Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 17:08:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238334.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_SRR6238334 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238334.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 17:08:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238334.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,890,354
Mapped reads	2,578,300 / 89.2%
Unmapped reads	312,054 / 10.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,517 / 0.85%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	113,058 / 3.91%
Duplication rate	3.13%
Clipped reads	1,348,515 / 46.66%

2.2. ACGT Content

Number/percentage of A's	48,139,165 / 28.59%
Number/percentage of C's	32,644,457 / 19.39%
Number/percentage of T's	50,964,659 / 30.27%
Number/percentage of G's	36,551,765 / 21.71%
Number/percentage of N's	51,764 / 0.03%
GC Percentage	41.1%

2.3. Coverage

Mean	0.0544

Standard Deviation	0.5288

2.4. Mapping Quality

Mean Mapping Quality	44.71

2.5. Mismatches and indels

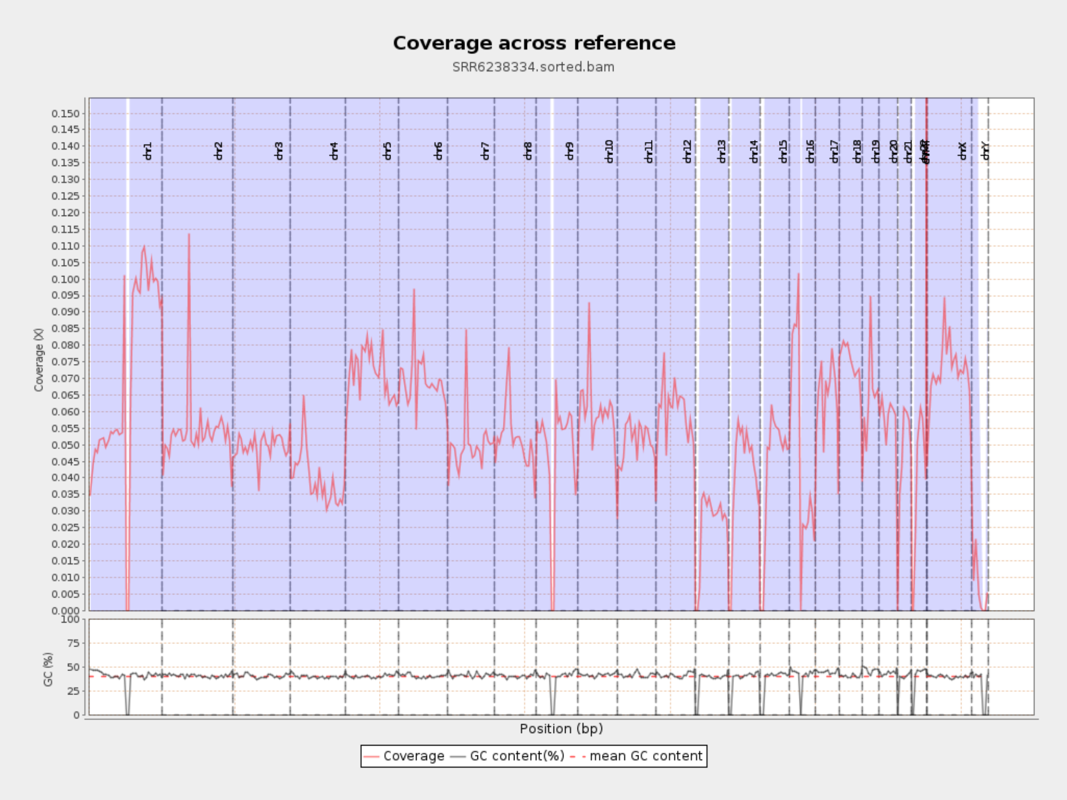
General error rate	0.88%
Mismatches	1,458,273
Insertions	12,540
Mapped reads with at least one insertion	0.48%
Deletions	45,177
Mapped reads with at least one deletion	1.73%
Homopolymer indels	45.18%

2.6. Chromosome stats

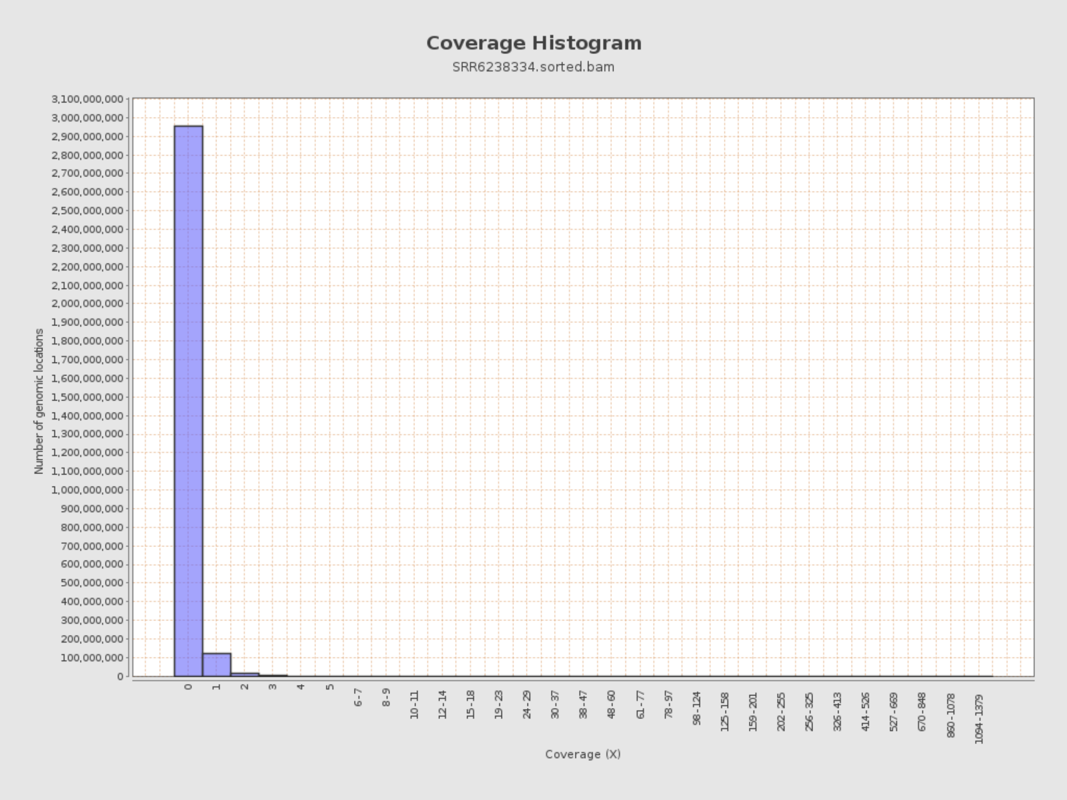
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17371673	0.0697	1.0908
chr2	243199373	13212697	0.0543	0.6233
chr3	198022430	9798136	0.0495	0.2564
chr4	191154276	7514821	0.0393	0.2575
chr5	180915260	12974826	0.0717	0.3148
chr6	171115067	11862599	0.0693	0.4199
chr7	159138663	7957351	0.05	0.5879

chr8	146364022	7577474	0.0518	0.7608
chr9	141213431	6756536	0.0478	0.487
chr10	135534747	8164821	0.0602	0.4759
chr11	135006516	6859750	0.0508	0.3849
chr12	133851895	8008733	0.0598	0.295
chr13	115169878	2954404	0.0257	0.1844
chr14	107349540	4393322	0.0409	0.2858
chr15	102531392	4403744	0.043	0.2492
chr16	90354753	4330811	0.0479	0.3047
chr17	81195210	5202685	0.0641	0.3502
chr18	78077248	5863649	0.0751	0.8457
chr19	59128983	3813698	0.0645	0.7949
chr20	63025520	3645639	0.0578	0.2844
chr21	48129895	2216710	0.0461	0.2815
chr22	51304566	1924328	0.0375	0.2214
chrMT	16571	5028	0.3034	0.612
chrX	155270560	11185782	0.072	0.3692
chrY	59373566	430510	0.0073	0.1659

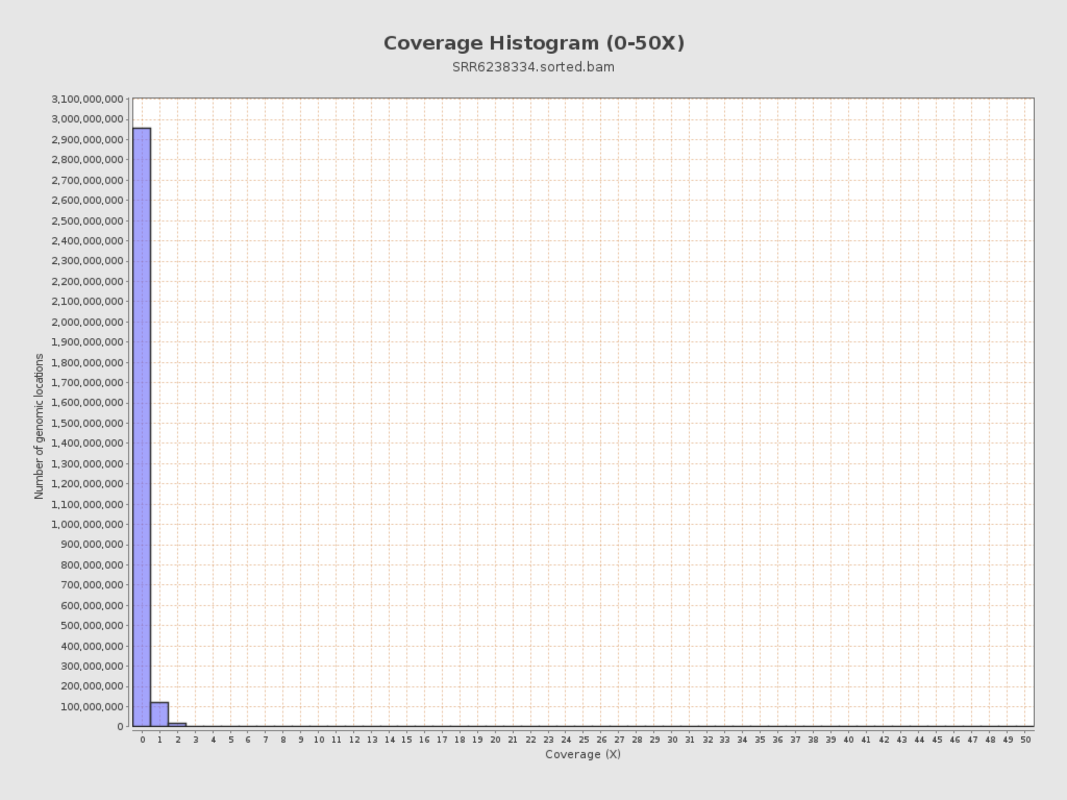
3. Results : Coverage across reference



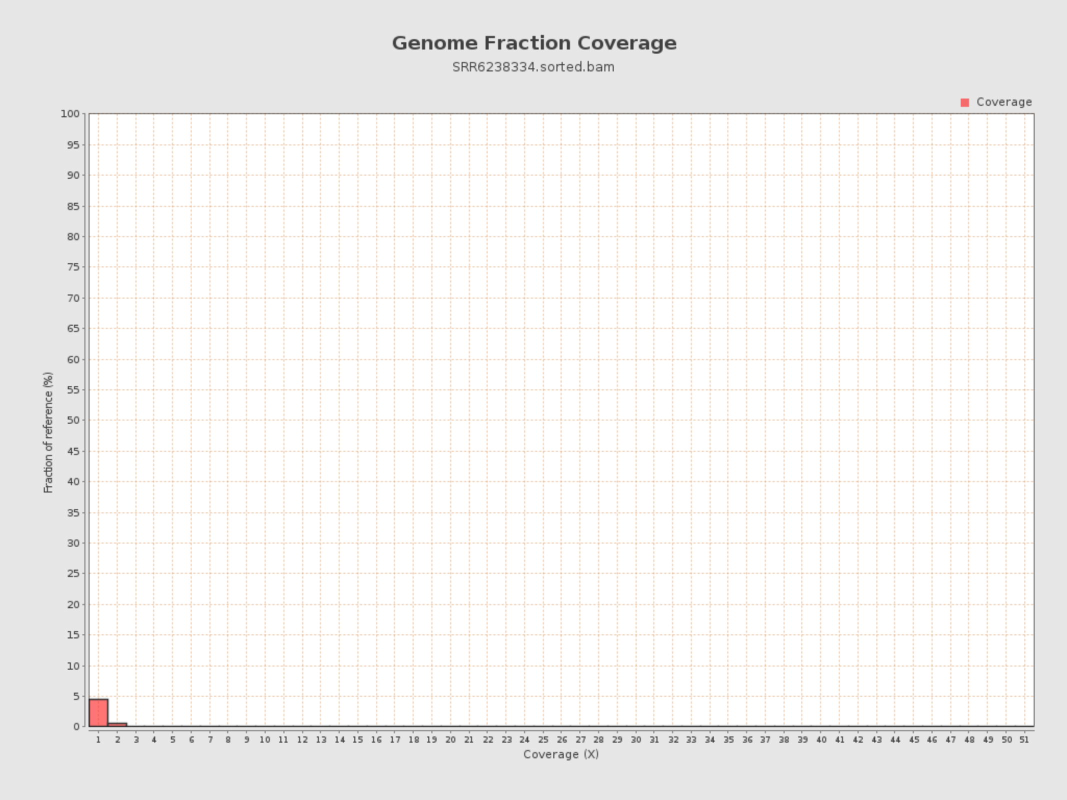
4. Results : Coverage Histogram



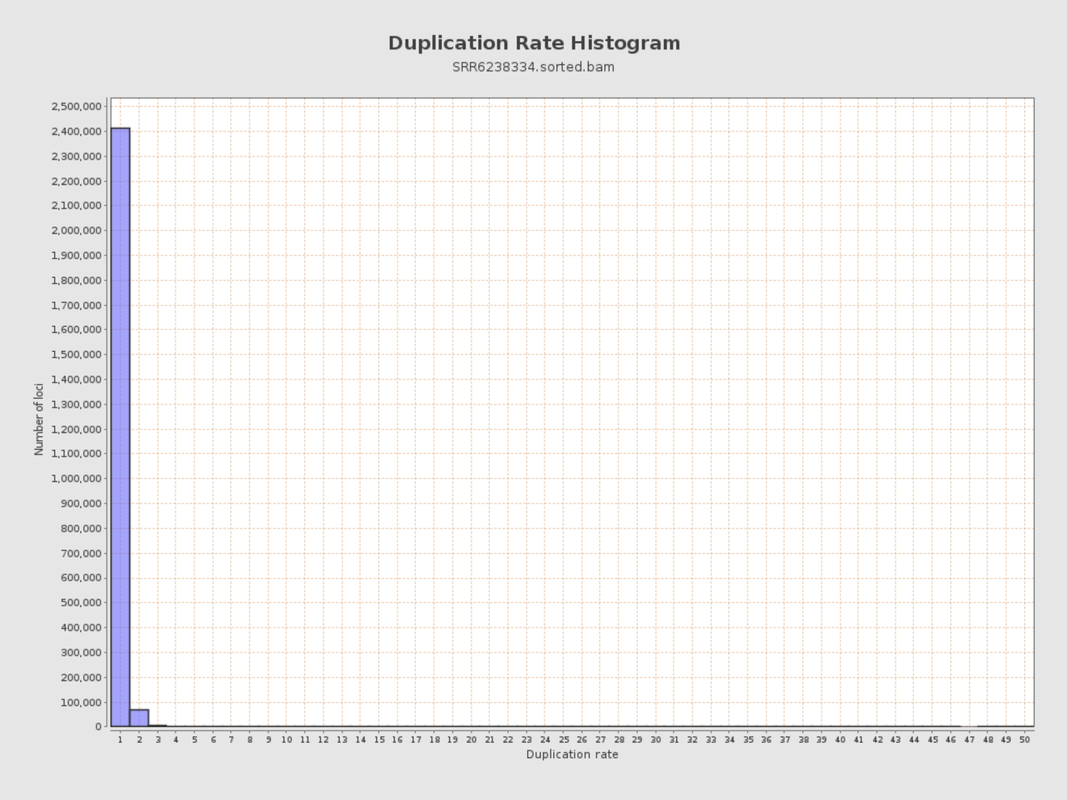
5. Results : Coverage Histogram (0-50X)



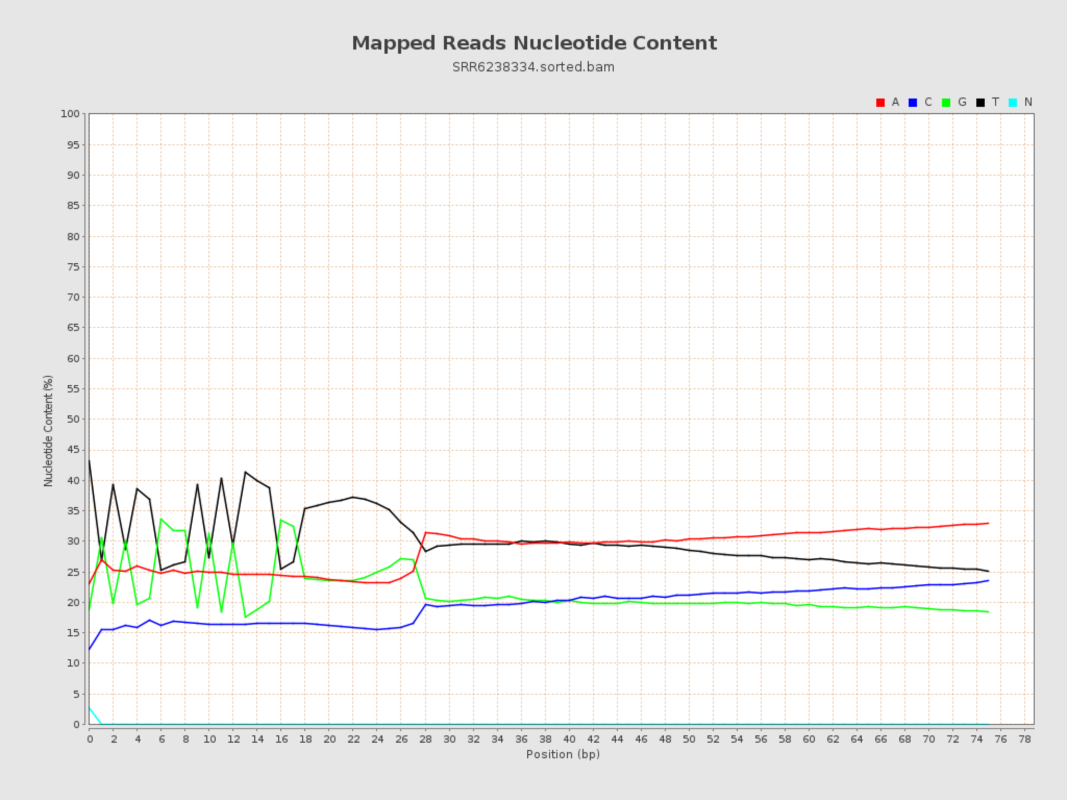
6. Results : Genome Fraction Coverage



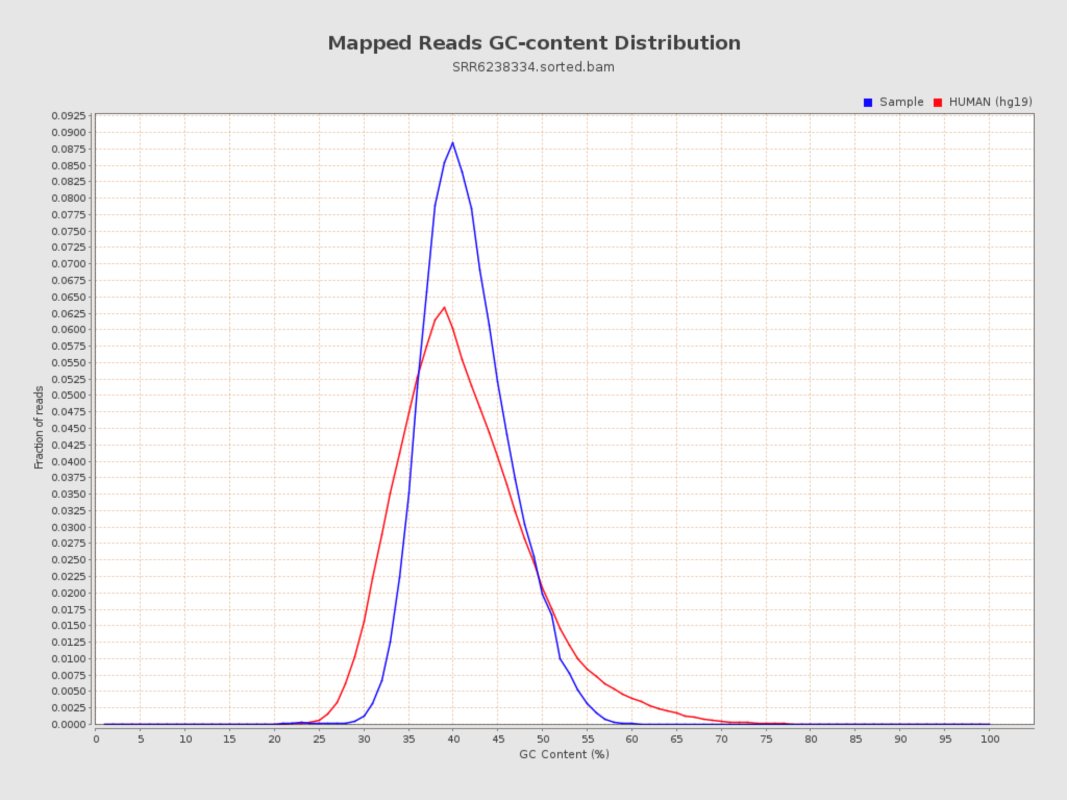
7. Results : Duplication Rate Histogram



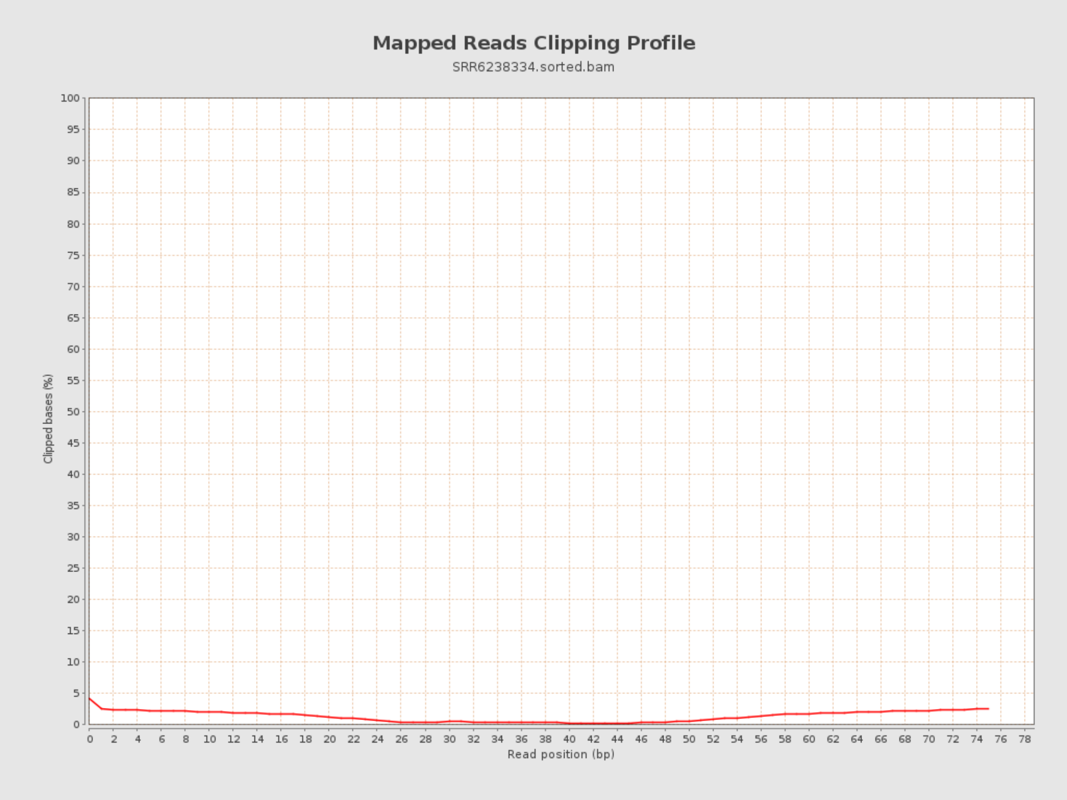
8. Results : Mapped Reads Nucleotide Content



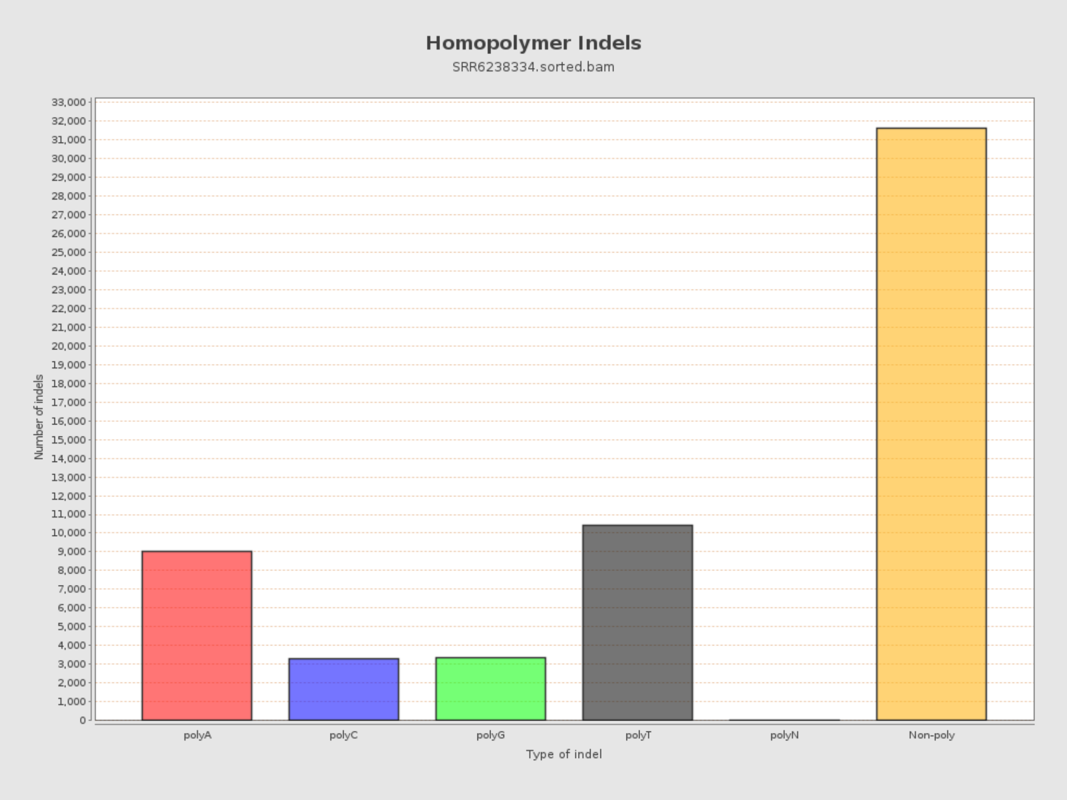
9. Results : Mapped Reads GC-content Distribution



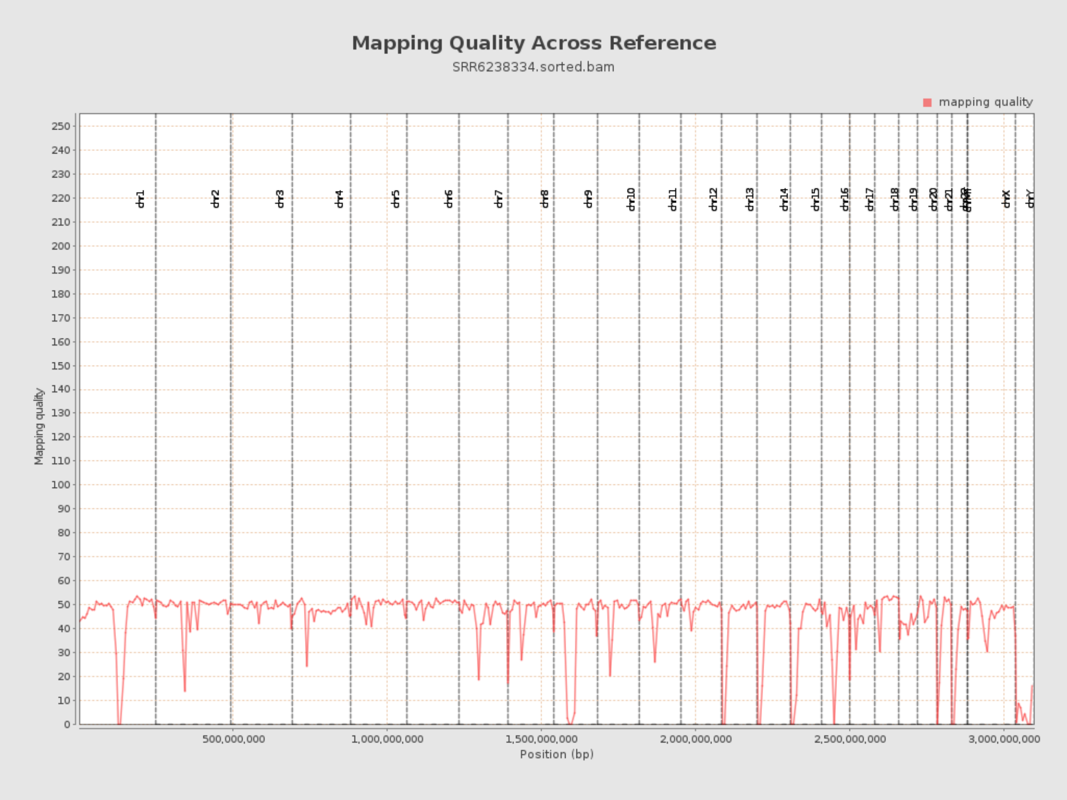
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram