Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:13:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240053.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_SRR6240053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:13:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,669,027
Mapped reads	1,299,254 / 77.84%
Unmapped reads	369,773 / 22.16%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,453 / 0.33%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	58,552 / 3.51%
Duplication rate	3.39%
Clipped reads	871,233 / 52.2%

2.2. ACGT Content

Number/percentage of A's	21,572,560 / 27.11%
Number/percentage of C's	13,639,920 / 17.14%
Number/percentage of T's	25,065,729 / 31.5%
Number/percentage of G's	19,249,391 / 24.19%
Number/percentage of N's	48,750 / 0.06%
GC Percentage	41.33%

2.3. Coverage

Mean	0.0257

Standard Deviation	0.2838

2.4. Mapping Quality

Mean Mapping Quality	42.26

2.5. Mismatches and indels

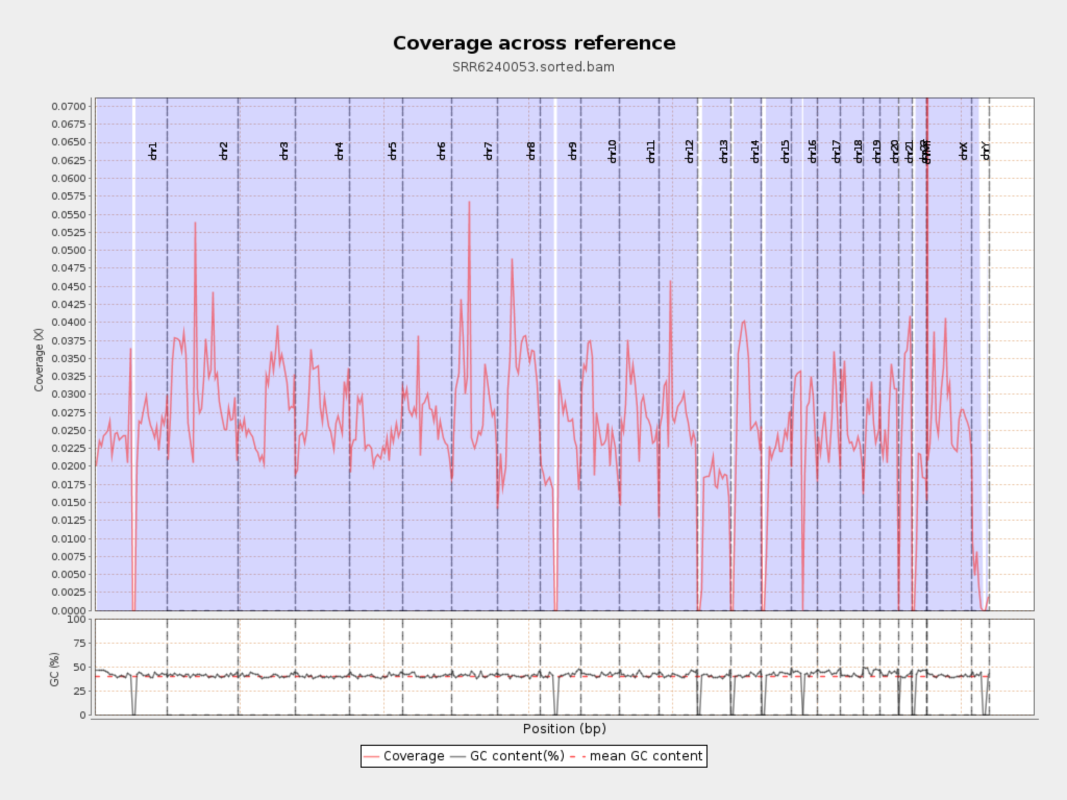
General error rate	1.1%
Mismatches	862,840
Insertions	5,907
Mapped reads with at least one insertion	0.45%
Deletions	26,883
Mapped reads with at least one deletion	2.05%
Homopolymer indels	48.92%

2.6. Chromosome stats

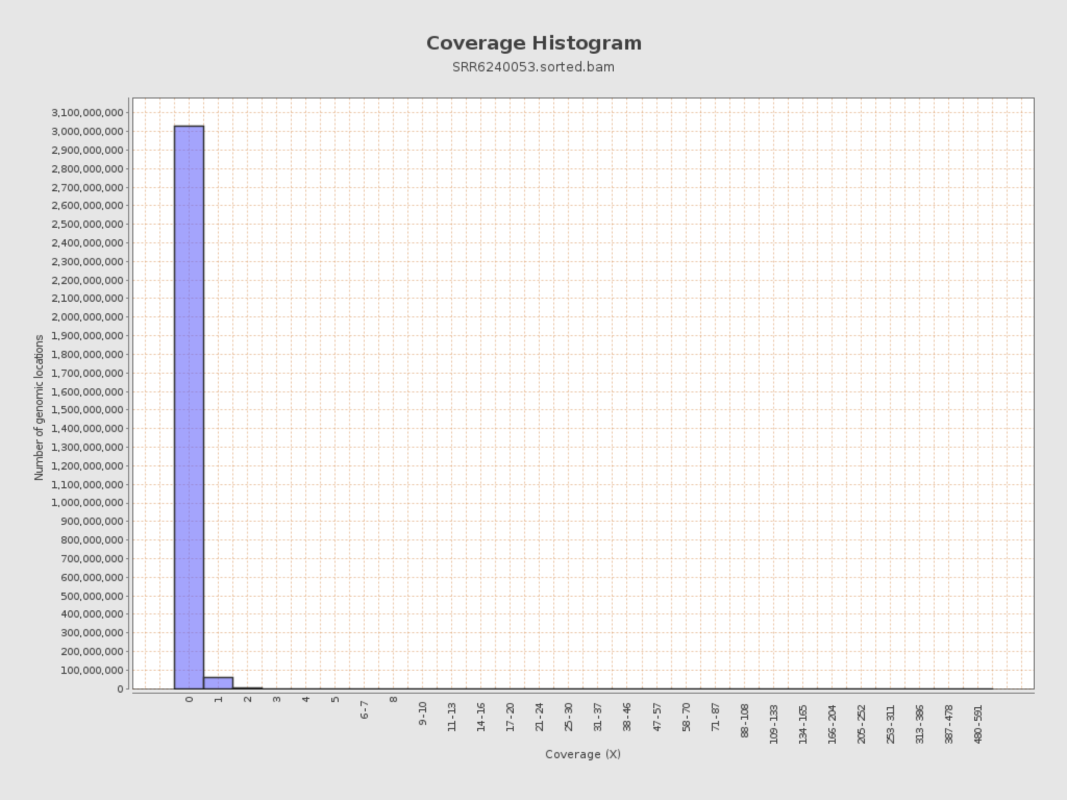
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5855508	0.0235	0.4056
chr2	243199373	7640199	0.0314	0.3633
chr3	198022430	5632243	0.0284	0.193
chr4	191154276	5253758	0.0275	0.1973
chr5	180915260	4299557	0.0238	0.1772
chr6	171115067	4634545	0.0271	0.2335
chr7	159138663	4775026	0.03	0.5439

chr8	146364022	4711242	0.0322	0.366
chr9	141213431	2910791	0.0206	0.272
chr10	135534747	3623789	0.0267	0.2242
chr11	135006516	3710731	0.0275	0.2655
chr12	133851895	3735997	0.0279	0.1918
chr13	115169878	1763748	0.0153	0.1391
chr14	107349540	2850260	0.0266	0.1968
chr15	102531392	1946191	0.019	0.1912
chr16	90354753	2328055	0.0258	0.1902
chr17	81195210	2091800	0.0258	0.2008
chr18	78077248	1972106	0.0253	0.3978
chr19	59128983	1547820	0.0262	0.3084
chr20	63025520	1664311	0.0264	0.1948
chr21	48129895	1409015	0.0293	0.1998
chr22	51304566	717153	0.014	0.1312
chrMT	16571	31649	1.9099	2.3096
chrX	155270560	4324575	0.0279	0.2215
chrY	59373566	192944	0.0032	0.0704

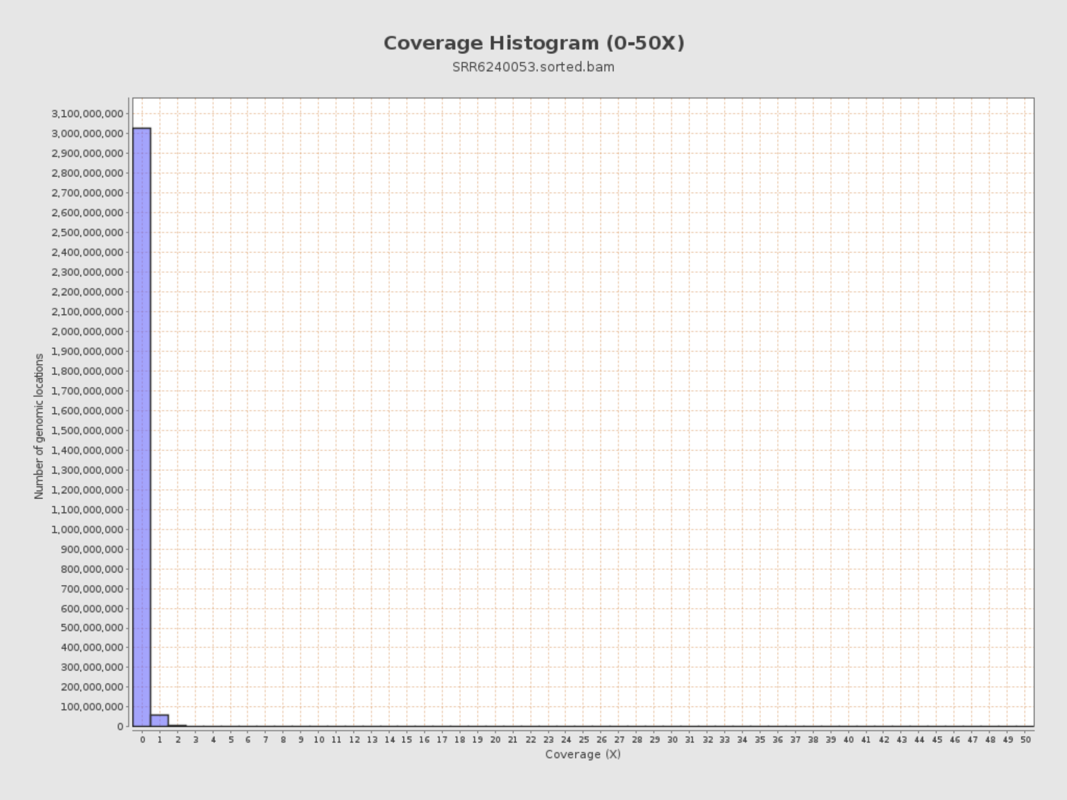
3. Results : Coverage across reference



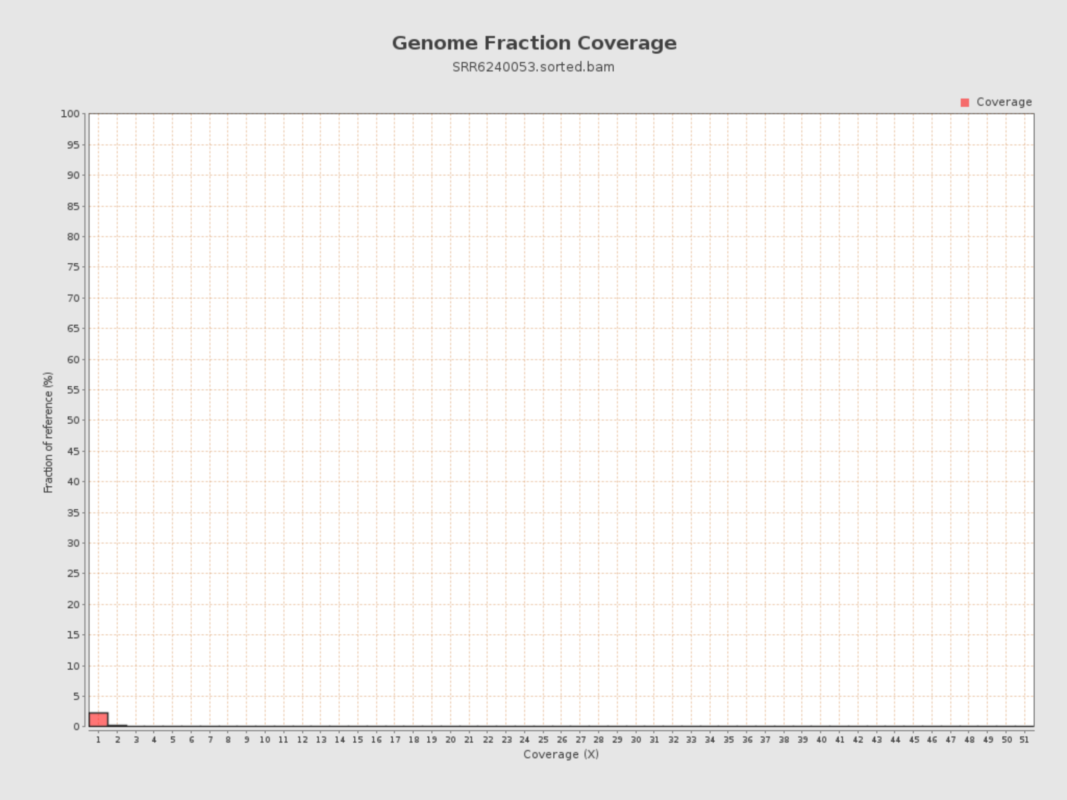
4. Results : Coverage Histogram



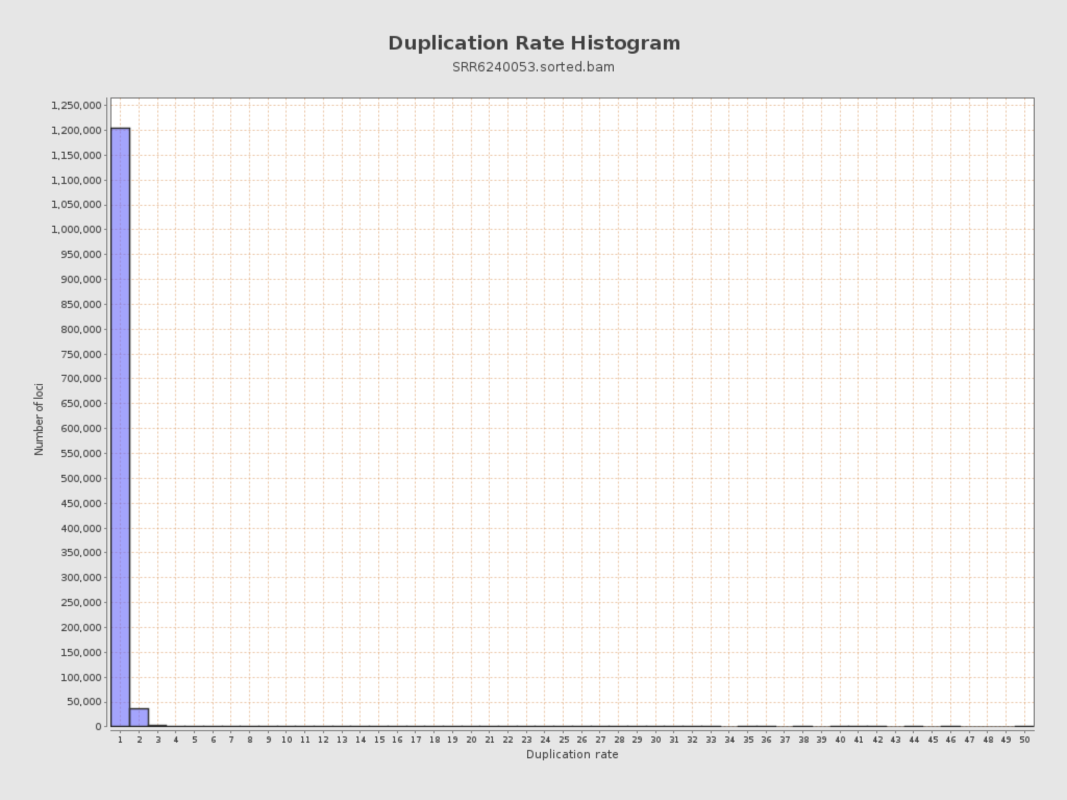
5. Results : Coverage Histogram (0-50X)



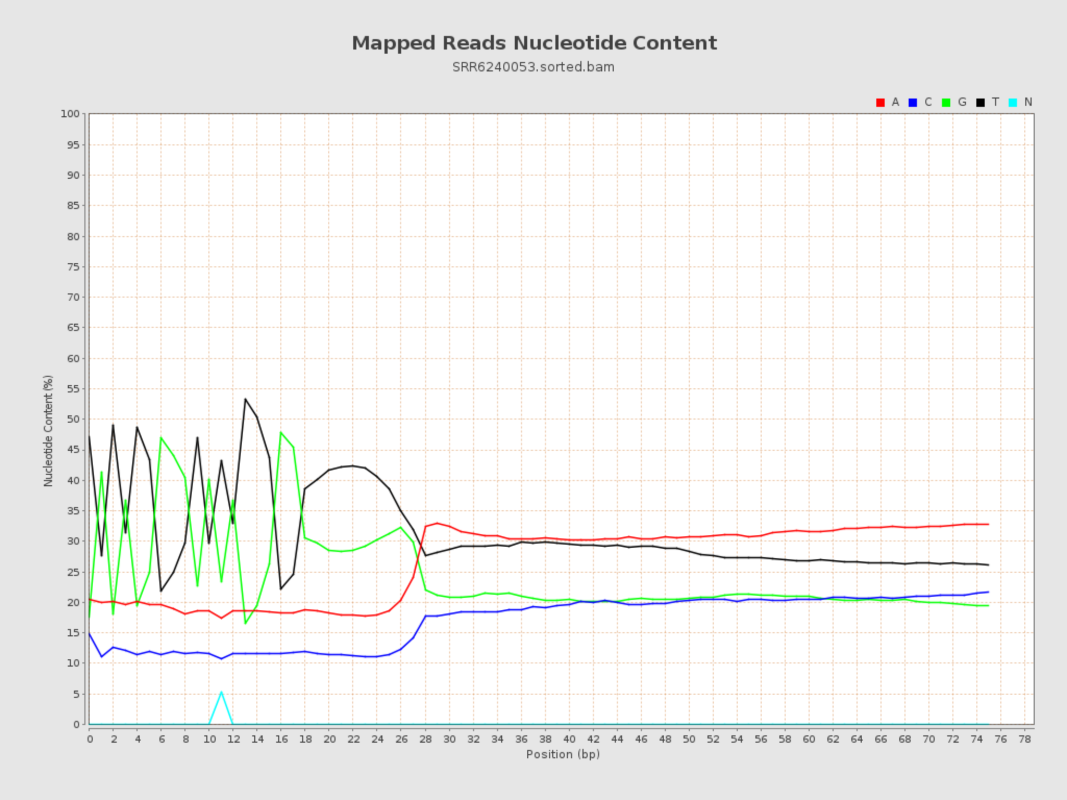
6. Results : Genome Fraction Coverage



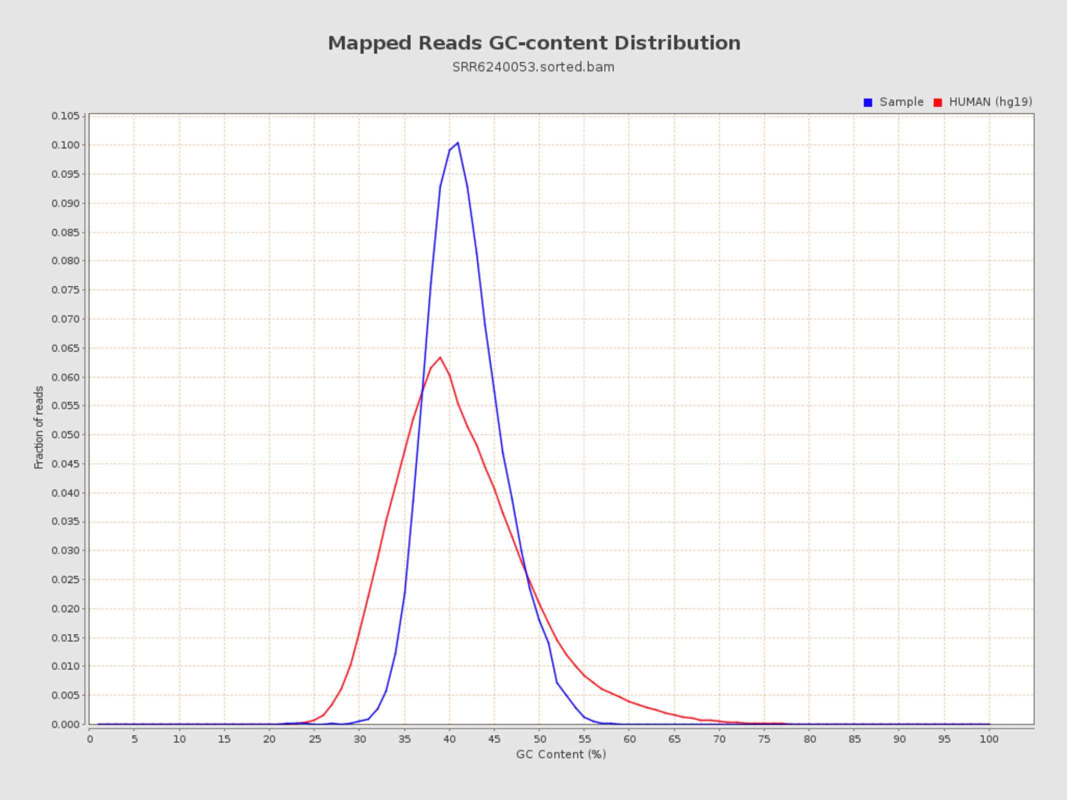
7. Results : Duplication Rate Histogram



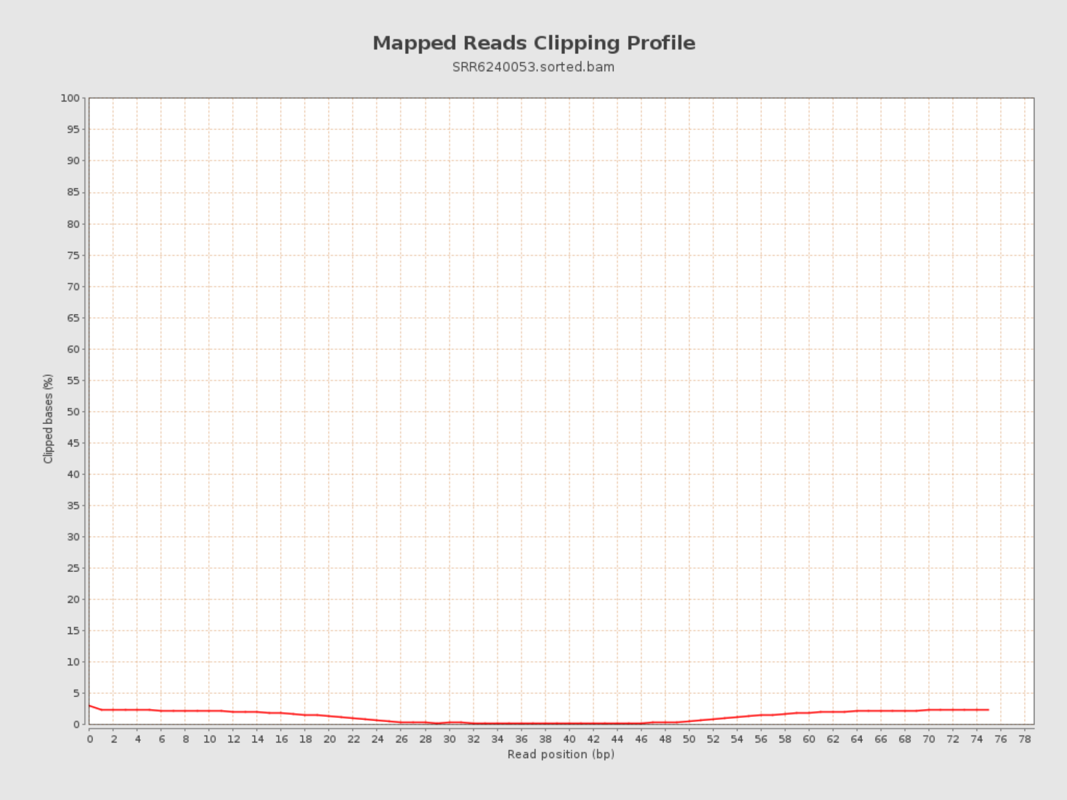
8. Results : Mapped Reads Nucleotide Content



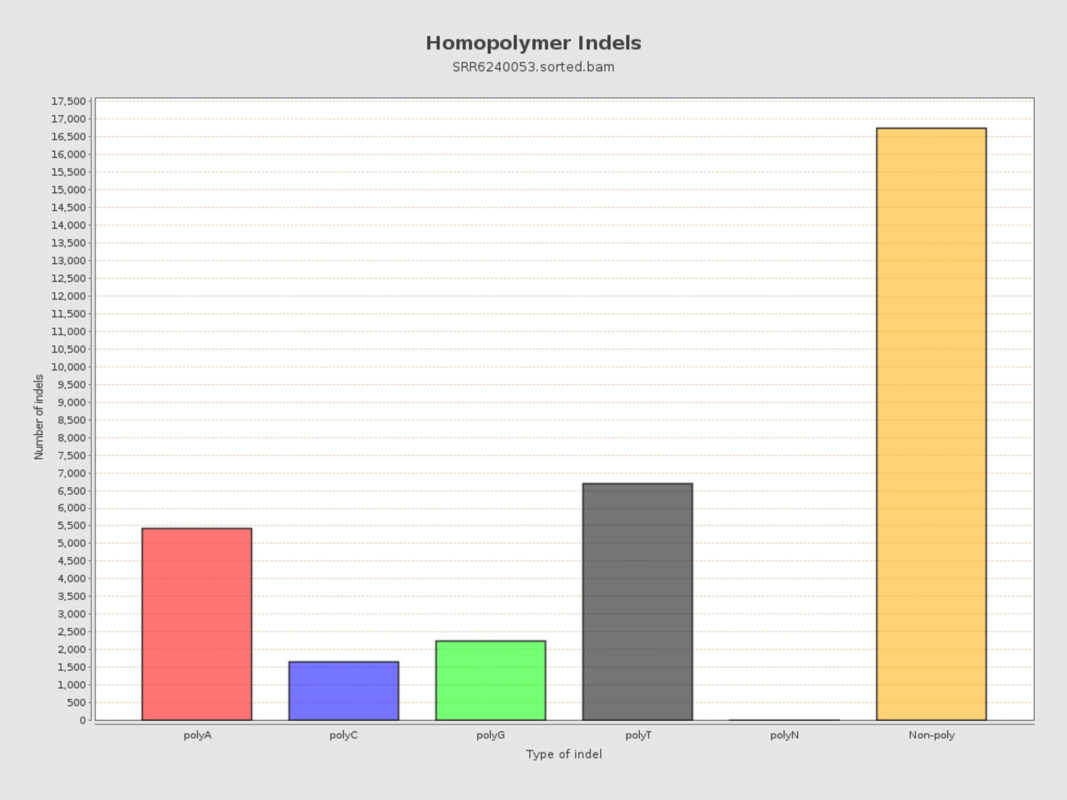
9. Results : Mapped Reads GC-content Distribution



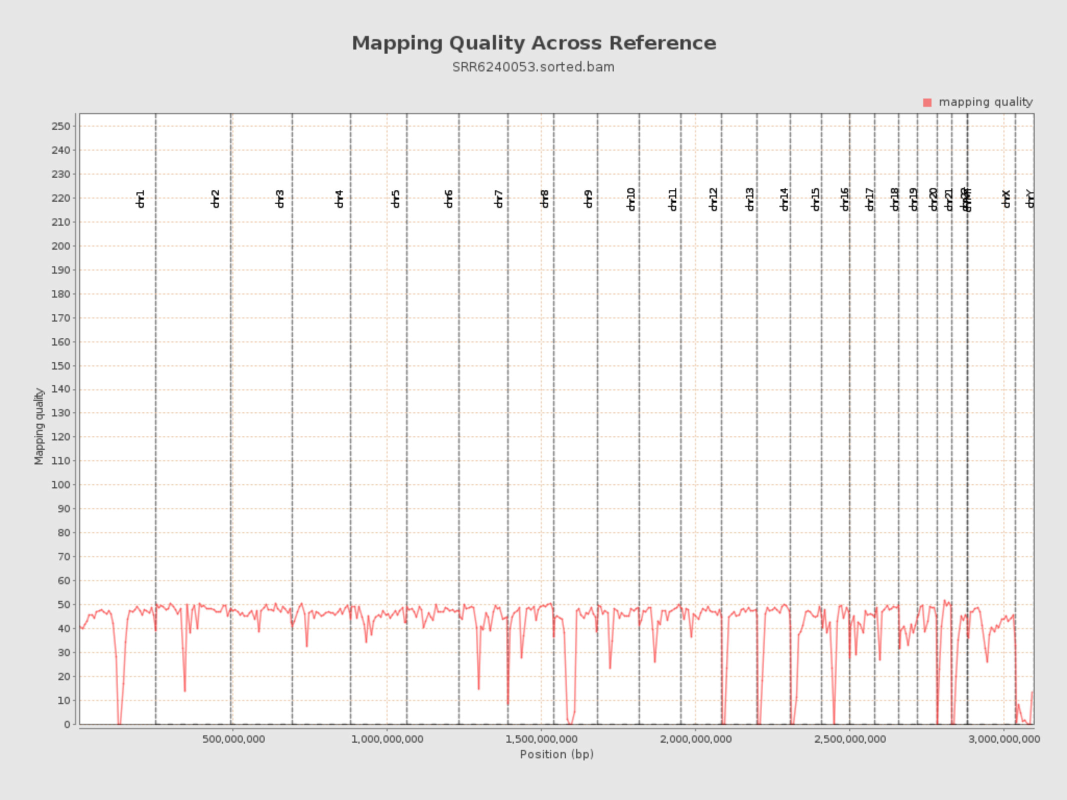
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram