

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/20 01:22:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1506125.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_SRR1506125 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1506125.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Dec 20 01:22:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1506125.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,656,556
Mapped reads	6,575,107 / 75.96%
Unmapped reads	2,081,449 / 24.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	102,803 / 1.19%
Read min/max/mean length	30 / 94 / 94.43
Duplicated reads (estimated)	1,129,026 / 13.04%
Duplication rate	11.6%
Clipped reads	3,948,940 / 45.62%

2.2. ACGT Content

Number/percentage of A's	141,638,867 / 27.38%
Number/percentage of C's	99,550,806 / 19.24%
Number/percentage of T's	141,980,295 / 27.44%
Number/percentage of G's	134,073,850 / 25.92%
Number/percentage of N's	90,027 / 0.02%
GC Percentage	45.16%

2.3. Coverage

Mean	0.1672

Standard Deviation	1.2111
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2.4. Mapping Quality

Mean Mapping Quality	46.66
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2.5. Mismatches and indels

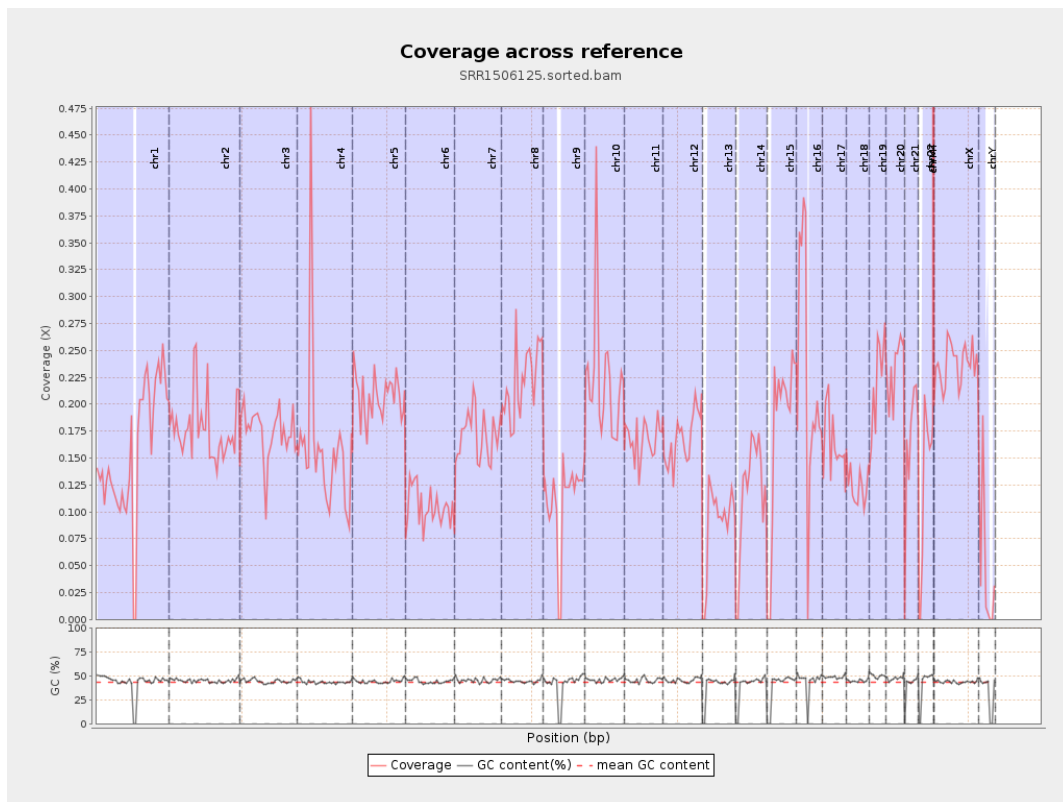
General error rate	0.79%
Mismatches	3,940,286
Insertions	49,327
Mapped reads with at least one insertion	0.73%
Deletions	106,019
Mapped reads with at least one deletion	1.57%
Homopolymer indels	40.46%

2.6. Chromosome stats

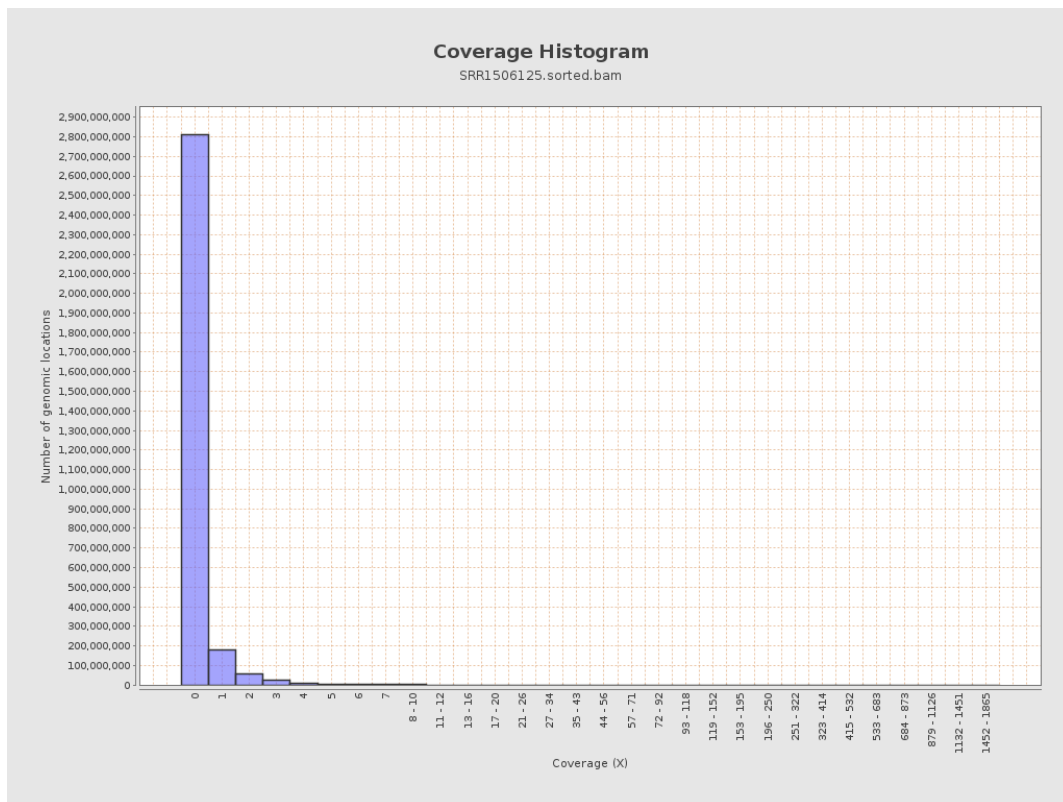
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	38813719	0.1557	1.6942
chr2	243199373	43022464	0.1769	1.416
chr3	198022430	34386663	0.1737	0.6992
chr4	191154276	29965883	0.1568	1.5345
chr5	180915260	37377902	0.2066	0.7787
chr6	171115067	17842495	0.1043	0.5759
chr7	159138663	27245956	0.1712	1.3323

chr8	146364022	32523317	0.2222	1.2106
chr9	141213431	15409763	0.1091	1.0917
chr10	135534747	30047528	0.2217	2.0335
chr11	135006516	22541329	0.167	1.0973
chr12	133851895	22449546	0.1677	0.7174
chr13	115169878	10273102	0.0892	0.4908
chr14	107349540	12663977	0.118	0.6795
chr15	102531392	18230447	0.1778	0.7319
chr16	90354753	20523255	0.2271	1.0989
chr17	81195210	13079257	0.1611	0.8875
chr18	78077248	9630759	0.1233	1.6775
chr19	59128983	13047065	0.2207	1.3972
chr20	63025520	14664095	0.2327	0.9765
chr21	48129895	7977033	0.1657	1.208
chr22	51304566	6309542	0.123	0.7017
chrMT	16571	99289	5.9917	6.436
chrX	155270560	36847879	0.2373	0.9563
chrY	59373566	2593753	0.0437	1.9334

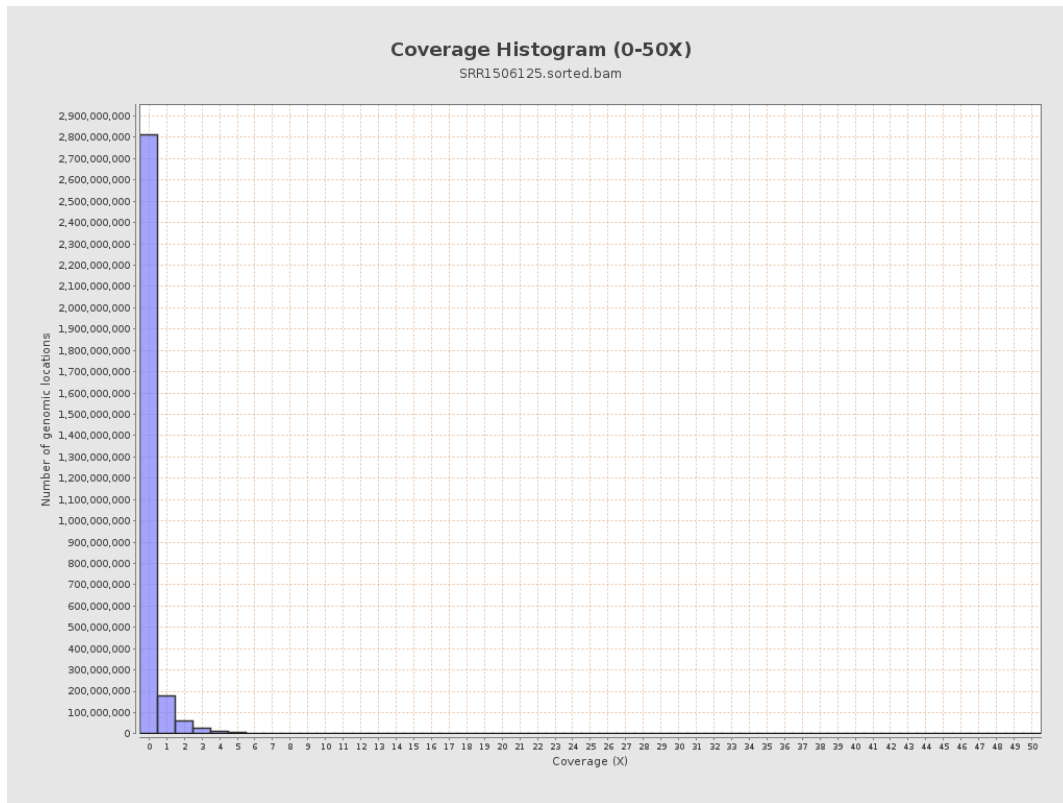
3. Results : Coverage across reference



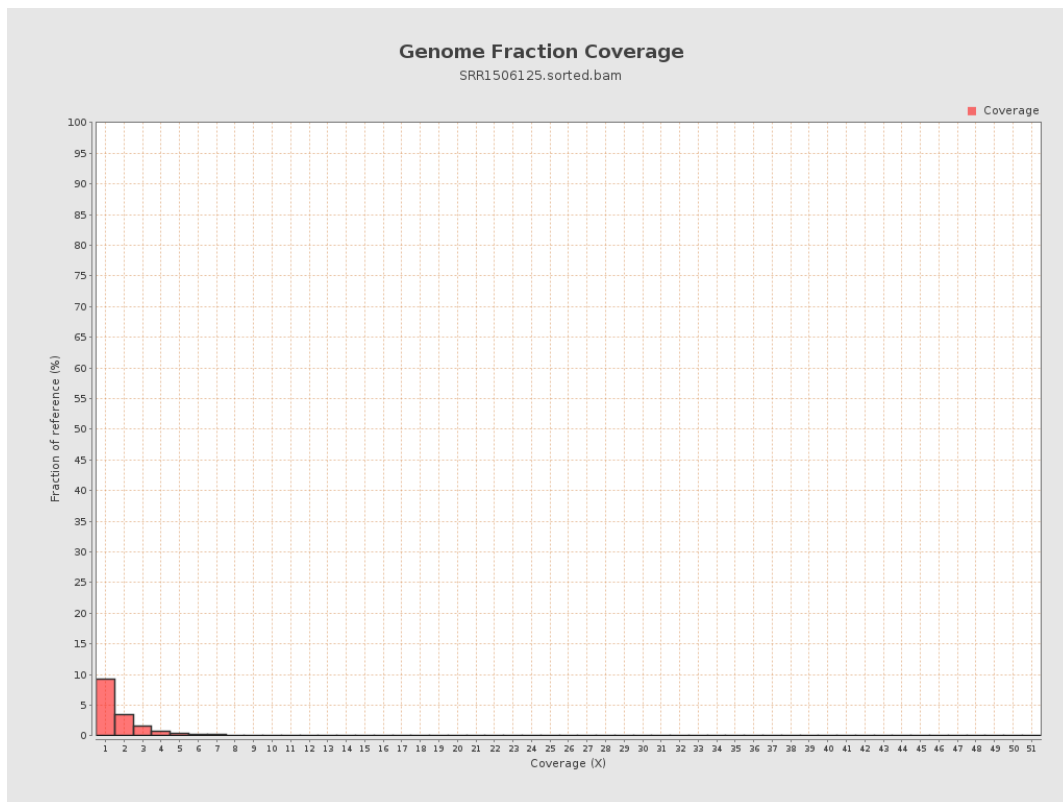
4. Results : Coverage Histogram



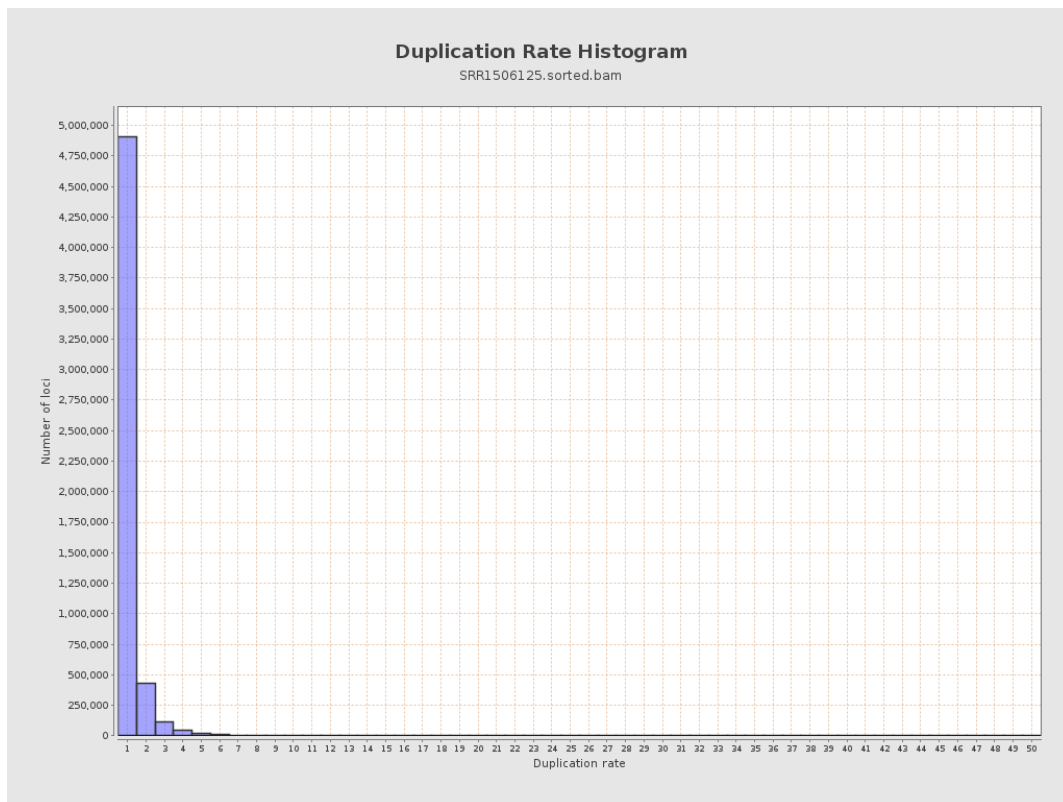
5. Results : Coverage Histogram (0-50X)



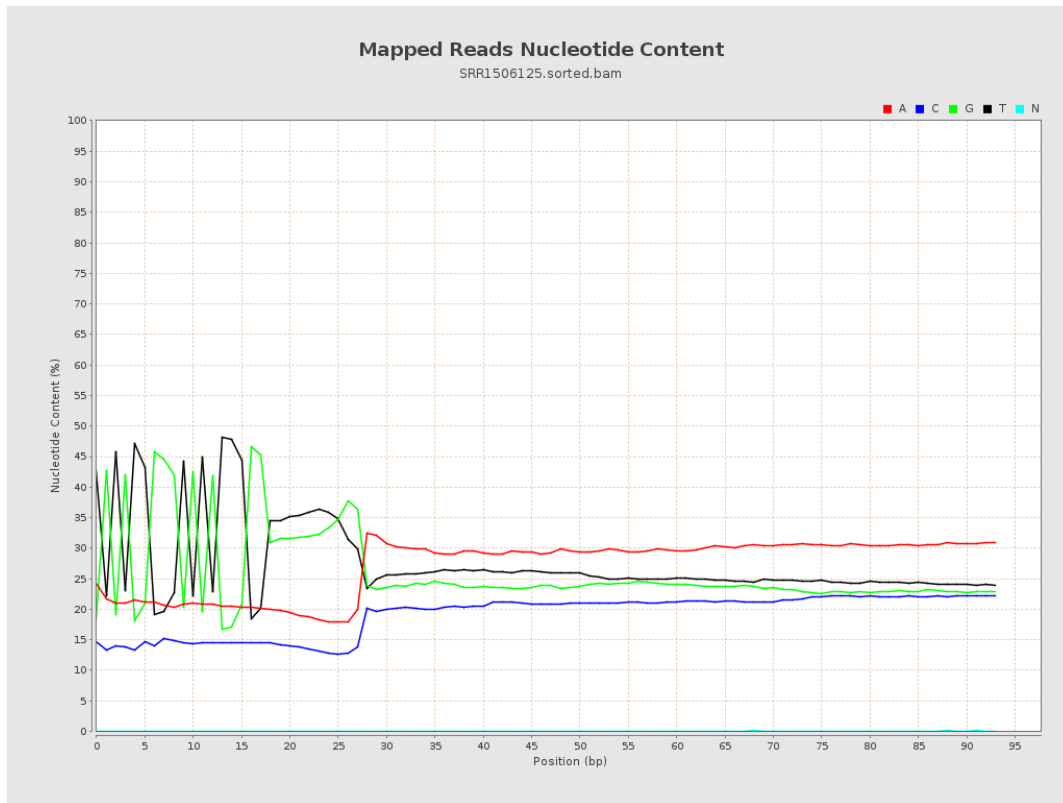
6. Results : Genome Fraction Coverage



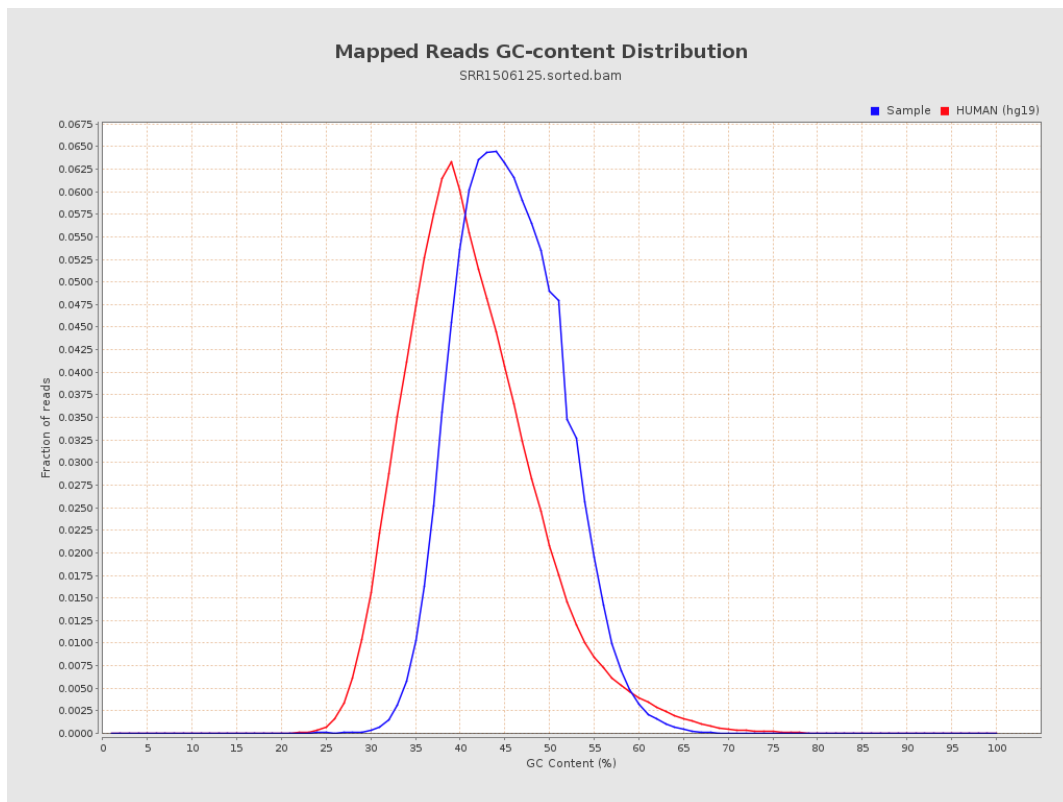
7. Results : Duplication Rate Histogram



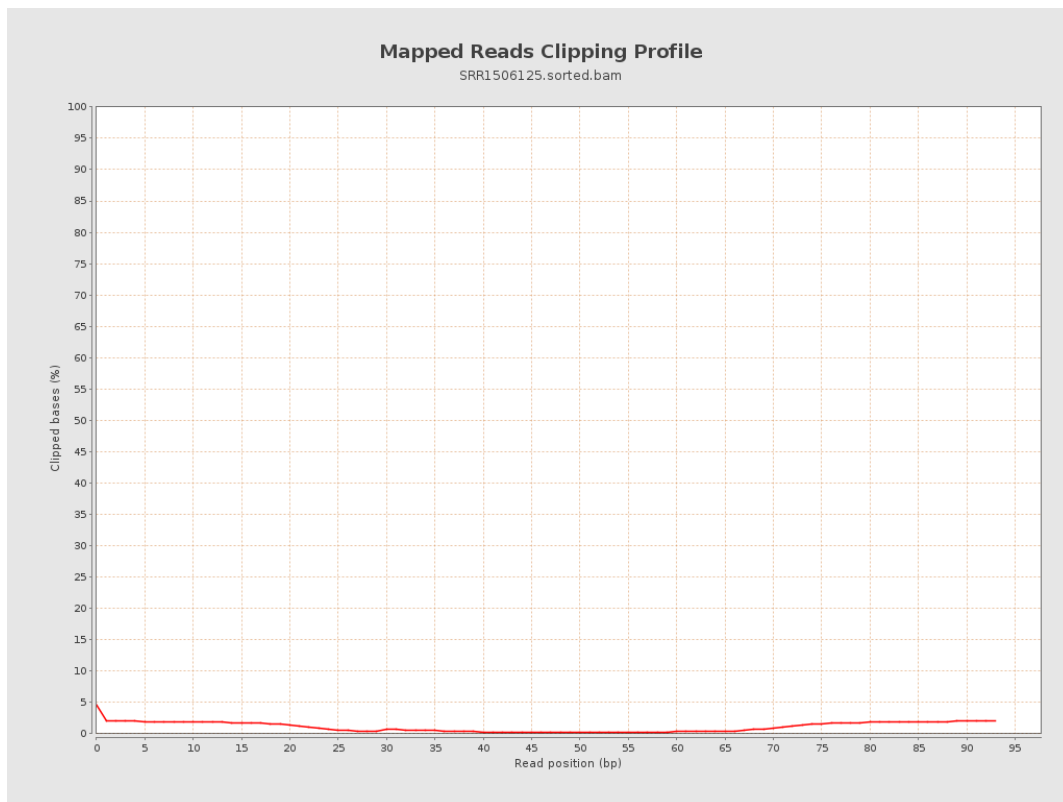
8. Results : Mapped Reads Nucleotide Content



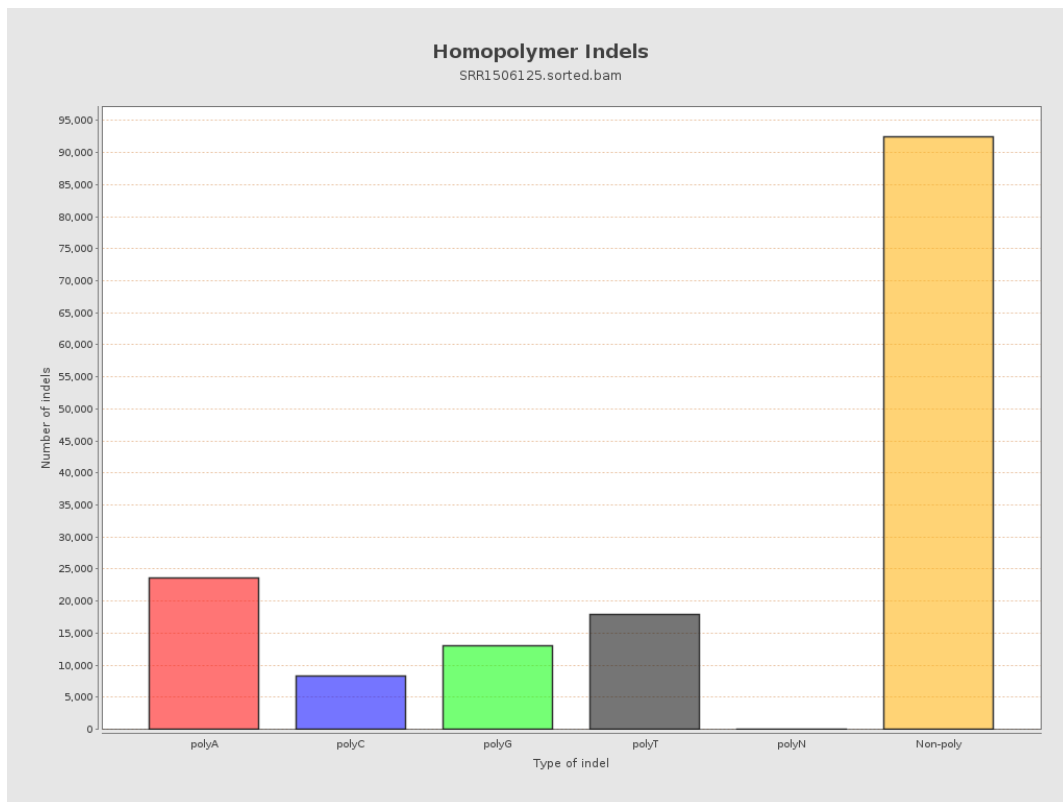
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

