Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 09:25:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153363.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_SRR1153363 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153363.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 09:25:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153363.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	152,537,200
Mapped reads	148,782,368 / 97.54%
Unmapped reads	3,754,832 / 2.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	939,302 / 0.62%
Read min/max/mean length	30 / 100 / 100.25
Duplicated reads (estimated)	76,356,598 / 50.06%
Duplication rate	32.96%
Clipped reads	14,455,454 / 9.48%

2.2. ACGT Content

Number/percentage of A's	3,702,111,278 / 25.38%
Number/percentage of C's	3,590,087,026 / 24.62%
Number/percentage of T's	3,736,104,854 / 25.62%
Number/percentage of G's	3,553,753,340 / 24.37%
Number/percentage of N's	2,378,942 / 0.02%
GC Percentage	48.98%

2.3. Coverage

Mean	4.712

Standard Deviation	35.5523

2.4. Mapping Quality

Mean Mapping Quality	49.4

2.5. Mismatches and indels

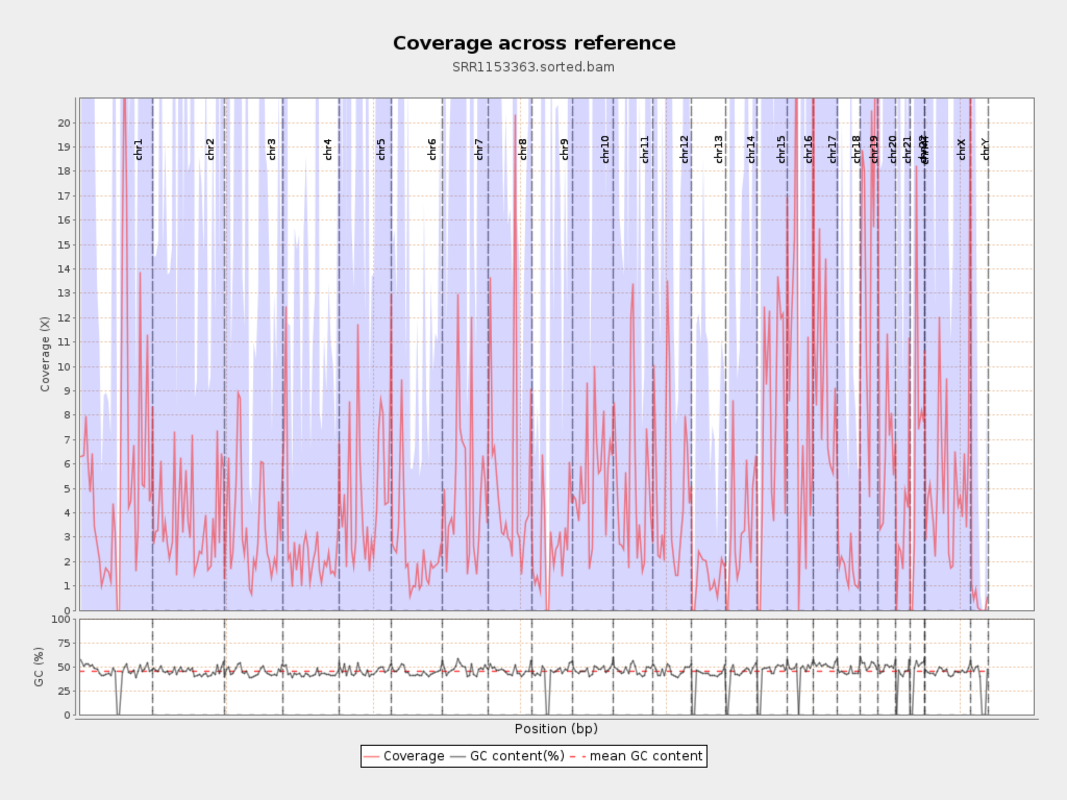
General error rate	0.4%
Mismatches	56,431,725
Insertions	847,732
Mapped reads with at least one insertion	0.56%
Deletions	1,103,813
Mapped reads with at least one deletion	0.73%
Homopolymer indels	45.33%

2.6. Chromosome stats

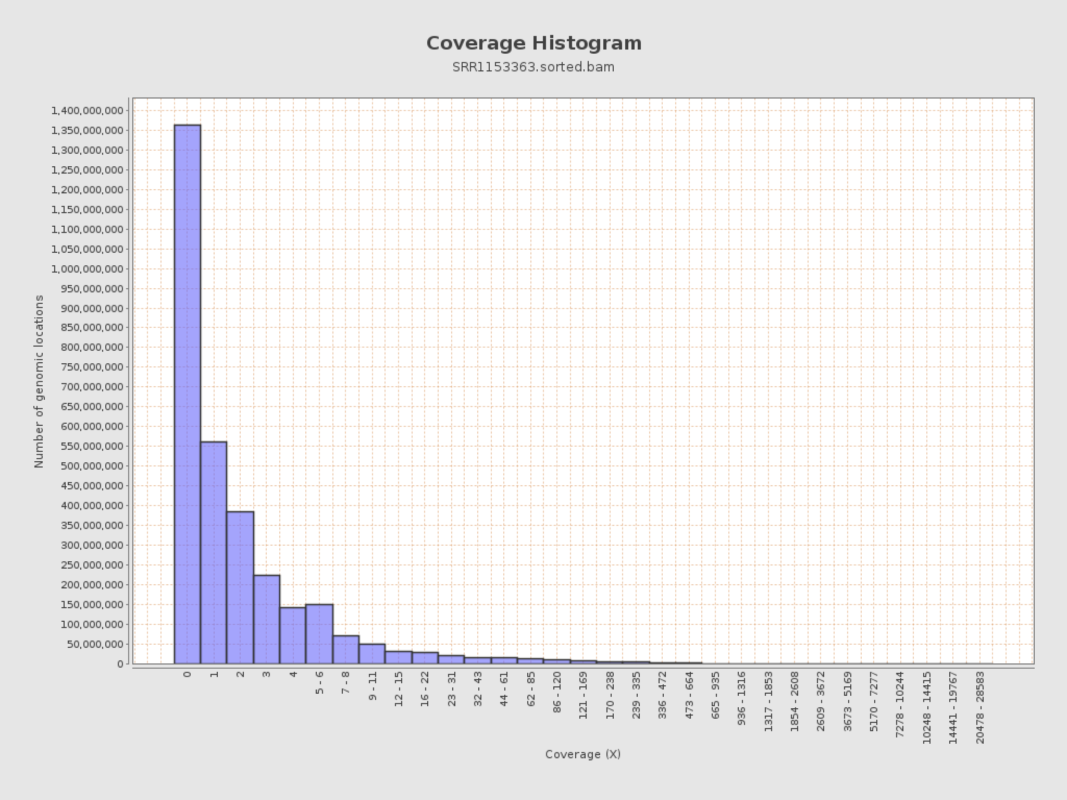
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1416790608	5.6842	35.6978
chr2	243199373	899054313	3.6968	20.6582
chr3	198022430	678812896	3.428	18.7383
chr4	191154276	507152827	2.6531	27.6494
chr5	180915260	879346930	4.8605	59.7075
chr6	171115067	391923026	2.2904	13.784
chr7	159138663	788010962	4.9517	50.2301

chr8	146364022	782919055	5.3491	58.3314
chr9	141213431	368775812	2.6115	16.3994
chr10	135534747	750416266	5.5367	28.0225
chr11	135006516	696413782	5.1584	25.1655
chr12	133851895	660465016	4.9343	24.5569
chr13	115169878	159709978	1.3867	8.3407
chr14	107349540	366797199	3.4168	18.9189
chr15	102531392	764388821	7.4552	41.7459
chr16	90354753	820287932	9.0785	54.6132
chr17	81195210	748303906	9.2161	61.1711
chr18	78077248	132879245	1.7019	12.3888
chr19	59128983	960226321	16.2395	60.7384
chr20	63025520	434004634	6.8862	31.8057
chr21	48129895	178036636	3.6991	30.0303
chr22	51304566	365076496	7.1159	43.5095
chrMT	16571	151413	9.1372	4.7278
chrX	155270560	815925932	5.2549	28.0031
chrY	59373566	21019690	0.354	15.4302

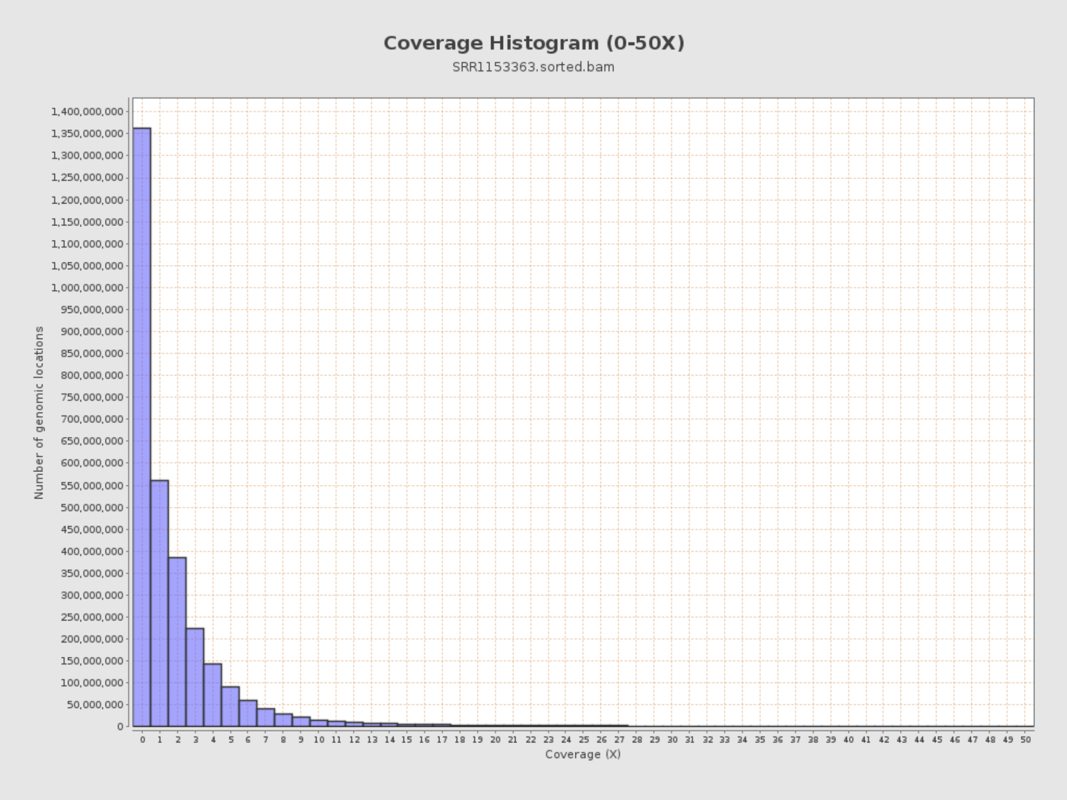
3. Results : Coverage across reference



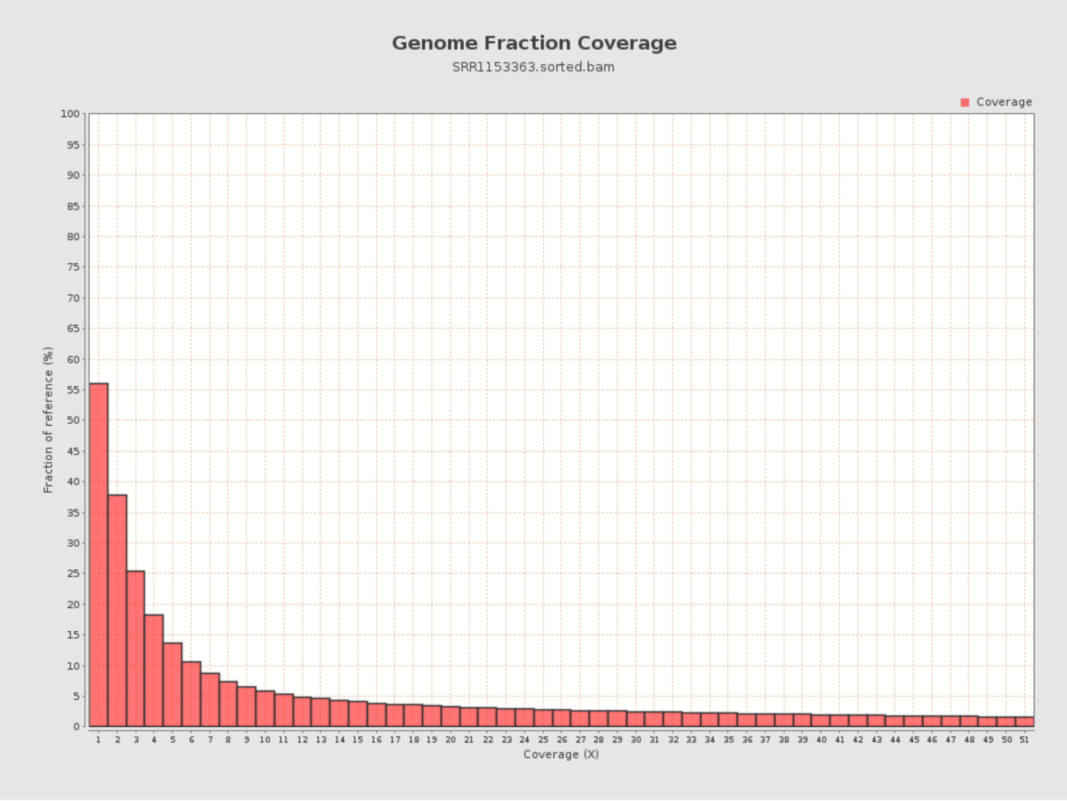
4. Results : Coverage Histogram



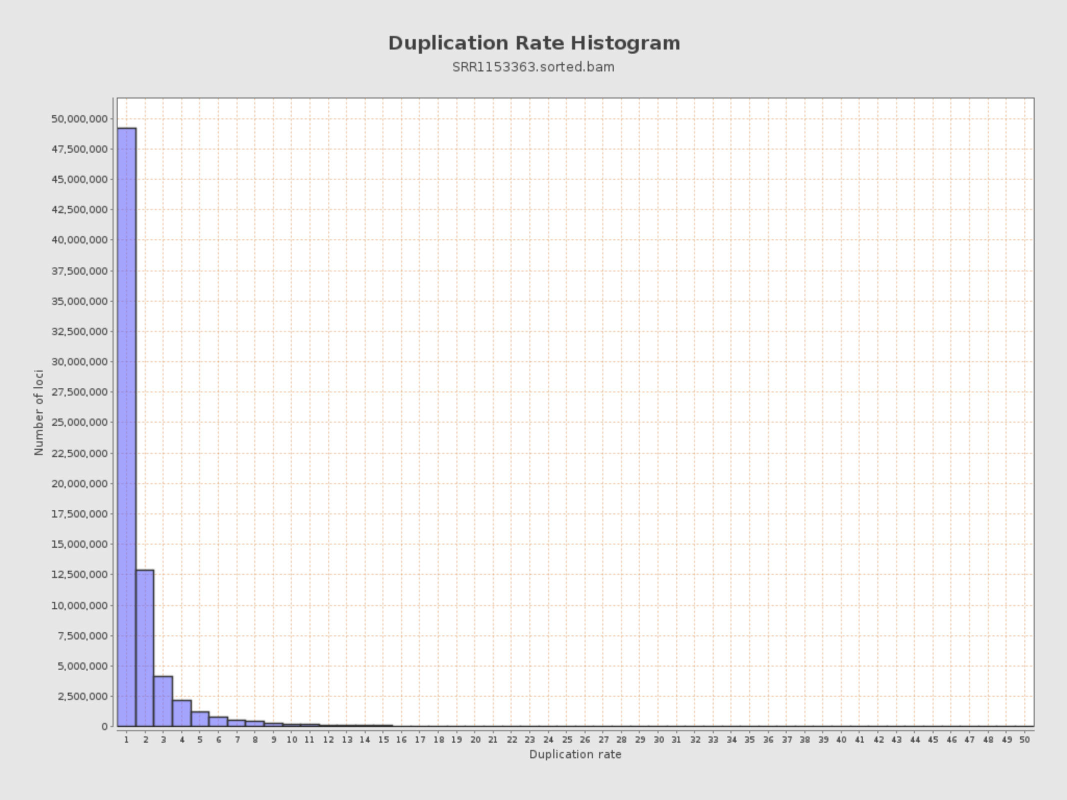
5. Results : Coverage Histogram (0-50X)



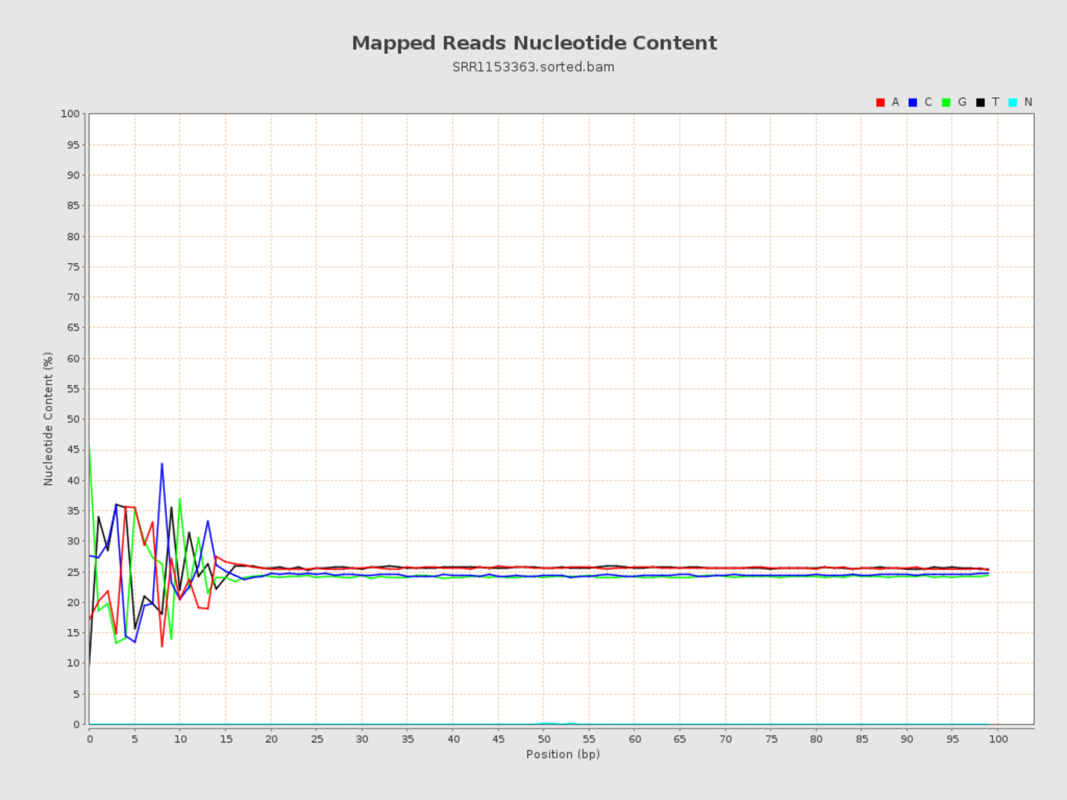
6. Results : Genome Fraction Coverage



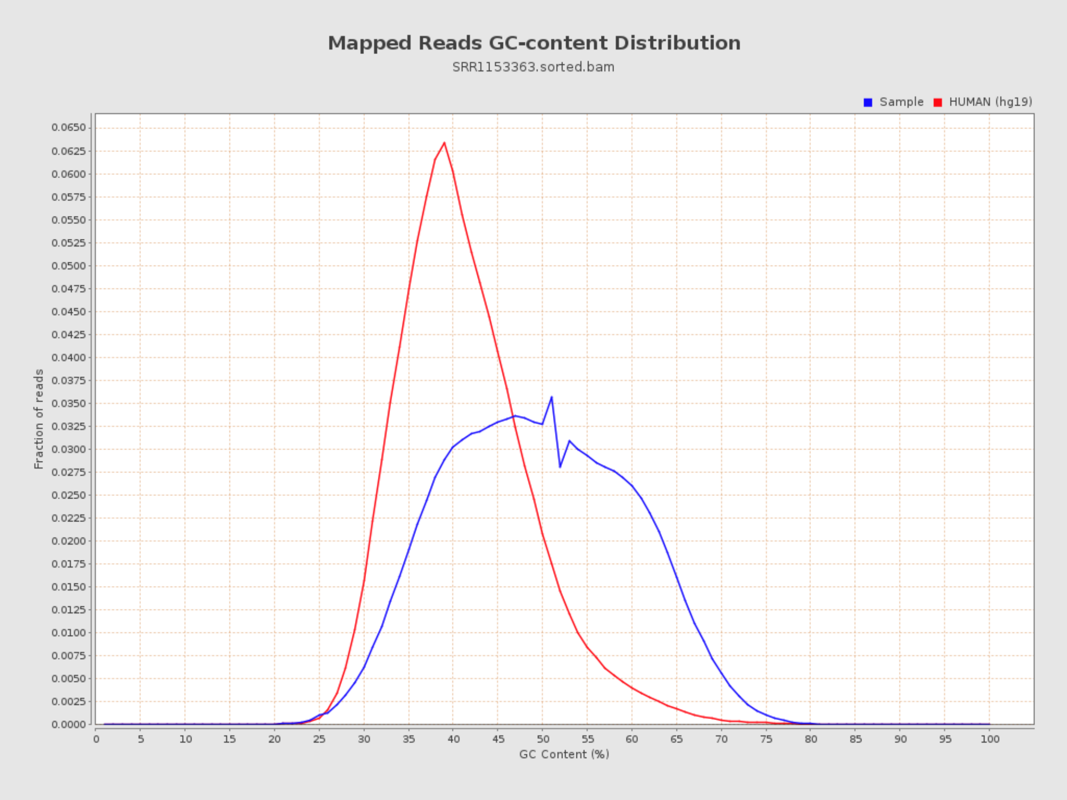
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

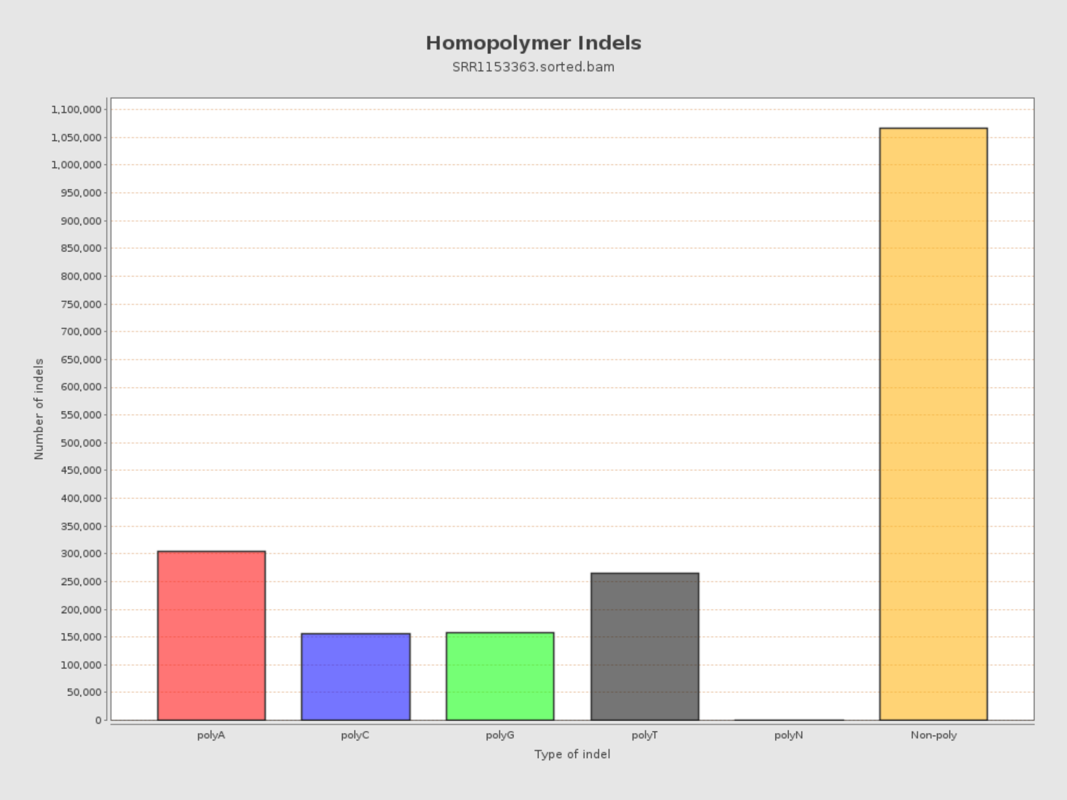


9. Results : Mapped Reads GC-content Distribution

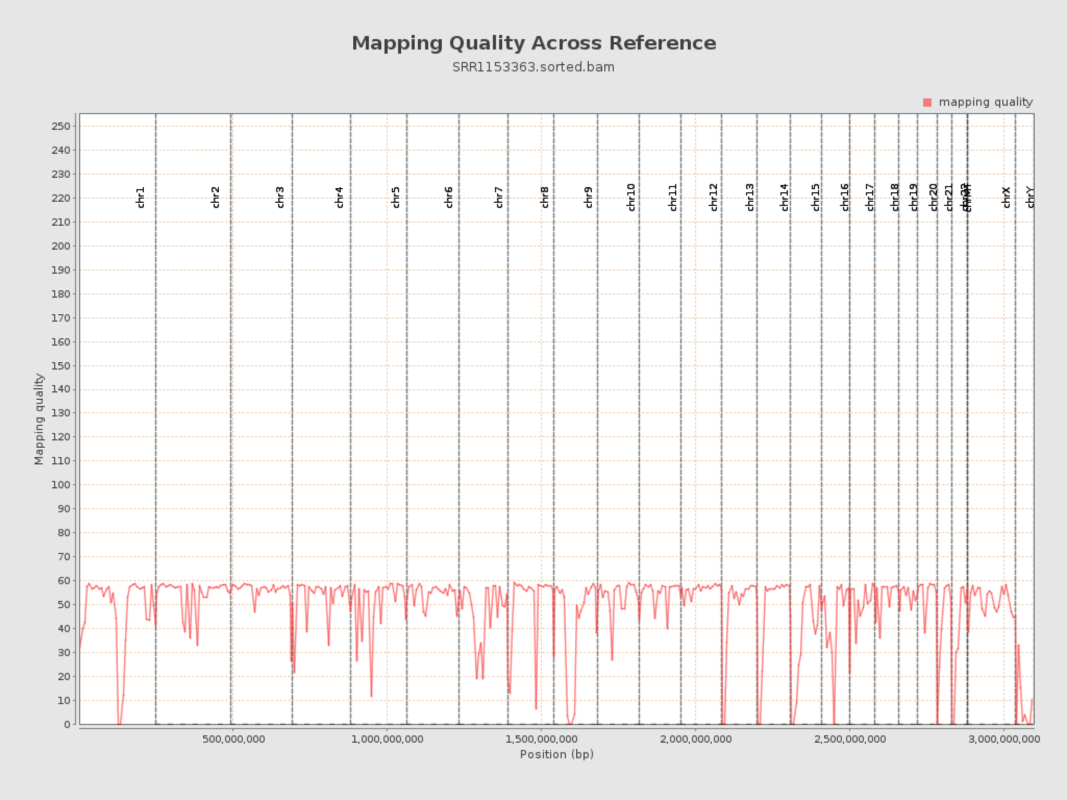


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram