Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 10:58:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238053.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_SRR6238053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 10:58:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,119,940
Mapped reads	1,902,340 / 89.74%
Unmapped reads	217,600 / 10.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,300 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	101,879 / 4.81%
Duplication rate	3.99%
Clipped reads	777,361 / 36.67%

2.2. ACGT Content

Number/percentage of A's	35,179,027 / 27.36%
Number/percentage of C's	24,725,897 / 19.23%
Number/percentage of T's	39,825,588 / 30.97%
Number/percentage of G's	28,830,105 / 22.42%
Number/percentage of N's	17,540 / 0.01%
GC Percentage	41.65%

2.3. Coverage

Mean	0.0415

Standard Deviation	0.4473

2.4. Mapping Quality

Mean Mapping Quality	46.51

2.5. Mismatches and indels

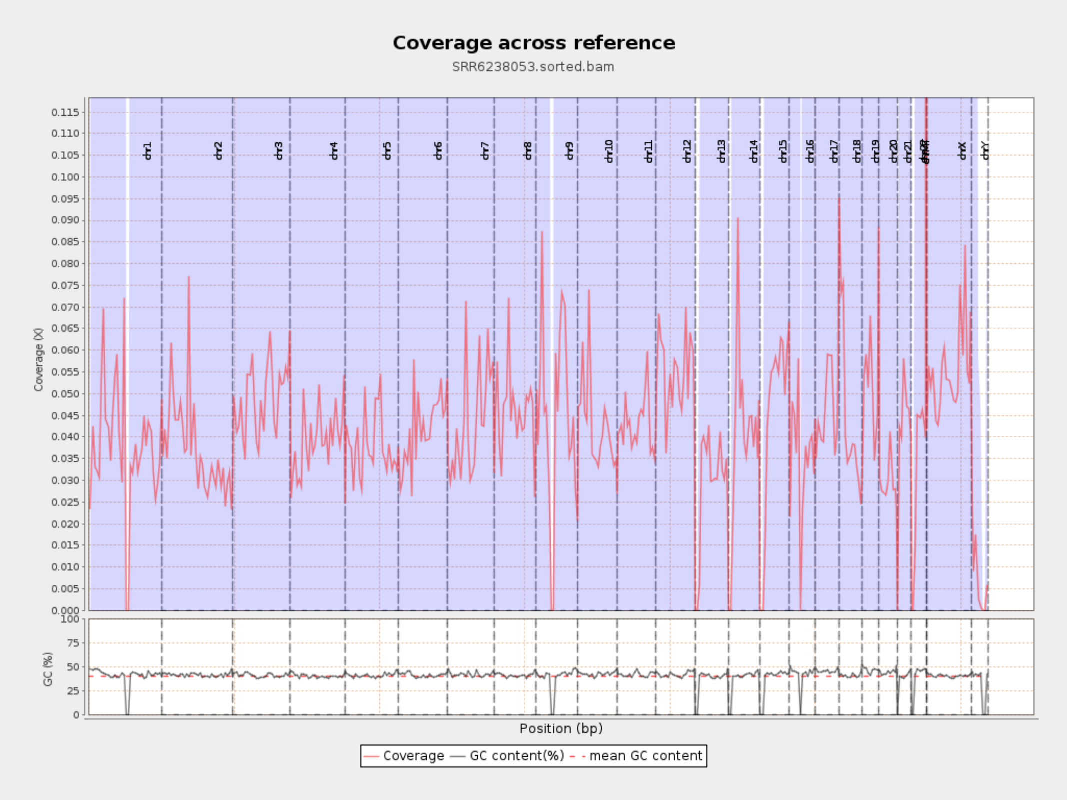
General error rate	0.75%
Mismatches	943,079
Insertions	9,023
Mapped reads with at least one insertion	0.47%
Deletions	26,973
Mapped reads with at least one deletion	1.4%
Homopolymer indels	46.58%

2.6. Chromosome stats

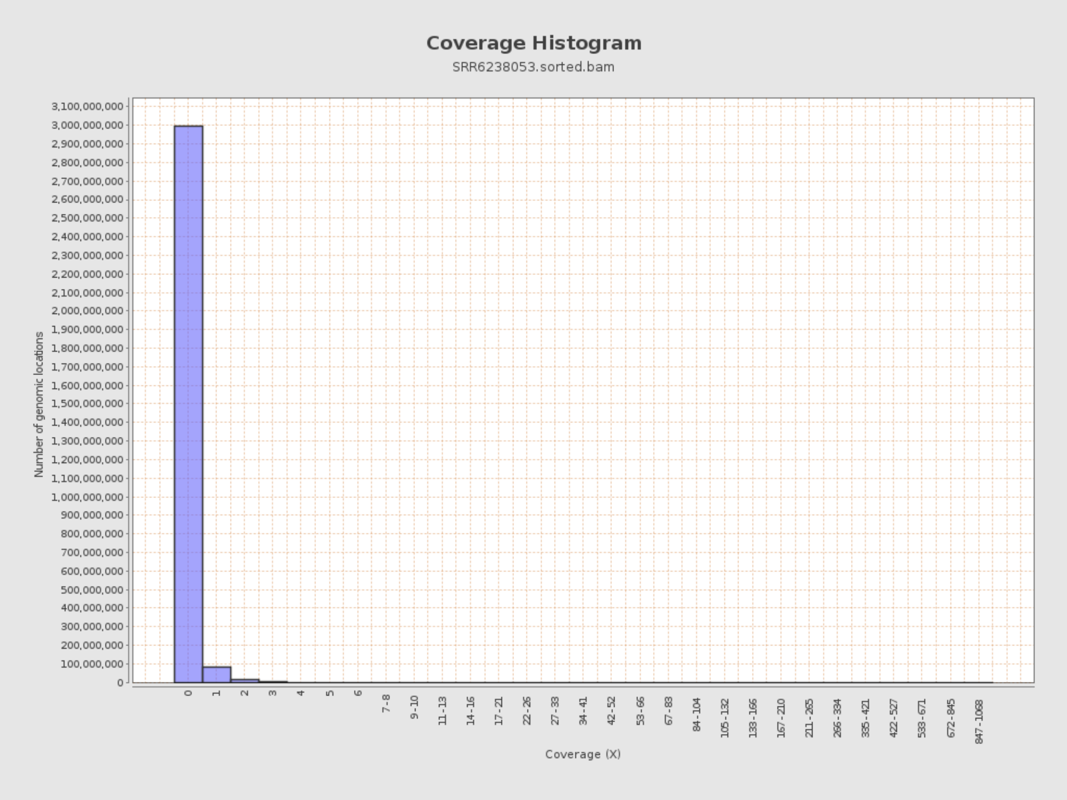
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9399720	0.0377	0.9295
chr2	243199373	9154853	0.0376	0.4781
chr3	198022430	9641064	0.0487	0.272
chr4	191154276	7456209	0.039	0.2555
chr5	180915260	6851347	0.0379	0.2414
chr6	171115067	7139298	0.0417	0.3029
chr7	159138663	6893726	0.0433	0.5052

chr8	146364022	6748679	0.0461	0.4171
chr9	141213431	6328186	0.0448	0.449
chr10	135534747	5821059	0.0429	0.4313
chr11	135006516	5760118	0.0427	0.3753
chr12	133851895	7338213	0.0548	0.3021
chr13	115169878	3318103	0.0288	0.2078
chr14	107349540	4252590	0.0396	0.2871
chr15	102531392	4567407	0.0445	0.2599
chr16	90354753	3163212	0.035	0.2898
chr17	81195210	3766040	0.0464	0.2989
chr18	78077248	3541119	0.0454	0.8724
chr19	59128983	3099167	0.0524	0.6114
chr20	63025520	1858175	0.0295	0.2224
chr21	48129895	2008180	0.0417	0.2938
chr22	51304566	1573626	0.0307	0.2134
chrMT	16571	40301	2.432	2.2189
chrX	155270560	8511194	0.0548	0.3194
chrY	59373566	394242	0.0066	0.1355

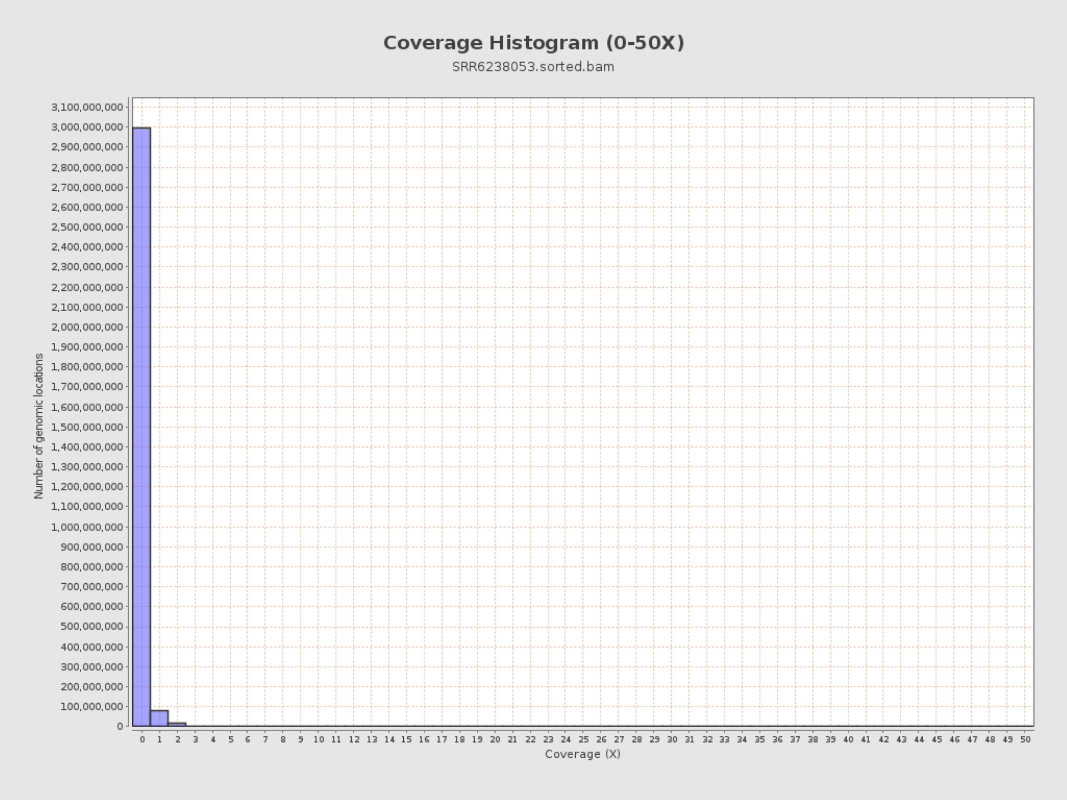
3. Results : Coverage across reference



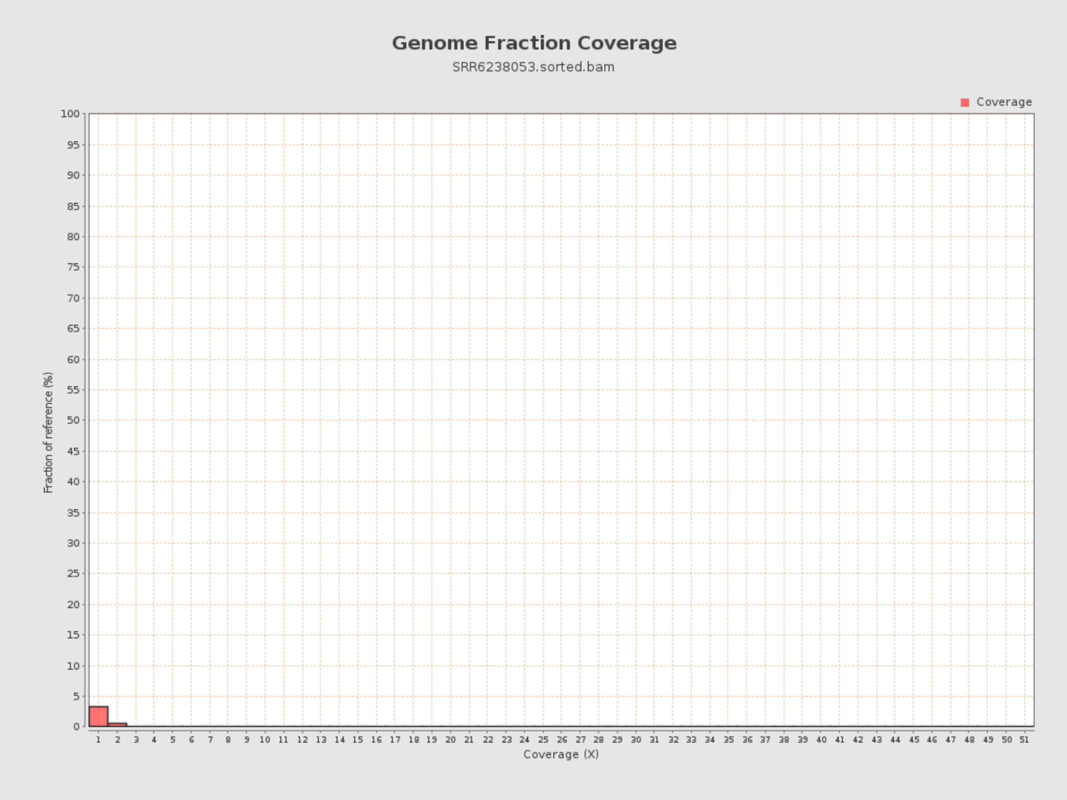
4. Results : Coverage Histogram



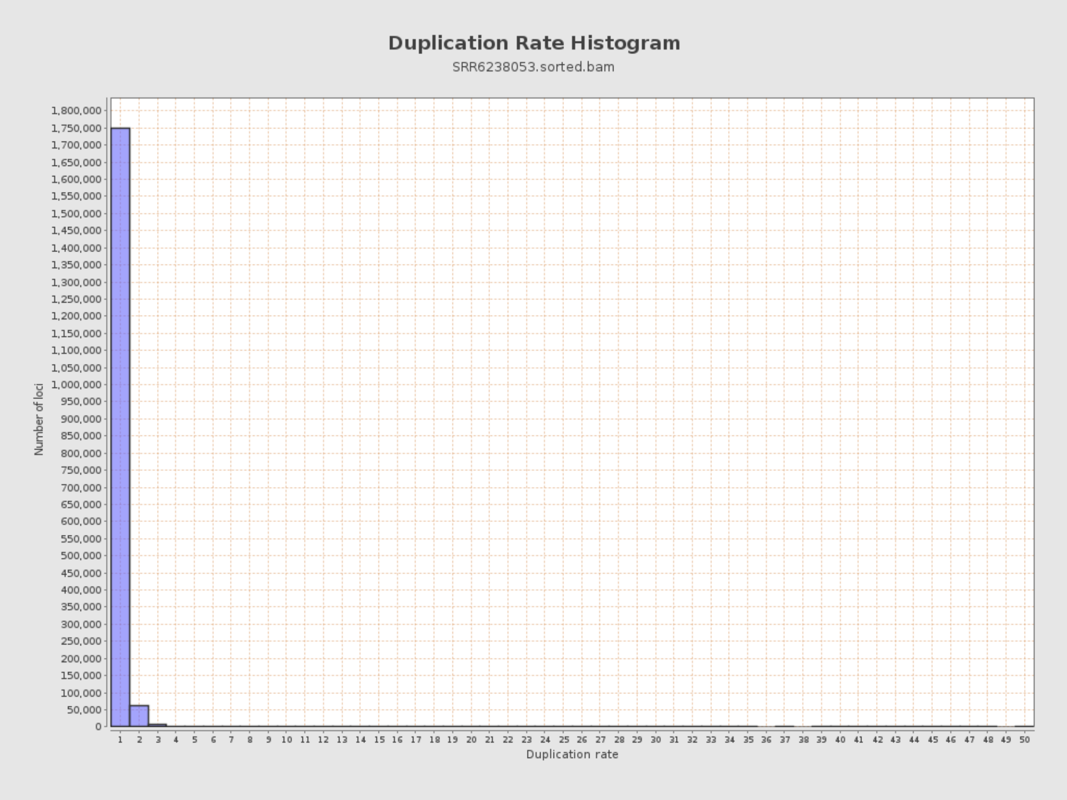
5. Results : Coverage Histogram (0-50X)



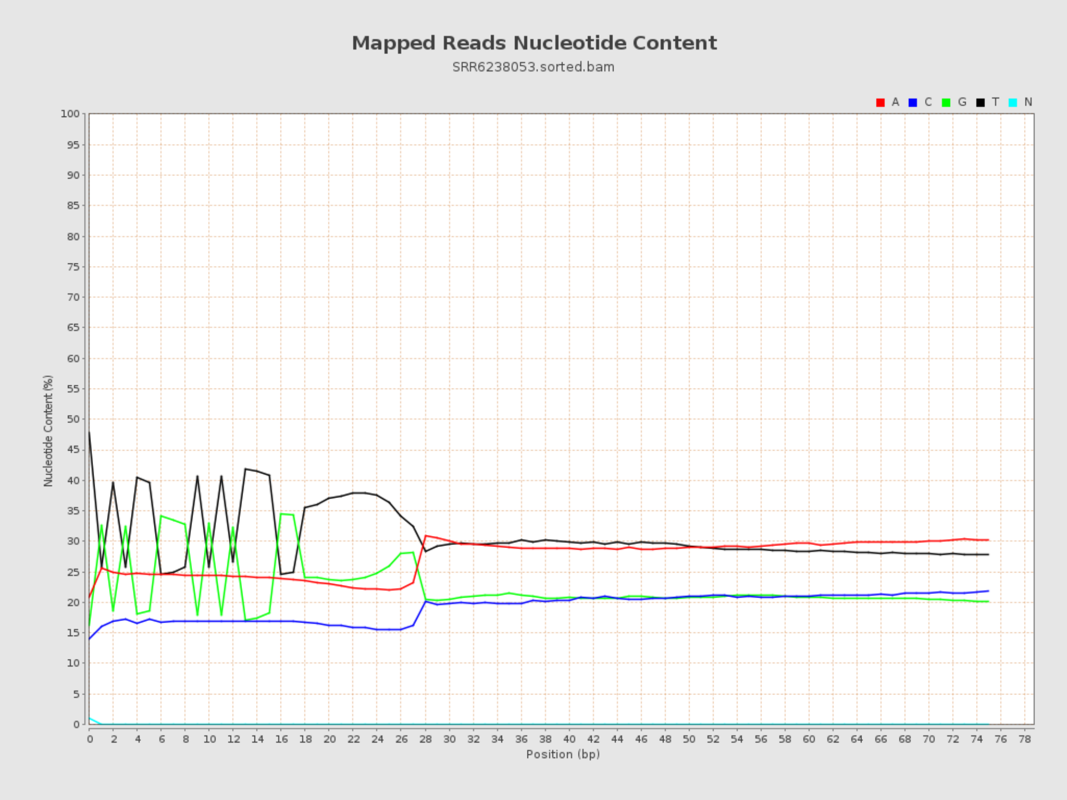
6. Results : Genome Fraction Coverage



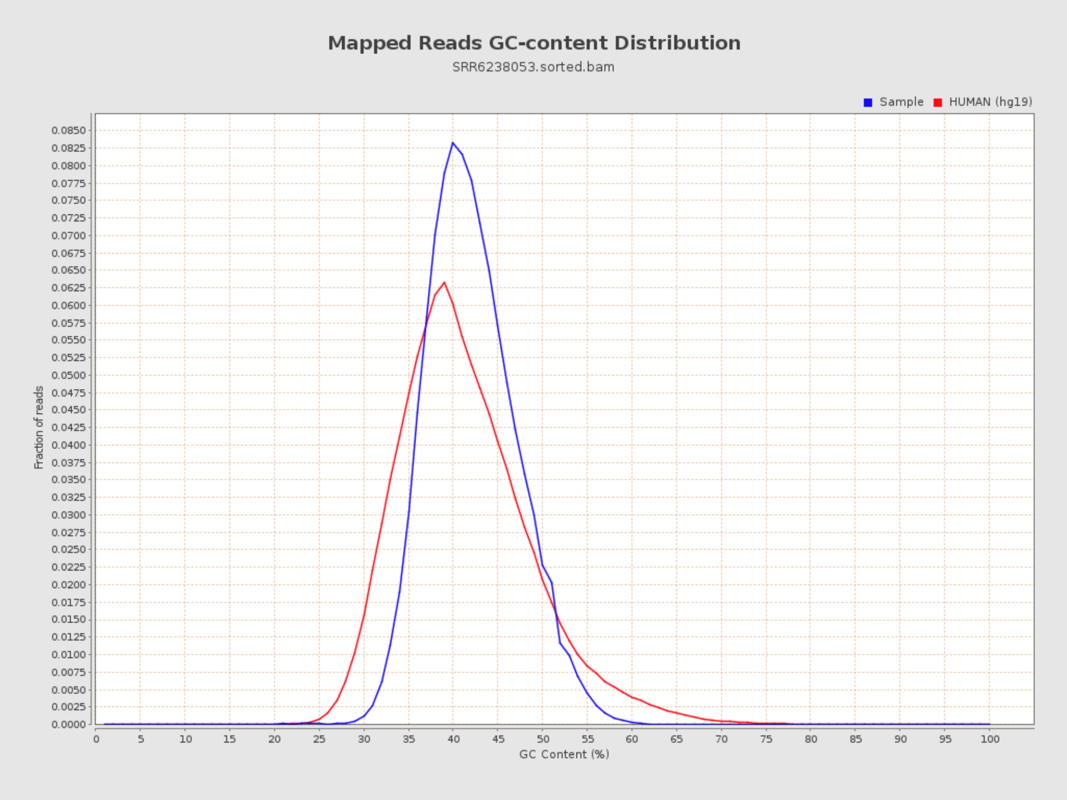
7. Results : Duplication Rate Histogram



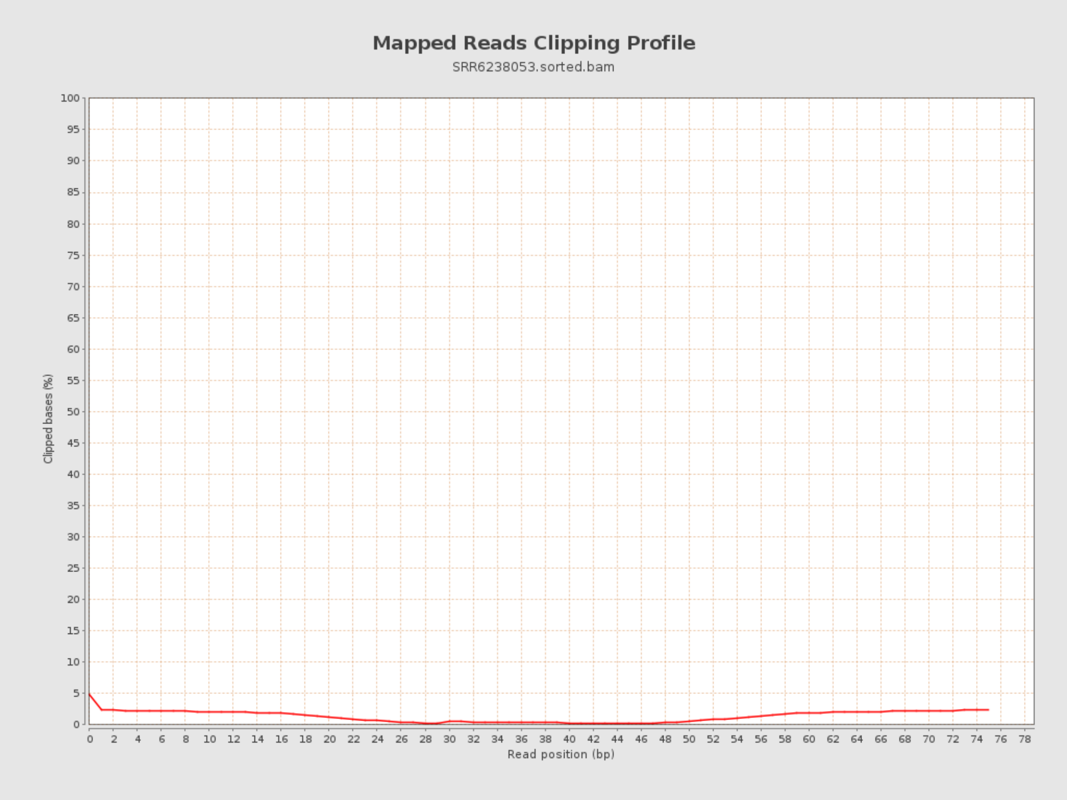
8. Results : Mapped Reads Nucleotide Content



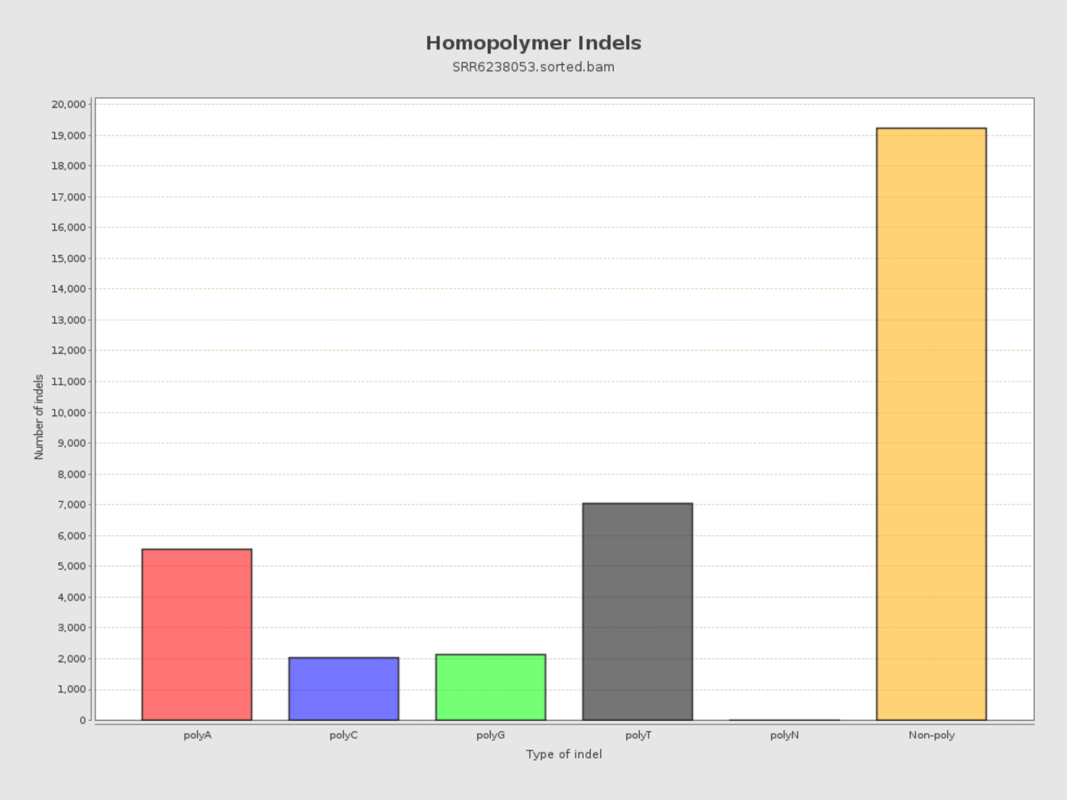
9. Results : Mapped Reads GC-content Distribution



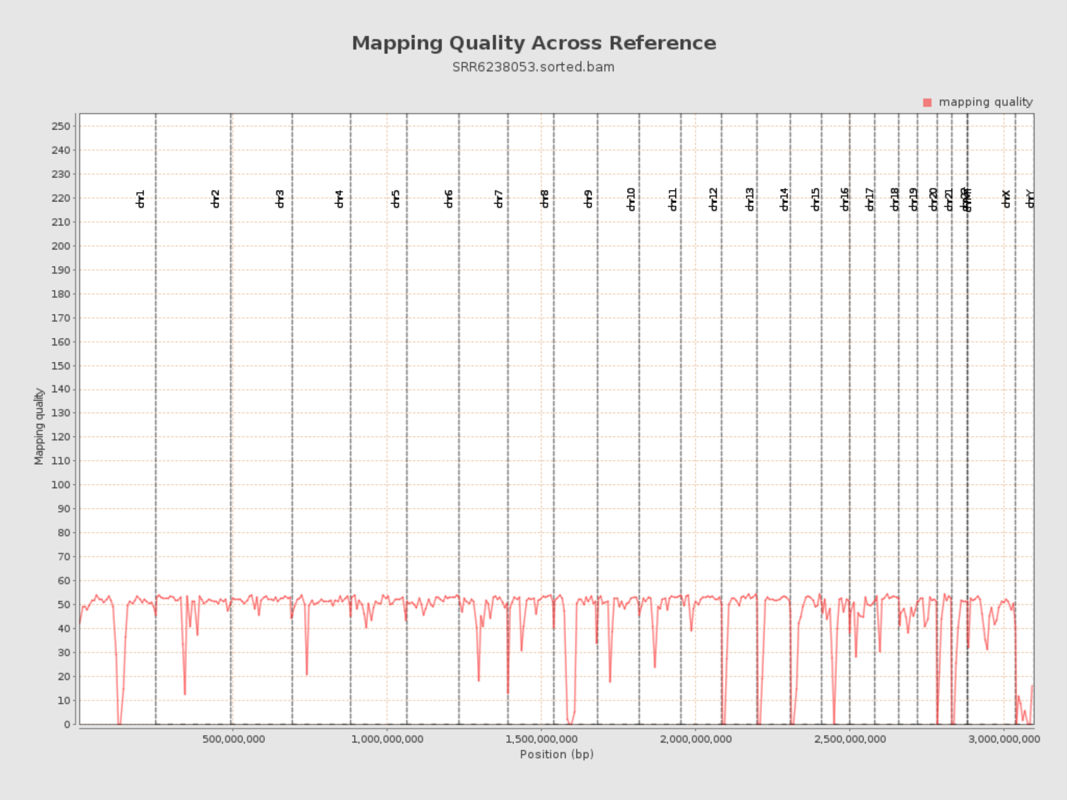
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram