Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:01:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819133.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_SRR1819133 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819133.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:01:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819133.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,734,237
Mapped reads	3,426,384 / 91.76%
Unmapped reads	307,853 / 8.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,403 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	405,709 / 10.86%
Duplication rate	8.55%
Clipped reads	3,434,982 / 91.99%

2.2. ACGT Content

Number/percentage of A's	47,711,917 / 23.82%
Number/percentage of C's	38,005,815 / 18.97%
Number/percentage of T's	63,898,593 / 31.9%
Number/percentage of G's	50,710,847 / 25.31%
Number/percentage of N's	2,753 / 0%
GC Percentage	44.29%

2.3. Coverage

Mean	0.0647

Standard Deviation	0.5804

2.4. Mapping Quality

Mean Mapping Quality	44.84

2.5. Mismatches and indels

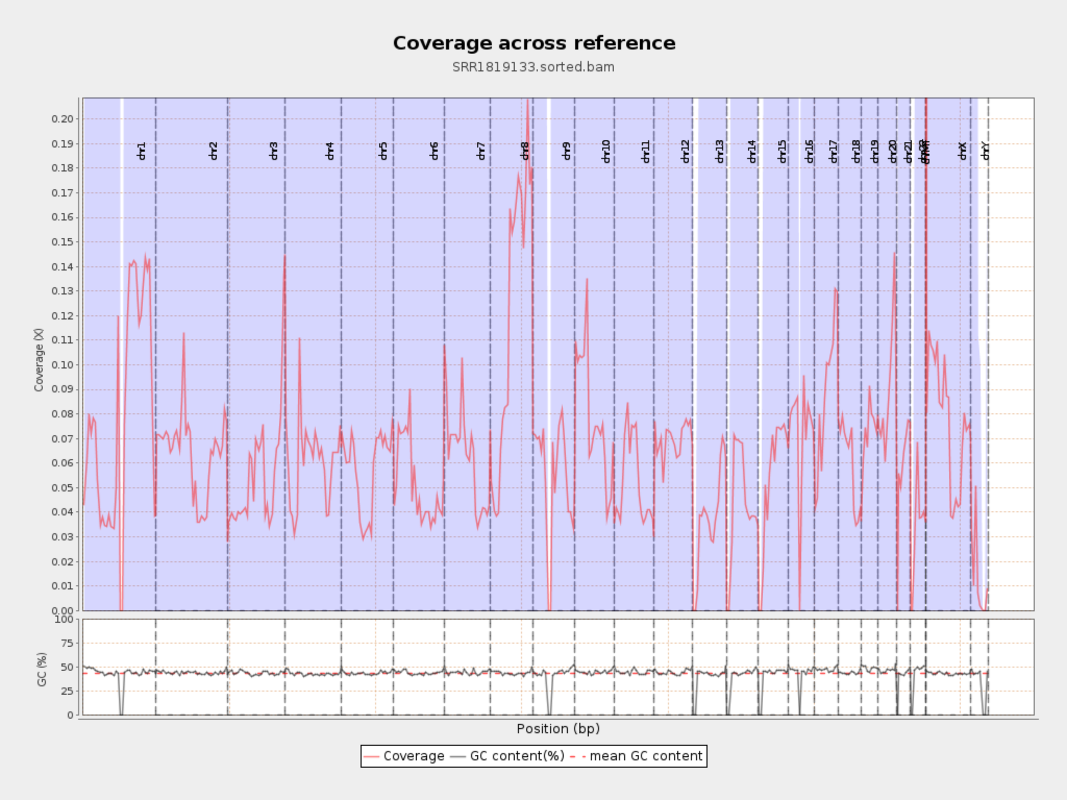
General error rate	0.53%
Mismatches	1,033,968
Insertions	12,648
Mapped reads with at least one insertion	0.37%
Deletions	35,430
Mapped reads with at least one deletion	1.03%
Homopolymer indels	44.1%

2.6. Chromosome stats

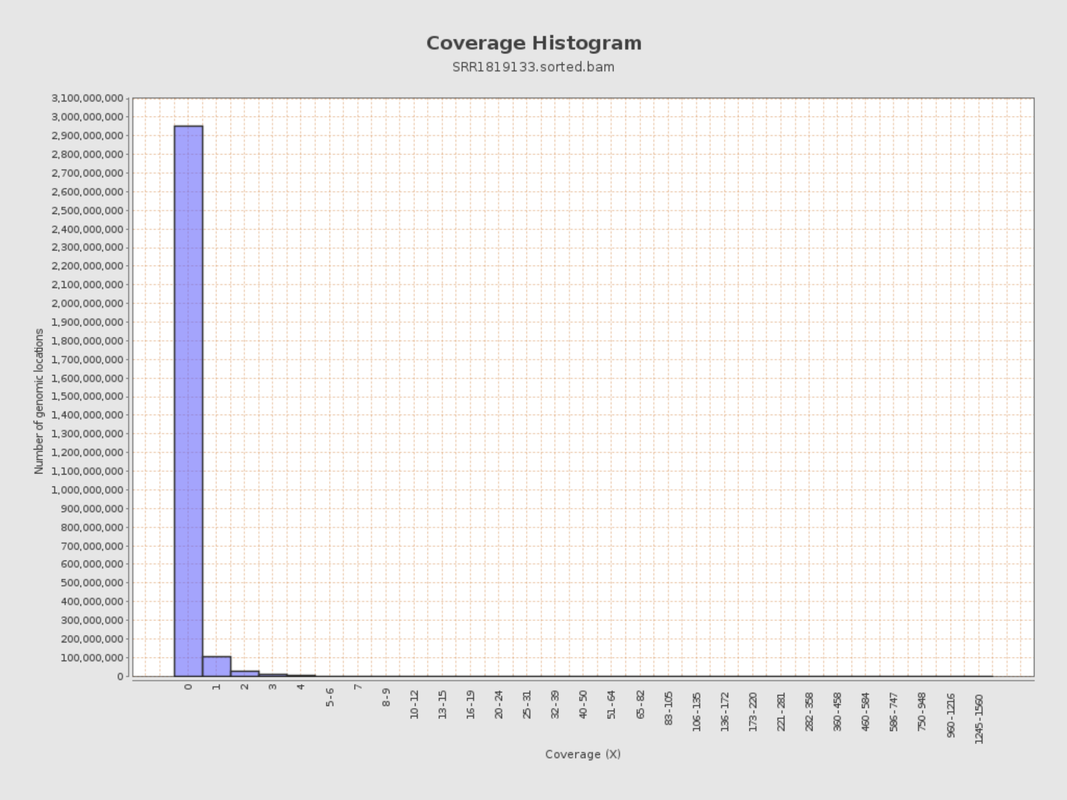
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19827861	0.0795	1.167
chr2	243199373	15709170	0.0646	0.7093
chr3	198022430	10853380	0.0548	0.313
chr4	191154276	11621531	0.0608	0.4439
chr5	180915260	10443929	0.0577	0.3217
chr6	171115067	8782113	0.0513	0.397
chr7	159138663	9957128	0.0626	0.6755

chr8	146364022	18022530	0.1231	0.6246
chr9	141213431	7676541	0.0544	0.4288
chr10	135534747	10613483	0.0783	0.6426
chr11	135006516	7036949	0.0521	0.4763
chr12	133851895	9376888	0.0701	0.3621
chr13	115169878	4309151	0.0374	0.2624
chr14	107349540	4752349	0.0443	0.2908
chr15	102531392	5336019	0.052	0.3051
chr16	90354753	6443355	0.0713	0.3941
chr17	81195210	7149685	0.0881	0.4323
chr18	78077248	4698098	0.0602	0.8927
chr19	59128983	4330670	0.0732	0.7821
chr20	63025520	5822550	0.0924	0.4286
chr21	48129895	2846787	0.0591	0.4054
chr22	51304566	1674756	0.0326	0.2402
chrMT	16571	183857	11.0951	7.1151
chrX	155270560	12146800	0.0782	0.4217
chrY	59373566	773900	0.013	0.4118

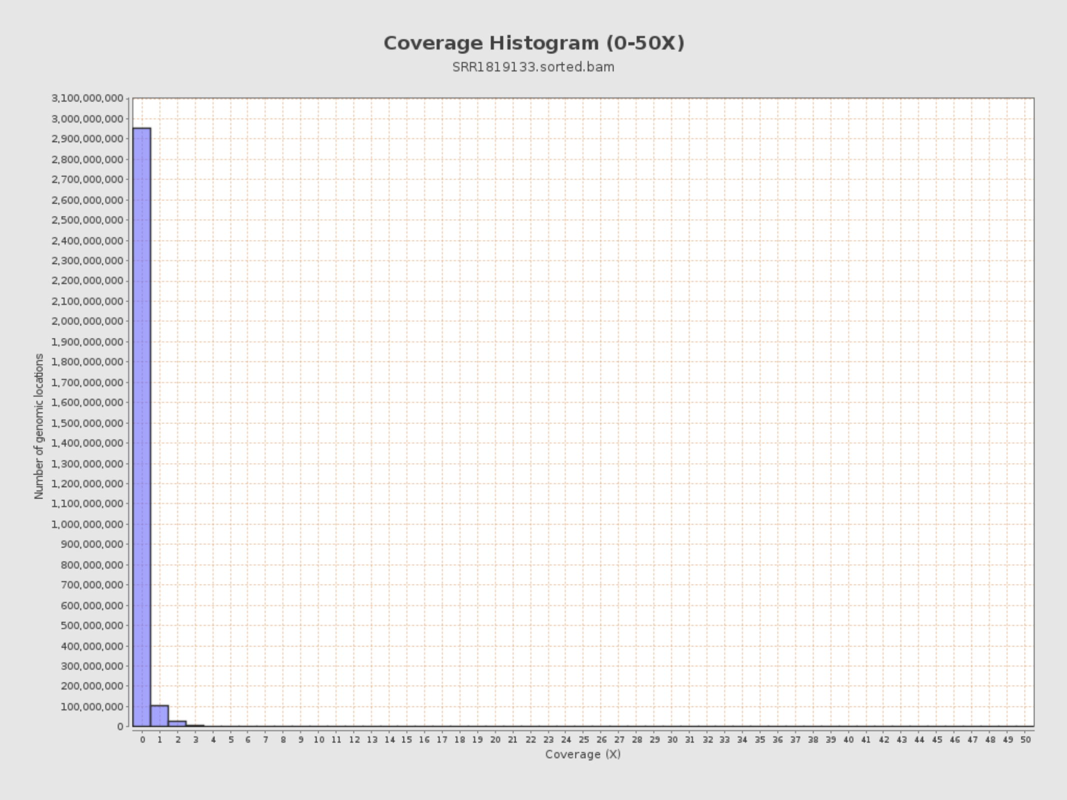
3. Results : Coverage across reference



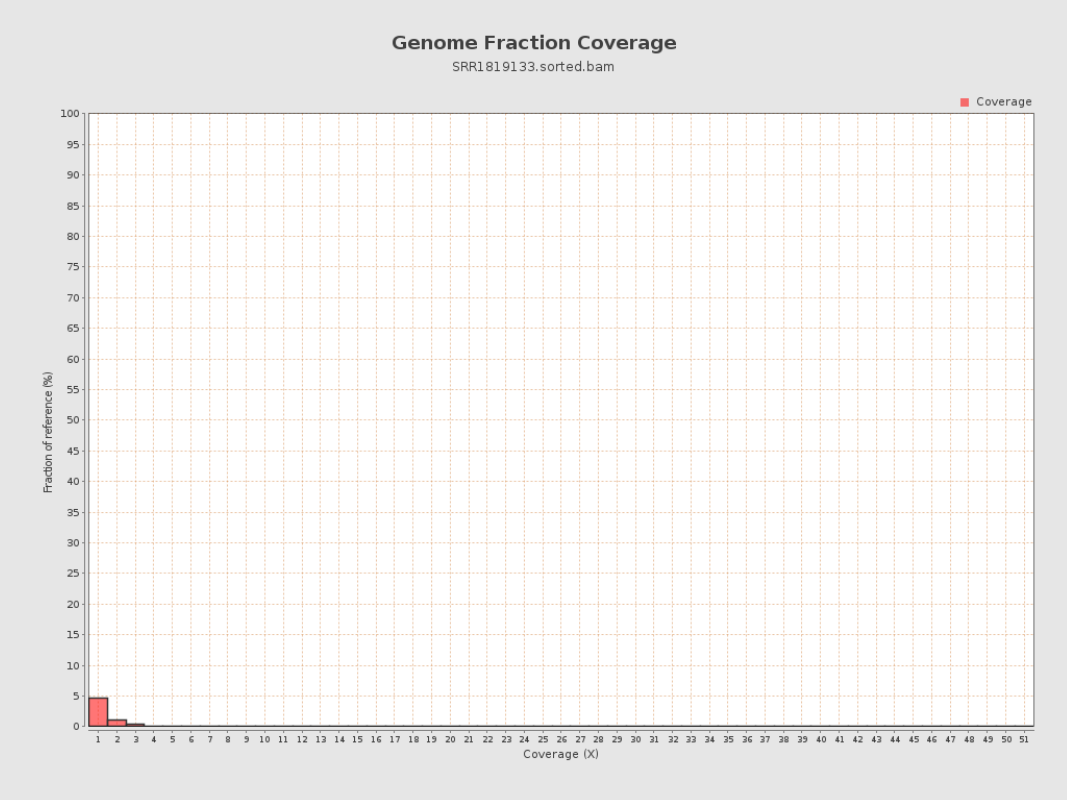
4. Results : Coverage Histogram



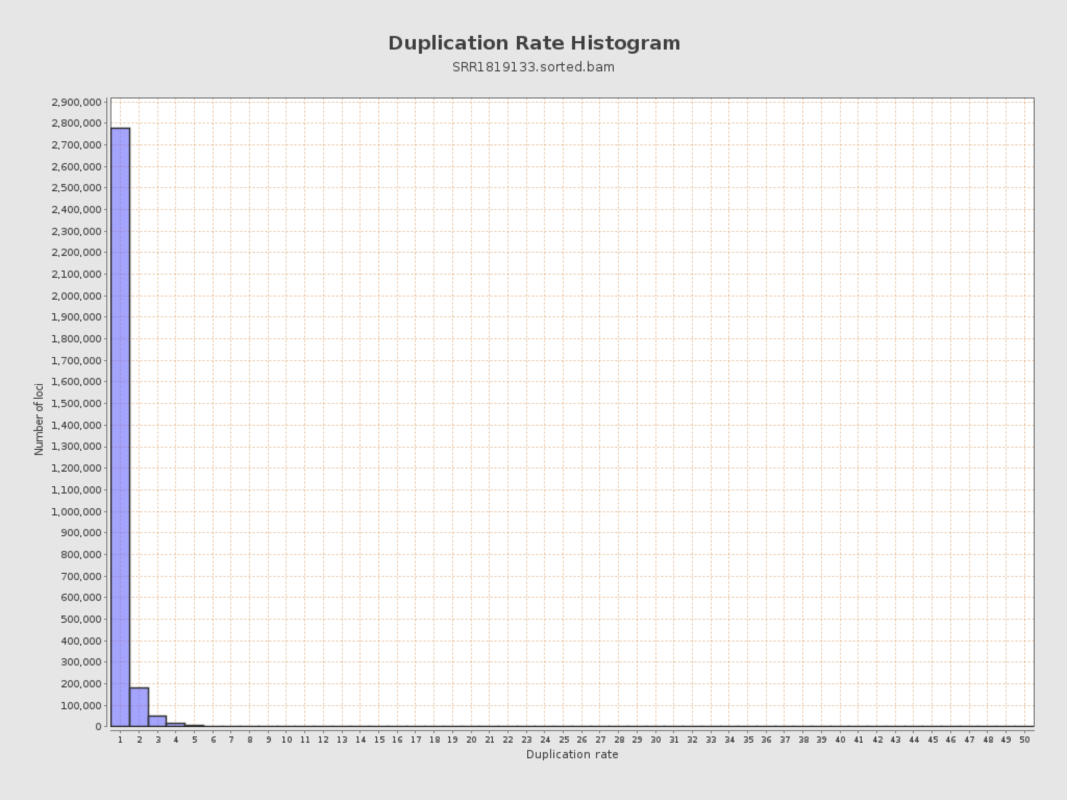
5. Results : Coverage Histogram (0-50X)



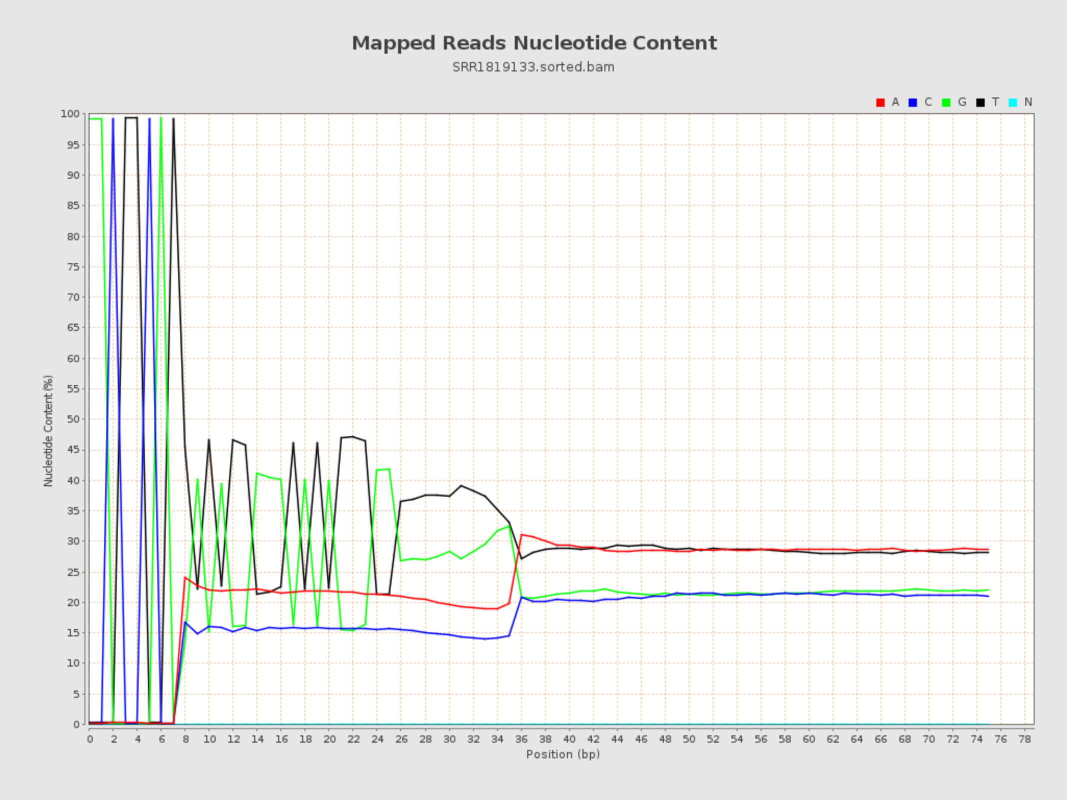
6. Results : Genome Fraction Coverage



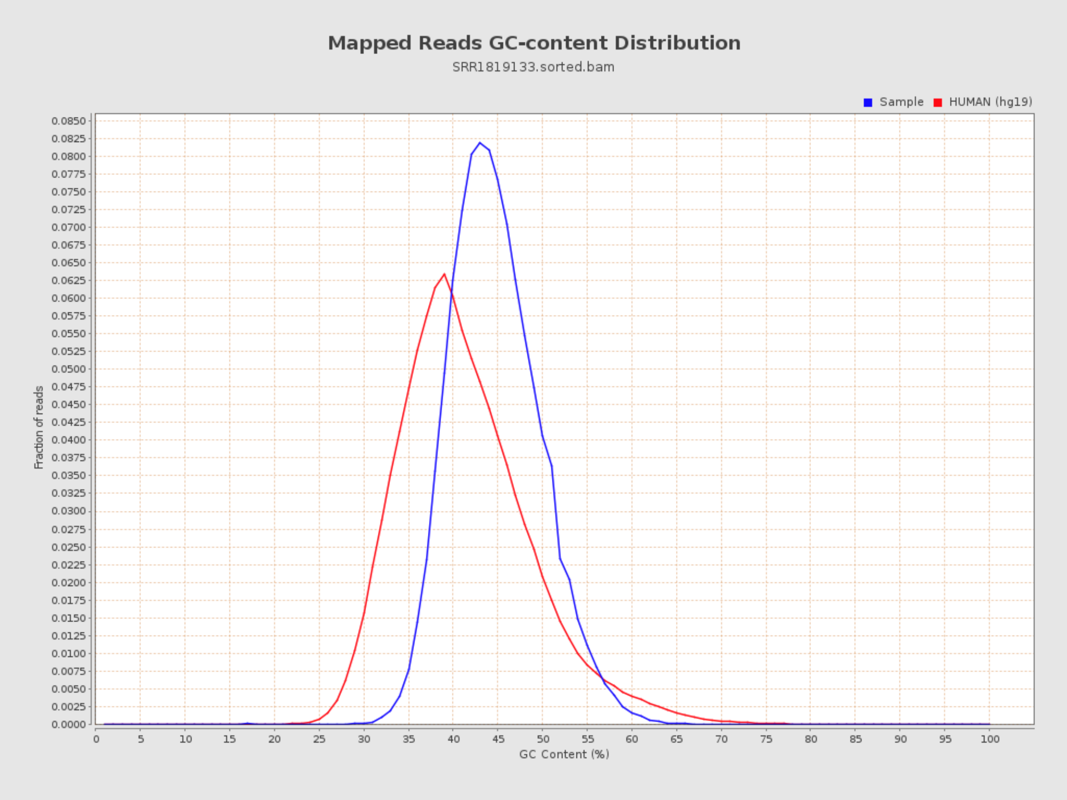
7. Results : Duplication Rate Histogram



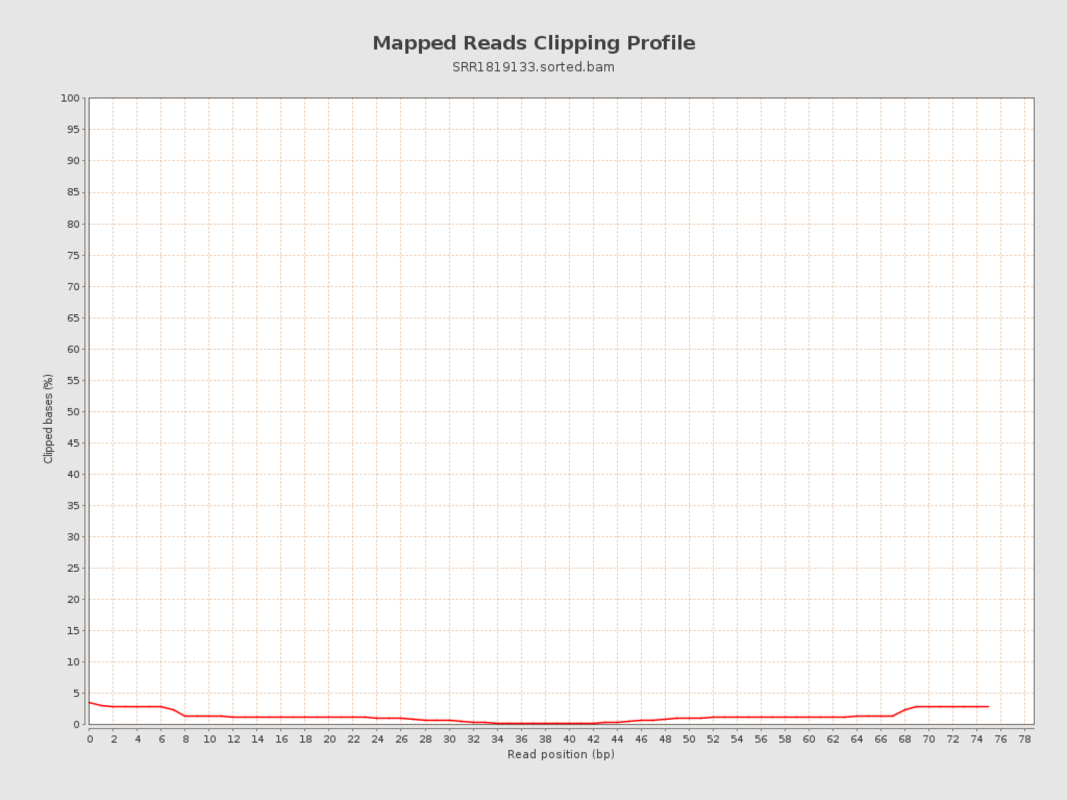
8. Results : Mapped Reads Nucleotide Content



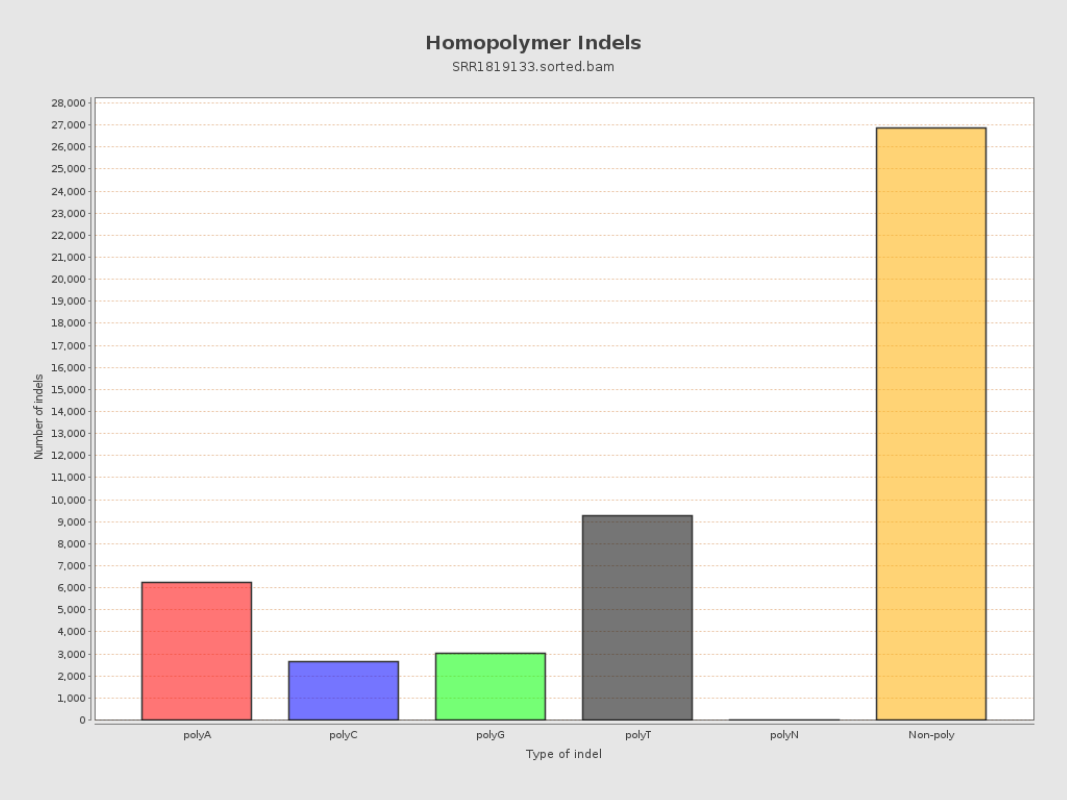
9. Results : Mapped Reads GC-content Distribution



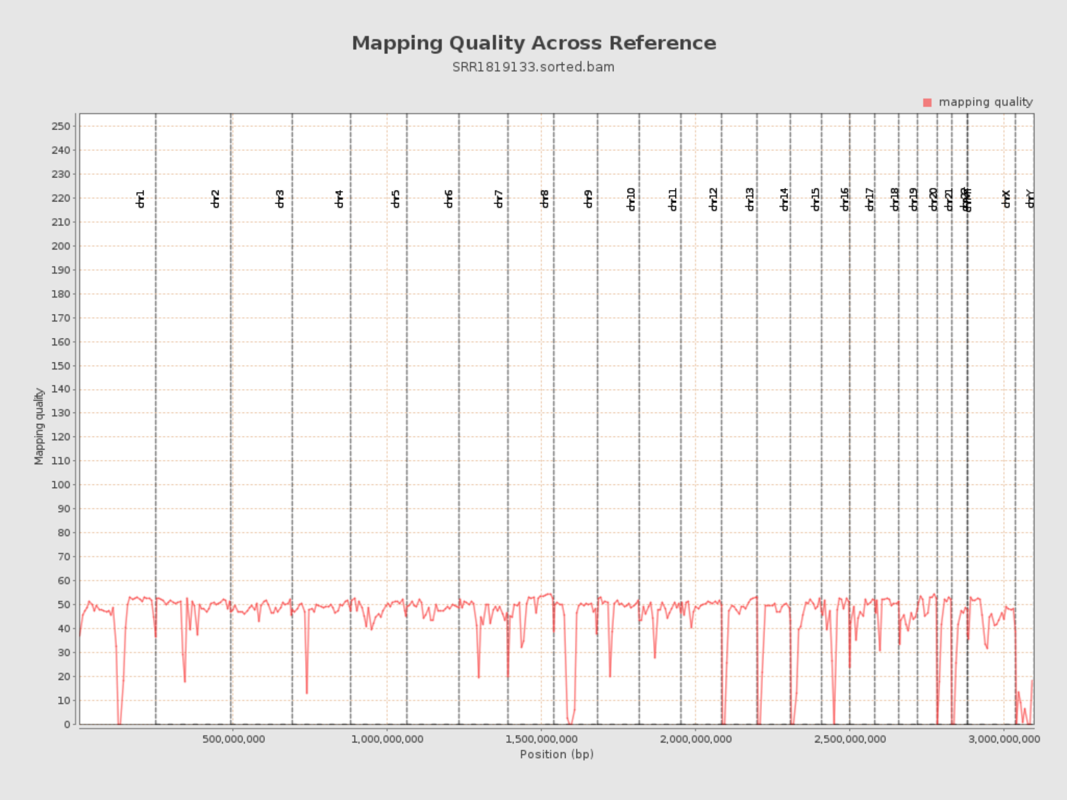
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram