Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 03:56:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153393.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_SRR1153393 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153393.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 03:56:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153393.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	87,261,464
Mapped reads	86,611,710 / 99.26%
Unmapped reads	649,754 / 0.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	464,297 / 0.53%
Read min/max/mean length	30 / 100 / 100.22
Duplicated reads (estimated)	51,139,901 / 58.61%
Duplication rate	46.1%
Clipped reads	15,203,986 / 17.42%

2.2. ACGT Content

Number/percentage of A's	2,064,079,003 / 24.66%
Number/percentage of C's	2,119,641,367 / 25.32%
Number/percentage of T's	2,057,080,418 / 24.58%
Number/percentage of G's	2,128,250,778 / 25.43%
Number/percentage of N's	1,111,163 / 0.01%
GC Percentage	50.75%

2.3. Coverage

Mean	2.7041

Standard Deviation	39.9519

2.4. Mapping Quality

Mean Mapping Quality	49.01

2.5. Mismatches and indels

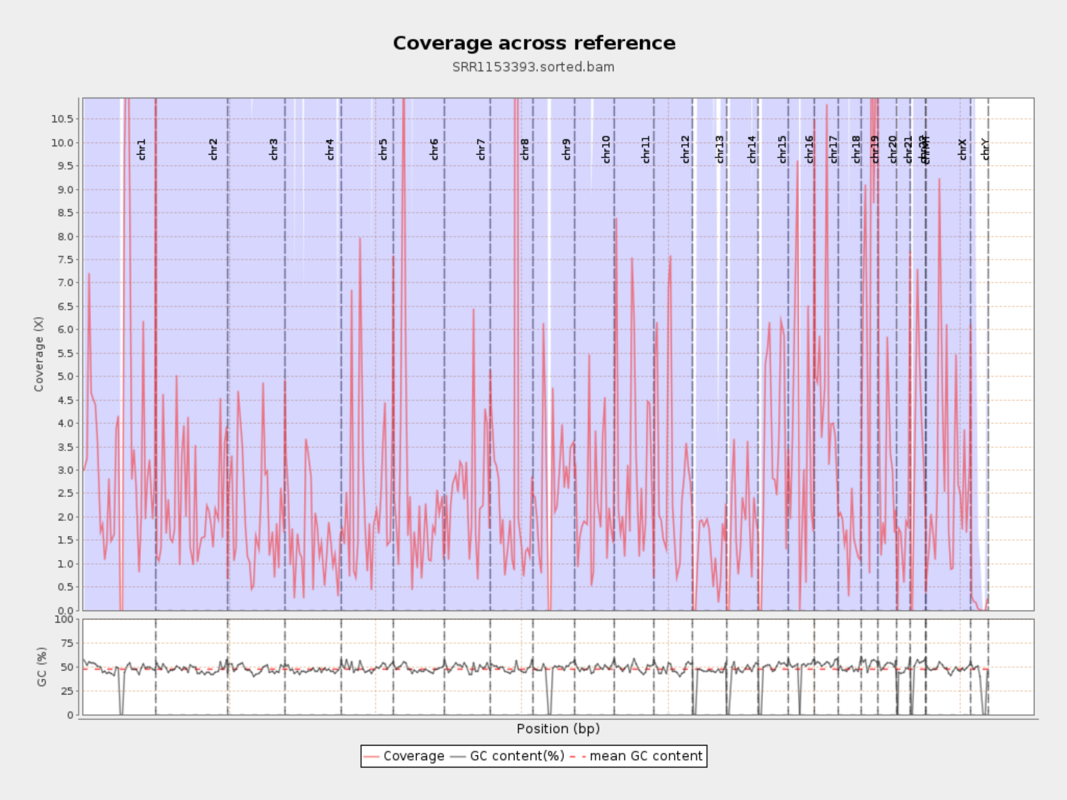
General error rate	0.29%
Mismatches	23,686,655
Insertions	604,731
Mapped reads with at least one insertion	0.69%
Deletions	393,280
Mapped reads with at least one deletion	0.45%
Homopolymer indels	45.42%

2.6. Chromosome stats

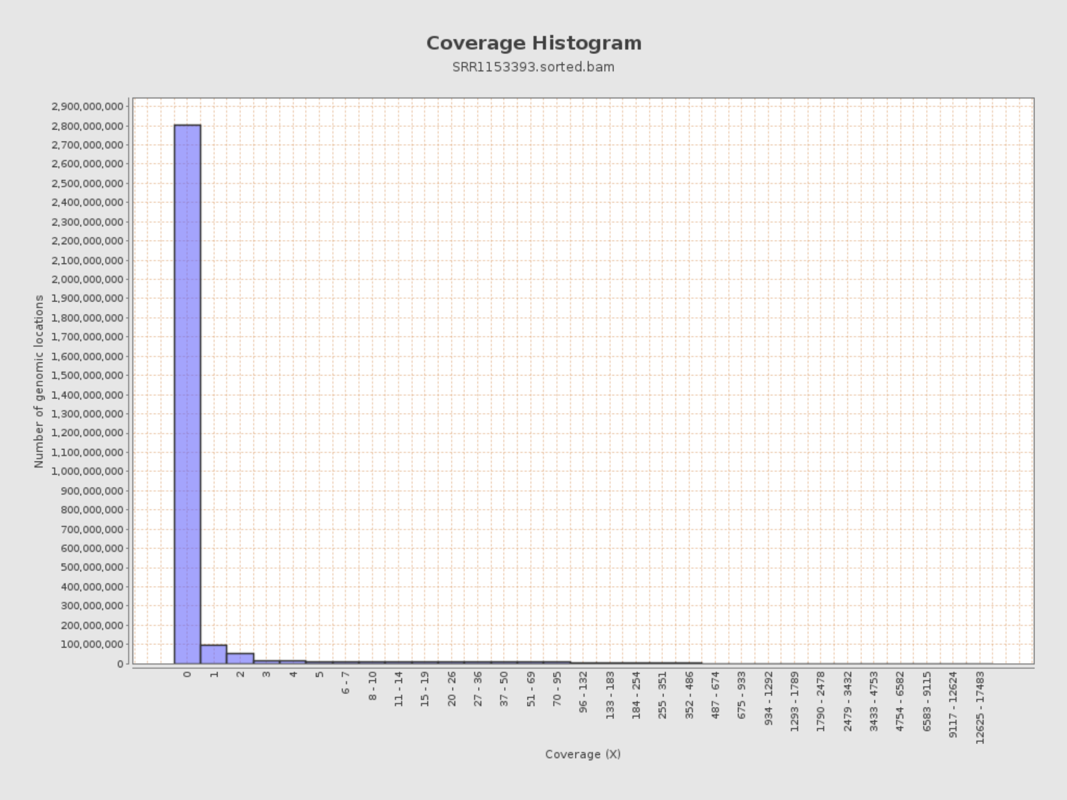
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	900626153	3.6133	38.1443
chr2	243199373	551786689	2.2689	26.5067
chr3	198022430	415508530	2.0983	28.918
chr4	191154276	296900727	1.5532	24.0998
chr5	180915260	444818051	2.4587	59.1796
chr6	171115067	408659504	2.3882	29.9836
chr7	159138663	406594067	2.555	33.5311

chr8	146364022	519639656	3.5503	97.7741
chr9	141213431	376729664	2.6678	31.0696
chr10	135534747	307746294	2.2706	24.375
chr11	135006516	434246081	3.2165	33.2311
chr12	133851895	411757654	3.0762	33.8444
chr13	115169878	138601173	1.2034	16.801
chr14	107349540	193629579	1.8037	22.5843
chr15	102531392	348375367	3.3977	34.7998
chr16	90354753	306273394	3.3897	33.4671
chr17	81195210	394970313	4.8645	43.2218
chr18	78077248	121904686	1.5613	21.785
chr19	59128983	487343821	8.242	65.3505
chr20	63025520	173553288	2.7537	28.123
chr21	48129895	97560414	2.027	31.3028
chr22	51304566	177484594	3.4594	34.5696
chrMT	16571	6173	0.3725	0.7726
chrX	155270560	449498644	2.8949	45.8917
chrY	59373566	6834673	0.1151	7.1607

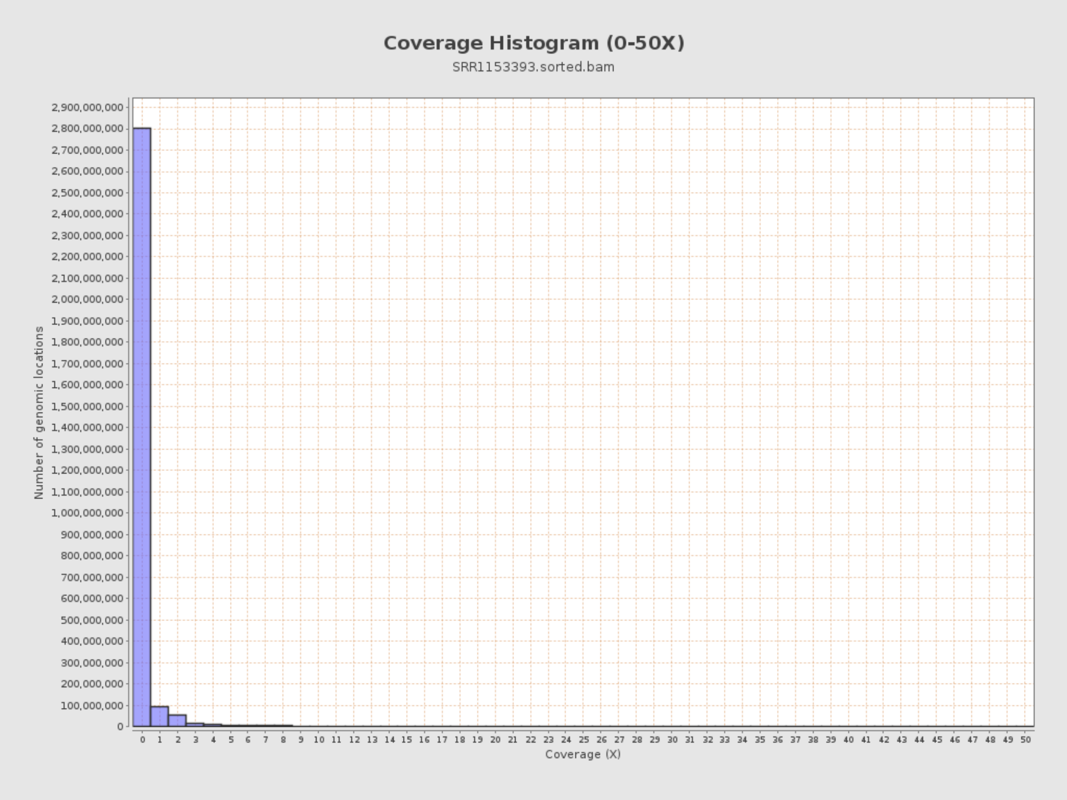
3. Results : Coverage across reference



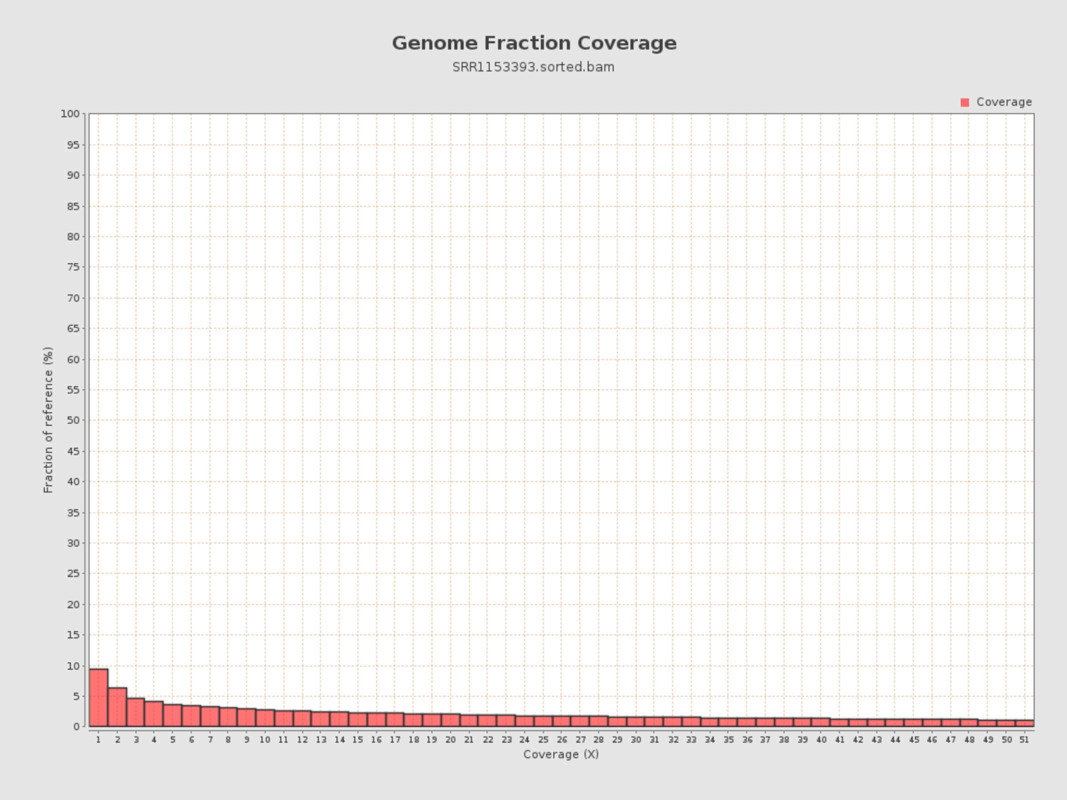
4. Results : Coverage Histogram



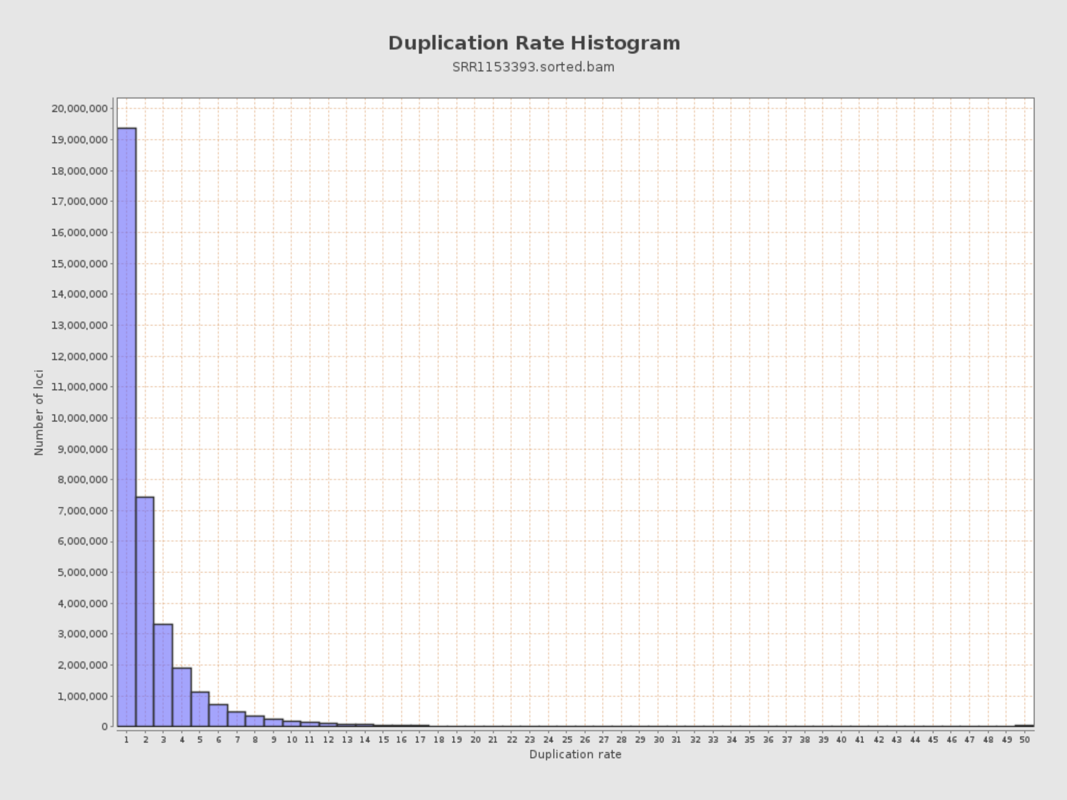
5. Results : Coverage Histogram (0-50X)



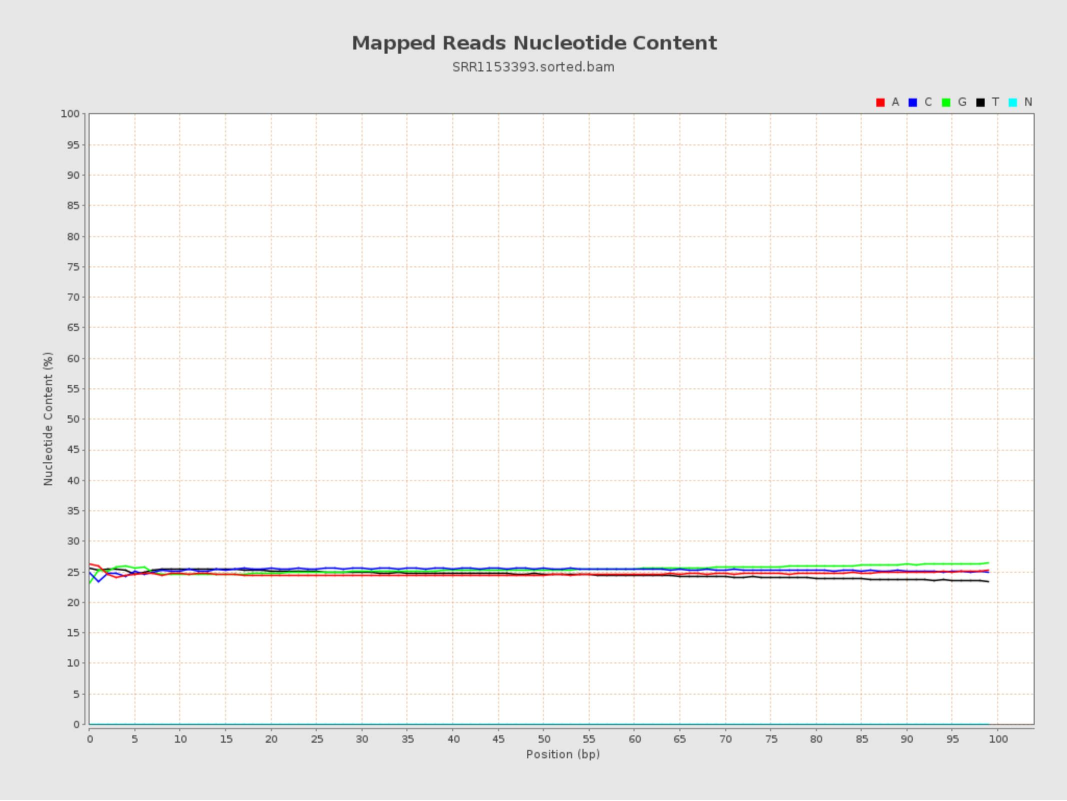
6. Results : Genome Fraction Coverage



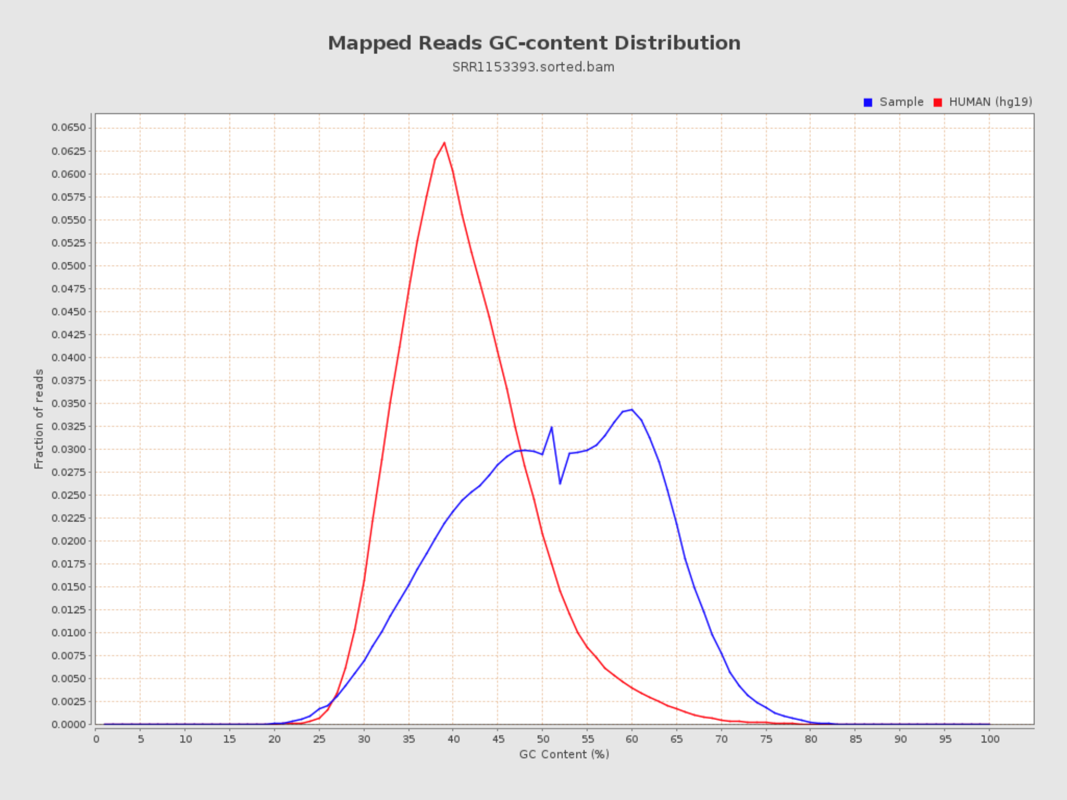
7. Results : Duplication Rate Histogram



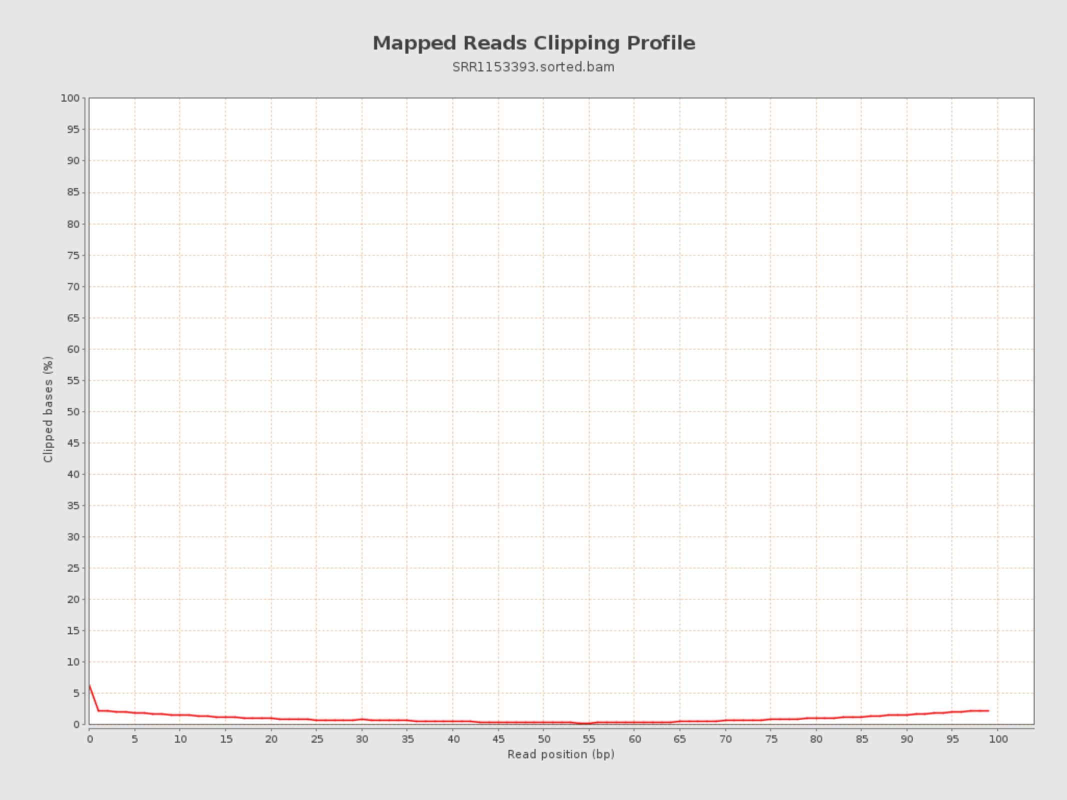
8. Results : Mapped Reads Nucleotide Content



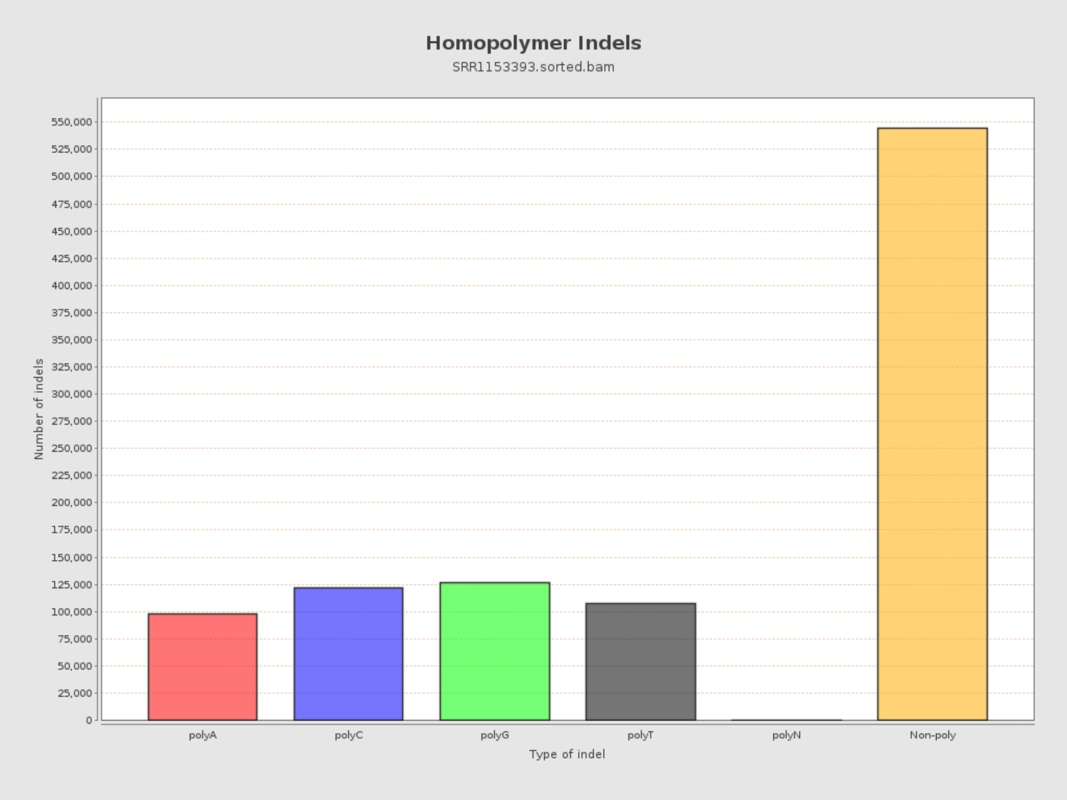
9. Results : Mapped Reads GC-content Distribution



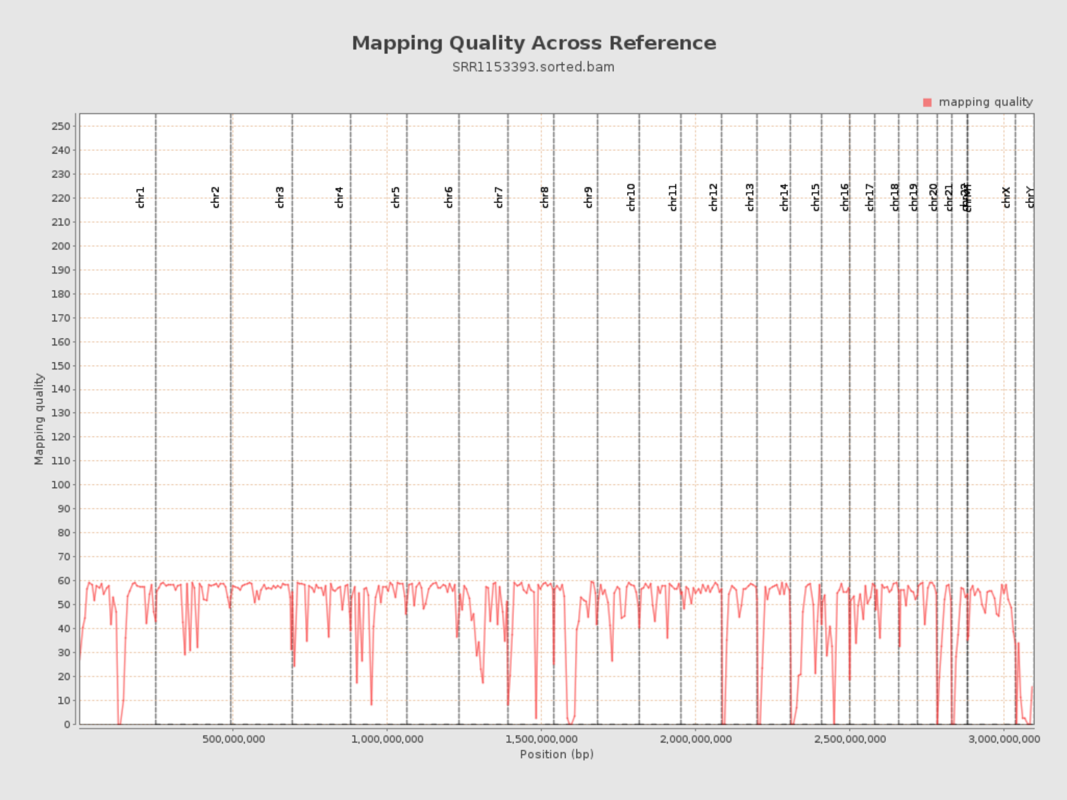
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram