Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:29:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751217.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_SRR8751217 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751217.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:29:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751217.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,354,033
Mapped reads	3,333,619 / 62.26%
Unmapped reads	2,020,414 / 37.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	196,099 / 3.66%
Read min/max/mean length	30 / 101 / 102.51
Duplicated reads (estimated)	125,720 / 2.35%
Duplication rate	1.77%
Clipped reads	832,155 / 15.54%

2.2. ACGT Content

Number/percentage of A's	97,321,270 / 29.72%
Number/percentage of C's	66,288,586 / 20.25%
Number/percentage of T's	97,921,316 / 29.91%
Number/percentage of G's	65,891,262 / 20.12%
Number/percentage of N's	2,333 / 0%
GC Percentage	40.37%

2.3. Coverage

Mean	0.1058

Standard Deviation	1.311

2.4. Mapping Quality

Mean Mapping Quality	50.89

2.5. Mismatches and indels

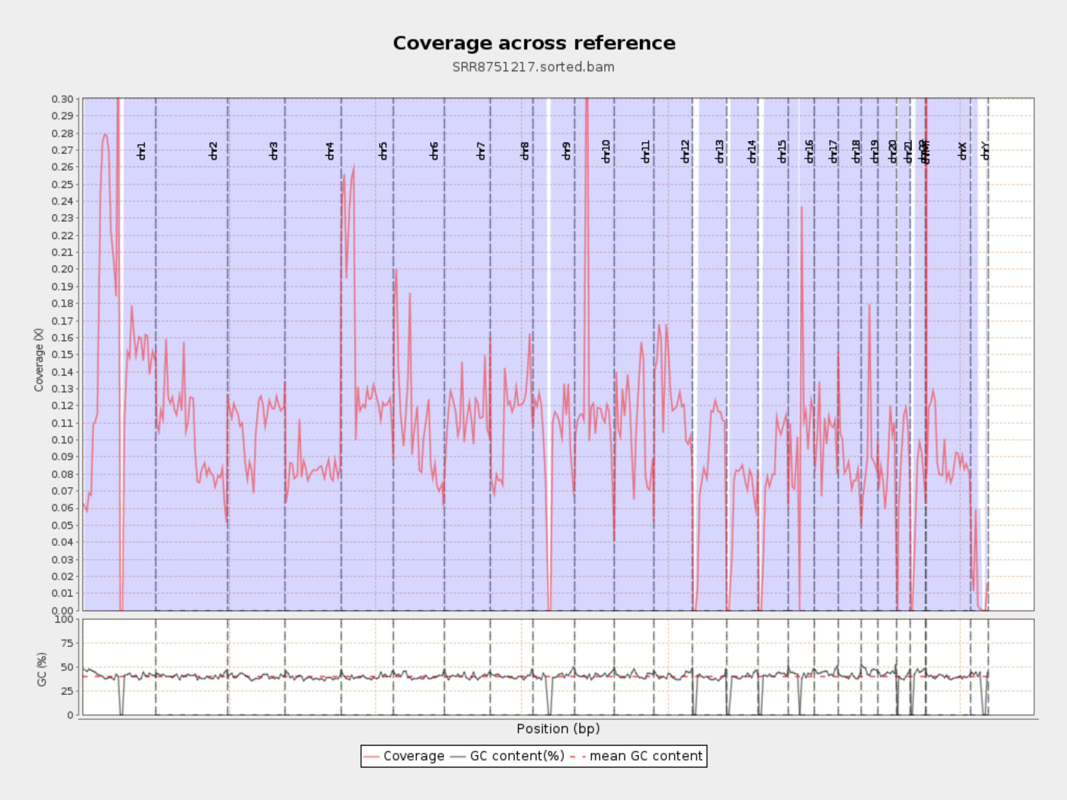
General error rate	0.53%
Mismatches	1,334,263
Insertions	291,578
Mapped reads with at least one insertion	8.32%
Deletions	52,021
Mapped reads with at least one deletion	1.53%
Homopolymer indels	53.81%

2.6. Chromosome stats

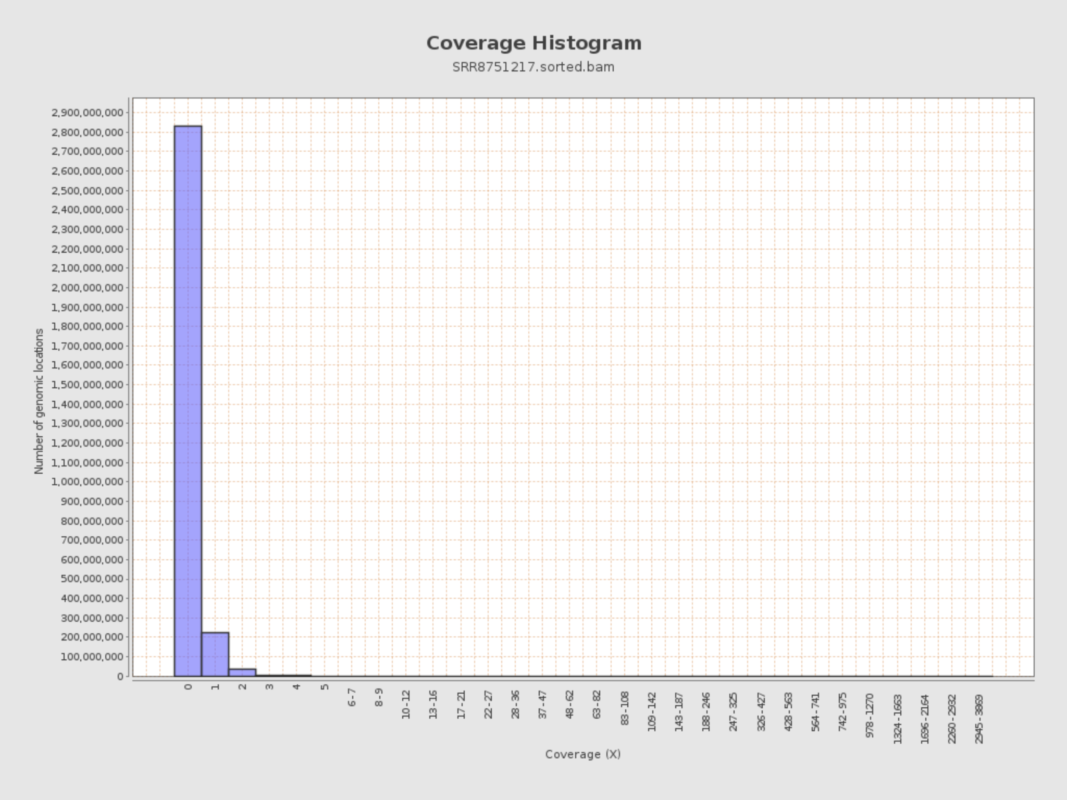
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	39223008	0.1574	3.5832
chr2	243199373	24712451	0.1016	0.5673
chr3	198022430	21852936	0.1104	0.5236
chr4	191154276	15727010	0.0823	0.4458
chr5	180915260	27348947	0.1512	0.4884
chr6	171115067	18743969	0.1095	0.8027
chr7	159138663	18240689	0.1146	0.8441

chr8	146364022	16281777	0.1112	0.5058
chr9	141213431	13878667	0.0983	0.6205
chr10	135534747	17087478	0.1261	2.3796
chr11	135006516	14609731	0.1082	0.6835
chr12	133851895	17105987	0.1278	0.4272
chr13	115169878	9600825	0.0834	0.3324
chr14	107349540	6847285	0.0638	0.3143
chr15	102531392	7734685	0.0754	0.3152
chr16	90354753	9276269	0.1027	1.0081
chr17	81195210	8358194	0.1029	0.6488
chr18	78077248	6743842	0.0864	1.1909
chr19	59128983	5577847	0.0943	2.4429
chr20	63025520	5453089	0.0865	0.3685
chr21	48129895	4113346	0.0855	0.3984
chr22	51304566	3135972	0.0611	0.2824
chrMT	16571	809445	48.8471	19.5085
chrX	155270560	14244090	0.0917	0.4204
chrY	59373566	828418	0.014	0.5427

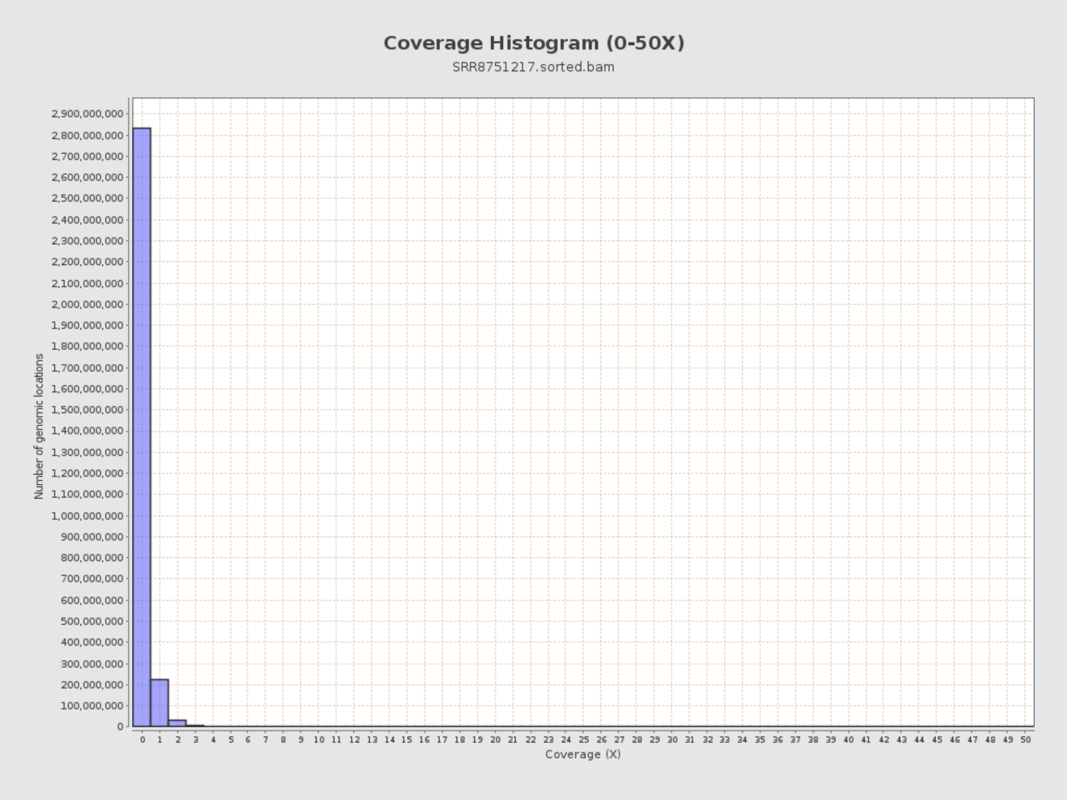
3. Results : Coverage across reference



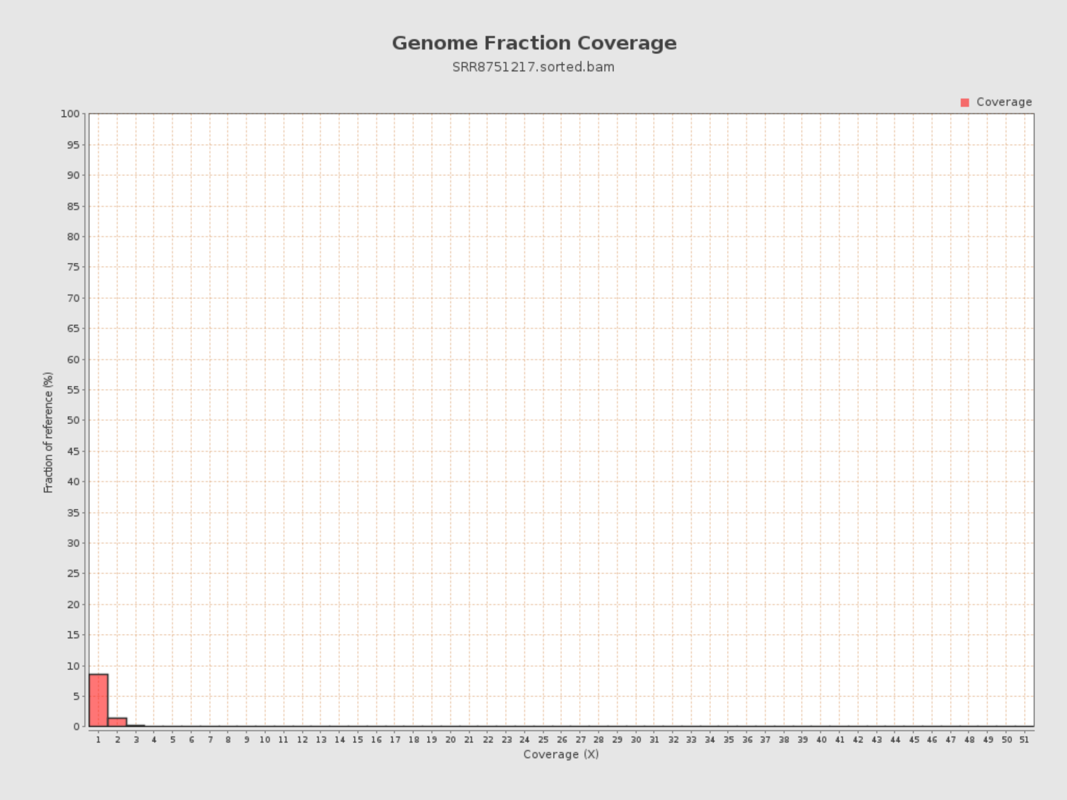
4. Results : Coverage Histogram



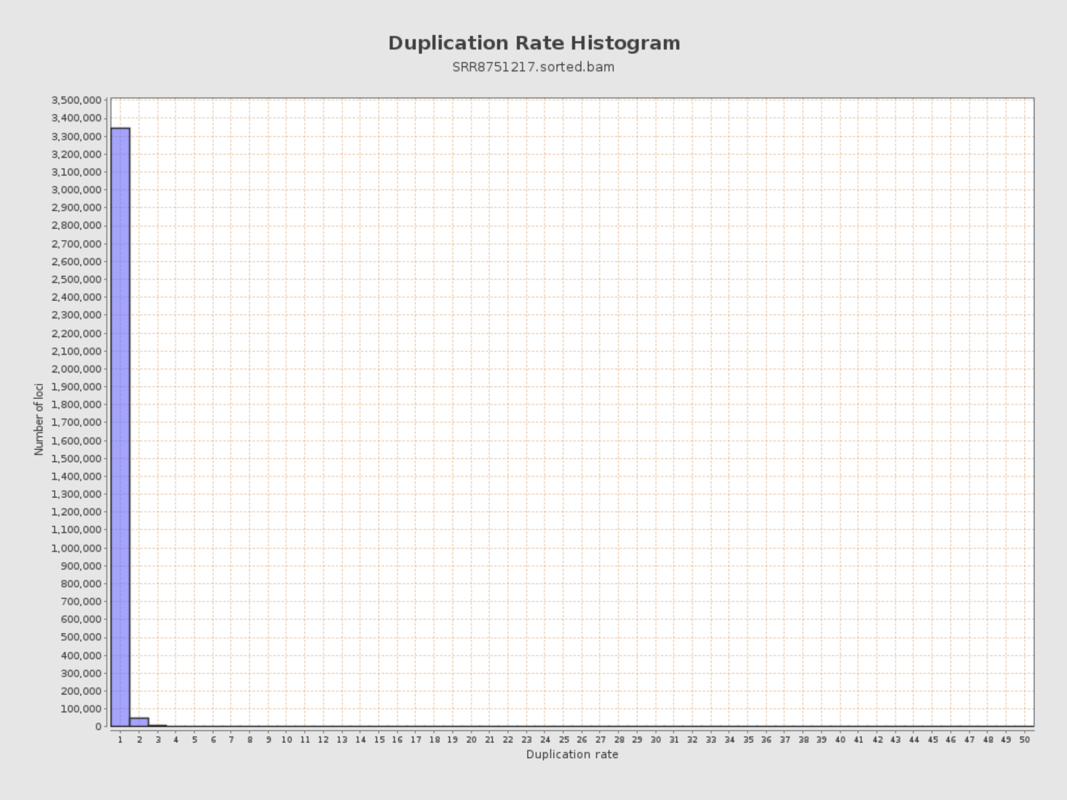
5. Results : Coverage Histogram (0-50X)



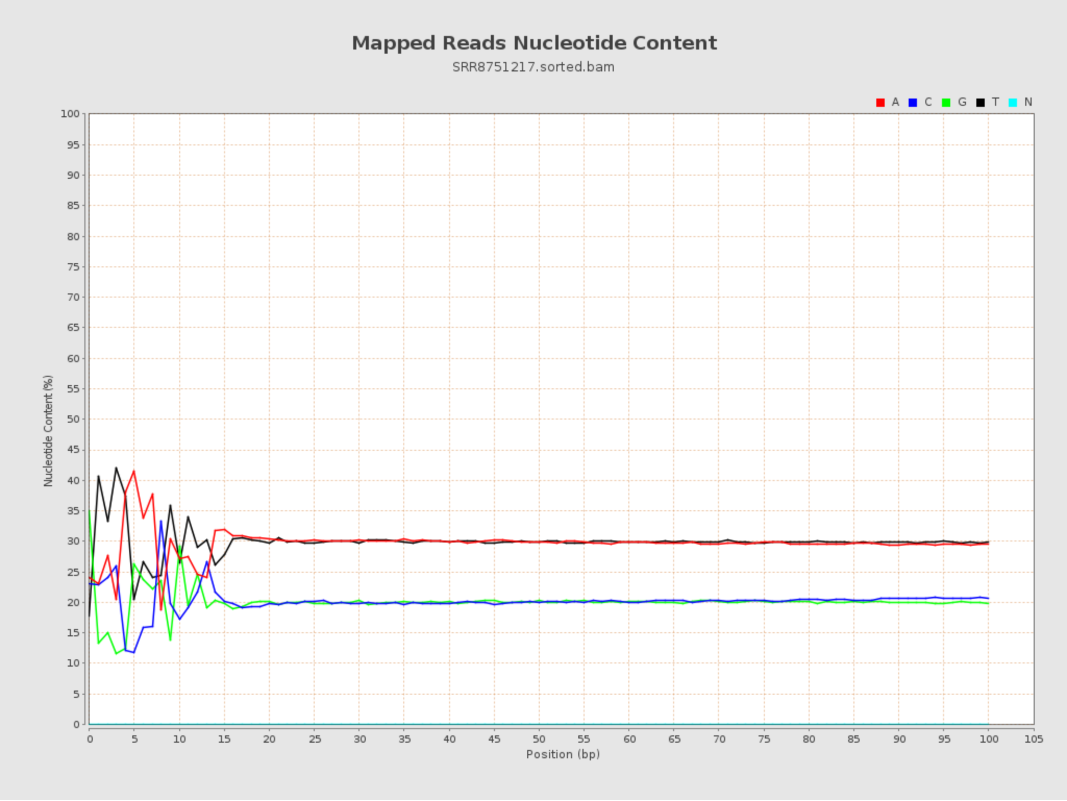
6. Results : Genome Fraction Coverage



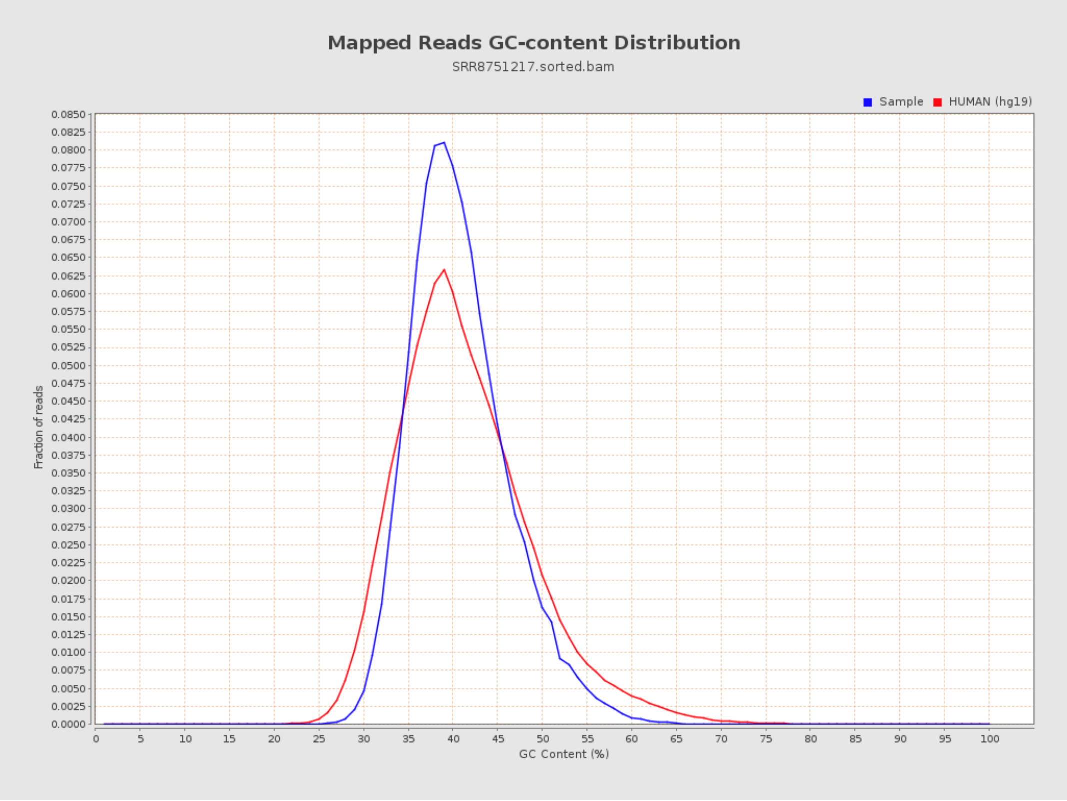
7. Results : Duplication Rate Histogram



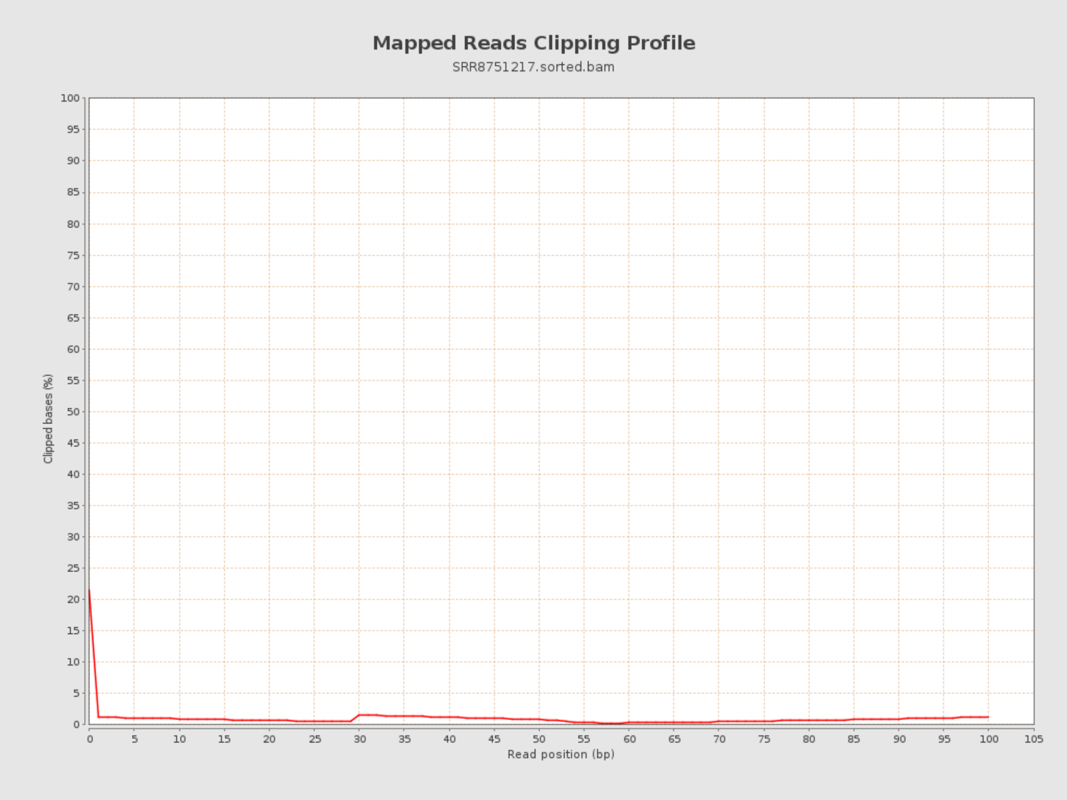
8. Results : Mapped Reads Nucleotide Content



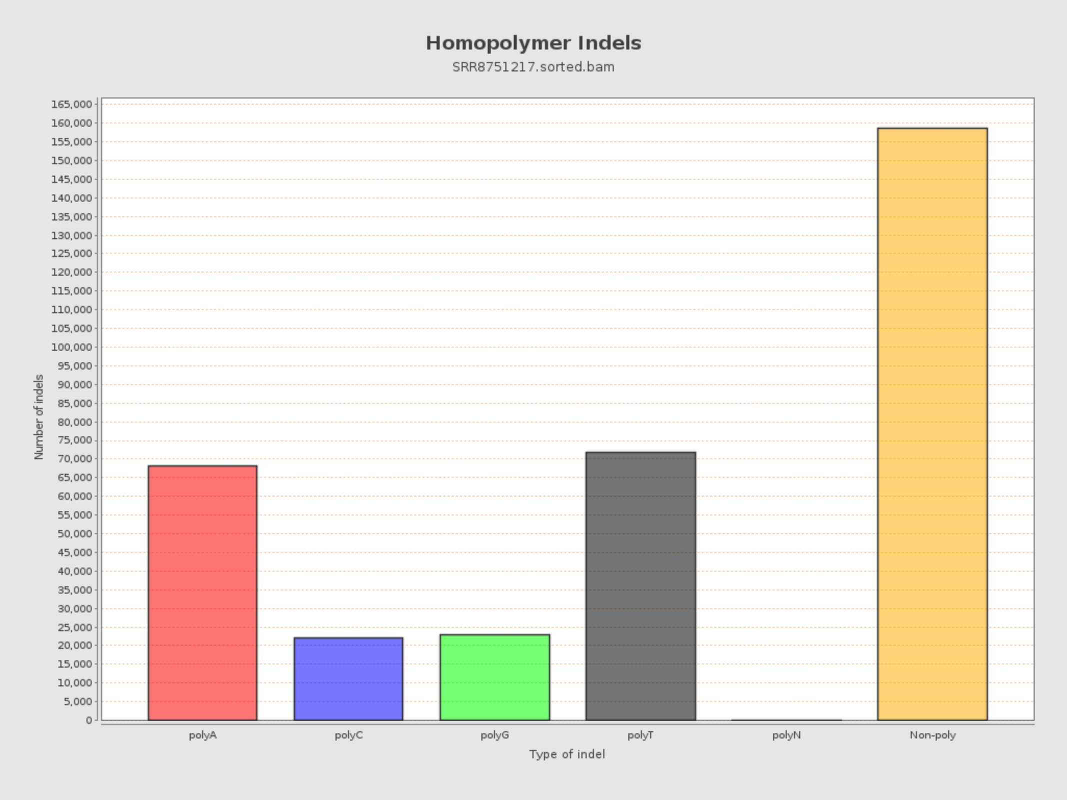
9. Results : Mapped Reads GC-content Distribution



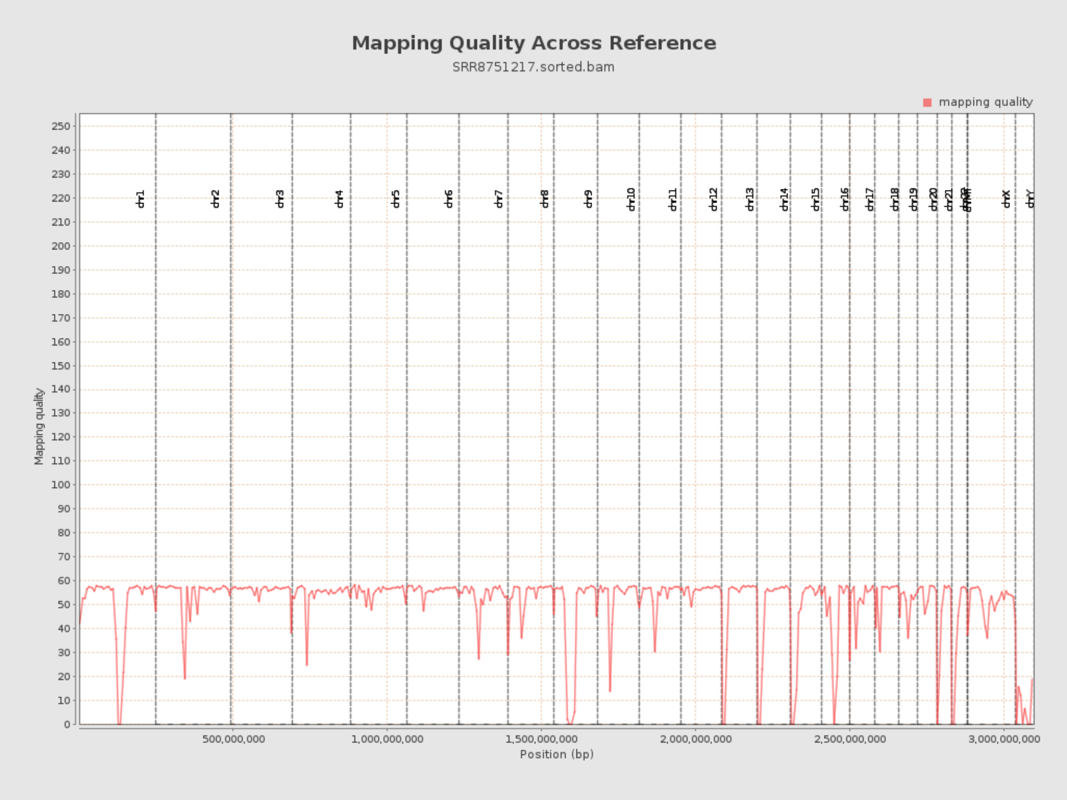
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram