Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 02:41:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004116.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_SRR6004116 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004116.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 02:41:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004116.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,980,065
Mapped reads	3,484,092 / 87.54%
Unmapped reads	495,973 / 12.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,371 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	231,935 / 5.83%
Duplication rate	5.15%
Clipped reads	1,318,134 / 33.12%

2.2. ACGT Content

Number/percentage of A's	67,800,972 / 28.39%
Number/percentage of C's	44,515,239 / 18.64%
Number/percentage of T's	76,595,446 / 32.07%
Number/percentage of G's	49,864,905 / 20.88%
Number/percentage of N's	33,471 / 0.01%
GC Percentage	39.52%

2.3. Coverage

Mean	0.0772

Standard Deviation	0.7853

2.4. Mapping Quality

Mean Mapping Quality	45.24

2.5. Mismatches and indels

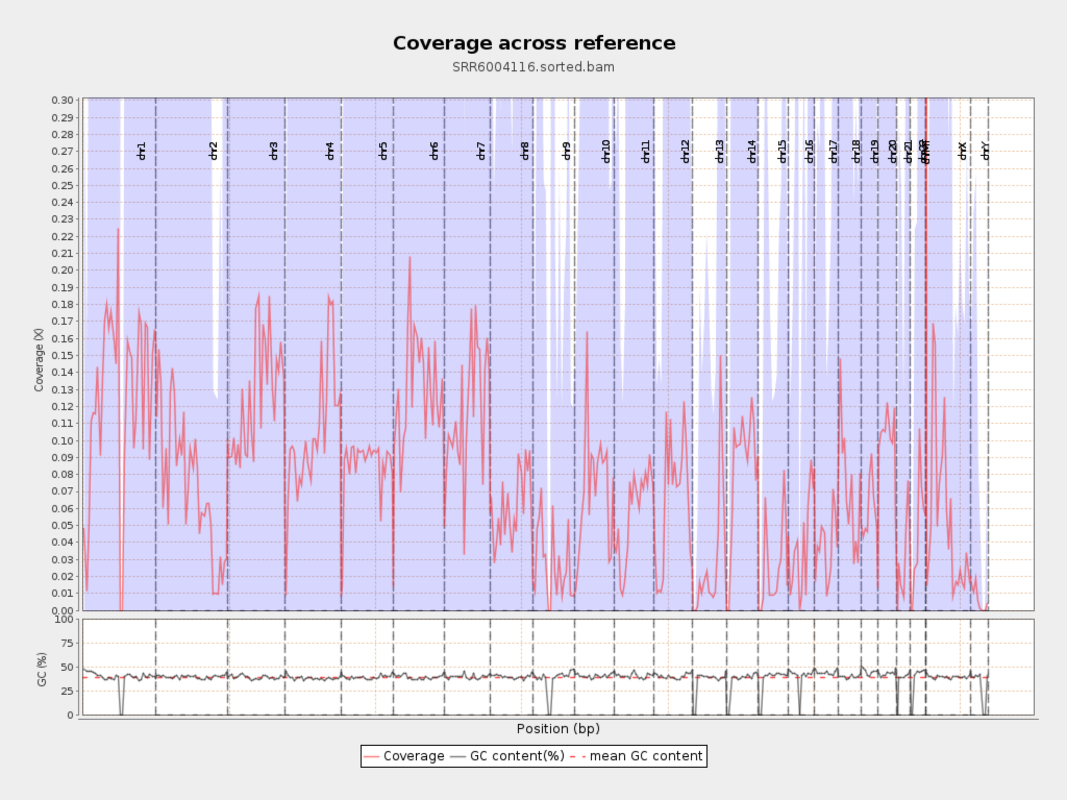
General error rate	0.93%
Mismatches	2,196,623
Insertions	17,978
Mapped reads with at least one insertion	0.51%
Deletions	58,936
Mapped reads with at least one deletion	1.67%
Homopolymer indels	47.2%

2.6. Chromosome stats

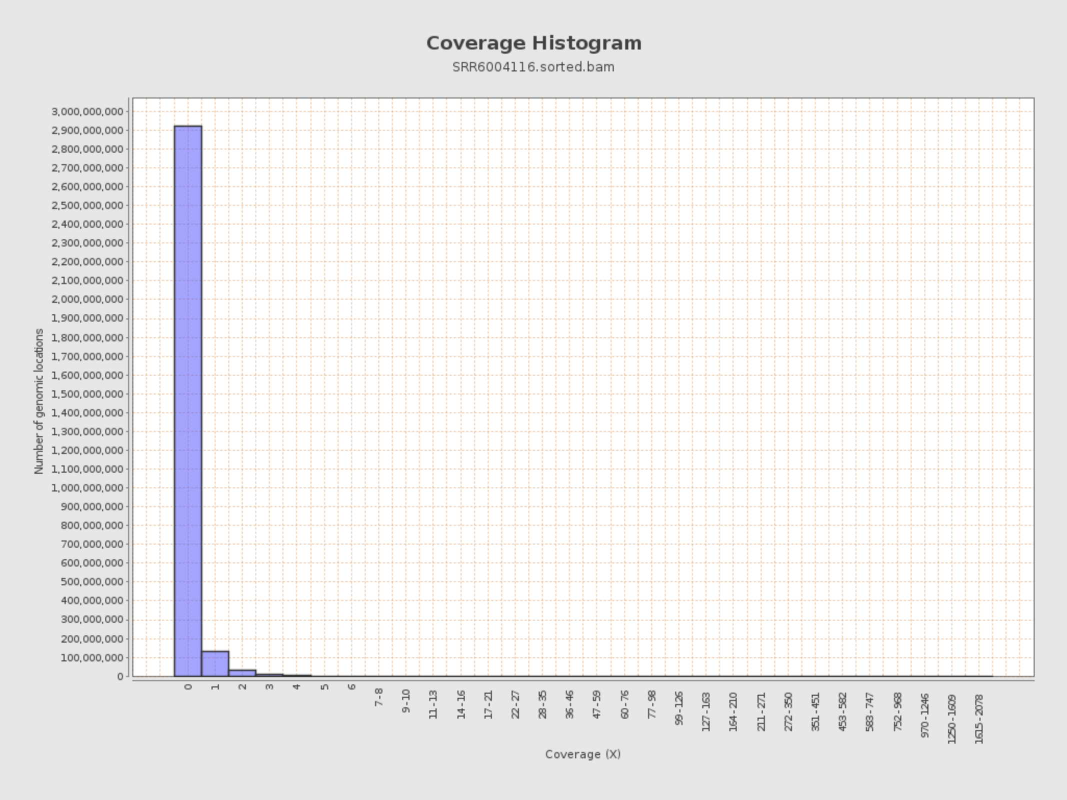
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31086475	0.1247	1.909
chr2	243199373	17958409	0.0738	0.609
chr3	198022430	24604376	0.1243	0.4887
chr4	191154276	20183960	0.1056	0.4192
chr5	180915260	15279485	0.0845	0.3741
chr6	171115067	22699391	0.1327	0.6911
chr7	159138663	18648050	0.1172	1.097

chr8	146364022	8846928	0.0604	0.5242
chr9	141213431	3882566	0.0275	0.4309
chr10	135534747	9532627	0.0703	0.9645
chr11	135006516	7707817	0.0571	0.6159
chr12	133851895	8664548	0.0647	0.3344
chr13	115169878	3486493	0.0303	0.2269
chr14	107349540	9099329	0.0848	0.3787
chr15	102531392	2650553	0.0259	0.2049
chr16	90354753	3290243	0.0364	0.3213
chr17	81195210	2984489	0.0368	0.2722
chr18	78077248	5579064	0.0715	1.1906
chr19	59128983	3471096	0.0587	1.1253
chr20	63025520	6573492	0.1043	0.4176
chr21	48129895	1535491	0.0319	0.2456
chr22	51304566	2373776	0.0463	0.2726
chrMT	16571	110028	6.6398	4.2849
chrX	155270560	8265874	0.0532	0.3773
chrY	59373566	392463	0.0066	0.1337

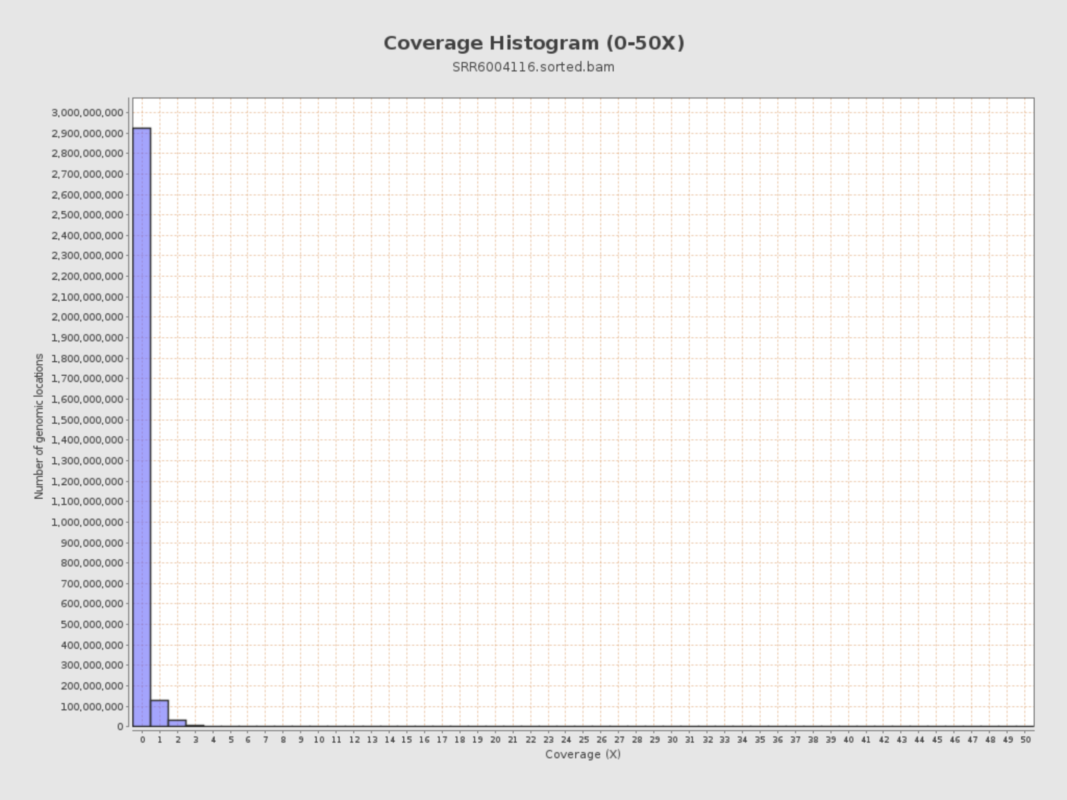
3. Results : Coverage across reference



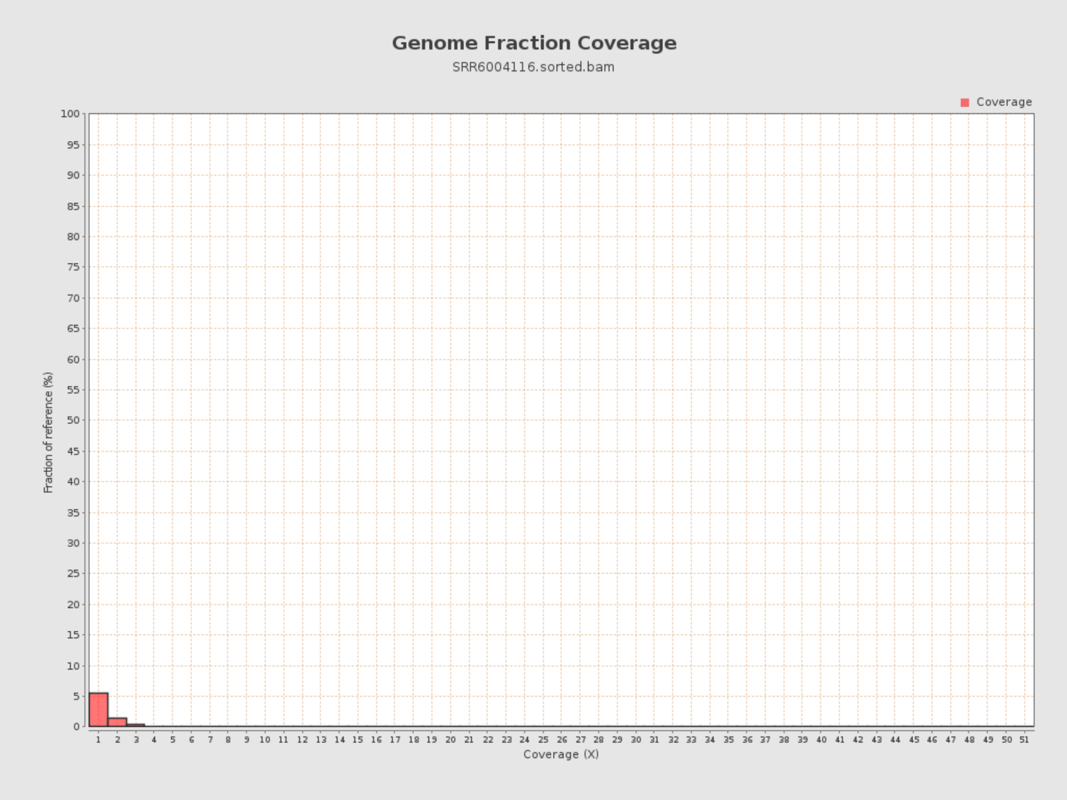
4. Results : Coverage Histogram



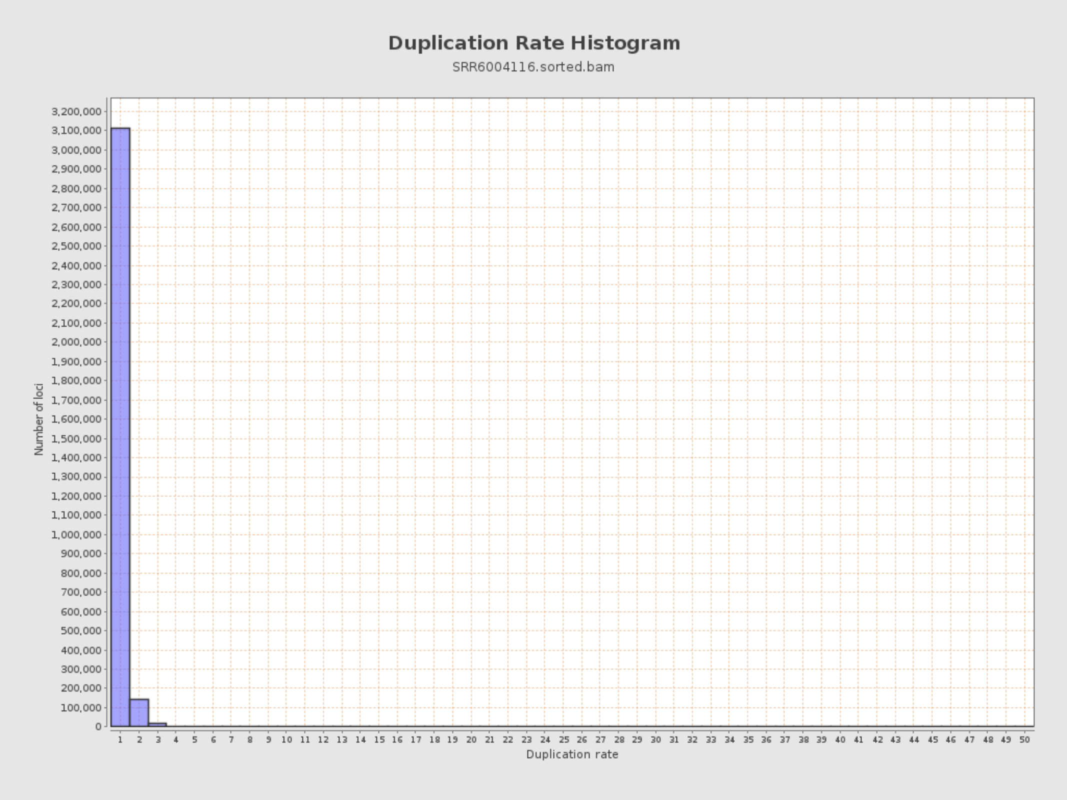
5. Results : Coverage Histogram (0-50X)



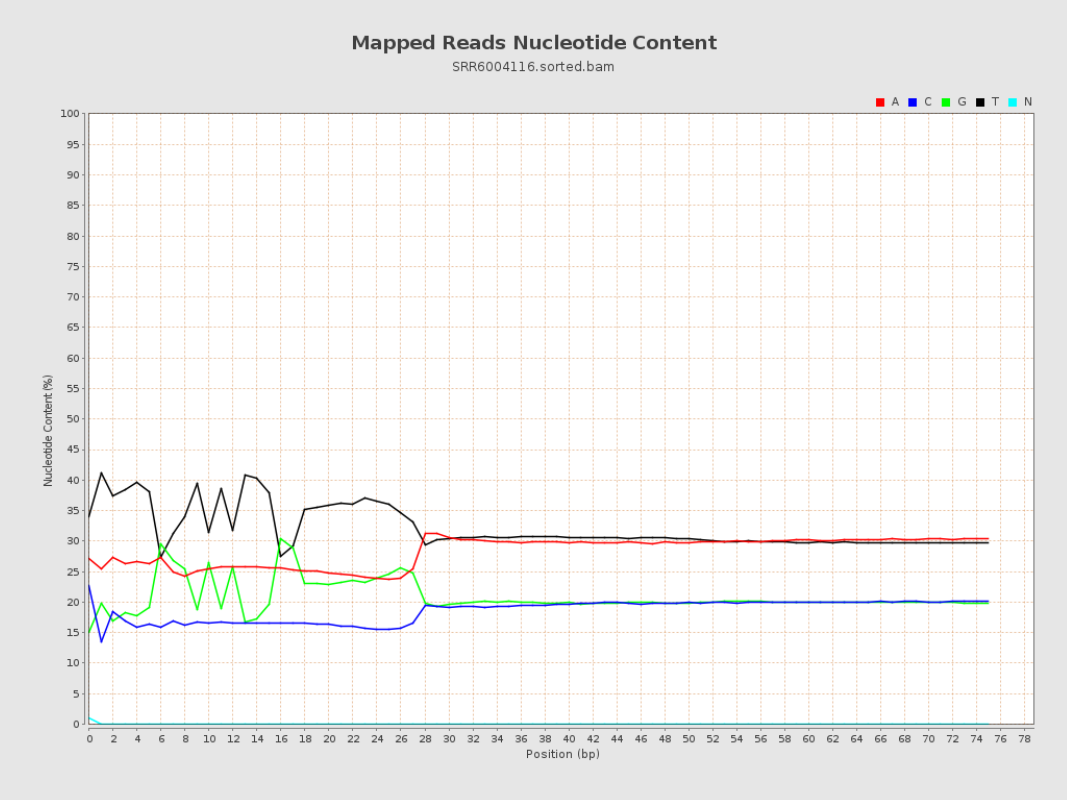
6. Results : Genome Fraction Coverage



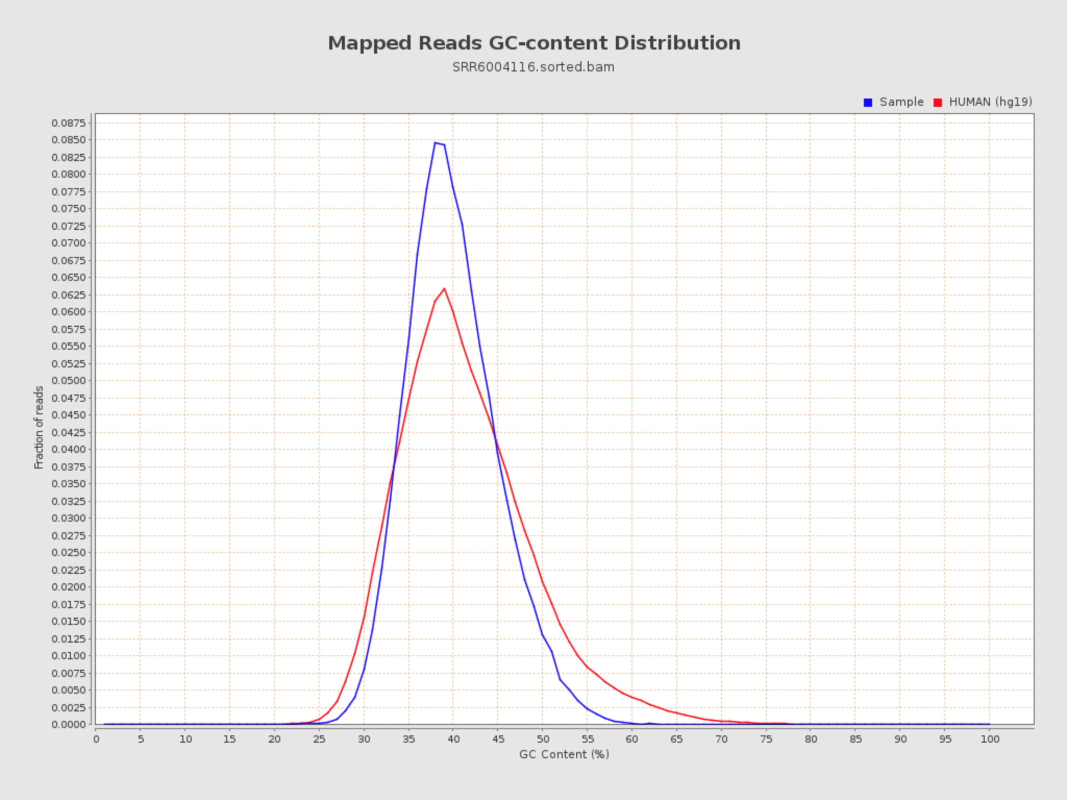
7. Results : Duplication Rate Histogram



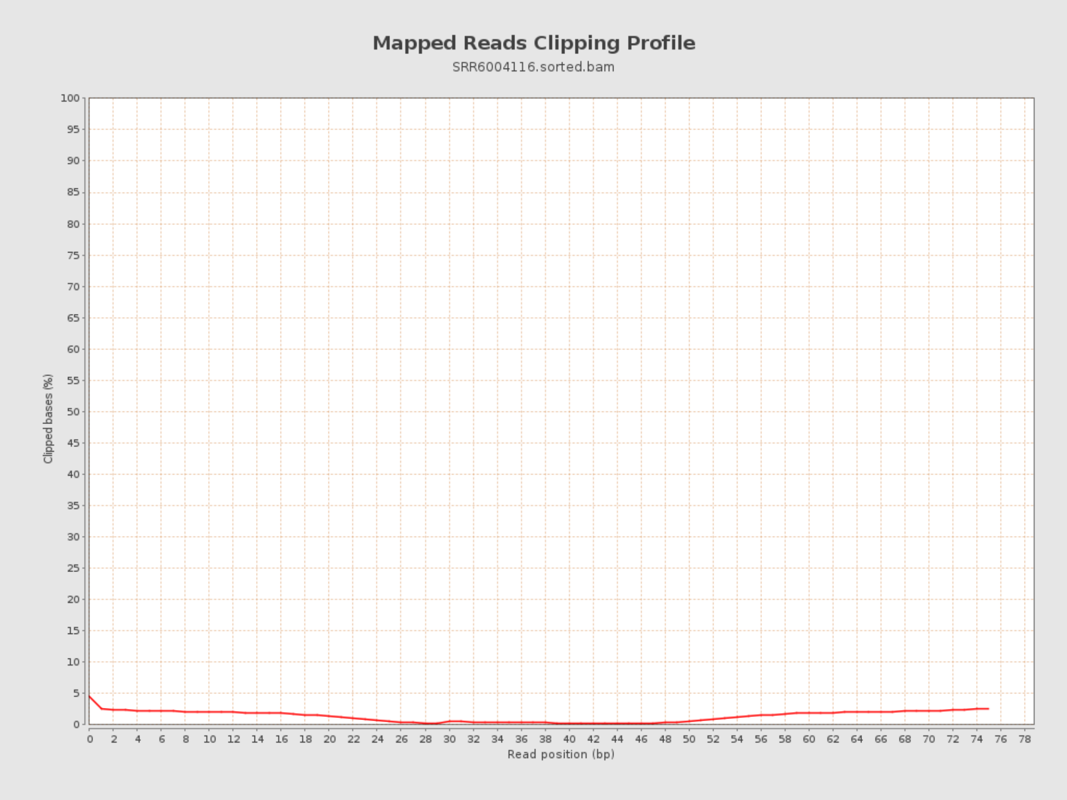
8. Results : Mapped Reads Nucleotide Content



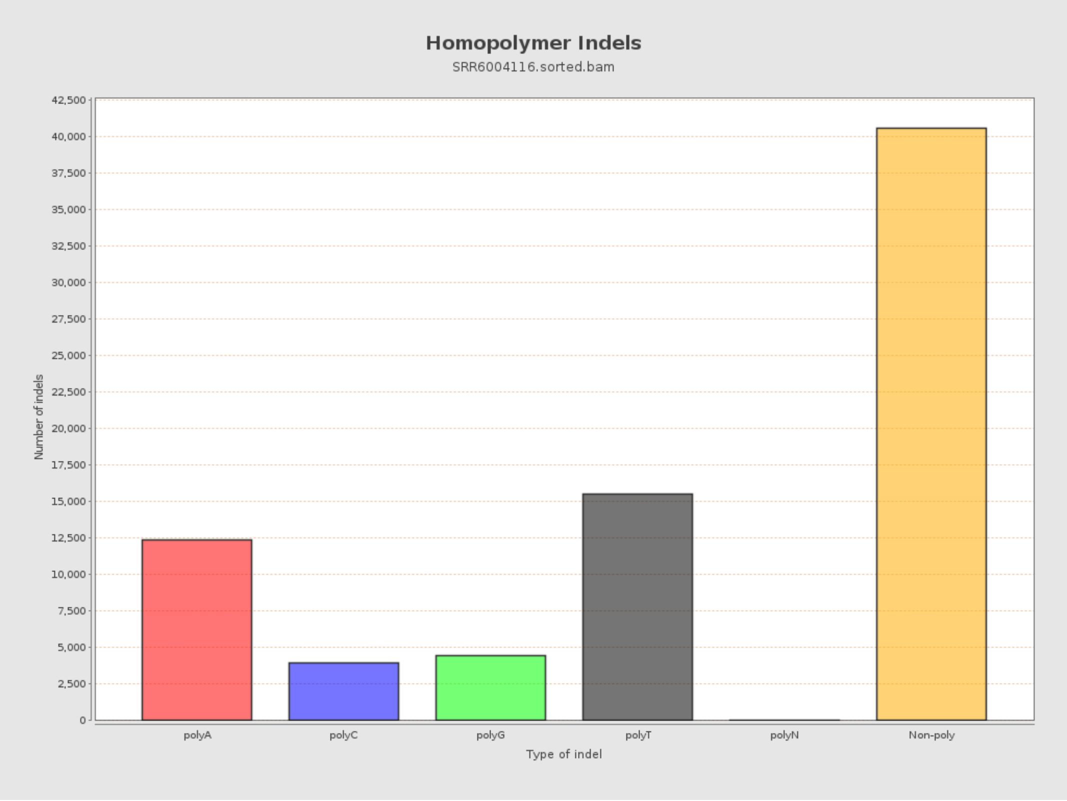
9. Results : Mapped Reads GC-content Distribution



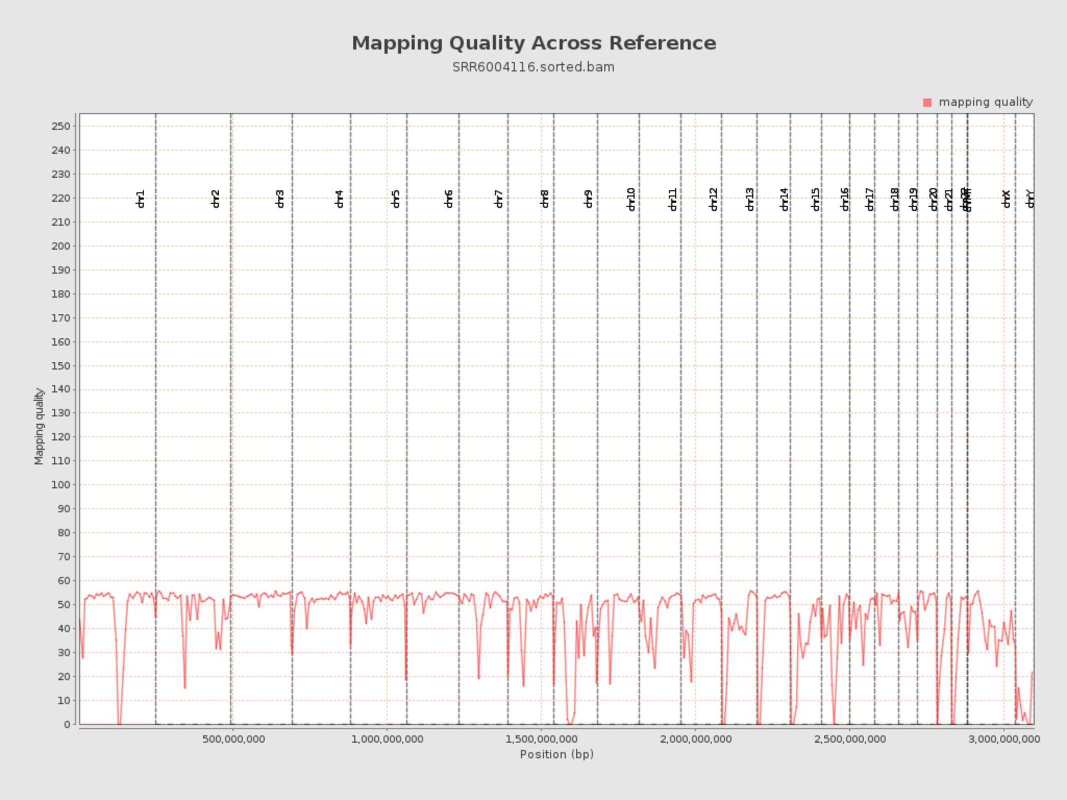
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram