Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/14 21:04:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153320.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_SRR1153320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 14 21:03:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	148,528,930
Mapped reads	146,292,189 / 98.49%
Unmapped reads	2,236,741 / 1.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	640,379 / 0.43%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	81,909,378 / 55.15%
Duplication rate	36.66%
Clipped reads	11,302,317 / 7.61%

2.2. ACGT Content

Number/percentage of A's	3,773,304,930 / 26.21%
Number/percentage of C's	3,421,536,158 / 23.77%
Number/percentage of T's	3,812,475,687 / 26.48%
Number/percentage of G's	3,387,016,487 / 23.53%
Number/percentage of N's	2,745,641 / 0.02%
GC Percentage	47.29%

2.3. Coverage

Mean	4.6514

Standard Deviation	38.1727

2.4. Mapping Quality

Mean Mapping Quality	49.19

2.5. Mismatches and indels

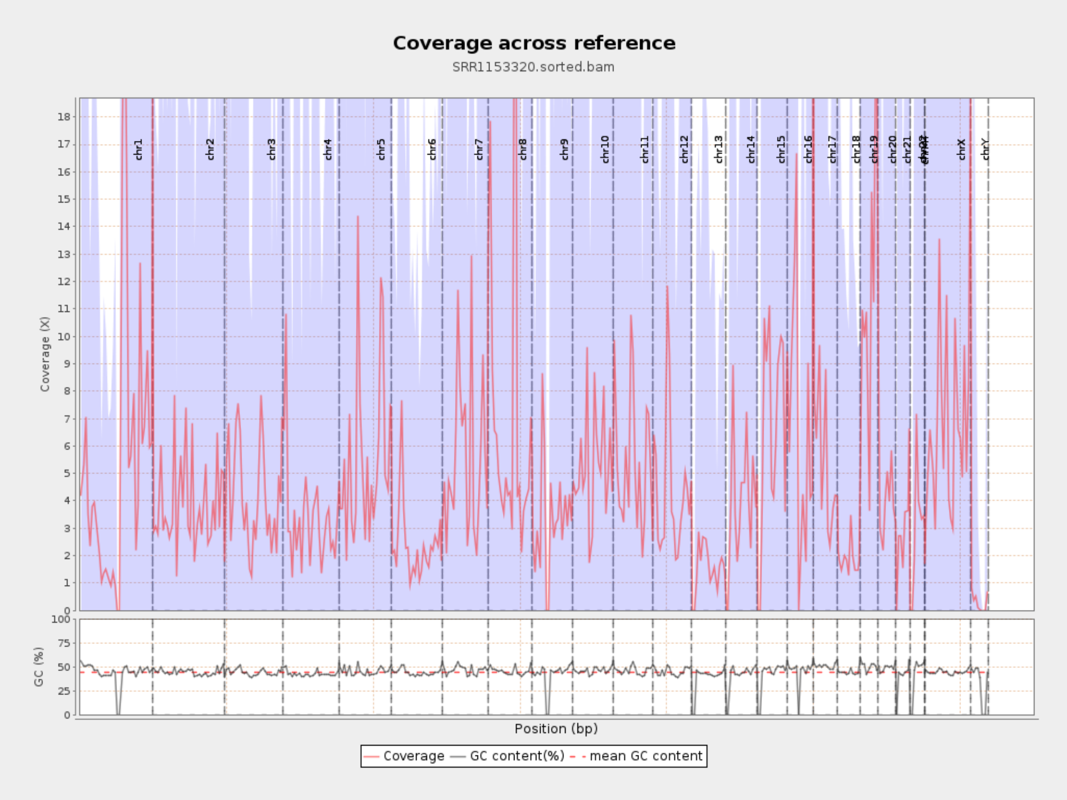
General error rate	0.37%
Mismatches	52,281,645
Insertions	754,162
Mapped reads with at least one insertion	0.51%
Deletions	1,010,715
Mapped reads with at least one deletion	0.68%
Homopolymer indels	45.46%

2.6. Chromosome stats

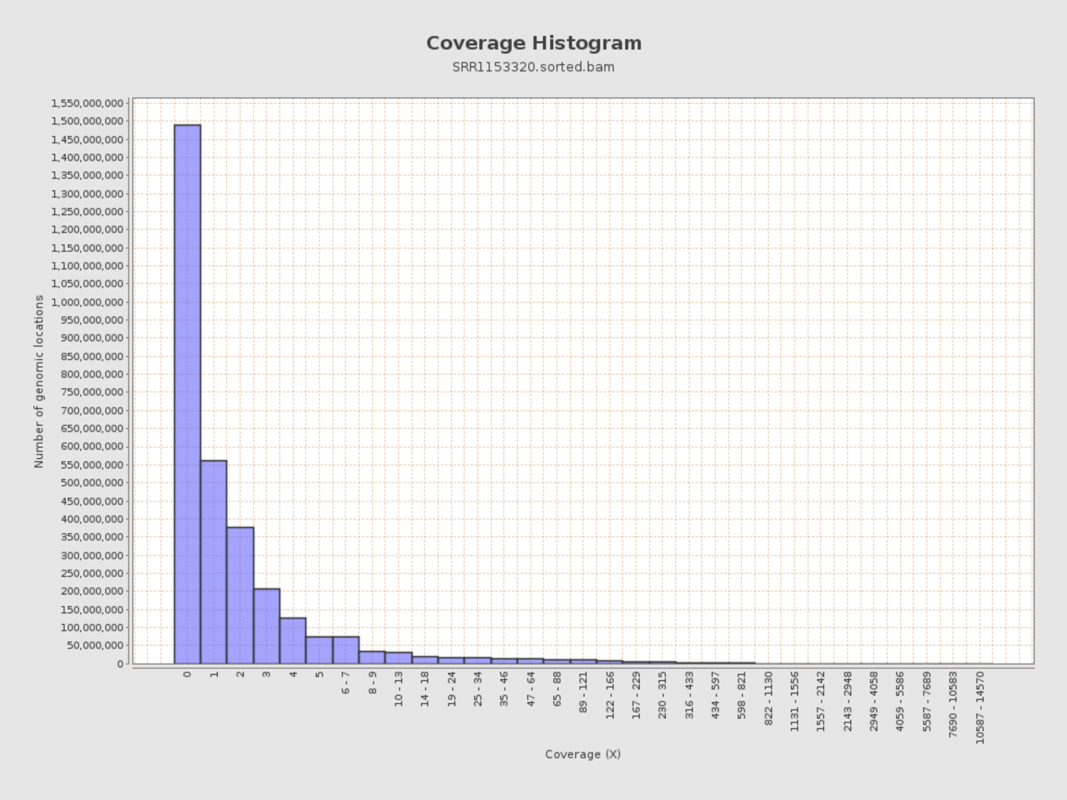
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1373712421	5.5114	40.366
chr2	243199373	950227319	3.9072	22.5865
chr3	198022430	825087914	4.1666	23.886
chr4	191154276	649911278	3.3999	29.9565
chr5	180915260	1007876433	5.571	63.0135
chr6	171115067	407899693	2.3838	16.1403
chr7	159138663	886731983	5.5721	43.5177

chr8	146364022	1008930320	6.8933	91.3237
chr9	141213431	466617786	3.3043	22.4948
chr10	135534747	725650009	5.354	32.6585
chr11	135006516	744257804	5.5128	28.2361
chr12	133851895	584162789	4.3642	23.2413
chr13	115169878	180063655	1.5635	11.81
chr14	107349540	417040741	3.8849	23.5907
chr15	102531392	655257499	6.3908	37.4495
chr16	90354753	596347413	6.6001	43.3138
chr17	81195210	440039376	5.4195	30.7846
chr18	78077248	147158468	1.8848	13.0424
chr19	59128983	696991211	11.7876	53.089
chr20	63025520	266026649	4.2209	22.696
chr21	48129895	142890245	2.9688	32.0578
chr22	51304566	159380505	3.1066	21.1008
chrMT	16571	27866	1.6816	1.6562
chrX	155270560	1049467889	6.759	39.8633
chrY	59373566	17525831	0.2952	11.0002

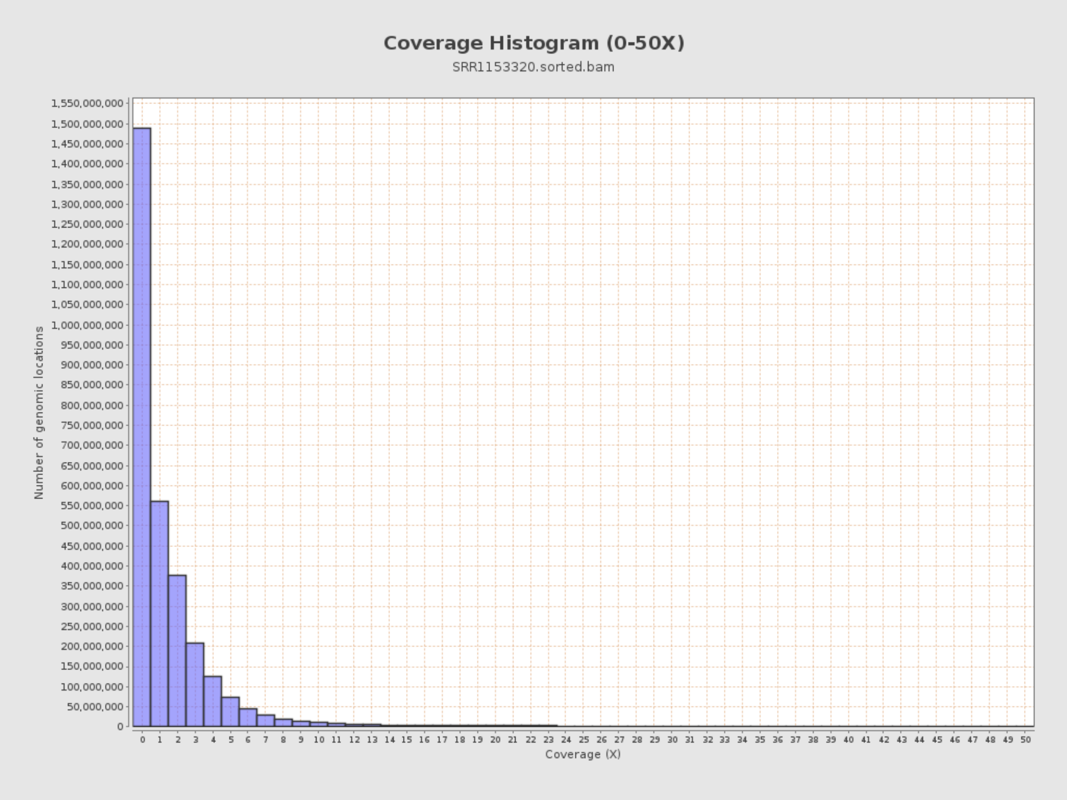
3. Results : Coverage across reference



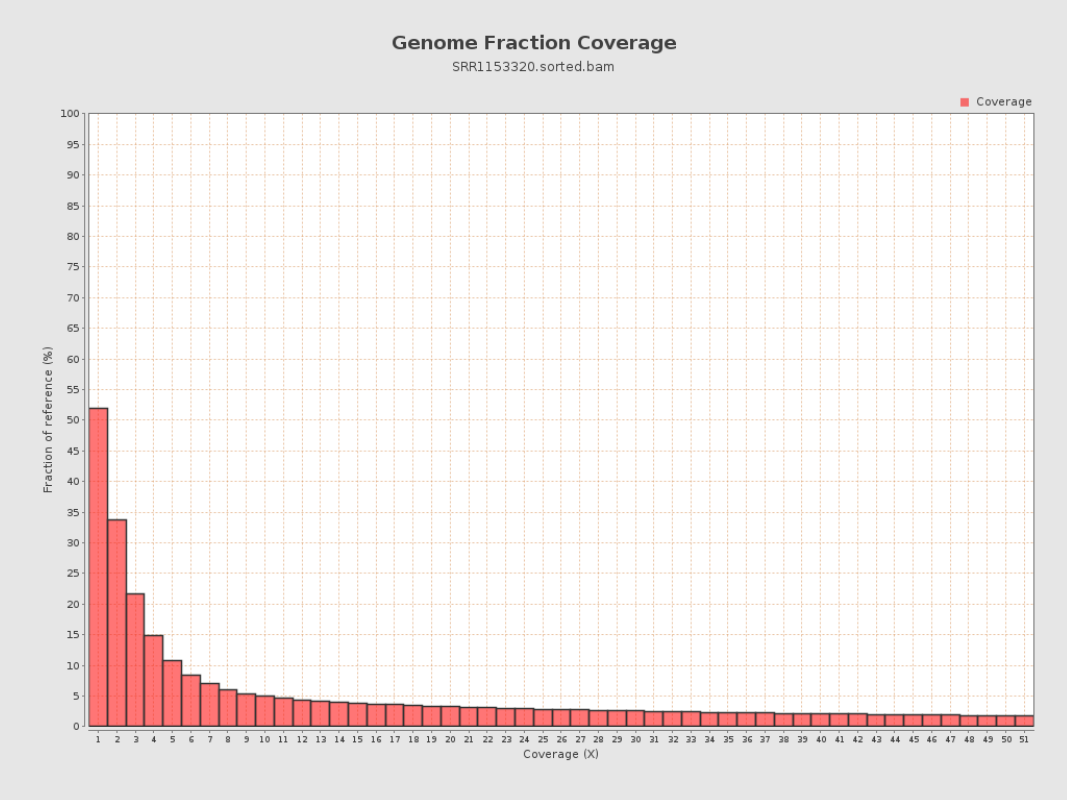
4. Results : Coverage Histogram



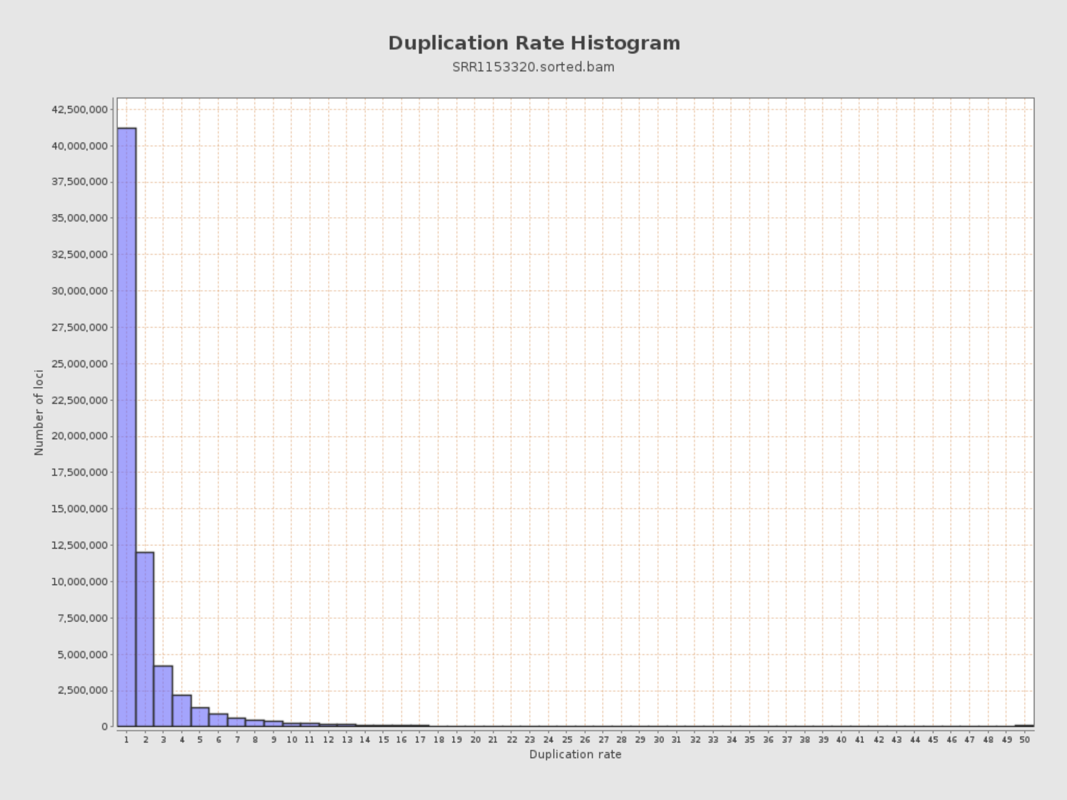
5. Results : Coverage Histogram (0-50X)



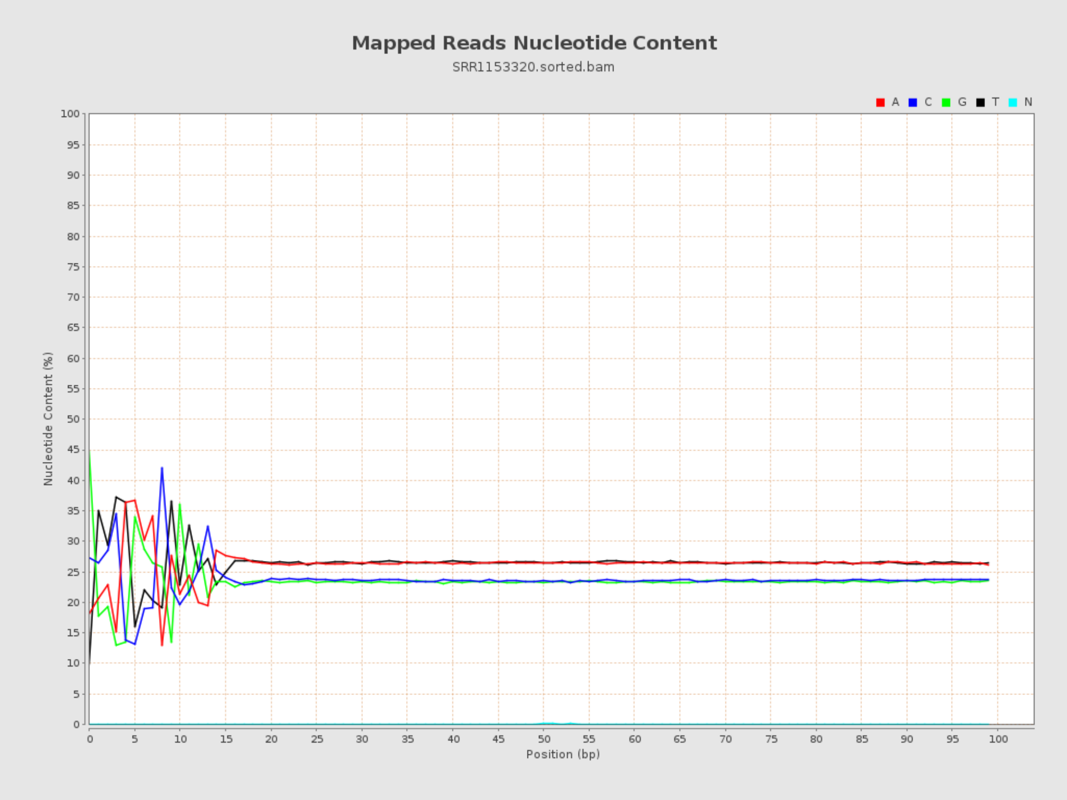
6. Results : Genome Fraction Coverage



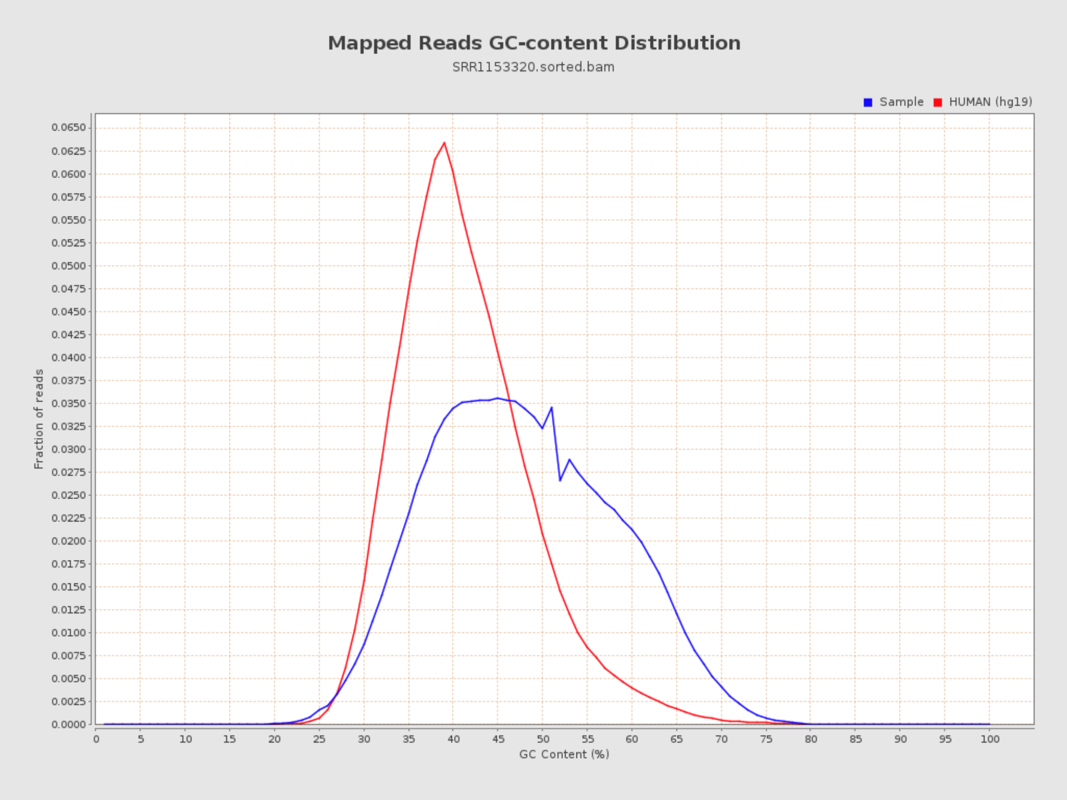
7. Results : Duplication Rate Histogram



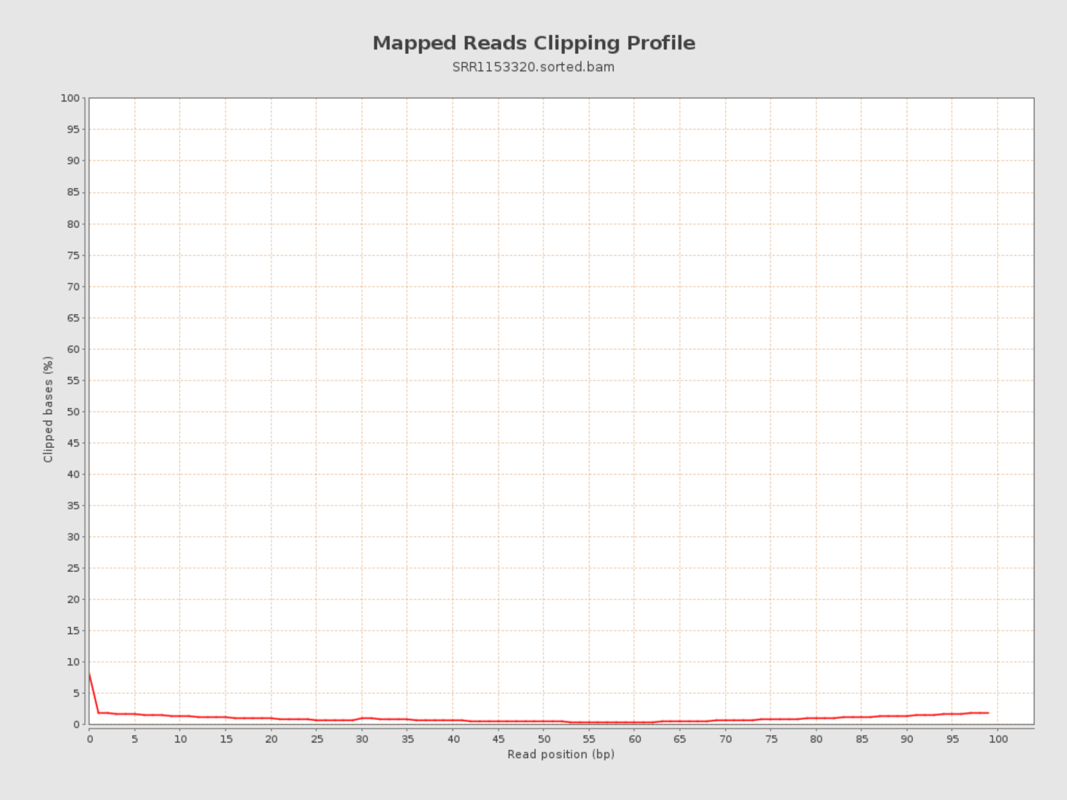
8. Results : Mapped Reads Nucleotide Content



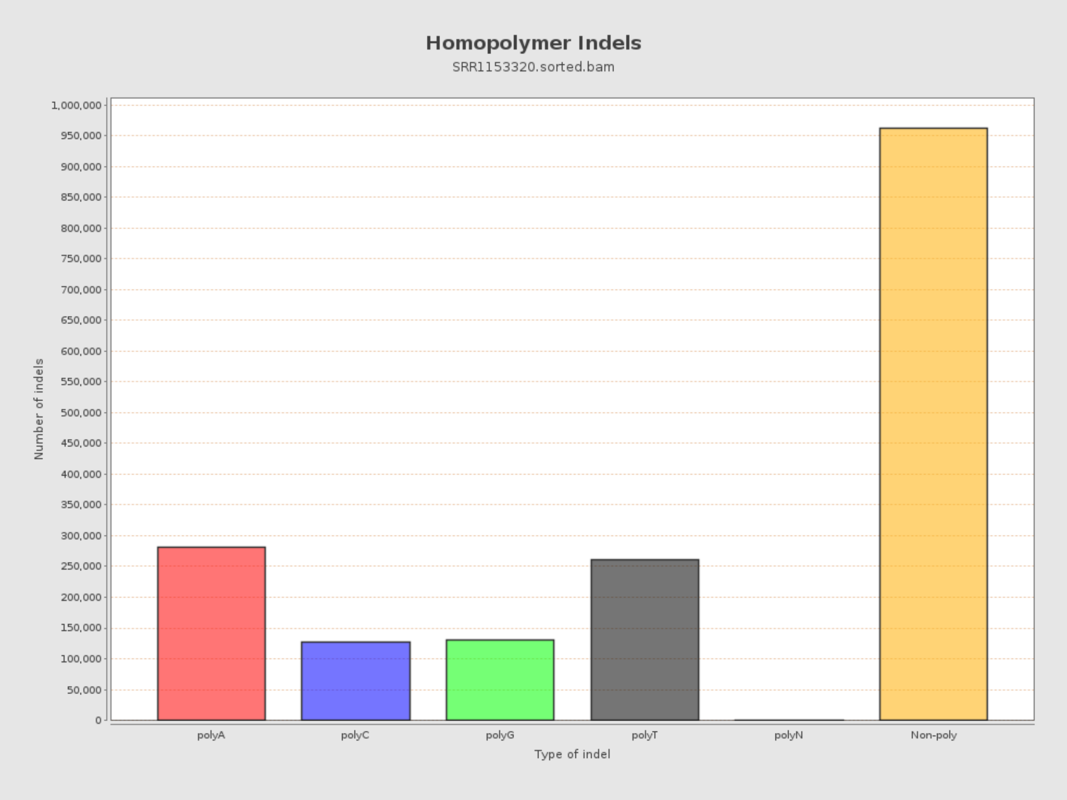
9. Results : Mapped Reads GC-content Distribution



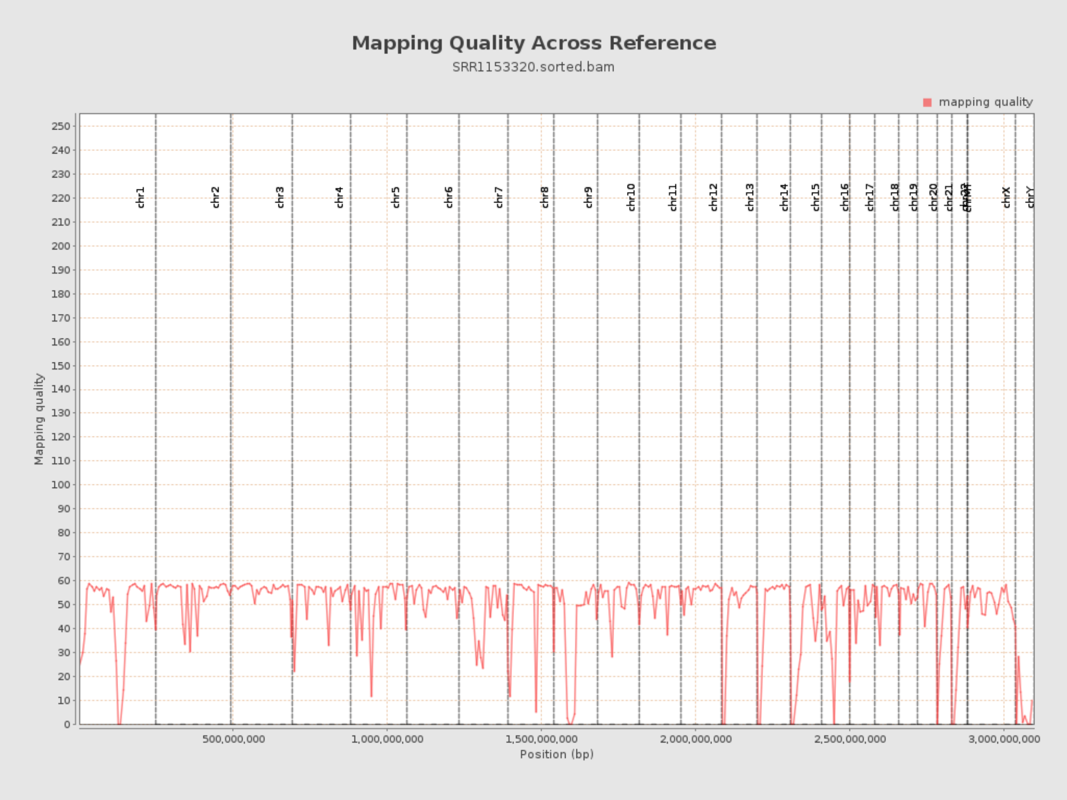
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram