Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 16:28:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153375.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_SRR1153375 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153375.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 16:28:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153375.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	46,448,628
Mapped reads	46,123,599 / 99.3%
Unmapped reads	325,029 / 0.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	237,774 / 0.51%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	30,972,499 / 66.68%
Duplication rate	59.68%
Clipped reads	6,167,655 / 13.28%

2.2. ACGT Content

Number/percentage of A's	1,179,456,709 / 26.31%
Number/percentage of C's	1,054,455,892 / 23.52%
Number/percentage of T's	1,215,163,091 / 27.11%
Number/percentage of G's	1,032,010,271 / 23.02%
Number/percentage of N's	1,432,761 / 0.03%
GC Percentage	46.55%

2.3. Coverage

Mean	1.4482

Standard Deviation	15.2975

2.4. Mapping Quality

Mean Mapping Quality	50.75

2.5. Mismatches and indels

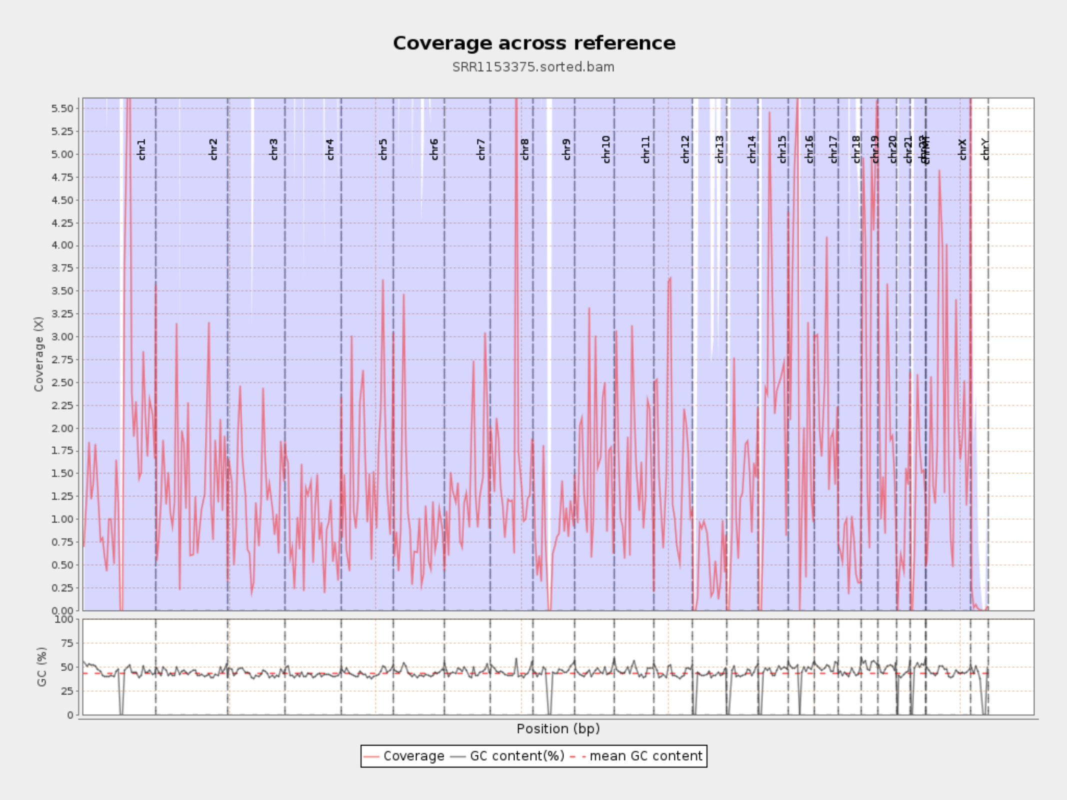
General error rate	0.27%
Mismatches	11,569,650
Insertions	310,812
Mapped reads with at least one insertion	0.67%
Deletions	269,448
Mapped reads with at least one deletion	0.58%
Homopolymer indels	49.71%

2.6. Chromosome stats

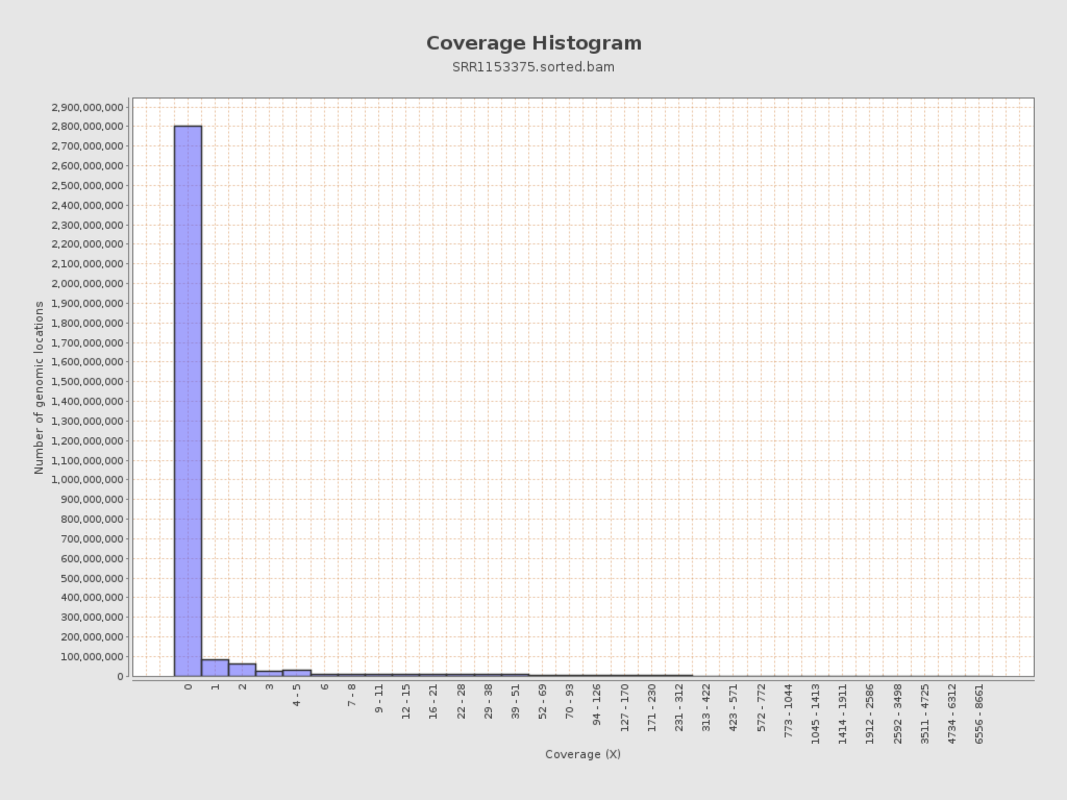
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	437372723	1.7548	15.8948
chr2	243199373	335917046	1.3812	13.2677
chr3	198022430	239321556	1.2086	11.6879
chr4	191154276	175666093	0.919	10.0178
chr5	180915260	284858235	1.5745	15.9659
chr6	171115067	155869293	0.9109	9.5349
chr7	159138663	216901858	1.363	16.1056

chr8	146364022	237374860	1.6218	26.6693
chr9	141213431	111610705	0.7904	8.4214
chr10	135534747	225248586	1.6619	15.6292
chr11	135006516	213856467	1.584	13.5985
chr12	133851895	224087701	1.6741	14.1355
chr13	115169878	57049891	0.4954	6.4326
chr14	107349540	132356636	1.233	11.5567
chr15	102531392	219194674	2.1378	18.7933
chr16	90354753	216836162	2.3998	22.7949
chr17	81195210	185292153	2.2821	16.4074
chr18	78077248	49323962	0.6317	7.3197
chr19	59128983	214136474	3.6215	24.9666
chr20	63025520	111846256	1.7746	16.0173
chr21	48129895	46016314	0.9561	10.5436
chr22	51304566	64412807	1.2555	11.8959
chrMT	16571	8307	0.5013	1.59
chrX	155270560	325886403	2.0988	22.0301
chrY	59373566	2615010	0.044	1.7029

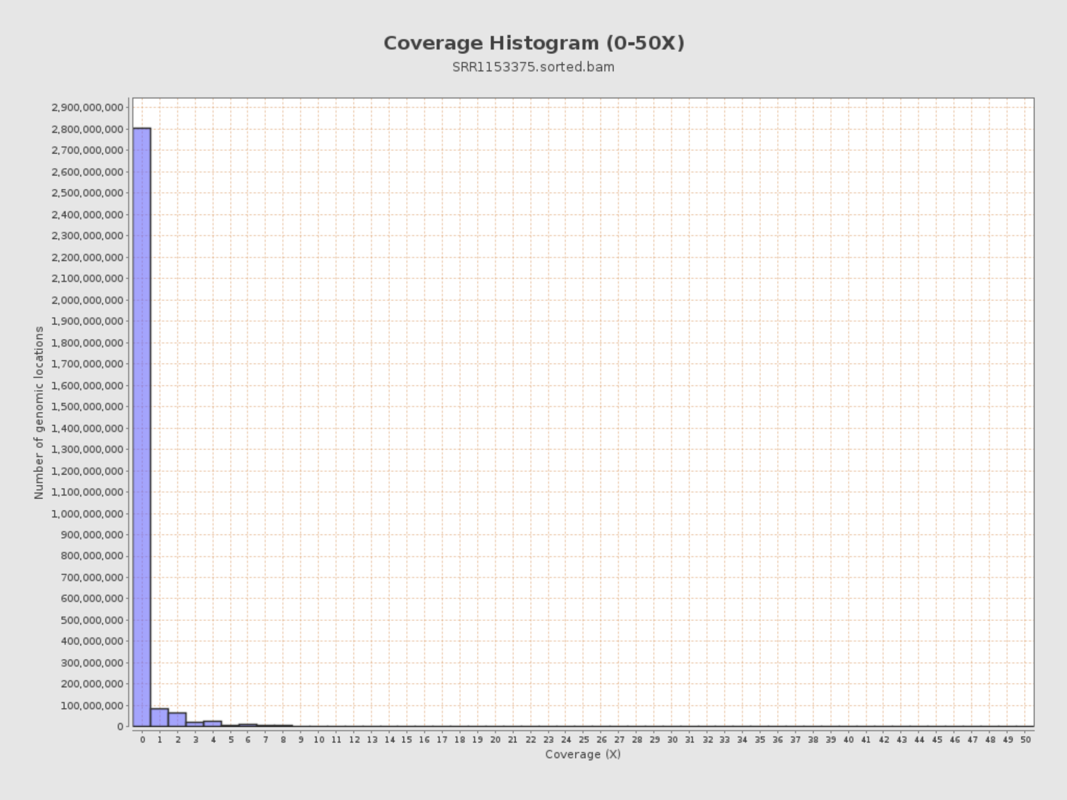
3. Results : Coverage across reference



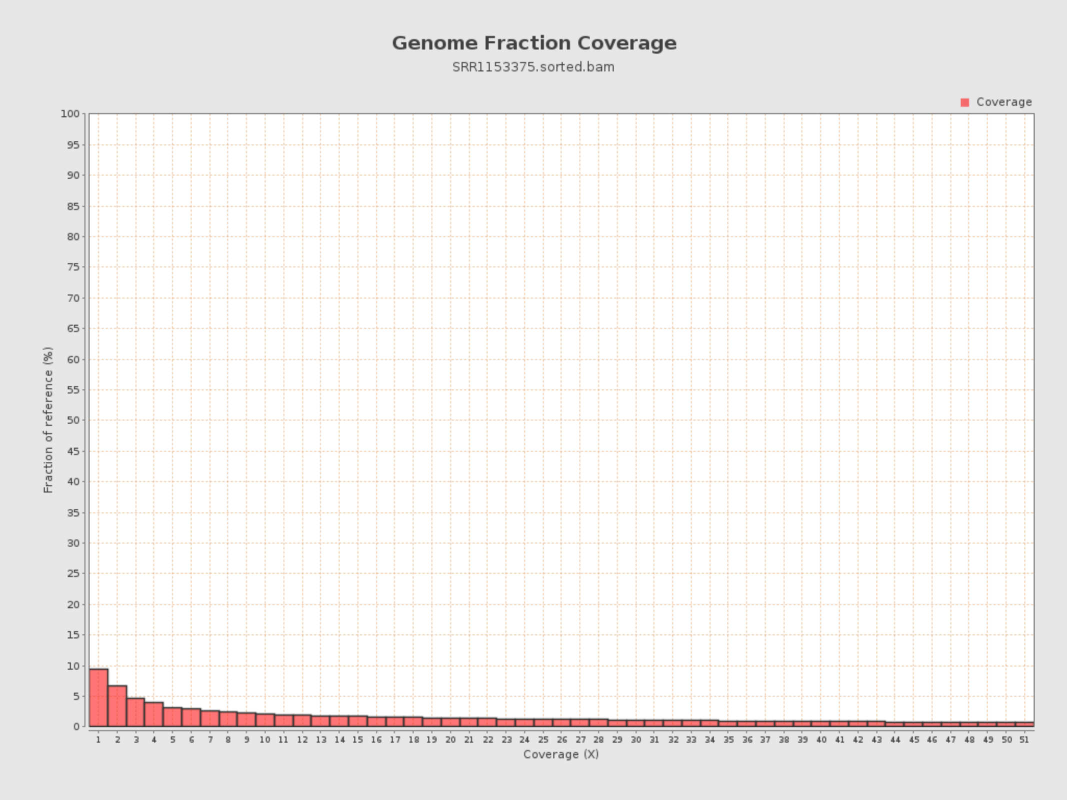
4. Results : Coverage Histogram



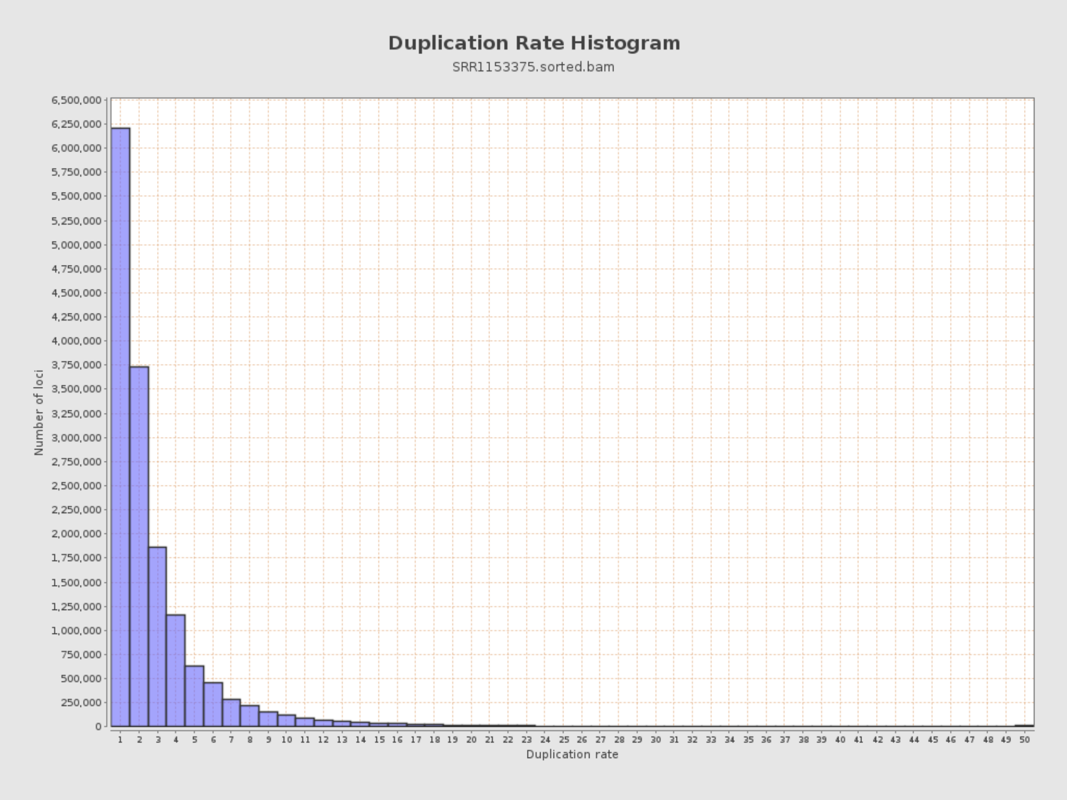
5. Results : Coverage Histogram (0-50X)



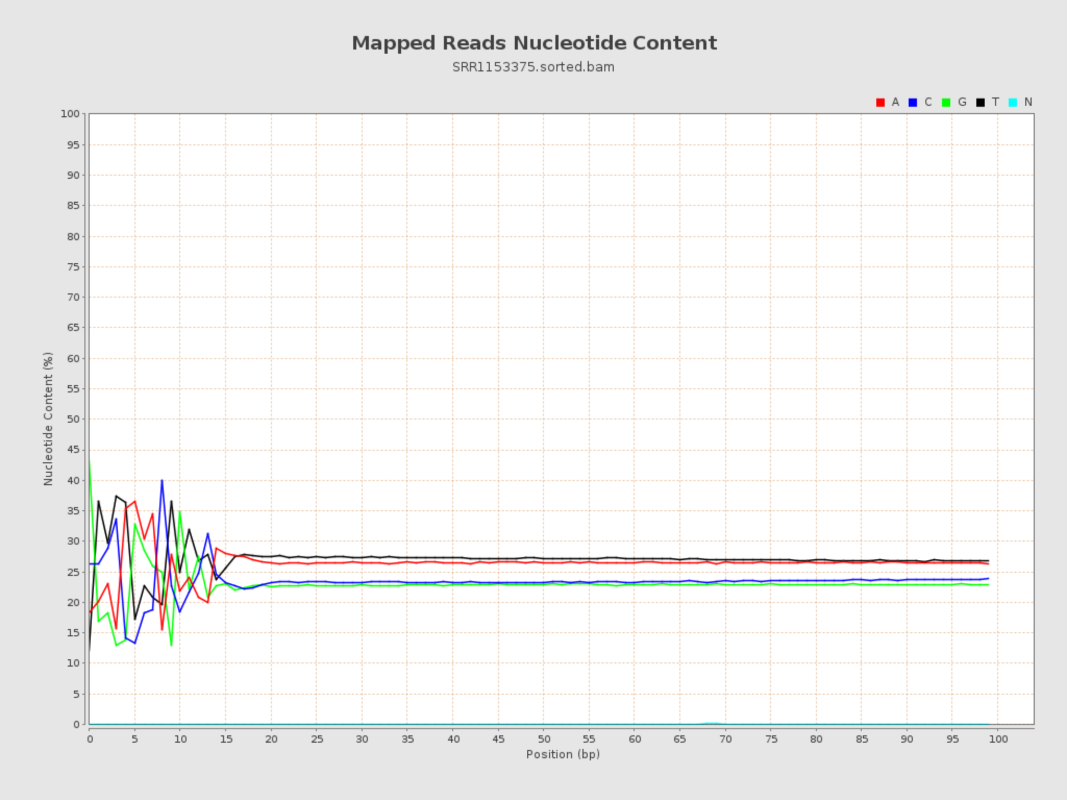
6. Results : Genome Fraction Coverage



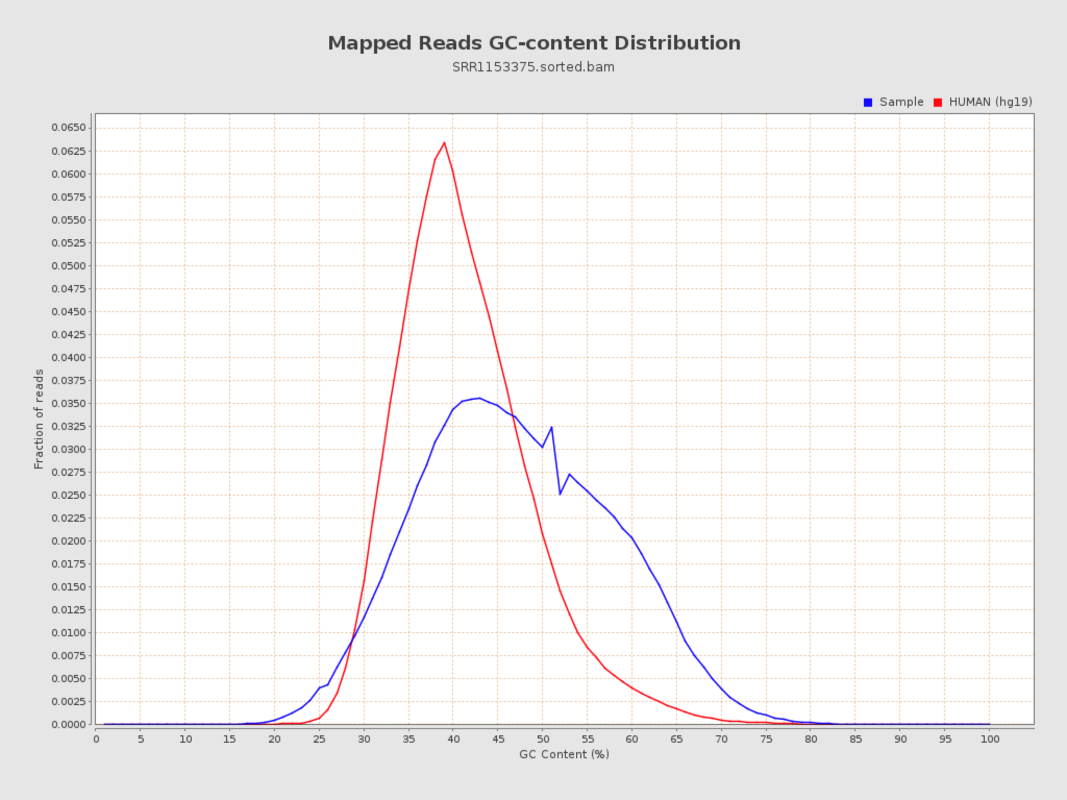
7. Results : Duplication Rate Histogram



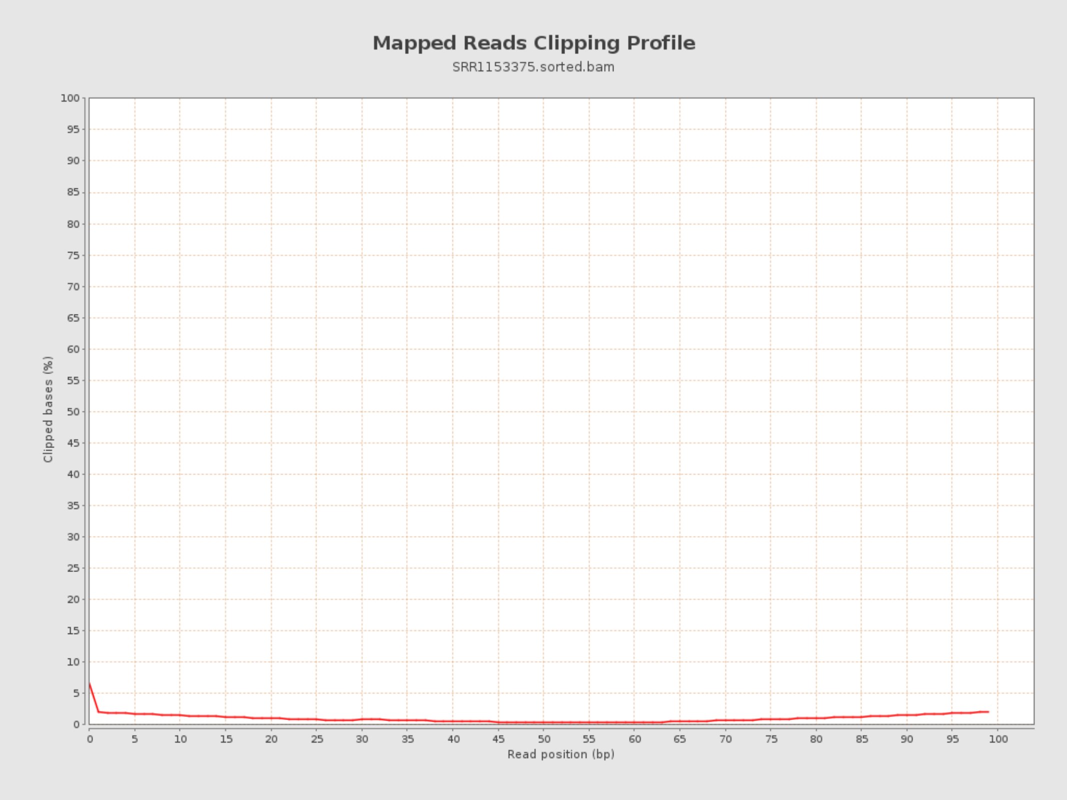
8. Results : Mapped Reads Nucleotide Content



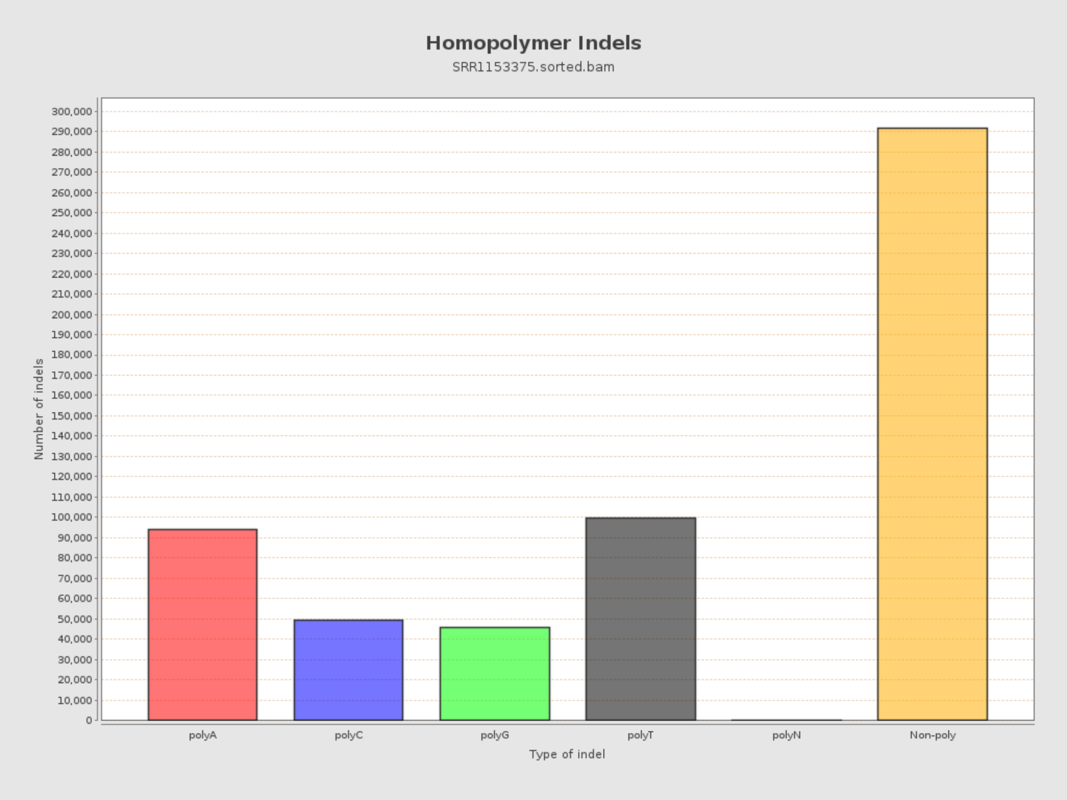
9. Results : Mapped Reads GC-content Distribution



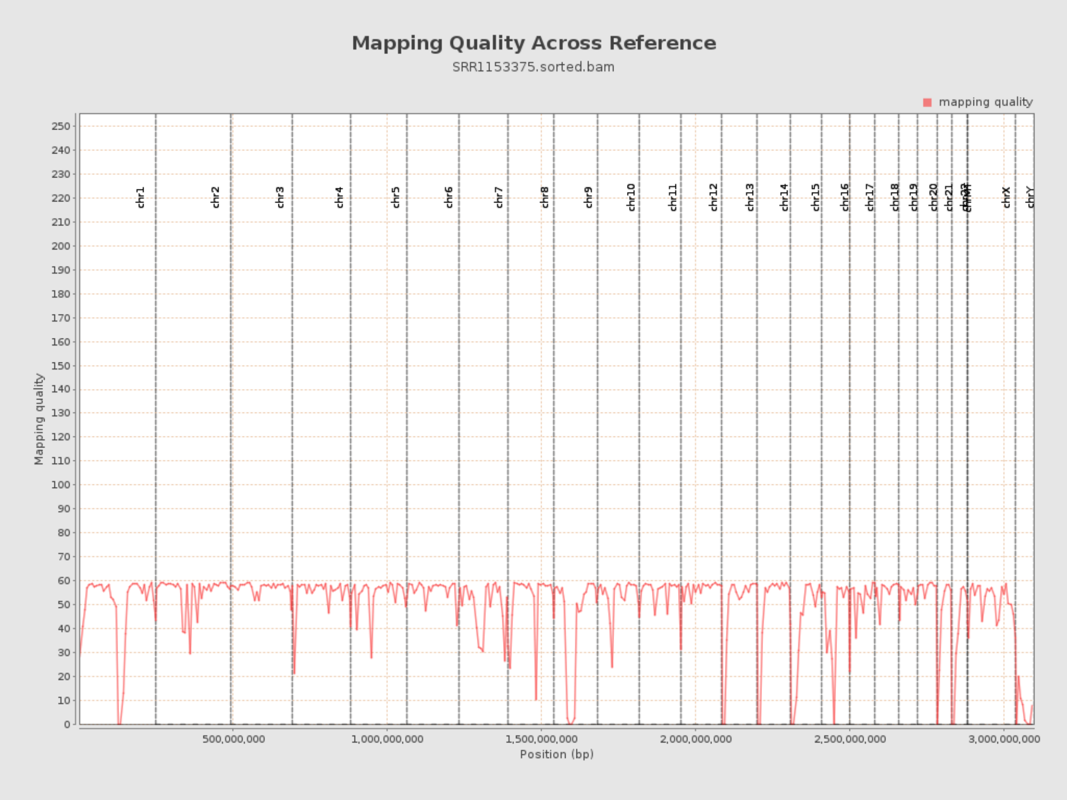
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram