Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 16:26:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238320.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_SRR6238320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 16:26:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,077,531
Mapped reads	2,802,923 / 91.08%
Unmapped reads	274,608 / 8.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	32,634 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	157,723 / 5.12%
Duplication rate	4.32%
Clipped reads	1,336,465 / 43.43%

2.2. ACGT Content

Number/percentage of A's	52,669,637 / 28.32%
Number/percentage of C's	34,758,557 / 18.69%
Number/percentage of T's	58,399,548 / 31.41%
Number/percentage of G's	40,064,574 / 21.55%
Number/percentage of N's	58,813 / 0.03%
GC Percentage	40.24%

2.3. Coverage

Mean	0.0601

Standard Deviation	0.5425

2.4. Mapping Quality

Mean Mapping Quality	46.42

2.5. Mismatches and indels

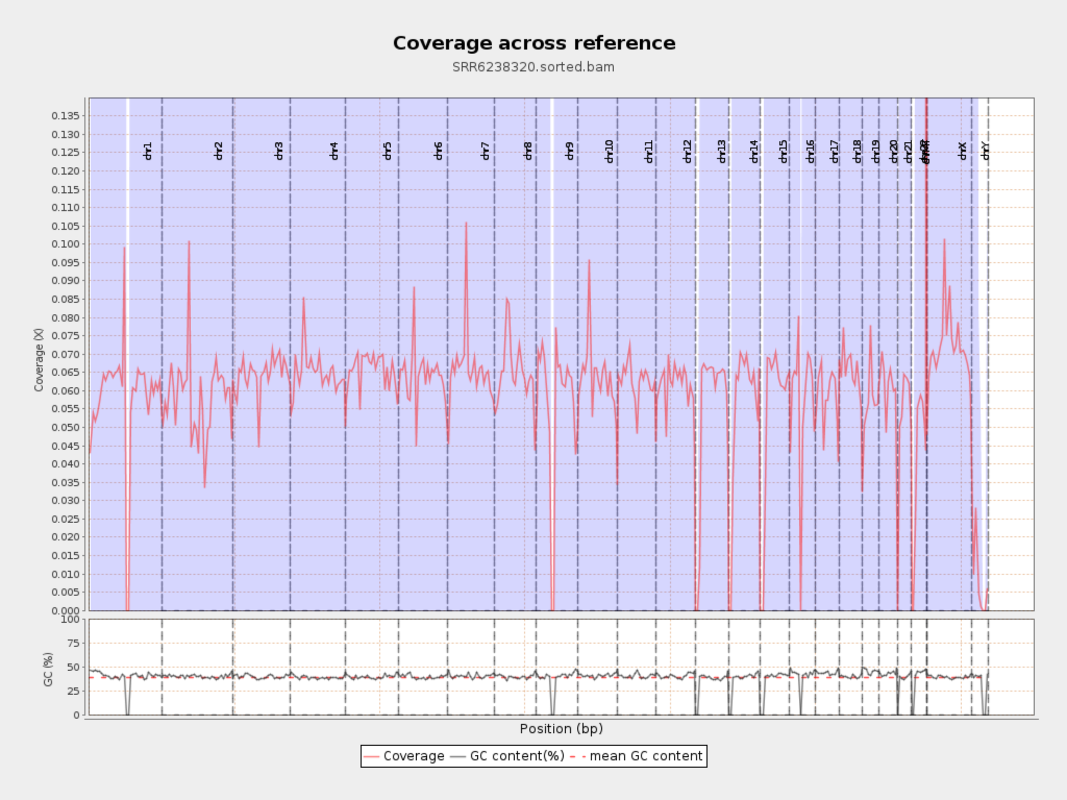
General error rate	0.85%
Mismatches	1,560,139
Insertions	14,381
Mapped reads with at least one insertion	0.51%
Deletions	47,553
Mapped reads with at least one deletion	1.68%
Homopolymer indels	46.95%

2.6. Chromosome stats

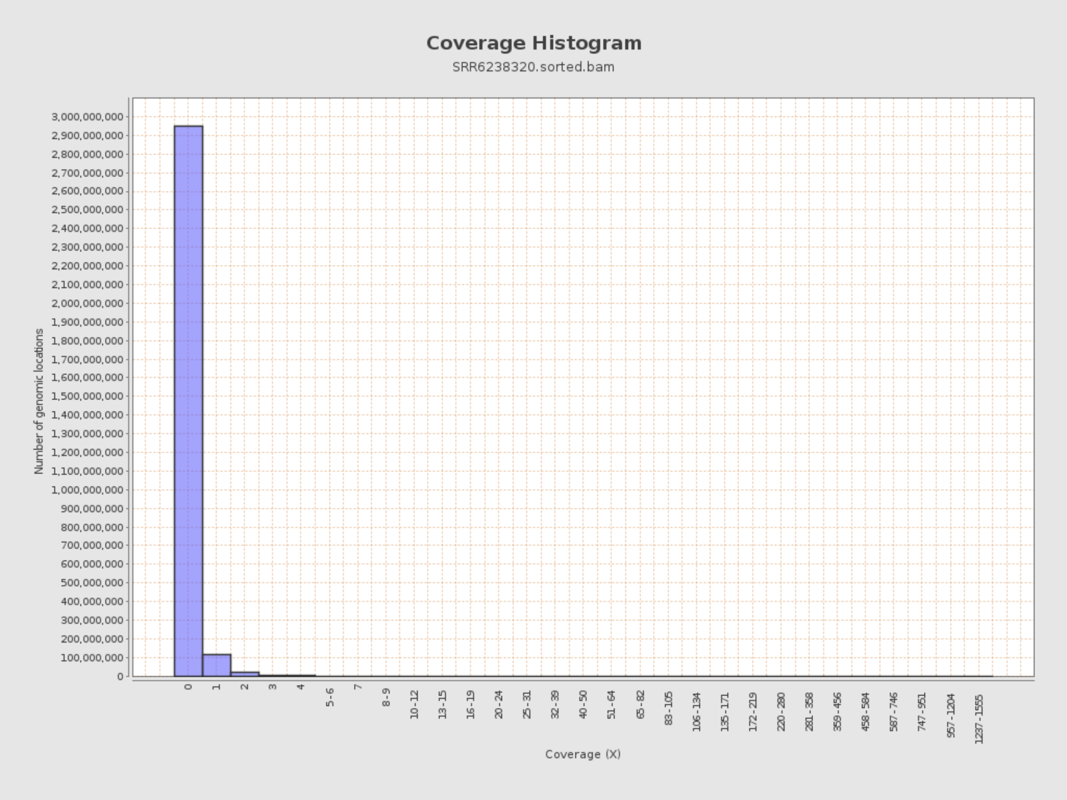
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14430409	0.0579	0.9847
chr2	243199373	14273494	0.0587	0.5693
chr3	198022430	12785074	0.0646	0.3099
chr4	191154276	12416800	0.065	0.3464
chr5	180915260	11902608	0.0658	0.3179
chr6	171115067	10960161	0.0641	0.3968
chr7	159138663	10570215	0.0664	0.7272

chr8	146364022	9462470	0.0647	0.9812
chr9	141213431	7991700	0.0566	0.4767
chr10	135534747	8701942	0.0642	0.4748
chr11	135006516	8408061	0.0623	0.4282
chr12	133851895	8240050	0.0616	0.318
chr13	115169878	6209933	0.0539	0.2857
chr14	107349540	5792637	0.054	0.3388
chr15	102531392	5476064	0.0534	0.287
chr16	90354753	5166287	0.0572	0.3309
chr17	81195210	4701175	0.0579	0.3464
chr18	78077248	5136060	0.0658	0.8929
chr19	59128983	3392985	0.0574	0.6592
chr20	63025520	3830680	0.0608	0.3211
chr21	48129895	2512315	0.0522	0.3274
chr22	51304566	1980201	0.0386	0.2378
chrMT	16571	16351	0.9867	1.235
chrX	155270560	11174244	0.072	0.3764
chrY	59373566	500968	0.0084	0.2171

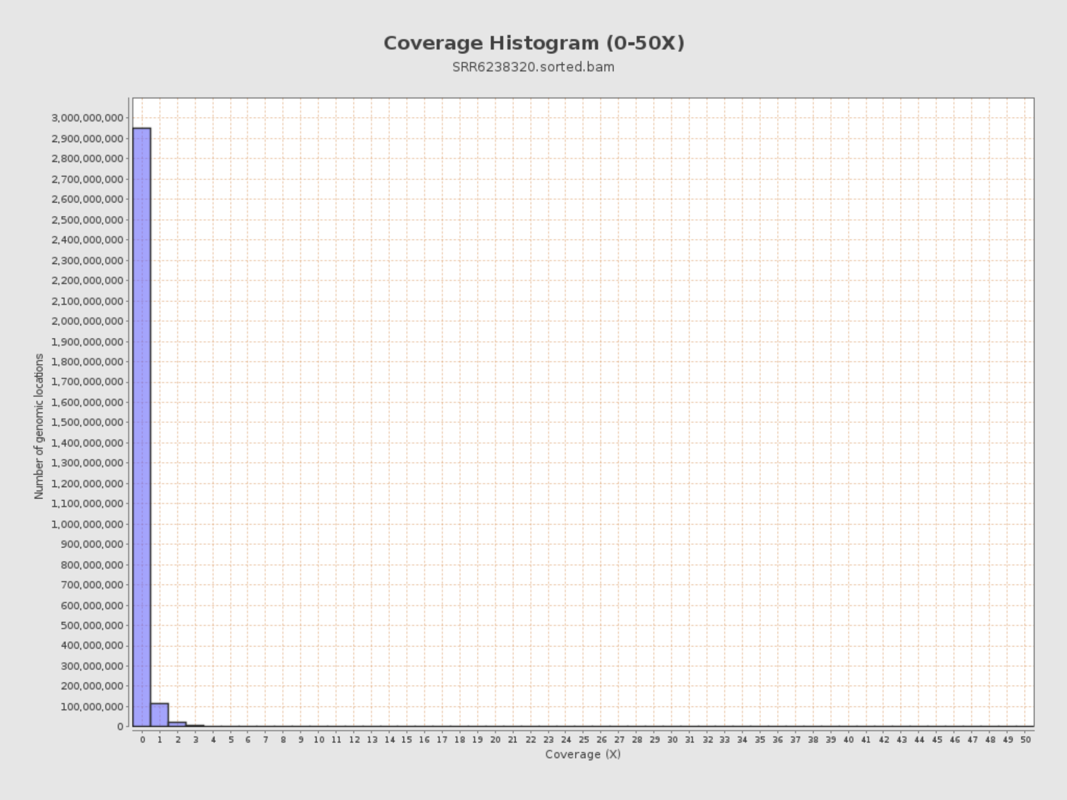
3. Results : Coverage across reference



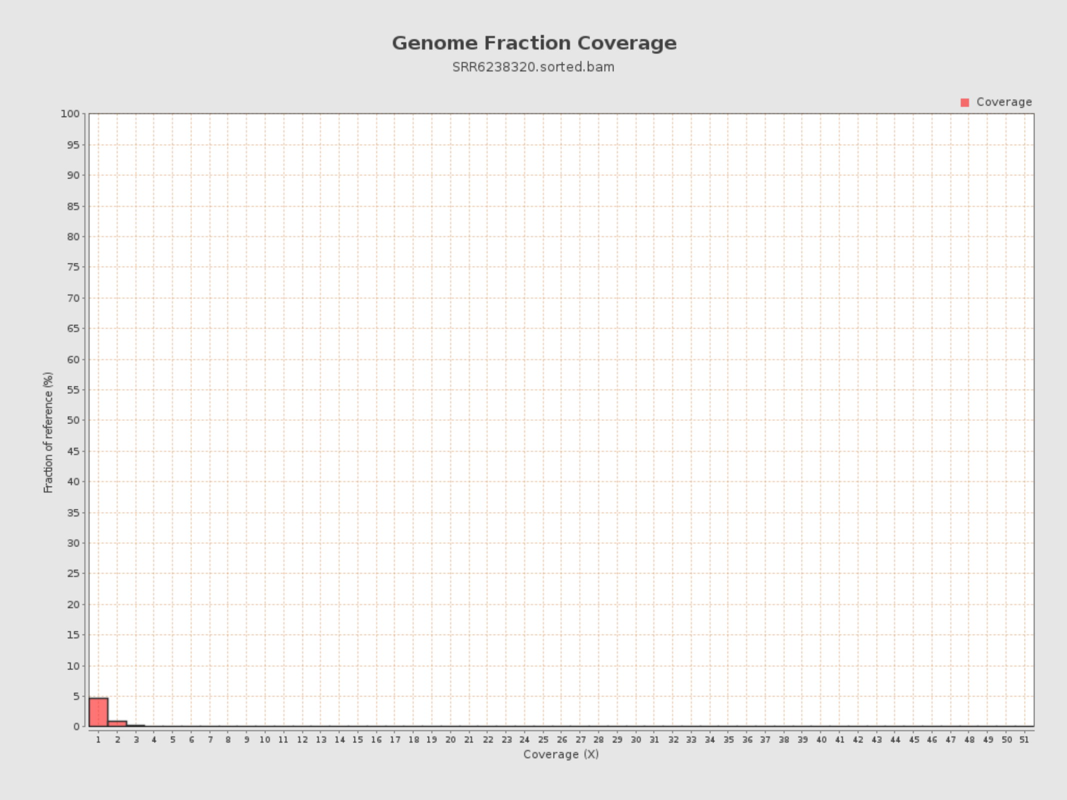
4. Results : Coverage Histogram



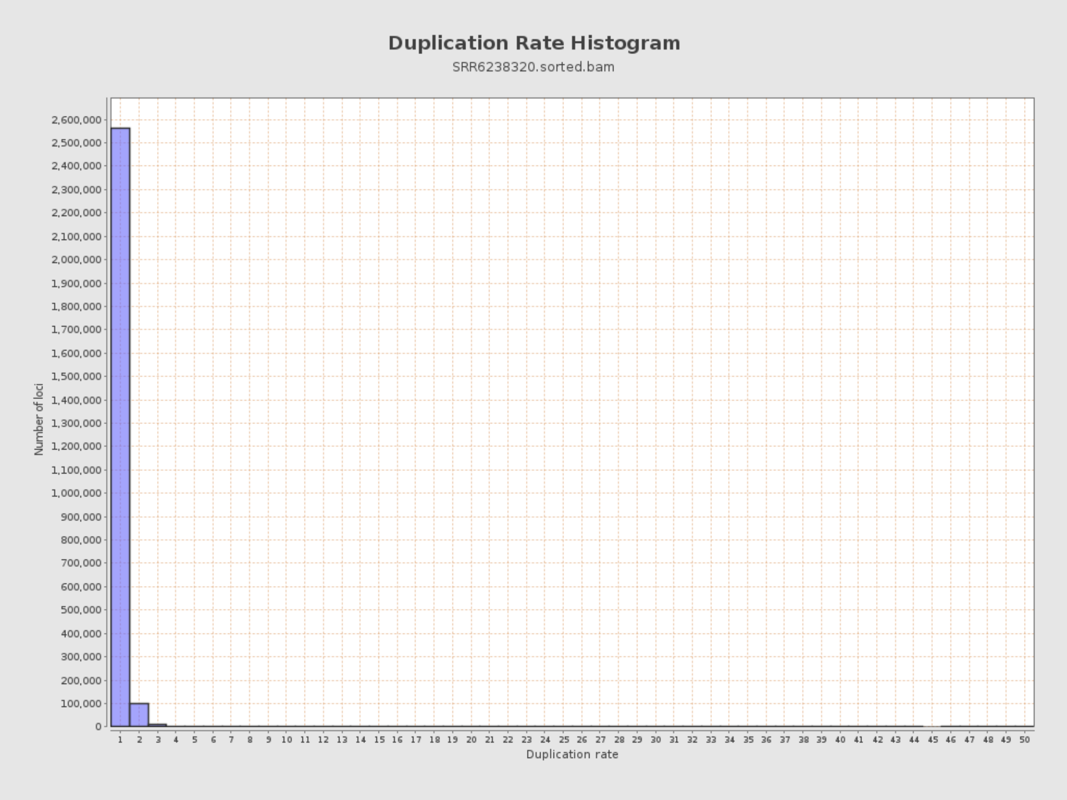
5. Results : Coverage Histogram (0-50X)



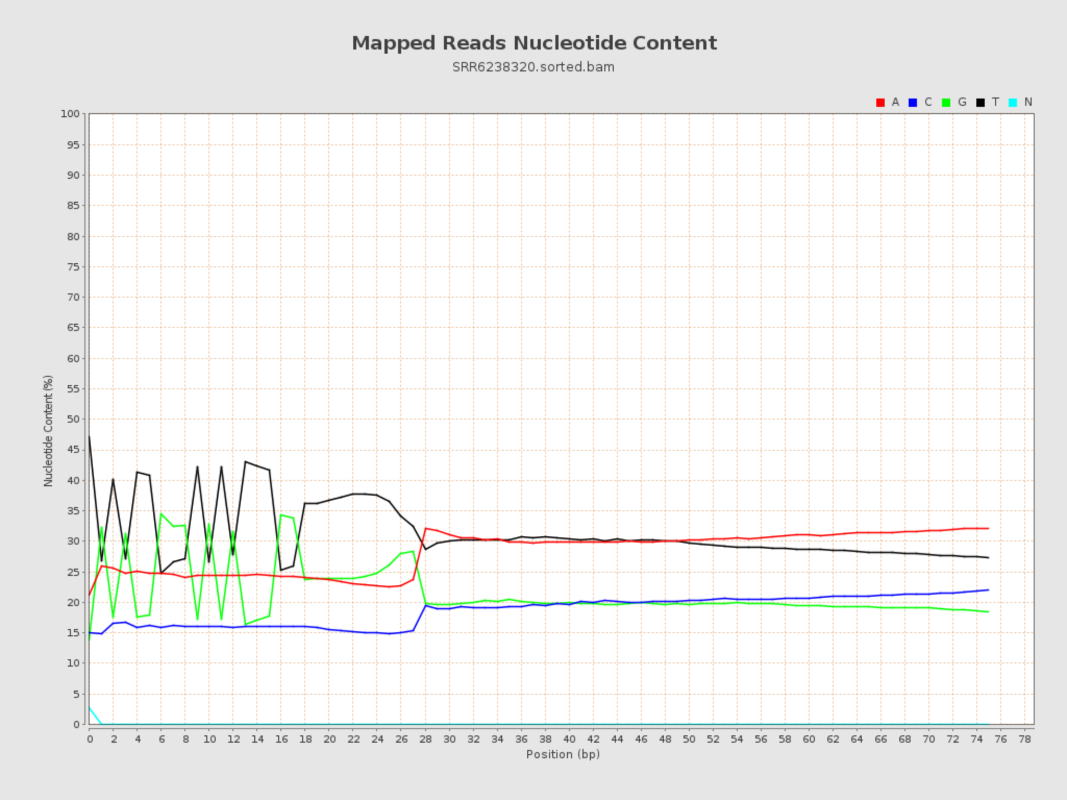
6. Results : Genome Fraction Coverage



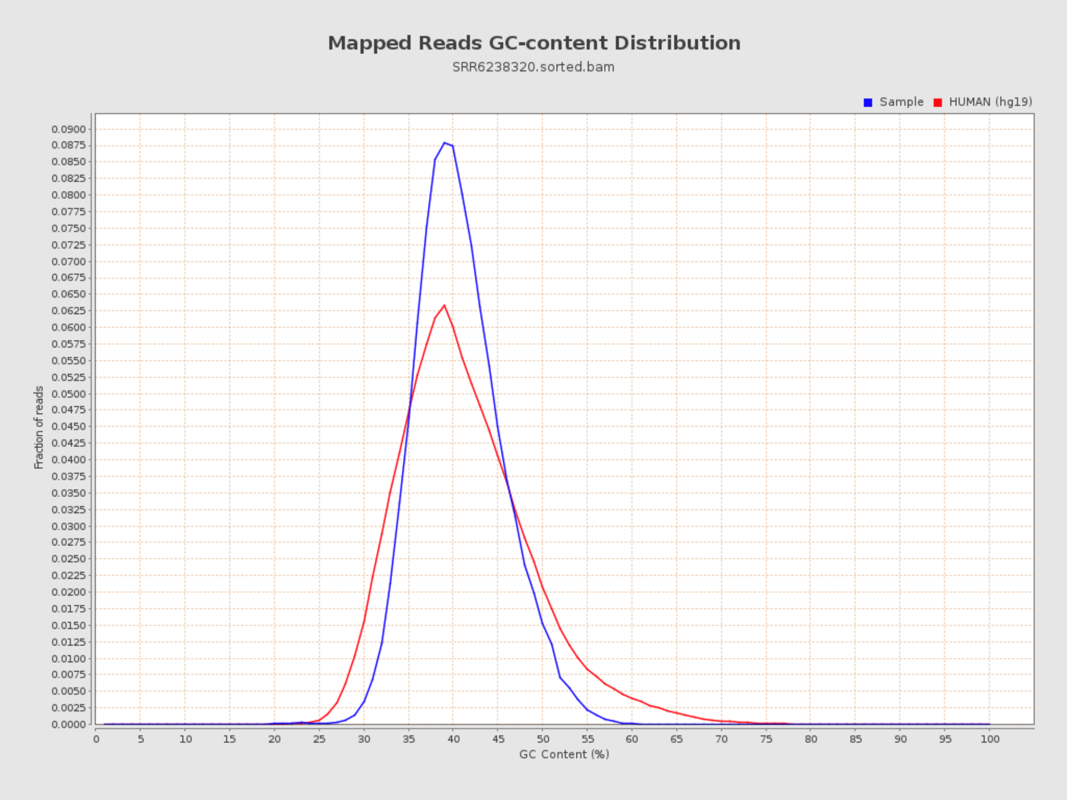
7. Results : Duplication Rate Histogram



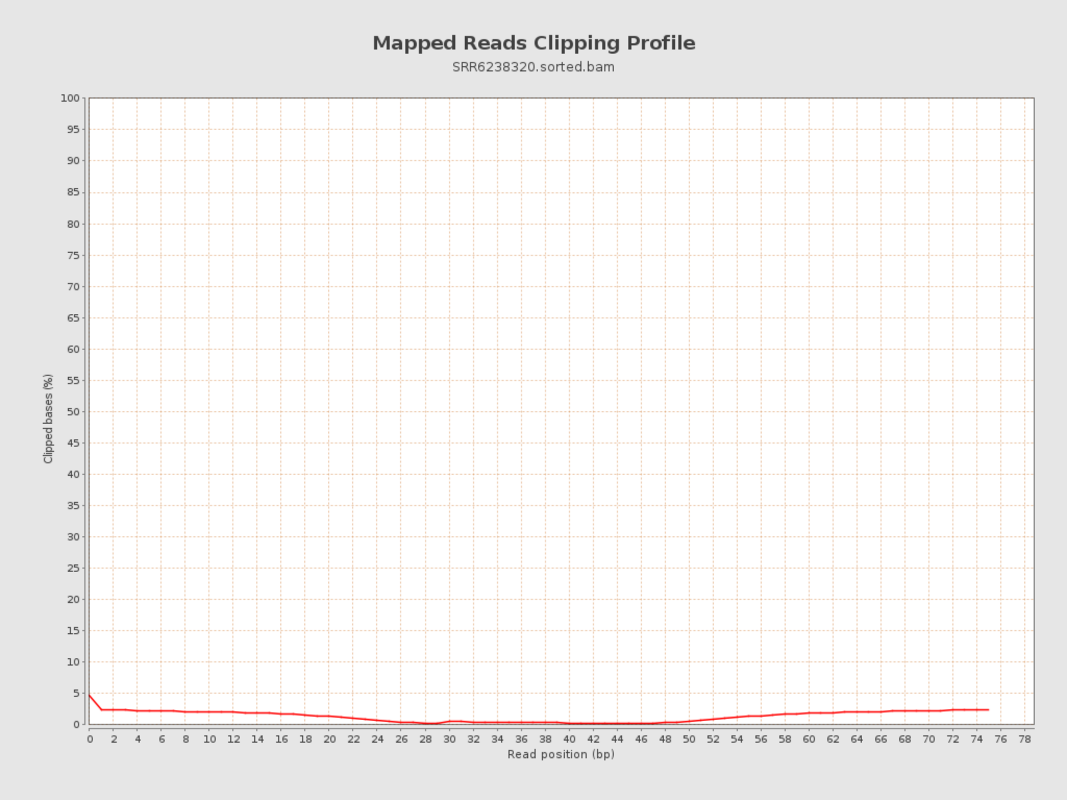
8. Results : Mapped Reads Nucleotide Content



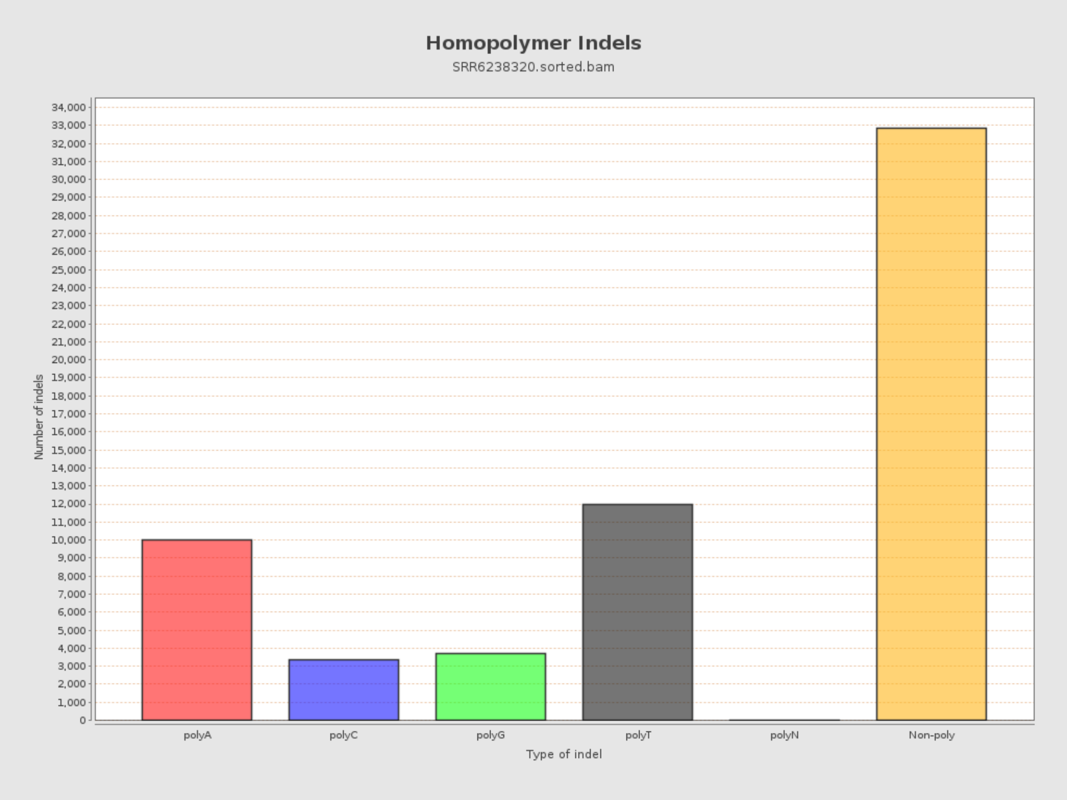
9. Results : Mapped Reads GC-content Distribution



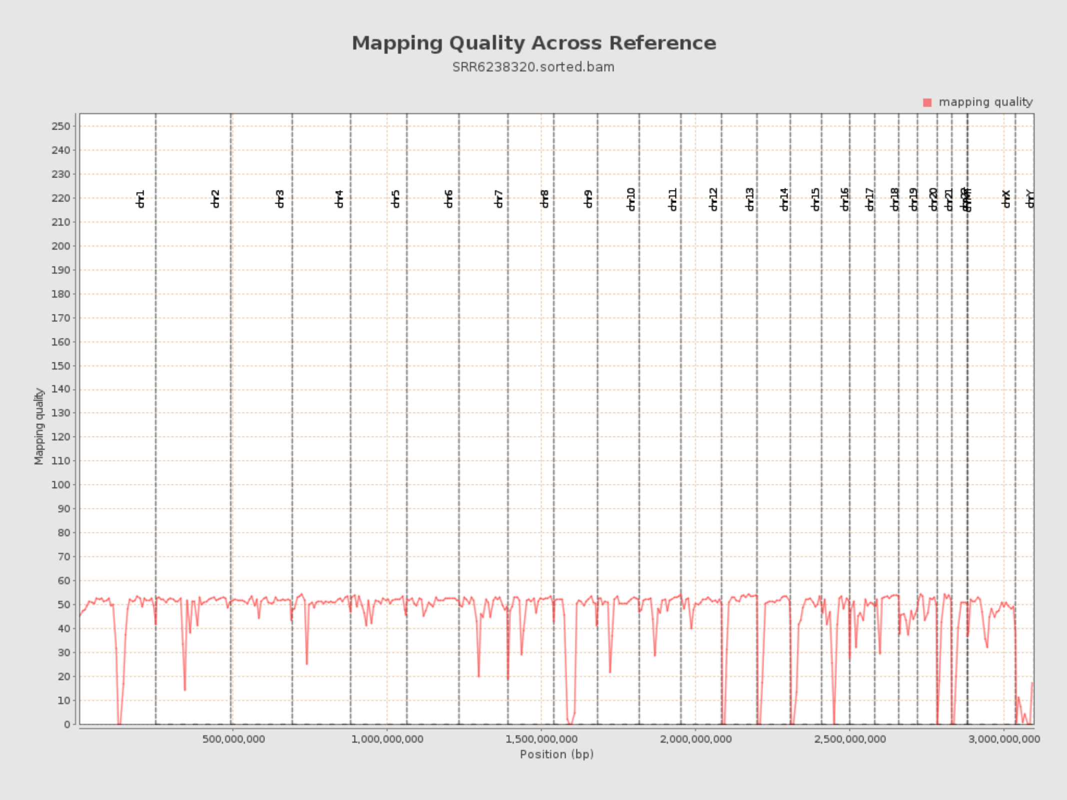
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram