Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:11:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013296.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_SRR6013296 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013296.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:11:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013296.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,671,817
Mapped reads	1,323,064 / 79.14%
Unmapped reads	348,753 / 20.86%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,088 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	128,814 / 7.71%
Duplication rate	8.05%
Clipped reads	718,481 / 42.98%

2.2. ACGT Content

Number/percentage of A's	23,015,013 / 27.01%
Number/percentage of C's	15,141,708 / 17.77%
Number/percentage of T's	27,843,735 / 32.68%
Number/percentage of G's	19,191,122 / 22.52%
Number/percentage of N's	17,711 / 0.02%
GC Percentage	40.29%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2939

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

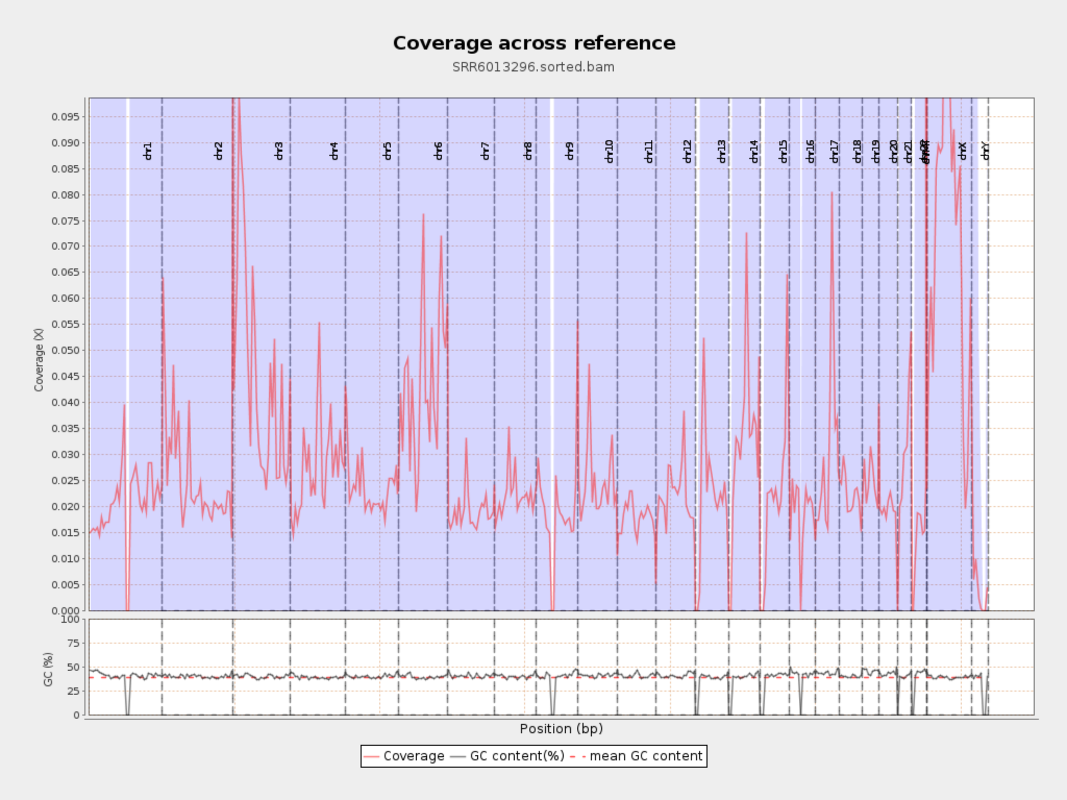
General error rate	0.85%
Mismatches	711,735
Insertions	5,876
Mapped reads with at least one insertion	0.44%
Deletions	20,872
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.76%

2.6. Chromosome stats

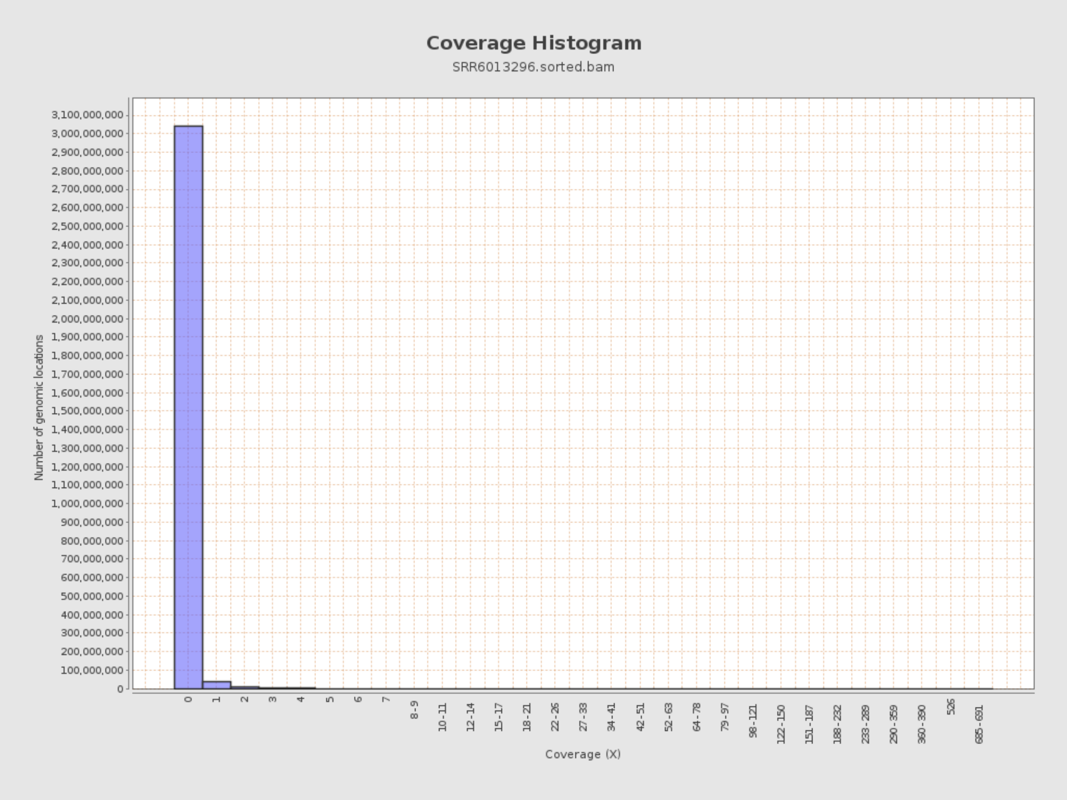
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5055080	0.0203	0.3813
chr2	243199373	6193255	0.0255	0.378
chr3	198022430	9243607	0.0467	0.3074
chr4	191154276	5264180	0.0275	0.2386
chr5	180915260	4247123	0.0235	0.2167
chr6	171115067	7473443	0.0437	0.3267
chr7	159138663	3045991	0.0191	0.2762

chr8	146364022	3229163	0.0221	0.2805
chr9	141213431	2517257	0.0178	0.2338
chr10	135534747	3350888	0.0247	0.3076
chr11	135006516	2408061	0.0178	0.2244
chr12	133851895	3014170	0.0225	0.2113
chr13	115169878	2509453	0.0218	0.2107
chr14	107349540	3389395	0.0316	0.2565
chr15	102531392	2278341	0.0222	0.2109
chr16	90354753	1686152	0.0187	0.2031
chr17	81195210	2525348	0.0311	0.2554
chr18	78077248	1762206	0.0226	0.4515
chr19	59128983	1505843	0.0255	0.3029
chr20	63025520	1213038	0.0192	0.1975
chr21	48129895	1415742	0.0294	0.2437
chr22	51304566	645067	0.0126	0.1511
chrMT	16571	33554	2.0249	2.1383
chrX	155270560	10943274	0.0705	0.4268
chrY	59373566	294439	0.005	0.1008

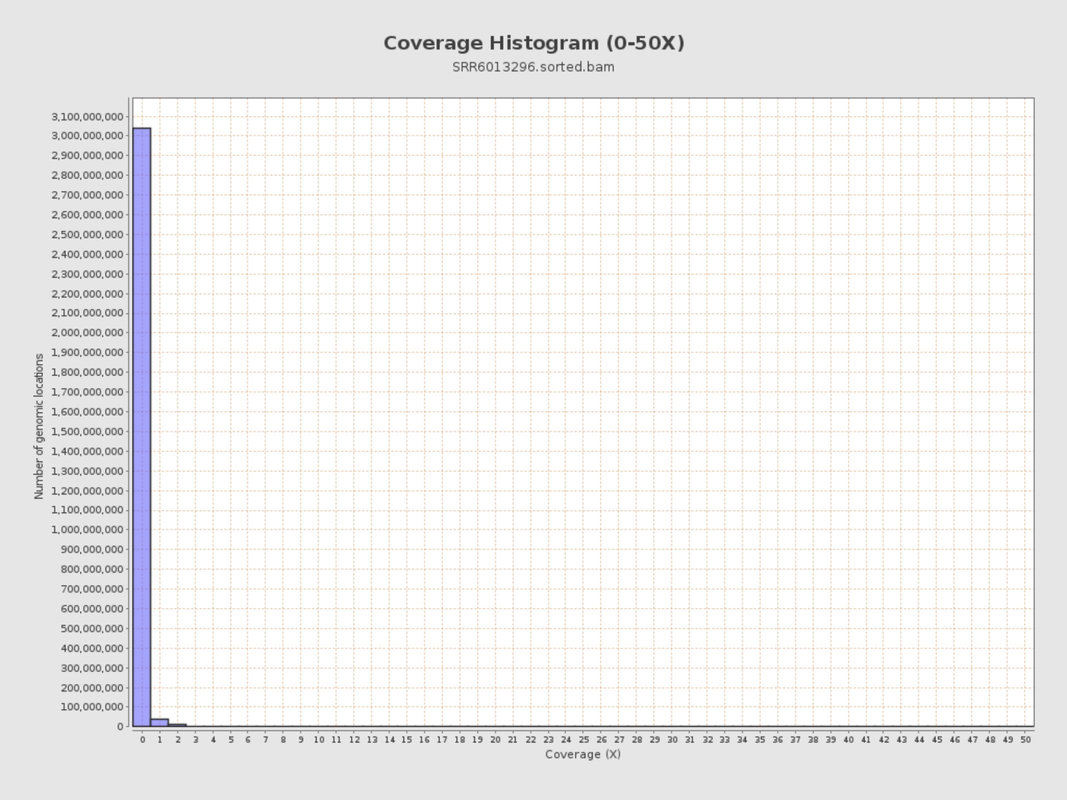
3. Results : Coverage across reference



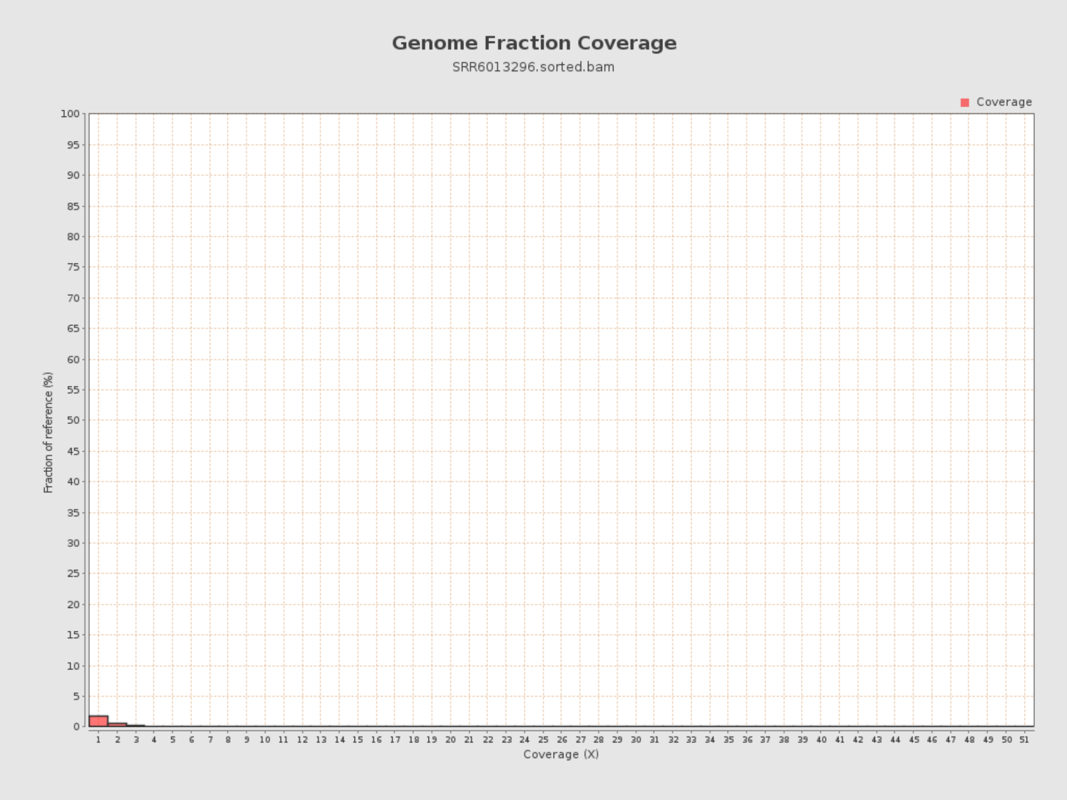
4. Results : Coverage Histogram



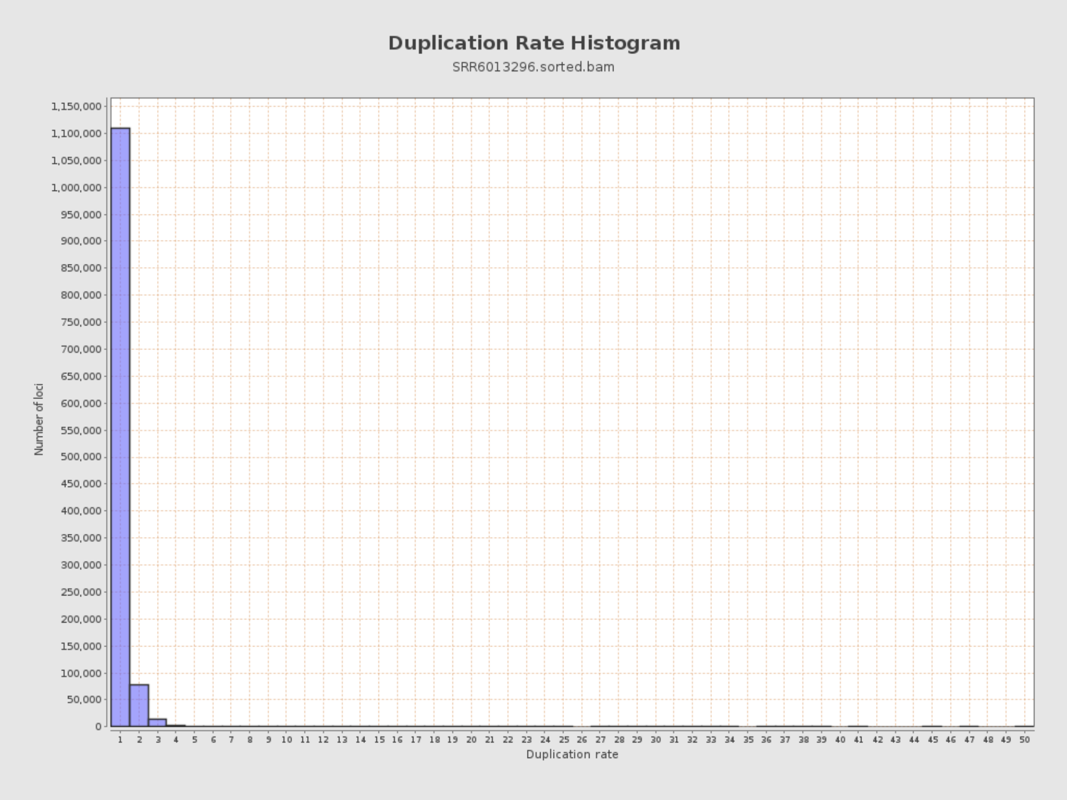
5. Results : Coverage Histogram (0-50X)



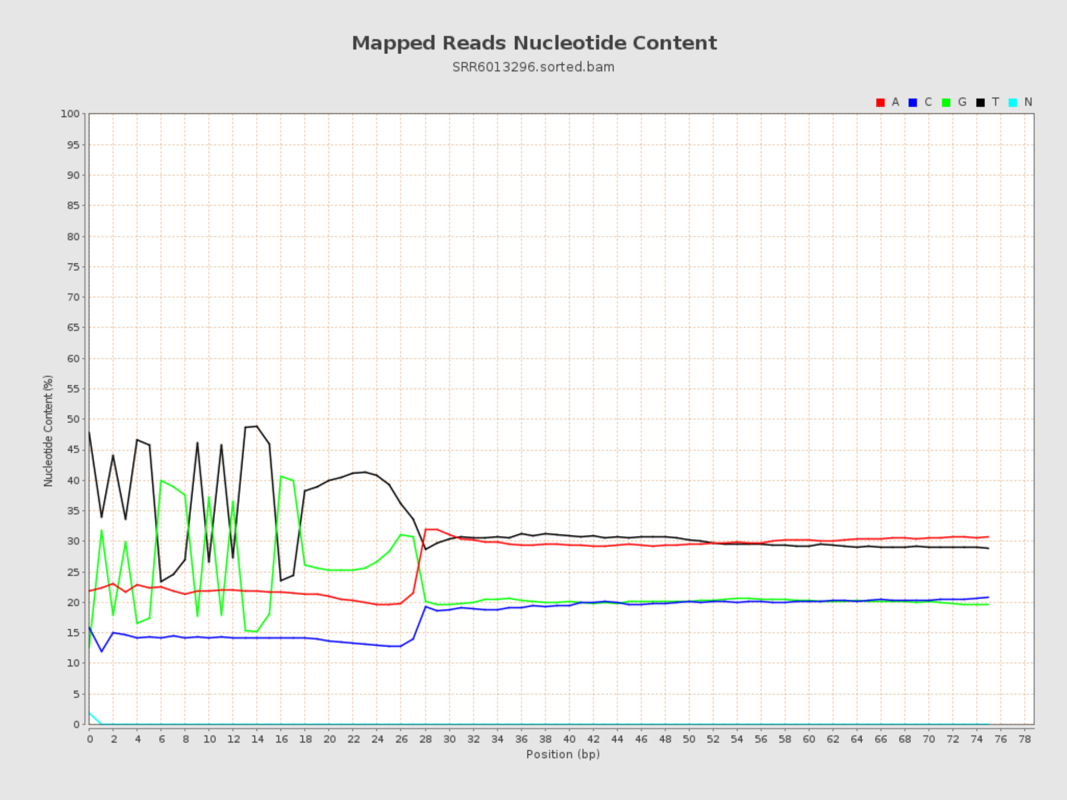
6. Results : Genome Fraction Coverage



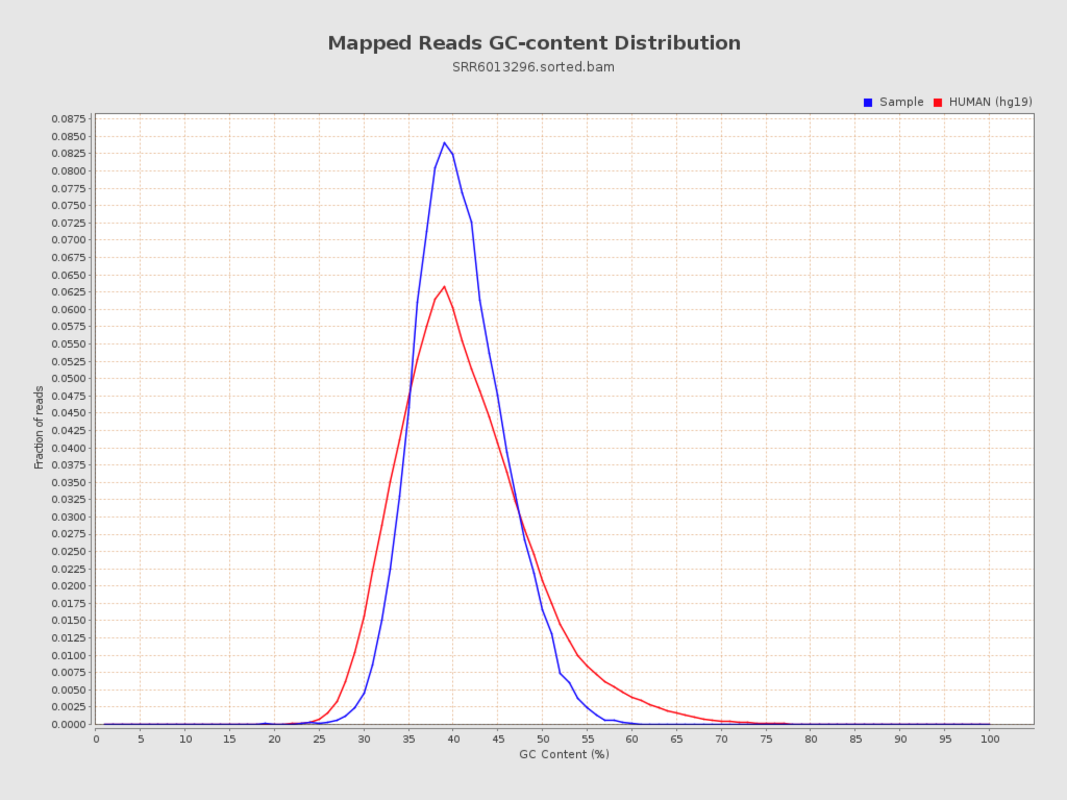
7. Results : Duplication Rate Histogram



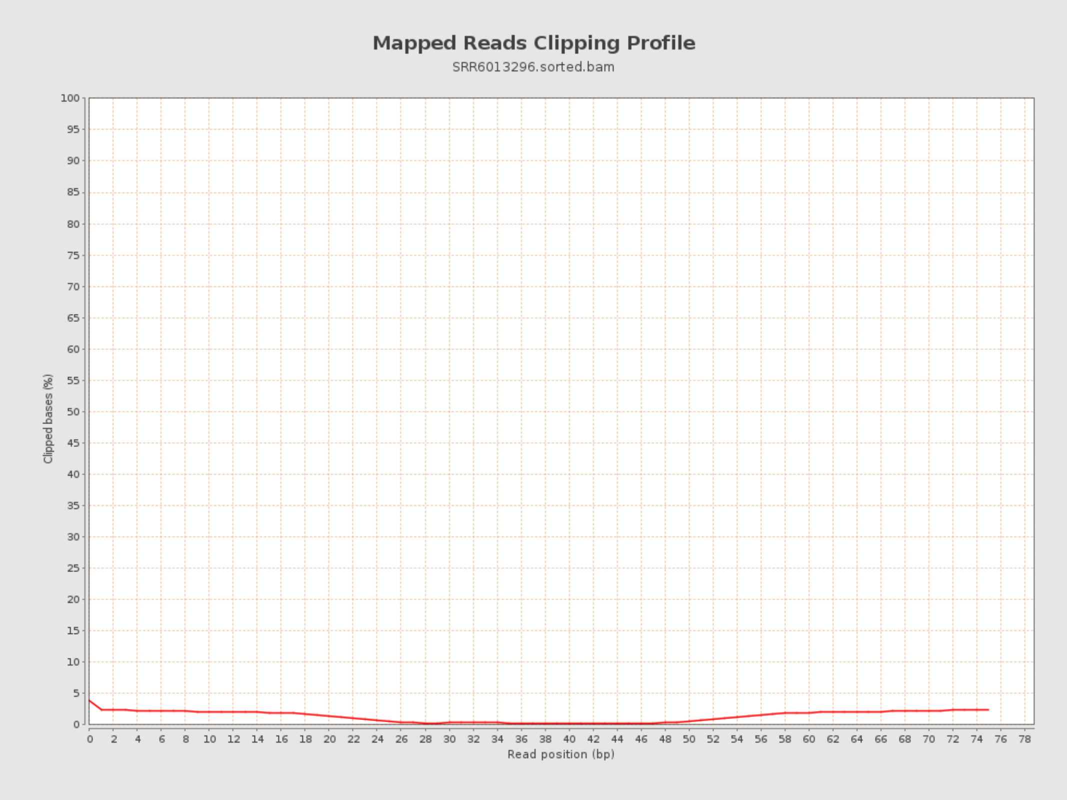
8. Results : Mapped Reads Nucleotide Content



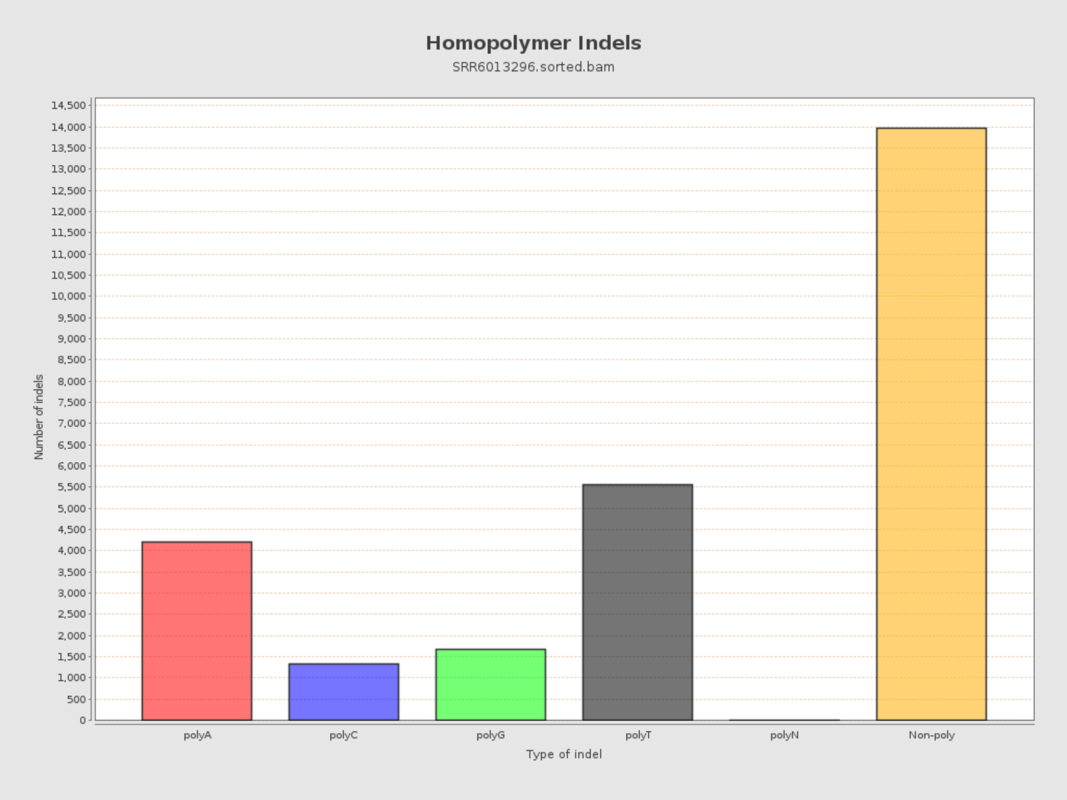
9. Results : Mapped Reads GC-content Distribution



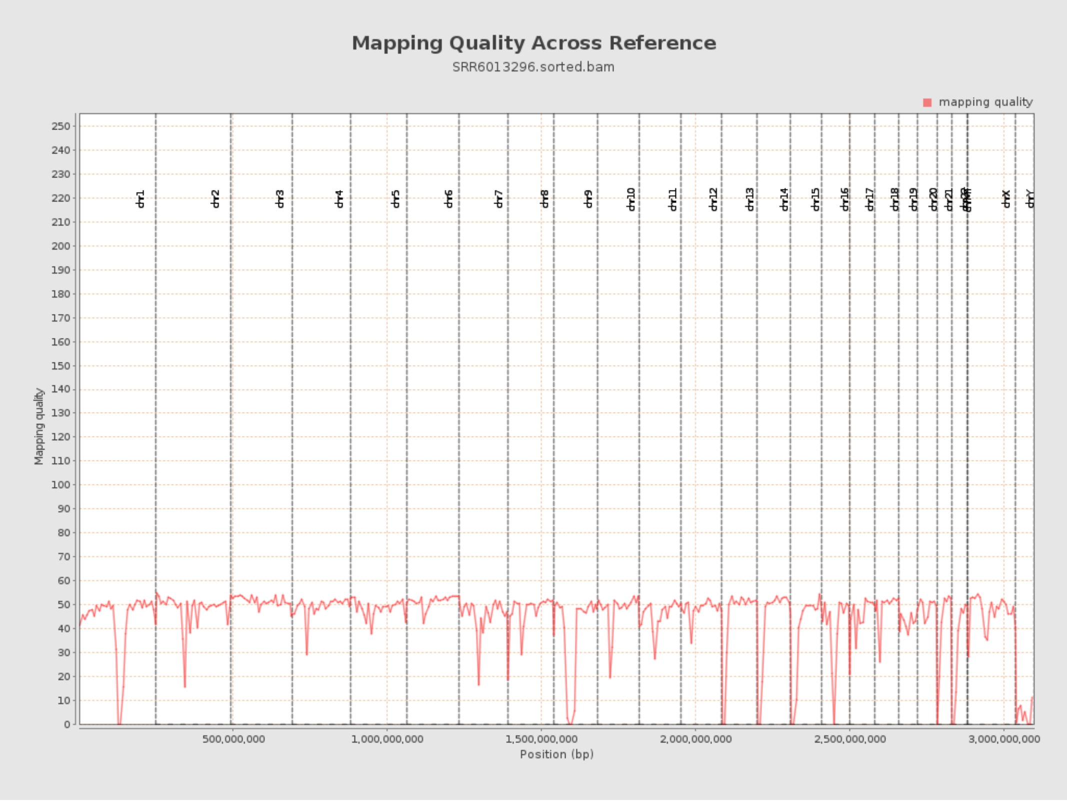
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram