Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 20:10:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238529.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_SRR6238529 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238529.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 20:10:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238529.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,812,102
Mapped reads	1,562,371 / 86.22%
Unmapped reads	249,731 / 13.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,833 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	442,379 / 24.41%
Duplication rate	18.9%
Clipped reads	1,029,087 / 56.79%

2.2. ACGT Content

Number/percentage of A's	23,419,707 / 24.62%
Number/percentage of C's	16,846,569 / 17.71%
Number/percentage of T's	31,960,362 / 33.6%
Number/percentage of G's	22,889,178 / 24.06%
Number/percentage of N's	6,335 / 0.01%
GC Percentage	41.77%

2.3. Coverage

Mean	0.0307

Standard Deviation	0.5763

2.4. Mapping Quality

Mean Mapping Quality	38.89

2.5. Mismatches and indels

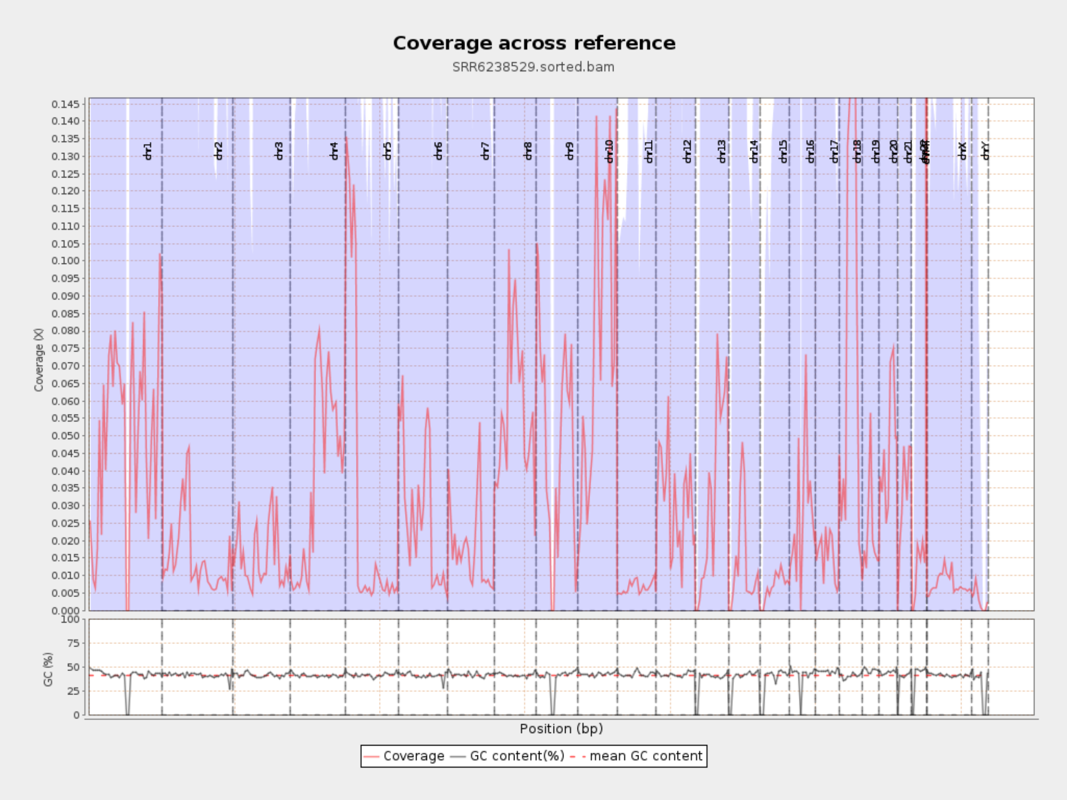
General error rate	0.69%
Mismatches	643,394
Insertions	5,769
Mapped reads with at least one insertion	0.37%
Deletions	32,609
Mapped reads with at least one deletion	2.06%
Homopolymer indels	39.14%

2.6. Chromosome stats

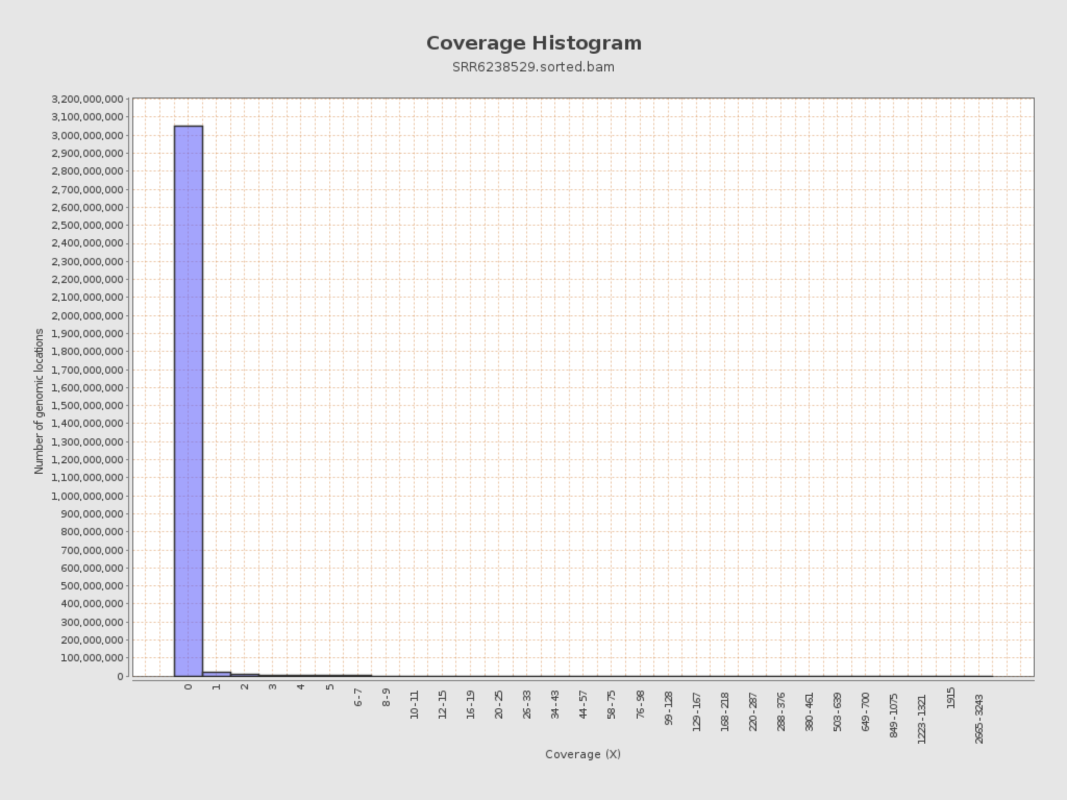
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12576995	0.0505	0.5656
chr2	243199373	3750155	0.0154	1.4244
chr3	198022430	3113421	0.0157	0.2419
chr4	191154276	7387989	0.0386	0.3773
chr5	180915260	5565168	0.0308	0.355
chr6	171115067	4724197	0.0276	0.55
chr7	159138663	2754559	0.0173	0.2958

chr8	146364022	8444532	0.0577	0.5198
chr9	141213431	6685849	0.0473	0.487
chr10	135534747	10467145	0.0772	0.5821
chr11	135006516	916289	0.0068	0.1563
chr12	133851895	4186401	0.0313	0.3521
chr13	115169878	3892954	0.0338	0.458
chr14	107349540	1509780	0.0141	0.264
chr15	102531392	707477	0.0069	0.3393
chr16	90354753	2476678	0.0274	0.3606
chr17	81195210	1238071	0.0152	0.2346
chr18	78077248	6872238	0.088	1.0869
chr19	59128983	1351019	0.0228	0.3802
chr20	63025520	2932899	0.0465	0.4295
chr21	48129895	1558447	0.0324	0.3554
chr22	51304566	590105	0.0115	0.1983
chrMT	16571	101550	6.1282	5.2274
chrX	155270560	1198853	0.0077	0.1684
chrY	59373566	173726	0.0029	0.1788

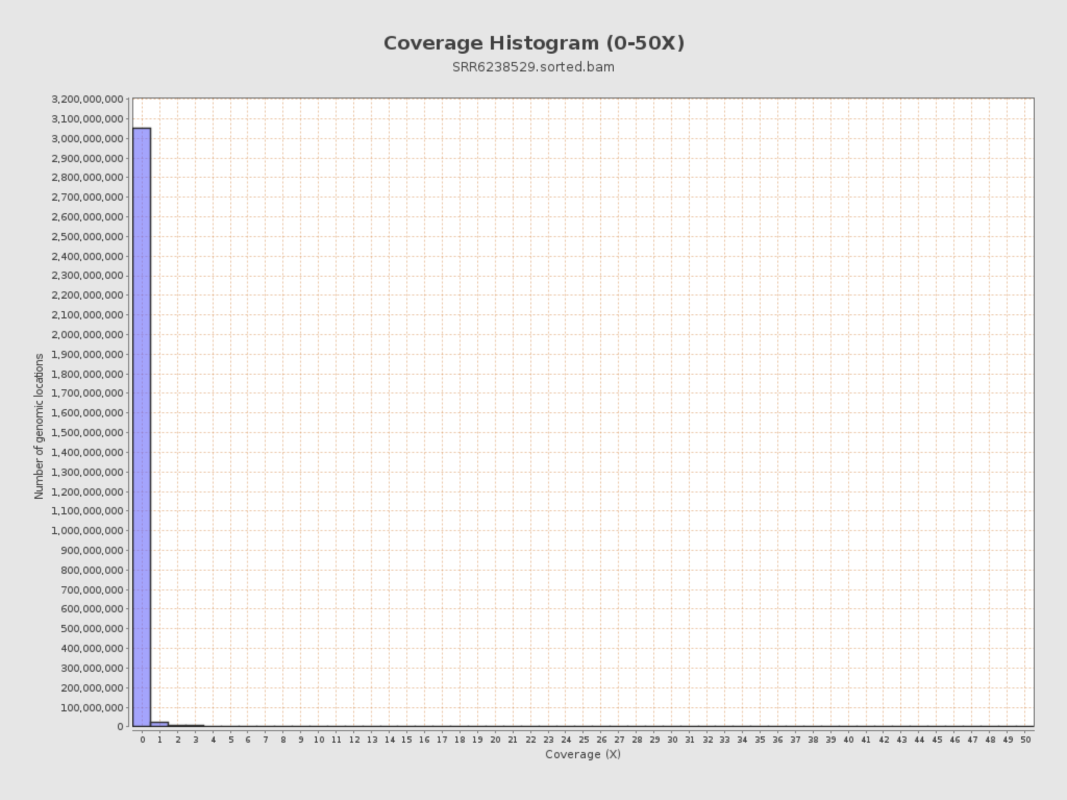
3. Results : Coverage across reference



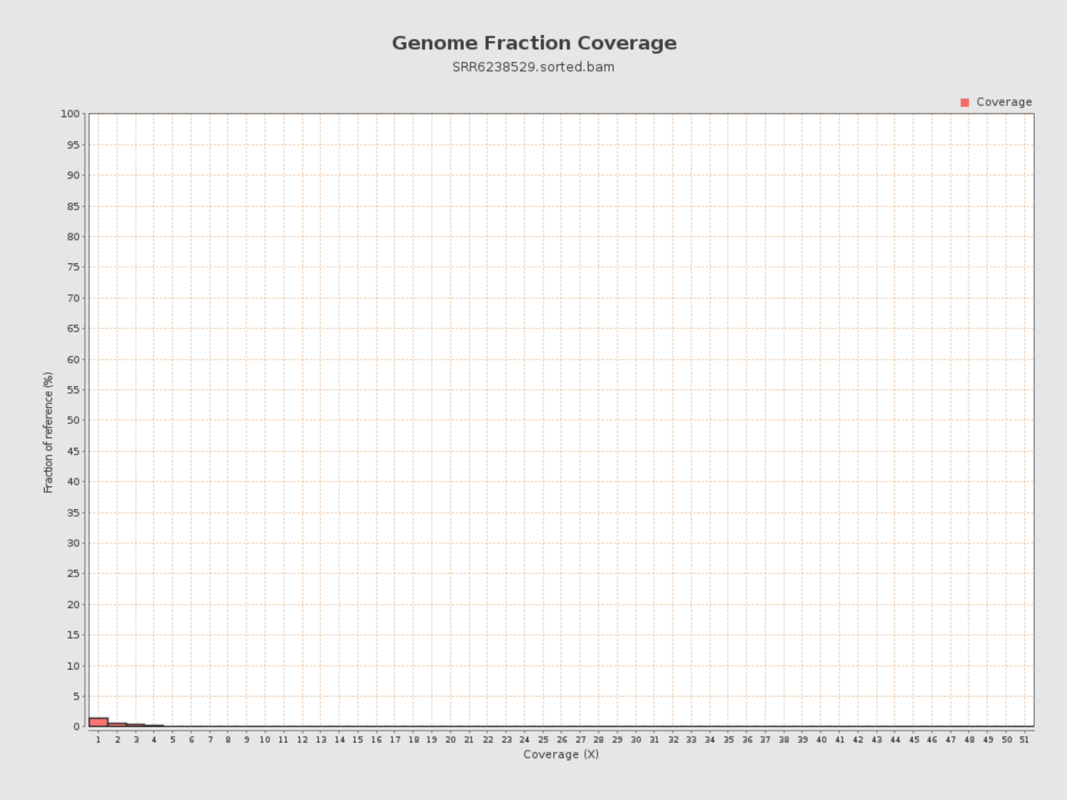
4. Results : Coverage Histogram



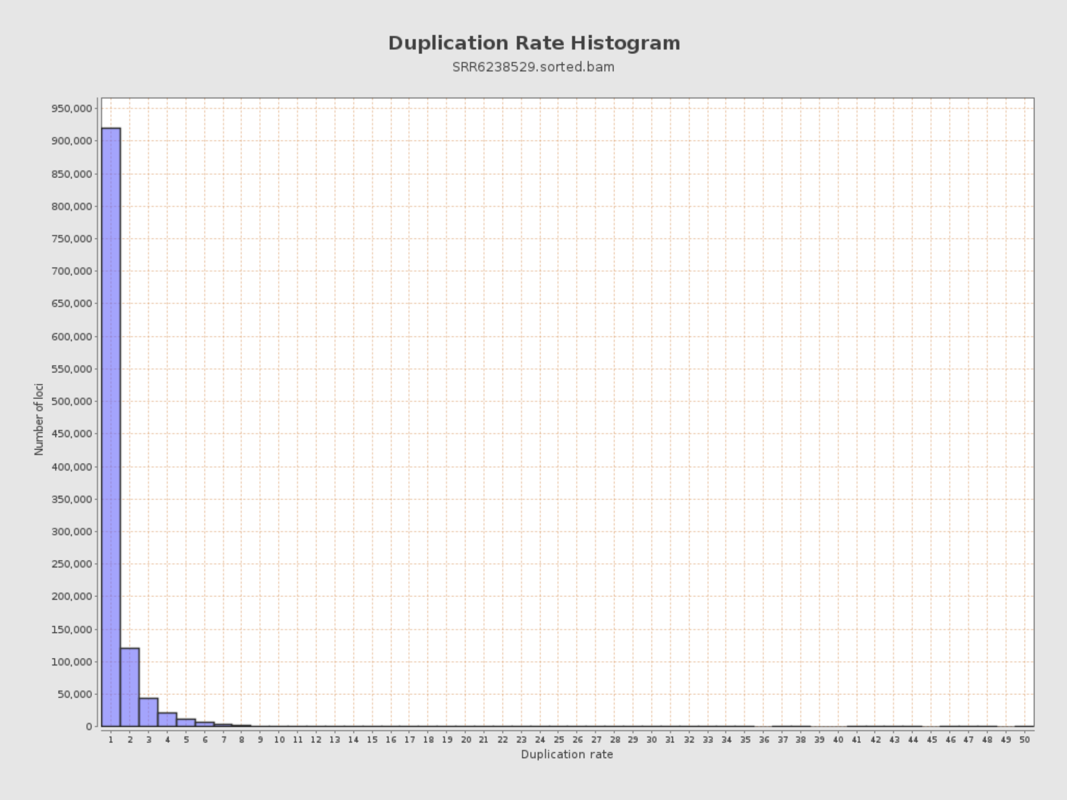
5. Results : Coverage Histogram (0-50X)



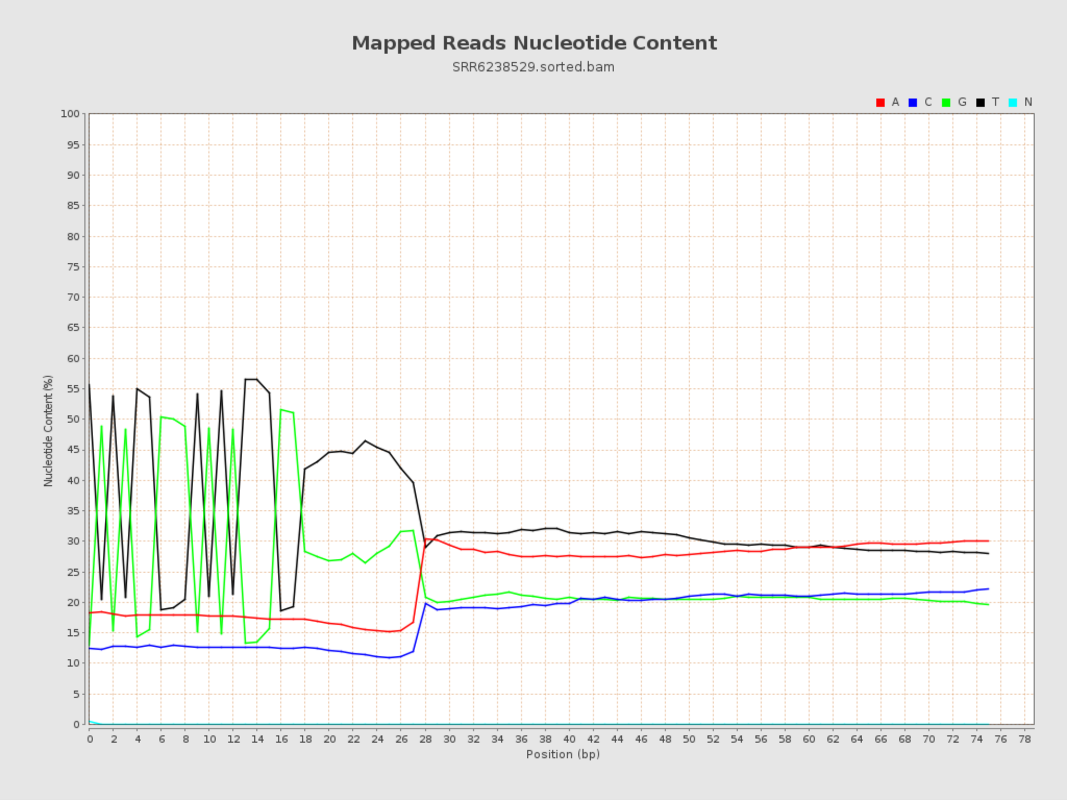
6. Results : Genome Fraction Coverage



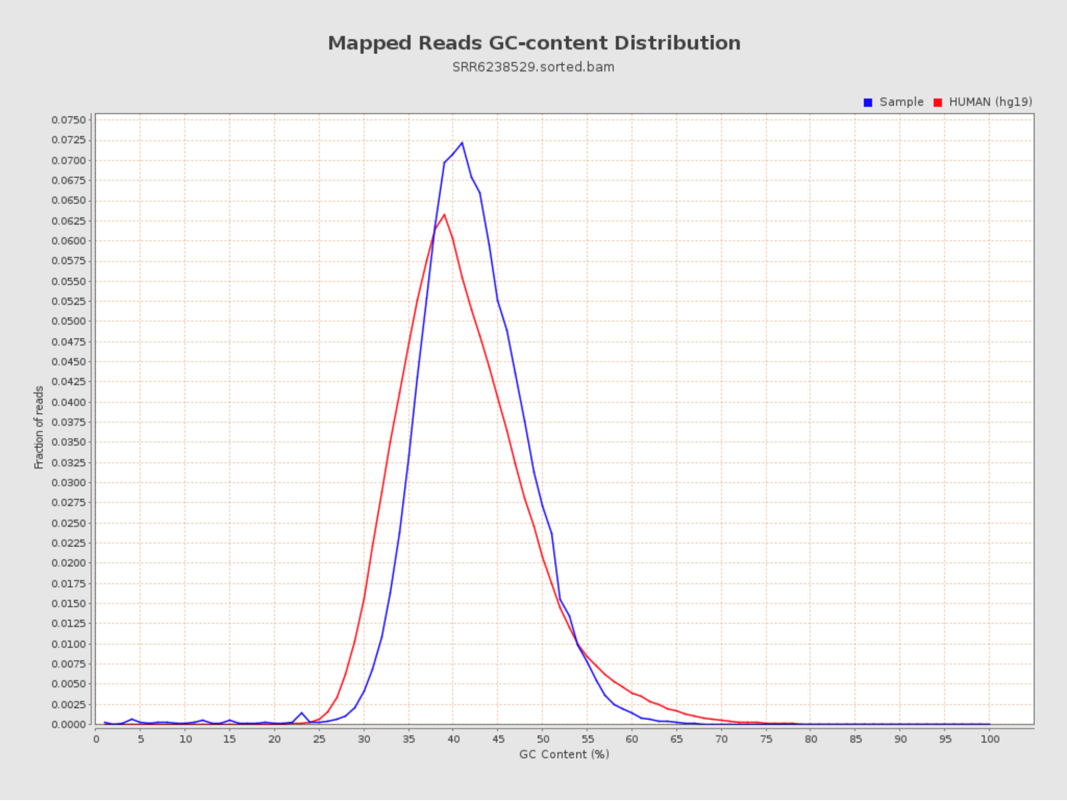
7. Results : Duplication Rate Histogram



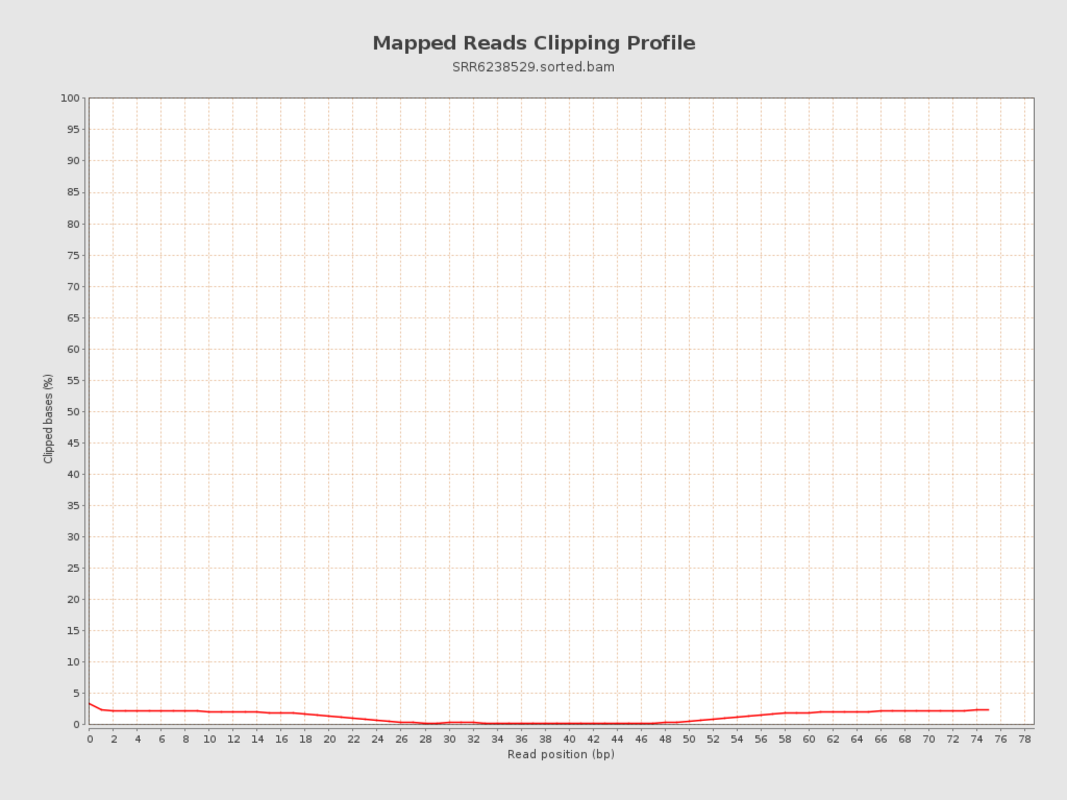
8. Results : Mapped Reads Nucleotide Content



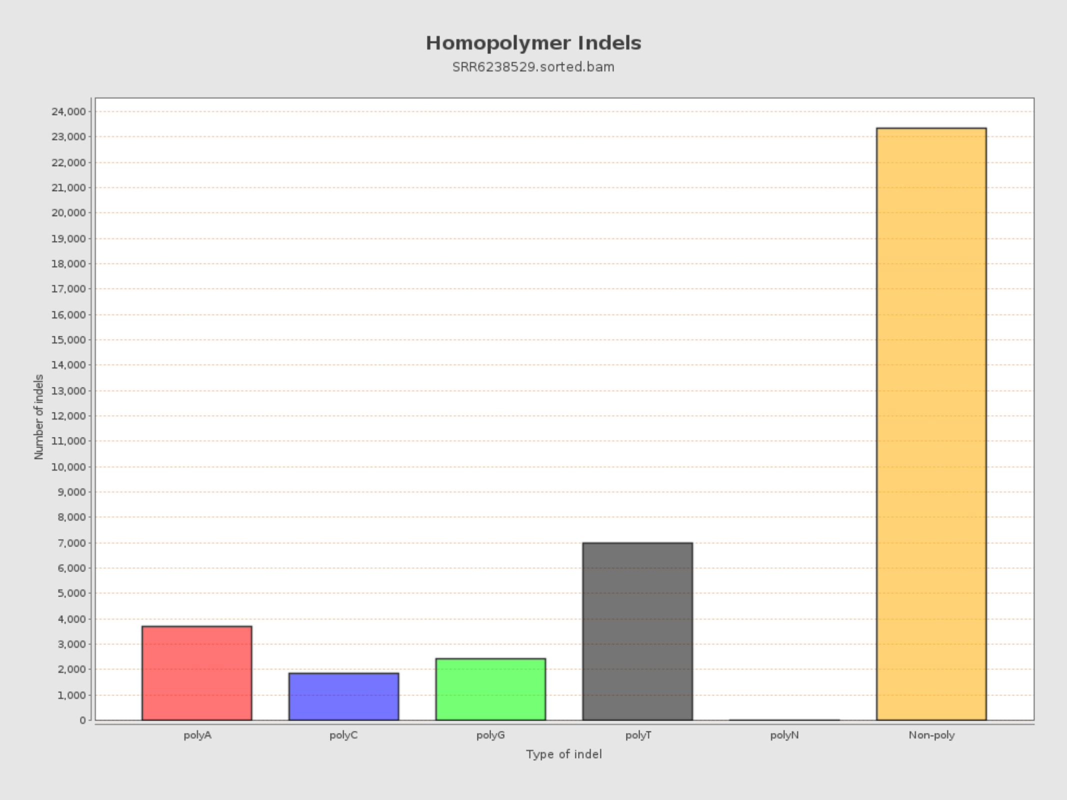
9. Results : Mapped Reads GC-content Distribution



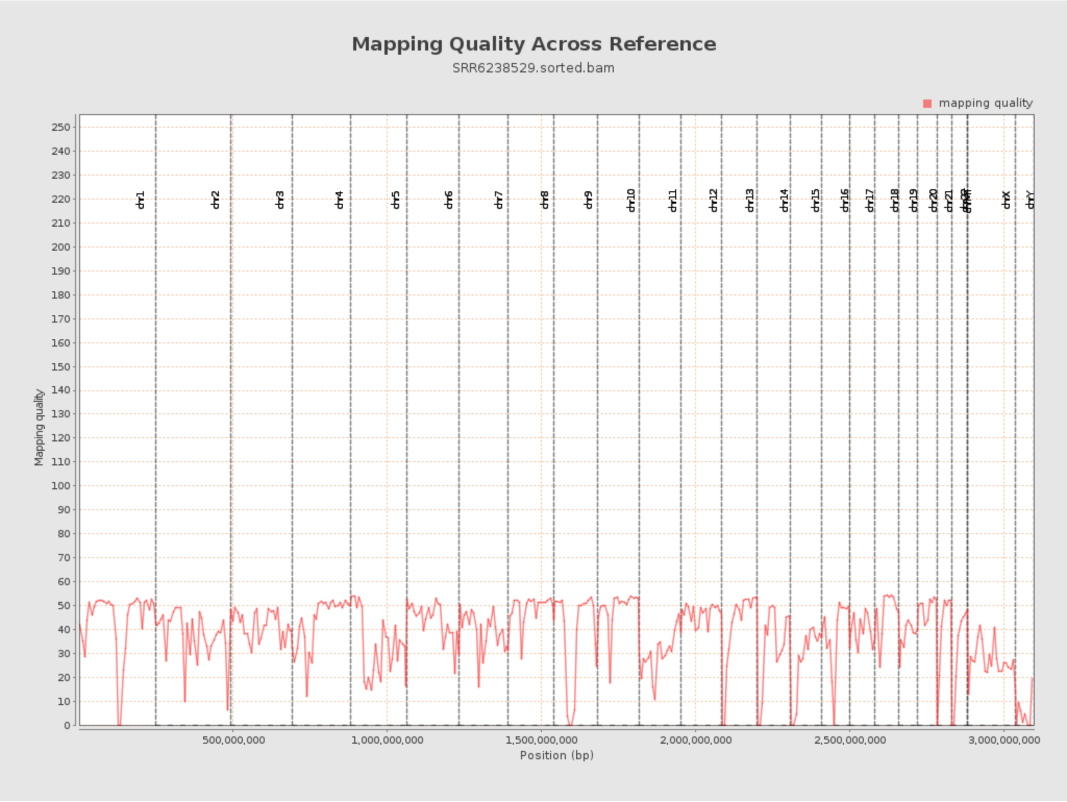
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram