Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/16 21:53:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1153385.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_SRR1153385 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1153385.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 16 21:53:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1153385.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	83,747,320
Mapped reads	83,156,296 / 99.29%
Unmapped reads	591,024 / 0.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	415,604 / 0.5%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	51,336,500 / 61.3%
Duplication rate	46.47%
Clipped reads	16,599,042 / 19.82%

2.2. ACGT Content

Number/percentage of A's	1,981,855,547 / 24.75%
Number/percentage of C's	2,022,464,575 / 25.25%
Number/percentage of T's	1,969,121,728 / 24.59%
Number/percentage of G's	2,034,235,089 / 25.4%
Number/percentage of N's	1,073,391 / 0.01%
GC Percentage	50.65%

2.3. Coverage

Mean	2.5873

Standard Deviation	40.6678

2.4. Mapping Quality

Mean Mapping Quality	49.41

2.5. Mismatches and indels

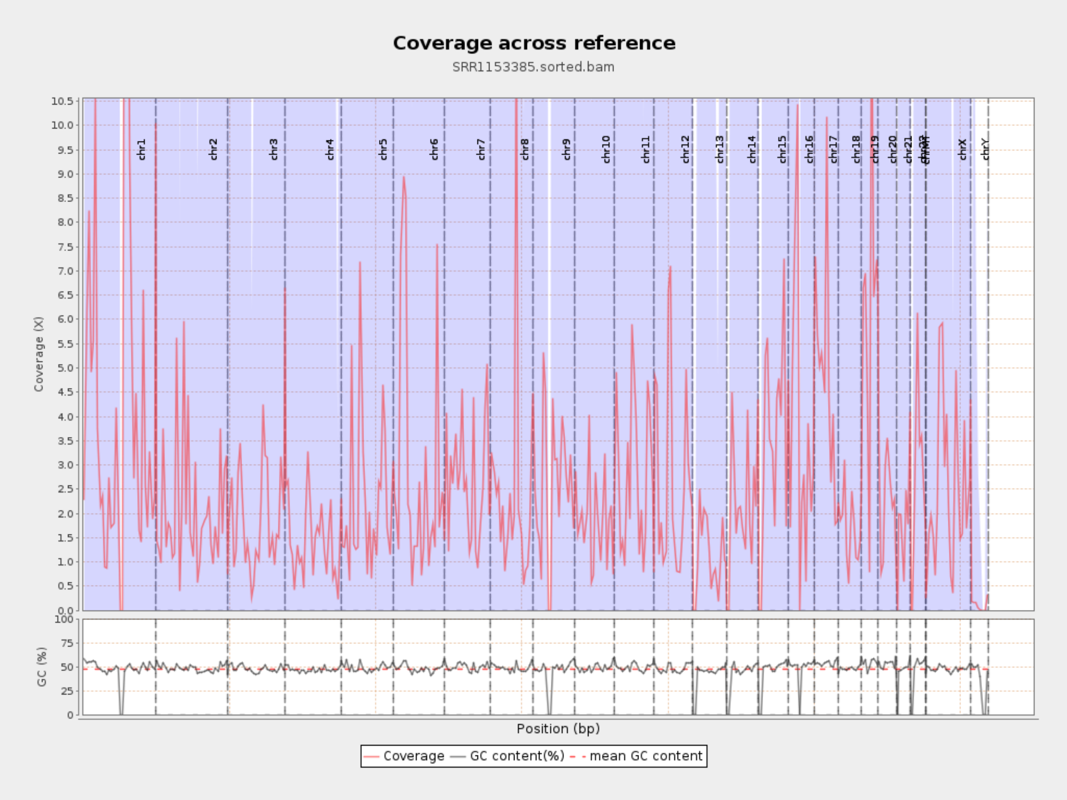
General error rate	0.29%
Mismatches	22,217,570
Insertions	544,398
Mapped reads with at least one insertion	0.65%
Deletions	360,916
Mapped reads with at least one deletion	0.43%
Homopolymer indels	44.16%

2.6. Chromosome stats

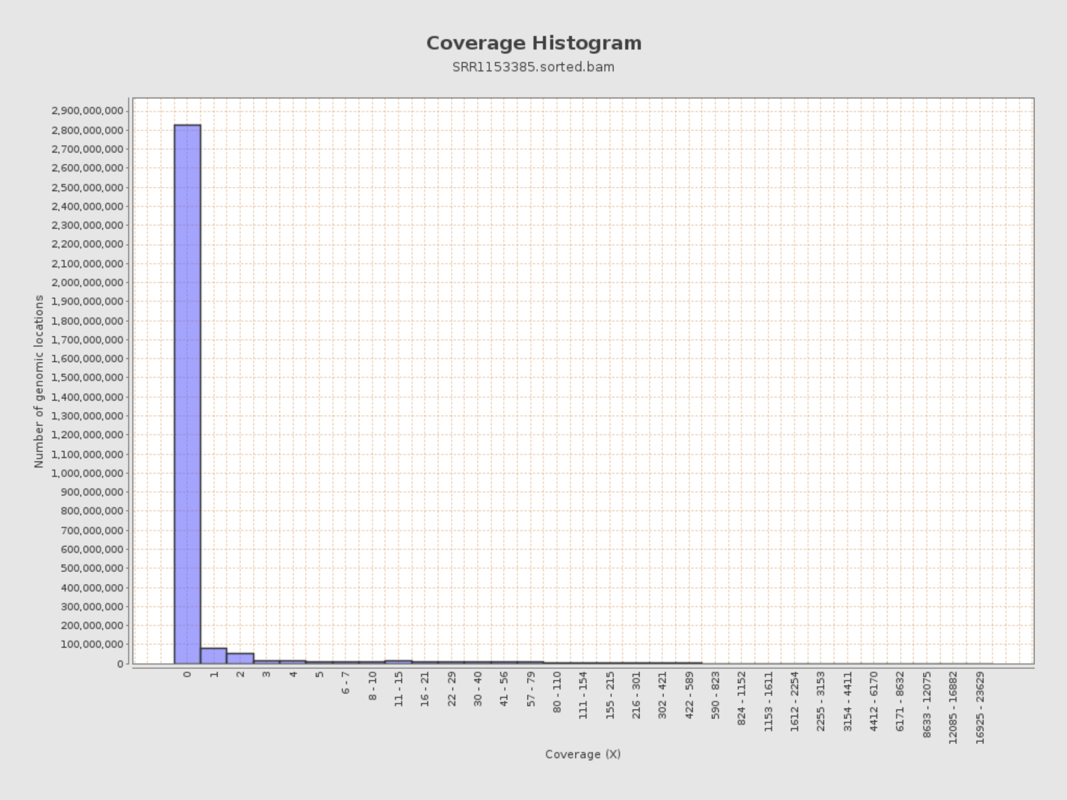
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1088887640	4.3686	59.1568
chr2	243199373	503042469	2.0684	33.9728
chr3	198022430	372910638	1.8832	28.94
chr4	191154276	275038826	1.4388	25.7905
chr5	180915260	414676968	2.2921	43.5182
chr6	171115067	489542976	2.8609	55.1833
chr7	159138663	427031001	2.6834	39.0105

chr8	146364022	357852009	2.4449	45.6198
chr9	141213431	363439392	2.5737	45.793
chr10	135534747	256687804	1.8939	26.2181
chr11	135006516	386218403	2.8607	34.4892
chr12	133851895	371951586	2.7788	34.8419
chr13	115169878	129228023	1.1221	20.6842
chr14	107349540	223799114	2.0848	37.486
chr15	102531392	347772710	3.3919	39.2515
chr16	90354753	326993450	3.619	49.9169
chr17	81195210	398502795	4.908	51.3667
chr18	78077248	132230684	1.6936	28.788
chr19	59128983	374502806	6.3337	72.6606
chr20	63025520	141679570	2.248	30.0319
chr21	48129895	88247135	1.8335	33.9912
chr22	51304566	140275061	2.7342	31.5761
chrMT	16571	4192	0.253	0.8282
chrX	155270560	392288150	2.5265	36.4864
chrY	59373566	6776104	0.1141	7.0125

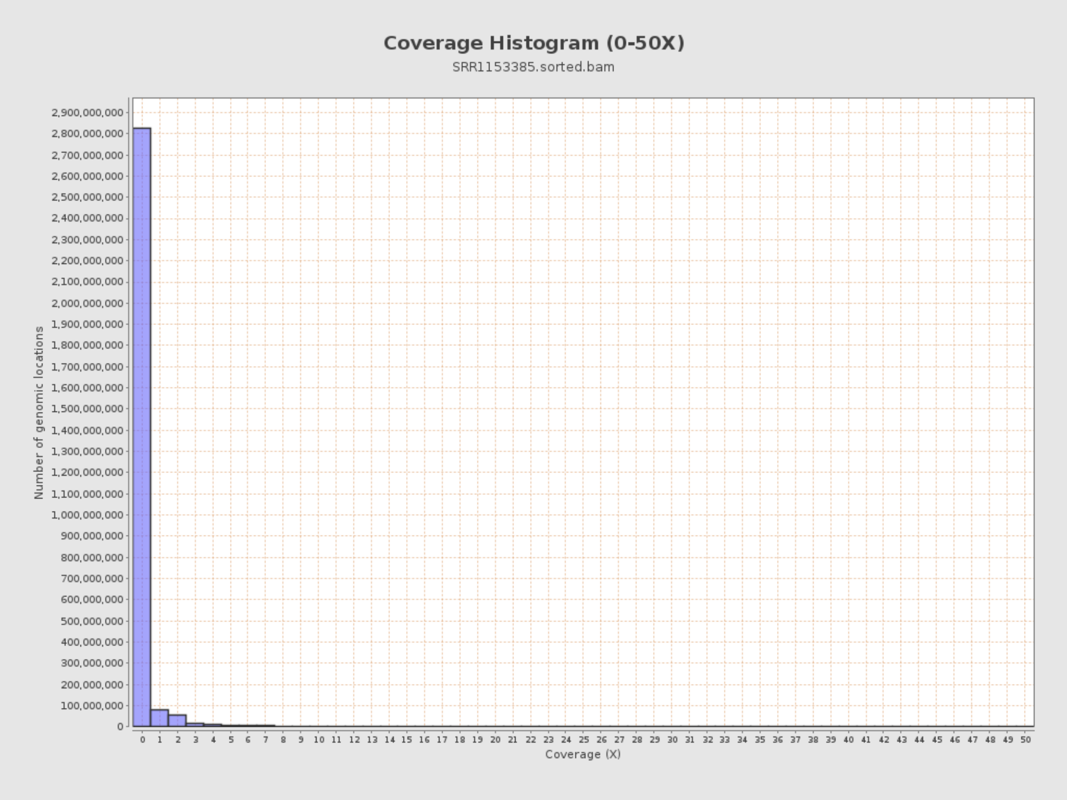
3. Results : Coverage across reference



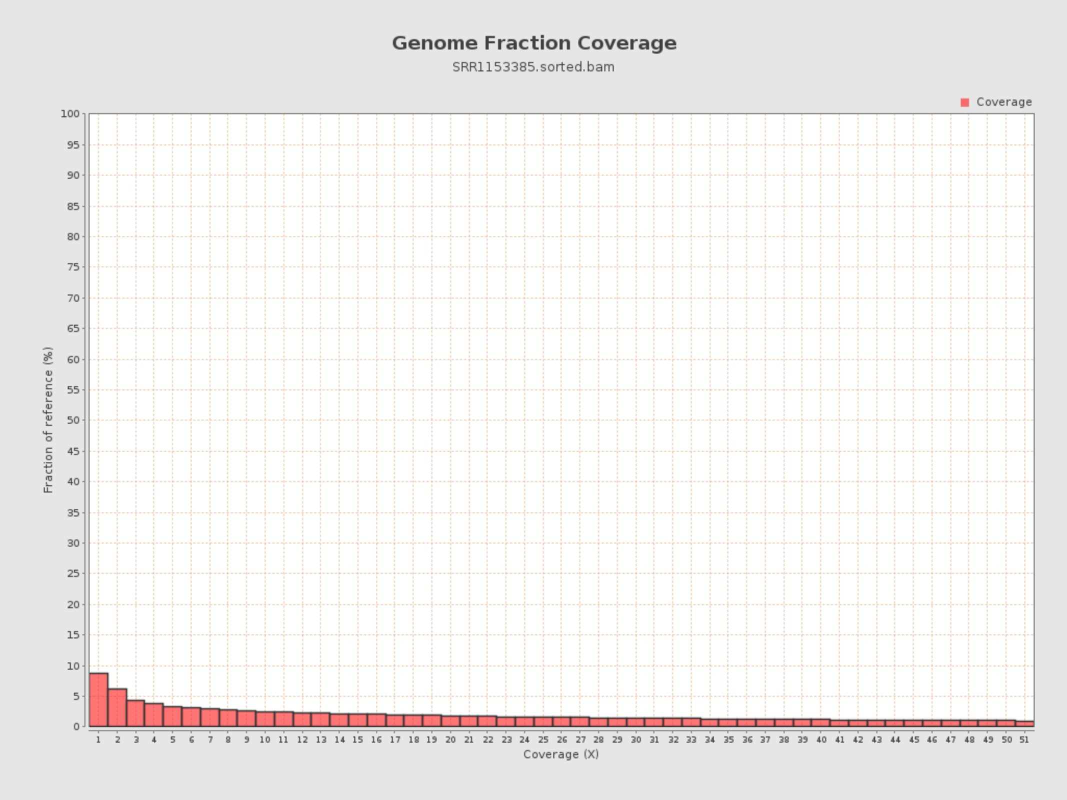
4. Results : Coverage Histogram



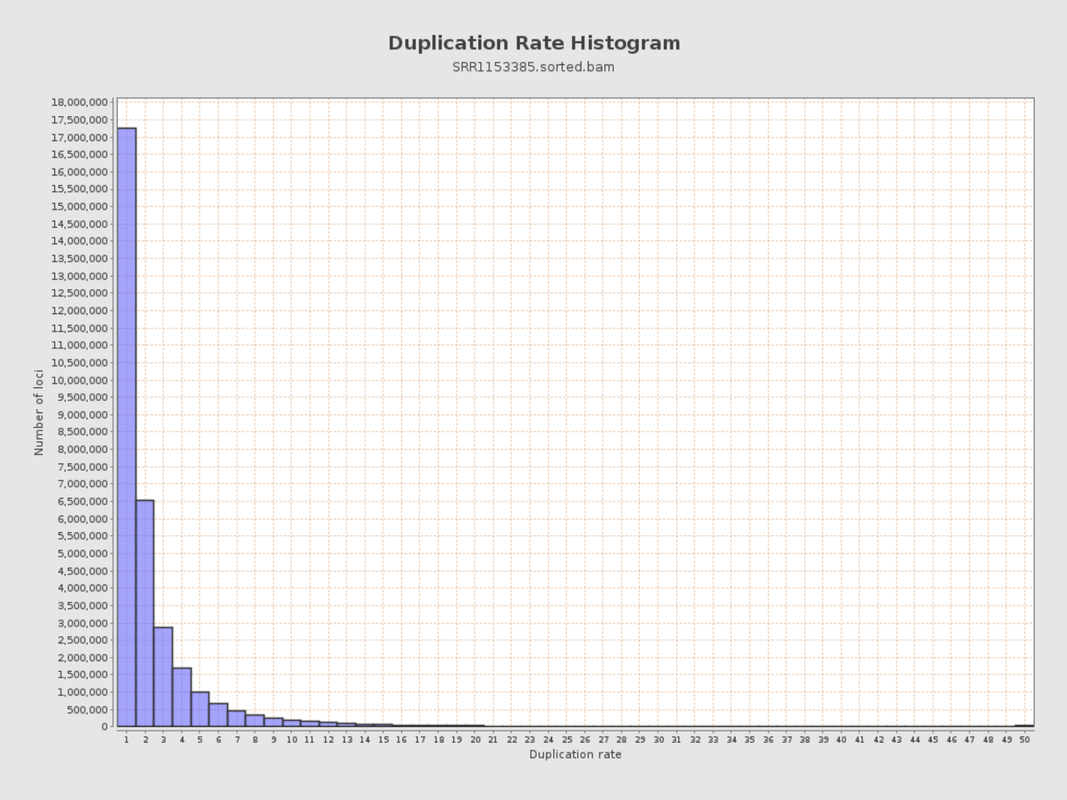
5. Results : Coverage Histogram (0-50X)



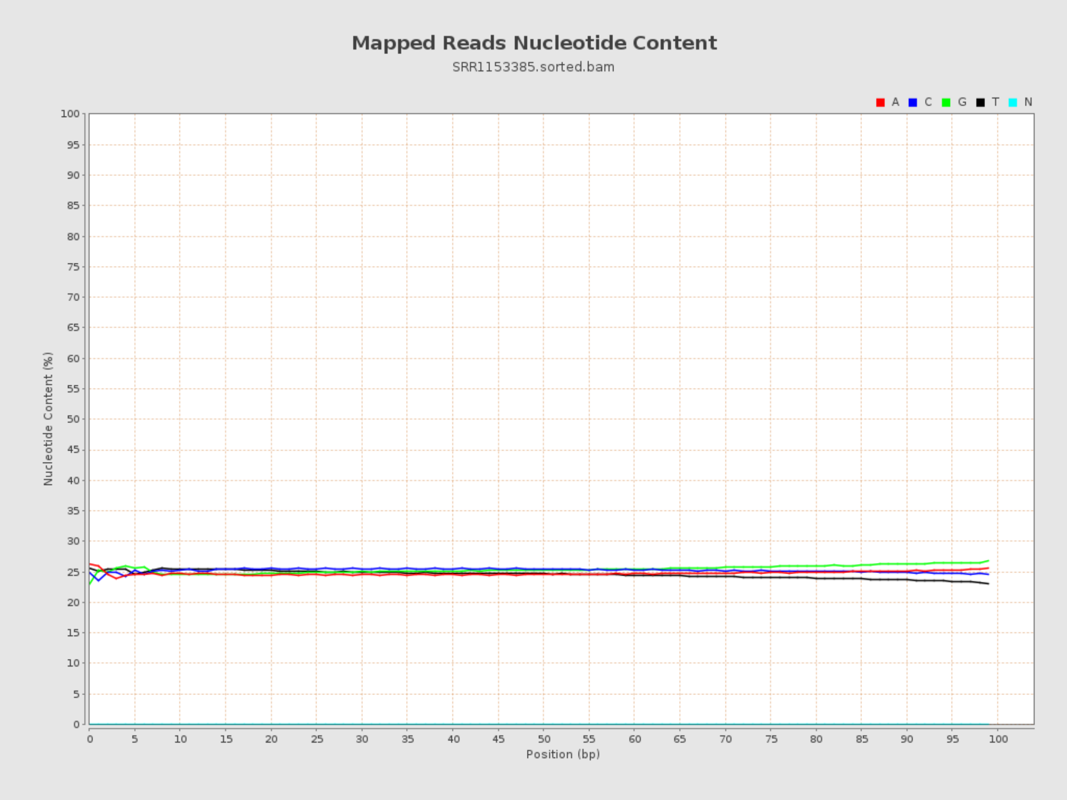
6. Results : Genome Fraction Coverage



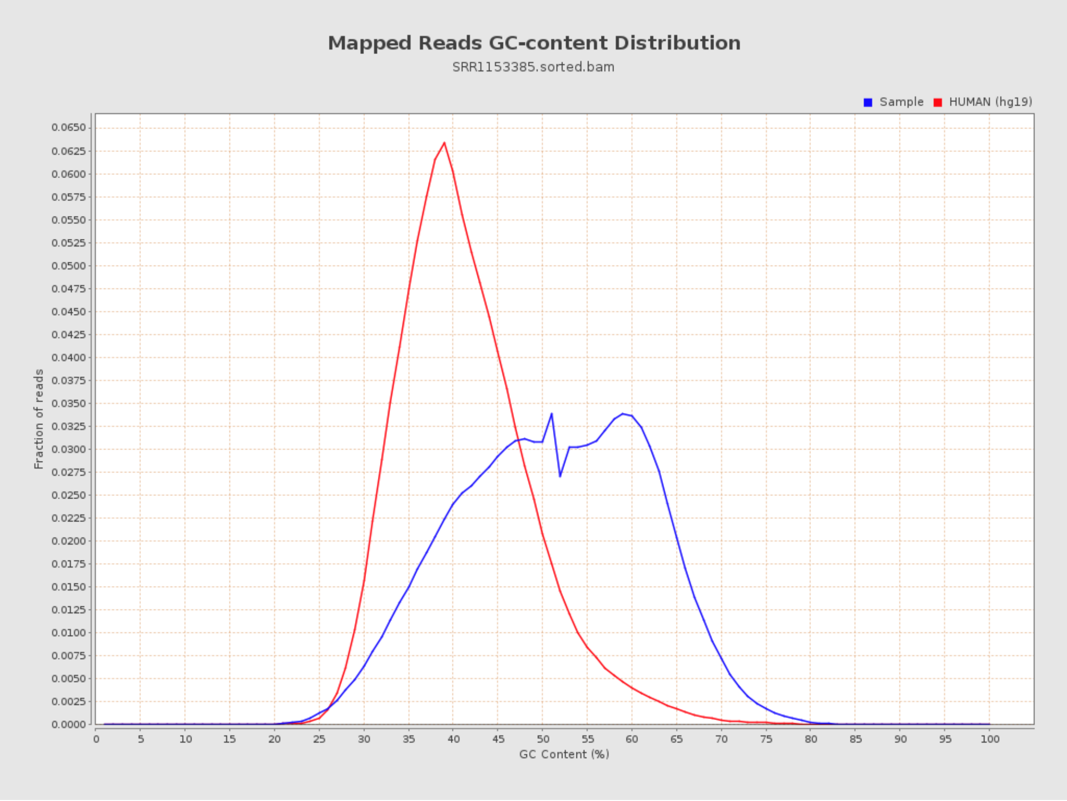
7. Results : Duplication Rate Histogram



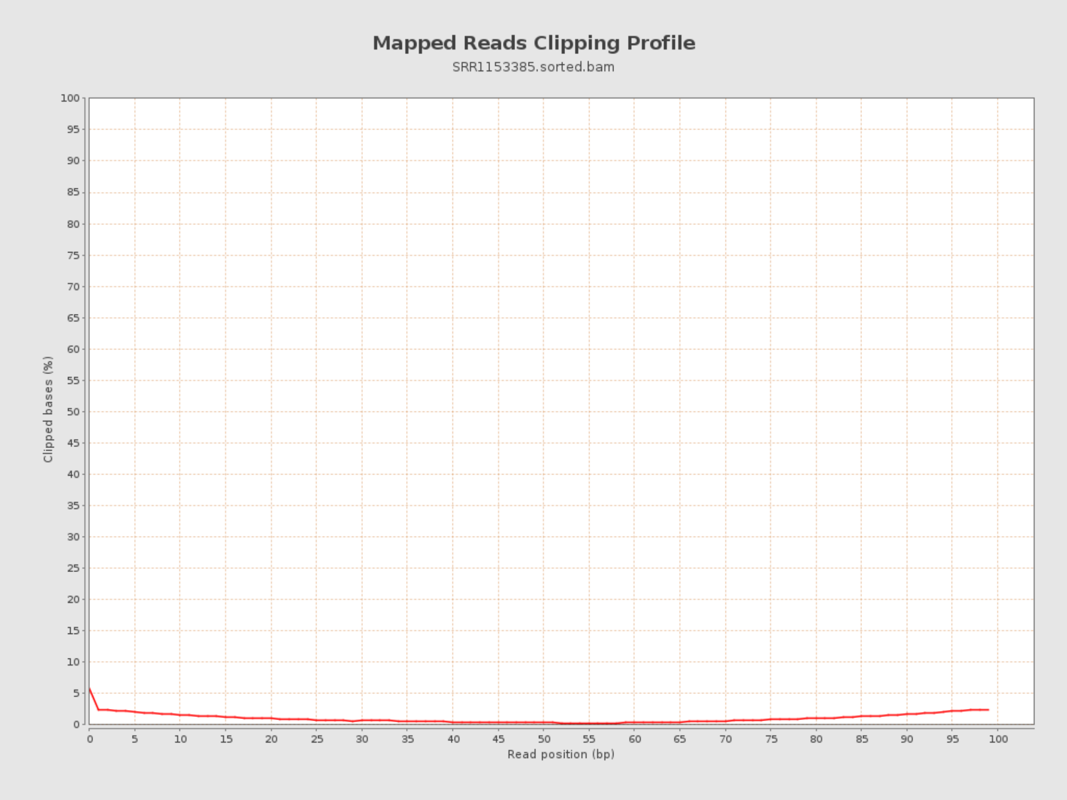
8. Results : Mapped Reads Nucleotide Content



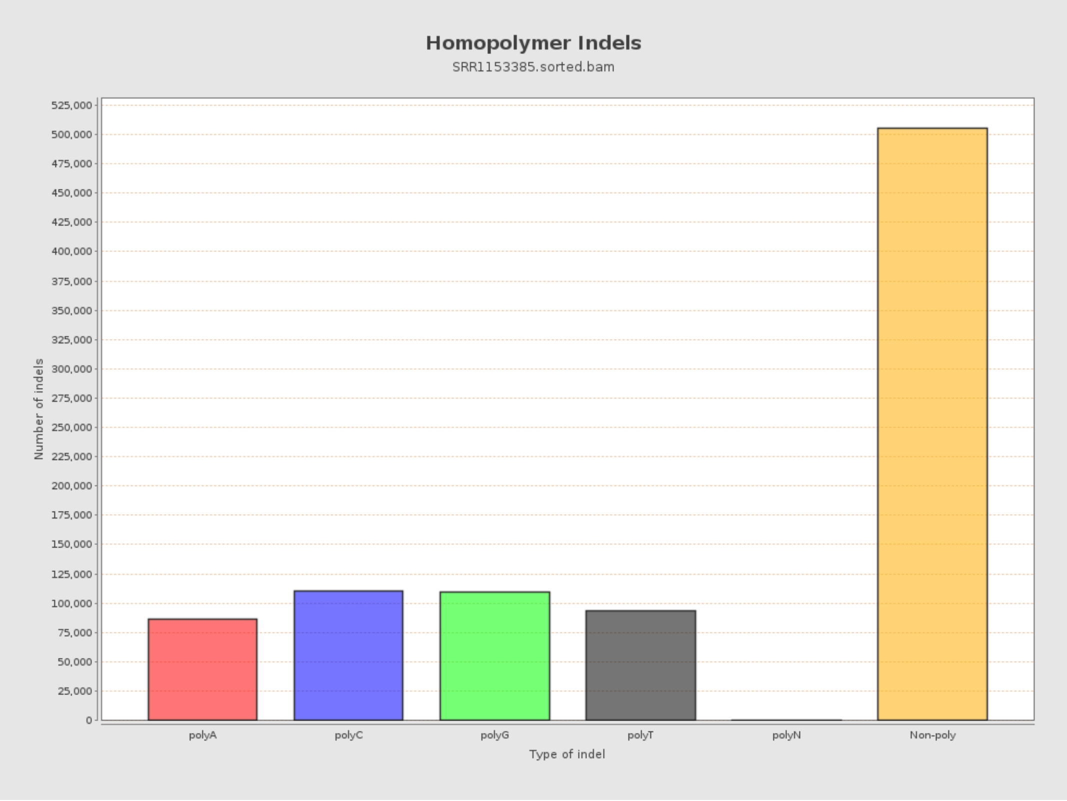
9. Results : Mapped Reads GC-content Distribution



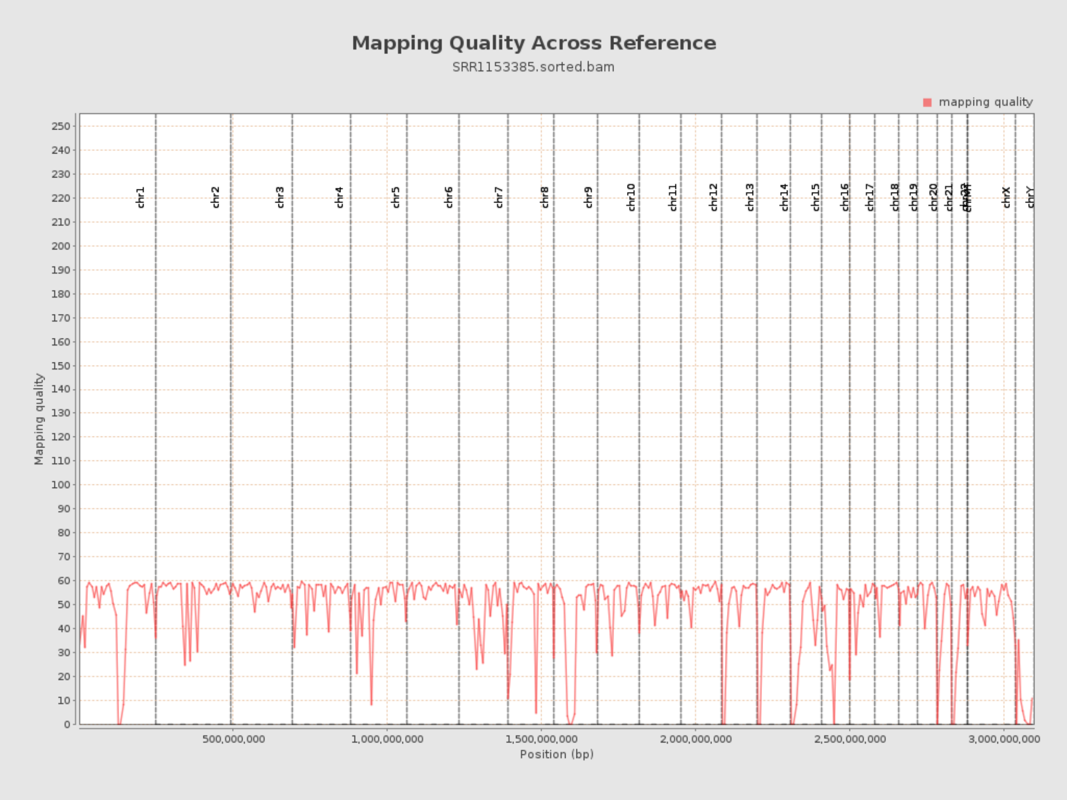
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram