Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:33:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008812.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_SRR6008812 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008812.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:33:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008812.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,559,480
Mapped reads	1,285,557 / 82.43%
Unmapped reads	273,923 / 17.57%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,079 / 0.9%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	161,820 / 10.38%
Duplication rate	9.59%
Clipped reads	647,659 / 41.53%

2.2. ACGT Content

Number/percentage of A's	22,453,735 / 26.66%
Number/percentage of C's	15,745,821 / 18.69%
Number/percentage of T's	26,387,532 / 31.33%
Number/percentage of G's	19,604,722 / 23.28%
Number/percentage of N's	38,072 / 0.05%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0272

Standard Deviation	0.3167

2.4. Mapping Quality

Mean Mapping Quality	43.99

2.5. Mismatches and indels

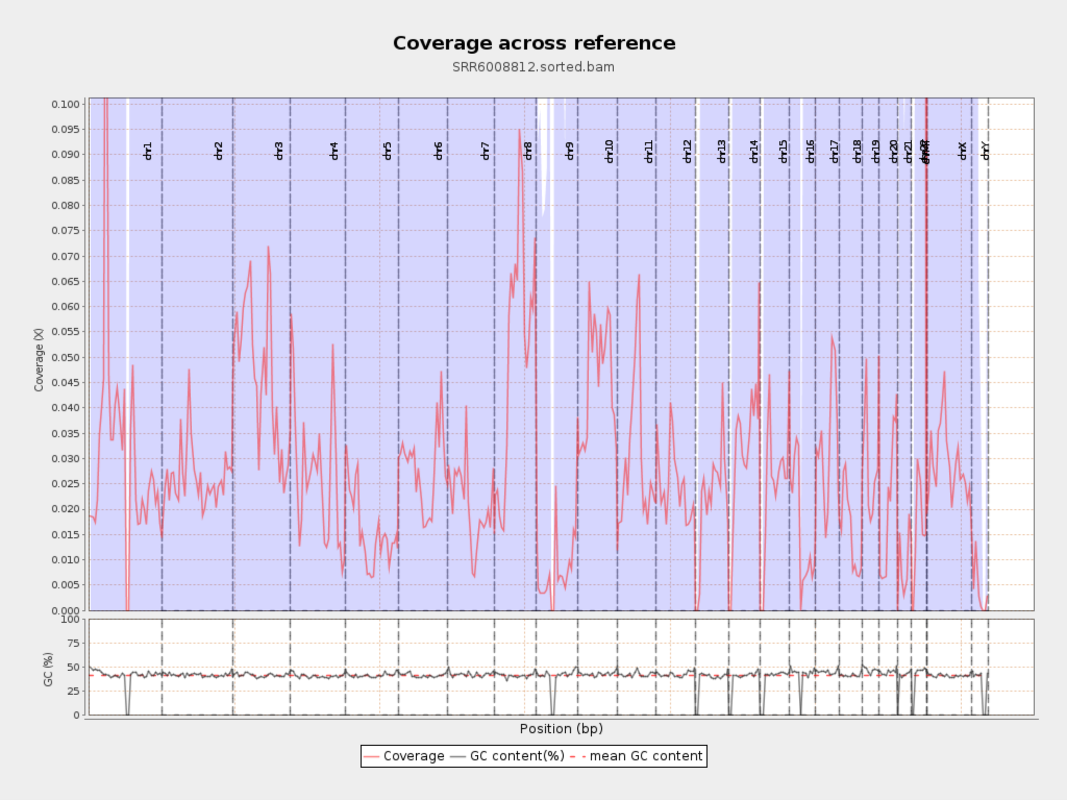
General error rate	0.83%
Mismatches	688,026
Insertions	5,725
Mapped reads with at least one insertion	0.44%
Deletions	20,214
Mapped reads with at least one deletion	1.56%
Homopolymer indels	46.83%

2.6. Chromosome stats

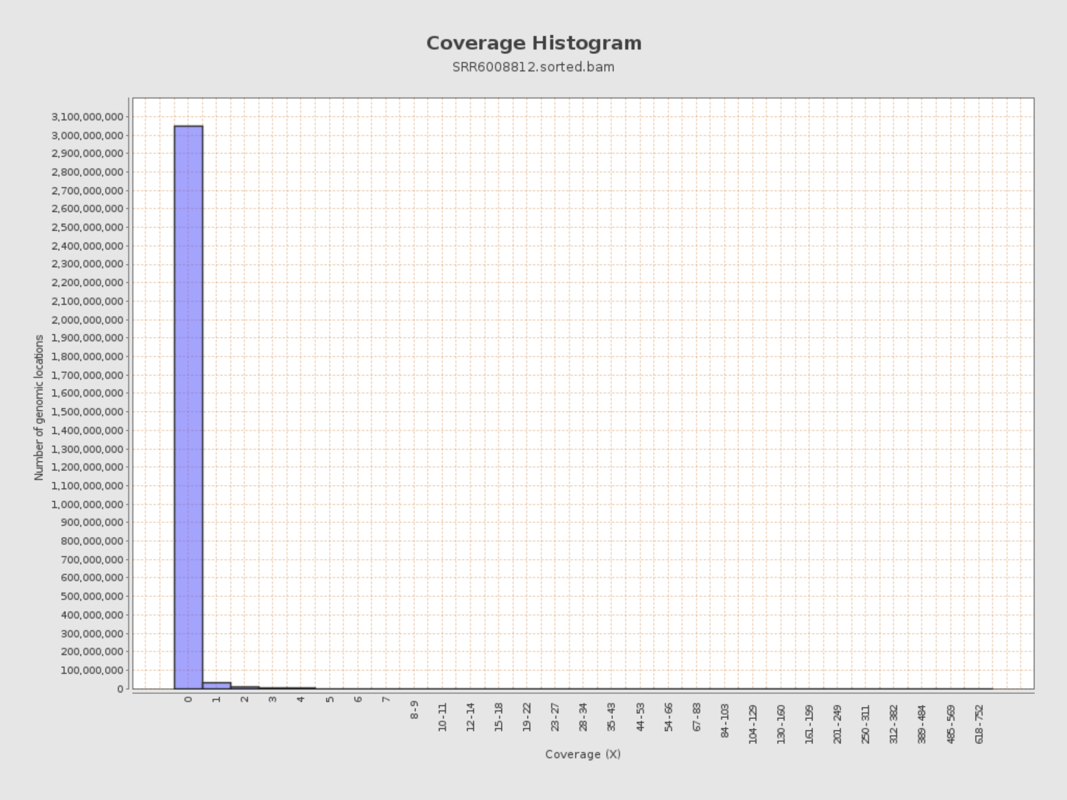
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7808366	0.0313	0.3933
chr2	243199373	6413914	0.0264	0.3343
chr3	198022430	9181201	0.0464	0.339
chr4	191154276	5011376	0.0262	0.2573
chr5	180915260	2826044	0.0156	0.1904
chr6	171115067	4780007	0.0279	0.2733
chr7	159138663	3306538	0.0208	0.335

chr8	146364022	7534284	0.0515	0.5588
chr9	141213431	1058840	0.0075	0.1846
chr10	135534747	6229584	0.046	0.3788
chr11	135006516	4097954	0.0304	0.4323
chr12	133851895	3354466	0.0251	0.247
chr13	115169878	2525920	0.0219	0.2282
chr14	107349540	3268081	0.0304	0.2725
chr15	102531392	2534432	0.0247	0.2457
chr16	90354753	1424980	0.0158	0.1932
chr17	81195210	2667670	0.0329	0.3227
chr18	78077248	1214435	0.0156	0.355
chr19	59128983	1715493	0.029	0.3136
chr20	63025520	1268793	0.0201	0.2205
chr21	48129895	453703	0.0094	0.1495
chr22	51304566	774619	0.0151	0.1845
chrMT	16571	31584	1.906	2.5001
chrX	155270560	4539762	0.0292	0.2973
chrY	59373566	243010	0.0041	0.1235

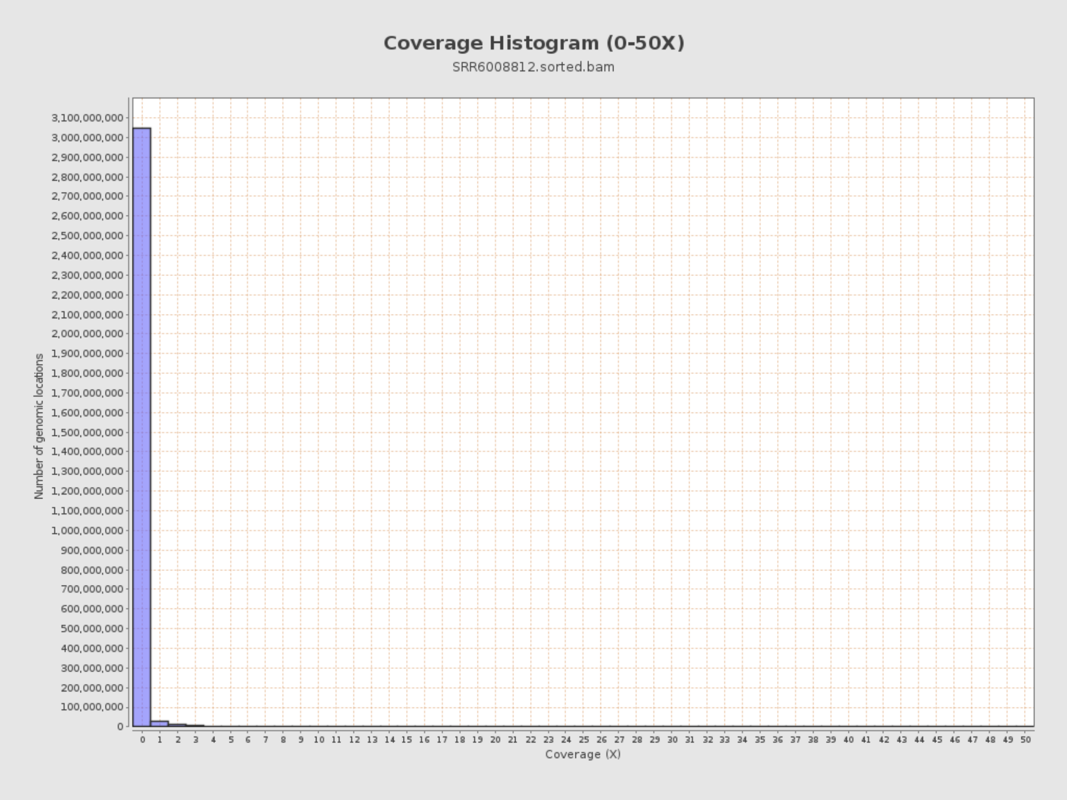
3. Results : Coverage across reference



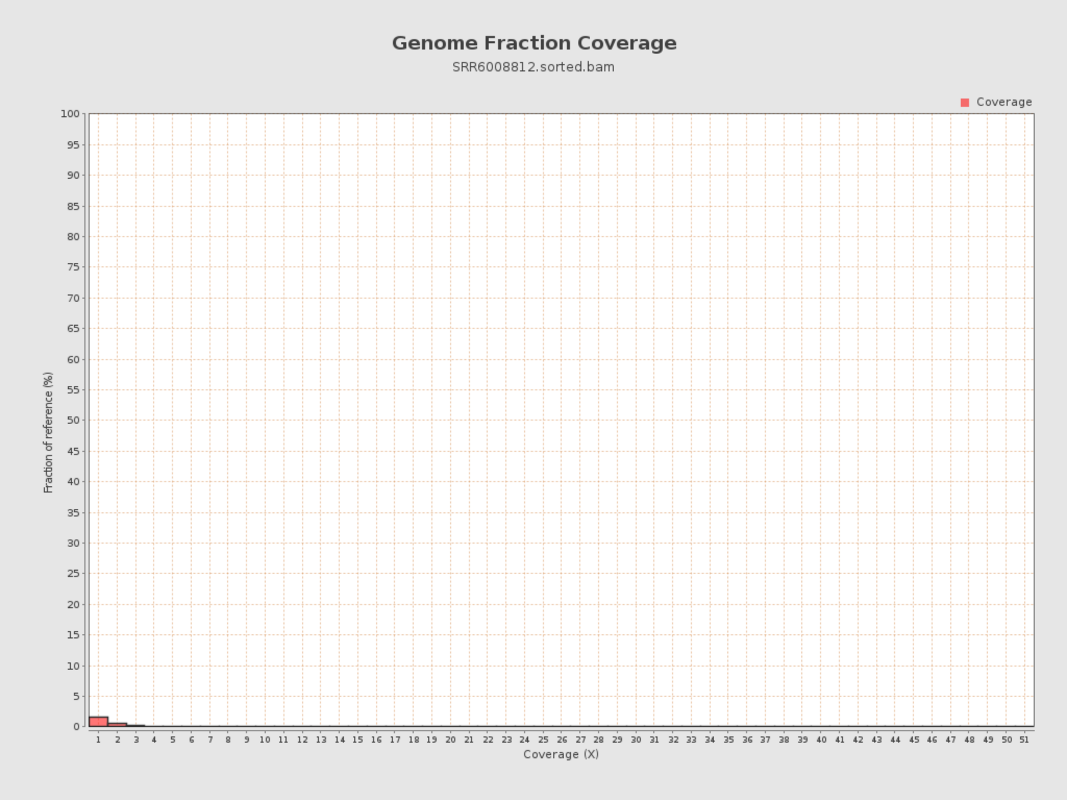
4. Results : Coverage Histogram



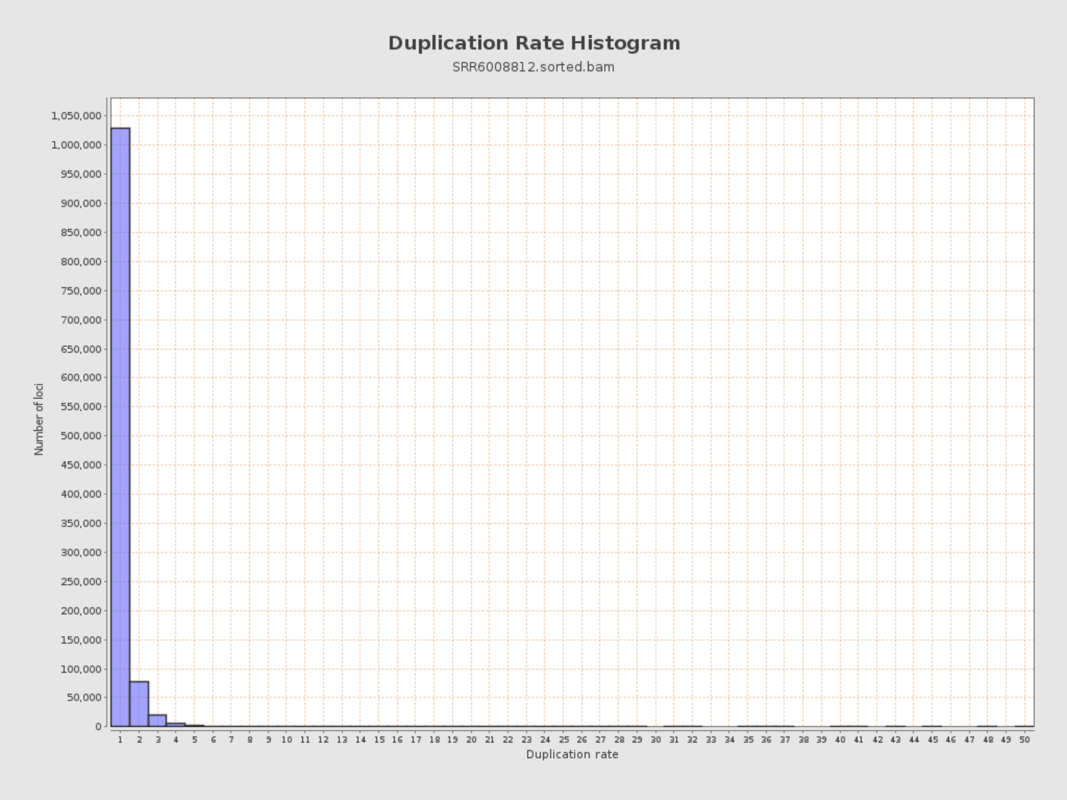
5. Results : Coverage Histogram (0-50X)



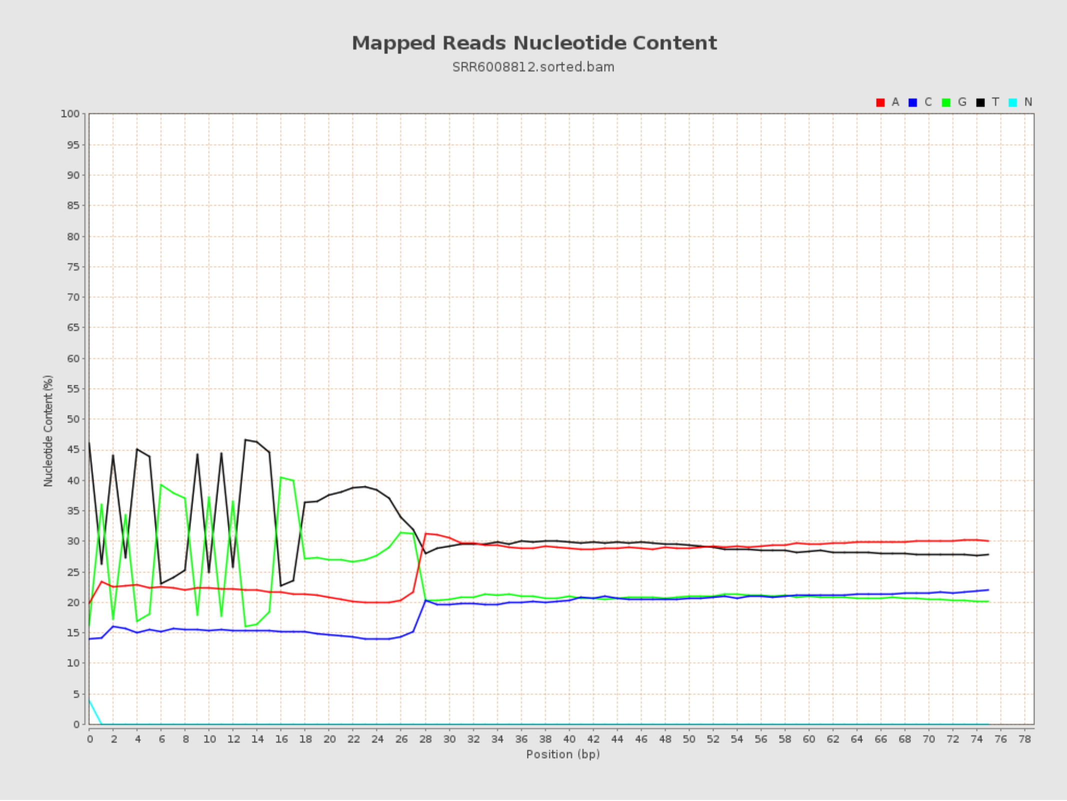
6. Results : Genome Fraction Coverage



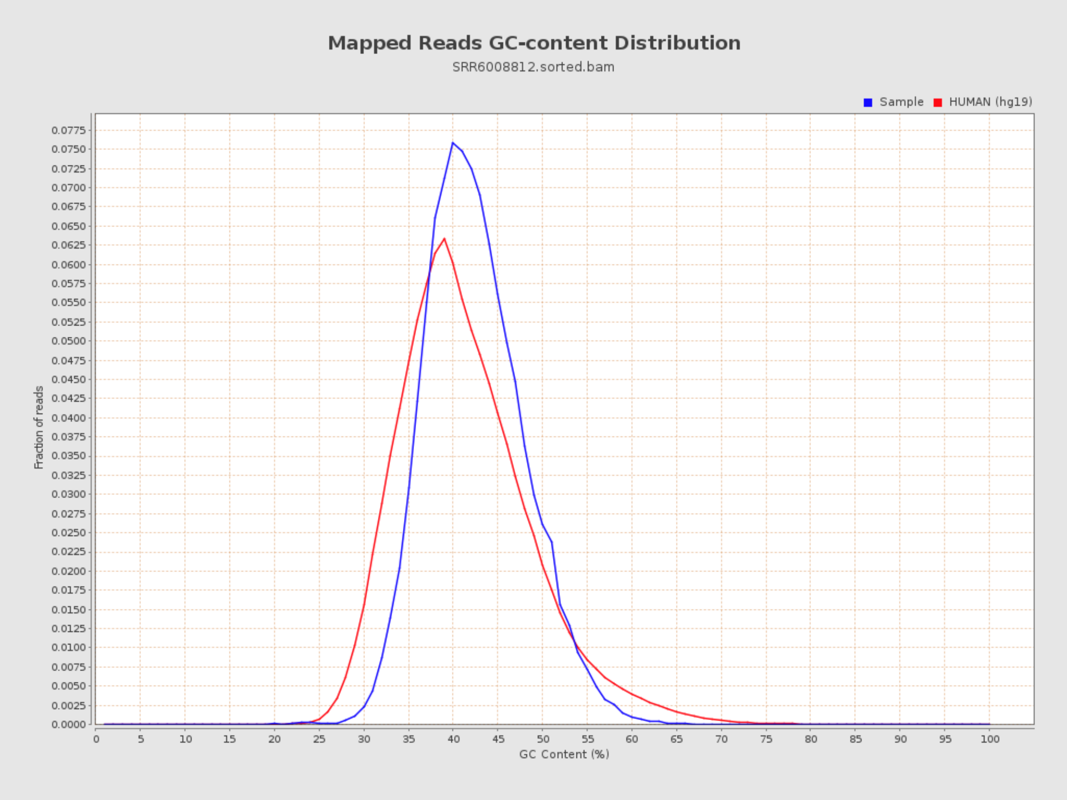
7. Results : Duplication Rate Histogram



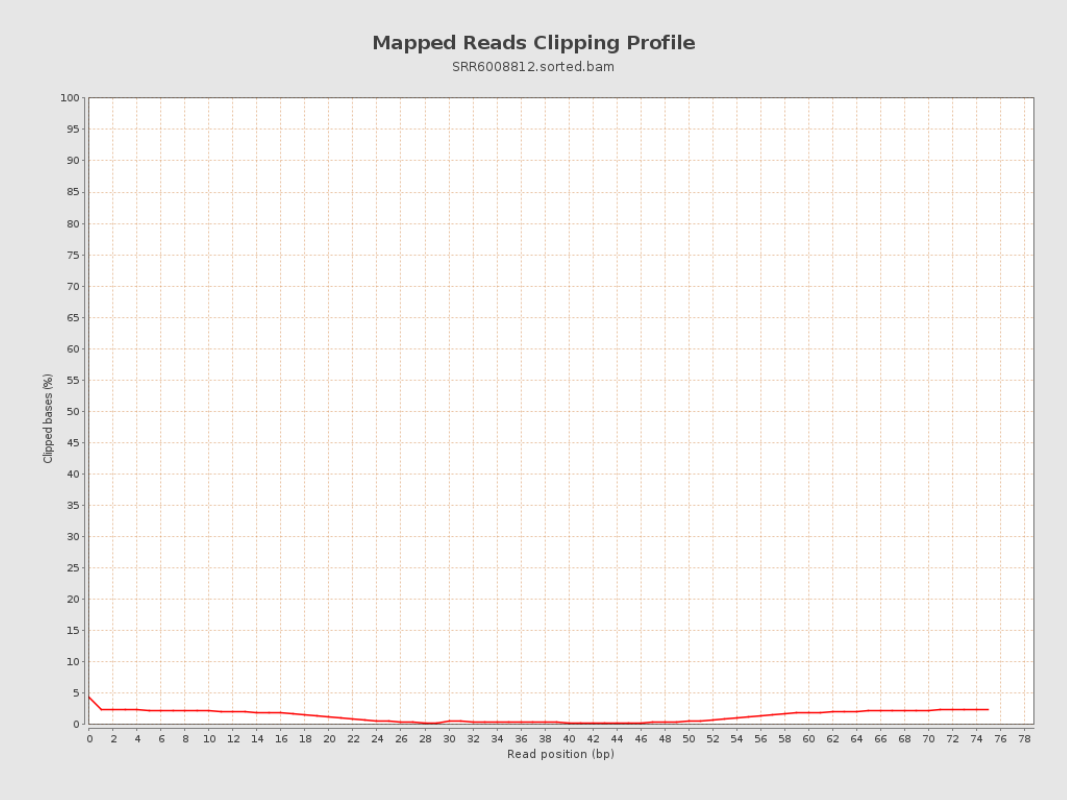
8. Results : Mapped Reads Nucleotide Content



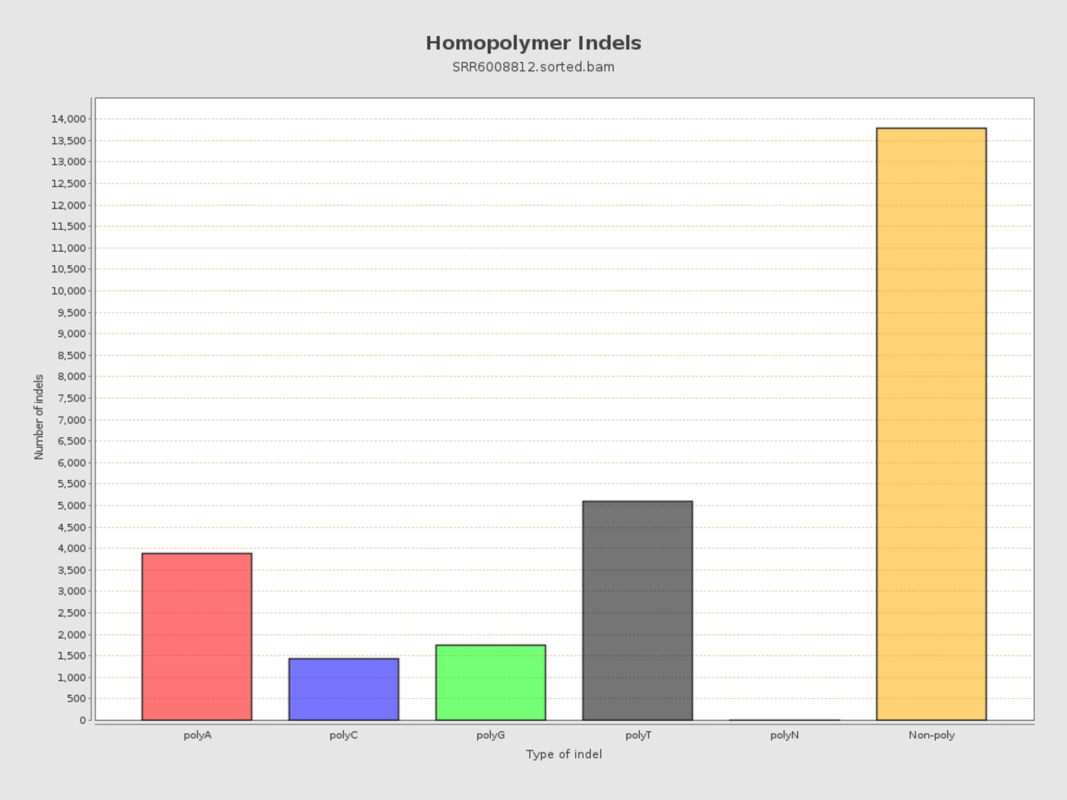
9. Results : Mapped Reads GC-content Distribution



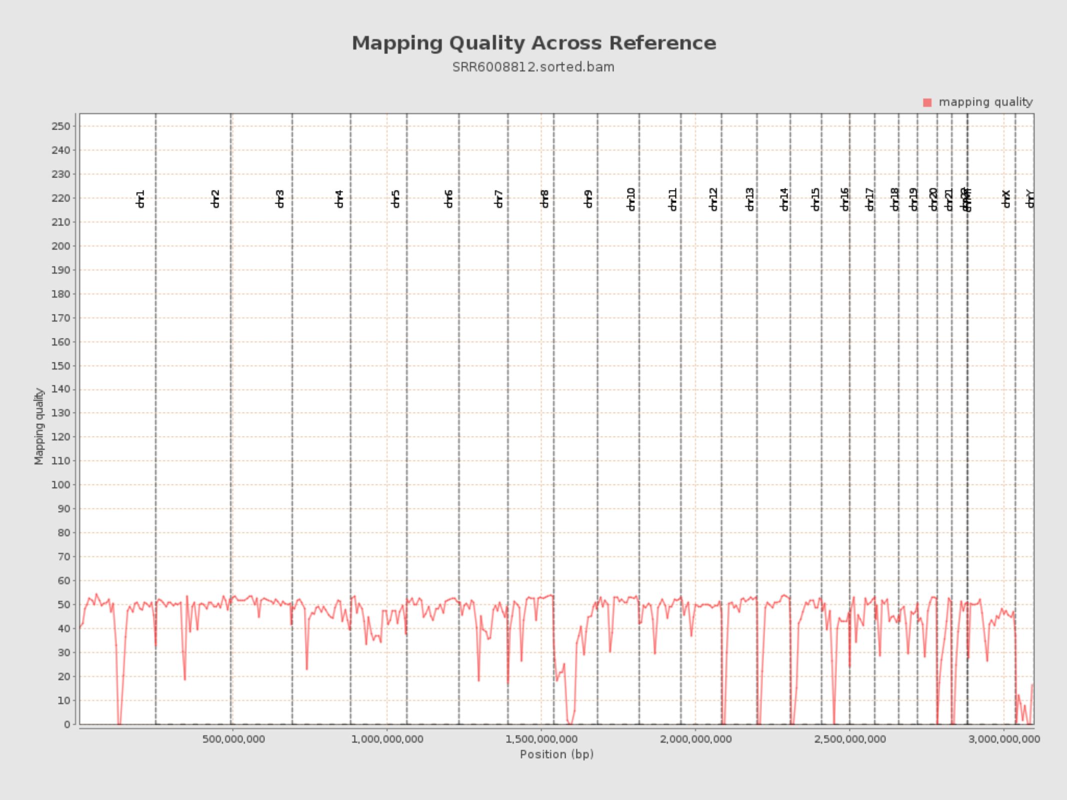
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram