Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 21:29:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163013.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_SRR1163013 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163013.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 21:29:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163013.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	102,798,974
Mapped reads	100,753,245 / 98.01%
Unmapped reads	2,045,729 / 1.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	743,405 / 0.72%
Read min/max/mean length	30 / 100 / 100.3
Duplicated reads (estimated)	56,224,272 / 54.69%
Duplication rate	45.05%
Clipped reads	10,730,106 / 10.44%

2.2. ACGT Content

Number/percentage of A's	2,421,532,151 / 24.45%
Number/percentage of C's	2,531,269,406 / 25.56%
Number/percentage of T's	2,414,942,458 / 24.38%
Number/percentage of G's	2,534,260,189 / 25.59%
Number/percentage of N's	2,305,700 / 0.02%
GC Percentage	51.14%

2.3. Coverage

Mean	3.1998

Standard Deviation	36.1471

2.4. Mapping Quality

Mean Mapping Quality	49.03

2.5. Mismatches and indels

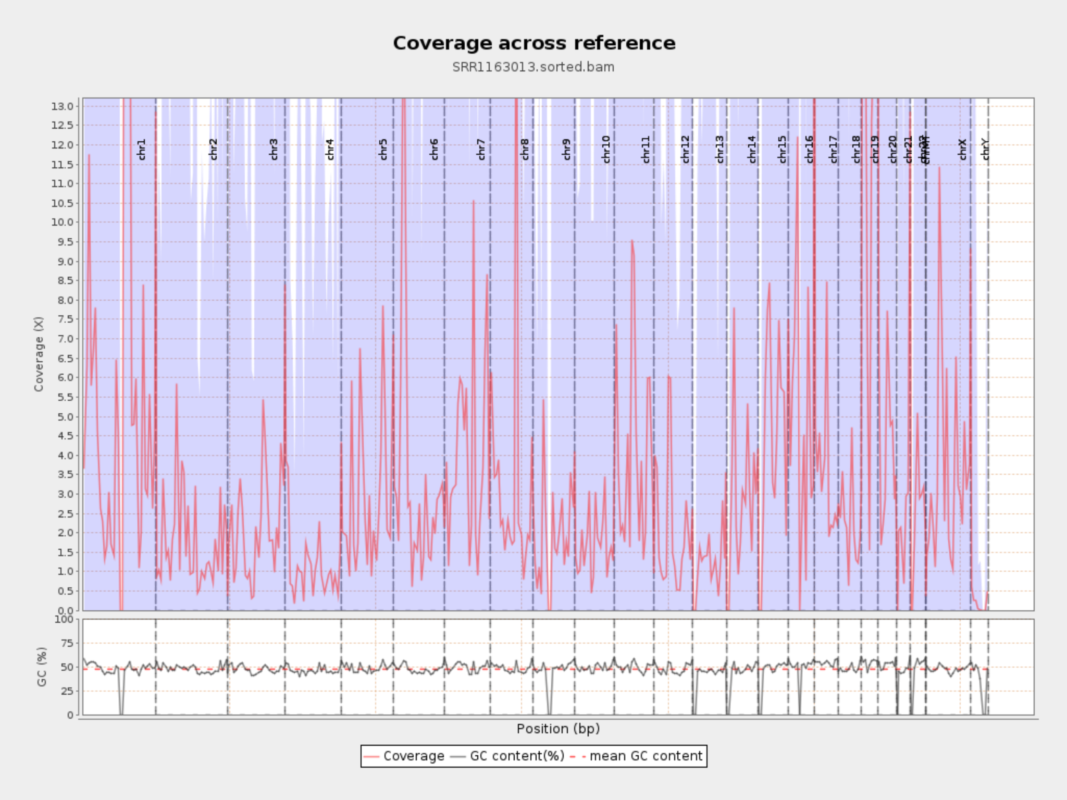
General error rate	0.46%
Mismatches	44,233,433
Insertions	688,799
Mapped reads with at least one insertion	0.67%
Deletions	603,357
Mapped reads with at least one deletion	0.59%
Homopolymer indels	46.91%

2.6. Chromosome stats

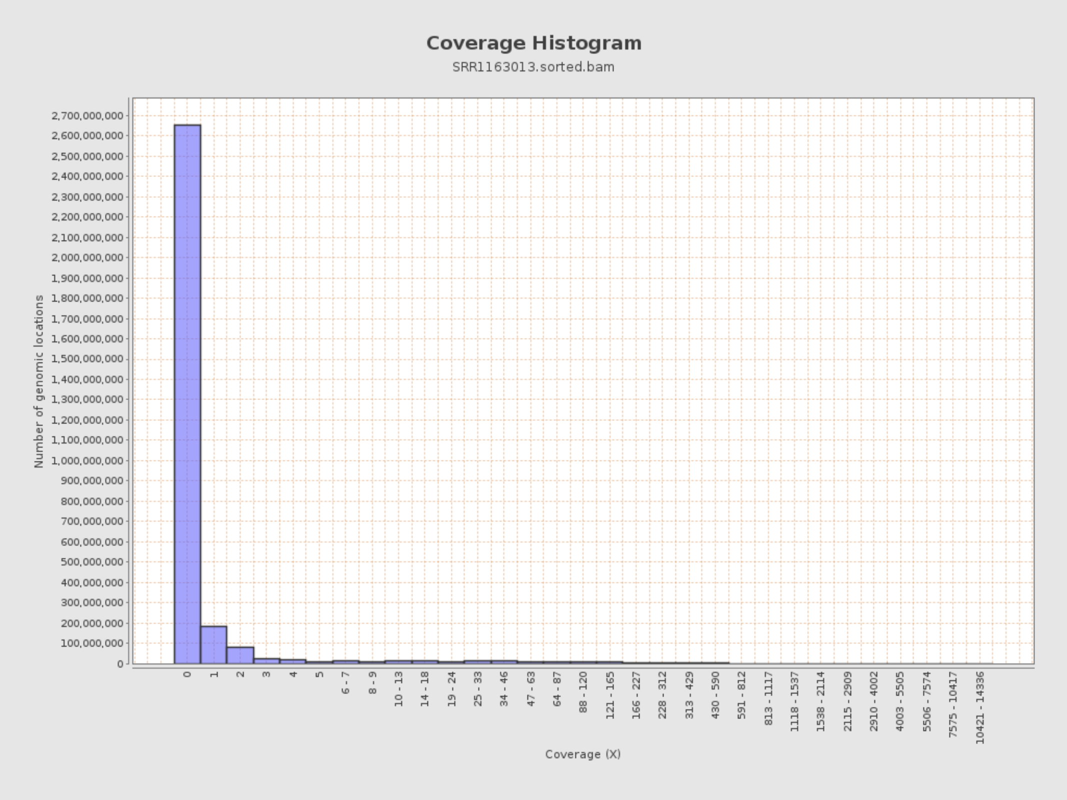
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1499555671	6.0163	53.445
chr2	243199373	427687951	1.7586	18.6342
chr3	198022430	426813171	2.1554	20.6779
chr4	191154276	219177145	1.1466	18.5015
chr5	180915260	540277382	2.9864	42.4774
chr6	171115067	574162164	3.3554	31.7176
chr7	159138663	645720332	4.0576	51.3993

chr8	146364022	494143642	3.3761	56.1907
chr9	141213431	262402298	1.8582	19.1892
chr10	135534747	229329292	1.692	16.8459
chr11	135006516	553618311	4.1007	32.5305
chr12	133851895	288080000	2.1522	20.5463
chr13	115169878	142780604	1.2397	15.3481
chr14	107349540	306685893	2.8569	25.5269
chr15	102531392	448621990	4.3755	33.8982
chr16	90354753	439681540	4.8662	35.9172
chr17	81195210	294415945	3.626	28.5873
chr18	78077248	176638253	2.2624	23.0453
chr19	59128983	832652389	14.082	89.4246
chr20	63025520	258015659	4.0938	33.2412
chr21	48129895	146893900	3.052	66.0413
chr22	51304566	126492506	2.4655	20.6265
chrMT	16571	6078	0.3668	0.8479
chrX	155270560	560183096	3.6078	35.3608
chrY	59373566	11571508	0.1949	10.6512

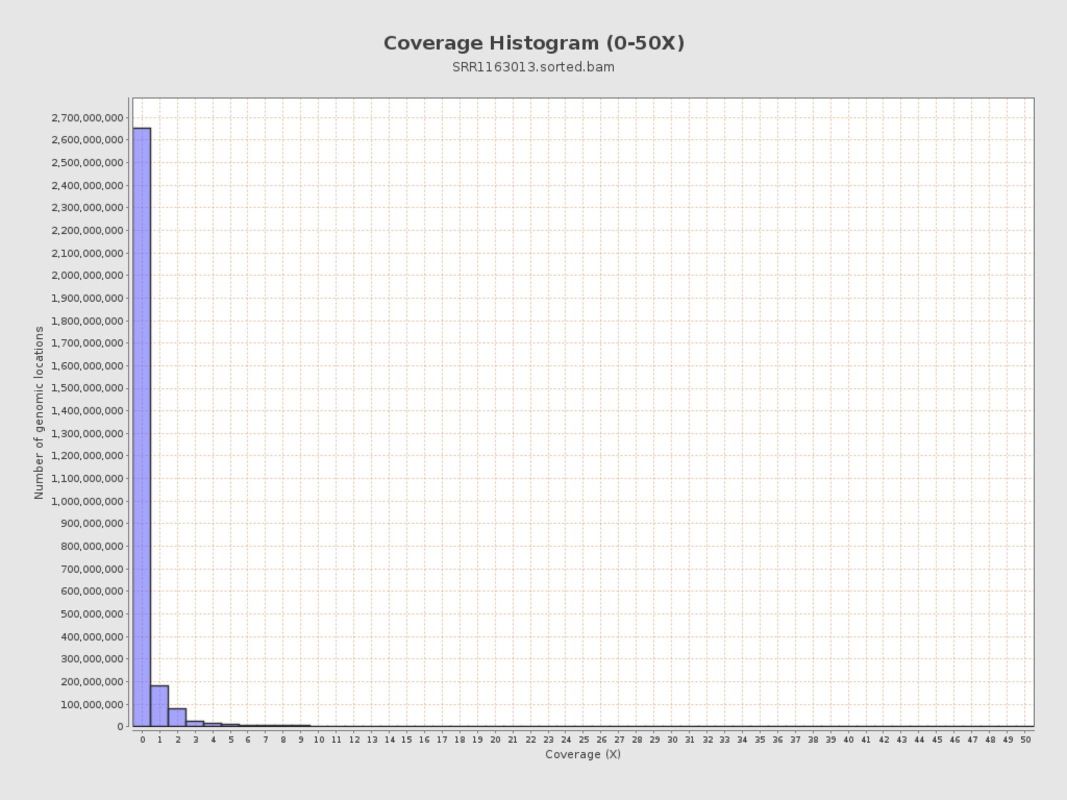
3. Results : Coverage across reference



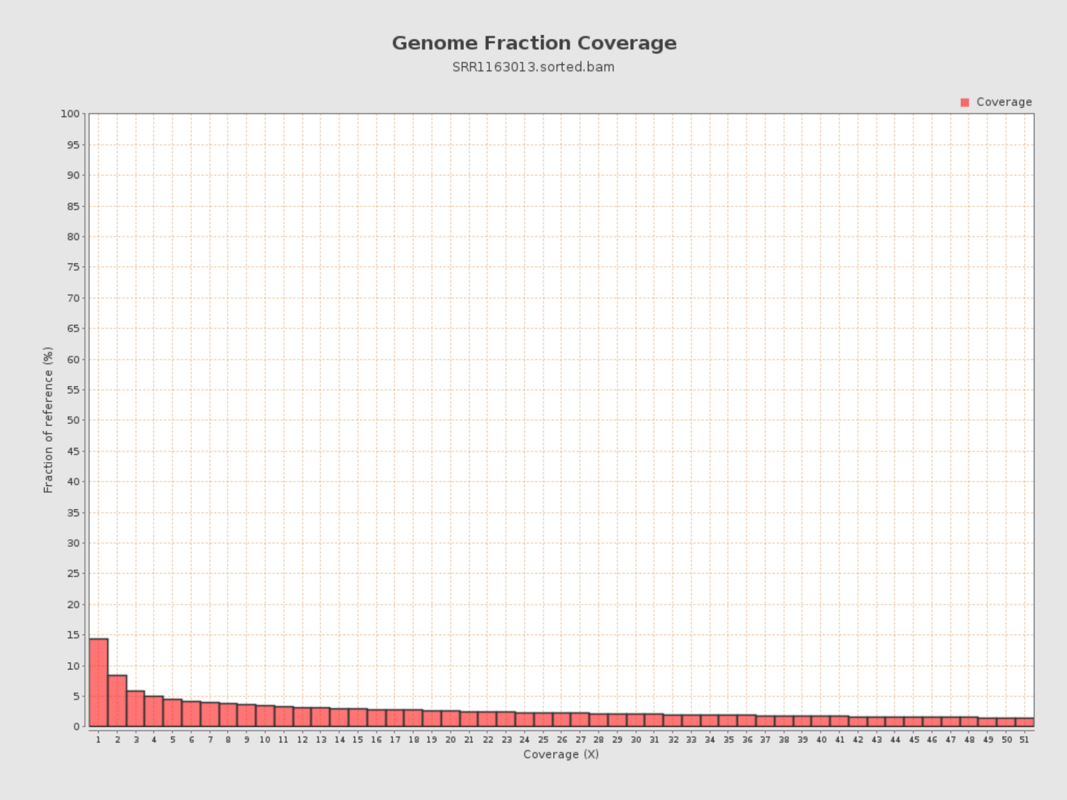
4. Results : Coverage Histogram



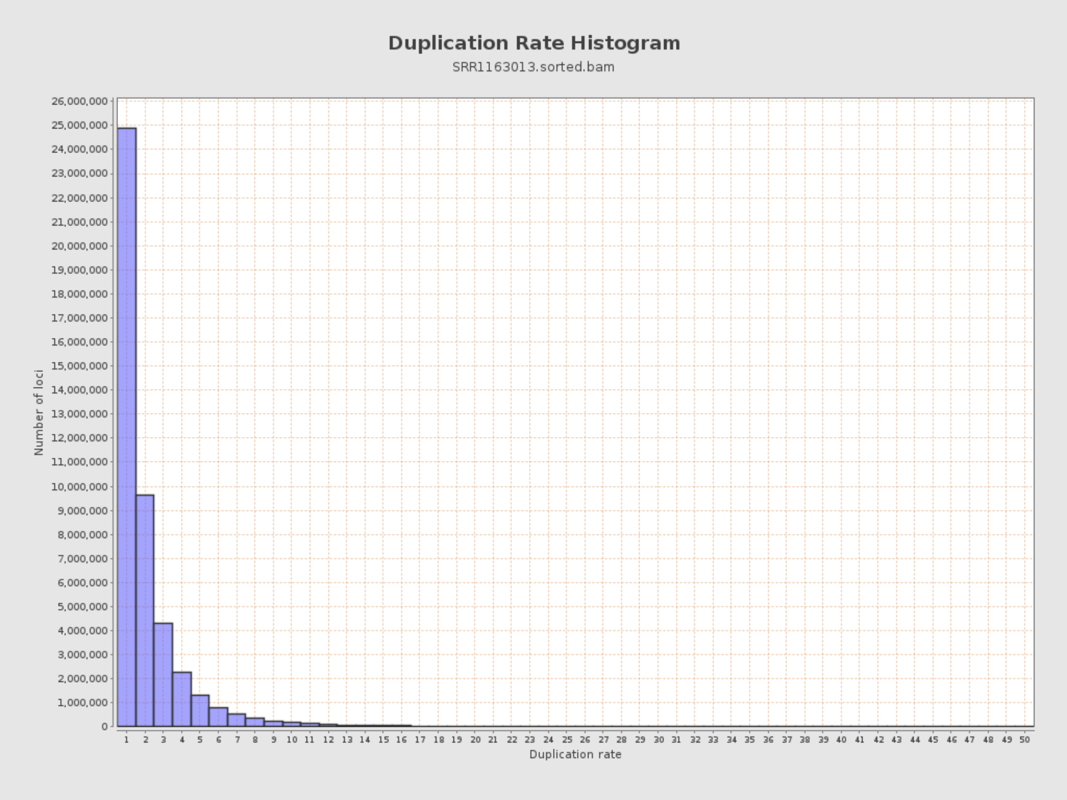
5. Results : Coverage Histogram (0-50X)



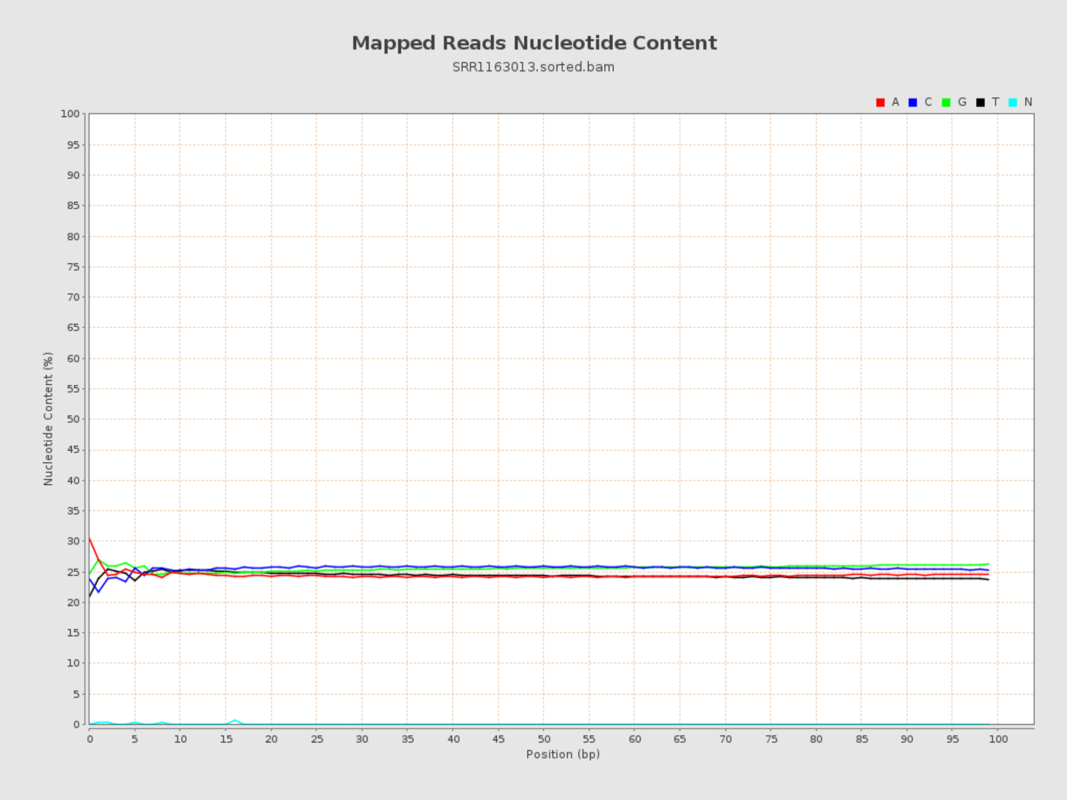
6. Results : Genome Fraction Coverage



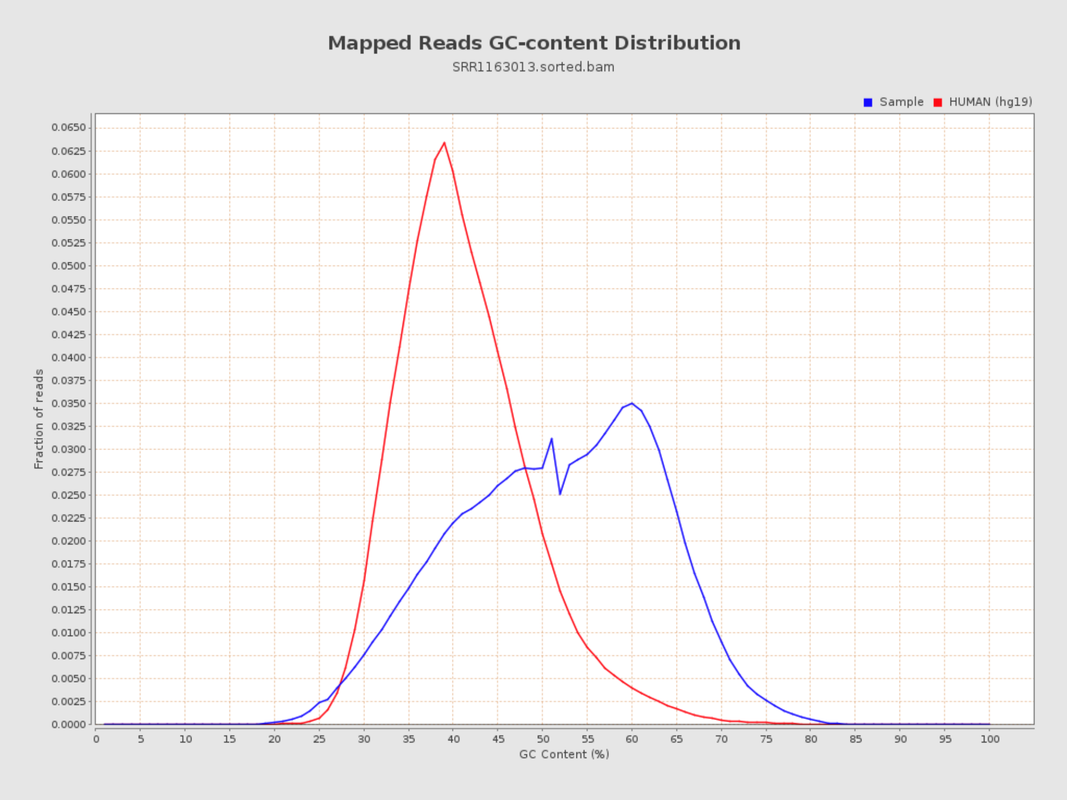
7. Results : Duplication Rate Histogram



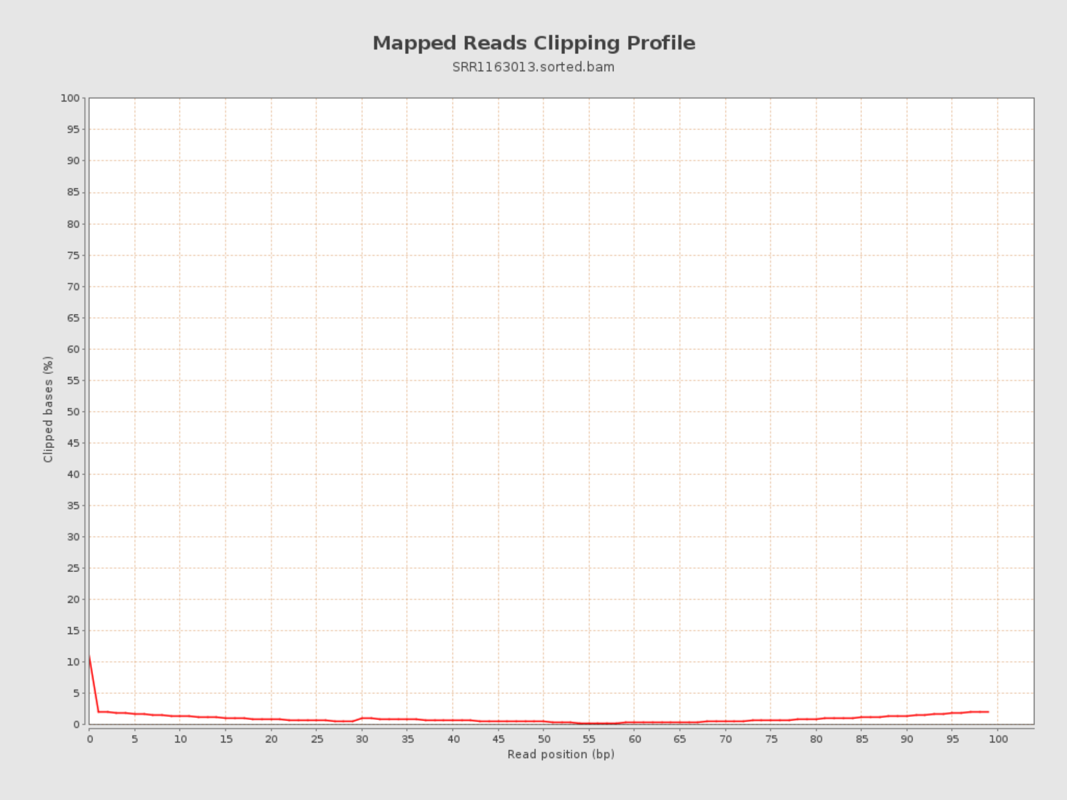
8. Results : Mapped Reads Nucleotide Content



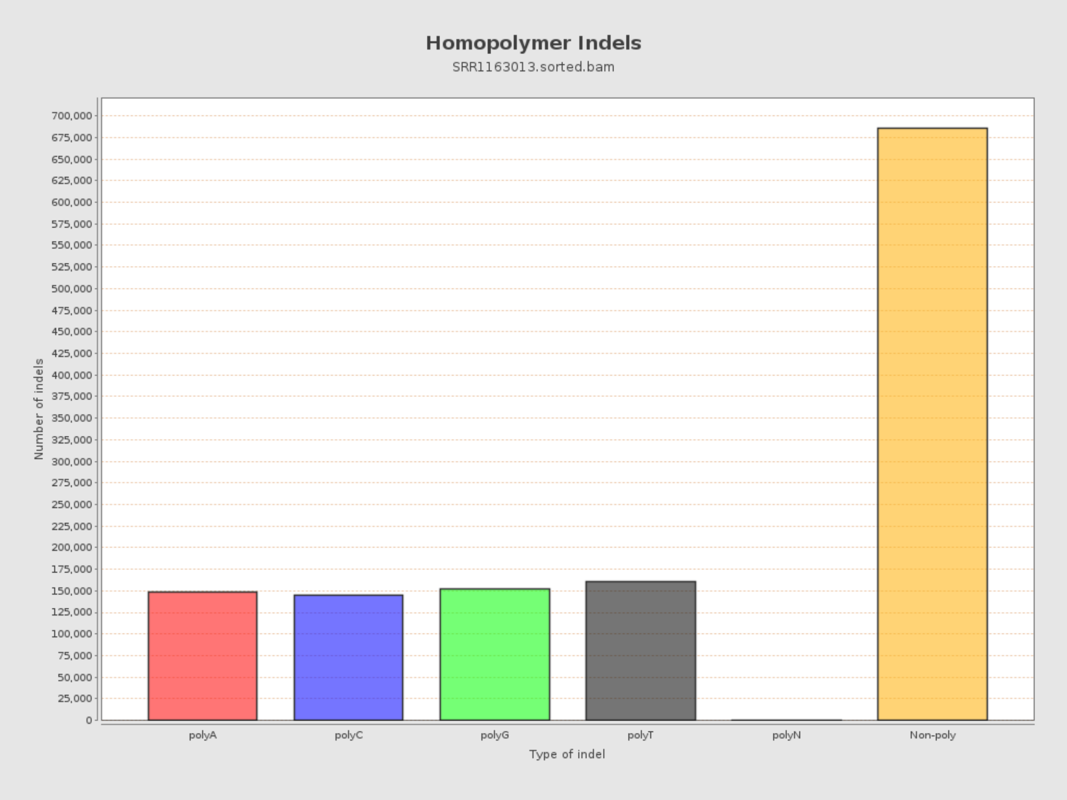
9. Results : Mapped Reads GC-content Distribution



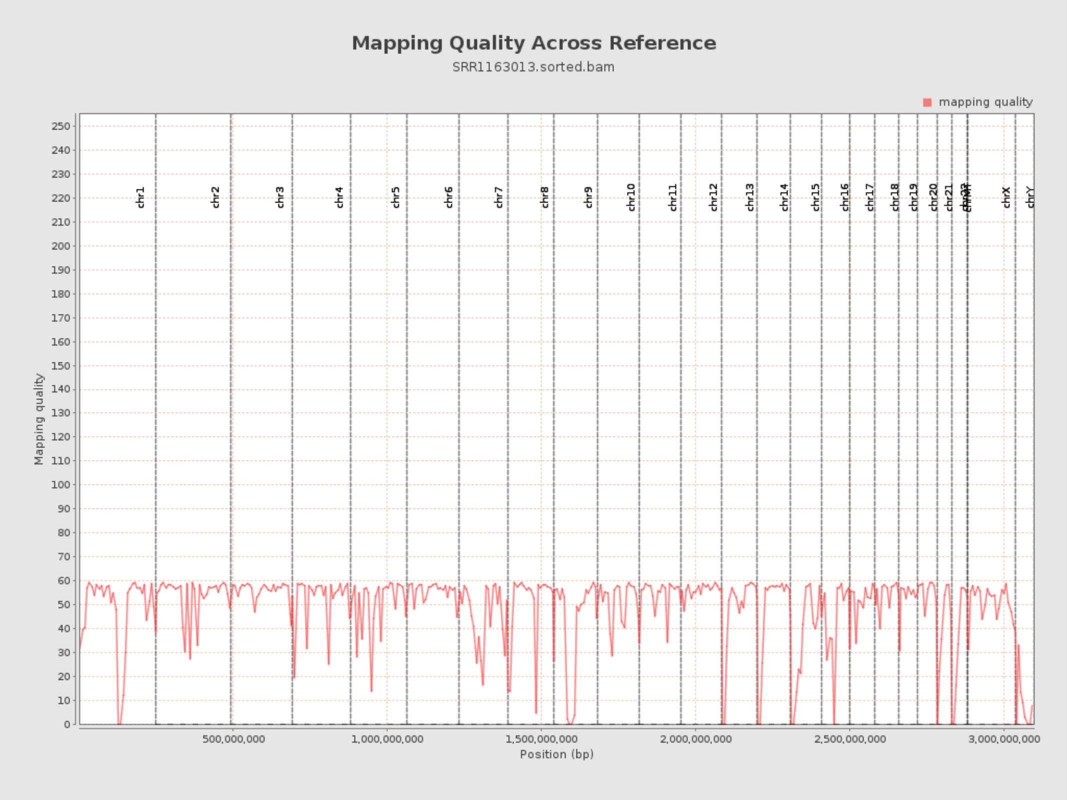
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram