Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/13 19:19:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153307.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_SRR1153307 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153307.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 13 19:19:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153307.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	75,821,710
Mapped reads	74,839,841 / 98.71%
Unmapped reads	981,869 / 1.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	486,723 / 0.64%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	34,687,120 / 45.75%
Duplication rate	36.71%
Clipped reads	3,705,945 / 4.89%

2.2. ACGT Content

Number/percentage of A's	1,916,582,584 / 25.77%
Number/percentage of C's	1,798,863,723 / 24.18%
Number/percentage of T's	1,916,367,145 / 25.76%
Number/percentage of G's	1,806,322,747 / 24.28%
Number/percentage of N's	336,766 / 0%
GC Percentage	48.47%

2.3. Coverage

Mean	2.4032

Standard Deviation	26.4316

2.4. Mapping Quality

Mean Mapping Quality	48.88

2.5. Mismatches and indels

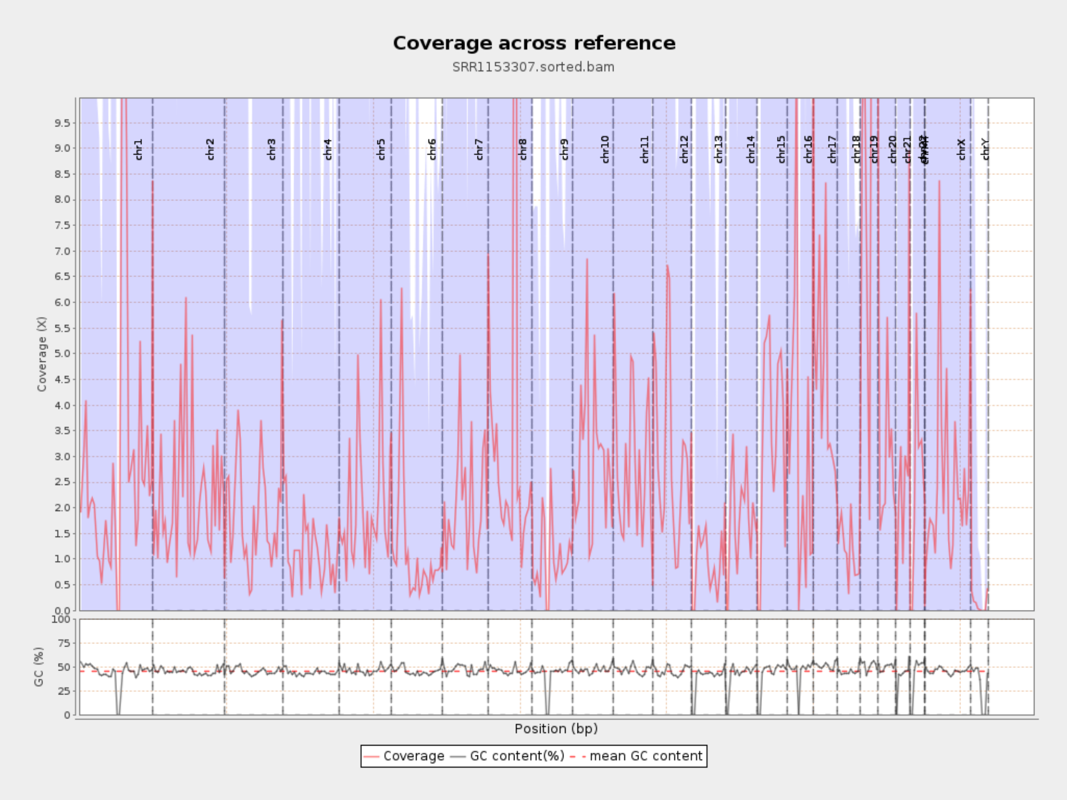
General error rate	0.32%
Mismatches	23,101,882
Insertions	638,217
Mapped reads with at least one insertion	0.84%
Deletions	432,959
Mapped reads with at least one deletion	0.57%
Homopolymer indels	47.45%

2.6. Chromosome stats

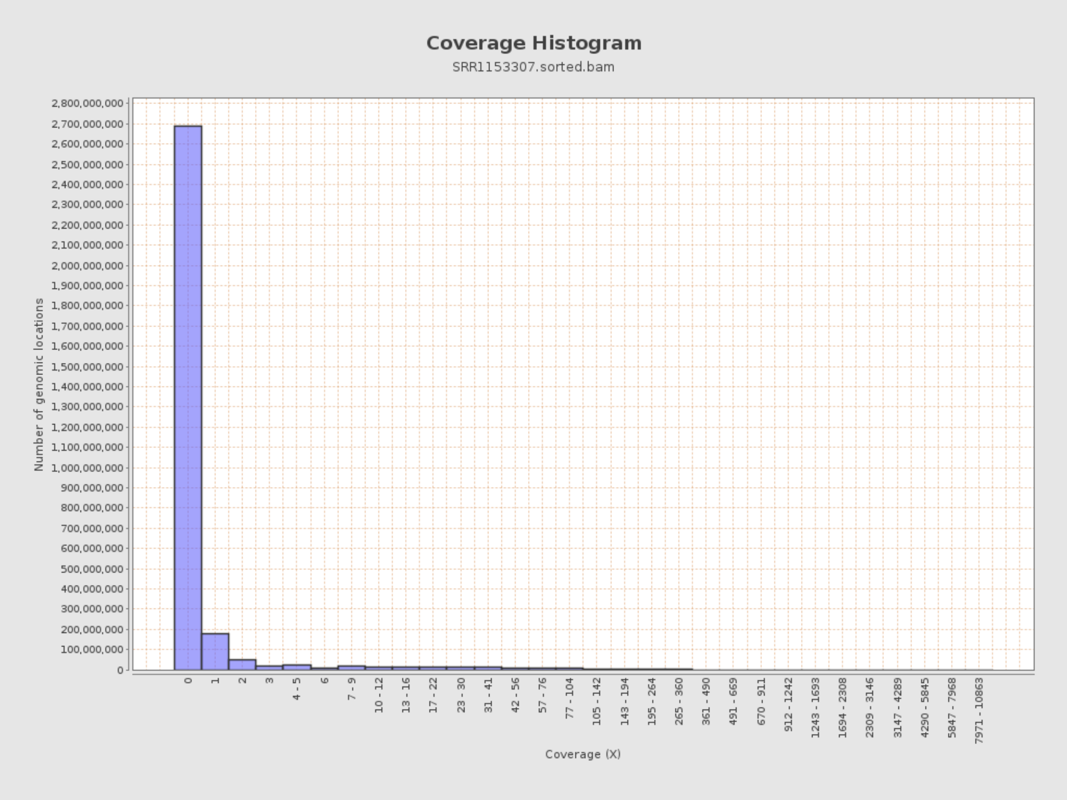
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	740748631	2.9719	26.263
chr2	243199373	554040524	2.2781	22.1062
chr3	198022430	371149459	1.8743	16.7394
chr4	191154276	222613863	1.1646	12.8498
chr5	180915260	375898849	2.0778	25.2291
chr6	171115067	193726048	1.1321	11.9708
chr7	159138663	324836442	2.0412	28.091

chr8	146364022	488709839	3.339	61.6578
chr9	141213431	139673693	0.9891	11.4161
chr10	135534747	417954317	3.0837	27.8911
chr11	135006516	392764711	2.9092	21.1599
chr12	133851895	402052095	3.0037	24.8253
chr13	115169878	103671771	0.9002	9.91
chr14	107349540	187737008	1.7488	15.7287
chr15	102531392	341767420	3.3333	26.1619
chr16	90354753	296749970	3.2843	26.2896
chr17	81195210	359014512	4.4216	28.3549
chr18	78077248	91233191	1.1685	11.8271
chr19	59128983	582969683	9.8593	58.5481
chr20	63025520	193012801	3.0625	23.4896
chr21	48129895	135788664	2.8213	43.9579
chr22	51304566	131953915	2.572	20.0384
chrMT	16571	1385	0.0836	0.3038
chrX	155270560	383244330	2.4682	24.1224
chrY	59373566	8138046	0.1371	6.5026

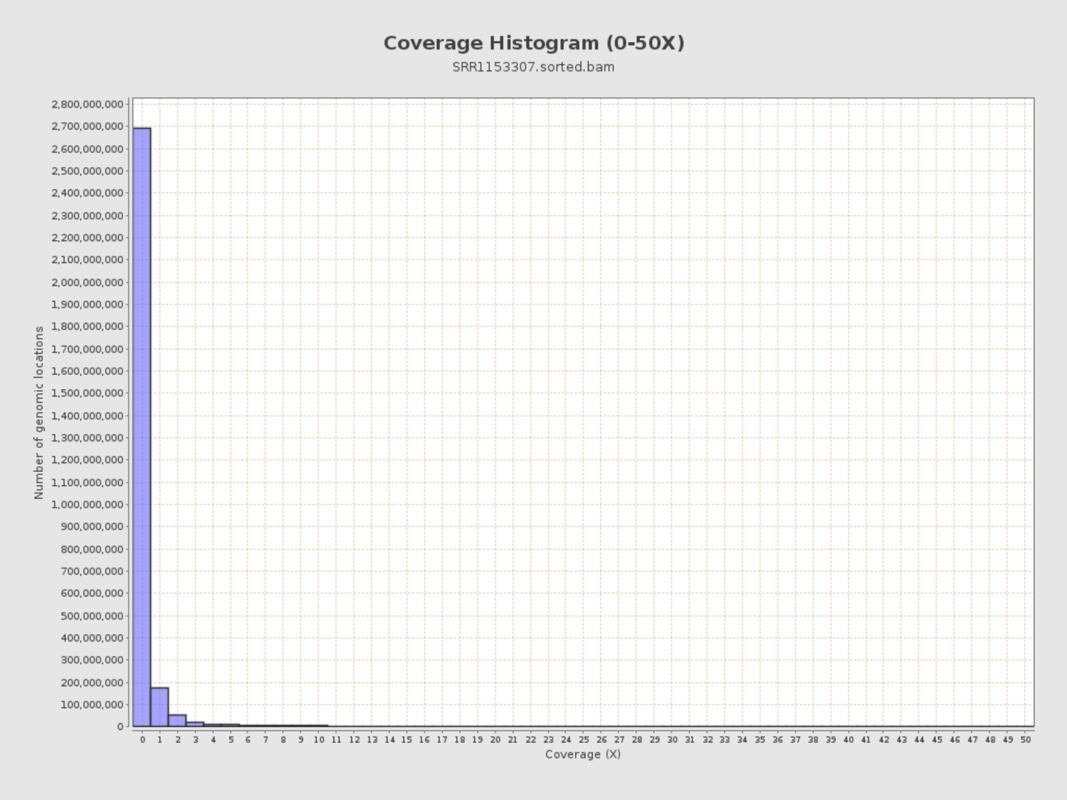
3. Results : Coverage across reference



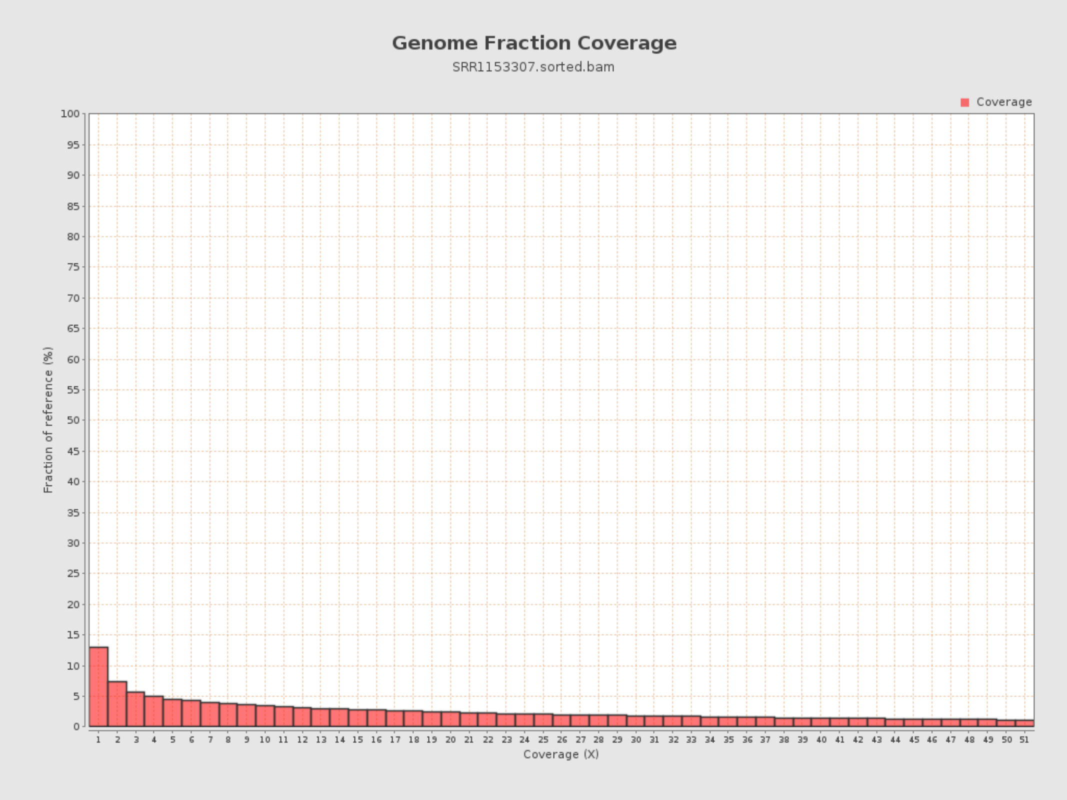
4. Results : Coverage Histogram



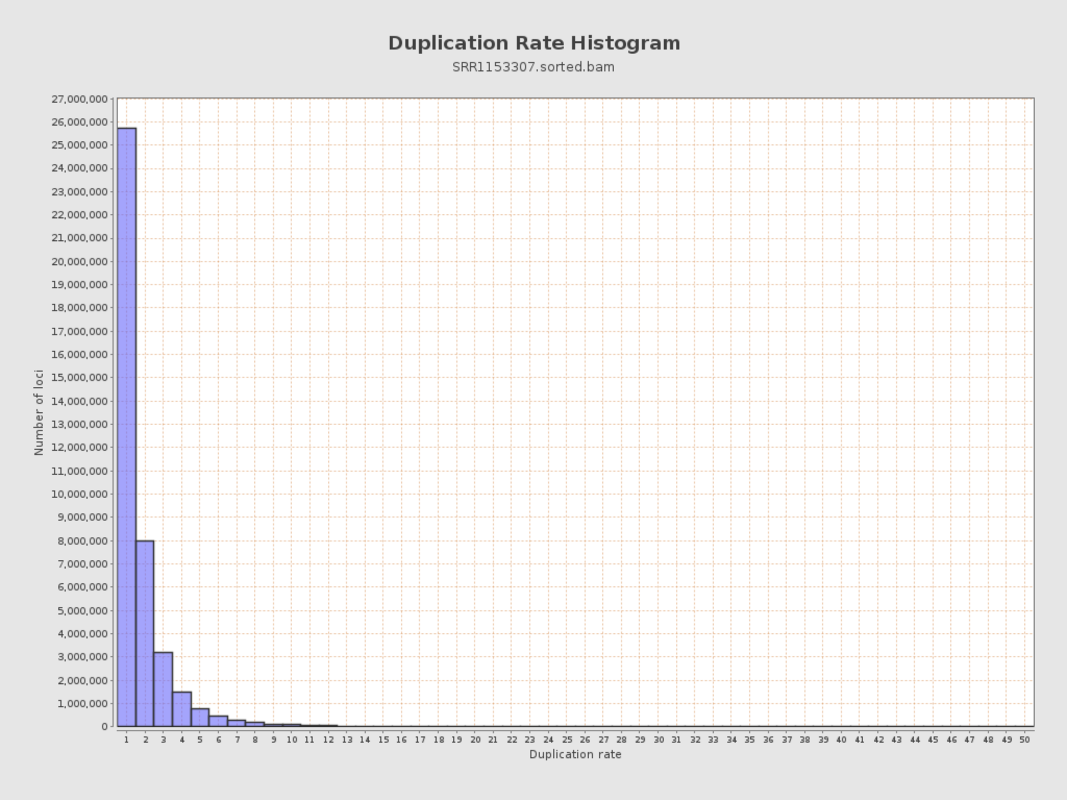
5. Results : Coverage Histogram (0-50X)



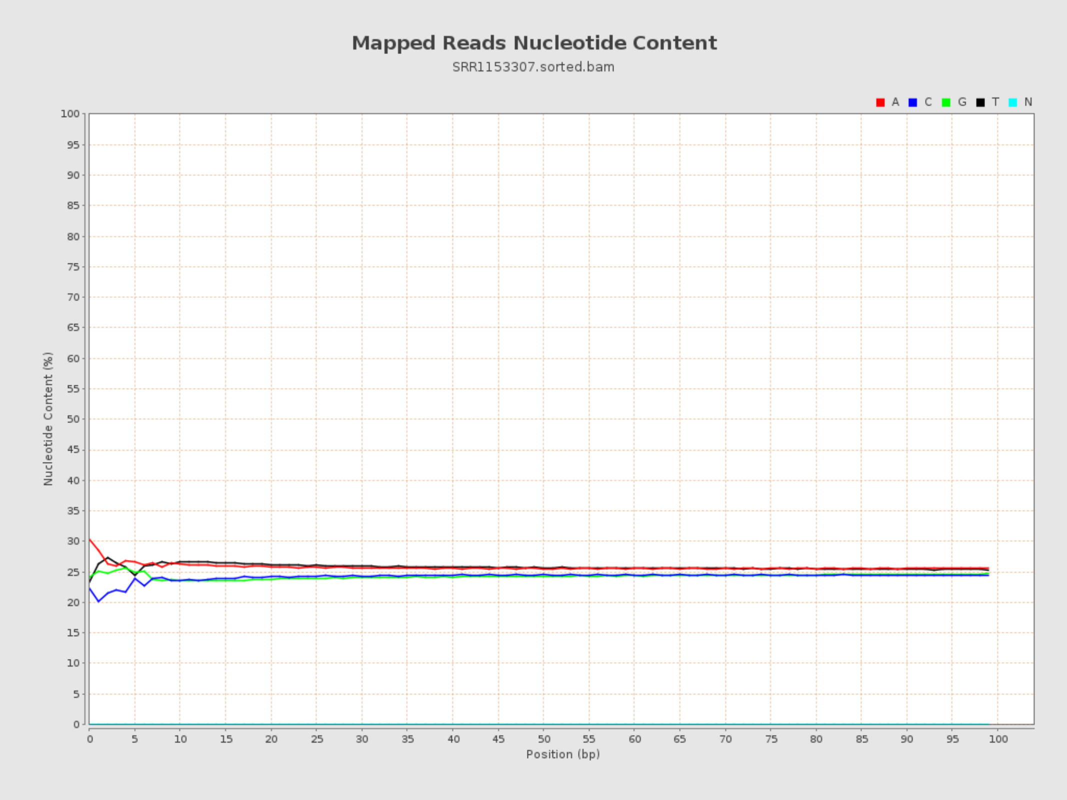
6. Results : Genome Fraction Coverage



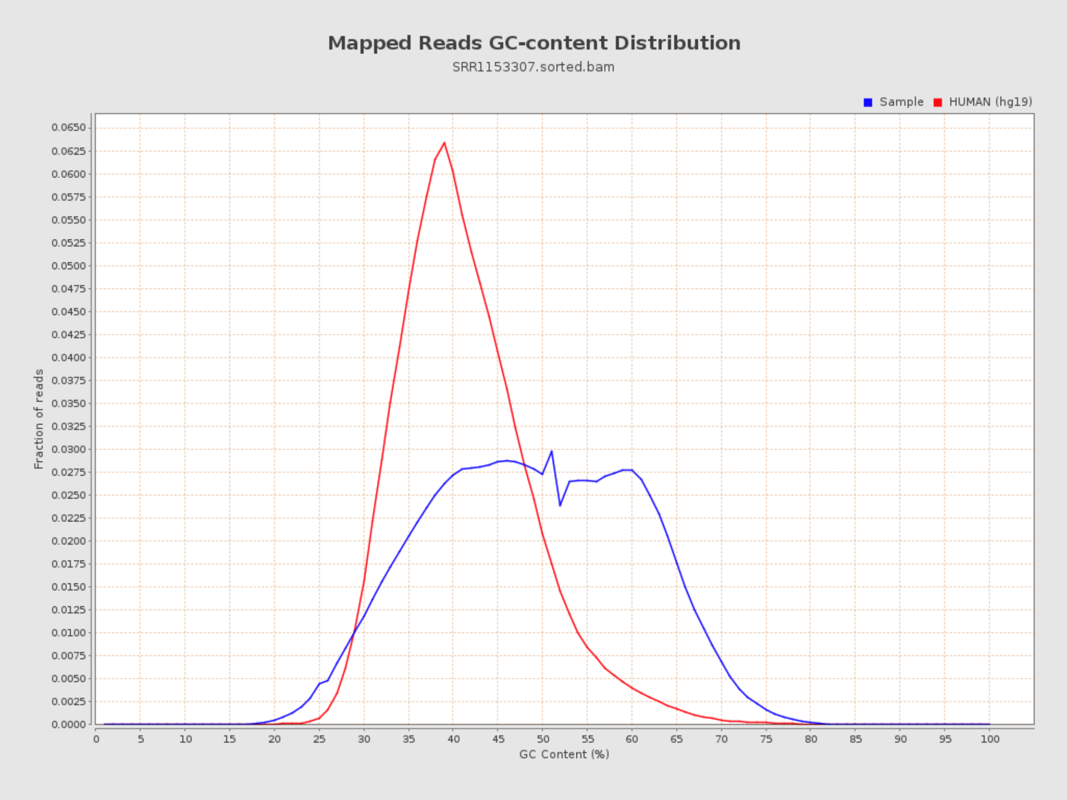
7. Results : Duplication Rate Histogram



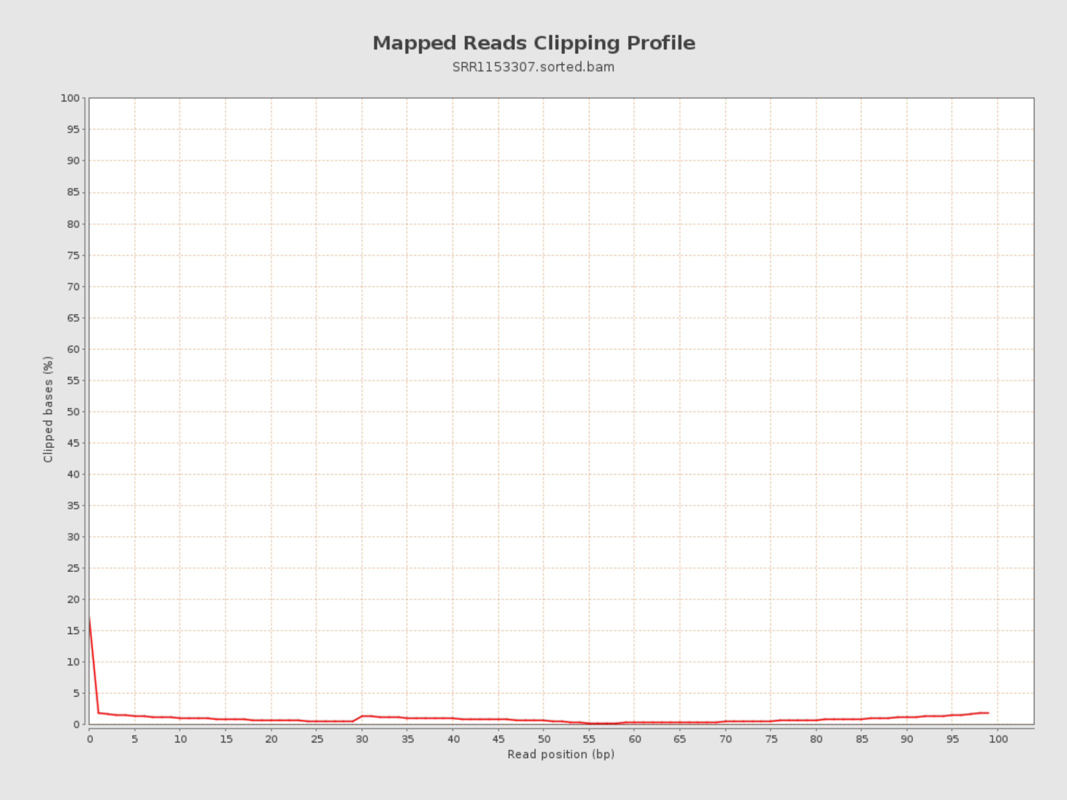
8. Results : Mapped Reads Nucleotide Content



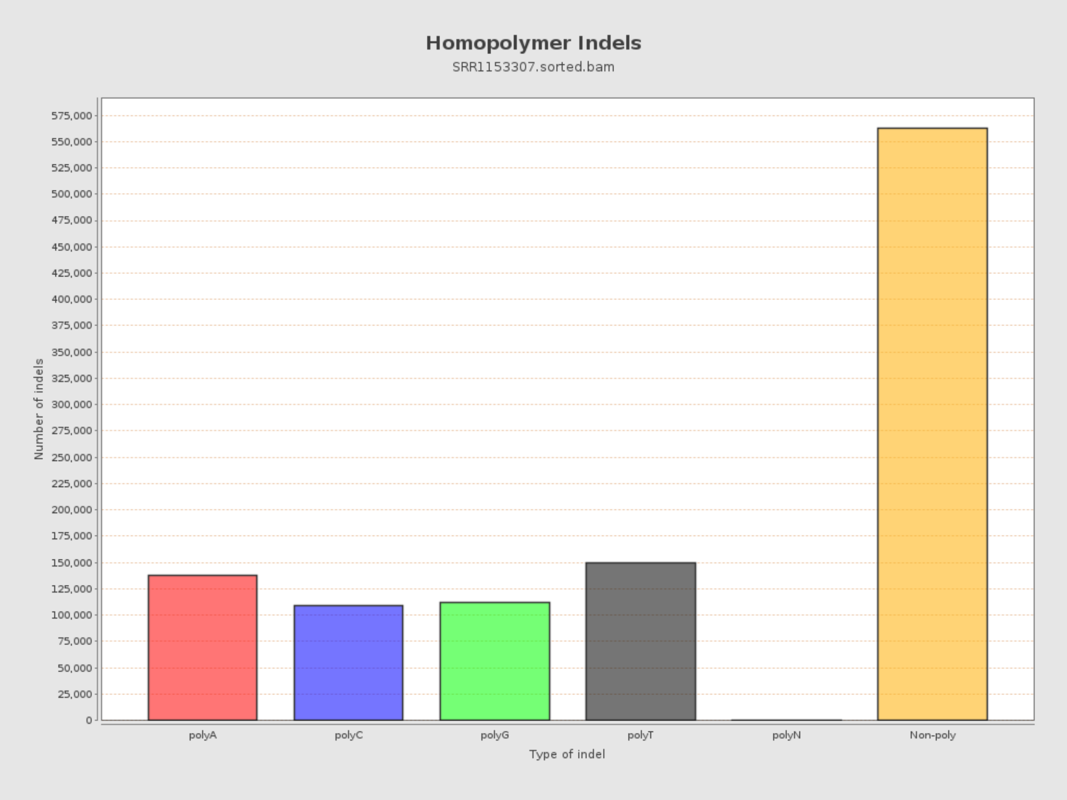
9. Results : Mapped Reads GC-content Distribution



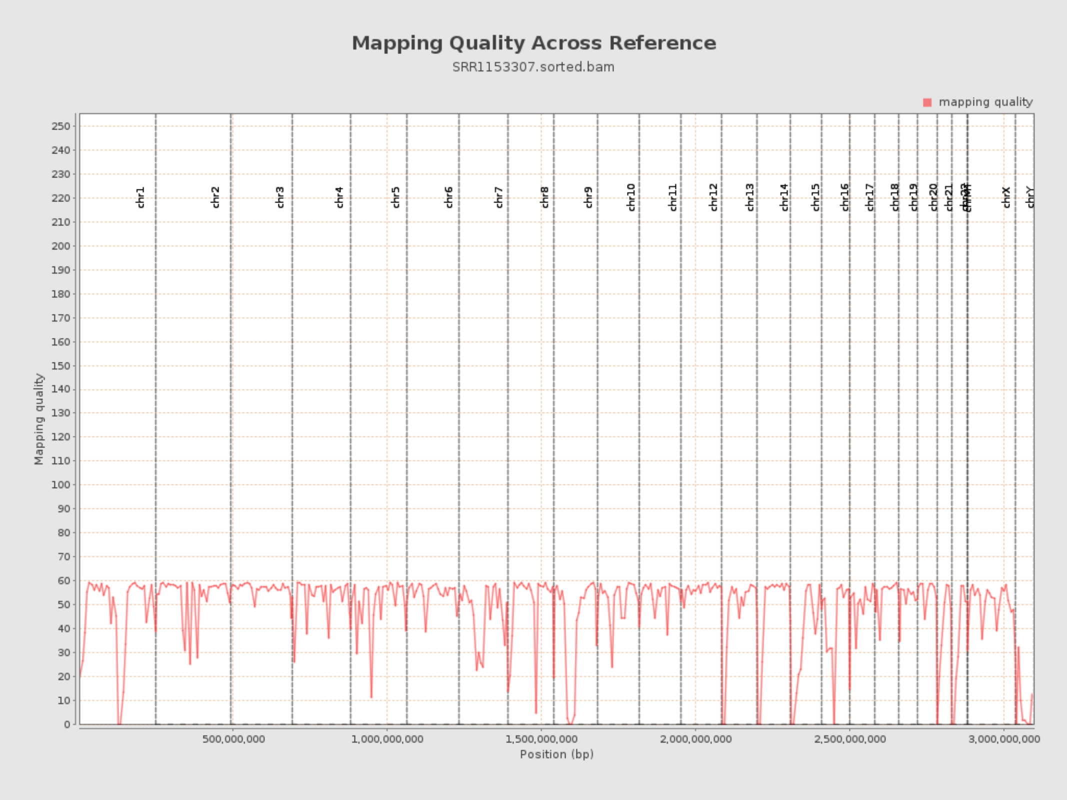
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram