Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:34:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751201.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_SRR8751201 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751201.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:34:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751201.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,795,459
Mapped reads	6,601,091 / 97.14%
Unmapped reads	194,368 / 2.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	91,429 / 1.35%
Read min/max/mean length	30 / 151 / 151.7
Duplicated reads (estimated)	1,036,886 / 15.26%
Duplication rate	15.24%
Clipped reads	1,423,072 / 20.94%

2.2. ACGT Content

Number/percentage of A's	269,706,564 / 28.25%
Number/percentage of C's	208,295,780 / 21.82%
Number/percentage of T's	272,554,979 / 28.55%
Number/percentage of G's	204,110,265 / 21.38%
Number/percentage of N's	9,396 / 0%
GC Percentage	43.2%

2.3. Coverage

Mean	0.3085

Standard Deviation	1.3436

2.4. Mapping Quality

Mean Mapping Quality	52.84

2.5. Mismatches and indels

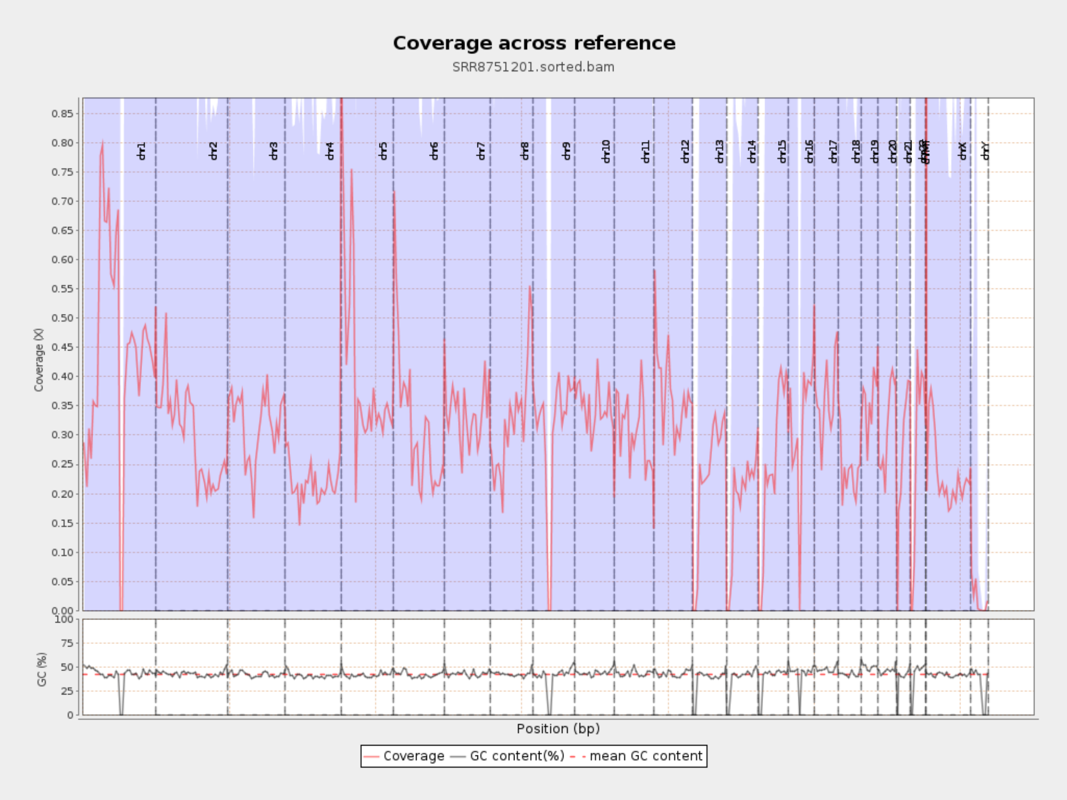
General error rate	0.72%
Mismatches	6,612,685
Insertions	113,697
Mapped reads with at least one insertion	1.68%
Deletions	108,472
Mapped reads with at least one deletion	1.6%
Homopolymer indels	47.41%

2.6. Chromosome stats

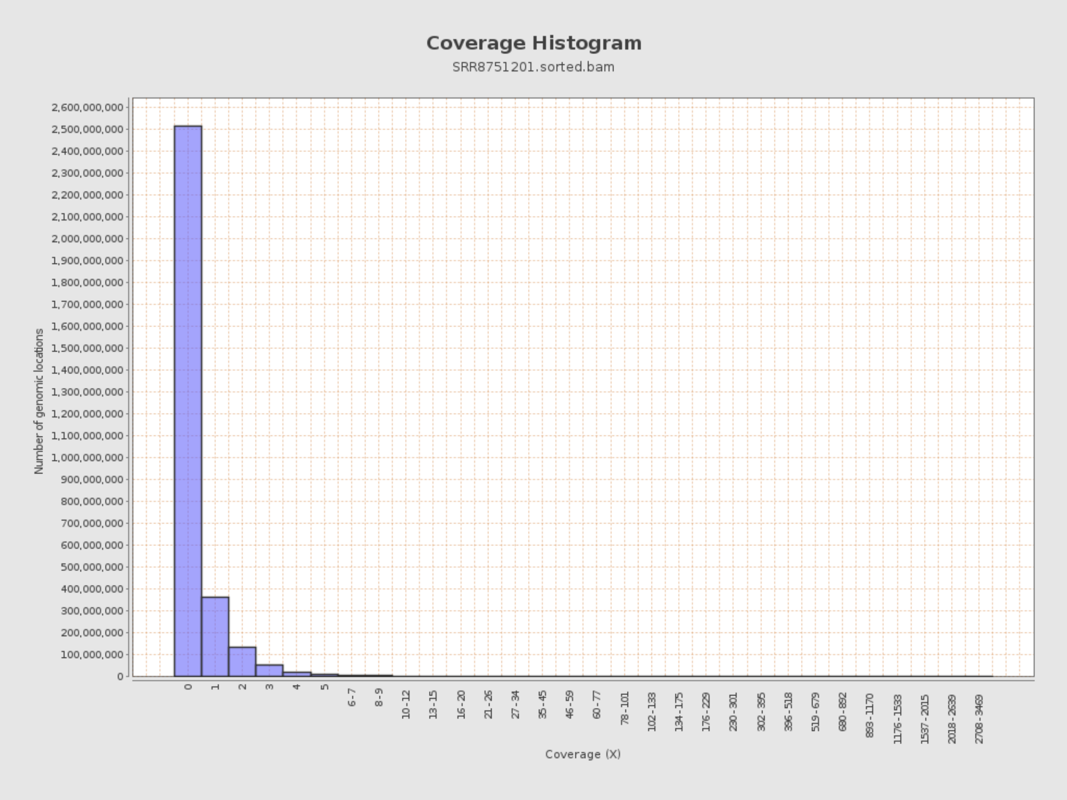
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	112220657	0.4502	3.2139
chr2	243199373	71778995	0.2951	0.906
chr3	198022430	62713384	0.3167	0.784
chr4	191154276	41778298	0.2186	0.6873
chr5	180915260	73556638	0.4066	0.9092
chr6	171115067	53808830	0.3145	1.1114
chr7	159138663	53835076	0.3383	0.9847

chr8	146364022	47593855	0.3252	0.8104
chr9	141213431	43646414	0.3091	0.9817
chr10	135534747	47071426	0.3473	1.7372
chr11	135006516	41322479	0.3061	1.0015
chr12	133851895	50207980	0.3751	0.9063
chr13	115169878	26577691	0.2308	0.6716
chr14	107349540	19927257	0.1856	0.6001
chr15	102531392	25234325	0.2461	0.7289
chr16	90354753	28298572	0.3132	0.8141
chr17	81195210	29425579	0.3624	1.1402
chr18	78077248	18632655	0.2386	1.0723
chr19	59128983	21055182	0.3561	2.1389
chr20	63025520	19775919	0.3138	0.8357
chr21	48129895	13130642	0.2728	0.8027
chr22	51304566	13694281	0.2669	0.7836
chrMT	16571	2074632	125.1965	56.718
chrX	155270560	36498597	0.2351	0.7192
chrY	59373566	1098325	0.0185	0.4662

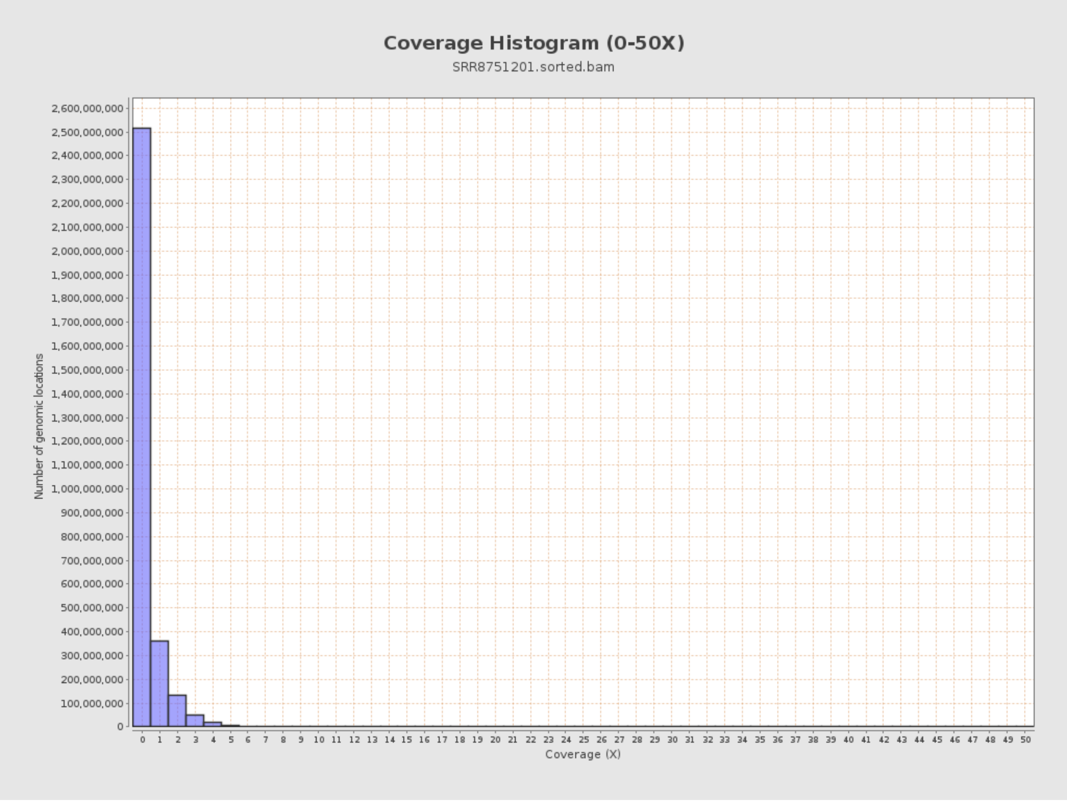
3. Results : Coverage across reference



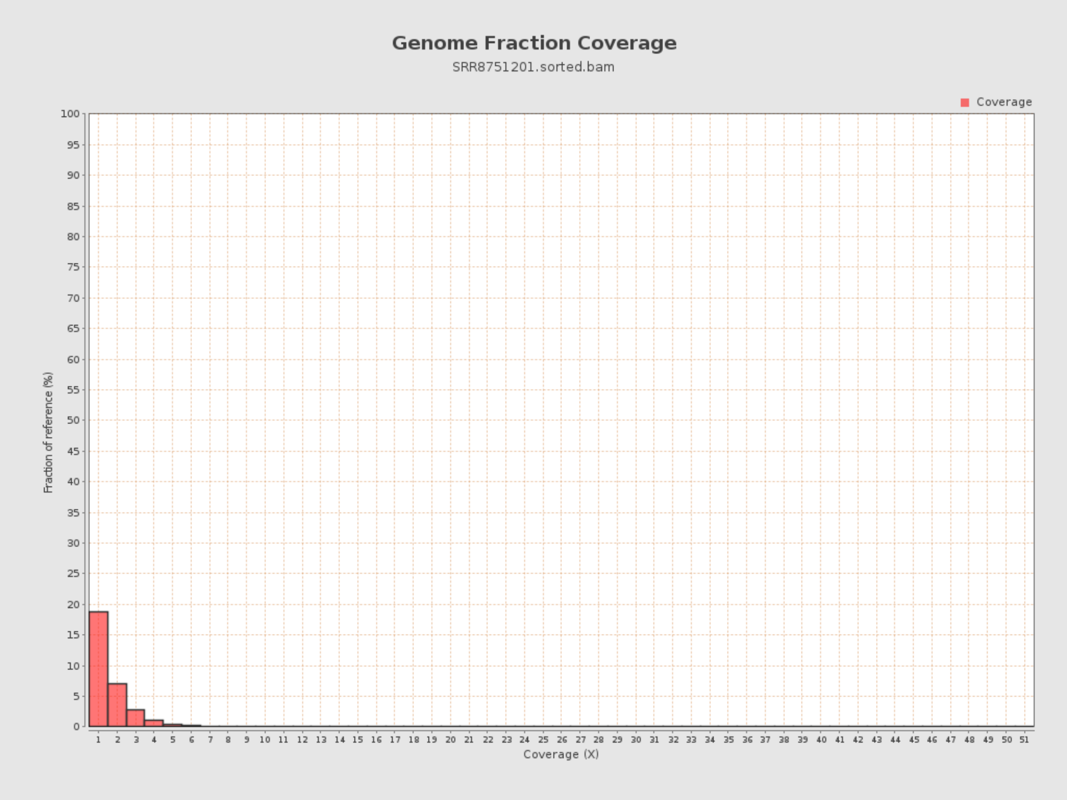
4. Results : Coverage Histogram



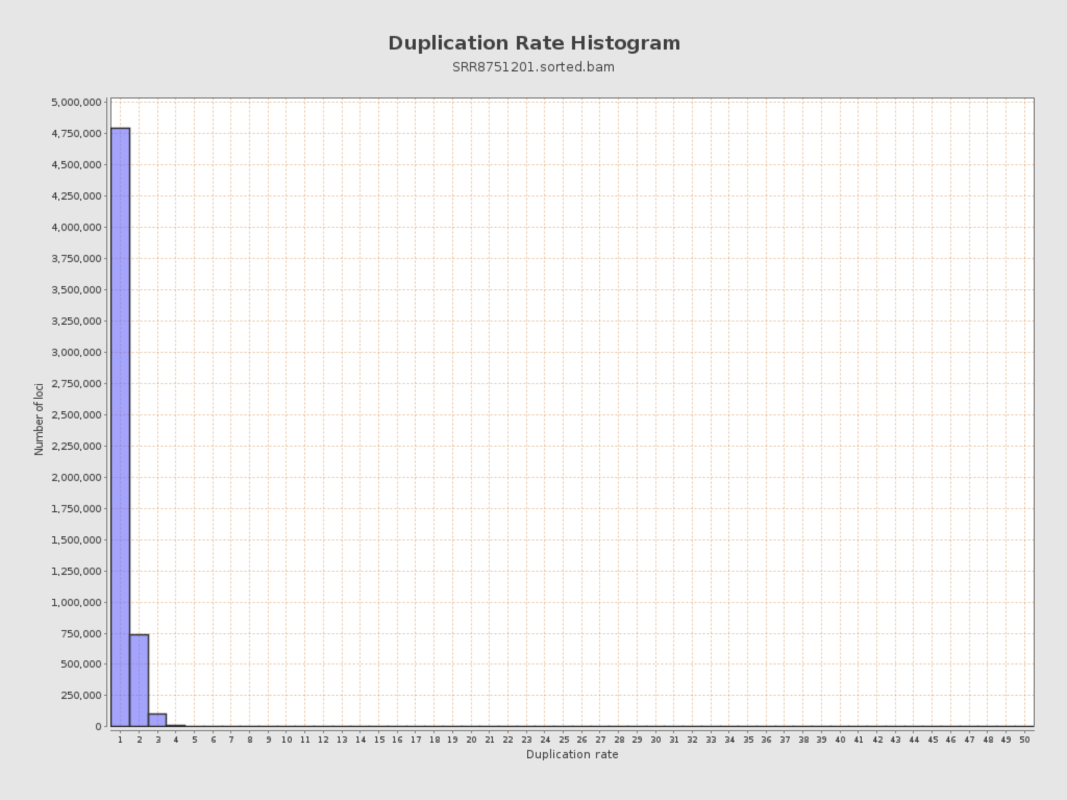
5. Results : Coverage Histogram (0-50X)



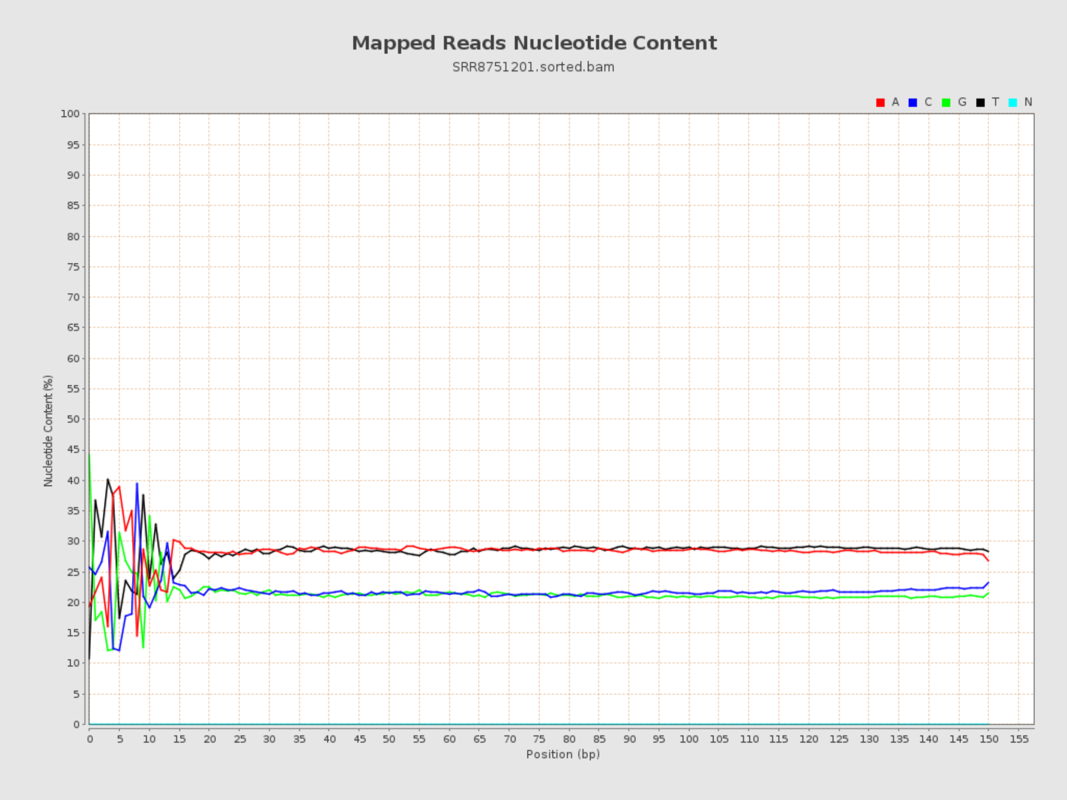
6. Results : Genome Fraction Coverage



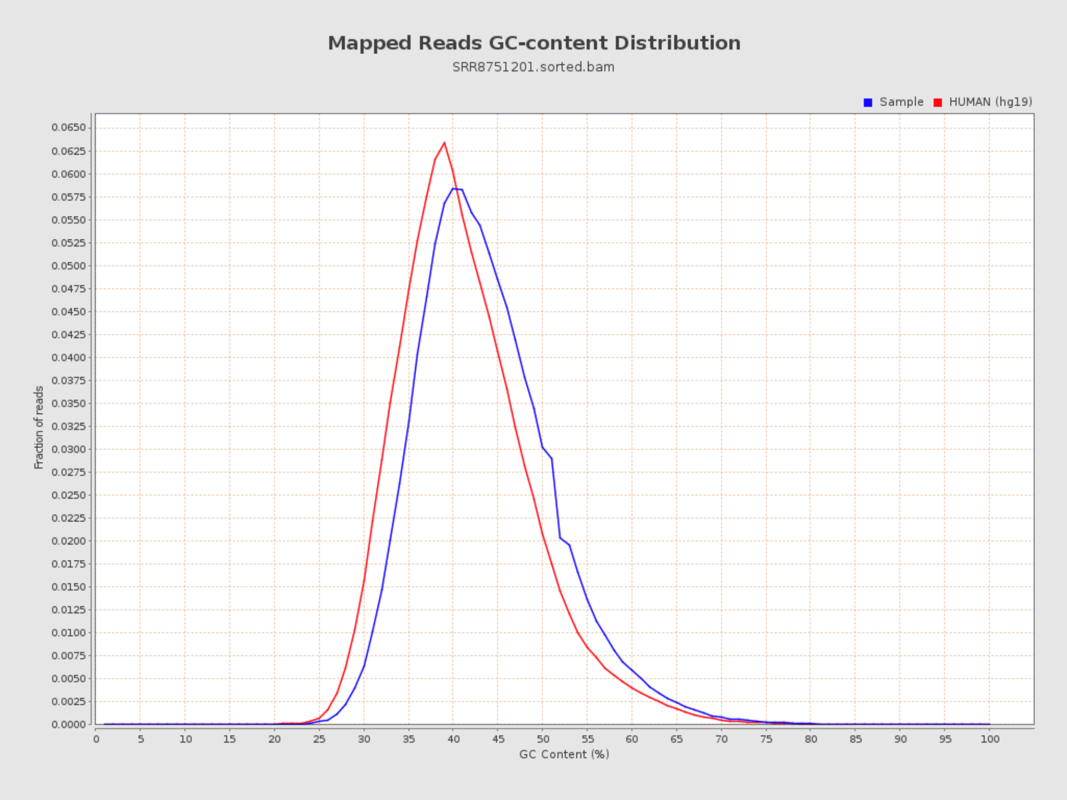
7. Results : Duplication Rate Histogram



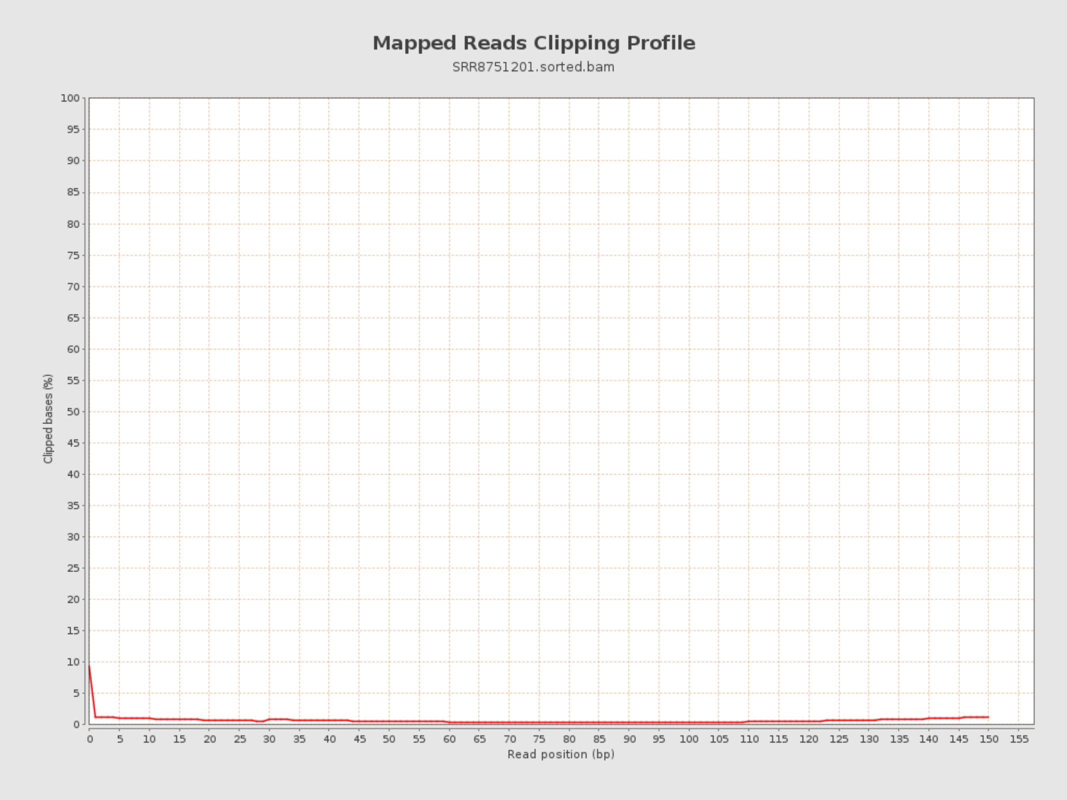
8. Results : Mapped Reads Nucleotide Content



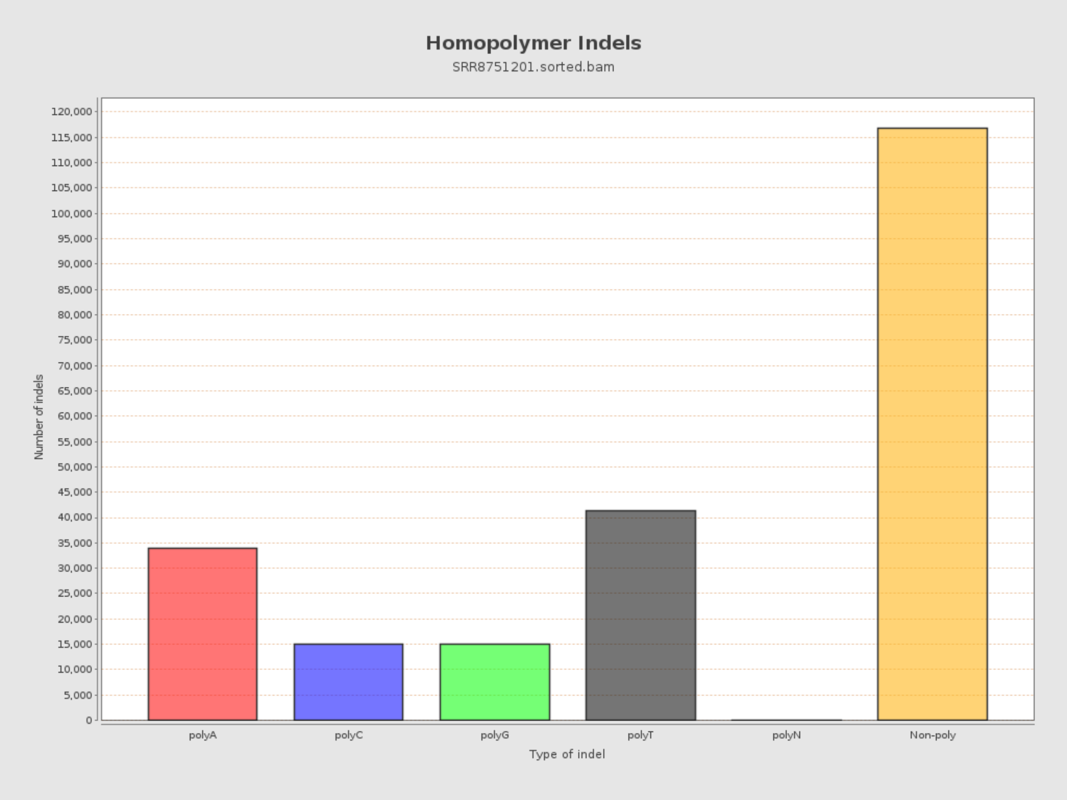
9. Results : Mapped Reads GC-content Distribution



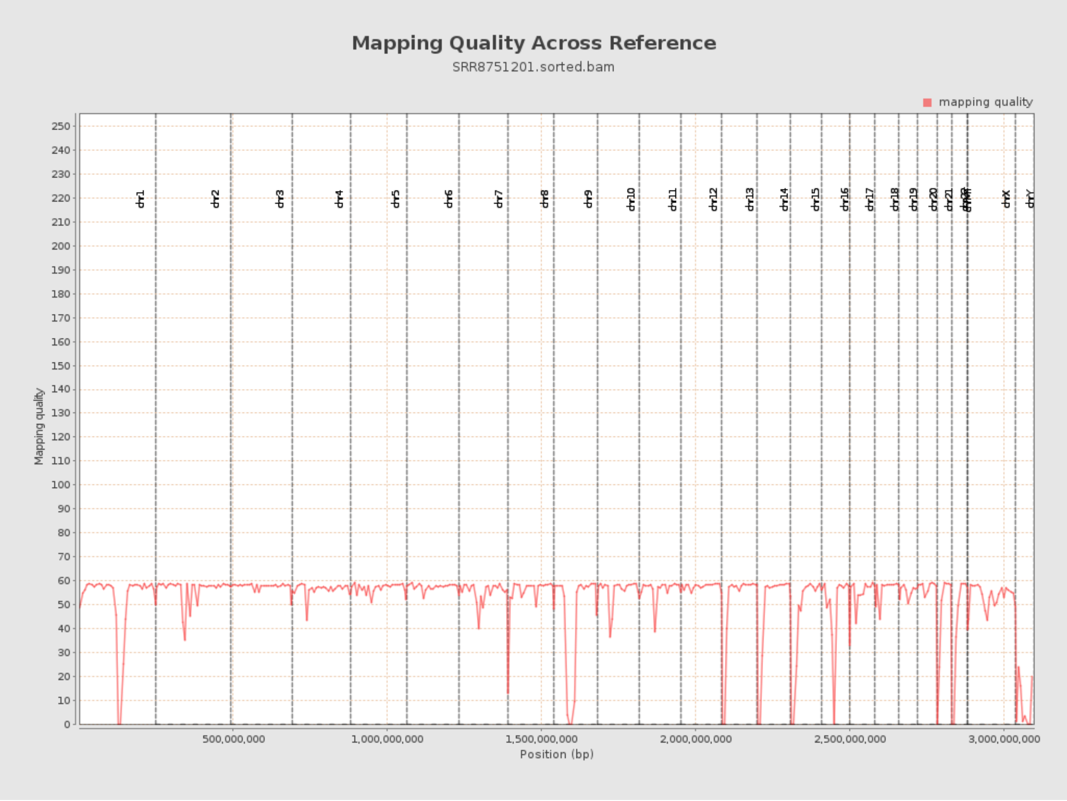
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram