Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 23:29:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153389.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_SRR1153389 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153389.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 23:29:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153389.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	92,024,220
Mapped reads	91,344,817 / 99.26%
Unmapped reads	679,403 / 0.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	477,824 / 0.52%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	58,941,818 / 64.05%
Duplication rate	49.38%
Clipped reads	18,547,746 / 20.16%

2.2. ACGT Content

Number/percentage of A's	2,169,811,488 / 24.69%
Number/percentage of C's	2,223,183,486 / 25.3%
Number/percentage of T's	2,158,090,111 / 24.56%
Number/percentage of G's	2,235,225,110 / 25.44%
Number/percentage of N's	1,165,899 / 0.01%
GC Percentage	50.74%

2.3. Coverage

Mean	2.8389

Standard Deviation	43.8131

2.4. Mapping Quality

Mean Mapping Quality	48.07

2.5. Mismatches and indels

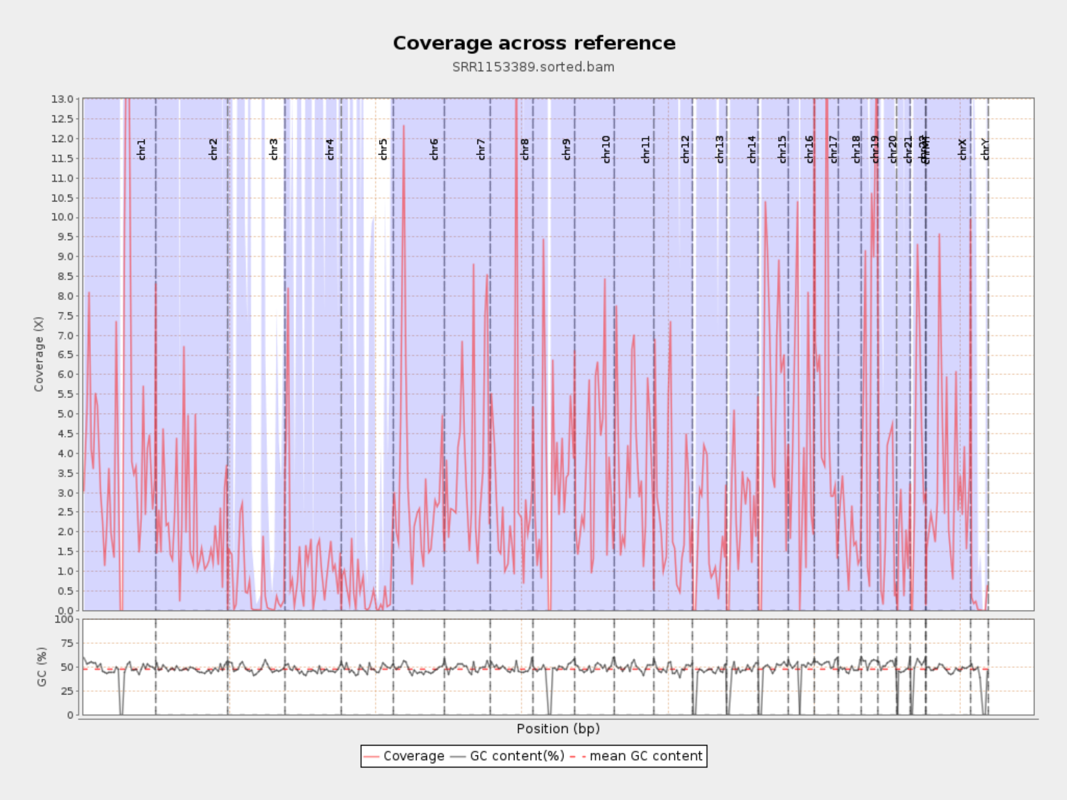
General error rate	0.29%
Mismatches	24,411,687
Insertions	614,852
Mapped reads with at least one insertion	0.66%
Deletions	397,981
Mapped reads with at least one deletion	0.43%
Homopolymer indels	44.69%

2.6. Chromosome stats

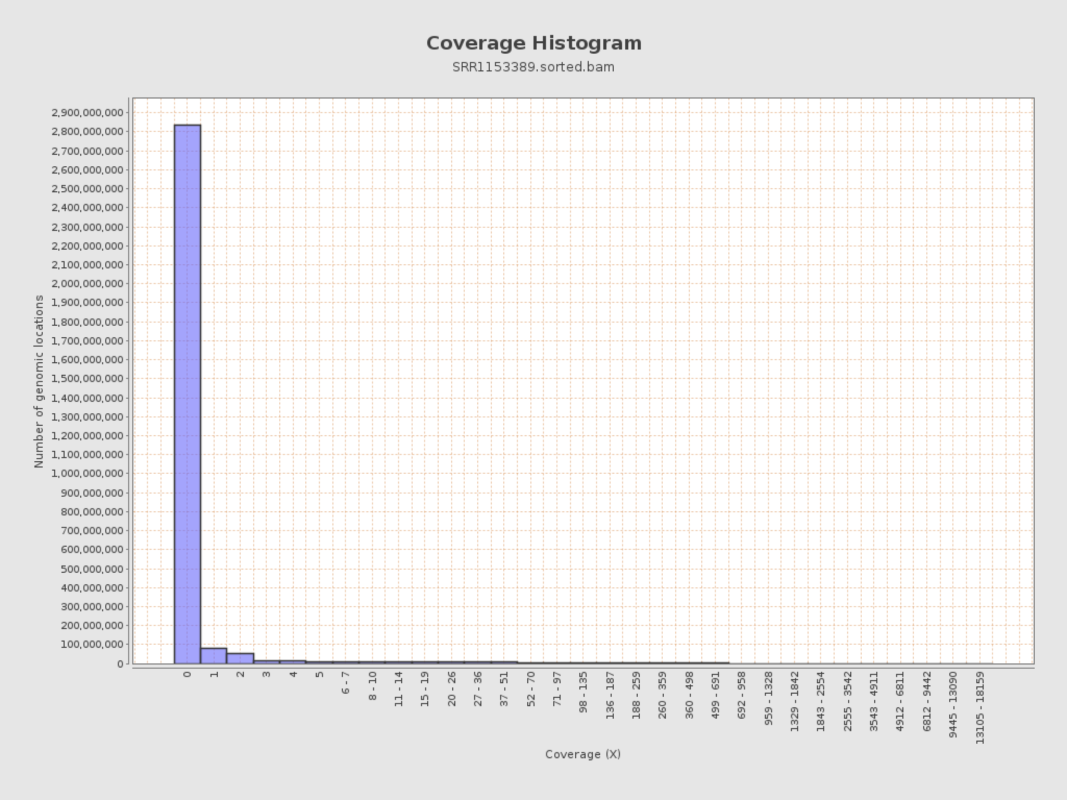
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1082191247	4.3418	56.3579
chr2	243199373	537999139	2.2122	31.6087
chr3	198022430	118262097	0.5972	14.2291
chr4	191154276	261008191	1.3654	31.764
chr5	180915260	96590627	0.5339	13.0657
chr6	171115067	521473231	3.0475	40.271
chr7	159138663	602044535	3.7831	61.8184

chr8	146364022	430610950	2.9421	53.0237
chr9	141213431	476747894	3.3761	46.0731
chr10	135534747	476026443	3.5122	50.2011
chr11	135006516	512359123	3.7951	49.6779
chr12	133851895	360782574	2.6954	40.4102
chr13	115169878	196271818	1.7042	31.6726
chr14	107349540	259240922	2.4149	32.418
chr15	102531392	530365496	5.1727	61.3818
chr16	90354753	352849839	3.9052	42.5562
chr17	81195210	446272180	5.4963	58.818
chr18	78077248	151208898	1.9367	28.7306
chr19	59128983	413425366	6.9919	70.6539
chr20	63025520	148726824	2.3598	47.1367
chr21	48129895	82372326	1.7115	34.4939
chr22	51304566	209944864	4.0921	70.4032
chrMT	16571	2261	0.1364	0.5503
chrX	155270560	511368825	3.2934	41.8183
chrY	59373566	10266464	0.1729	9.4167

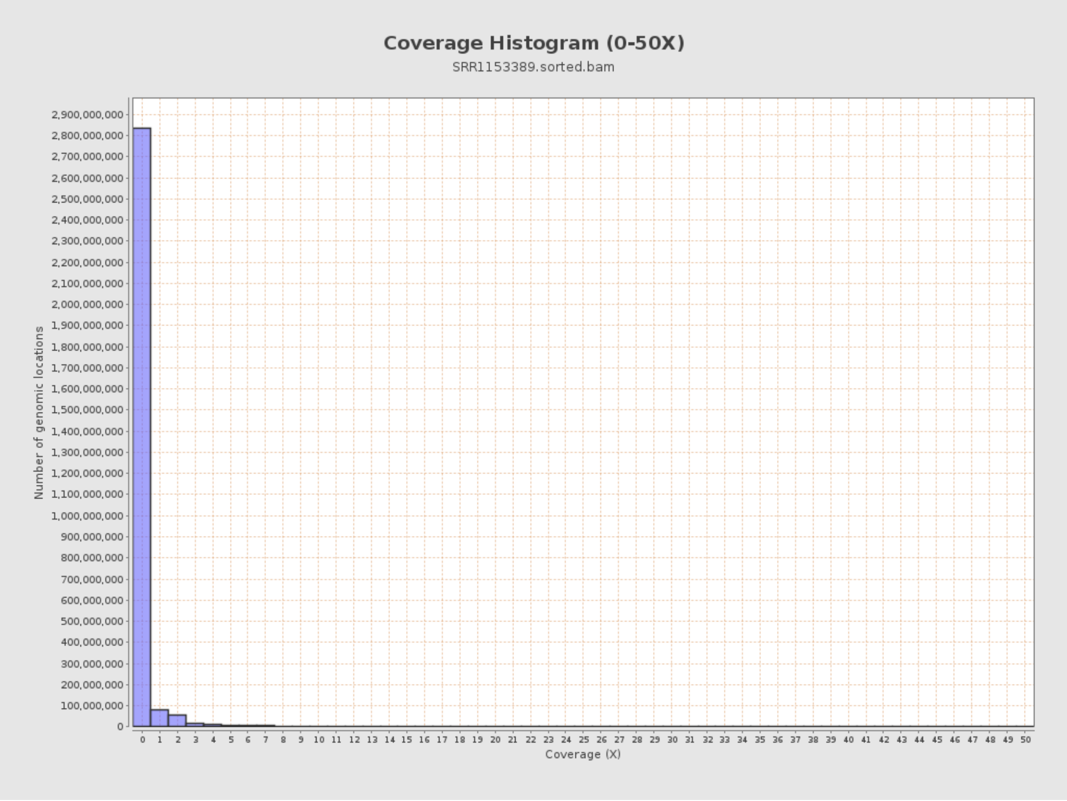
3. Results : Coverage across reference



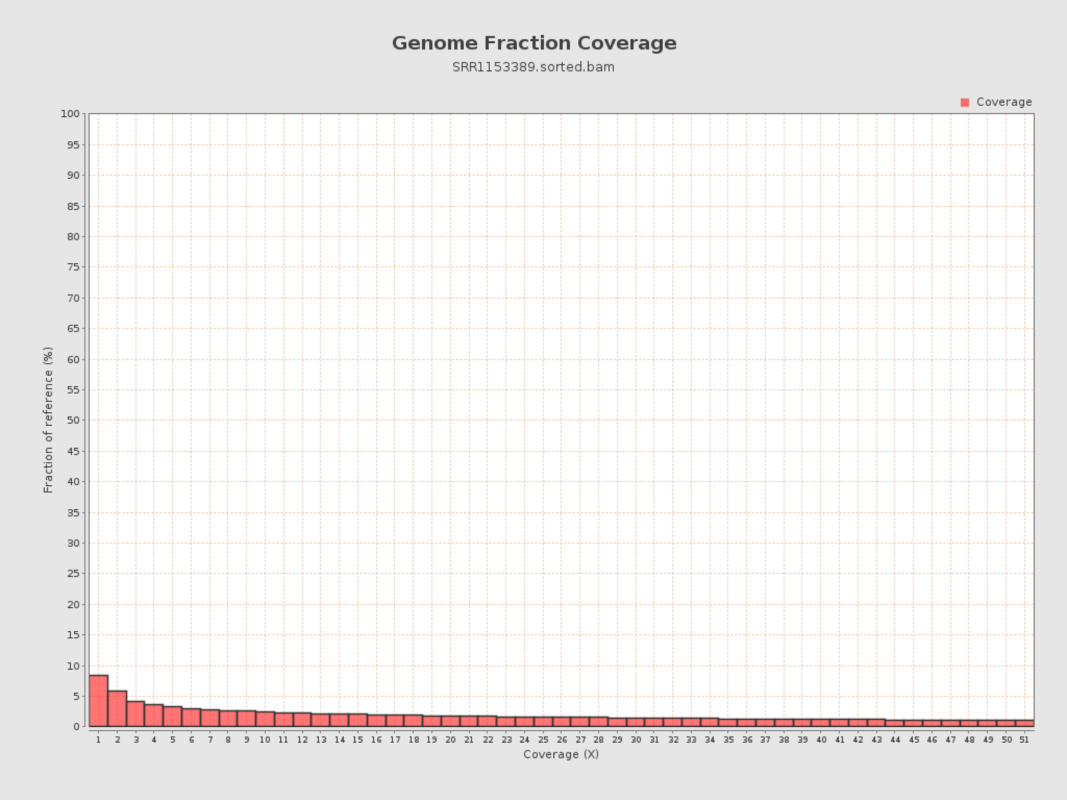
4. Results : Coverage Histogram



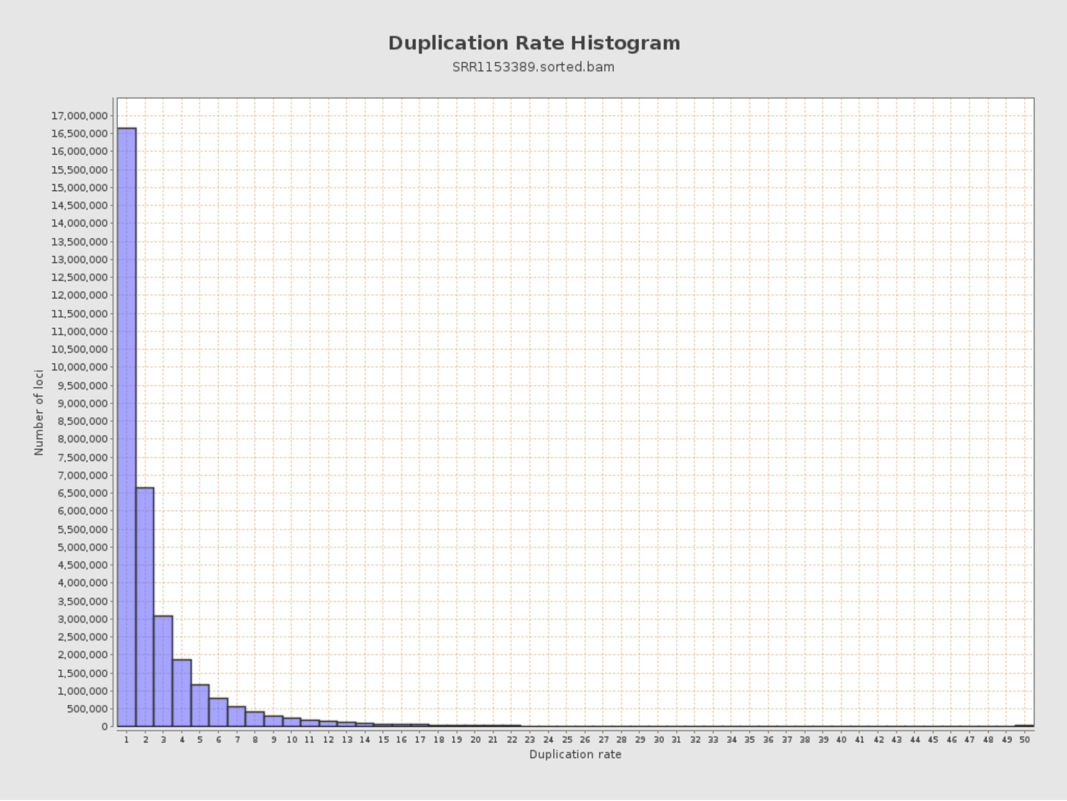
5. Results : Coverage Histogram (0-50X)



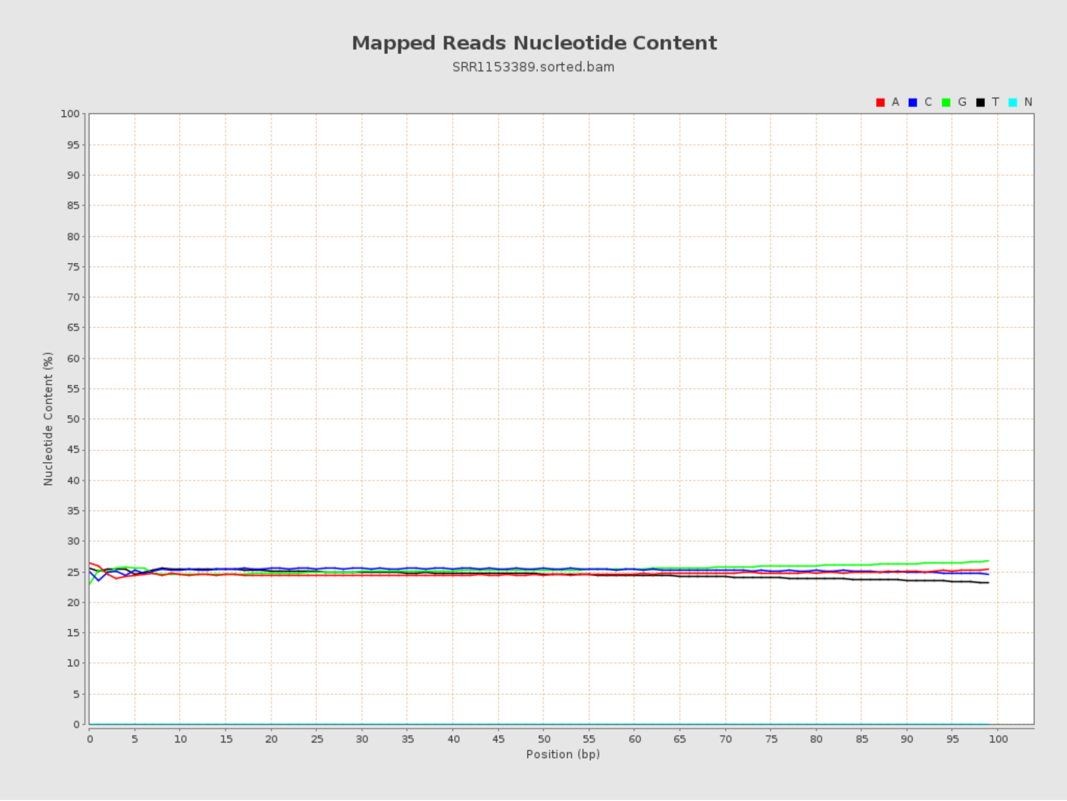
6. Results : Genome Fraction Coverage



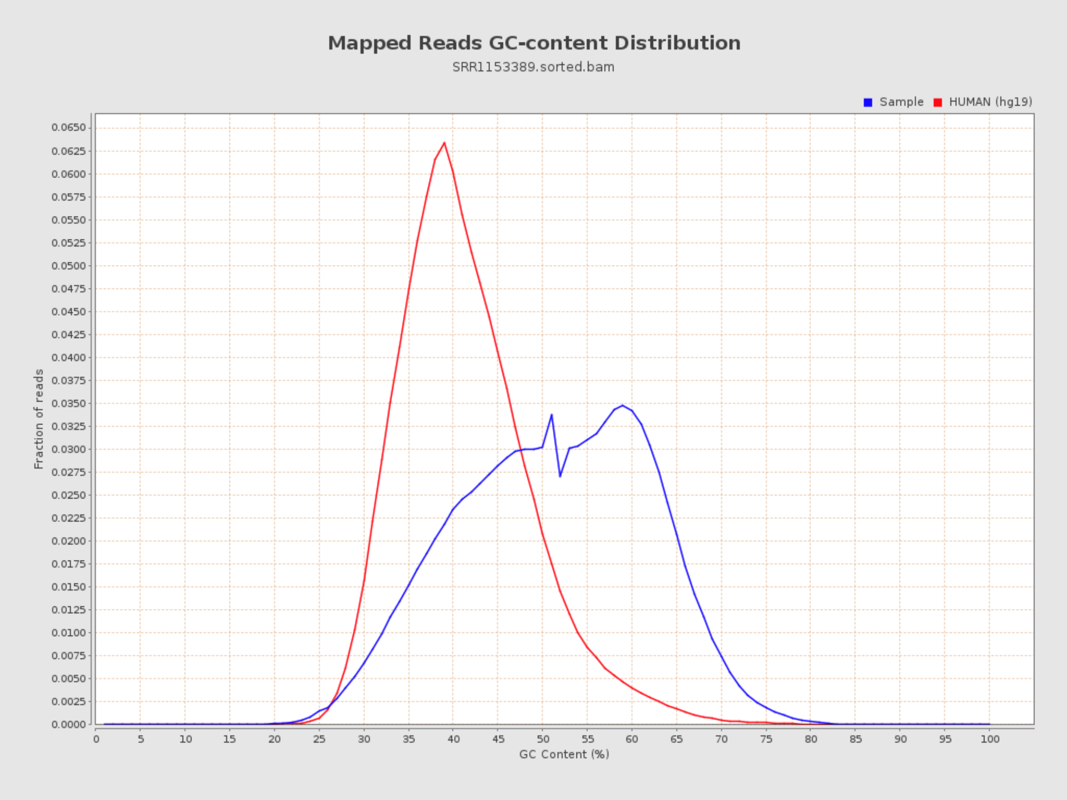
7. Results : Duplication Rate Histogram



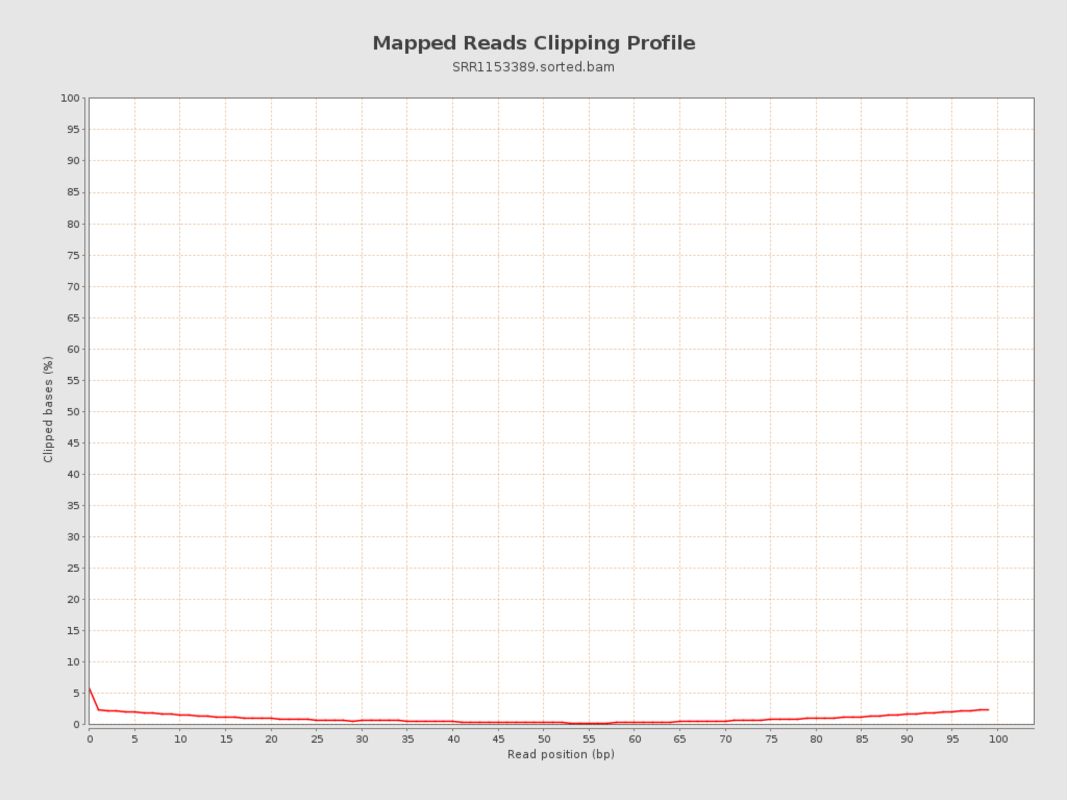
8. Results : Mapped Reads Nucleotide Content



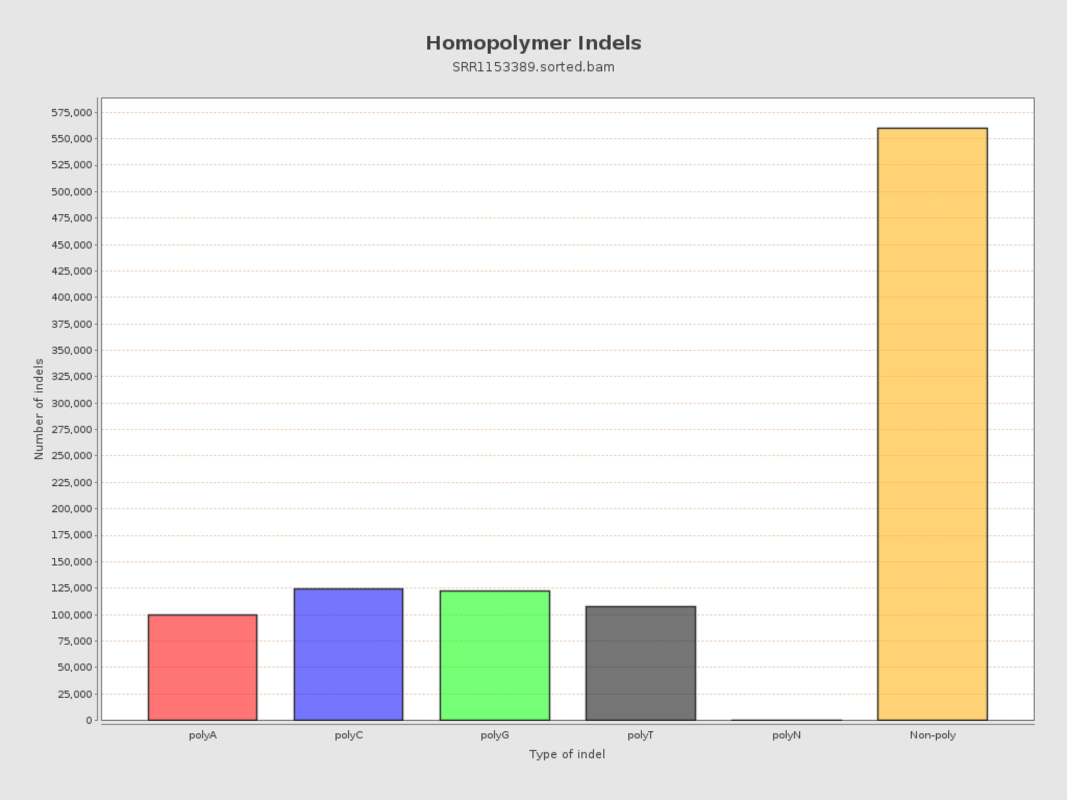
9. Results : Mapped Reads GC-content Distribution



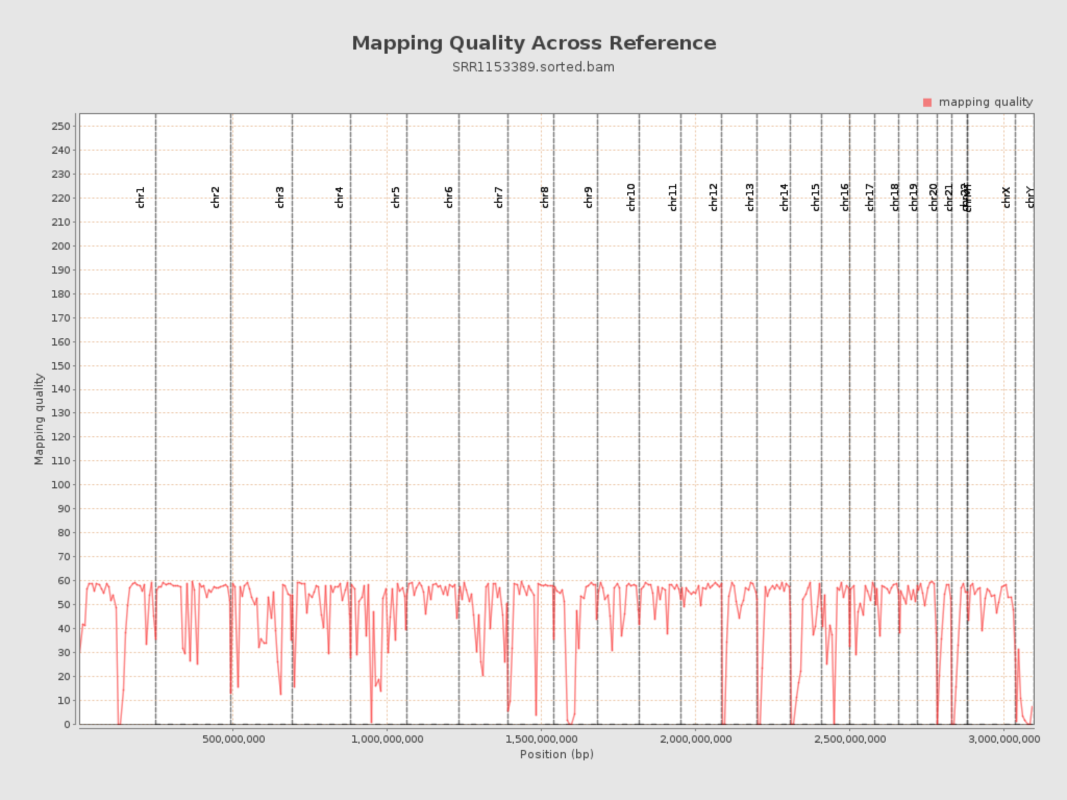
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram