Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 10:56:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163148.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_SRR1163148 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163148.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 10:56:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163148.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	97,880,114
Mapped reads	96,570,149 / 98.66%
Unmapped reads	1,309,965 / 1.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	403,145 / 0.41%
Read min/max/mean length	30 / 100 / 100.17
Duplicated reads (estimated)	58,272,264 / 59.53%
Duplication rate	48.76%
Clipped reads	21,730,679 / 22.2%

2.2. ACGT Content

Number/percentage of A's	2,233,944,647 / 24.37%
Number/percentage of C's	2,349,720,646 / 25.64%
Number/percentage of T's	2,217,438,551 / 24.19%
Number/percentage of G's	2,364,008,235 / 25.79%
Number/percentage of N's	358,413 / 0%
GC Percentage	51.43%

2.3. Coverage

Mean	2.9611

Standard Deviation	37.5035

2.4. Mapping Quality

Mean Mapping Quality	49.11

2.5. Mismatches and indels

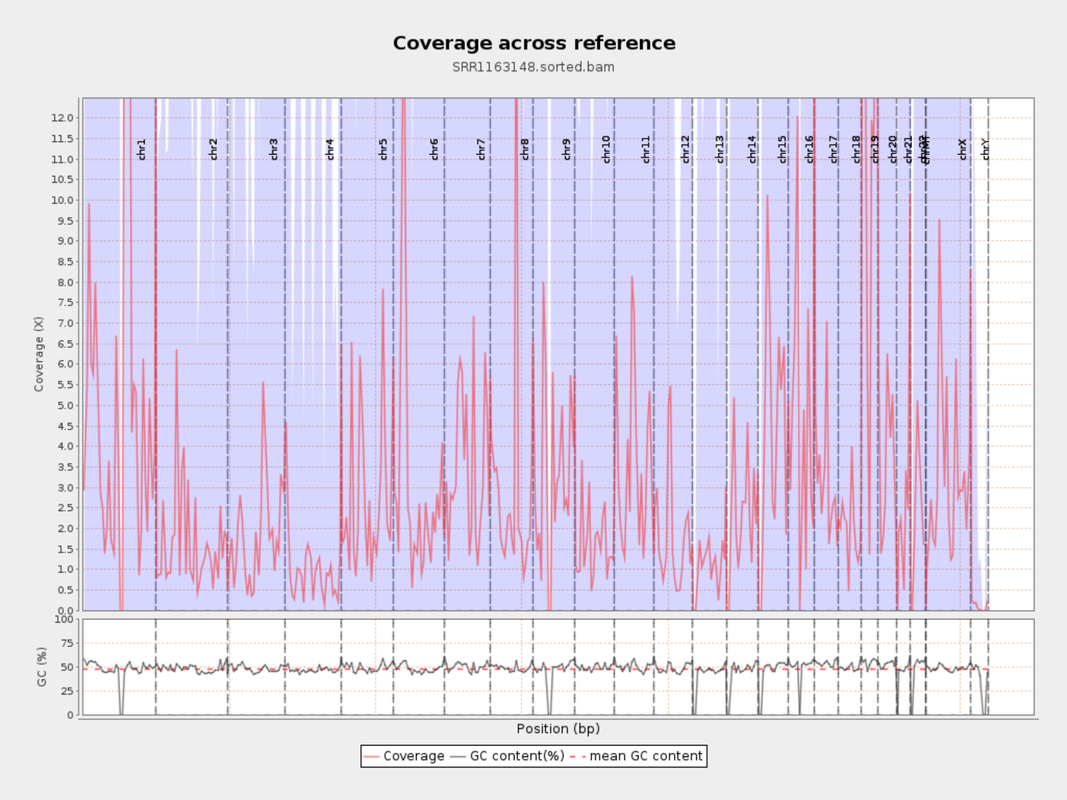
General error rate	0.38%
Mismatches	33,711,616
Insertions	584,855
Mapped reads with at least one insertion	0.6%
Deletions	488,263
Mapped reads with at least one deletion	0.5%
Homopolymer indels	45.91%

2.6. Chromosome stats

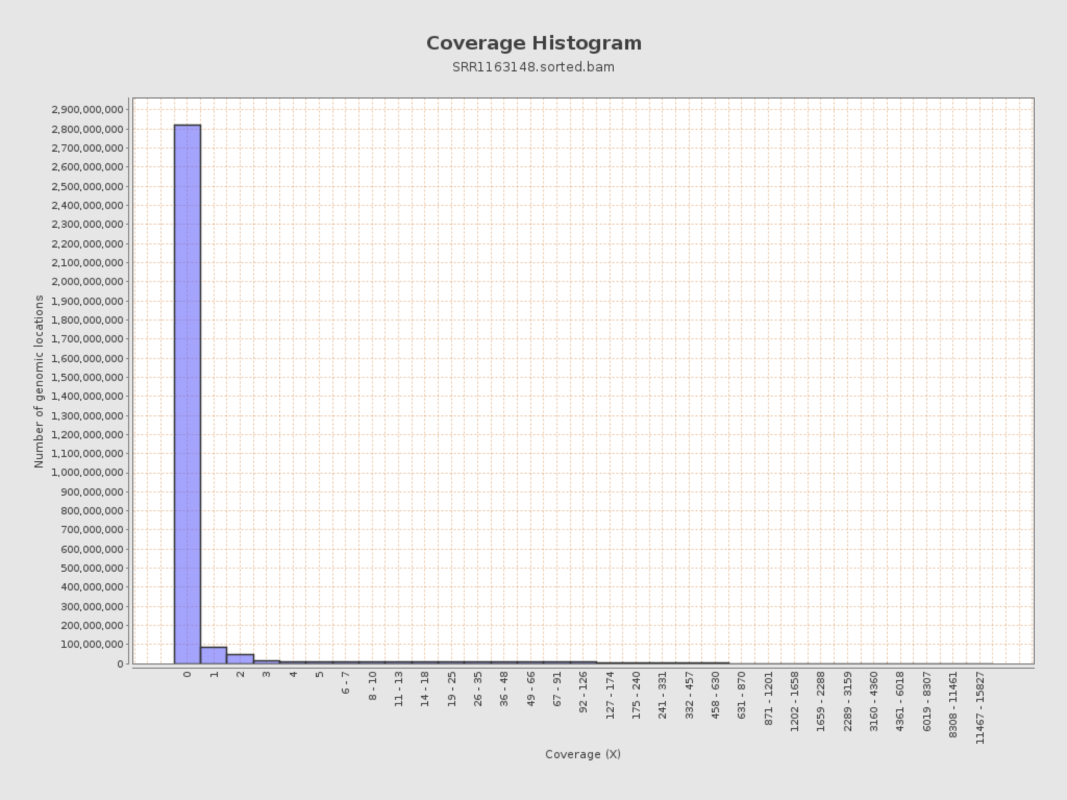
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1371140871	5.5011	52.315
chr2	243199373	401568495	1.6512	19.8549
chr3	198022430	369919335	1.8681	20.7116
chr4	191154276	189210450	0.9898	16.4188
chr5	180915260	513695830	2.8394	49.3828
chr6	171115067	537269085	3.1398	37.1158
chr7	159138663	559453071	3.5155	42.3715

chr8	146364022	441223297	3.0146	54.02
chr9	141213431	457653527	3.2409	35.1601
chr10	135534747	217932452	1.6079	25.3098
chr11	135006516	484529706	3.5889	32.8515
chr12	133851895	252164435	1.8839	20.4035
chr13	115169878	125657000	1.0911	16.9741
chr14	107349540	248245860	2.3125	23.83
chr15	102531392	440706815	4.2983	41.8169
chr16	90354753	392501776	4.344	38.6016
chr17	81195210	267761742	3.2978	27.2751
chr18	78077248	157461491	2.0167	25.4474
chr19	59128983	739480188	12.5062	95.8784
chr20	63025520	229891014	3.6476	36.9395
chr21	48129895	131691712	2.7362	57.6637
chr22	51304566	117395215	2.2882	29.0177
chrMT	16571	544	0.0328	0.2344
chrX	155270560	513624250	3.3079	37.873
chrY	59373566	6365000	0.1072	6.0283

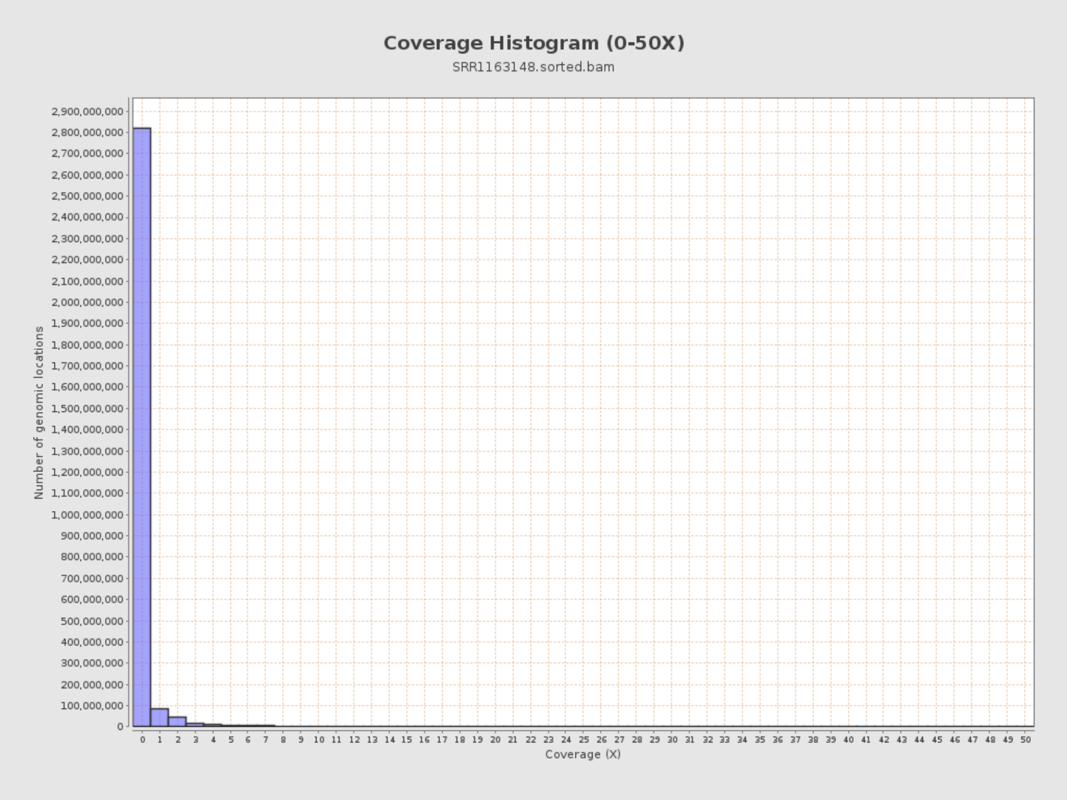
3. Results : Coverage across reference



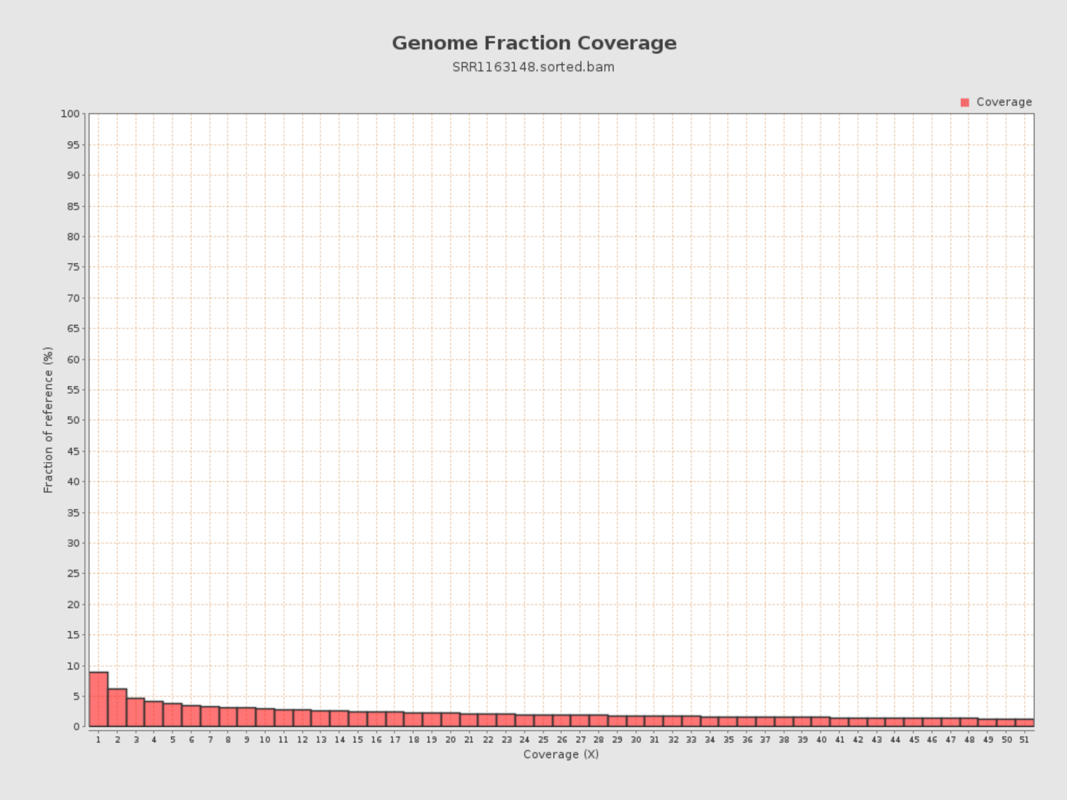
4. Results : Coverage Histogram



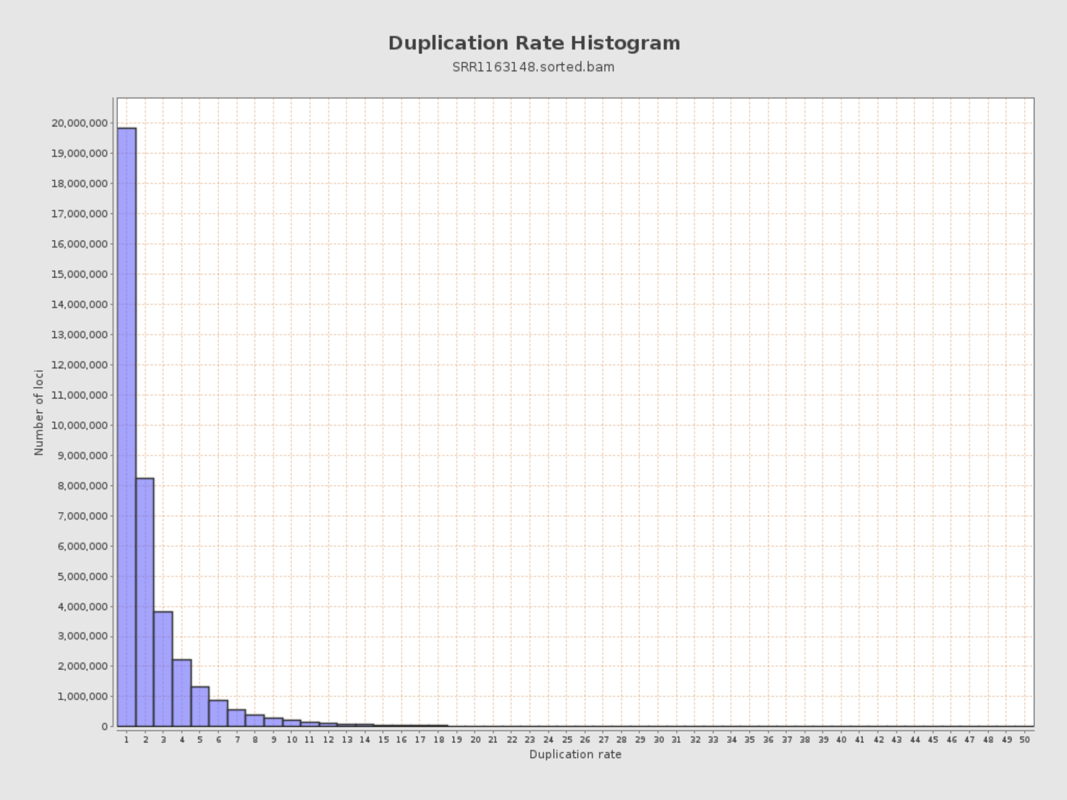
5. Results : Coverage Histogram (0-50X)



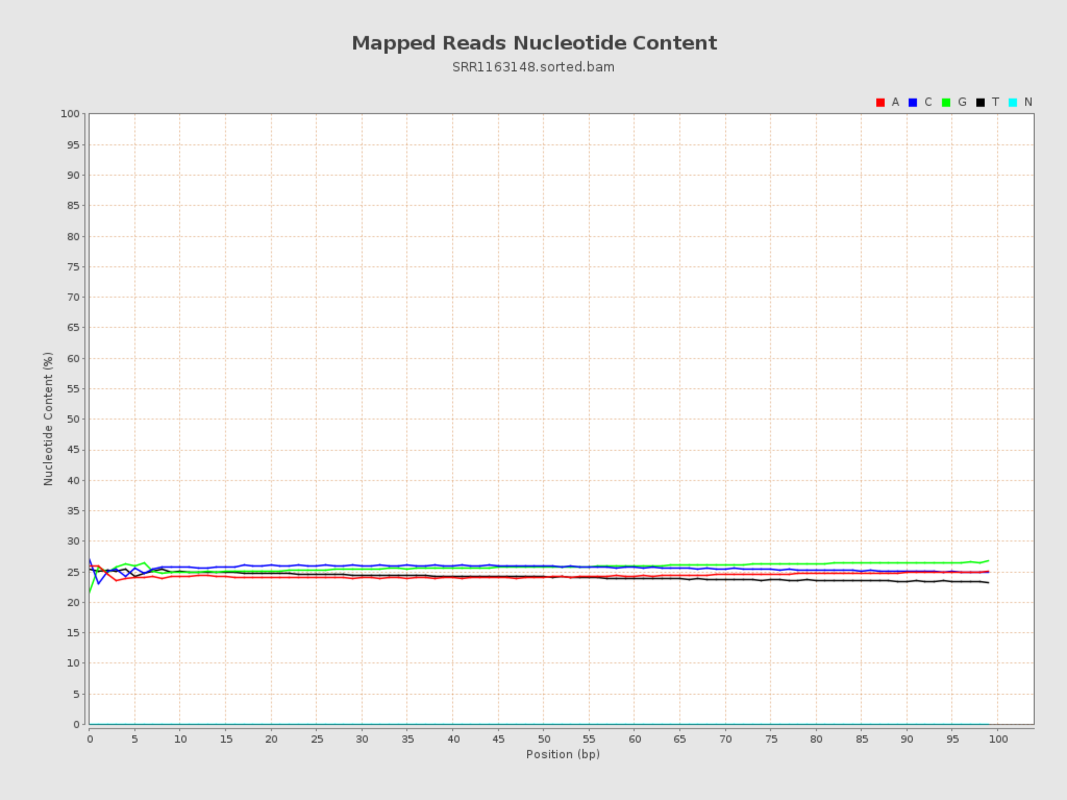
6. Results : Genome Fraction Coverage



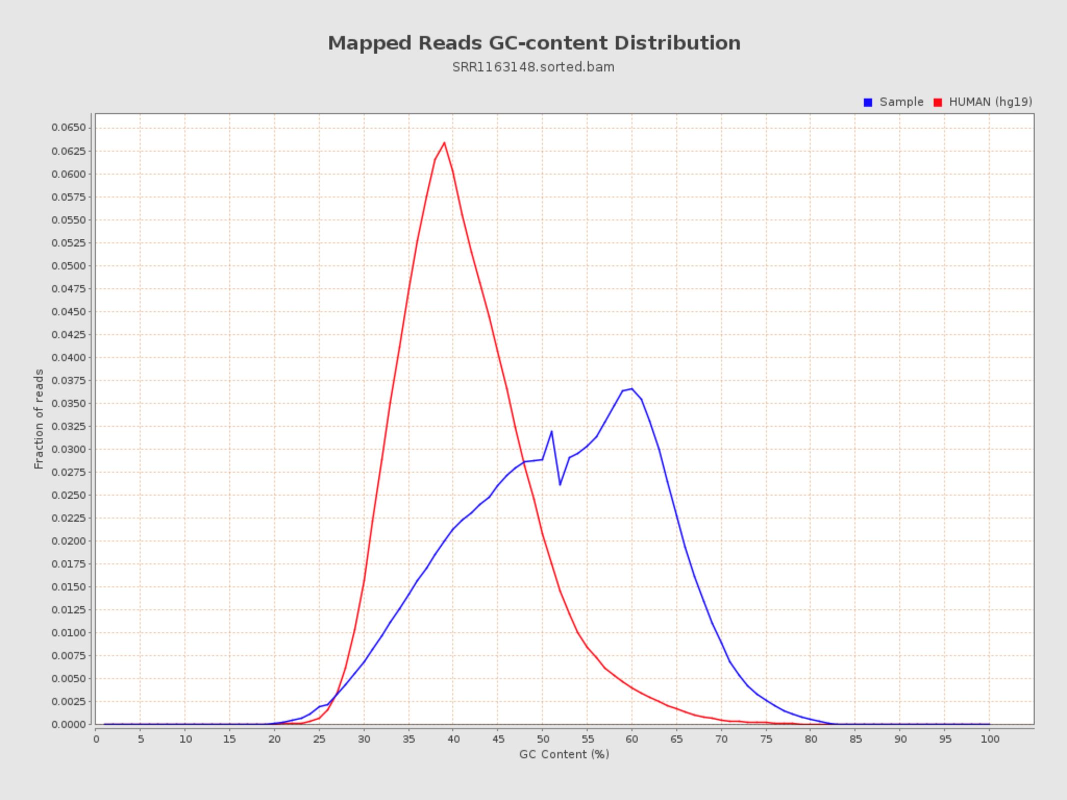
7. Results : Duplication Rate Histogram



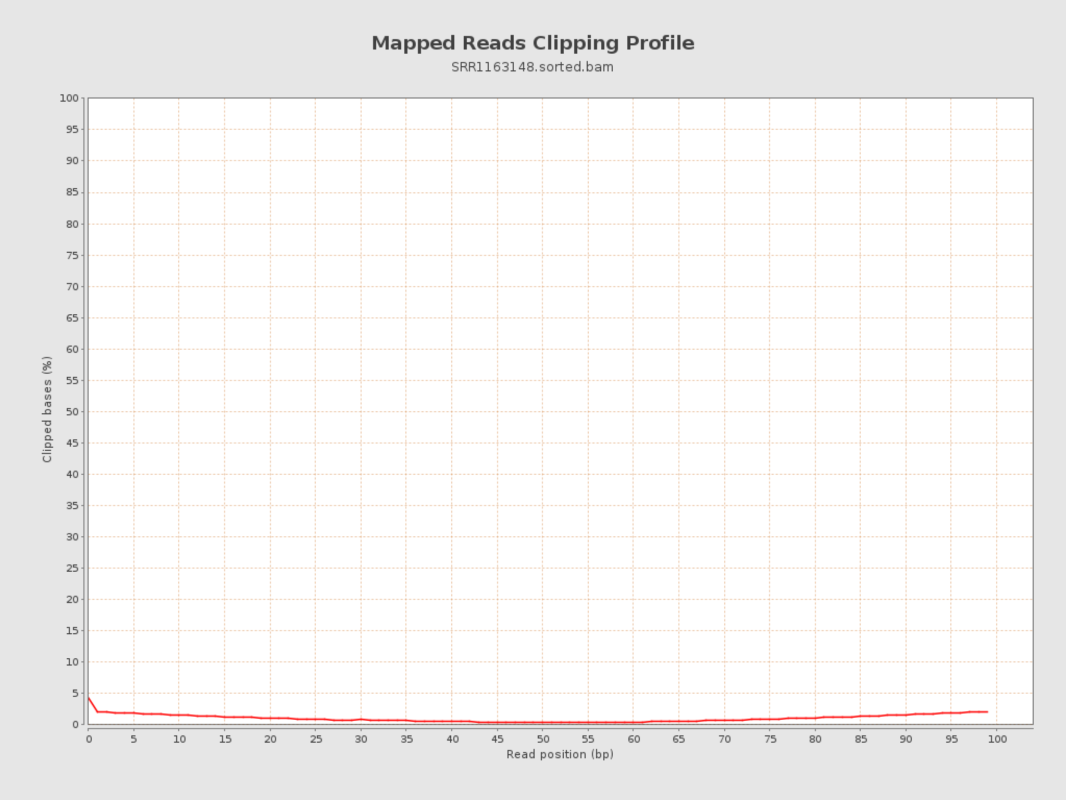
8. Results : Mapped Reads Nucleotide Content



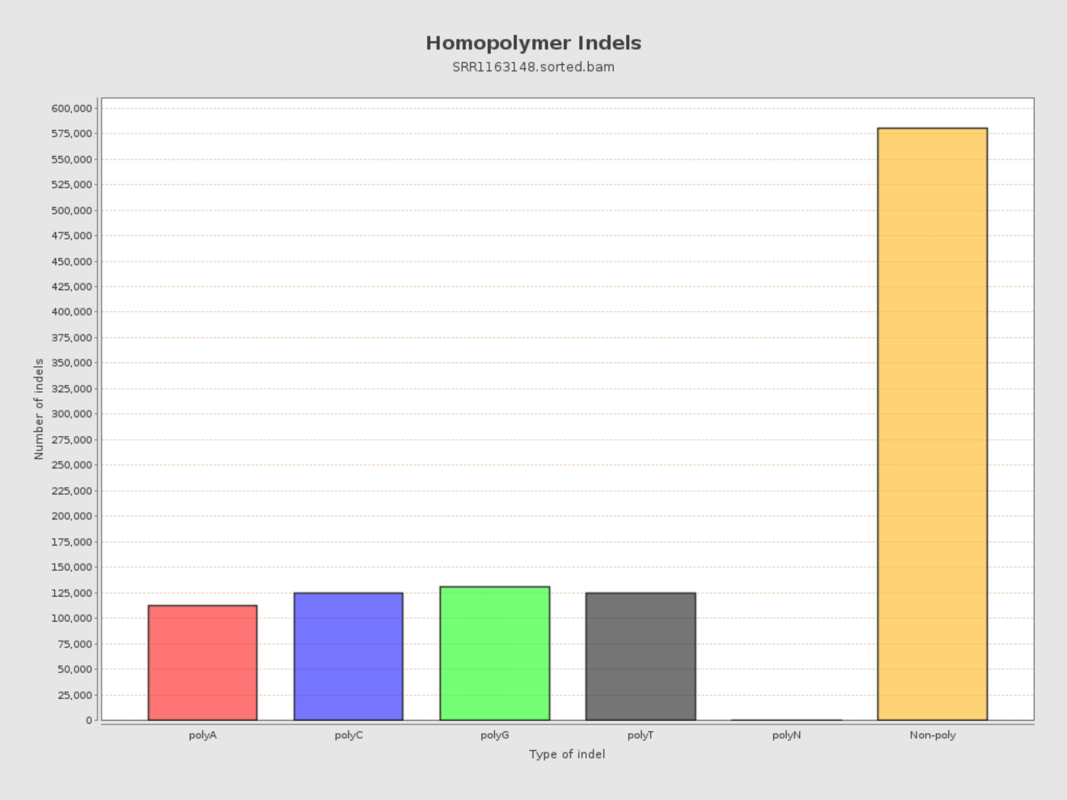
9. Results : Mapped Reads GC-content Distribution



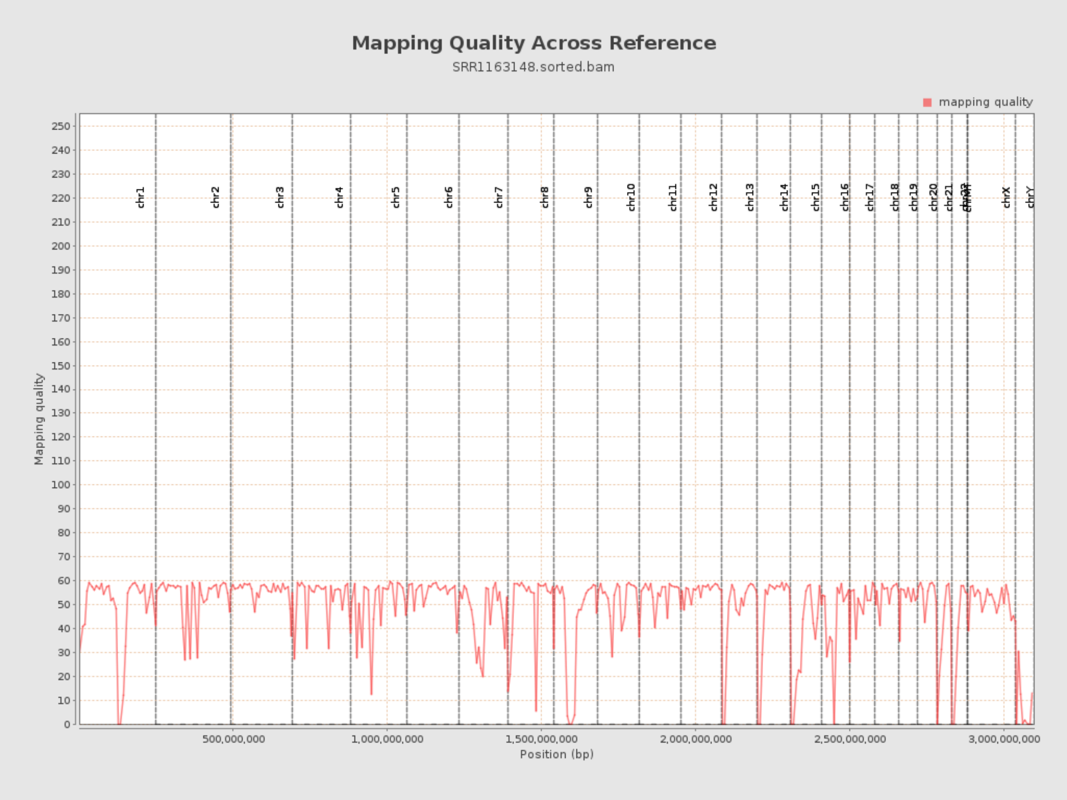
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram