Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 02:55:30

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153312.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_SRR1153312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153312.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 02:55:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	223,286,584
Mapped reads	218,198,999 / 97.72%
Unmapped reads	5,087,585 / 2.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,333,368 / 0.6%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	131,360,465 / 58.83%
Duplication rate	38.32%
Clipped reads	19,108,693 / 8.56%

2.2. ACGT Content

Number/percentage of A's	5,385,427,324 / 25.13%
Number/percentage of C's	5,328,716,462 / 24.86%
Number/percentage of T's	5,434,525,587 / 25.36%
Number/percentage of G's	5,280,062,955 / 24.64%
Number/percentage of N's	4,039,118 / 0.02%
GC Percentage	49.5%

2.3. Coverage

Mean	6.9245

Standard Deviation	56.7443

2.4. Mapping Quality

Mean Mapping Quality	49.32

2.5. Mismatches and indels

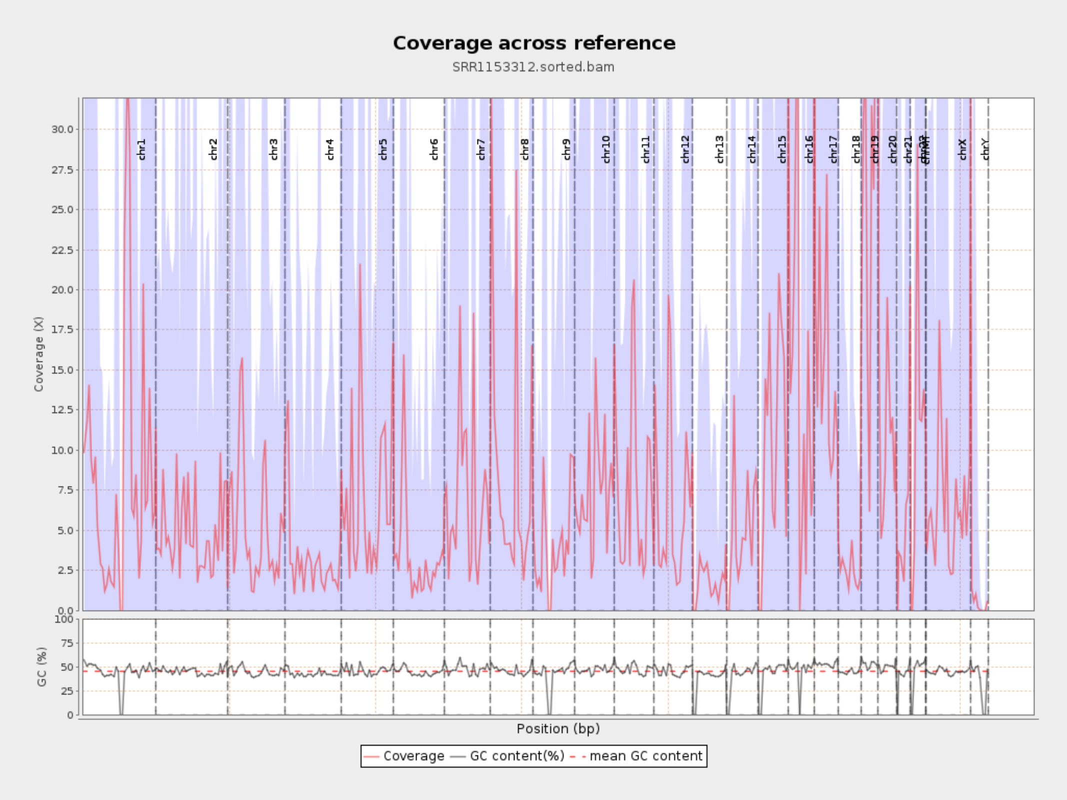
General error rate	0.42%
Mismatches	88,214,974
Insertions	1,207,989
Mapped reads with at least one insertion	0.55%
Deletions	1,546,249
Mapped reads with at least one deletion	0.7%
Homopolymer indels	45.02%

2.6. Chromosome stats

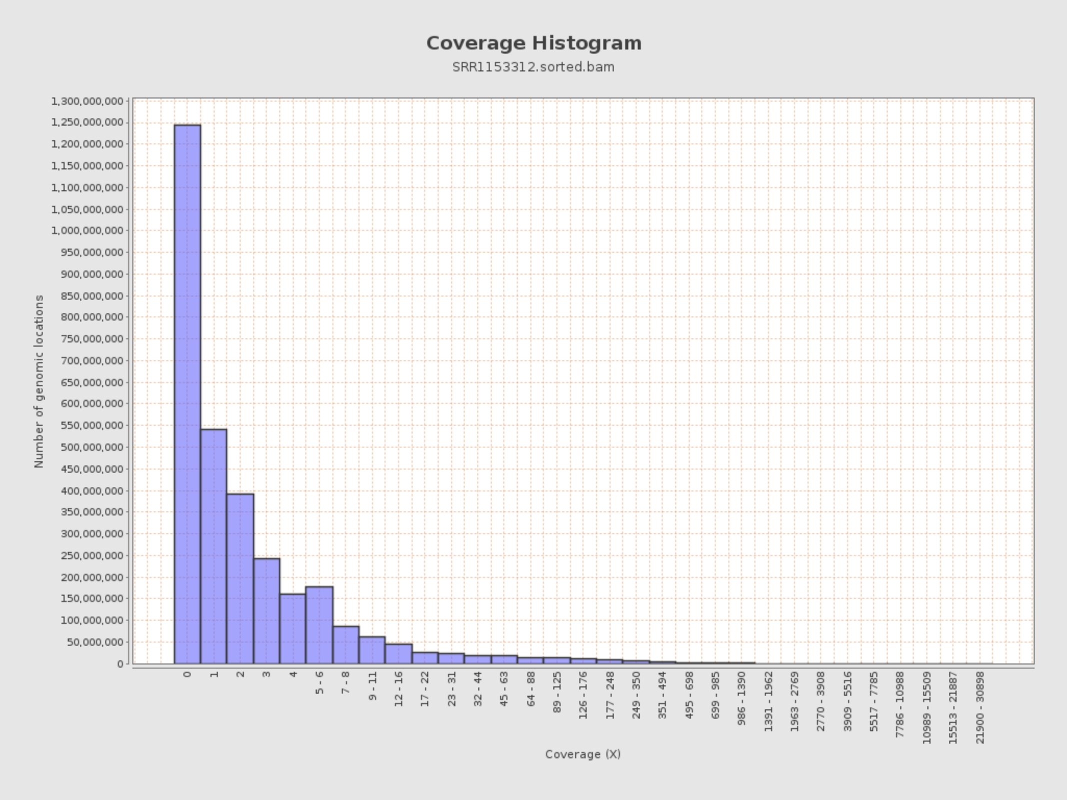
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2079684096	8.3437	55.1076
chr2	243199373	1183662508	4.867	28.1357
chr3	198022430	1037406957	5.2388	30.4448
chr4	191154276	615936070	3.2222	29.1824
chr5	180915260	1288117545	7.12	108.4101
chr6	171115067	572487900	3.3456	22.2862
chr7	159138663	1139268659	7.159	79.2233

chr8	146364022	1236025076	8.4449	96.7019
chr9	141213431	556965599	3.9441	23.9717
chr10	135534747	1015070164	7.4894	40.9598
chr11	135006516	1032375119	7.6469	40.0626
chr12	133851895	935427501	6.9885	36.0633
chr13	115169878	201319993	1.748	11.0617
chr14	107349540	534888580	4.9827	28.2
chr15	102531392	1063529961	10.3727	58.5008
chr16	90354753	1285967282	14.2324	85.9282
chr17	81195210	1243676820	15.3171	91.5404
chr18	78077248	193481388	2.4781	16.5747
chr19	59128983	1625292549	27.4872	106.4752
chr20	63025520	661815273	10.5008	50.9853
chr21	48129895	275186324	5.7176	61.4023
chr22	51304566	566087962	11.0339	68.2712
chrMT	16571	72048	4.3478	2.981
chrX	155270560	1066867044	6.871	39.6574
chrY	59373566	25549516	0.4303	18.8341

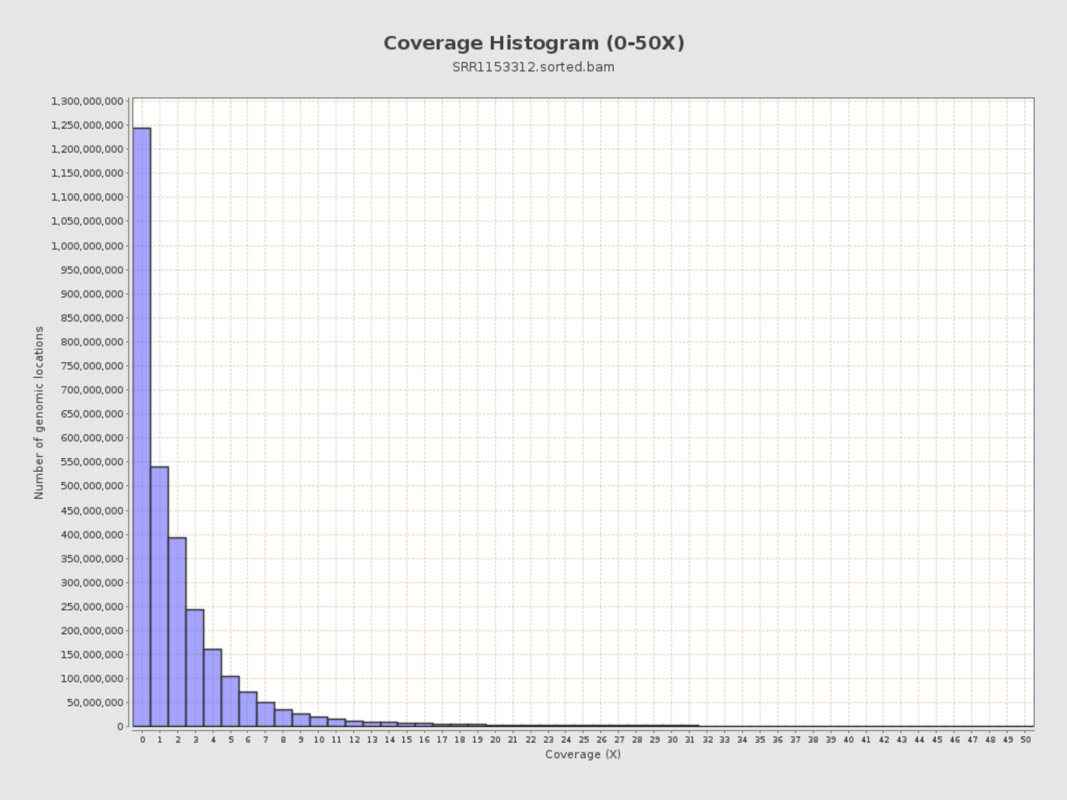
3. Results : Coverage across reference



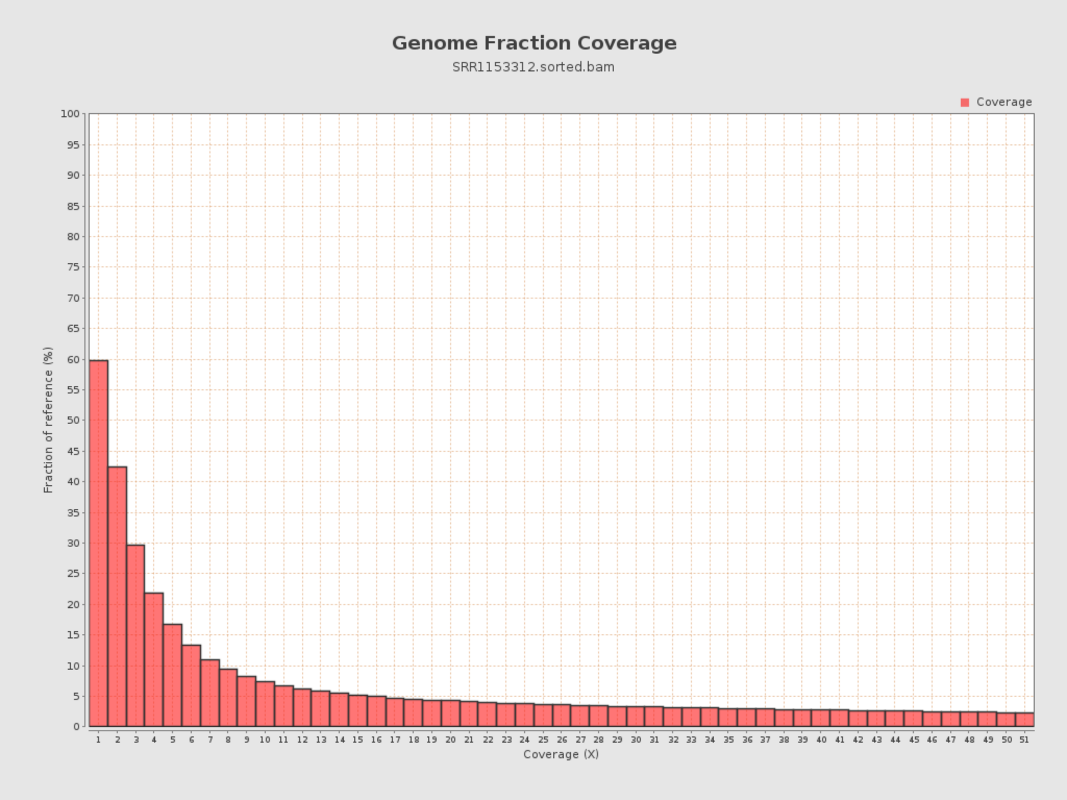
4. Results : Coverage Histogram



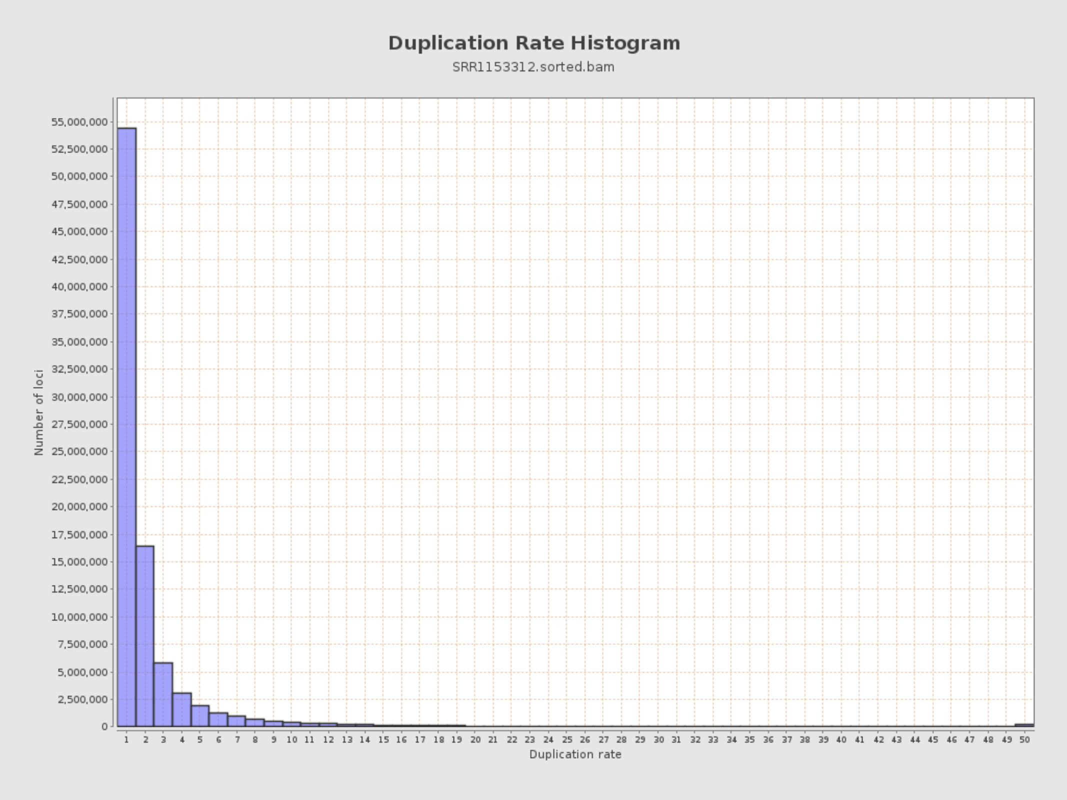
5. Results : Coverage Histogram (0-50X)



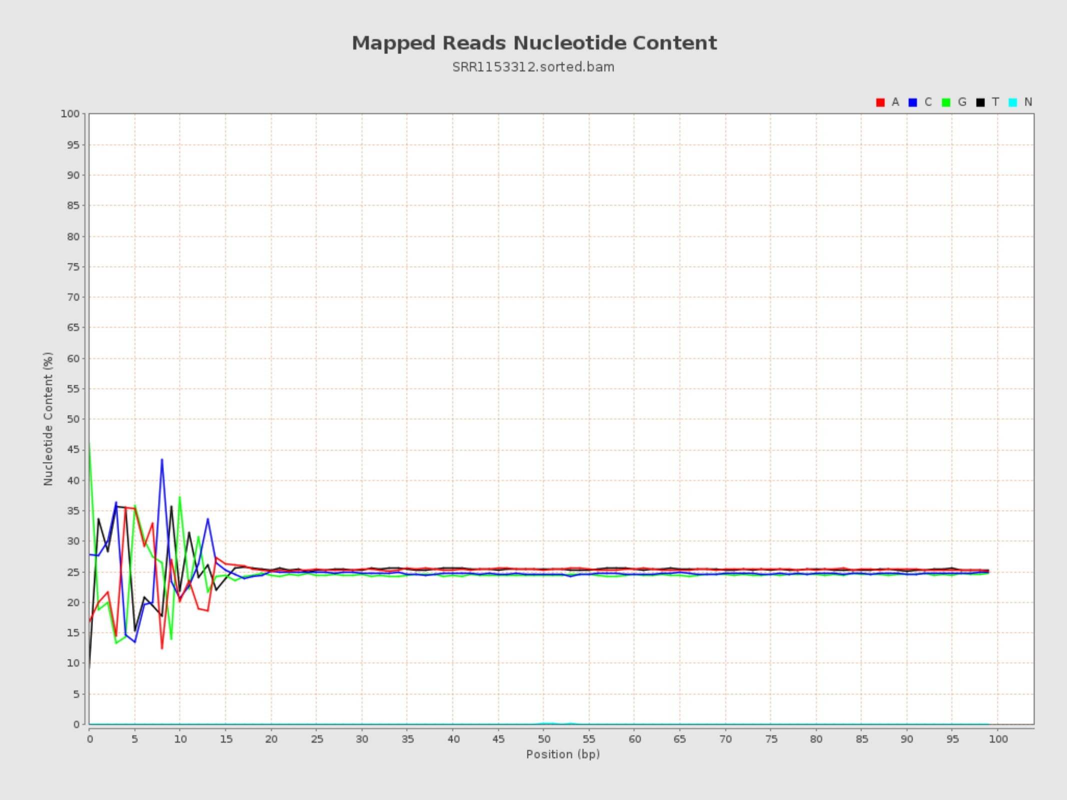
6. Results : Genome Fraction Coverage



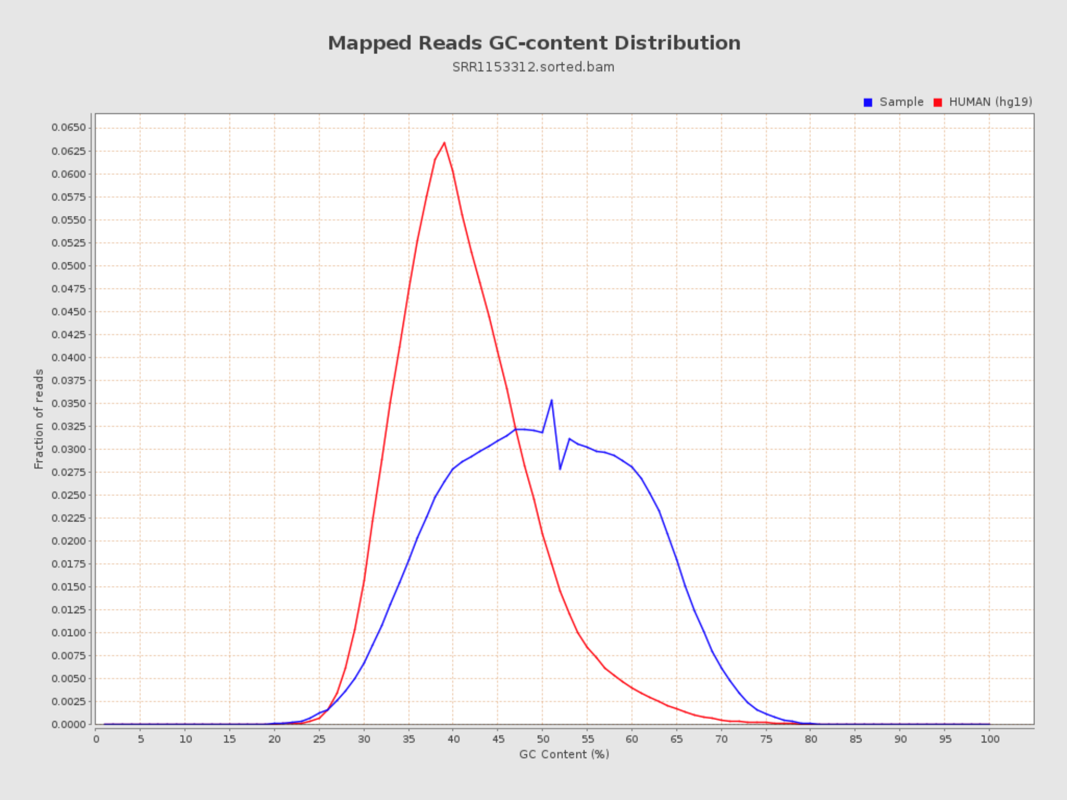
7. Results : Duplication Rate Histogram



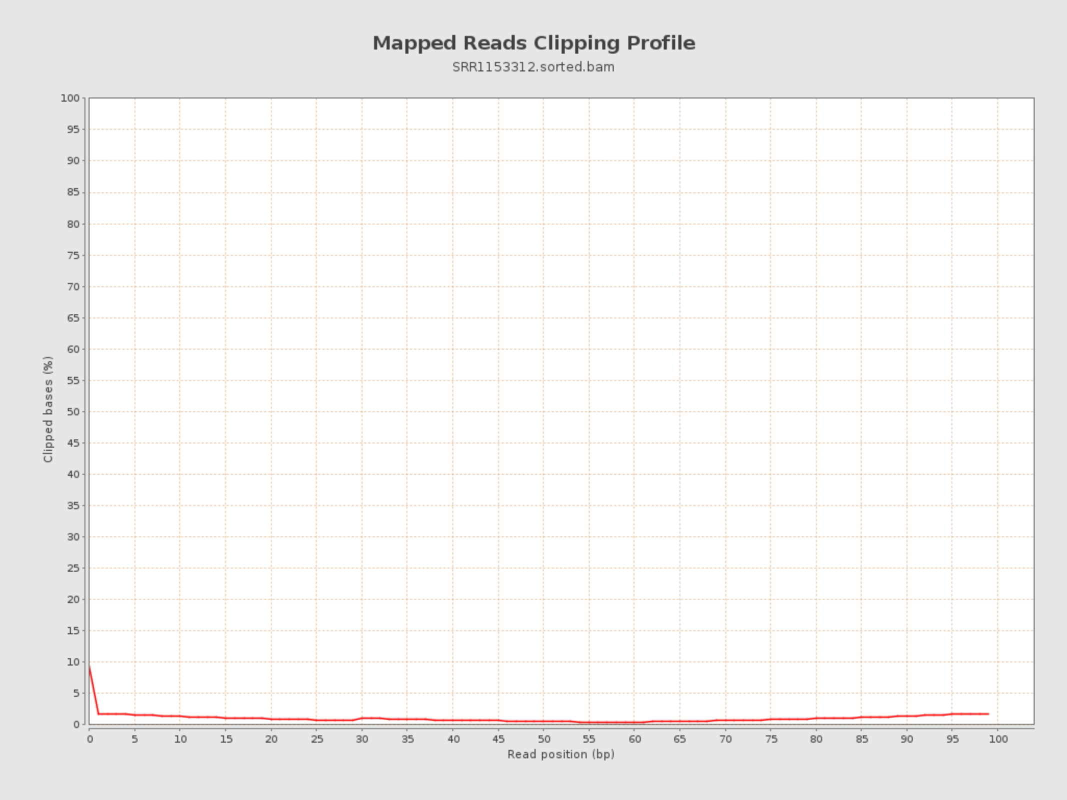
8. Results : Mapped Reads Nucleotide Content



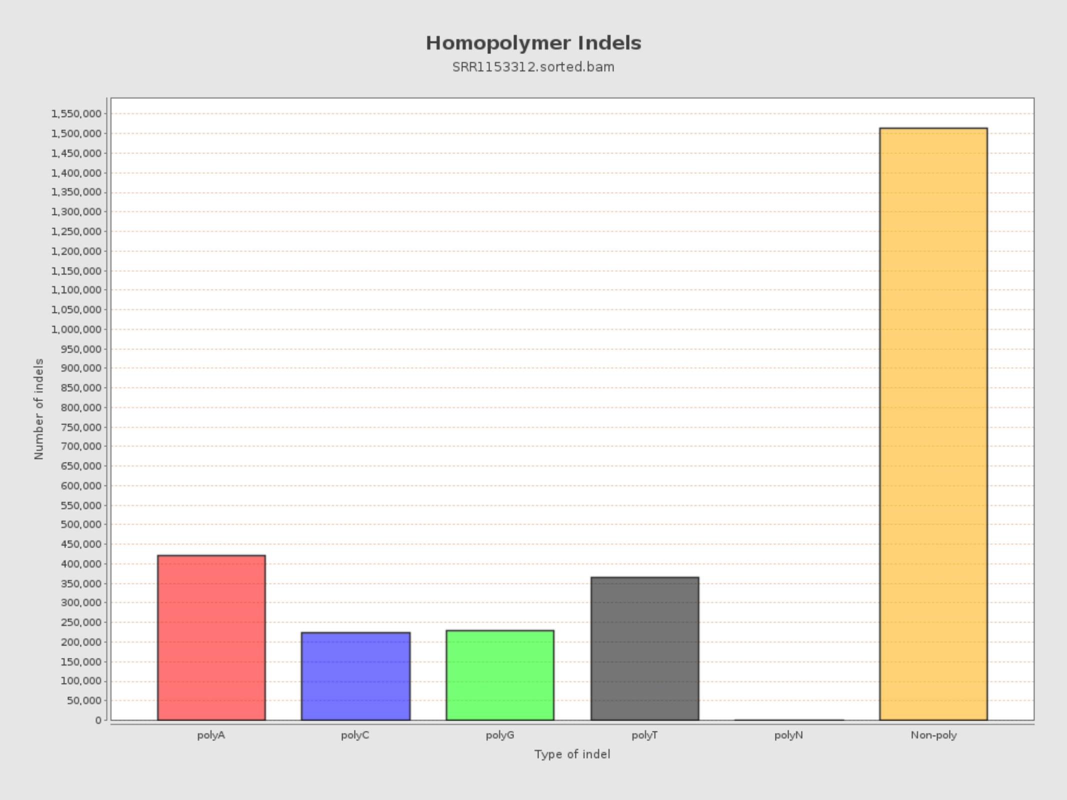
9. Results : Mapped Reads GC-content Distribution



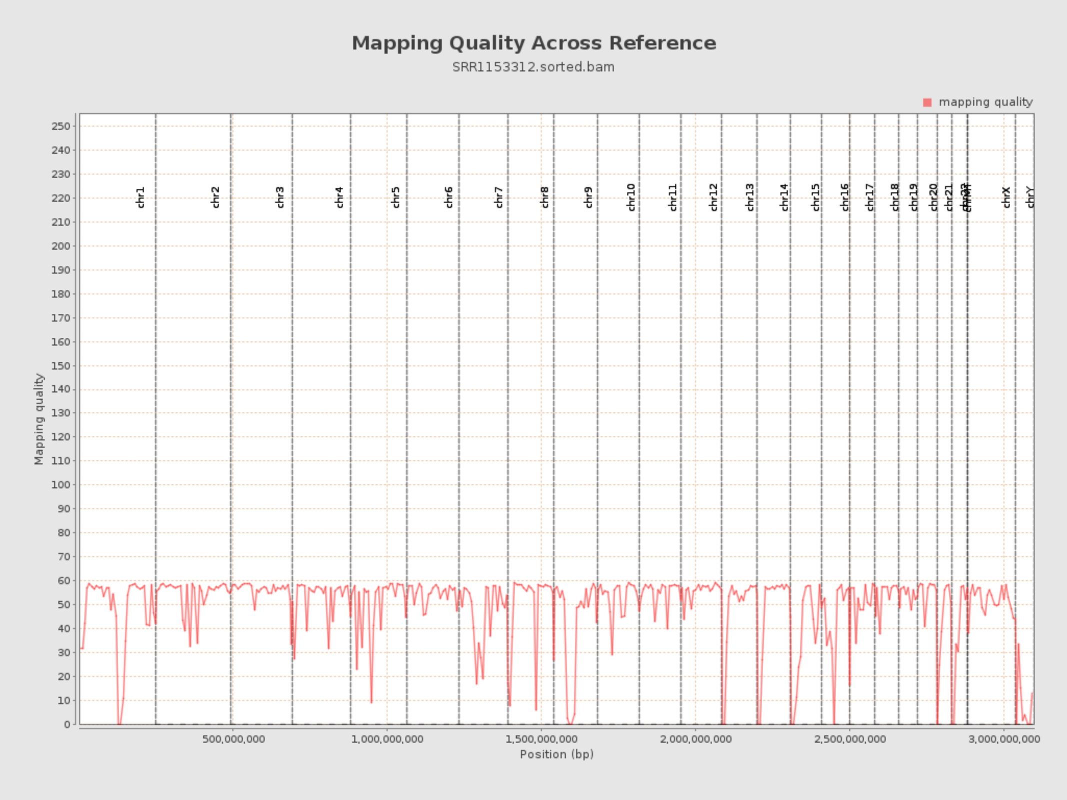
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram