Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 03:12:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163508.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_SRR1163508 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163508.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 03:12:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163508.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	205,534,476
Mapped reads	198,826,736 / 96.74%
Unmapped reads	6,707,740 / 3.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	81,128 / 0.04%
Read min/max/mean length	30 / 100 / 100.02
Duplicated reads (estimated)	116,502,557 / 56.68%
Duplication rate	52.81%
Clipped reads	5,109,214 / 2.49%

2.2. ACGT Content

Number/percentage of A's	4,874,066,234 / 24.64%
Number/percentage of C's	5,011,681,167 / 25.34%
Number/percentage of T's	4,960,913,575 / 25.08%
Number/percentage of G's	4,927,335,230 / 24.91%
Number/percentage of N's	5,078,715 / 0.03%
GC Percentage	50.25%

2.3. Coverage

Mean	6.3902

Standard Deviation	56.9903

2.4. Mapping Quality

Mean Mapping Quality	48.86

2.5. Mismatches and indels

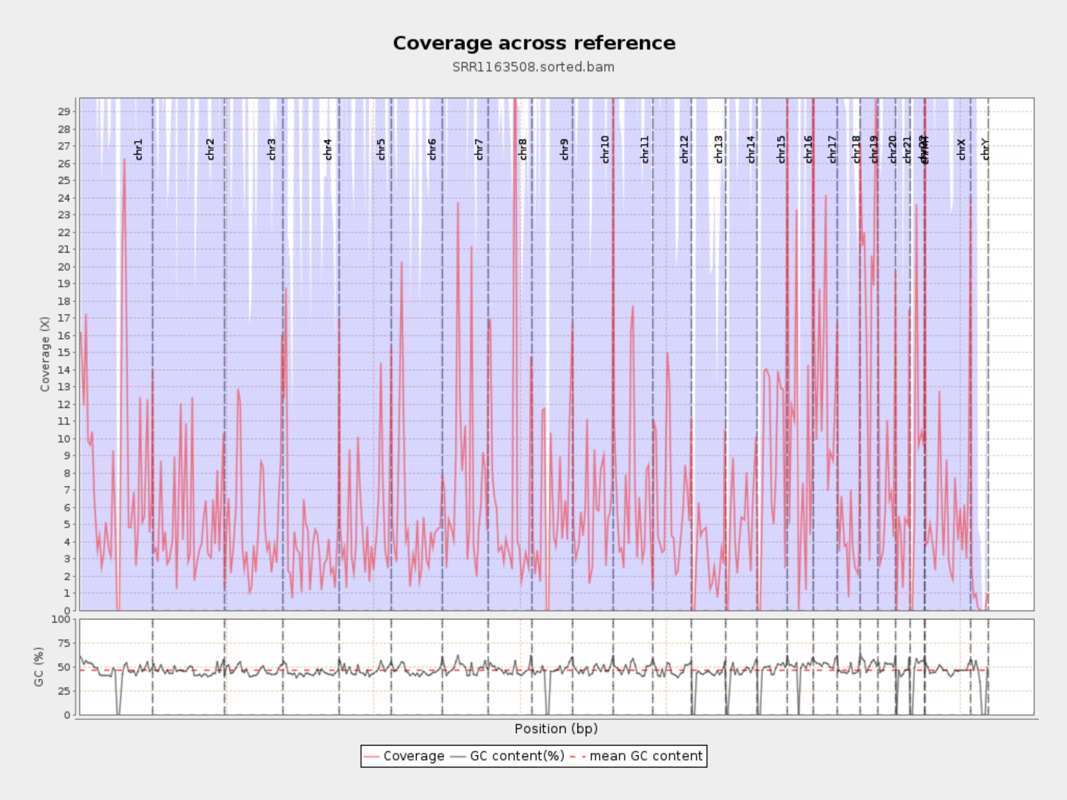
General error rate	0.64%
Mismatches	125,299,537
Insertions	948,910
Mapped reads with at least one insertion	0.47%
Deletions	1,306,565
Mapped reads with at least one deletion	0.65%
Homopolymer indels	44.56%

2.6. Chromosome stats

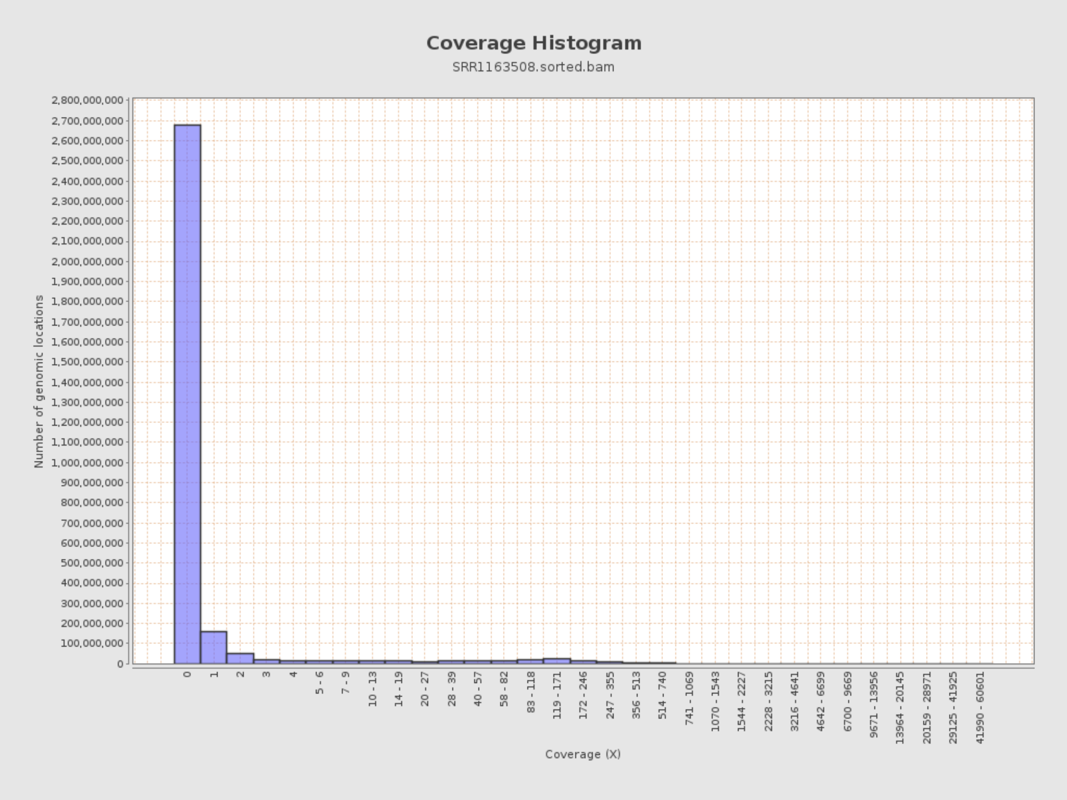
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2002155724	8.0327	52.9109
chr2	243199373	1267242238	5.2107	39.3745
chr3	198022430	985161303	4.975	37.8397
chr4	191154276	787404562	4.1192	52.9265
chr5	180915260	946628485	5.2324	56.1726
chr6	171115067	855583537	5	33.9467
chr7	159138663	1232972234	7.7478	127.7853

chr8	146364022	1009562181	6.8976	108.319
chr9	141213431	861401298	6.1	41.8635
chr10	135534747	764800387	5.6428	36.5943
chr11	135006516	984328461	7.291	41.7948
chr12	133851895	867555590	6.4815	36.5336
chr13	115169878	337312090	2.9288	24.0064
chr14	107349540	530093578	4.938	34.4329
chr15	102531392	881455283	8.5969	53.138
chr16	90354753	878204594	9.7195	53.6003
chr17	81195210	1091724272	13.4457	67.9444
chr18	78077248	297621374	3.8119	40.3394
chr19	59128983	1154283384	19.5214	72.6502
chr20	63025520	435460467	6.9093	41.2553
chr21	48129895	254577447	5.2894	49.1845
chr22	51304566	486449840	9.4816	56.2477
chrMT	16571	1002811	60.516	19.8605
chrX	155270560	833480509	5.3679	36.8796
chrY	59373566	35531912	0.5984	30.4897

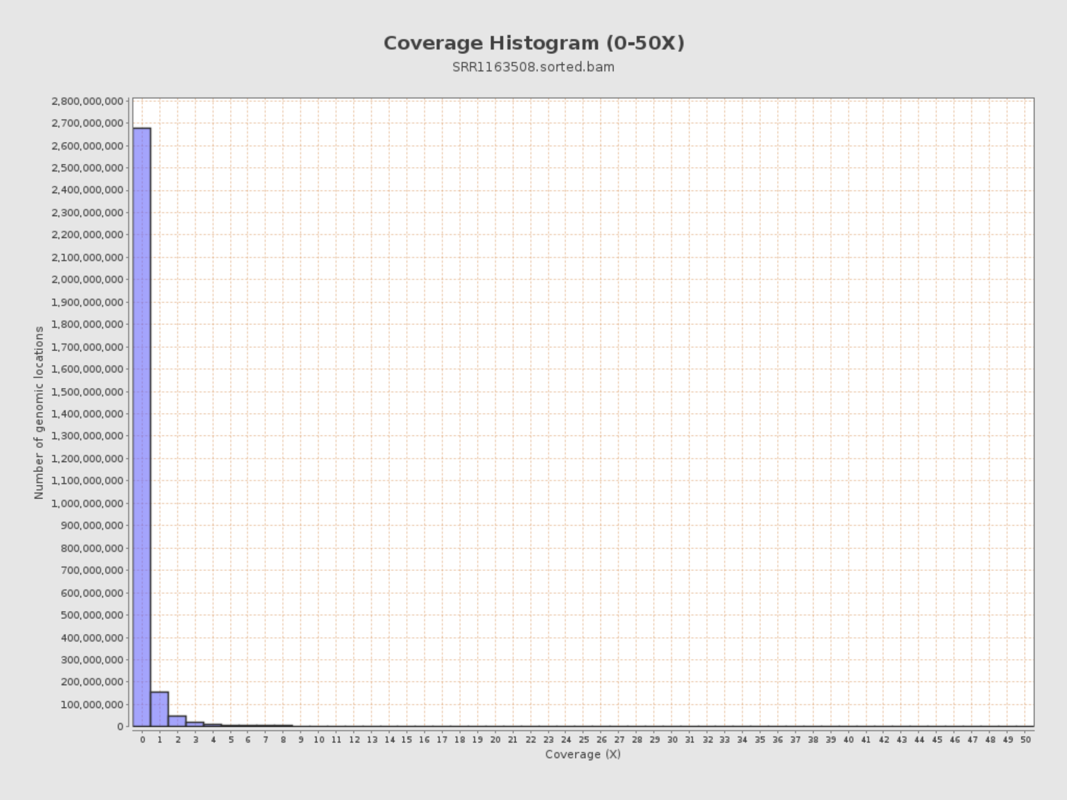
3. Results : Coverage across reference



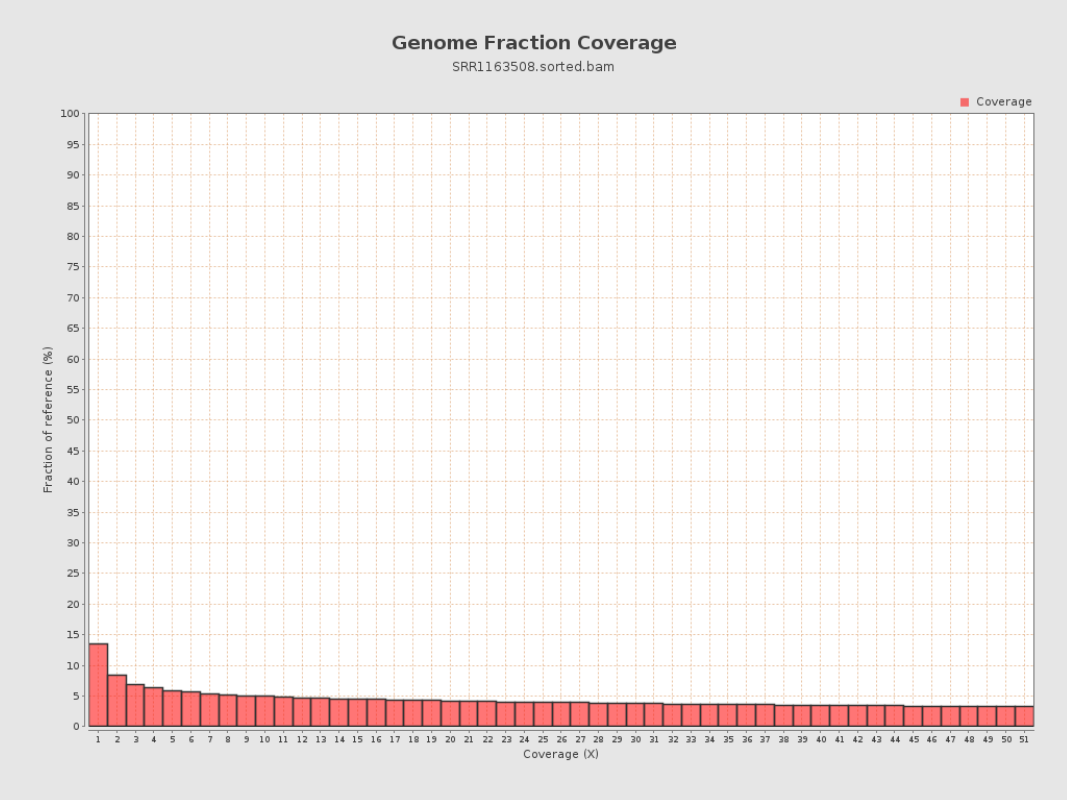
4. Results : Coverage Histogram



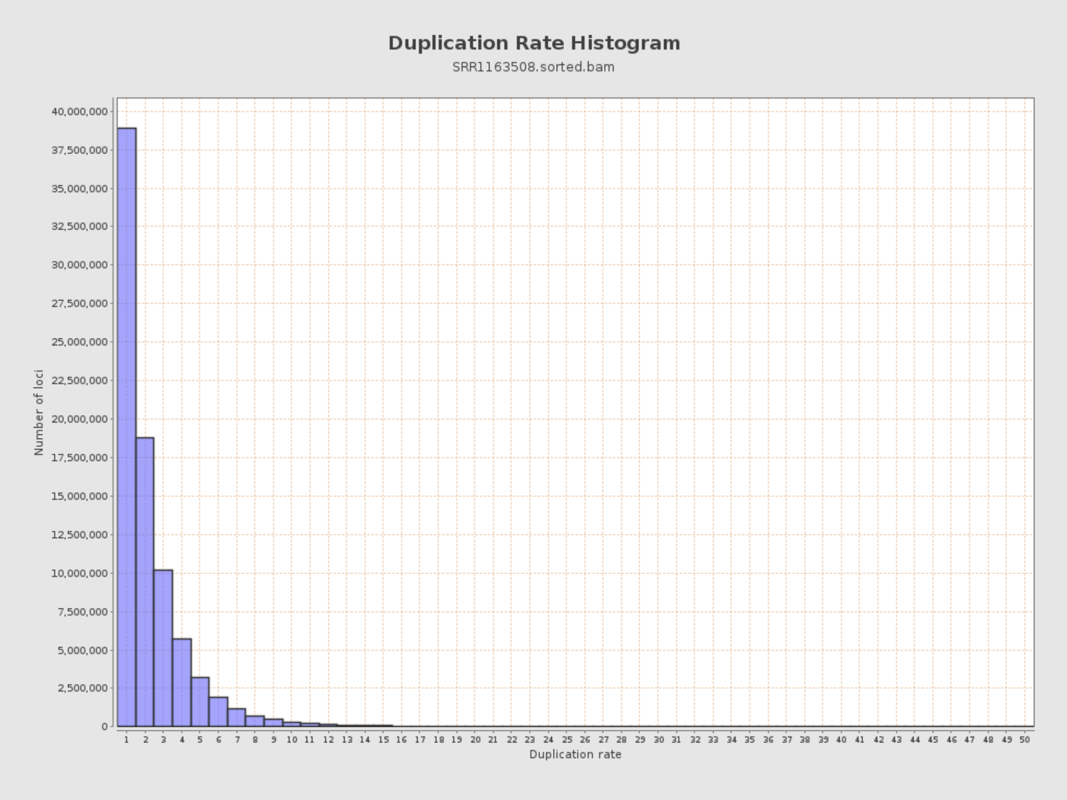
5. Results : Coverage Histogram (0-50X)



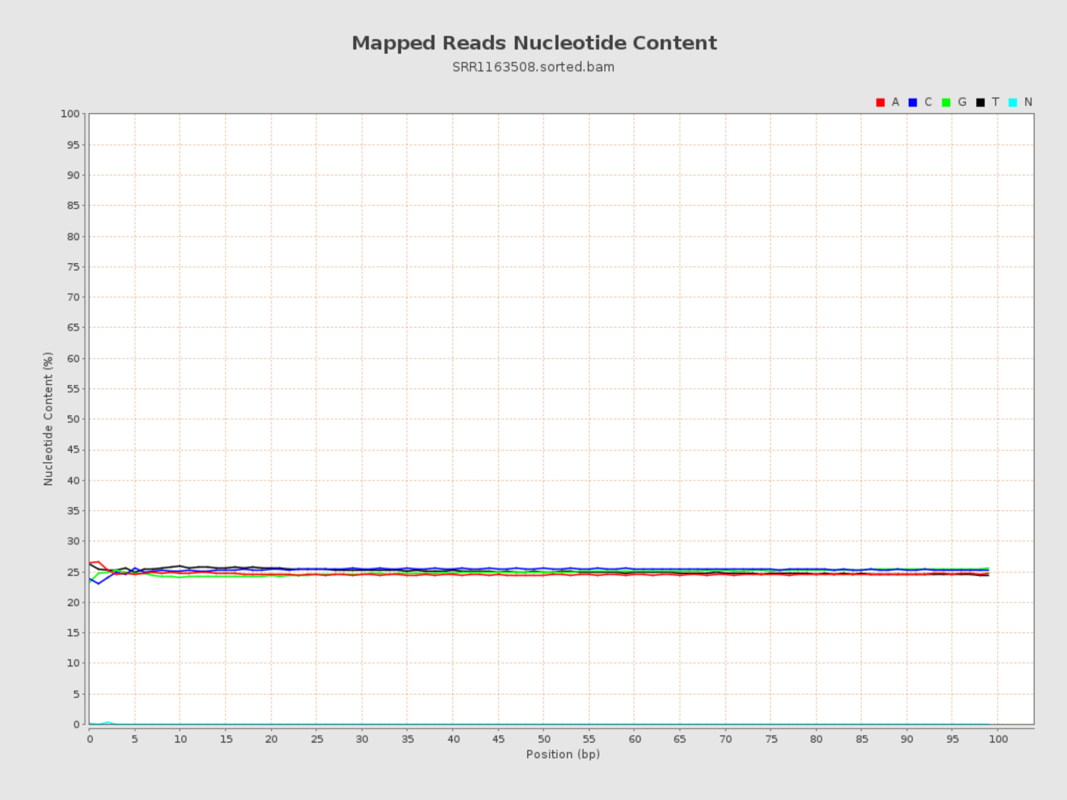
6. Results : Genome Fraction Coverage



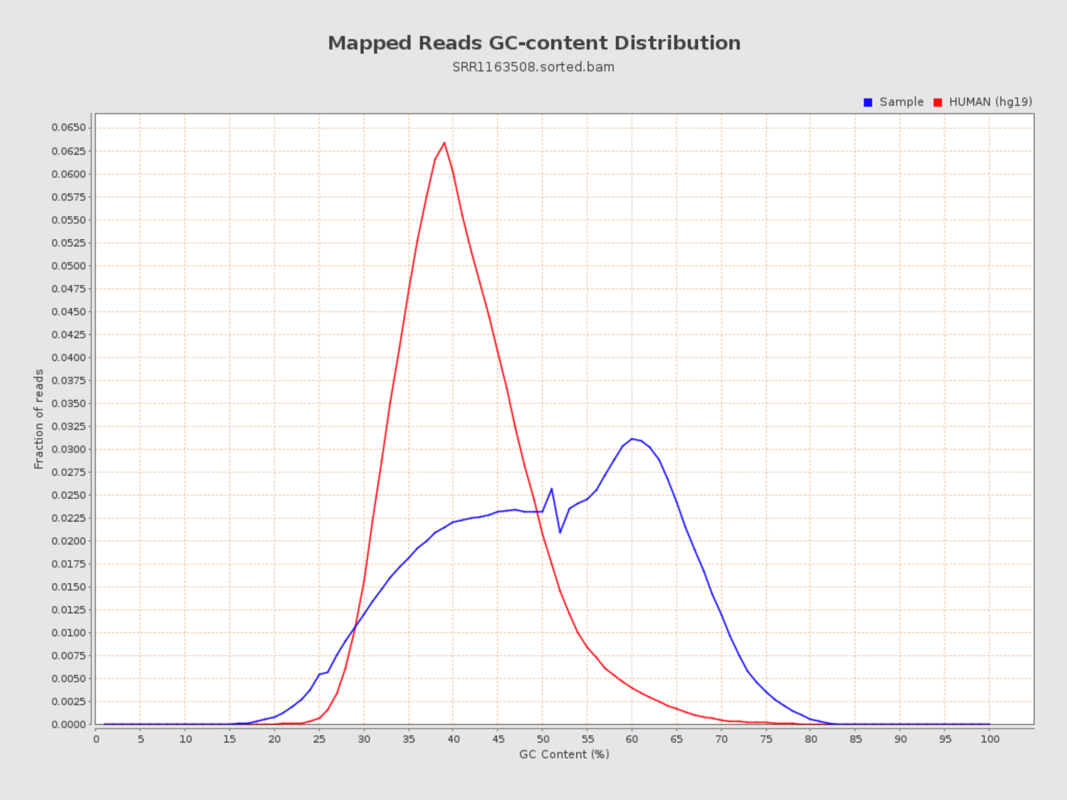
7. Results : Duplication Rate Histogram



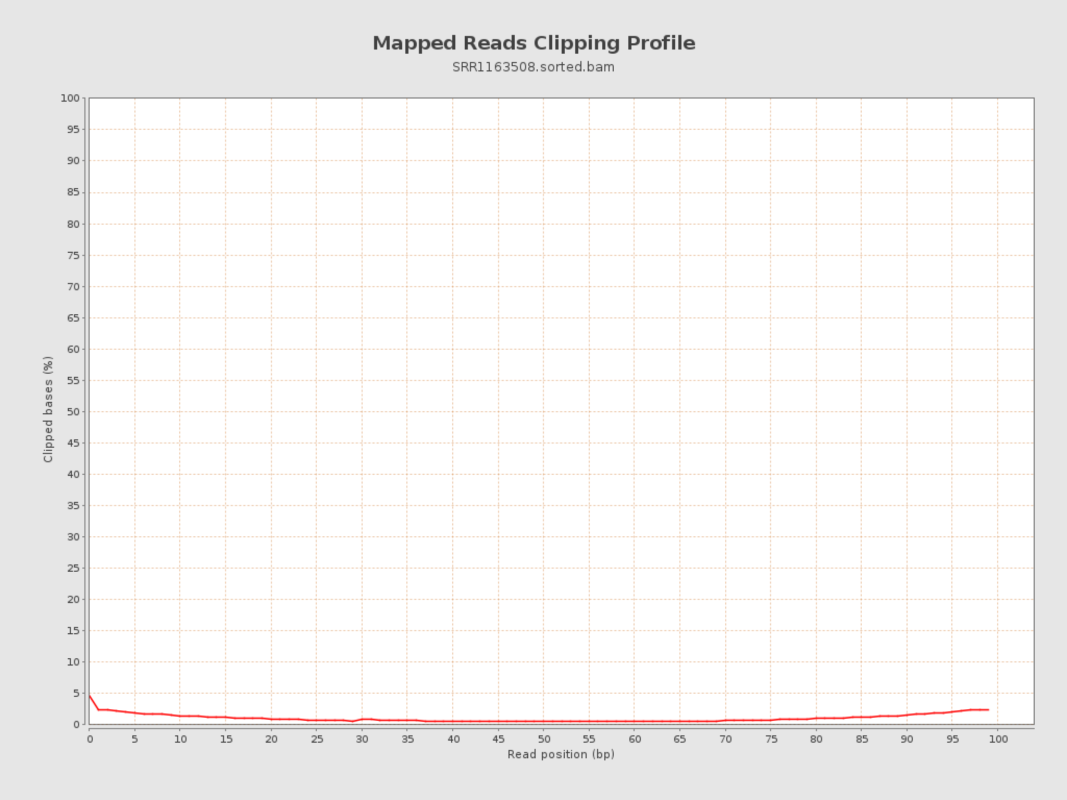
8. Results : Mapped Reads Nucleotide Content



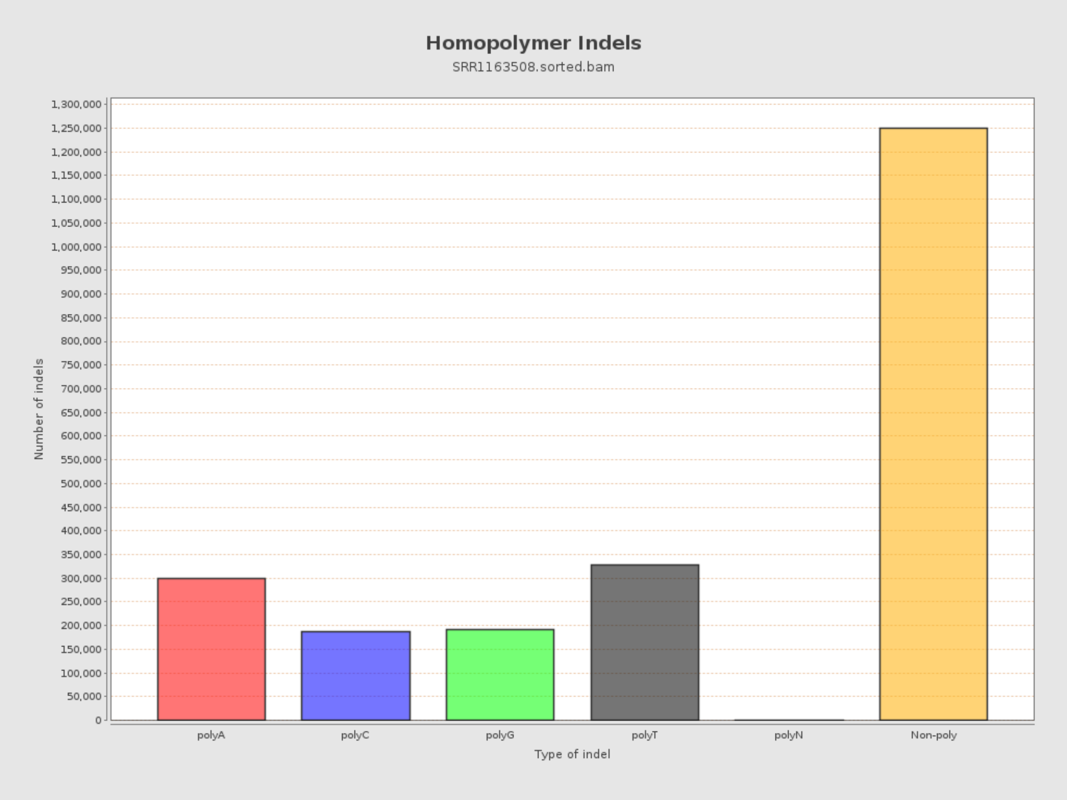
9. Results : Mapped Reads GC-content Distribution



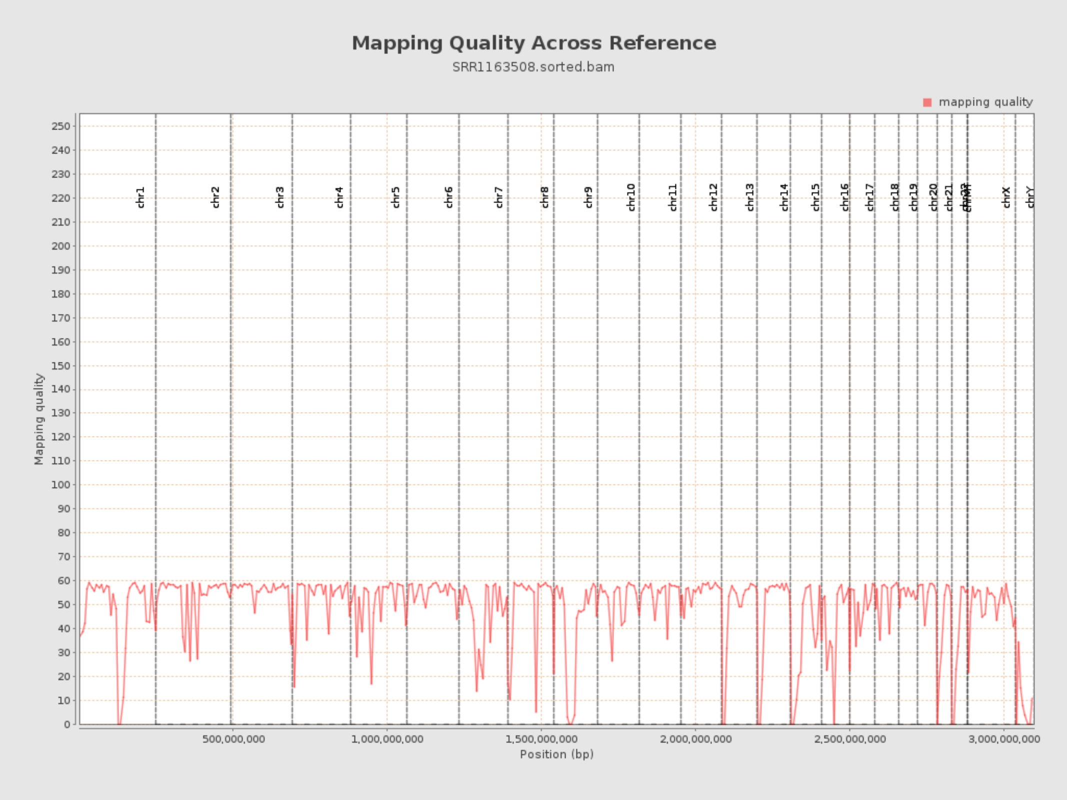
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram