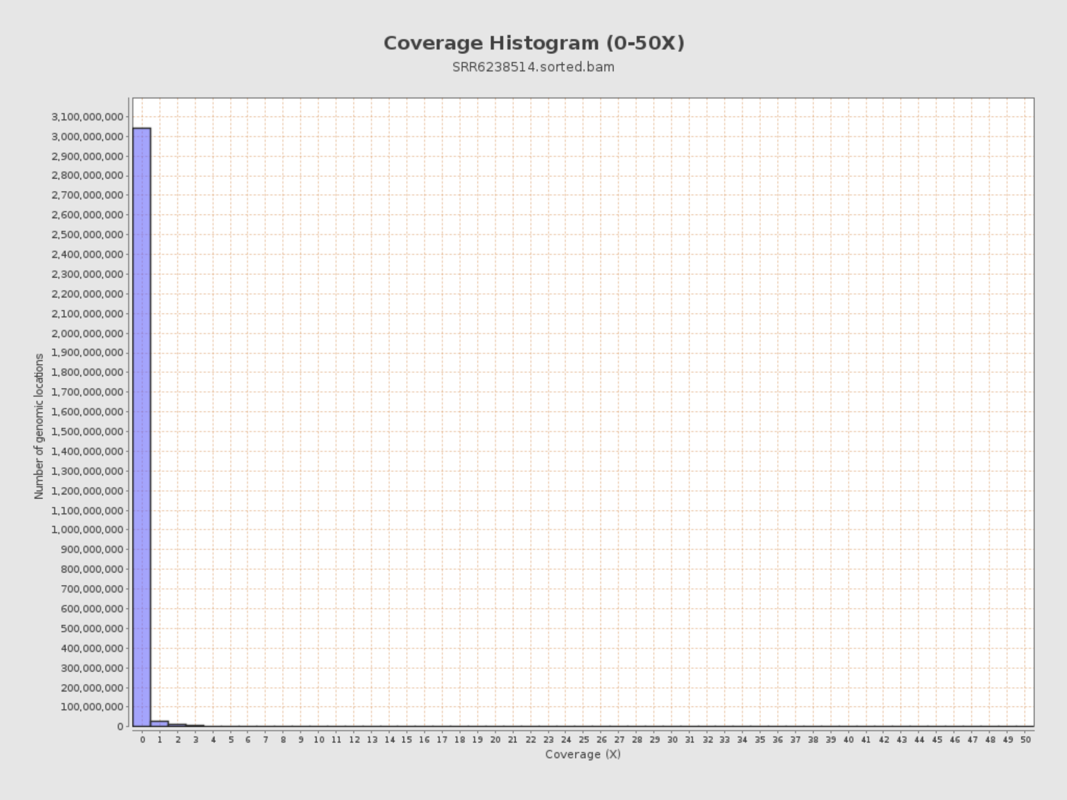
3. Results : Coverage across reference



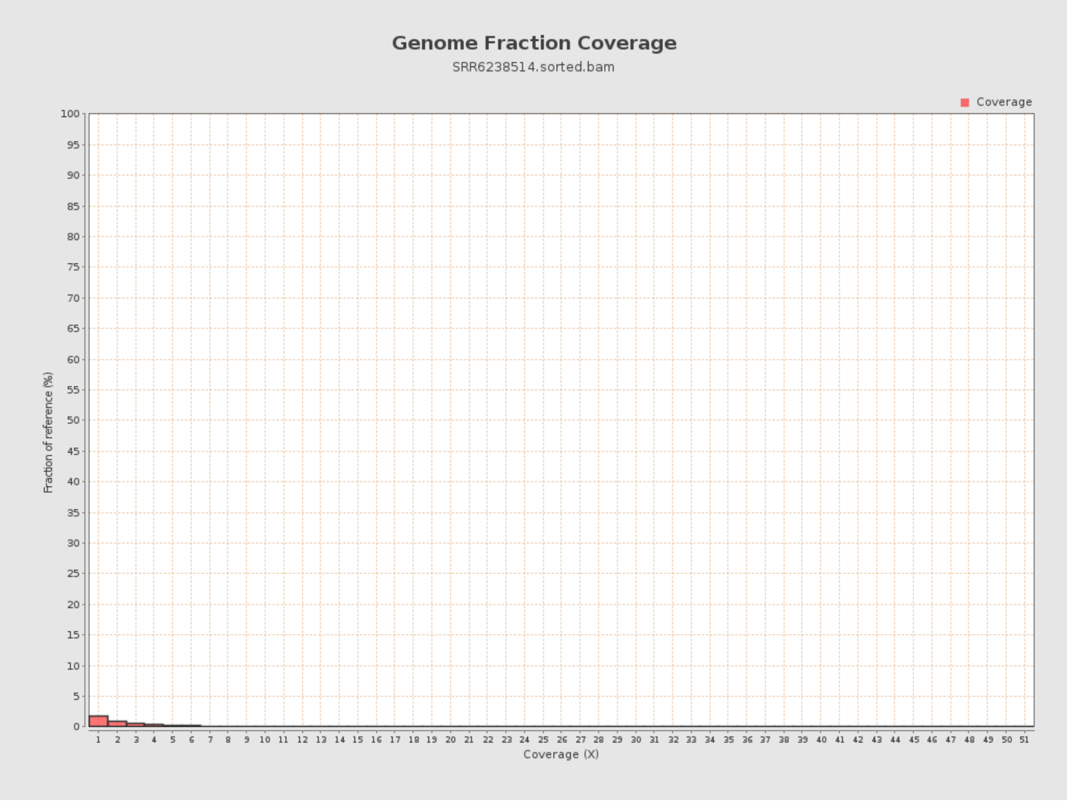
4. Results : Coverage Histogram



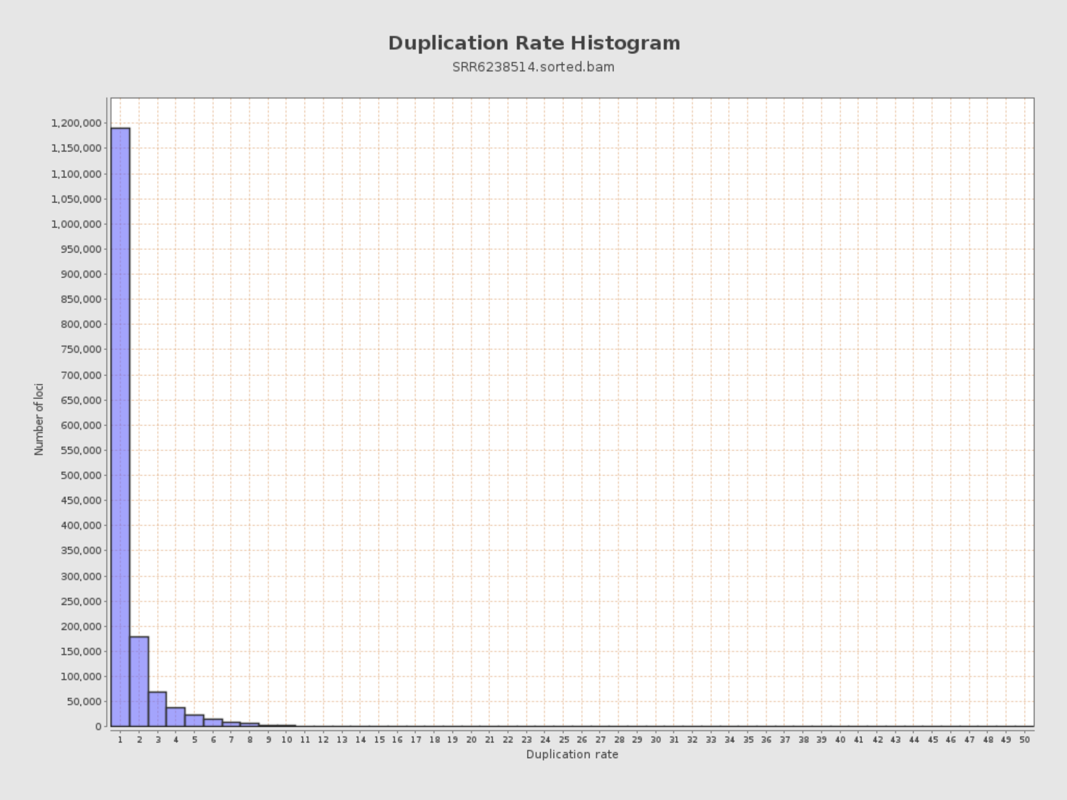
5. Results : Coverage Histogram (0-50X)



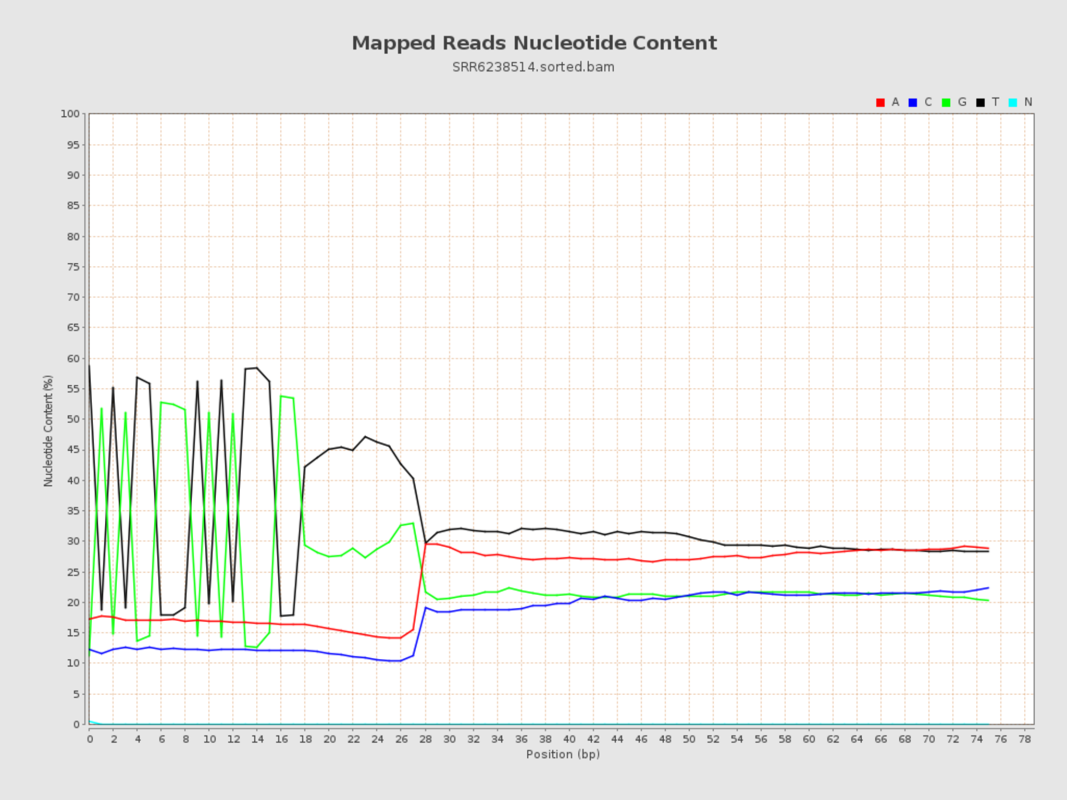
6. Results : Genome Fraction Coverage



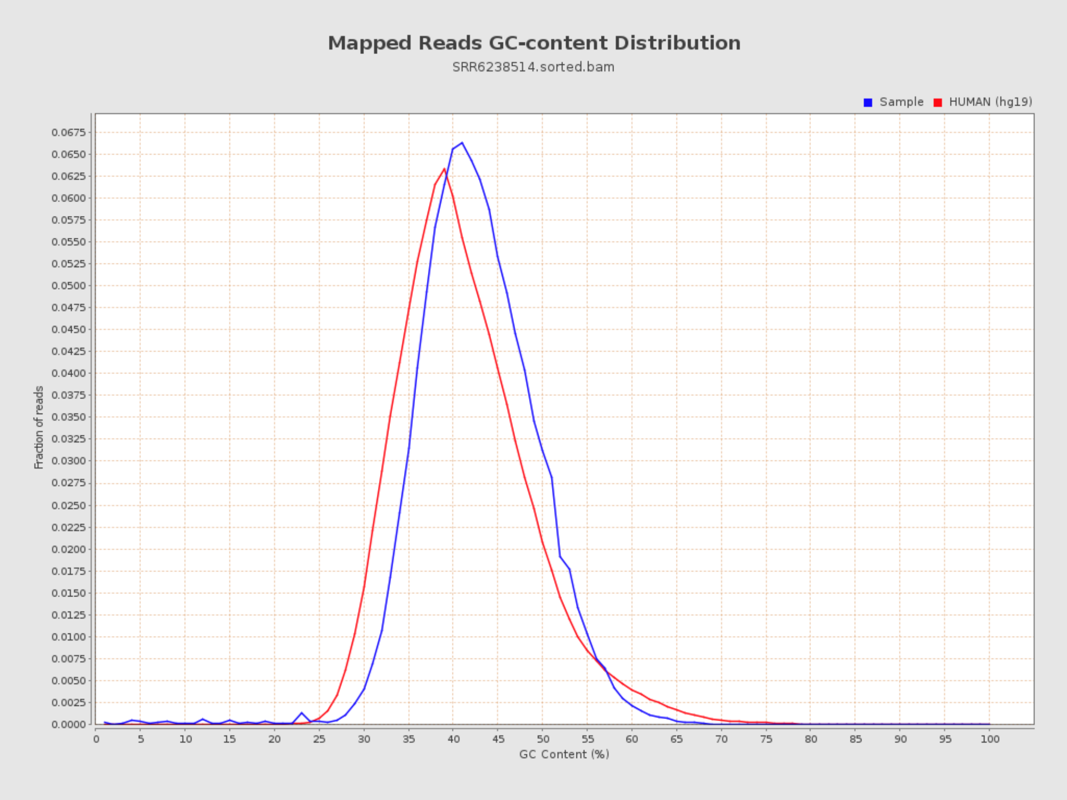
7. Results : Duplication Rate Histogram



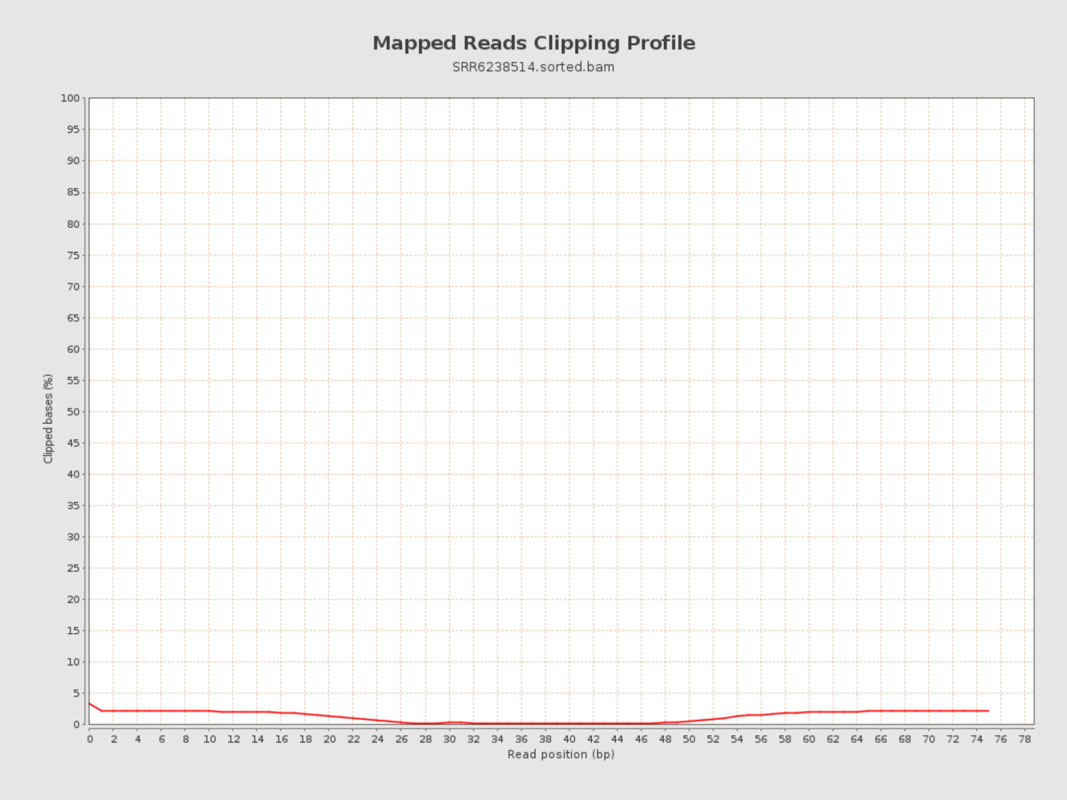
8. Results : Mapped Reads Nucleotide Content



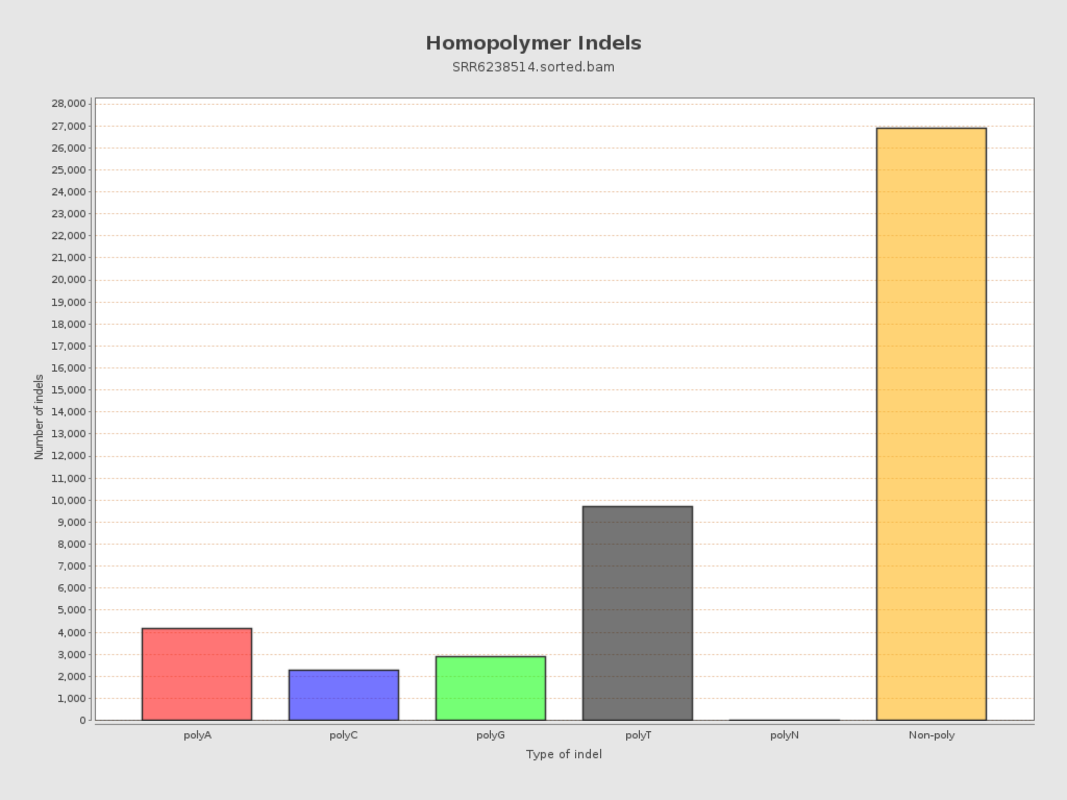
9. Results : Mapped Reads GC-content Distribution



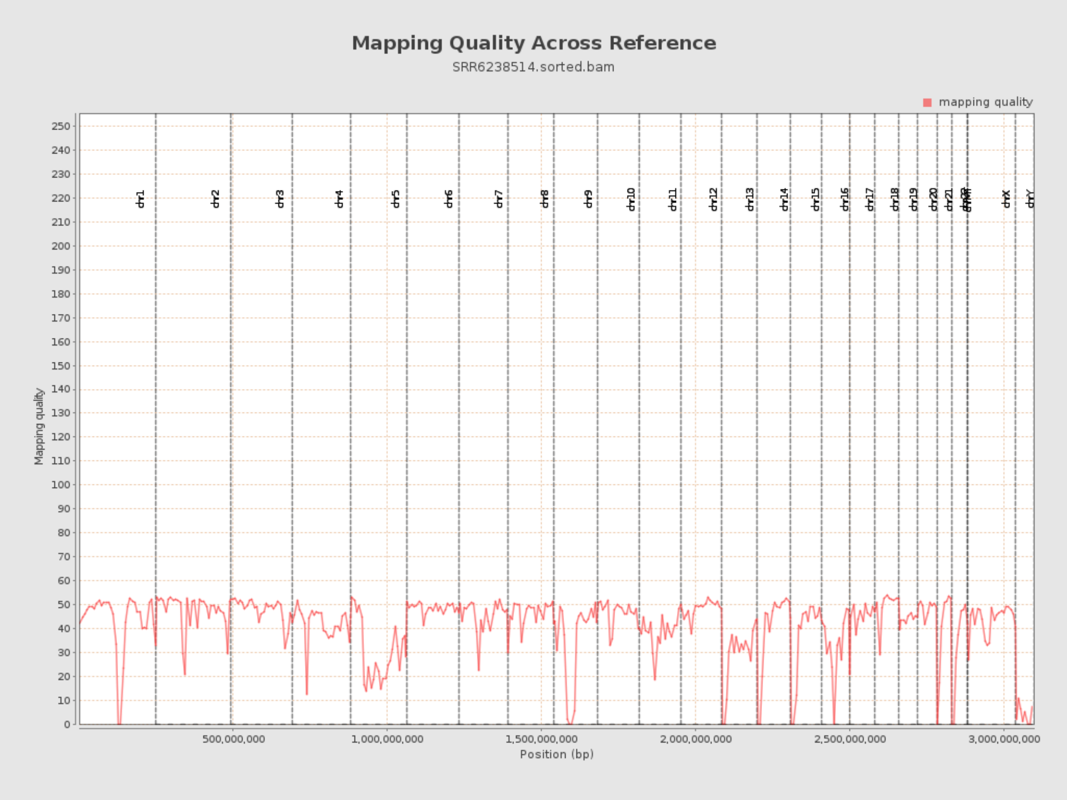
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram