

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:37:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124788.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_SRR3124788 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124788.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:37:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124788.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	679,163
Mapped reads	677,878 / 99.81%
Unmapped reads	1,285 / 0.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	319,494 / 47.04%
Read min/max/mean length	30 / 151 / 182.02
Duplicated reads (estimated)	984,002 / 144.88%
Duplication rate	2.84%
Clipped reads	669,702 / 98.61%

2.2. ACGT Content

Number/percentage of A's	28,136,871 / 27.86%
Number/percentage of C's	17,307,876 / 17.14%
Number/percentage of T's	34,353,774 / 34.02%
Number/percentage of G's	21,178,641 / 20.97%
Number/percentage of N's	0 / 0%
GC Percentage	38.11%

2.3. Coverage

Mean	0.0326

Standard Deviation	100.7518
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2.4. Mapping Quality

Mean Mapping Quality	50.19
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2.5. Mismatches and indels

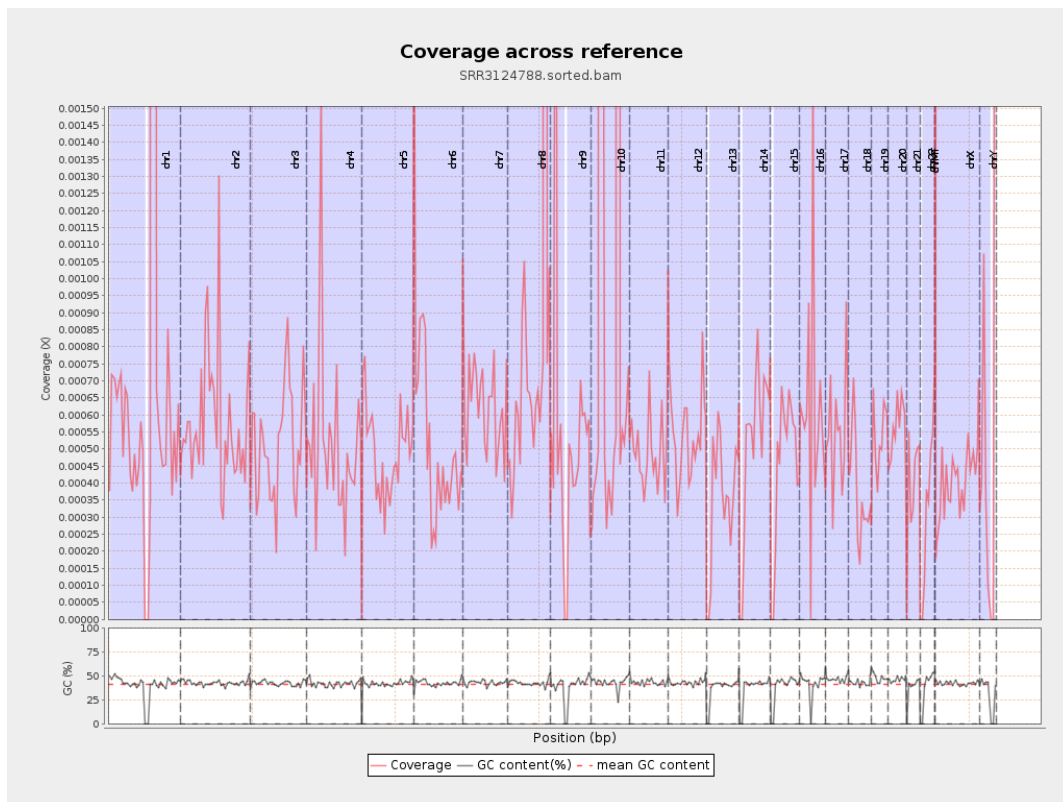
General error rate	0.79%
Mismatches	789,525
Insertions	7,140
Mapped reads with at least one insertion	1.05%
Deletions	32,801
Mapped reads with at least one deletion	4.79%
Homopolymer indels	53.57%

2.6. Chromosome stats

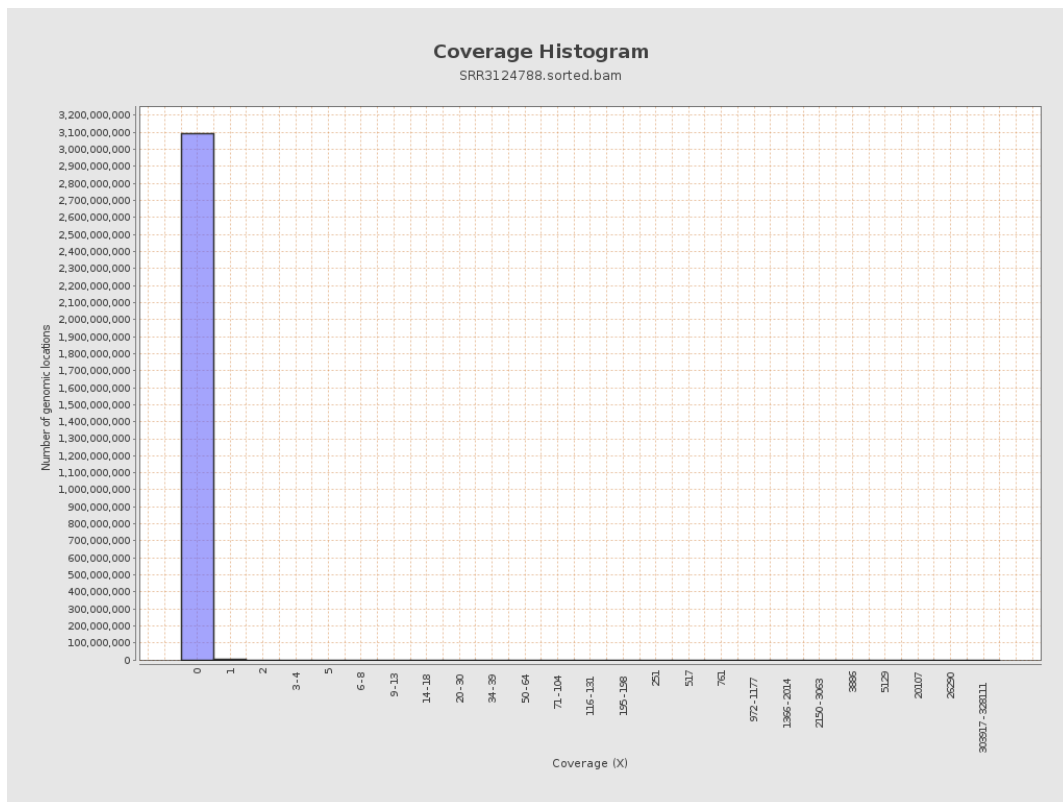
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1193870	0.0048	3.0977
chr2	243199373	140935	0.0006	0.0271
chr3	198022430	102129	0.0005	0.0242
chr4	191154276	97186	0.0005	0.0273
chr5	180915260	88757	0.0005	0.0229
chr6	171115067	90437	0.0005	0.0879
chr7	159138663	99977	0.0006	0.0253

chr8	146364022	911795	0.0062	3.846
chr9	141213431	79280	0.0006	0.0958
chr10	135534747	97592233	0.7201	481.4759
chr11	135006516	66492	0.0005	0.0303
chr12	133851895	73135	0.0005	0.0235
chr13	115169878	41276	0.0004	0.0191
chr14	107349540	55863	0.0005	0.0238
chr15	102531392	46024	0.0004	0.0216
chr16	90354753	56605	0.0006	0.0271
chr17	81195210	44761	0.0006	0.0259
chr18	78077248	28751	0.0004	0.0197
chr19	59128983	31152	0.0005	0.0232
chr20	63025520	35449	0.0006	0.024
chr21	48129895	19019	0.0004	0.0202
chr22	51304566	16092	0.0003	0.018
chrMT	16571	761	0.0459	0.227
chrX	155270560	62195	0.0004	0.0205
chrY	59373566	37310	0.0006	0.0303

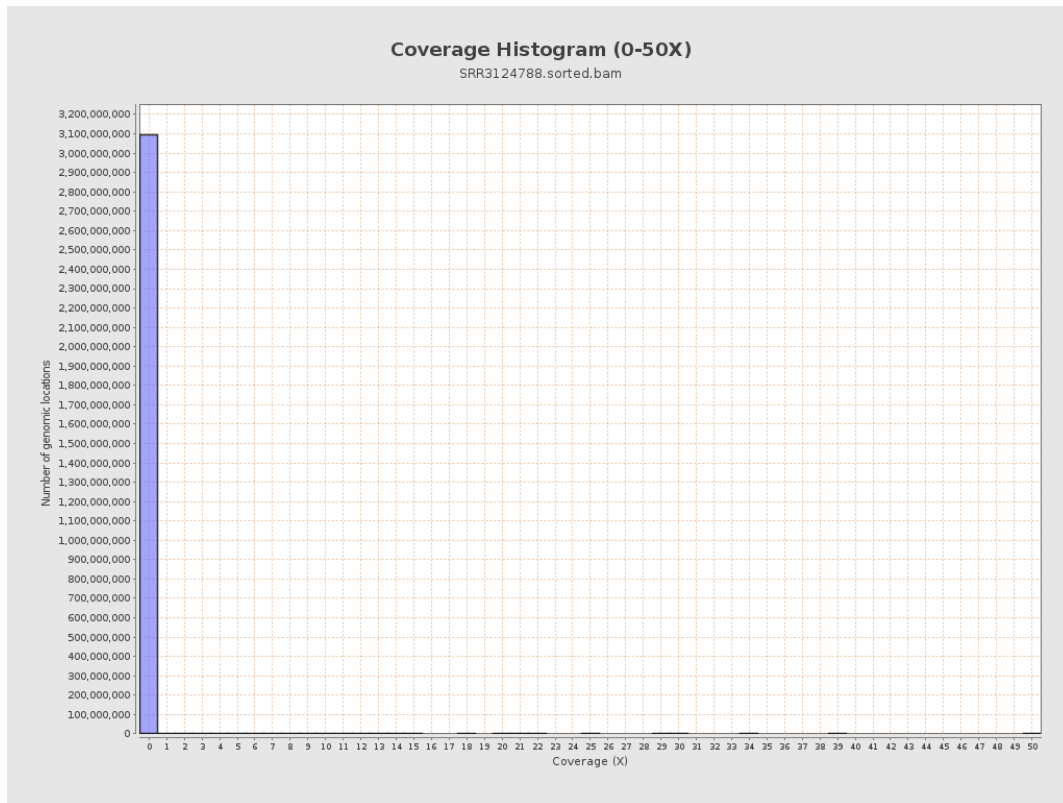
3. Results : Coverage across reference



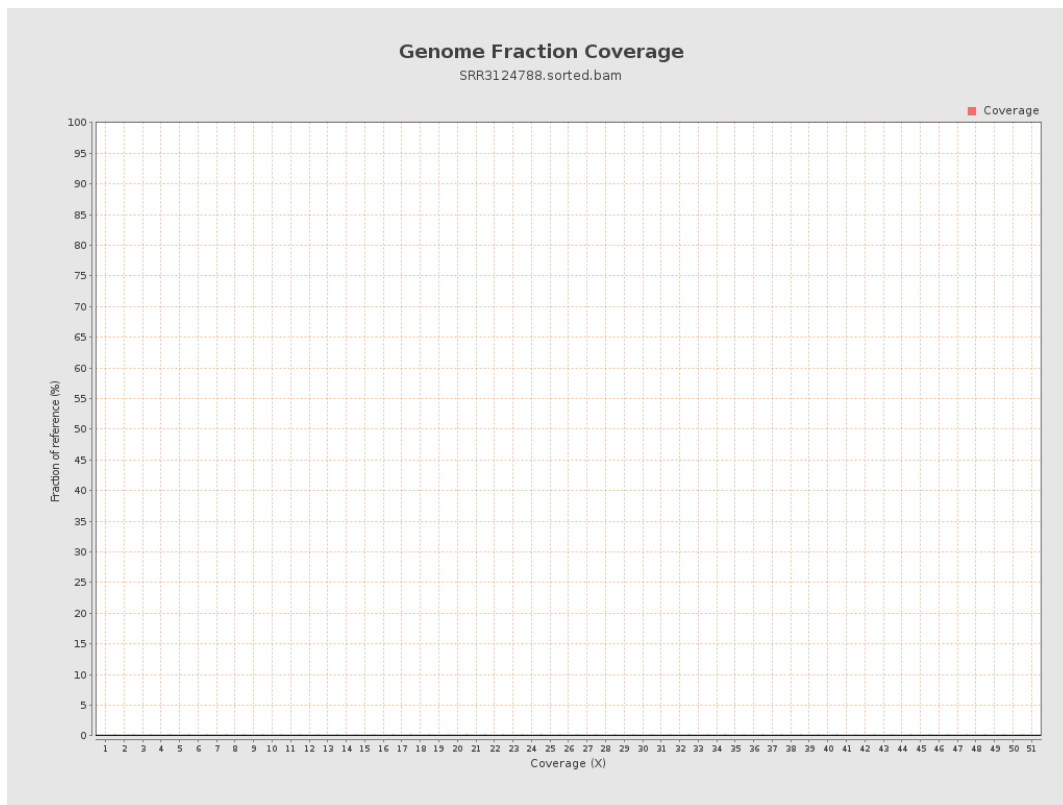
4. Results : Coverage Histogram



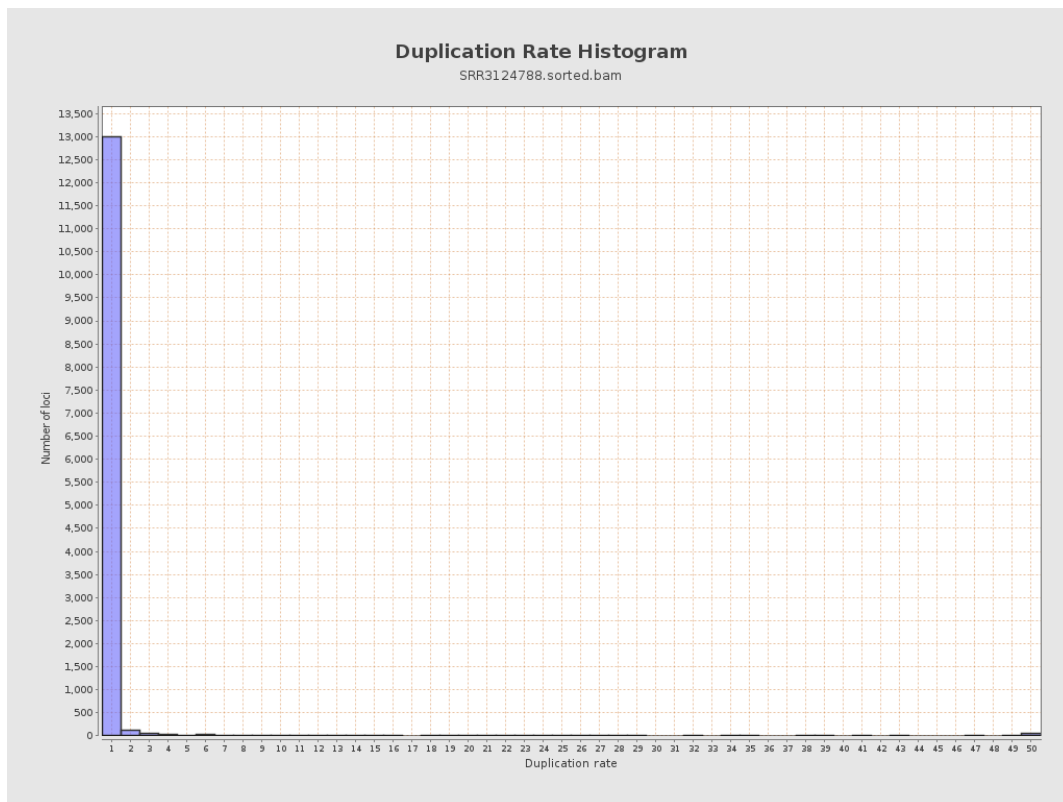
5. Results : Coverage Histogram (0-50X)



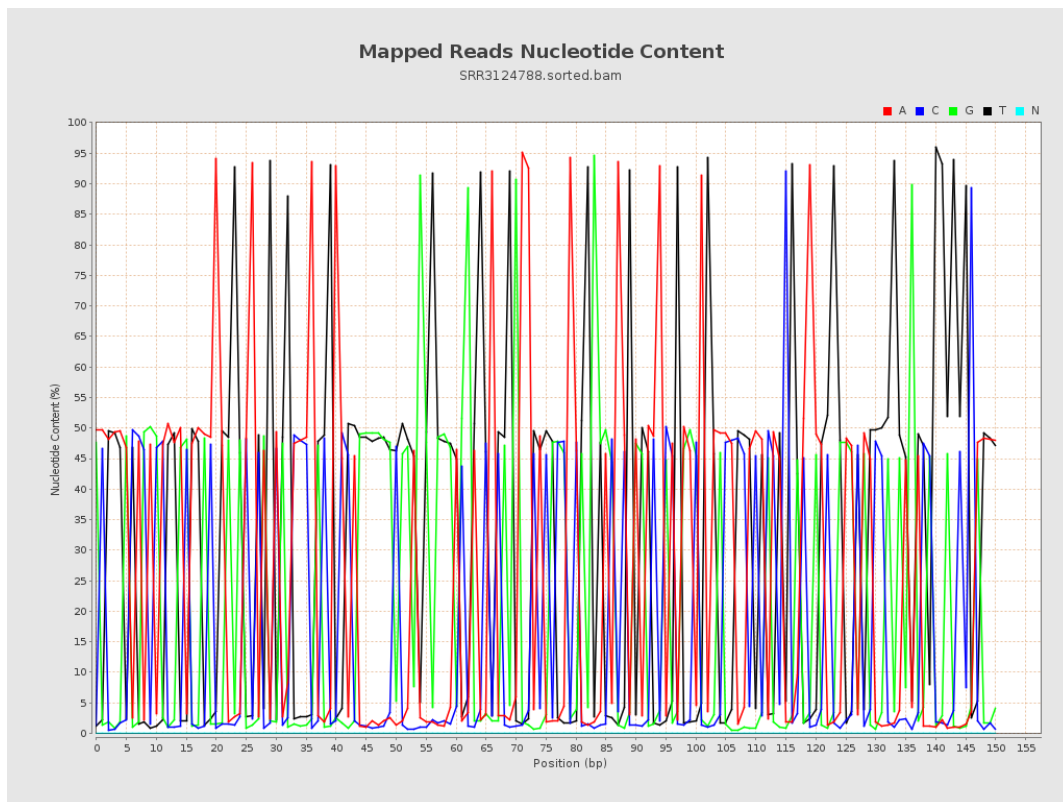
6. Results : Genome Fraction Coverage



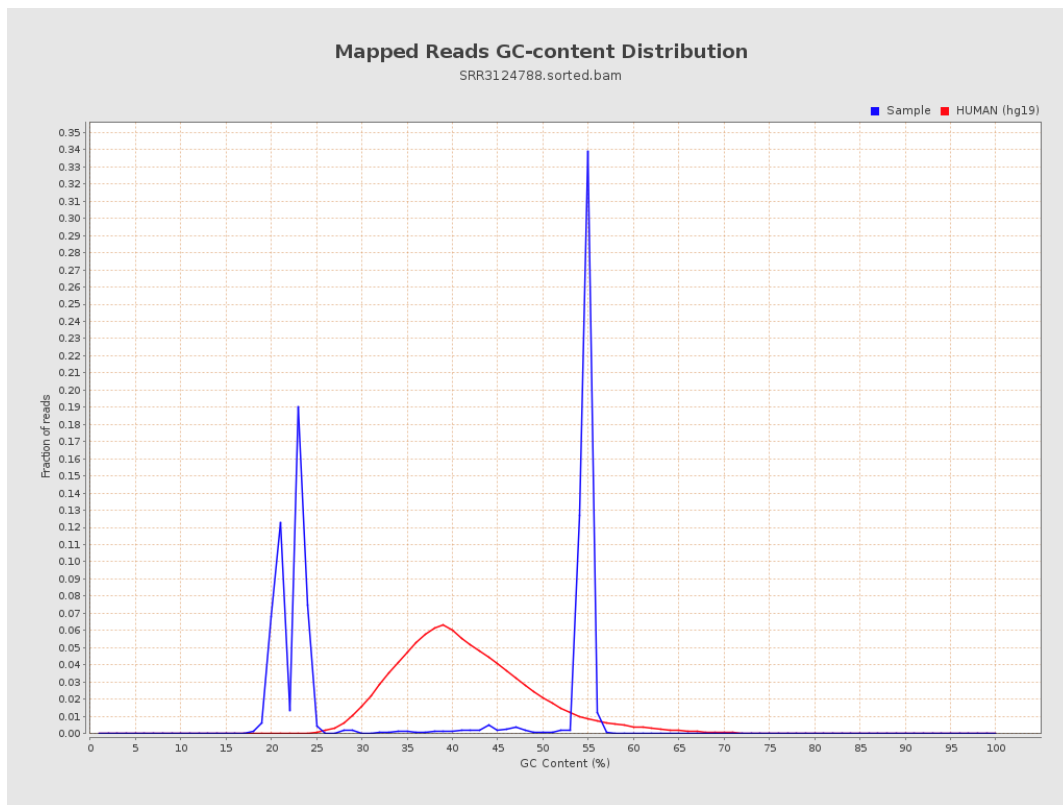
7. Results : Duplication Rate Histogram



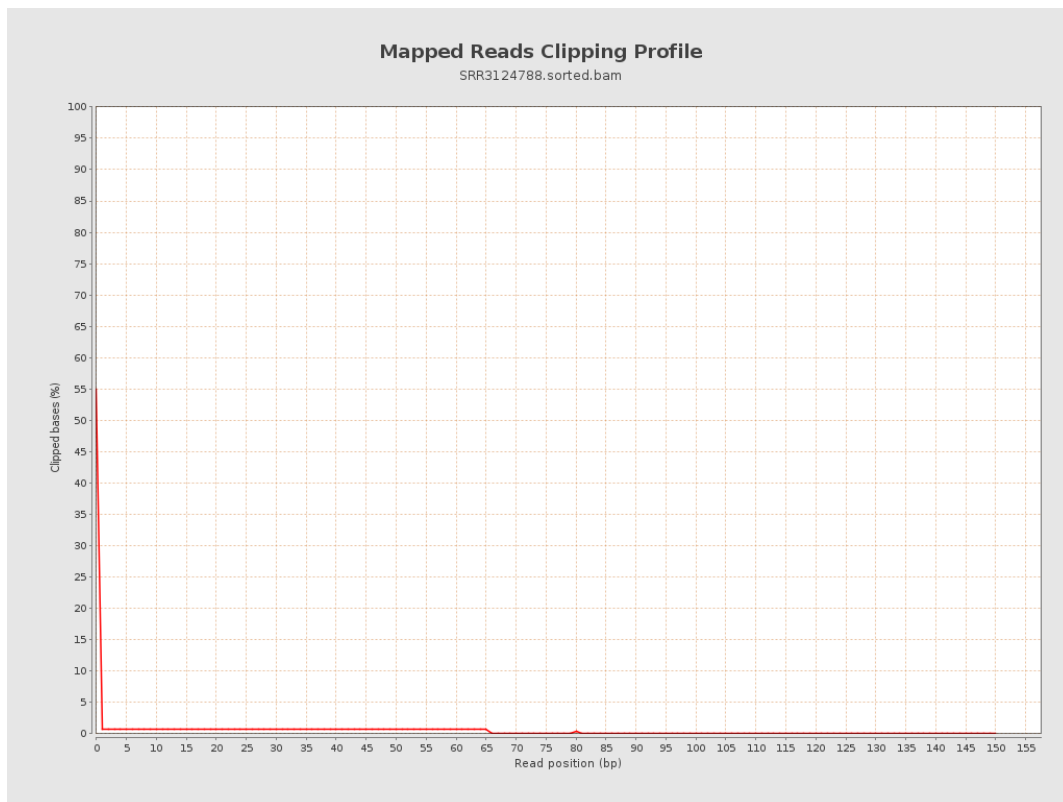
8. Results : Mapped Reads Nucleotide Content



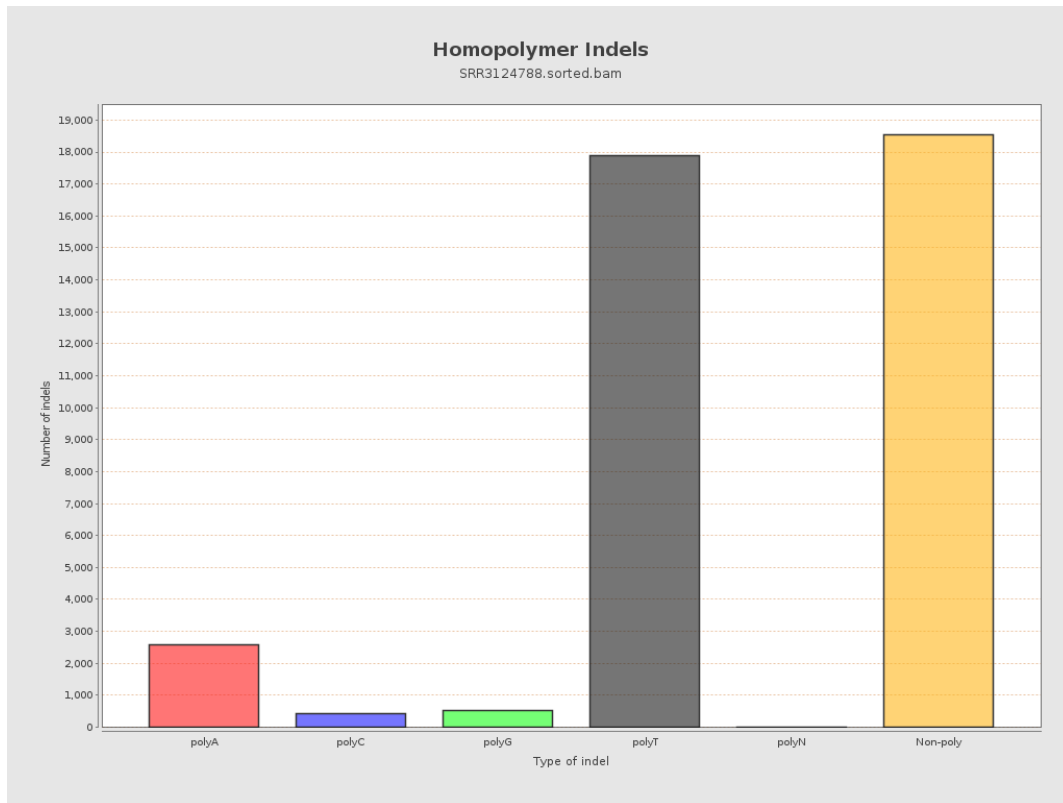
9. Results : Mapped Reads GC-content Distribution



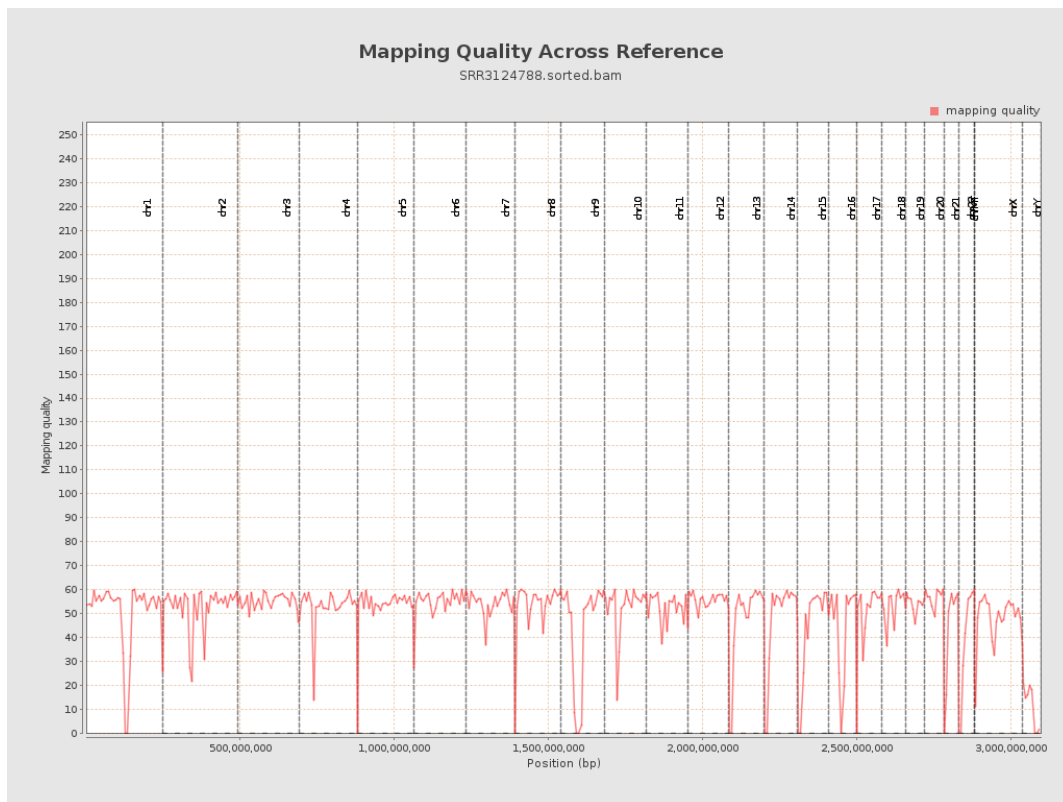
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

