Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:45:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238288.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_SRR6238288 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238288.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:45:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238288.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,412,999
Mapped reads	2,122,119 / 87.95%
Unmapped reads	290,880 / 12.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,632 / 1.02%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	133,756 / 5.54%
Duplication rate	5.12%
Clipped reads	1,039,215 / 43.07%

2.2. ACGT Content

Number/percentage of A's	38,774,607 / 27.7%
Number/percentage of C's	26,962,471 / 19.26%
Number/percentage of T's	42,963,121 / 30.69%
Number/percentage of G's	31,249,019 / 22.32%
Number/percentage of N's	28,965 / 0.02%
GC Percentage	41.59%

2.3. Coverage

Mean	0.0452

Standard Deviation	0.38

2.4. Mapping Quality

Mean Mapping Quality	45.83

2.5. Mismatches and indels

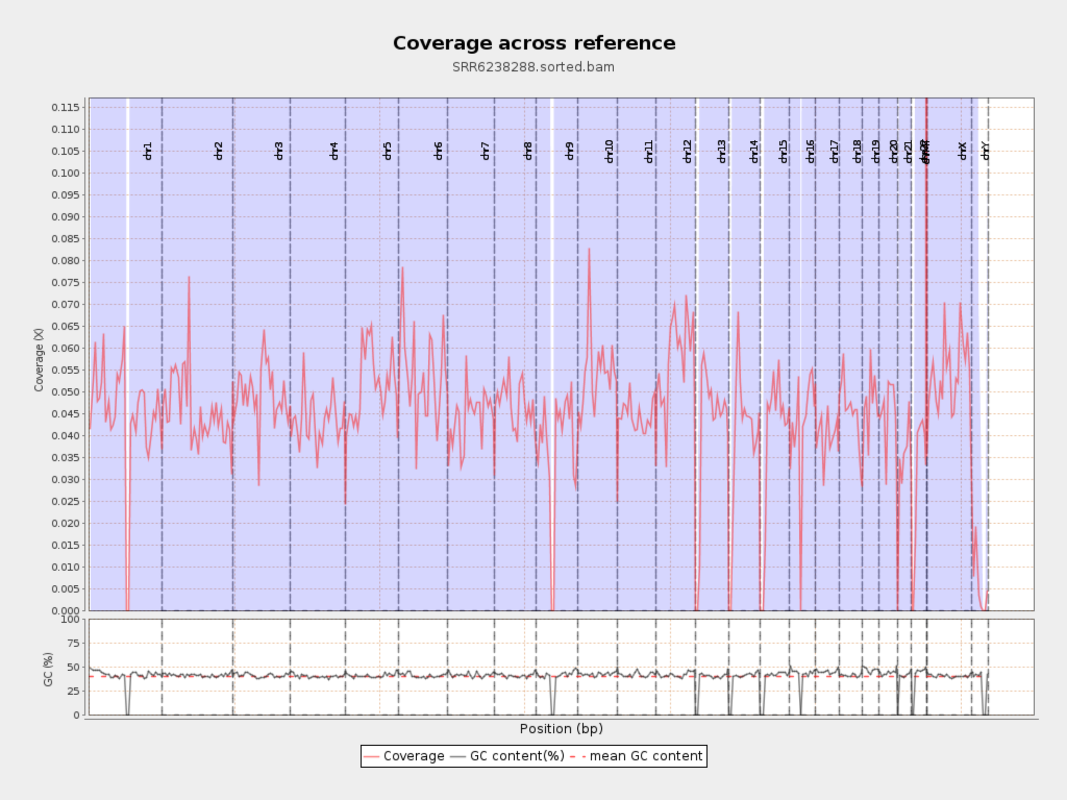
General error rate	0.89%
Mismatches	1,229,951
Insertions	11,193
Mapped reads with at least one insertion	0.52%
Deletions	40,774
Mapped reads with at least one deletion	1.9%
Homopolymer indels	47.41%

2.6. Chromosome stats

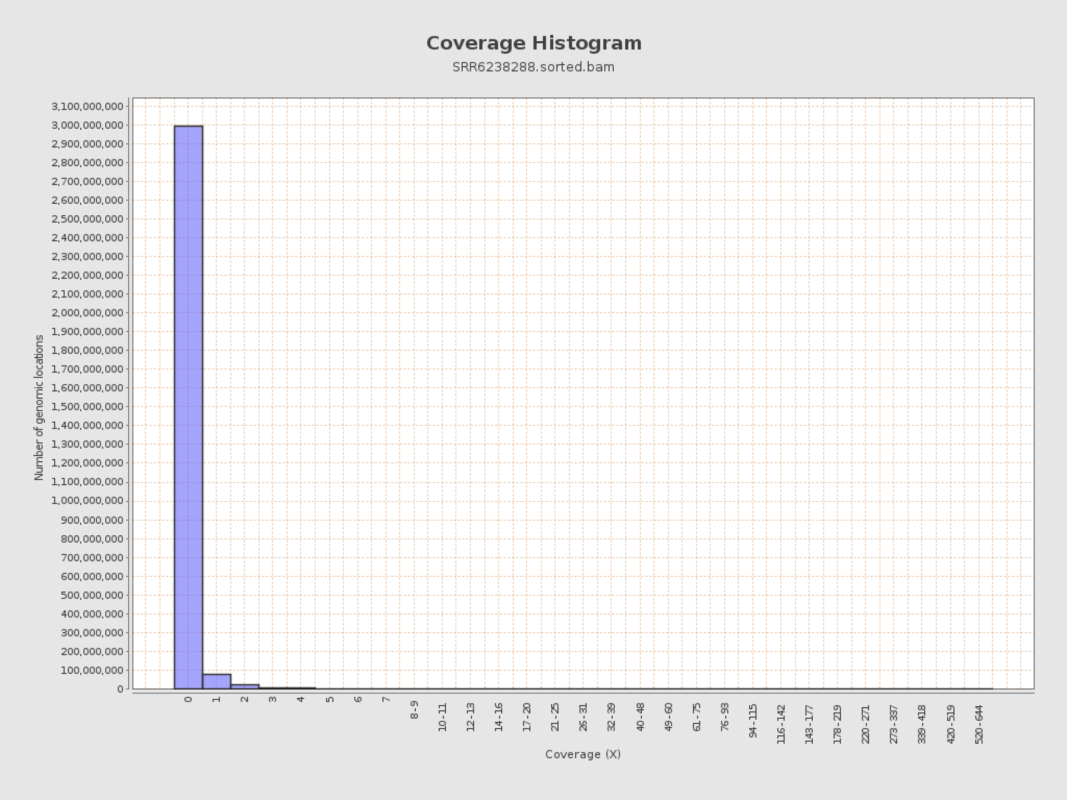
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11185207	0.0449	0.6137
chr2	243199373	11160107	0.0459	0.4355
chr3	198022430	9786894	0.0494	0.2917
chr4	191154276	8288093	0.0434	0.2831
chr5	180915260	9315892	0.0515	0.296
chr6	171115067	9210844	0.0538	0.3524
chr7	159138663	7075922	0.0445	0.4208

chr8	146364022	6901977	0.0472	0.4164
chr9	141213431	5219351	0.037	0.346
chr10	135534747	7383520	0.0545	0.4219
chr11	135006516	5961716	0.0442	0.3479
chr12	133851895	7767229	0.058	0.3194
chr13	115169878	4703699	0.0408	0.2632
chr14	107349540	4159229	0.0387	0.2801
chr15	102531392	3931638	0.0383	0.2625
chr16	90354753	3803335	0.0421	0.2893
chr17	81195210	3214146	0.0396	0.2862
chr18	78077248	3599033	0.0461	0.6448
chr19	59128983	2770320	0.0469	0.4917
chr20	63025520	2840920	0.0451	0.2855
chr21	48129895	1584306	0.0329	0.2492
chr22	51304566	1476365	0.0288	0.2182
chrMT	16571	9921	0.5987	0.9495
chrX	155270560	8326280	0.0536	0.3279
chrY	59373566	369714	0.0062	0.1439

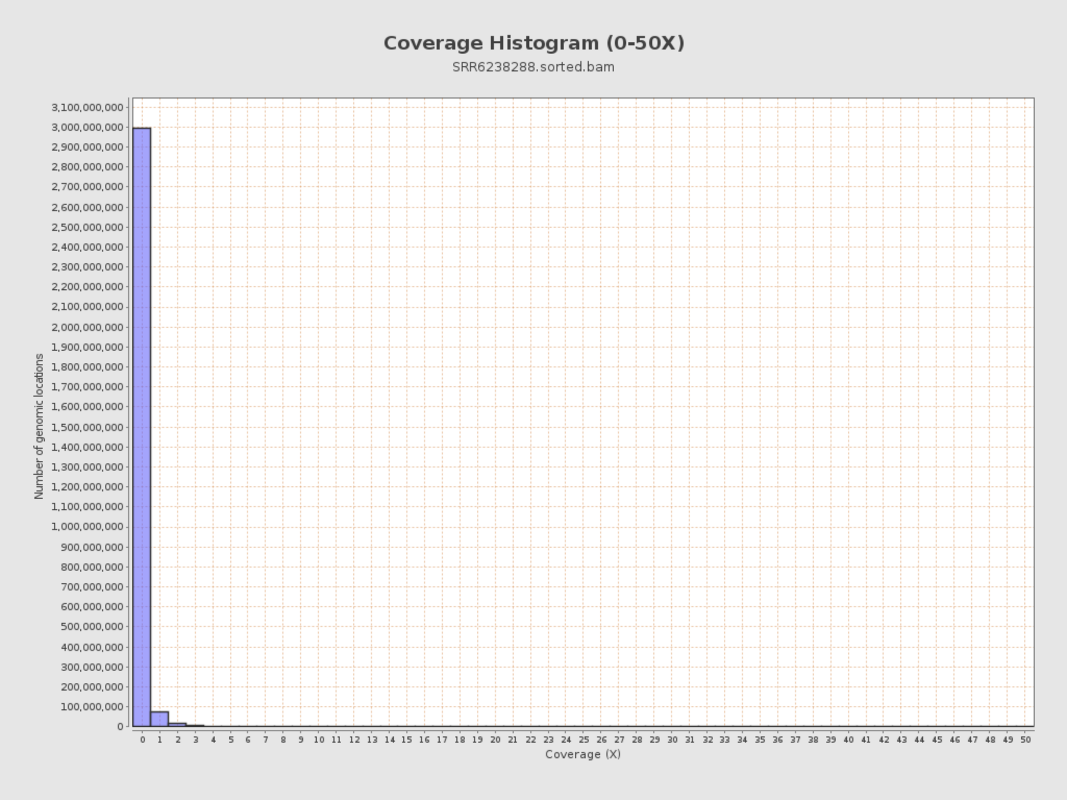
3. Results : Coverage across reference



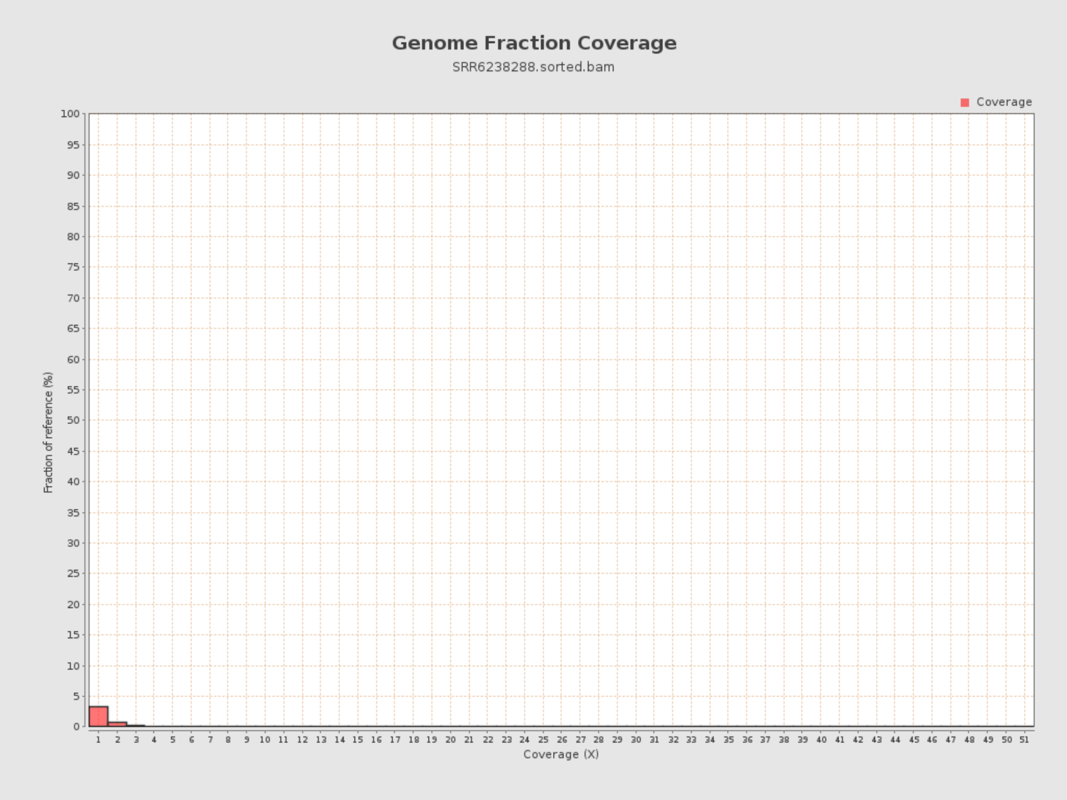
4. Results : Coverage Histogram



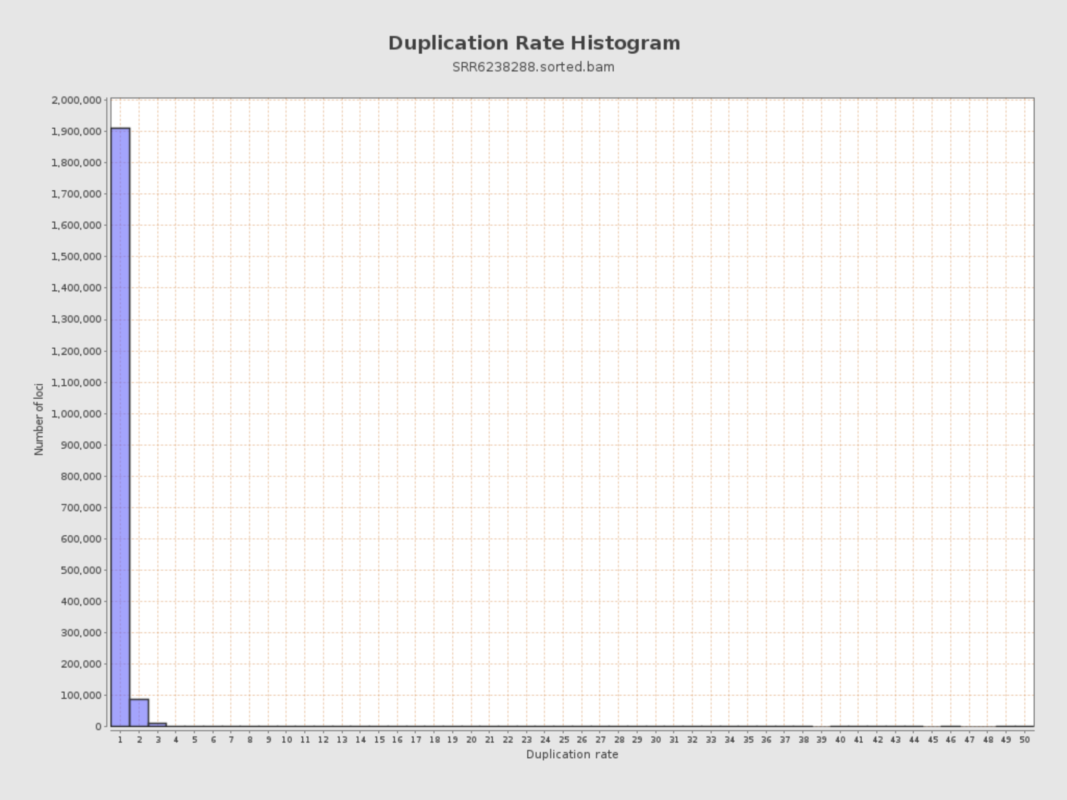
5. Results : Coverage Histogram (0-50X)



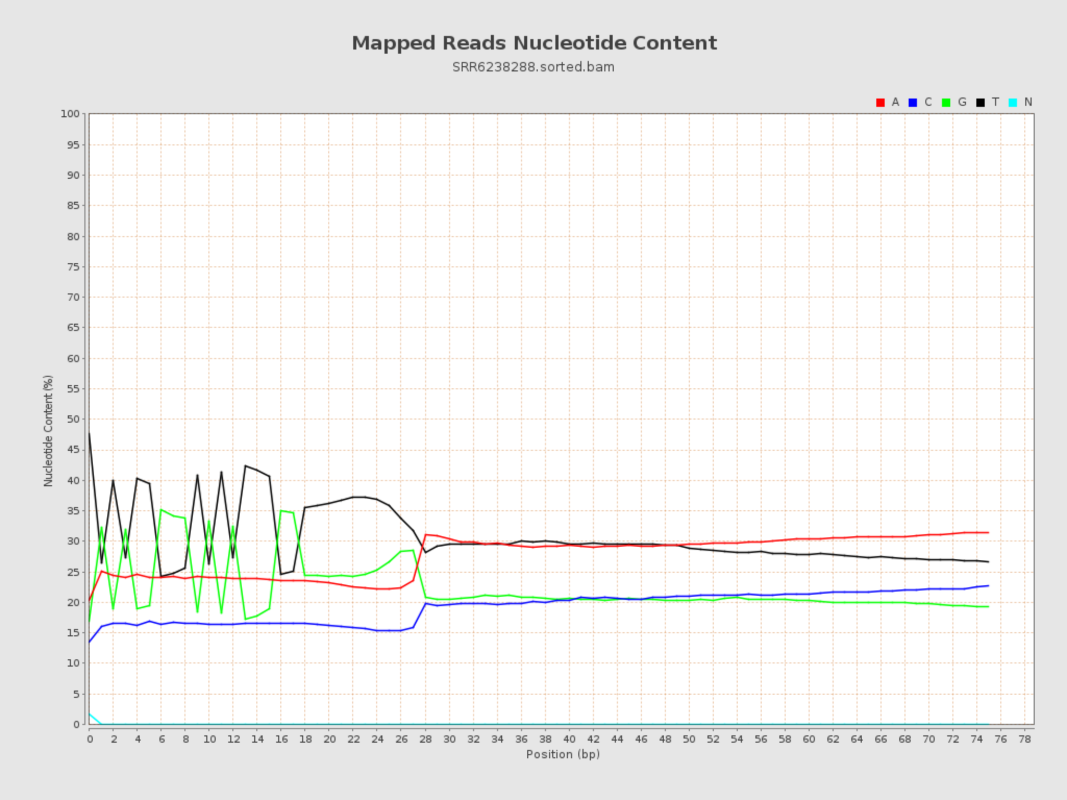
6. Results : Genome Fraction Coverage



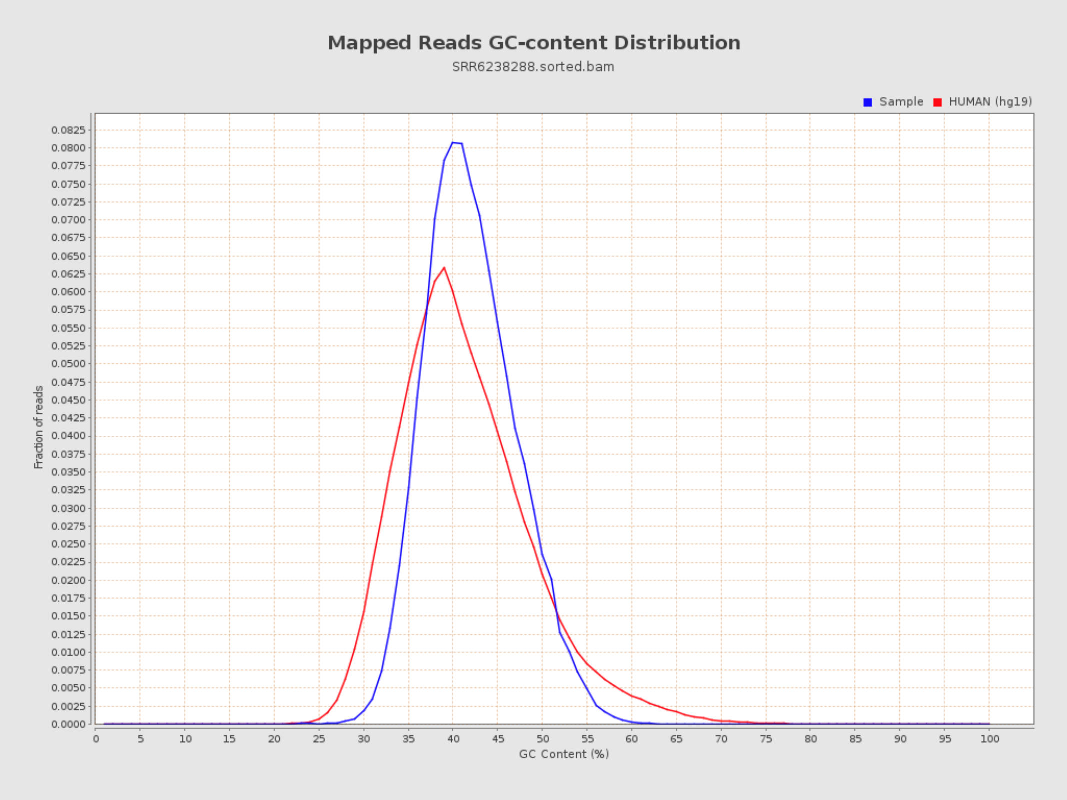
7. Results : Duplication Rate Histogram



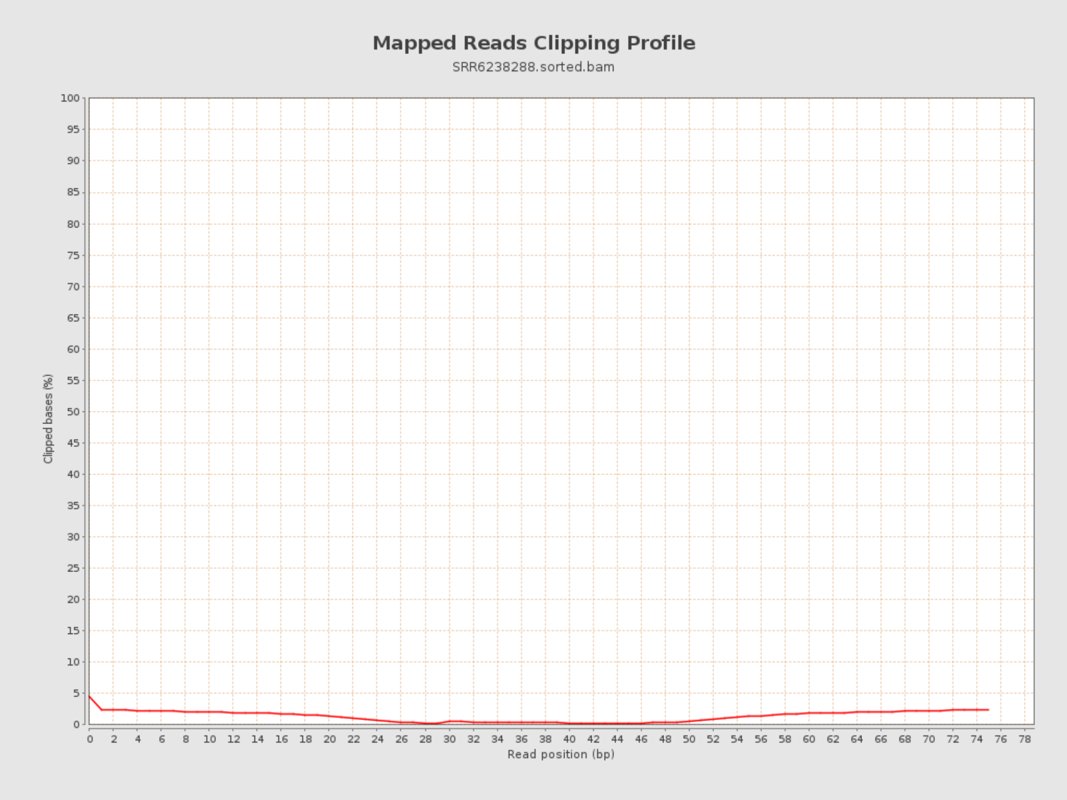
8. Results : Mapped Reads Nucleotide Content



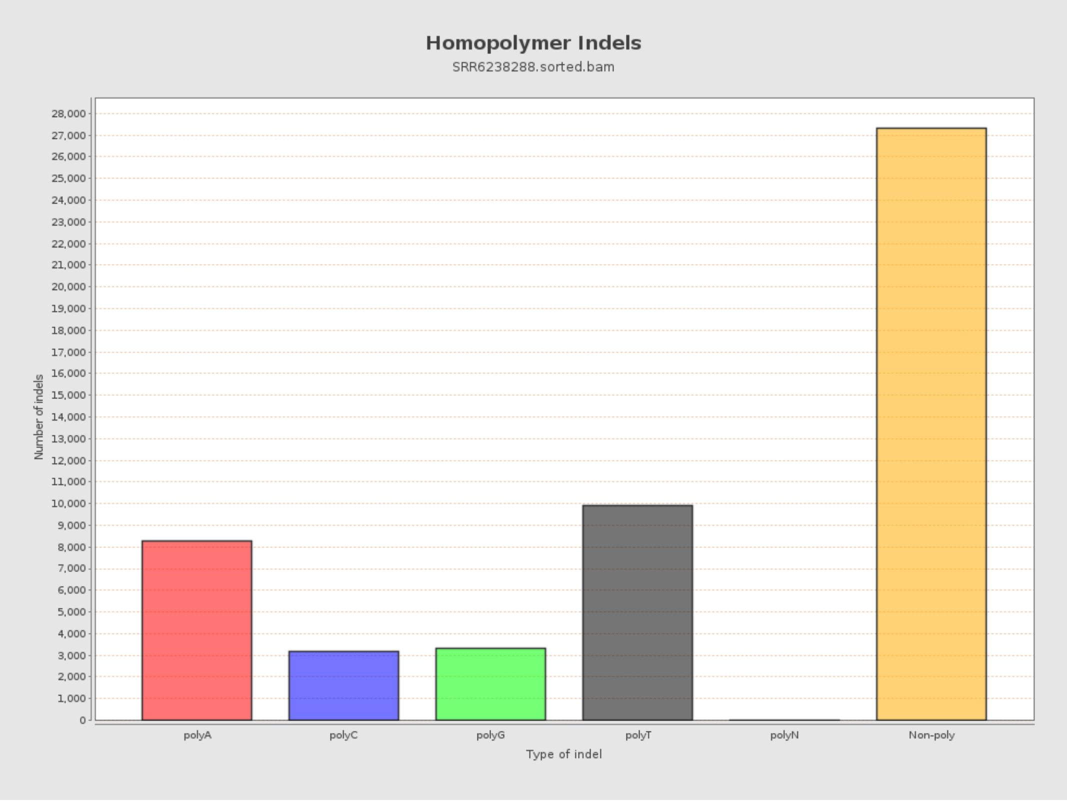
9. Results : Mapped Reads GC-content Distribution



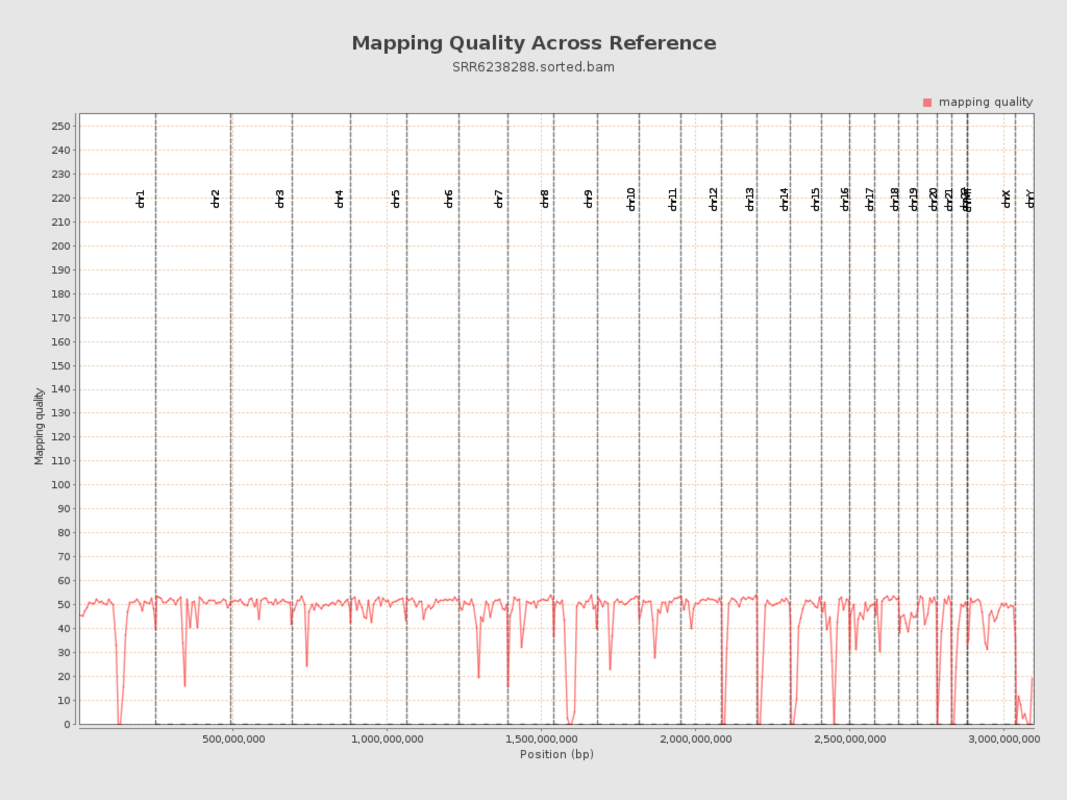
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram