Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 02:04:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506320.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_SRR1506320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 02:04:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,912,300
Mapped reads	10,348,438 / 69.4%
Unmapped reads	4,563,862 / 30.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	172,789 / 1.16%
Read min/max/mean length	30 / 94 / 94.42
Duplicated reads (estimated)	2,572,957 / 17.25%
Duplication rate	14.7%
Clipped reads	6,072,701 / 40.72%

2.2. ACGT Content

Number/percentage of A's	222,206,650 / 26.99%
Number/percentage of C's	158,239,366 / 19.22%
Number/percentage of T's	239,339,353 / 29.07%
Number/percentage of G's	203,452,431 / 24.71%
Number/percentage of N's	194,635 / 0.02%
GC Percentage	43.92%

2.3. Coverage

Mean	0.2661

Standard Deviation	1.817

2.4. Mapping Quality

Mean Mapping Quality	47.63

2.5. Mismatches and indels

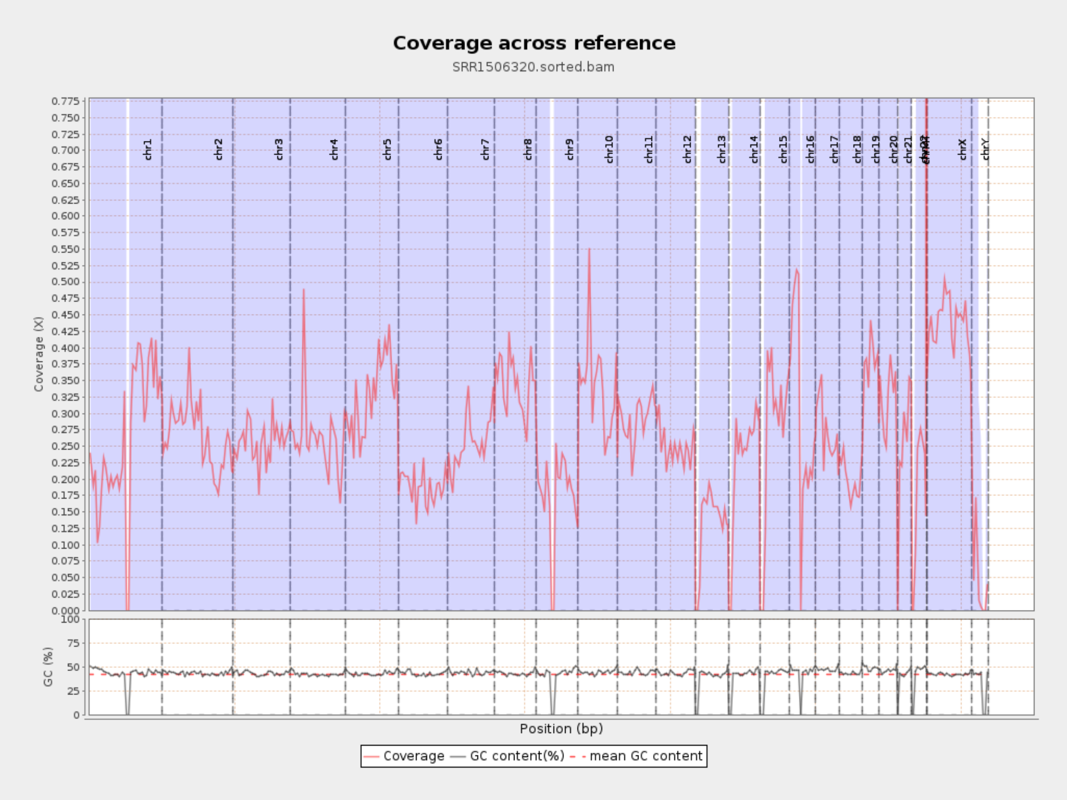
General error rate	0.71%
Mismatches	5,699,711
Insertions	65,413
Mapped reads with at least one insertion	0.62%
Deletions	167,509
Mapped reads with at least one deletion	1.59%
Homopolymer indels	42.91%

2.6. Chromosome stats

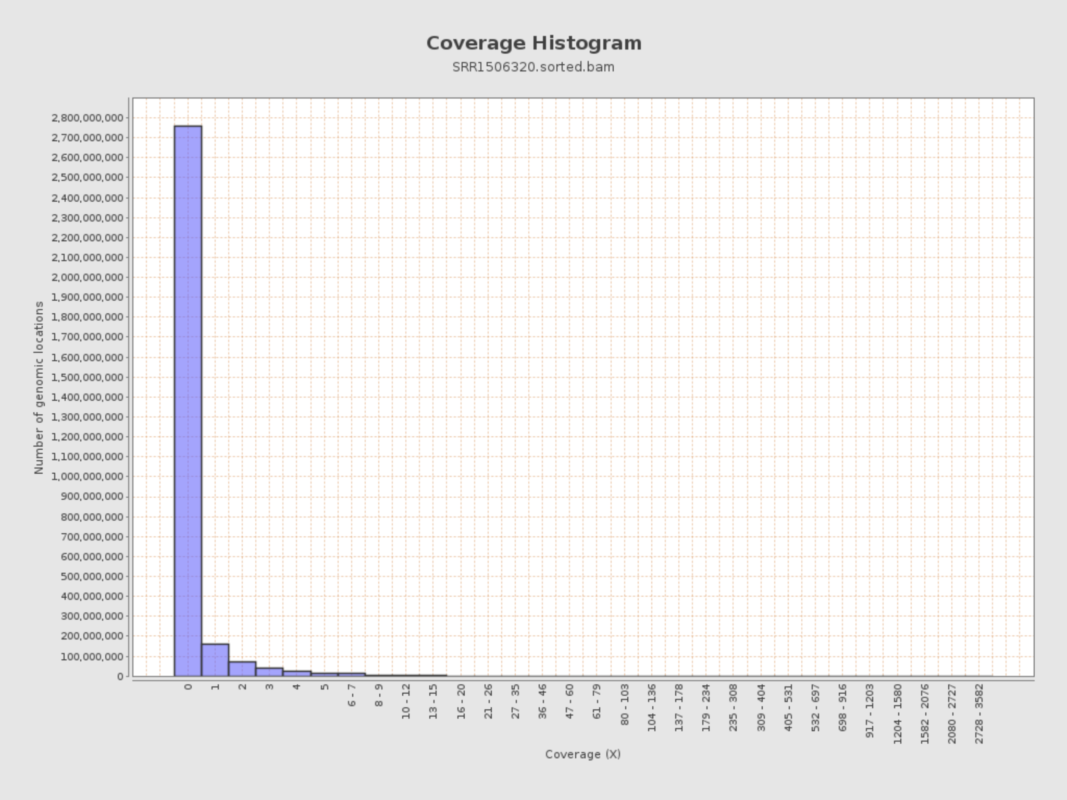
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	64513226	0.2588	3.3189
chr2	243199373	65008144	0.2673	1.9299
chr3	198022430	50590708	0.2555	1.0459
chr4	191154276	49714109	0.2601	1.5284
chr5	180915260	59821641	0.3307	1.2103
chr6	171115067	32131941	0.1878	0.9949
chr7	159138663	40824349	0.2565	2.0873

chr8	146364022	50861612	0.3475	2.3221
chr9	141213431	24479079	0.1733	1.7471
chr10	135534747	46574752	0.3436	2.2418
chr11	135006516	39351667	0.2915	1.719
chr12	133851895	33369866	0.2493	1.0772
chr13	115169878	15183784	0.1318	0.7252
chr14	107349540	24229326	0.2257	1.1364
chr15	102531392	27706123	0.2702	1.0986
chr16	90354753	27159637	0.3006	1.4253
chr17	81195210	22121199	0.2724	1.3795
chr18	78077248	15487260	0.1984	2.5958
chr19	59128983	22278900	0.3768	2.4603
chr20	63025520	20124360	0.3193	1.3069
chr21	48129895	12249310	0.2545	1.373
chr22	51304566	8865719	0.1728	0.9889
chrMT	16571	261291	15.768	10.6274
chrX	155270560	67950692	0.4376	1.5832
chrY	59373566	2915660	0.0491	1.4062

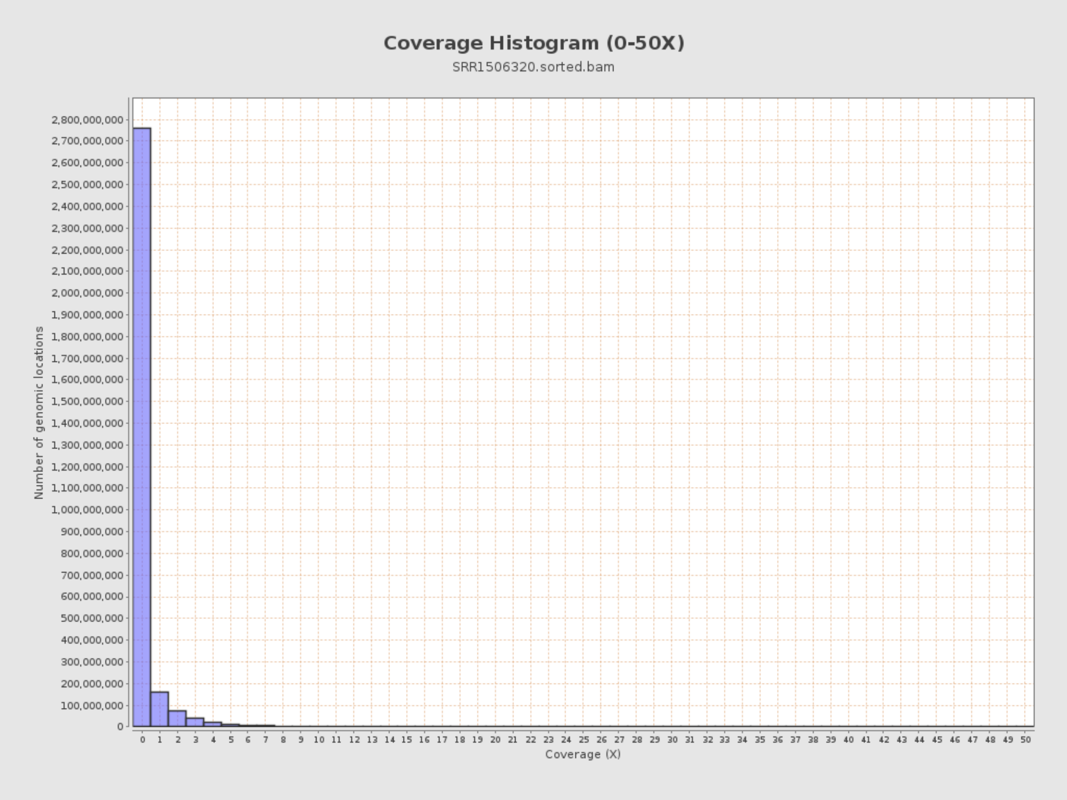
3. Results : Coverage across reference



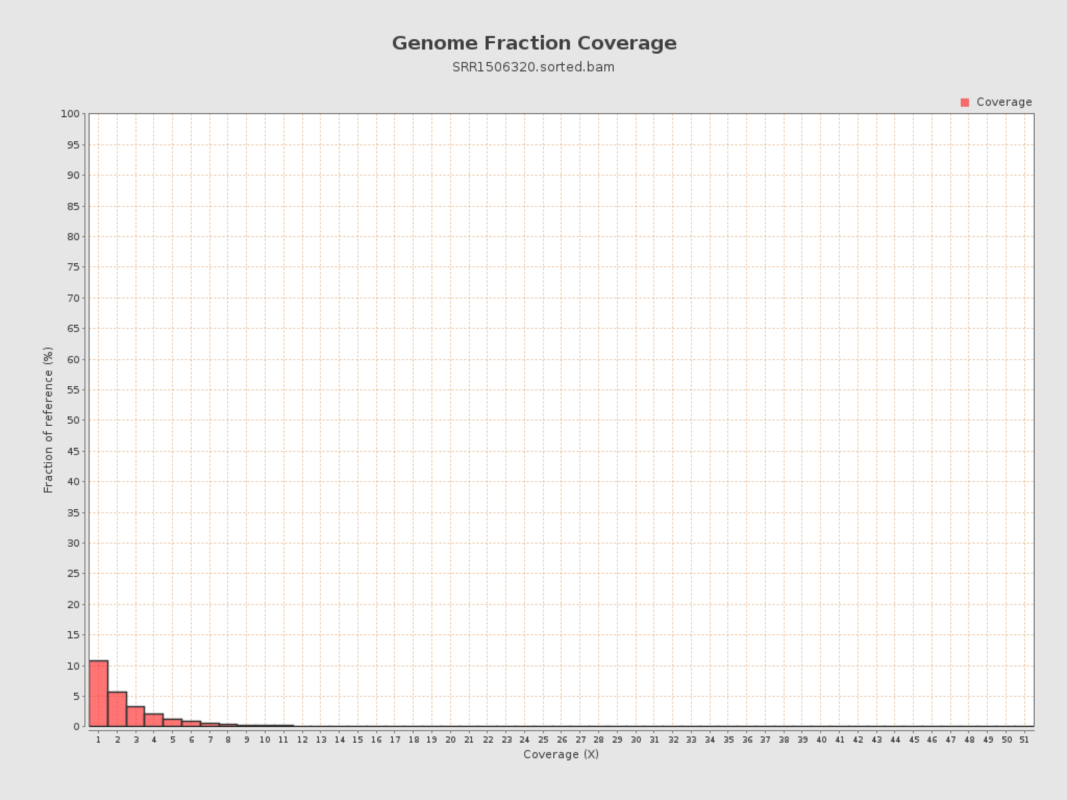
4. Results : Coverage Histogram



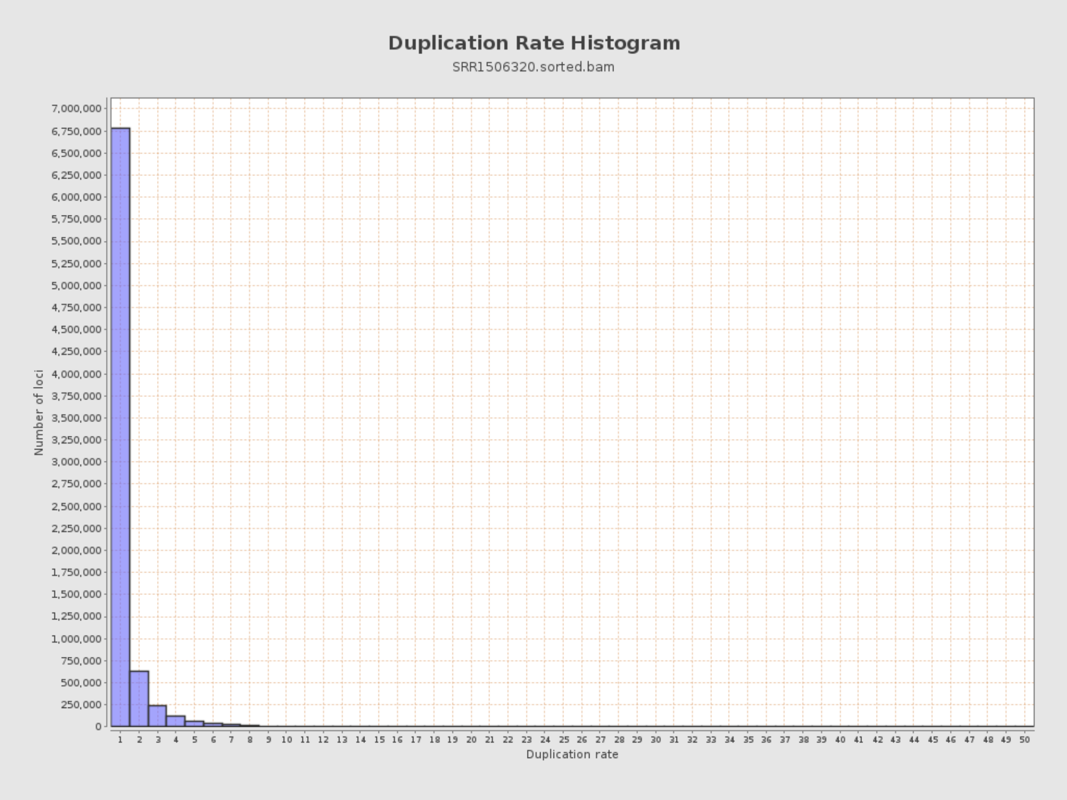
5. Results : Coverage Histogram (0-50X)



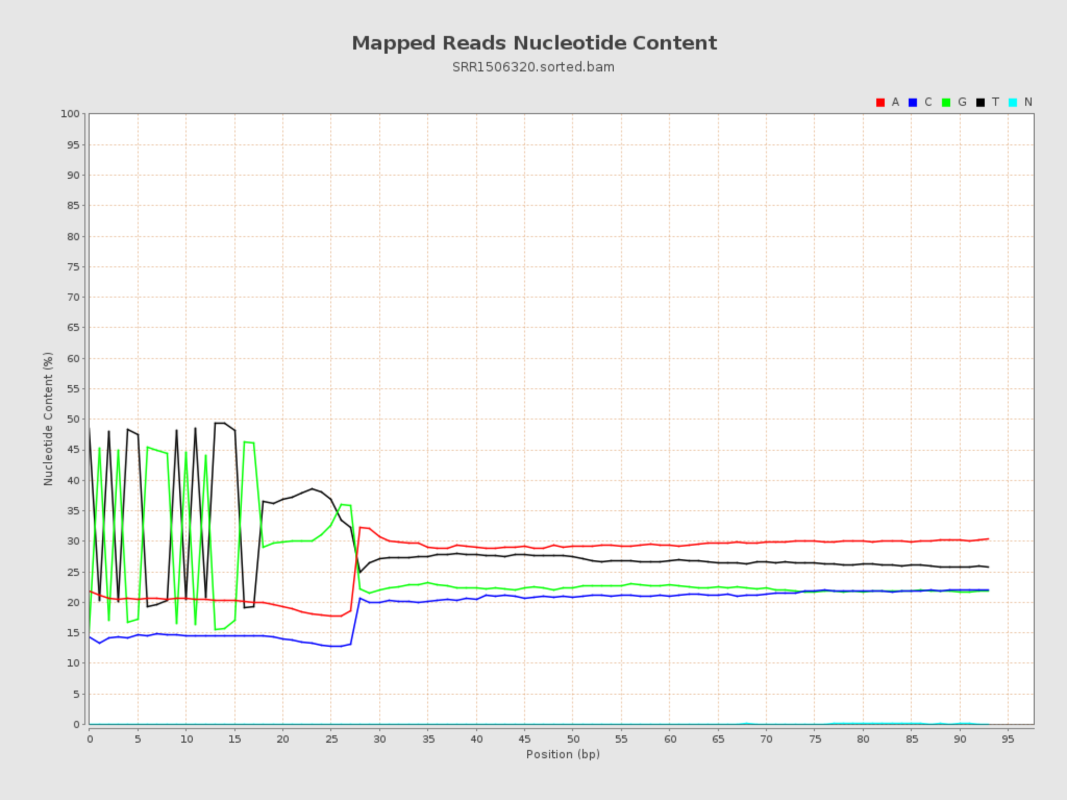
6. Results : Genome Fraction Coverage



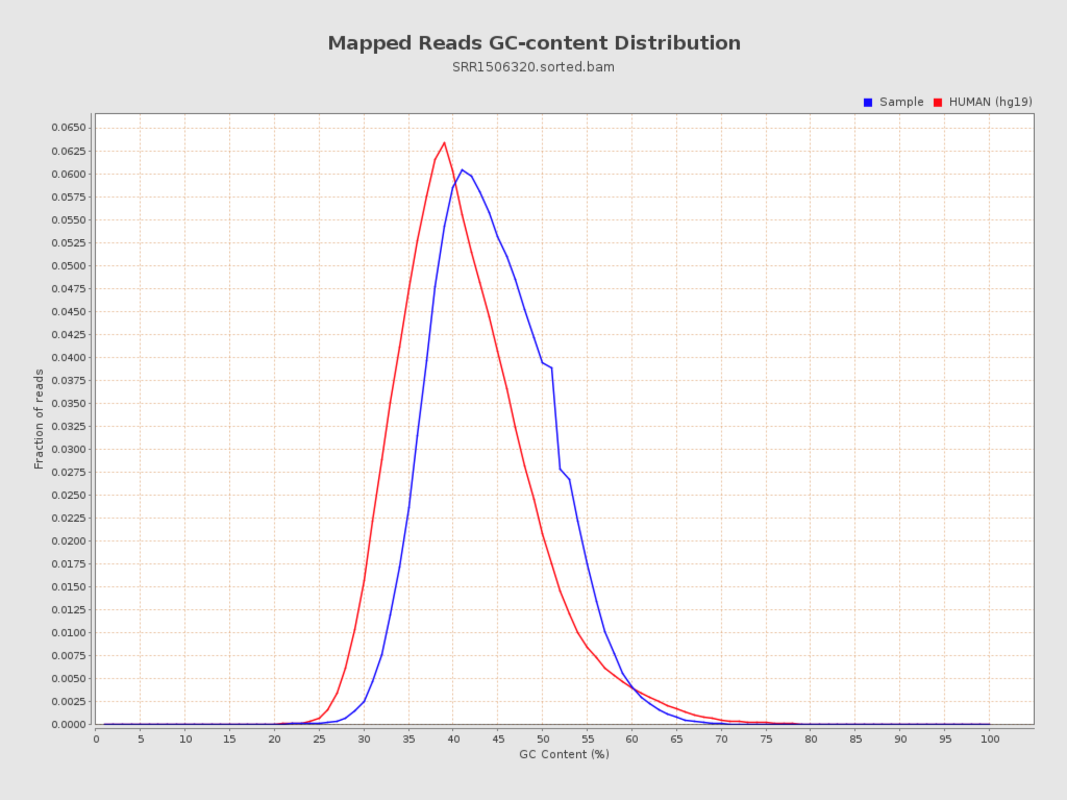
7. Results : Duplication Rate Histogram



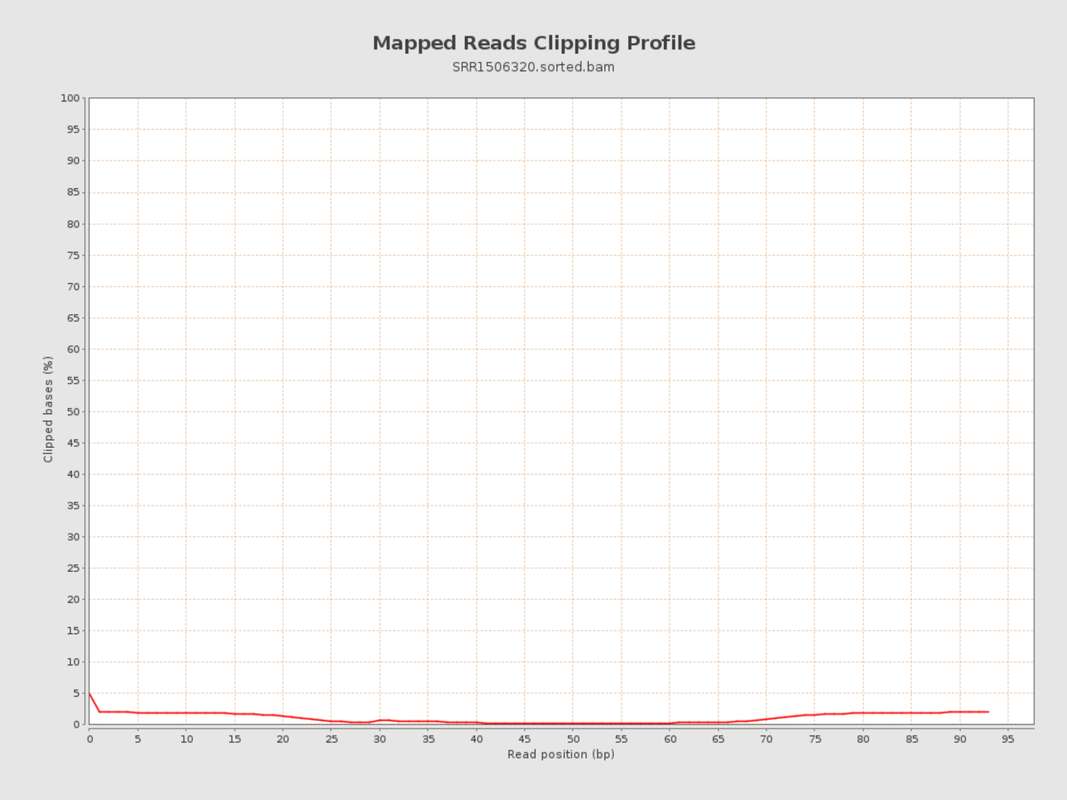
8. Results : Mapped Reads Nucleotide Content



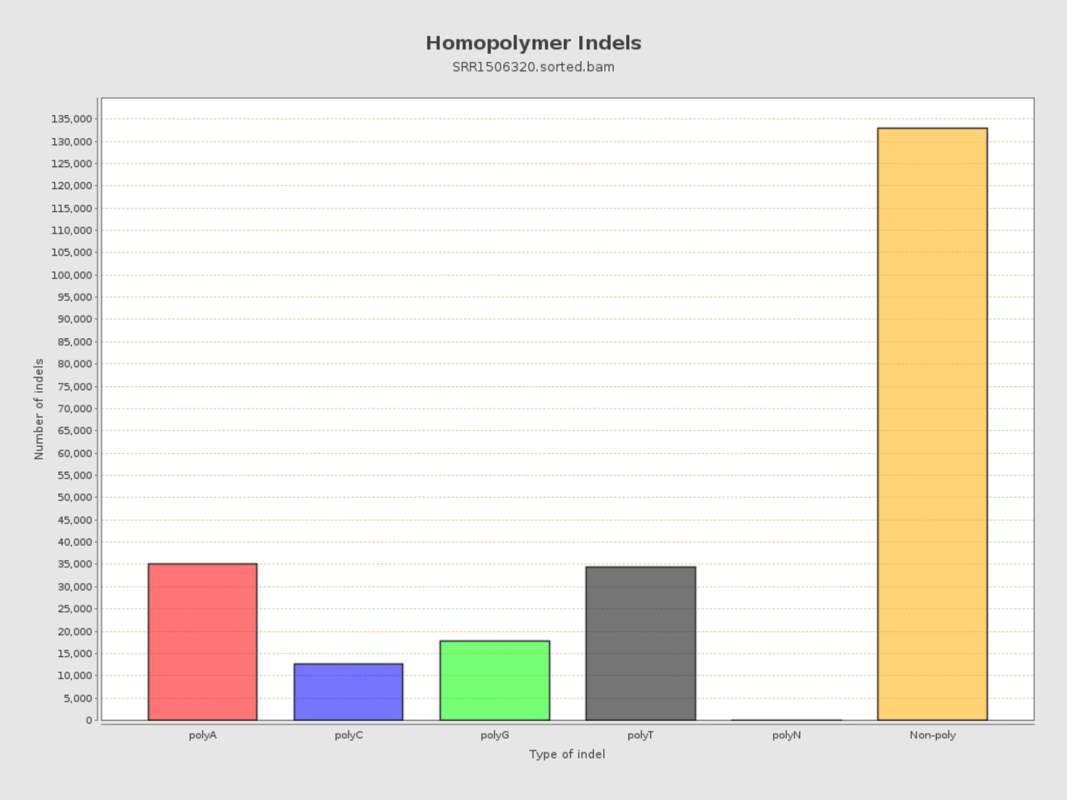
9. Results : Mapped Reads GC-content Distribution



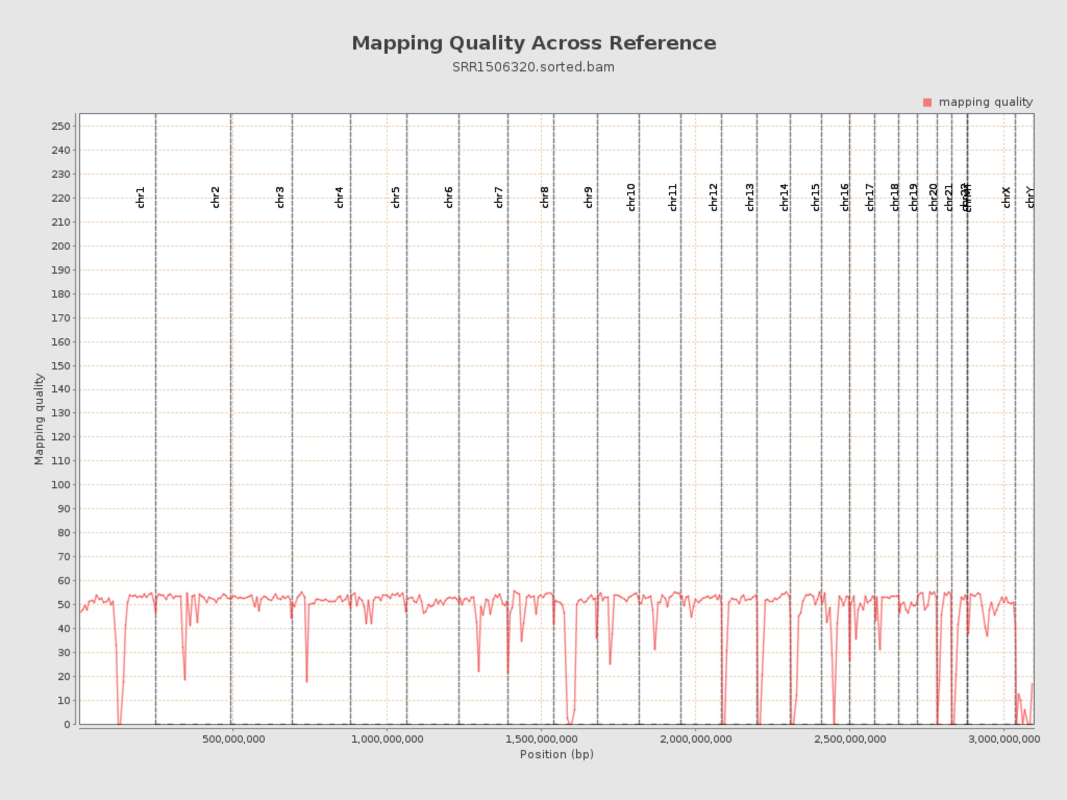
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram