Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/20 09:09:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR090159.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_SRR090159 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR090159.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Apr 20 09:09:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR090159.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,877,082
Mapped reads	17,885,237 / 81.75%
Unmapped reads	3,991,845 / 18.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,004 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	2,282,553 / 10.43%
Duplication rate	9.37%
Clipped reads	2,494,077 / 11.4%

2.2. ACGT Content

Number/percentage of A's	270,295,869 / 32.38%
Number/percentage of C's	163,509,411 / 19.59%
Number/percentage of T's	221,754,251 / 26.56%
Number/percentage of G's	179,139,114 / 21.46%
Number/percentage of N's	94,548 / 0.01%
GC Percentage	41.05%

2.3. Coverage

Mean	0.2697

Standard Deviation	1.7503

2.4. Mapping Quality

Mean Mapping Quality	43.53

2.5. Mismatches and indels

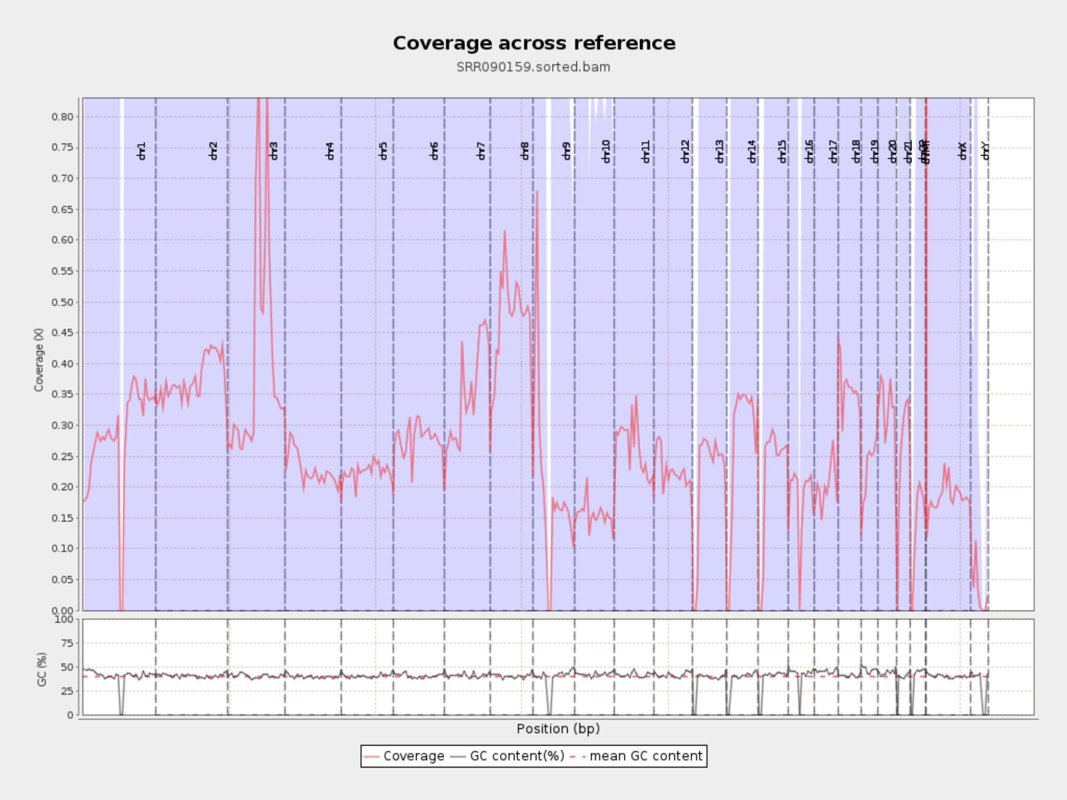
General error rate	0.45%
Mismatches	3,685,812
Insertions	35,533
Mapped reads with at least one insertion	0.2%
Deletions	111,988
Mapped reads with at least one deletion	0.62%
Homopolymer indels	45.07%

2.6. Chromosome stats

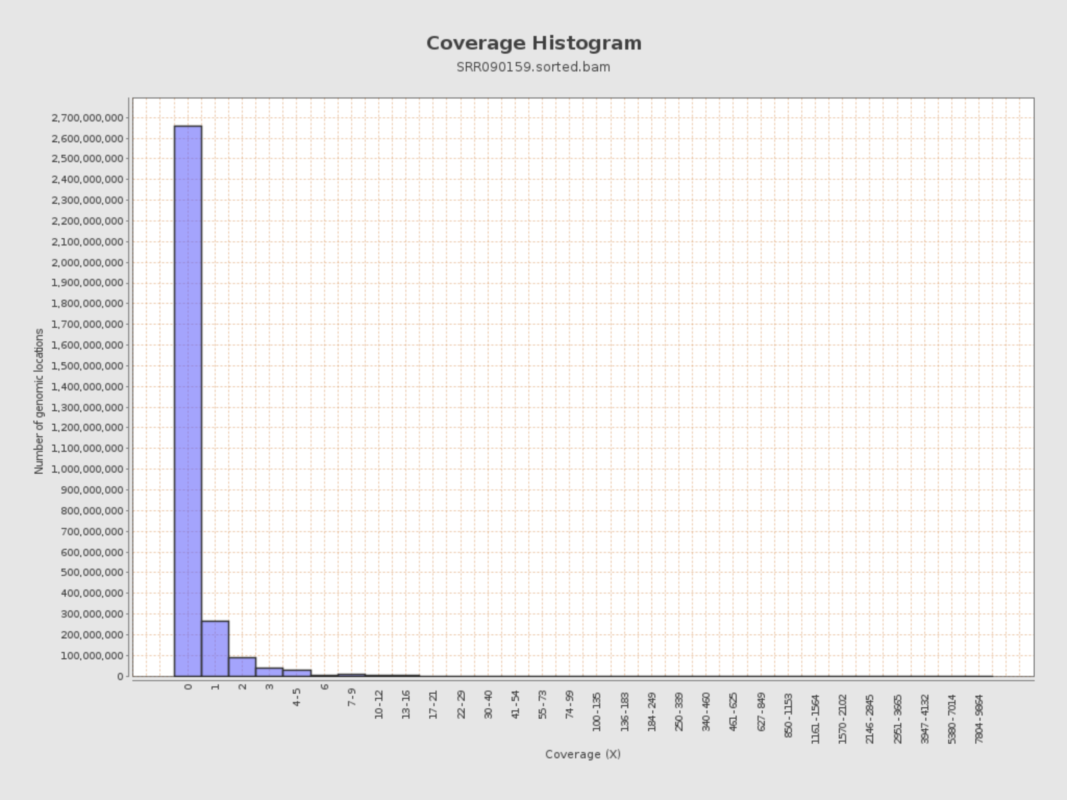
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	69969030	0.2807	1.8614
chr2	243199373	91271550	0.3753	1.607
chr3	198022430	79151544	0.3997	1.3114
chr4	191154276	43711427	0.2287	0.9069
chr5	180915260	40580221	0.2243	0.868
chr6	171115067	47762654	0.2791	1.0807
chr7	159138663	55733395	0.3502	2.4548

chr8	146364022	69003713	0.4715	5.4633
chr9	141213431	28180028	0.1996	1.0959
chr10	135534747	21009099	0.155	0.9278
chr11	135006516	35580294	0.2635	1.1688
chr12	133851895	30370706	0.2269	0.8845
chr13	115169878	24699768	0.2145	0.8618
chr14	107349540	29627189	0.276	1.037
chr15	102531392	21950086	0.2141	0.8576
chr16	90354753	16070792	0.1779	0.7913
chr17	81195210	16606087	0.2045	0.888
chr18	78077248	28161739	0.3607	1.6942
chr19	59128983	13916948	0.2354	1.457
chr20	63025520	20757043	0.3293	1.1227
chr21	48129895	12142904	0.2523	1.0663
chr22	51304566	6874133	0.134	0.6427
chrMT	16571	1244950	75.1282	54.9518
chrX	155270560	28550065	0.1839	0.8599
chrY	59373566	2037716	0.0343	1.0952

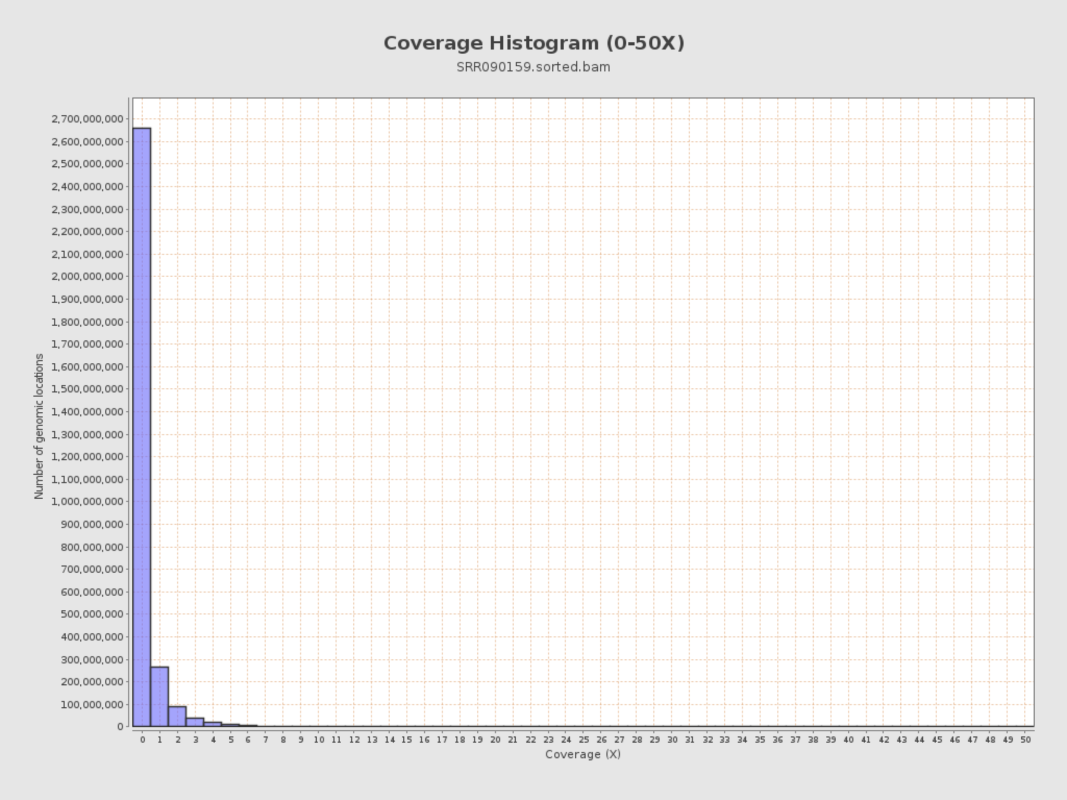
3. Results : Coverage across reference



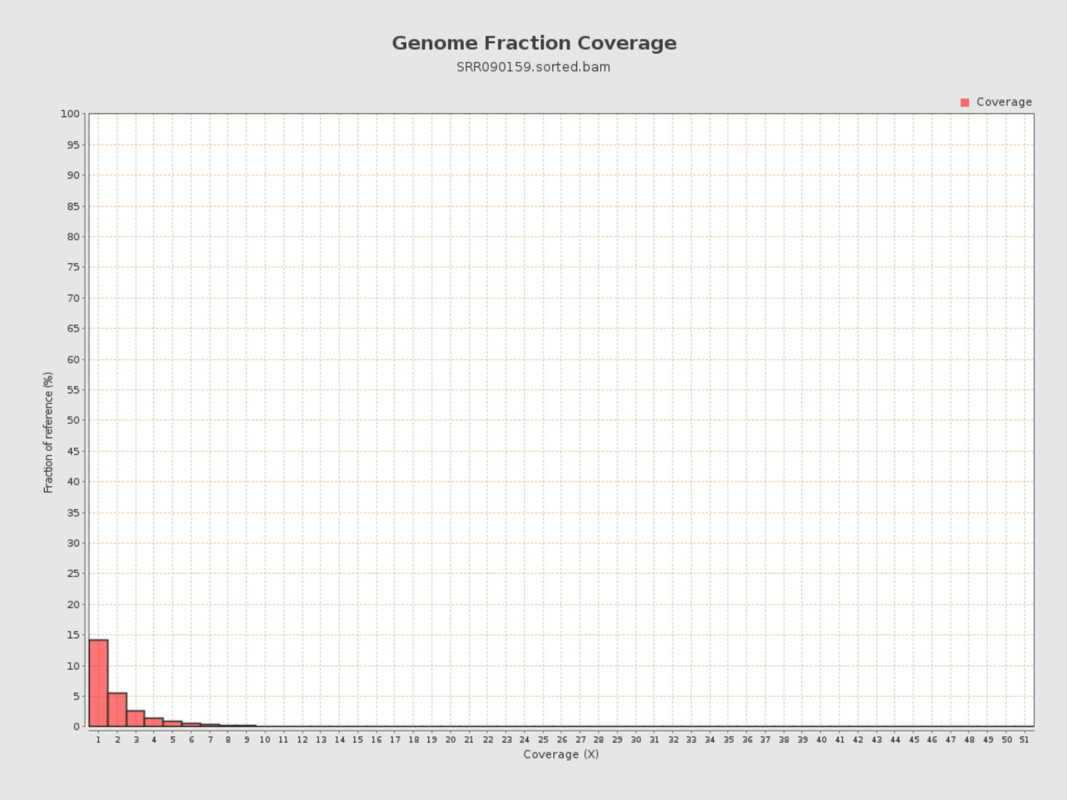
4. Results : Coverage Histogram



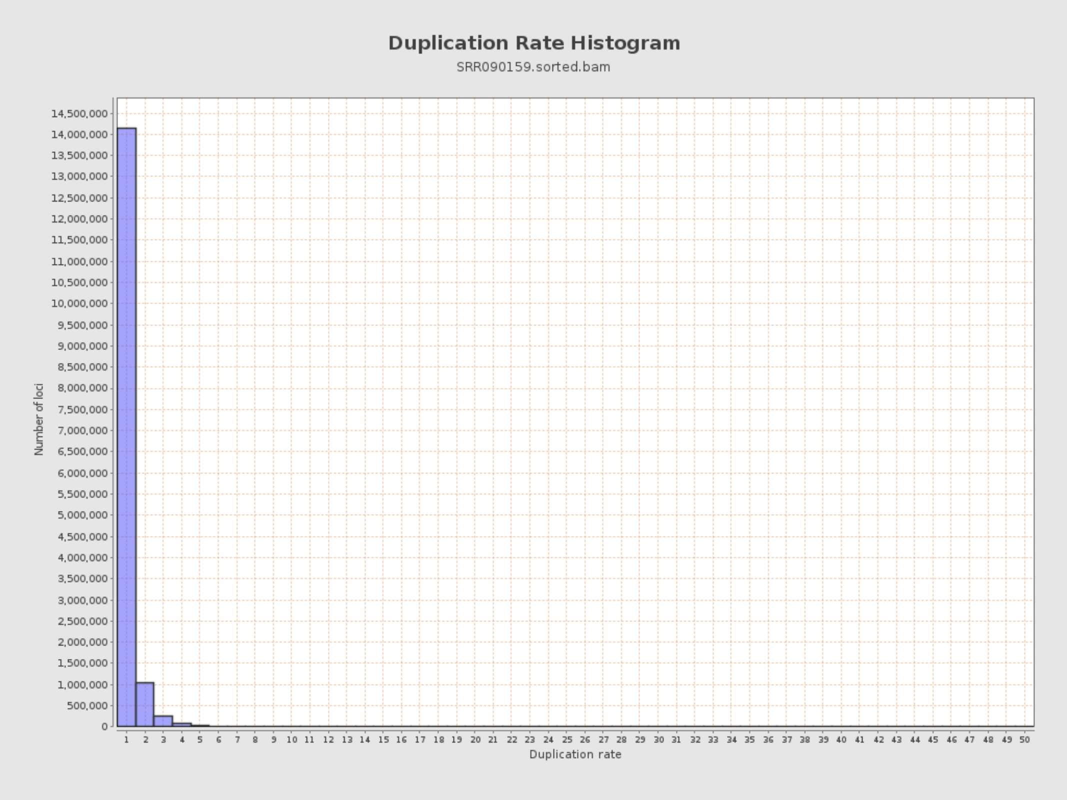
5. Results : Coverage Histogram (0-50X)



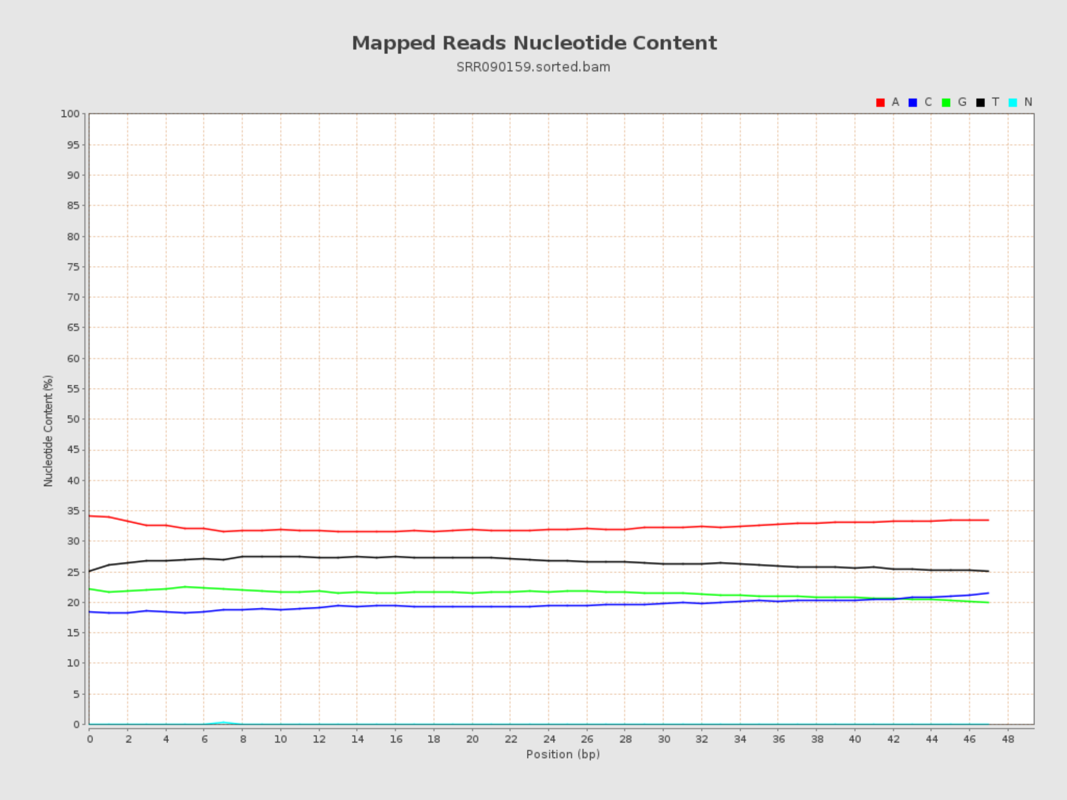
6. Results : Genome Fraction Coverage



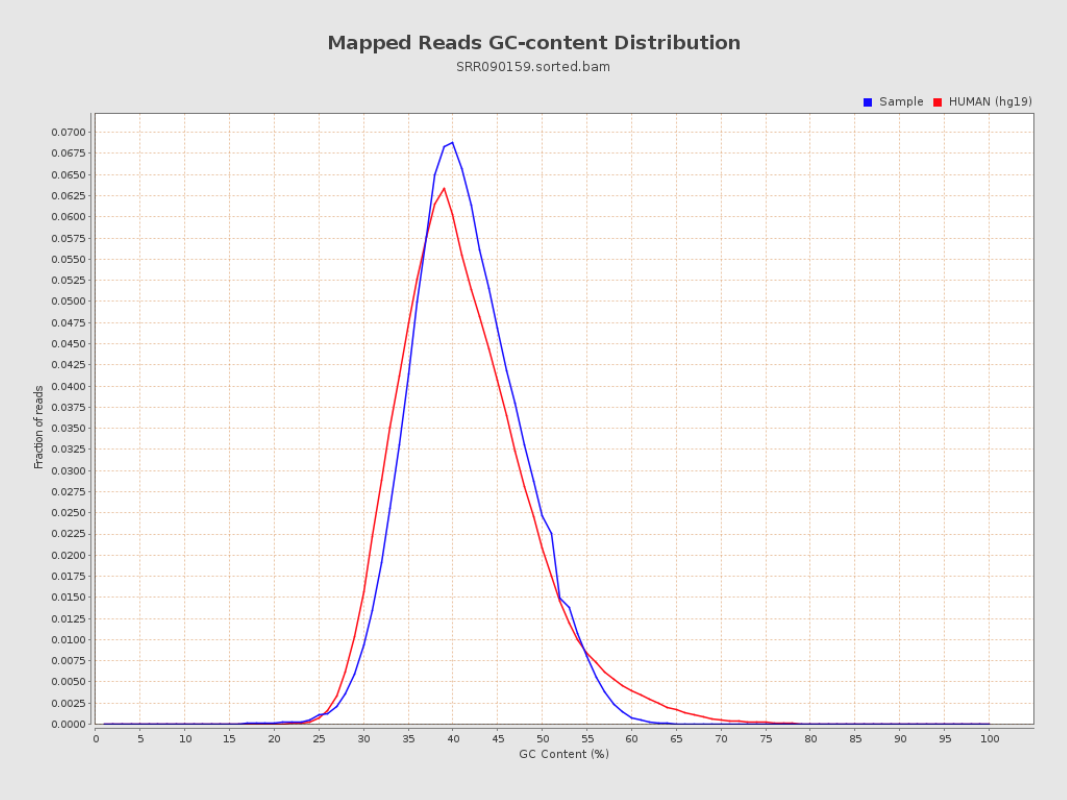
7. Results : Duplication Rate Histogram



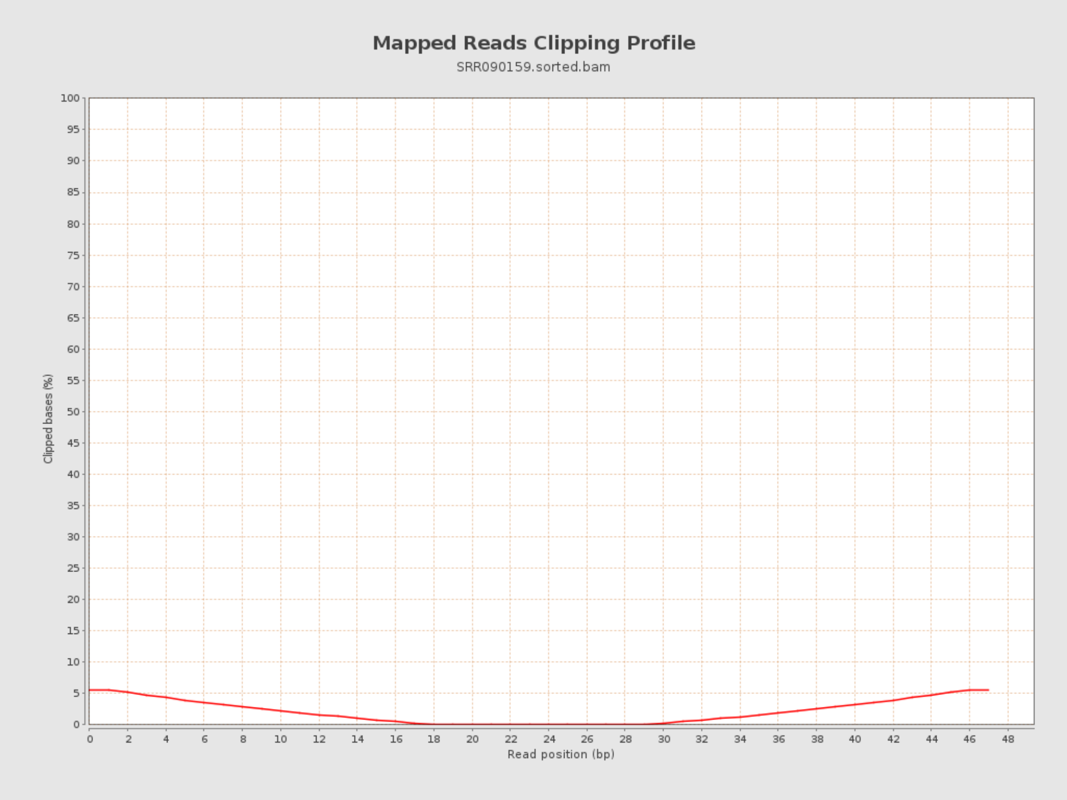
8. Results : Mapped Reads Nucleotide Content



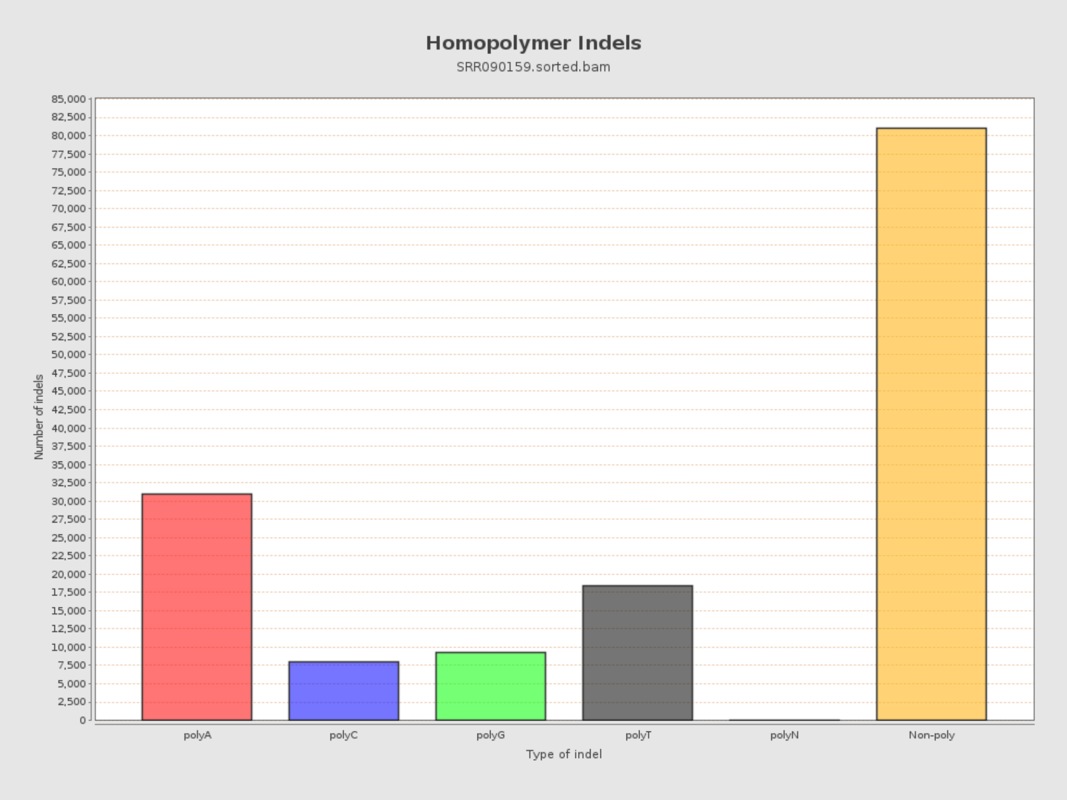
9. Results : Mapped Reads GC-content Distribution



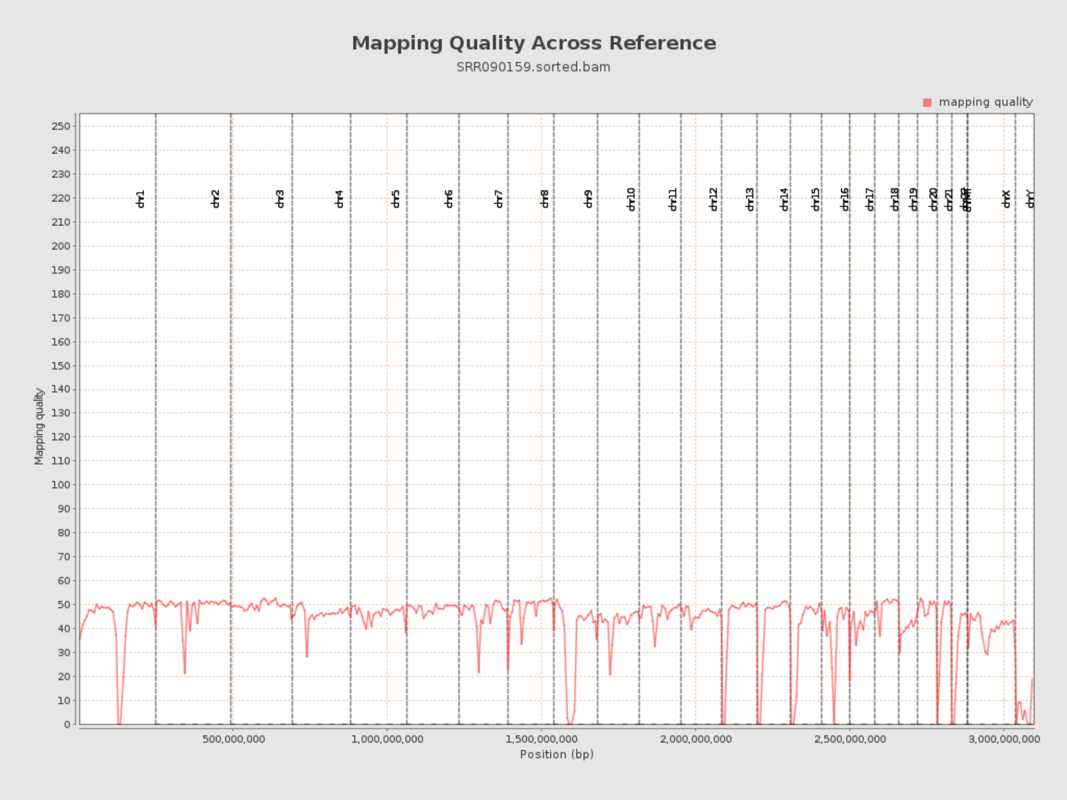
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram