Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:43:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240042.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_SRR6240042 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240042.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:43:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240042.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,110,322
Mapped reads	1,755,698 / 83.2%
Unmapped reads	354,624 / 16.8%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,694 / 0.6%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	216,155 / 10.24%
Duplication rate	9.63%
Clipped reads	926,687 / 43.91%

2.2. ACGT Content

Number/percentage of A's	31,811,138 / 28.07%
Number/percentage of C's	20,528,706 / 18.11%
Number/percentage of T's	36,268,811 / 32%
Number/percentage of G's	24,643,773 / 21.75%
Number/percentage of N's	73,283 / 0.06%
GC Percentage	39.86%

2.3. Coverage

Mean	0.0366

Standard Deviation	0.3906

2.4. Mapping Quality

Mean Mapping Quality	46.29

2.5. Mismatches and indels

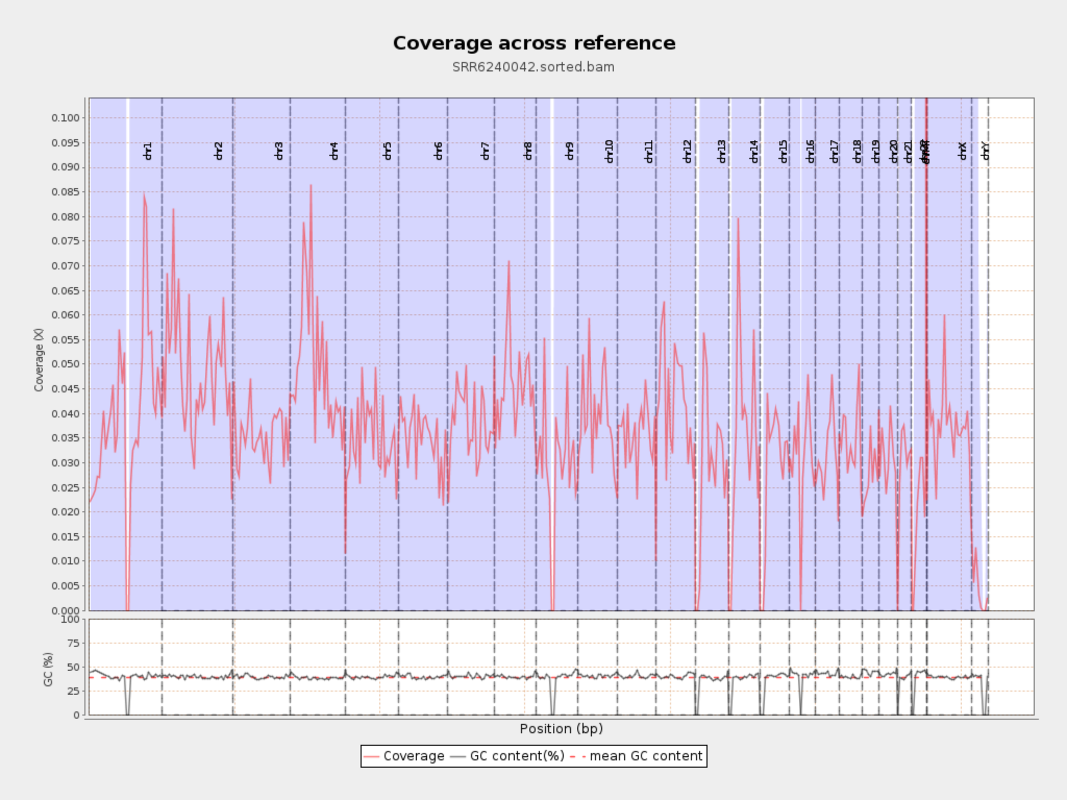
General error rate	0.87%
Mismatches	973,952
Insertions	8,169
Mapped reads with at least one insertion	0.46%
Deletions	26,115
Mapped reads with at least one deletion	1.47%
Homopolymer indels	48.03%

2.6. Chromosome stats

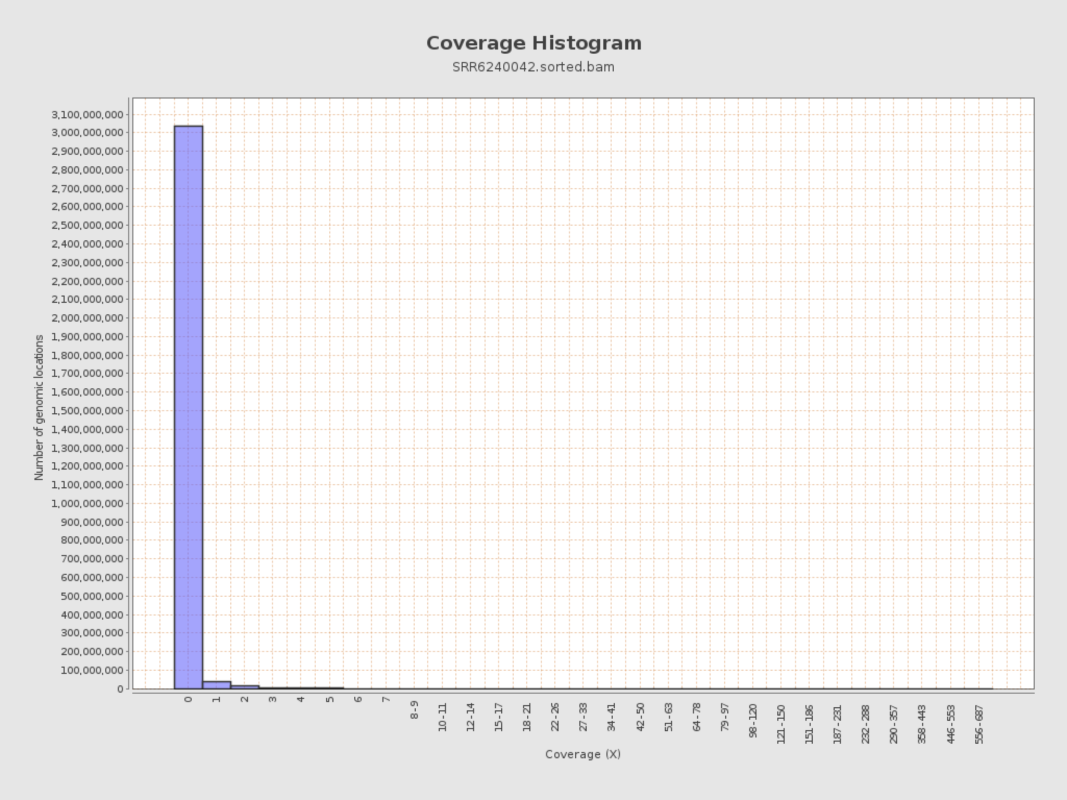
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9769647	0.0392	0.5884
chr2	243199373	11911540	0.049	0.4472
chr3	198022430	7038606	0.0355	0.3138
chr4	191154276	9527893	0.0498	0.3839
chr5	180915260	6251605	0.0346	0.3062
chr6	171115067	6014564	0.0351	0.3293
chr7	159138663	6078512	0.0382	0.4441

chr8	146364022	6657497	0.0455	0.5423
chr9	141213431	4155714	0.0294	0.3378
chr10	135534747	5345927	0.0394	0.4066
chr11	135006516	4834836	0.0358	0.3422
chr12	133851895	5701856	0.0426	0.3454
chr13	115169878	3241022	0.0281	0.2777
chr14	107349540	3815235	0.0355	0.3374
chr15	102531392	2929010	0.0286	0.2949
chr16	90354753	2820145	0.0312	0.2926
chr17	81195210	2541007	0.0313	0.2988
chr18	78077248	2756068	0.0353	0.5541
chr19	59128983	1638104	0.0277	0.3991
chr20	63025520	1920678	0.0305	0.2953
chr21	48129895	1410830	0.0293	0.2906
chr22	51304566	937414	0.0183	0.213
chrMT	16571	16234	0.9797	1.4333
chrX	155270560	5812077	0.0374	0.3411
chrY	59373566	244489	0.0041	0.1195

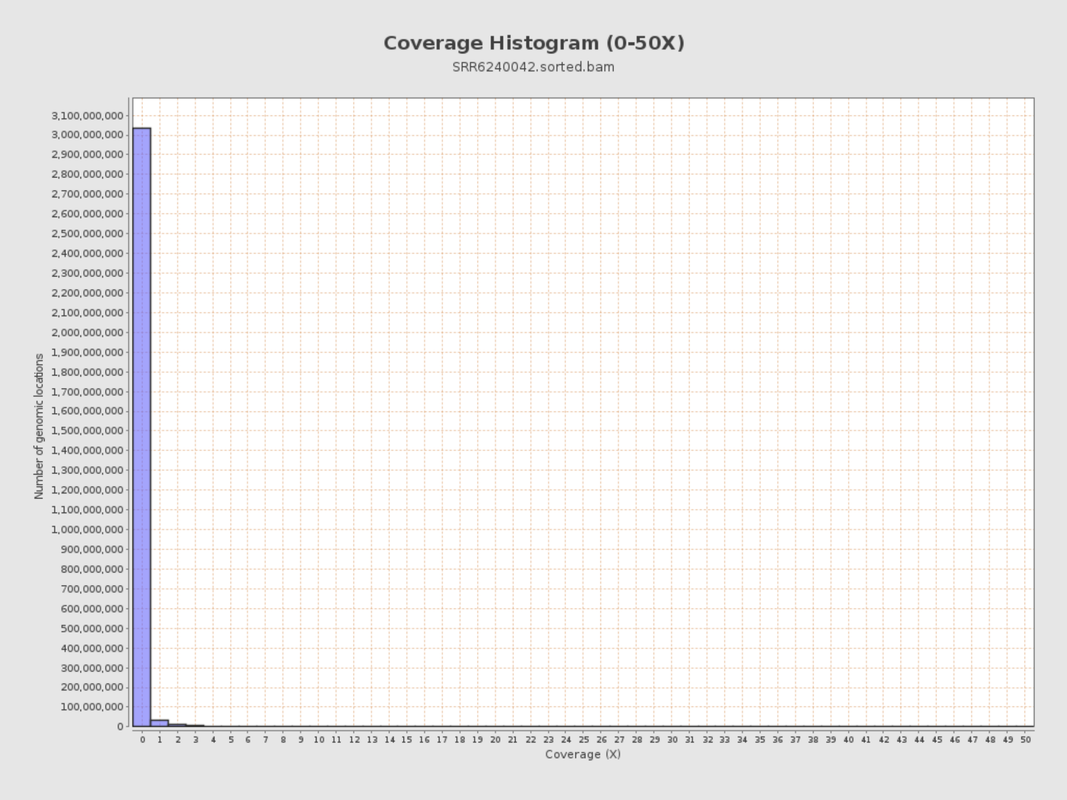
3. Results : Coverage across reference



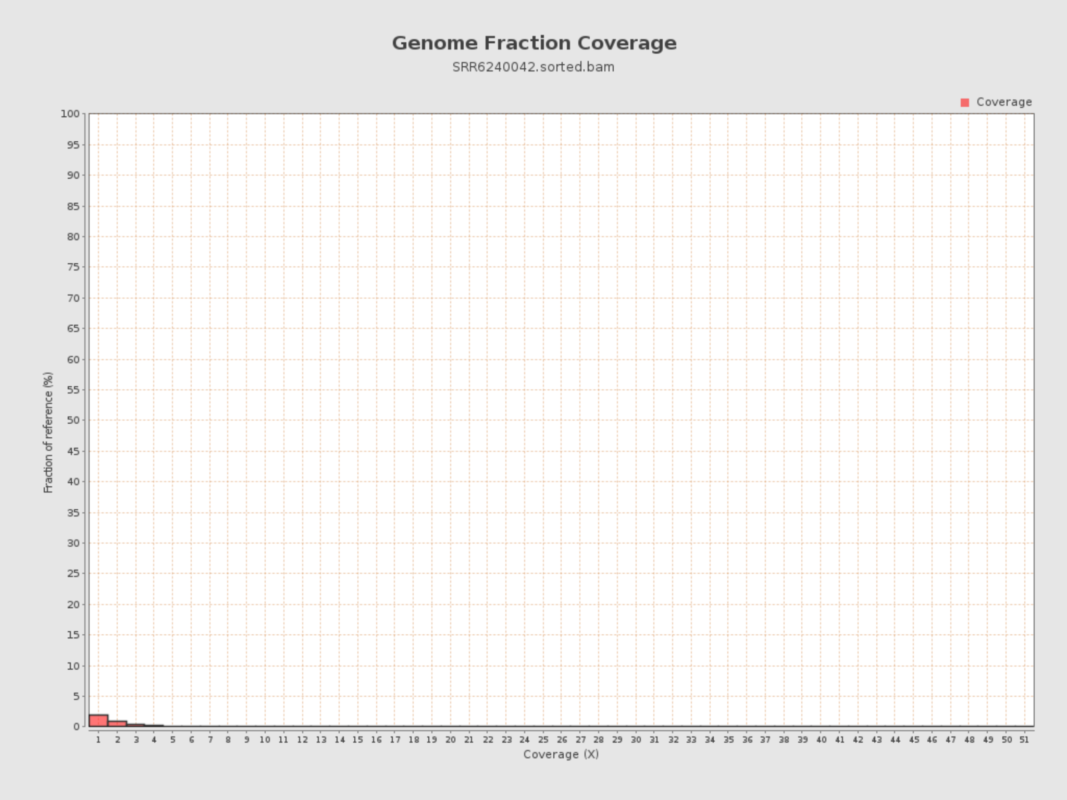
4. Results : Coverage Histogram



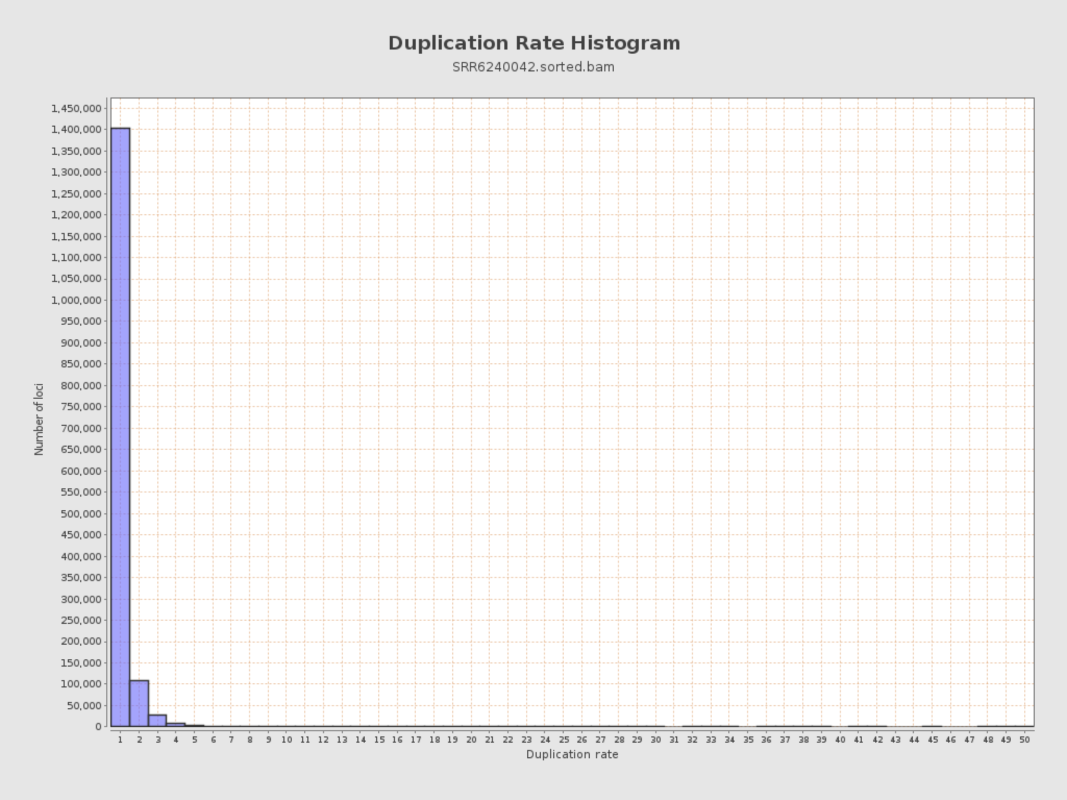
5. Results : Coverage Histogram (0-50X)



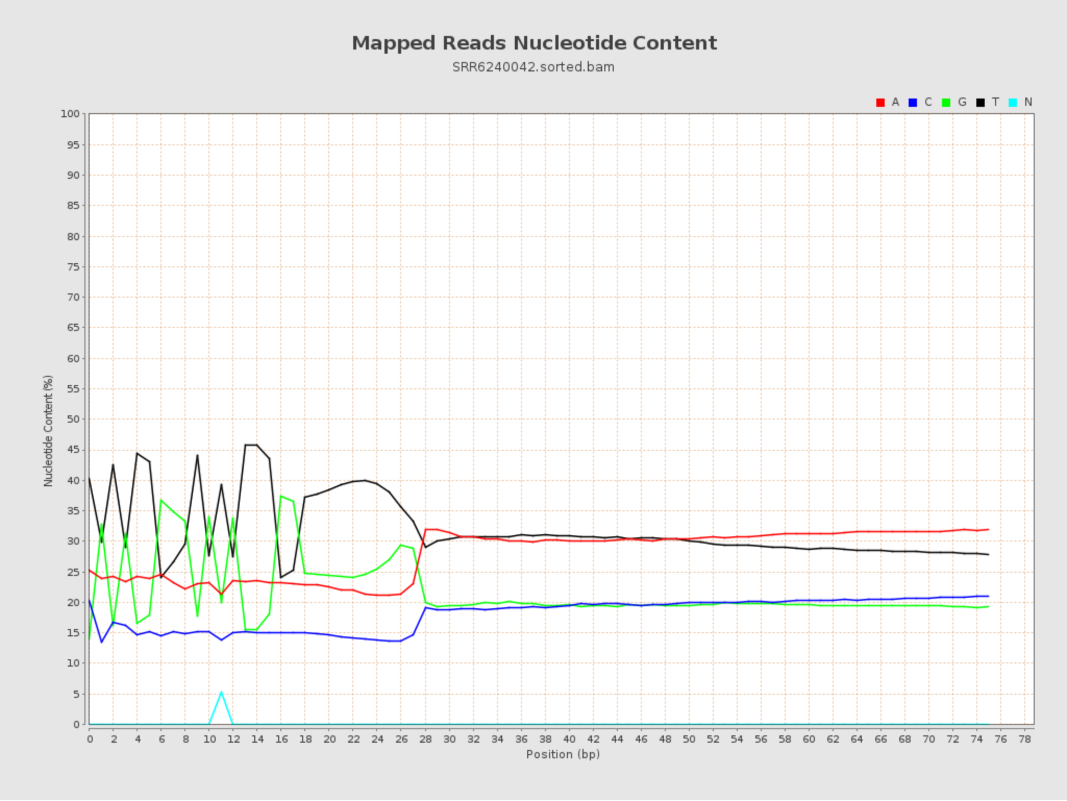
6. Results : Genome Fraction Coverage



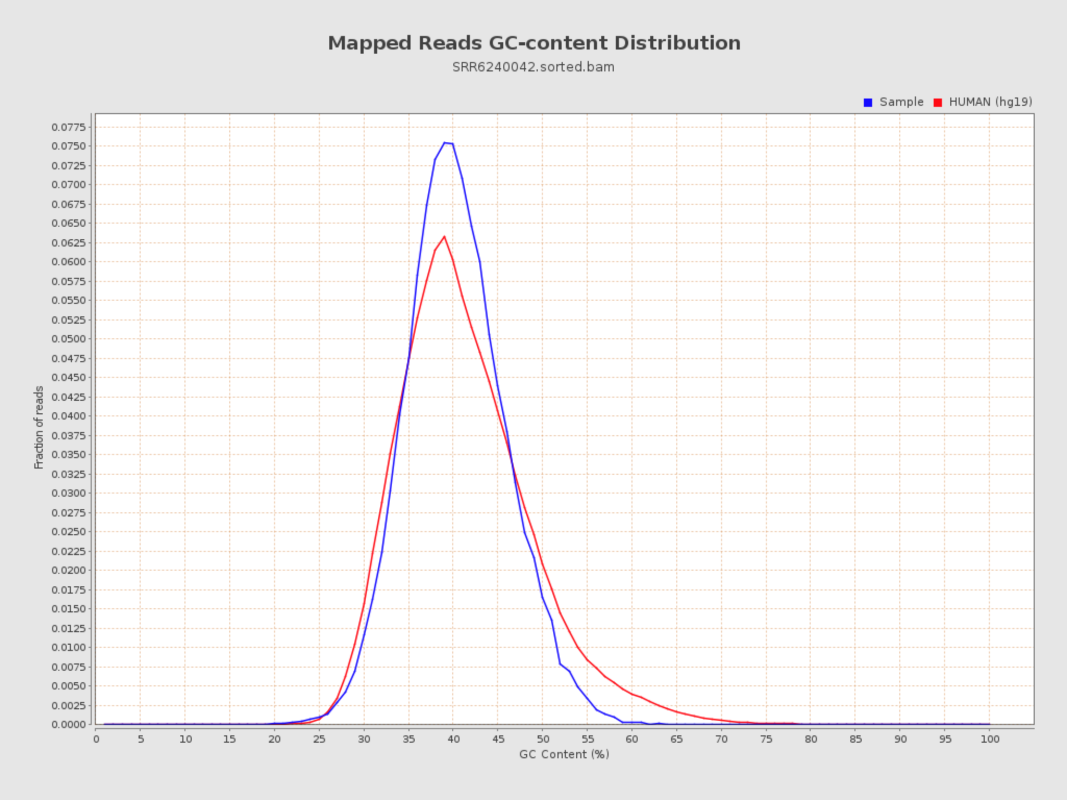
7. Results : Duplication Rate Histogram



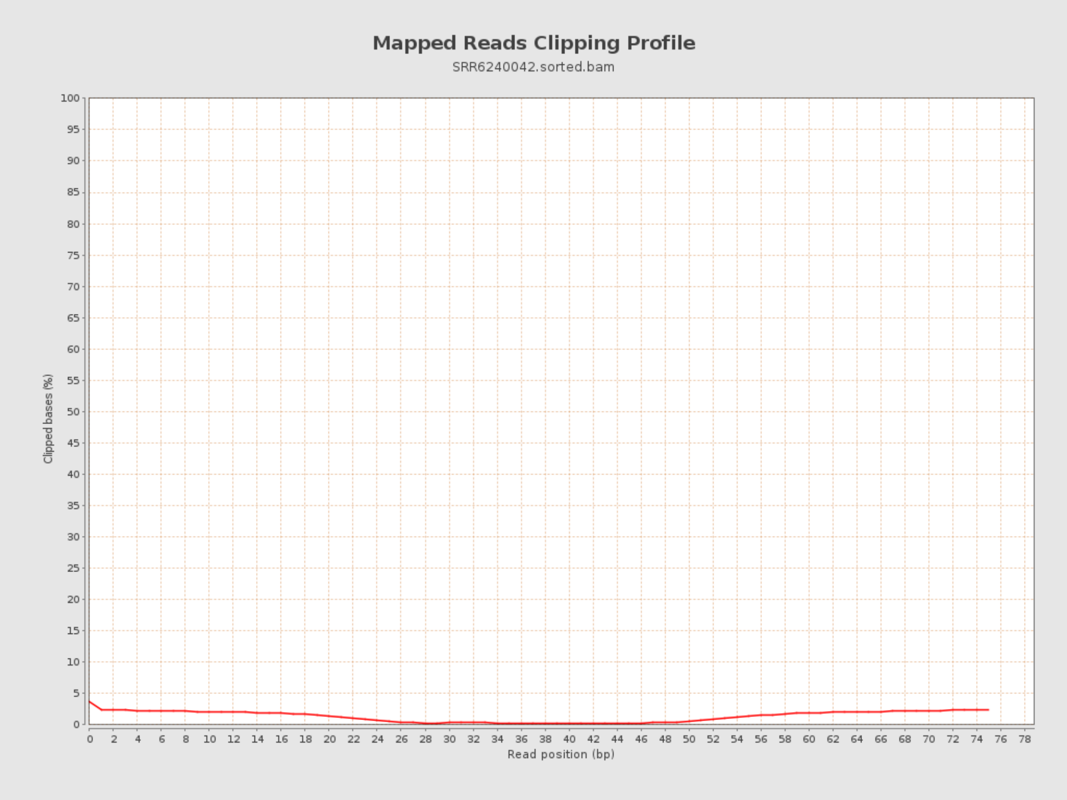
8. Results : Mapped Reads Nucleotide Content



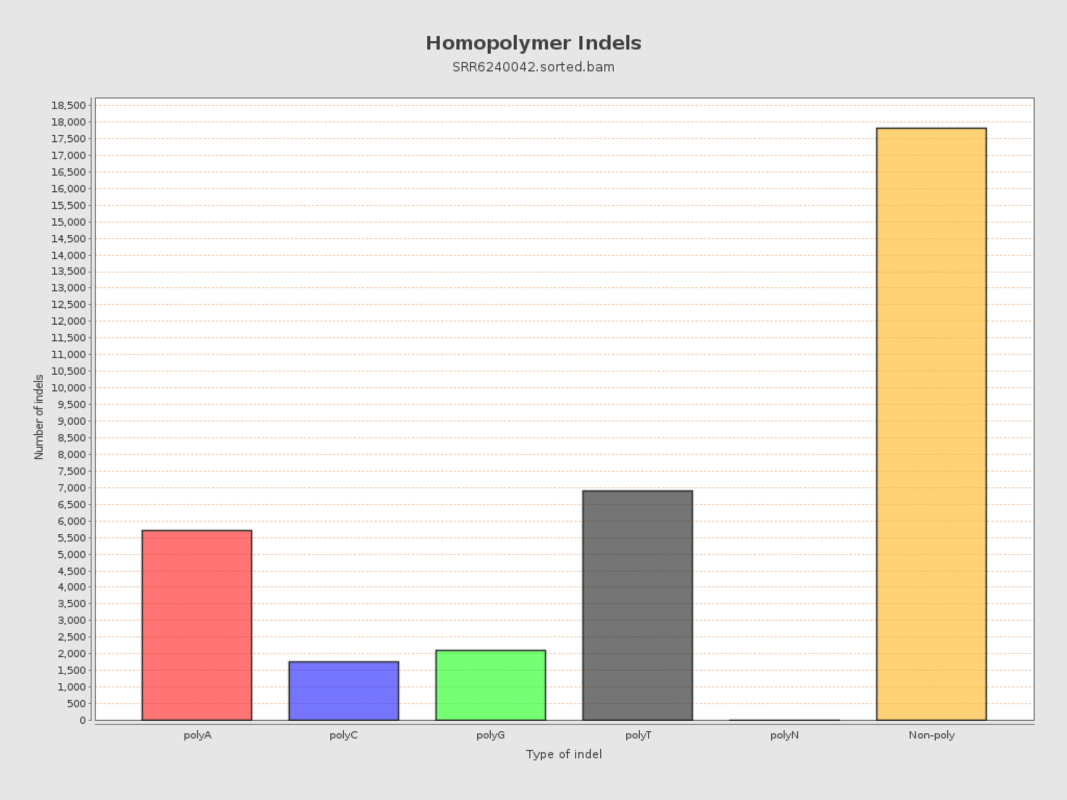
9. Results : Mapped Reads GC-content Distribution



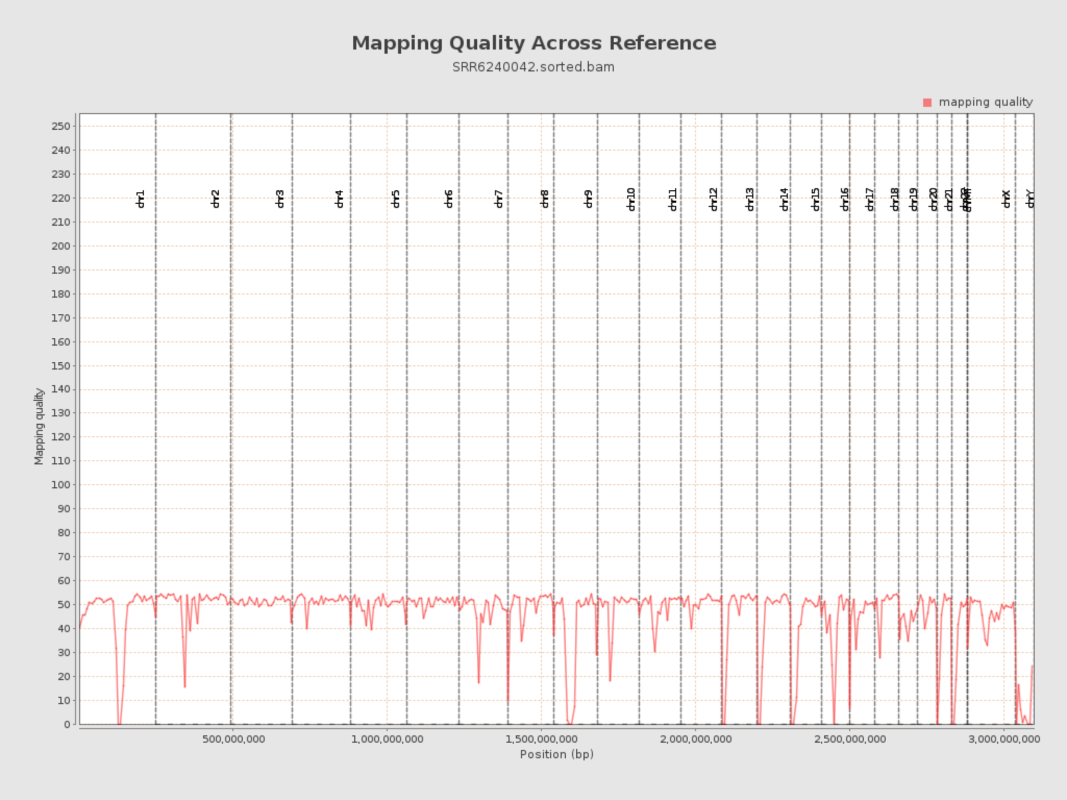
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram