

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:16:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008693.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_SRR6008693 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008693.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:16:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008693.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,683,638
Mapped reads	1,299,376 / 77.18%
Unmapped reads	384,262 / 22.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,768 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	120,341 / 7.15%
Duplication rate	7.62%
Clipped reads	763,185 / 45.33%

2.2. ACGT Content

Number/percentage of A's	22,049,684 / 26.95%
Number/percentage of C's	14,342,354 / 17.53%
Number/percentage of T's	26,458,297 / 32.34%
Number/percentage of G's	18,949,161 / 23.16%
Number/percentage of N's	13,672 / 0.02%
GC Percentage	40.69%

2.3. Coverage

Mean	0.0264

Standard Deviation	0.2574
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2.4. Mapping Quality

Mean Mapping Quality	46.97
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2.5. Mismatches and indels

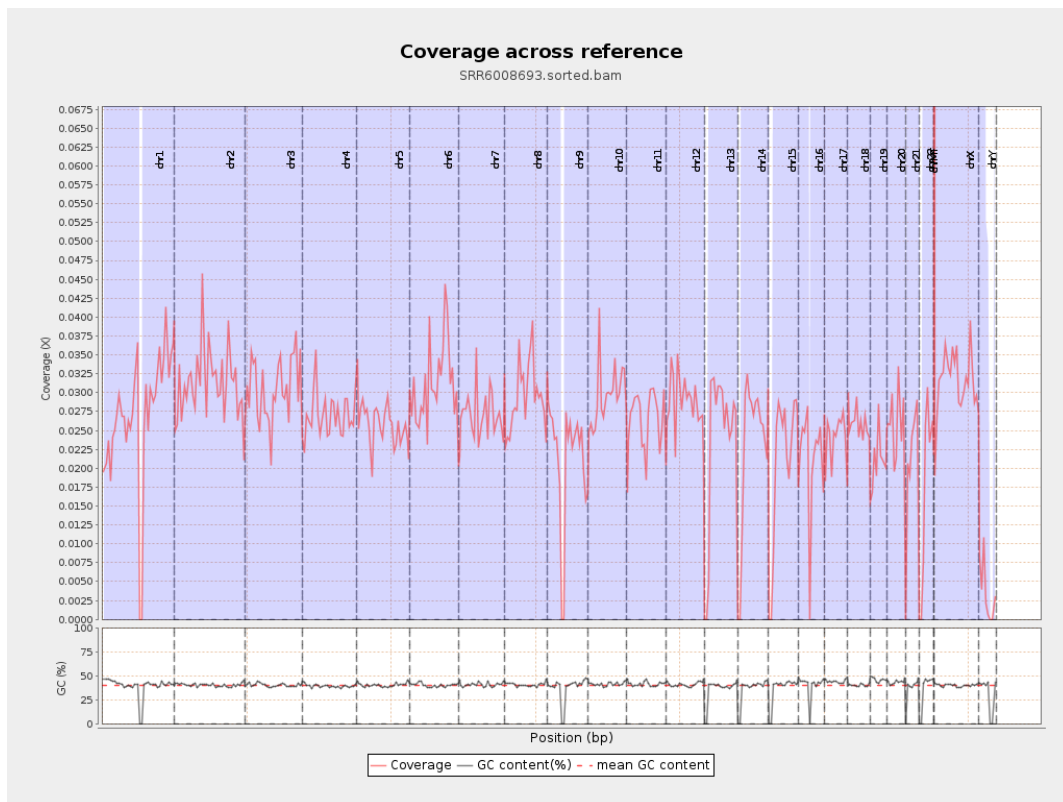
General error rate	0.77%
Mismatches	622,702
Insertions	6,432
Mapped reads with at least one insertion	0.49%
Deletions	25,886
Mapped reads with at least one deletion	1.97%
Homopolymer indels	48.58%

2.6. Chromosome stats

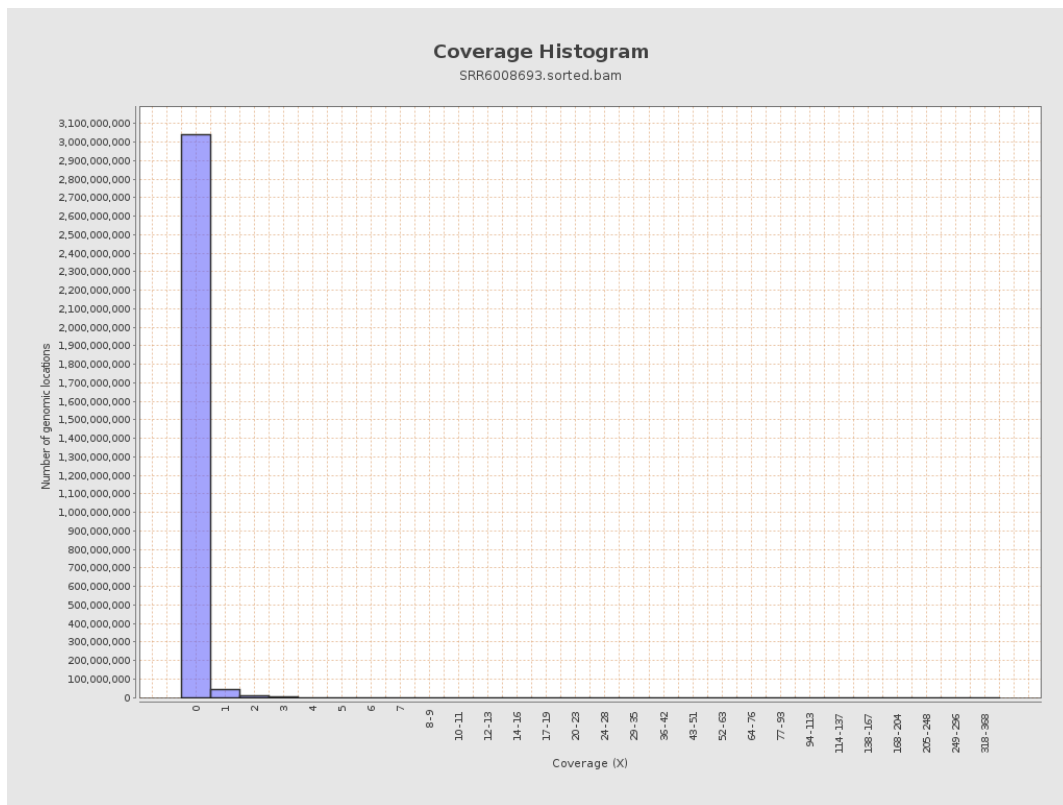
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6733967	0.027	0.3329
chr2	243199373	7617139	0.0313	0.2886
chr3	198022430	6048087	0.0305	0.2427
chr4	191154276	5156292	0.027	0.2303
chr5	180915260	4651459	0.0257	0.2179
chr6	171115067	5349617	0.0313	0.2537
chr7	159138663	4302461	0.027	0.2937

chr8	146364022	4325766	0.0296	0.329
chr9	141213431	3009207	0.0213	0.2275
chr10	135534747	4012769	0.0296	0.2737
chr11	135006516	3573990	0.0265	0.2499
chr12	133851895	3880598	0.029	0.2366
chr13	115169878	2718671	0.0236	0.2095
chr14	107349540	2452256	0.0228	0.2206
chr15	102531392	2143591	0.0209	0.1969
chr16	90354753	1886768	0.0209	0.2067
chr17	81195210	1939562	0.0239	0.2185
chr18	78077248	2024614	0.0259	0.3427
chr19	59128983	1257870	0.0213	0.2476
chr20	63025520	1611190	0.0256	0.2193
chr21	48129895	1000895	0.0208	0.2009
chr22	51304566	926316	0.0181	0.179
chrMT	16571	109016	6.5787	4.5211
chrX	155270560	4919376	0.0317	0.2516
chrY	59373566	202668	0.0034	0.0899

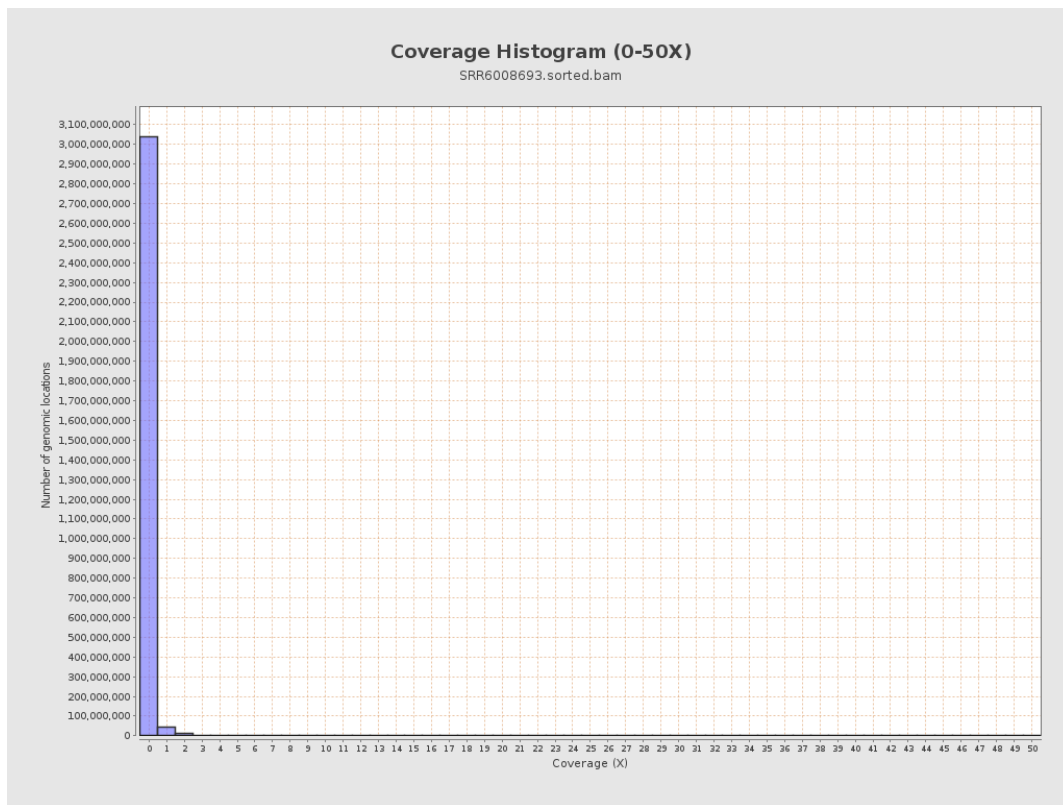
3. Results : Coverage across reference



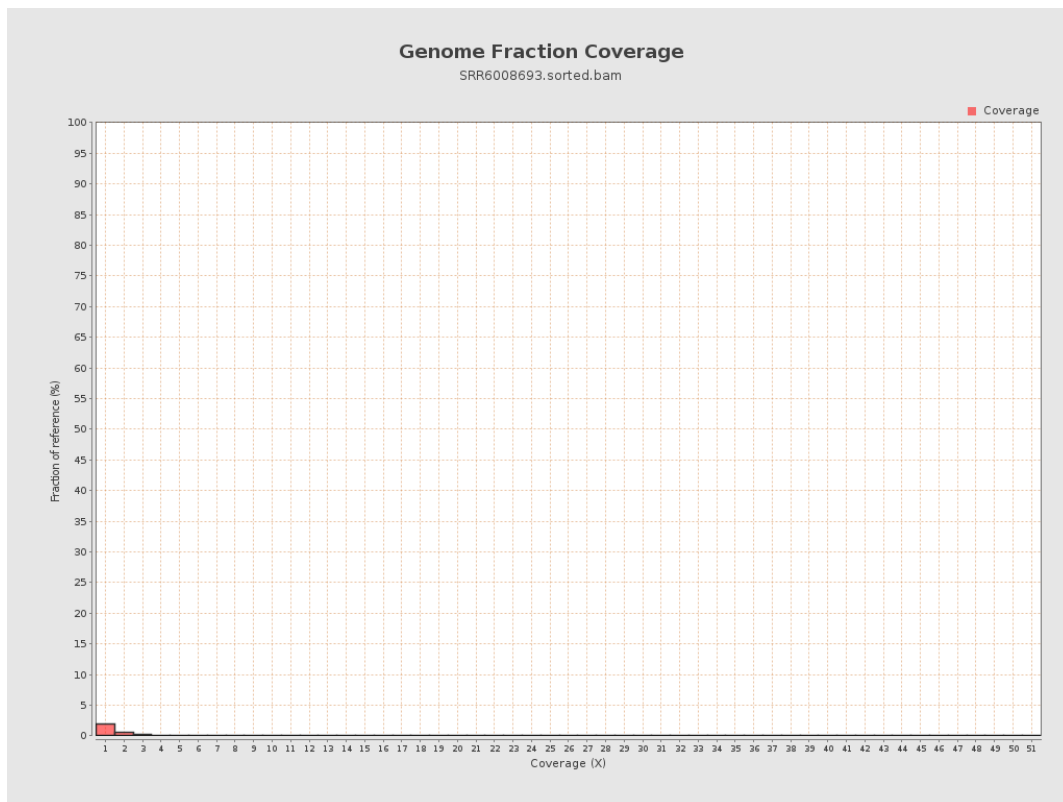
4. Results : Coverage Histogram



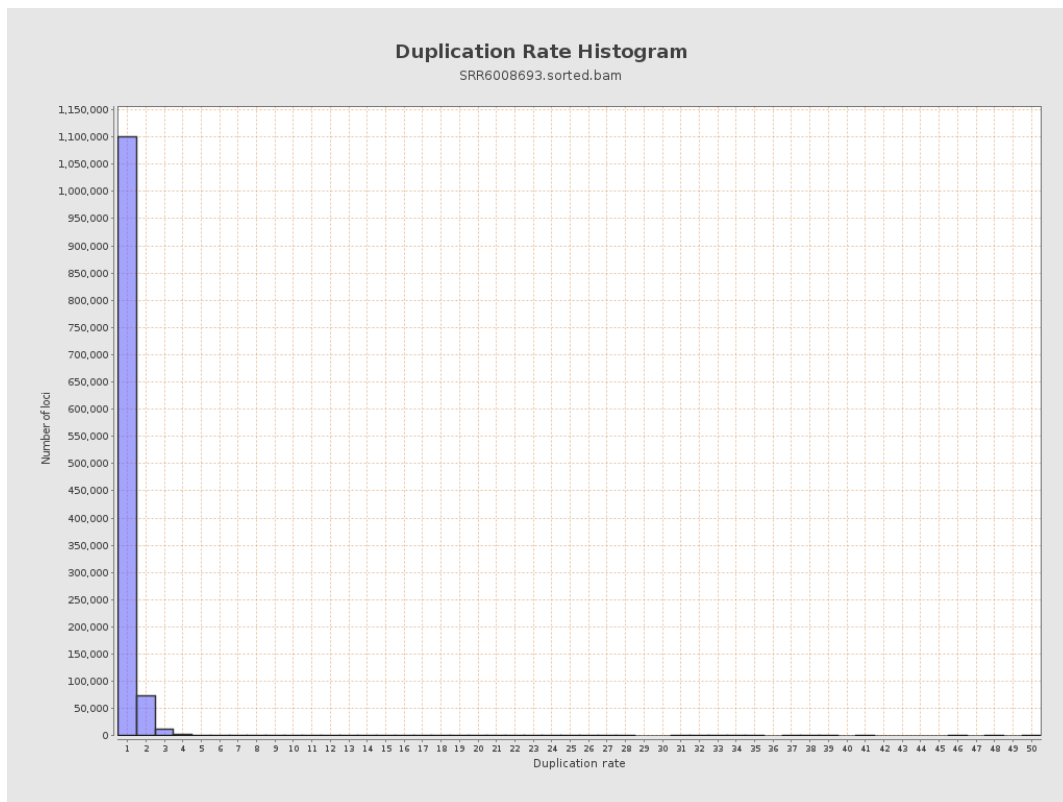
5. Results : Coverage Histogram (0-50X)



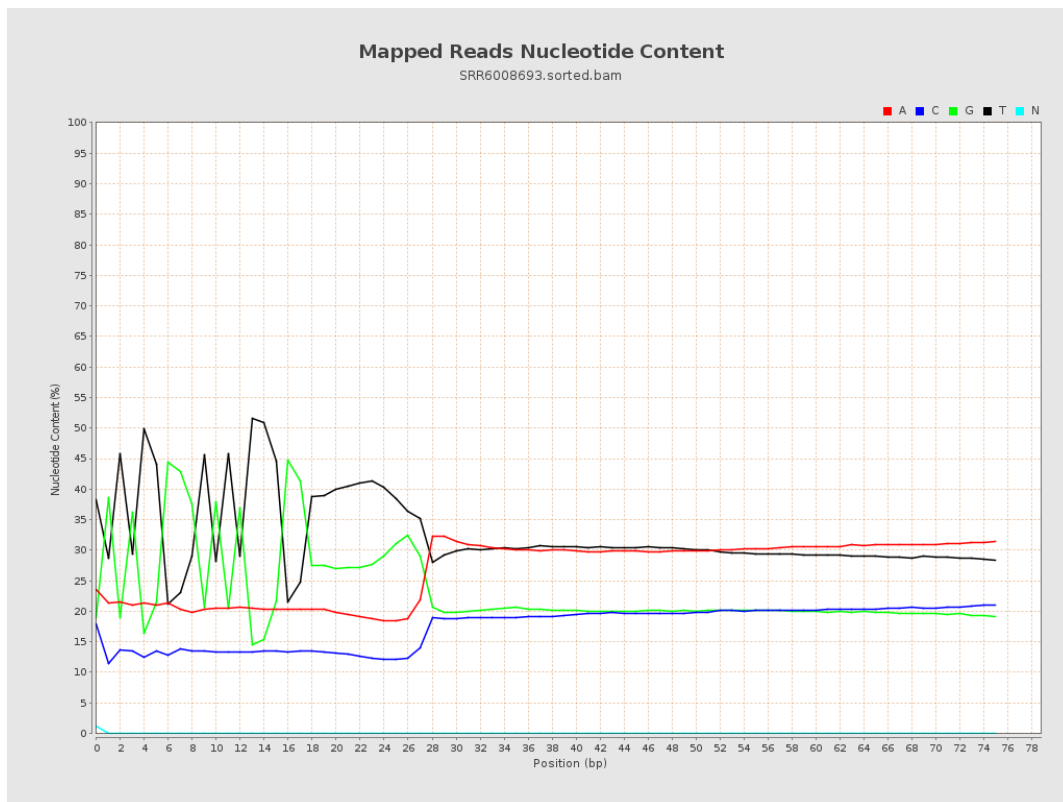
6. Results : Genome Fraction Coverage



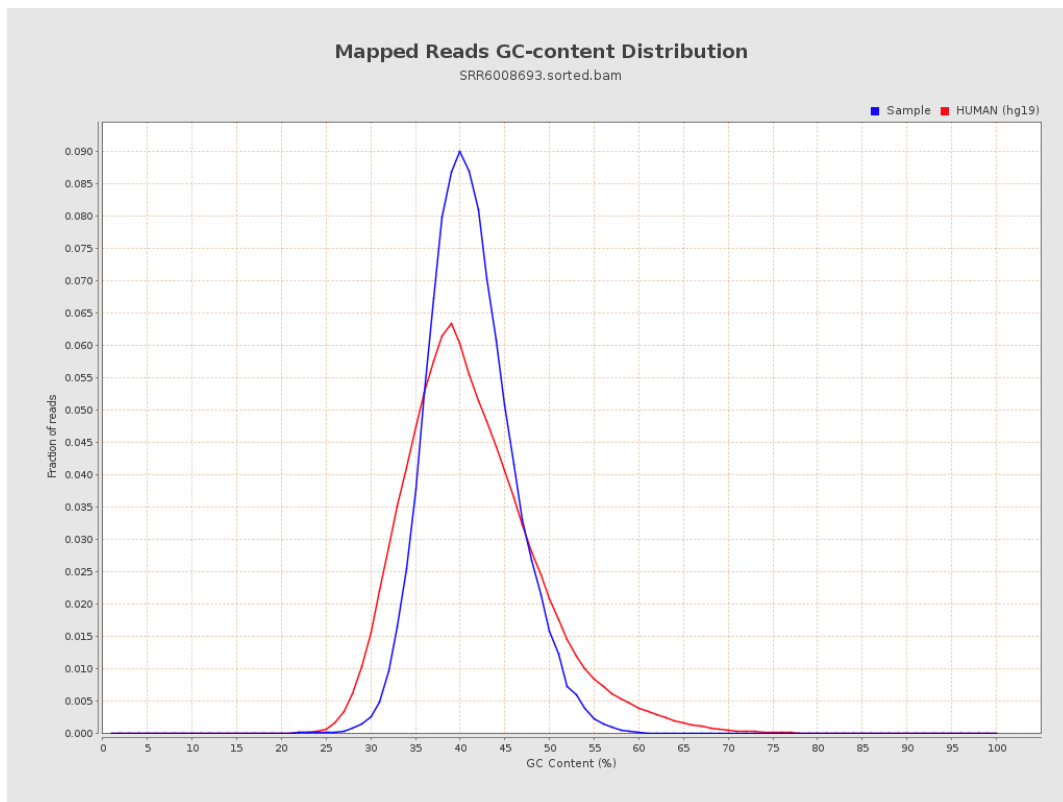
7. Results : Duplication Rate Histogram



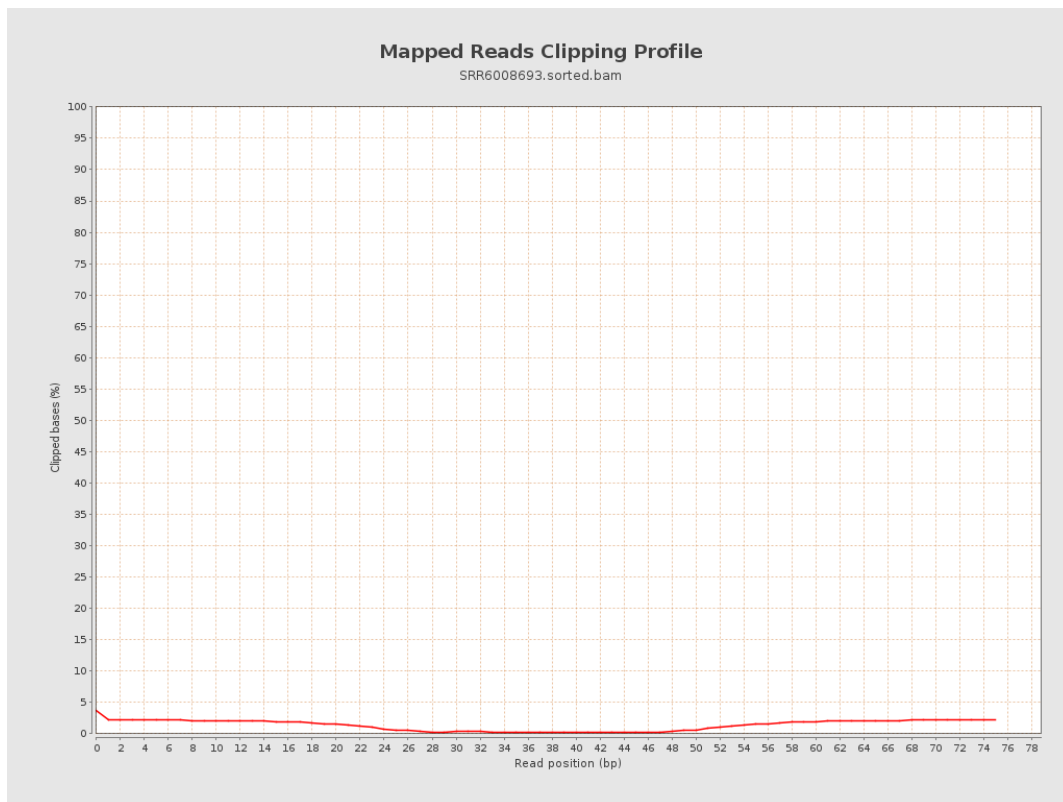
8. Results : Mapped Reads Nucleotide Content



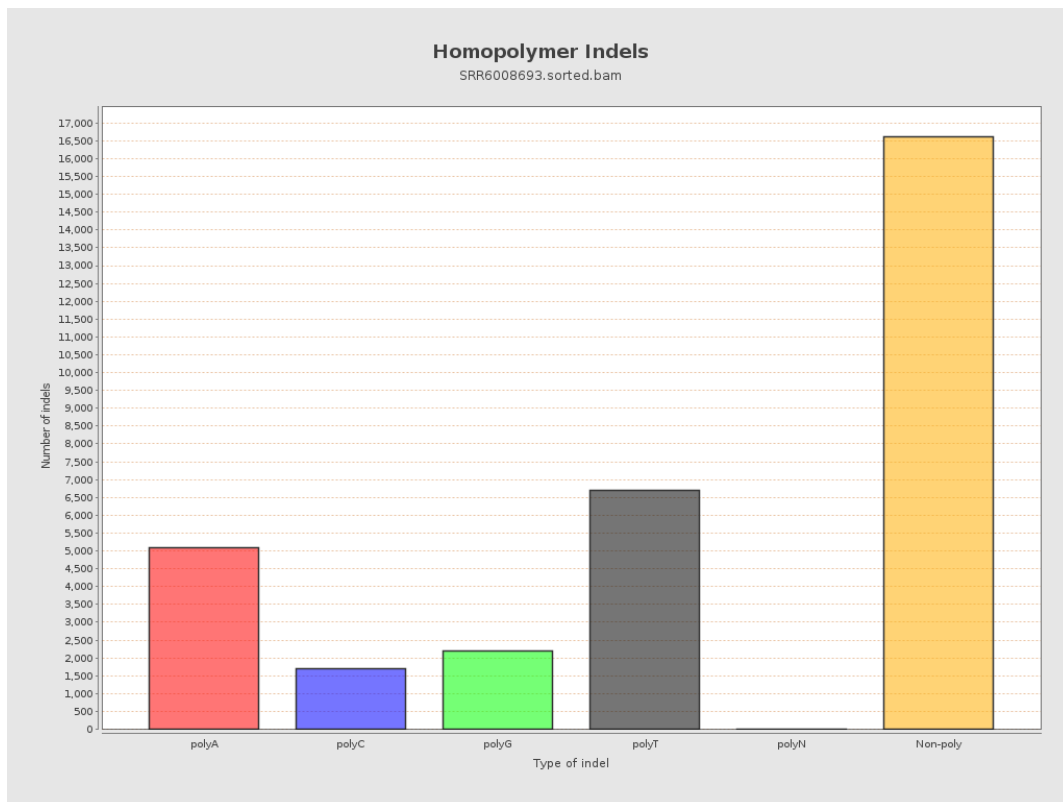
9. Results : Mapped Reads GC-content Distribution



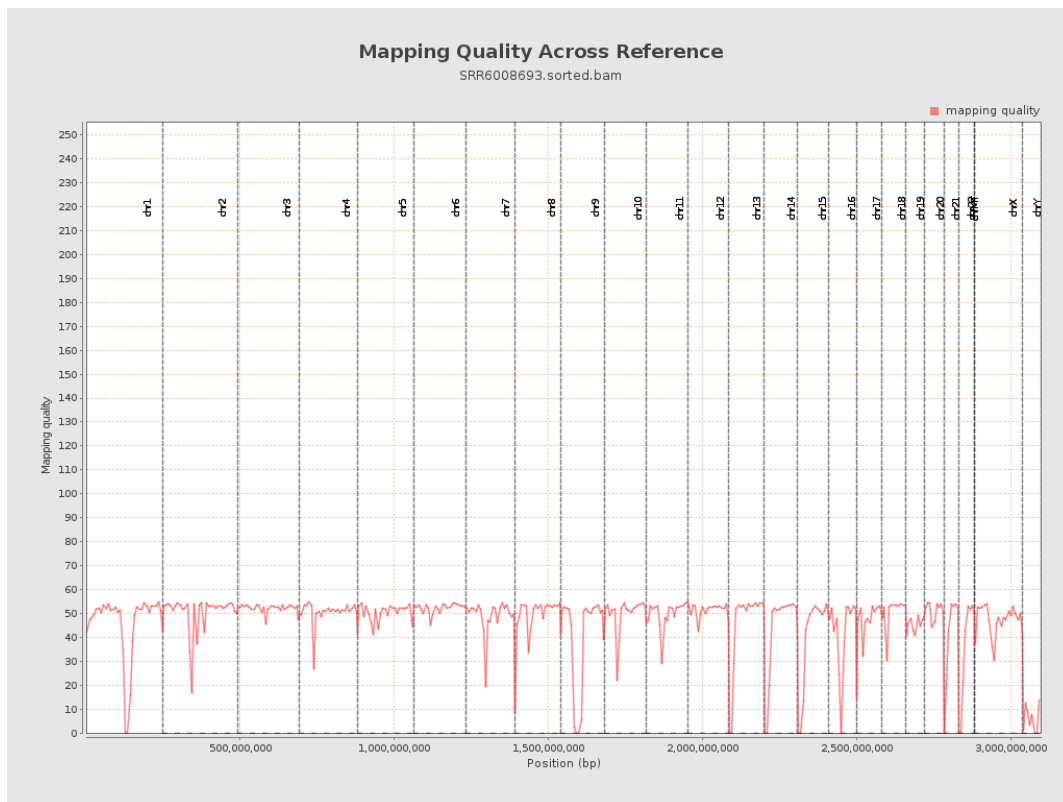
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

