Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:28:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068060.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_SRR6068060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:28:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,888,412
Mapped reads	1,516,350 / 80.3%
Unmapped reads	372,062 / 19.7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,638 / 0.72%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	307,572 / 16.29%
Duplication rate	13.52%
Clipped reads	767,416 / 40.64%

2.2. ACGT Content

Number/percentage of A's	26,691,852 / 27.04%
Number/percentage of C's	17,431,508 / 17.66%
Number/percentage of T's	32,124,670 / 32.55%
Number/percentage of G's	22,348,936 / 22.64%
Number/percentage of N's	100,007 / 0.1%
GC Percentage	40.31%

2.3. Coverage

Mean	0.0319

Standard Deviation	0.4652

2.4. Mapping Quality

Mean Mapping Quality	46.03

2.5. Mismatches and indels

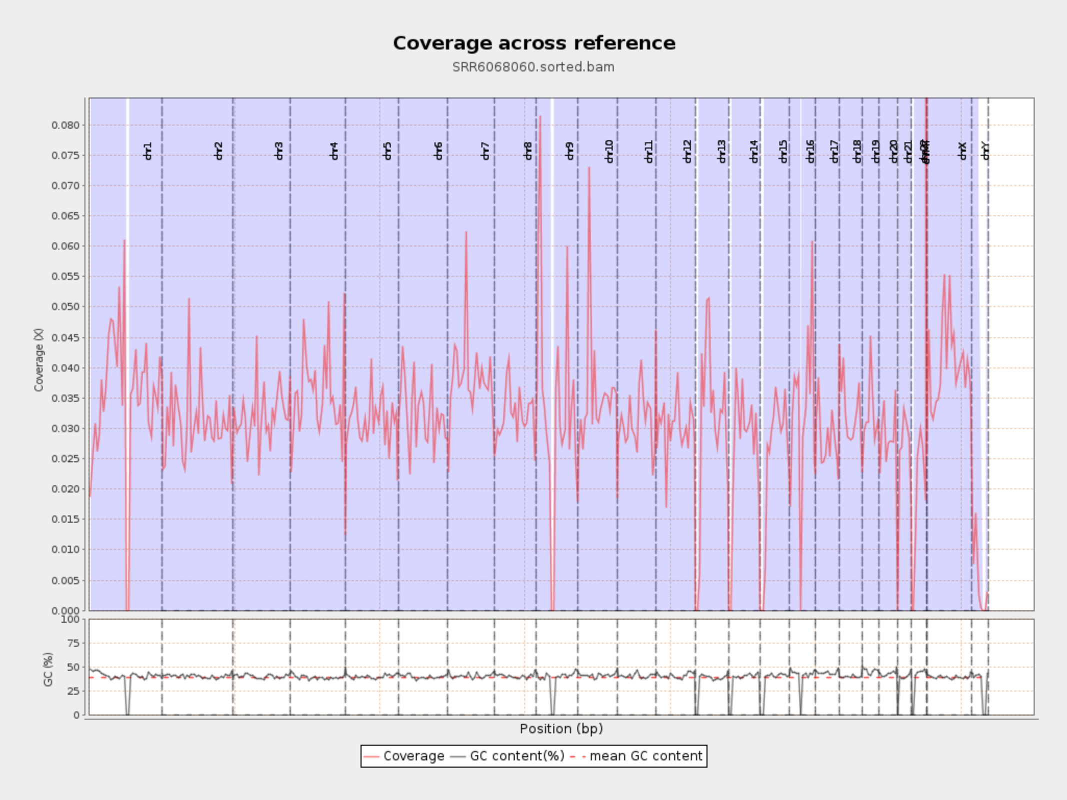
General error rate	0.87%
Mismatches	842,321
Insertions	7,934
Mapped reads with at least one insertion	0.52%
Deletions	22,753
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.9%

2.6. Chromosome stats

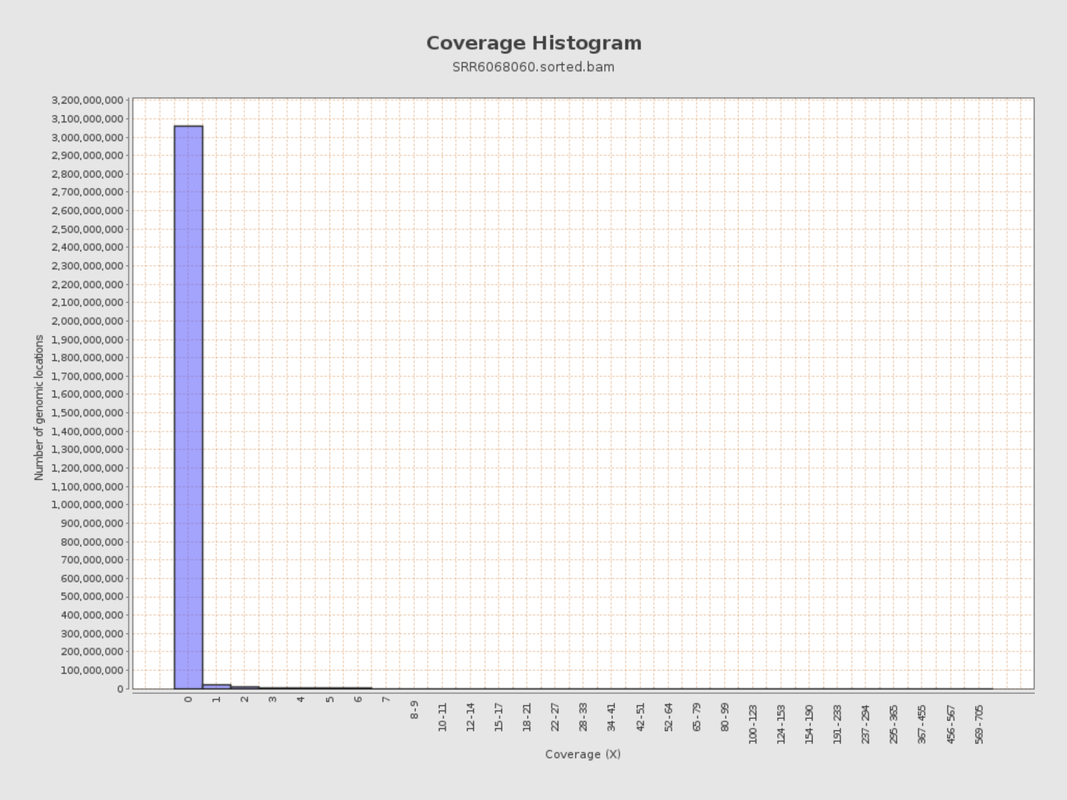
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8769268	0.0352	0.7059
chr2	243199373	7563031	0.0311	0.5128
chr3	198022430	6332036	0.032	0.4035
chr4	191154276	6841410	0.0358	0.4299
chr5	180915260	5717234	0.0316	0.3946
chr6	171115067	5589920	0.0327	0.4276
chr7	159138663	6147986	0.0386	0.5659

chr8	146364022	4710252	0.0322	0.4532
chr9	141213431	4825406	0.0342	0.4569
chr10	135534747	4819629	0.0356	0.4975
chr11	135006516	4170564	0.0309	0.4205
chr12	133851895	4021035	0.03	0.3796
chr13	115169878	3443720	0.0299	0.3919
chr14	107349540	2850226	0.0266	0.3753
chr15	102531392	2511314	0.0245	0.3425
chr16	90354753	3006793	0.0333	0.405
chr17	81195210	2285451	0.0281	0.3744
chr18	78077248	2584346	0.0331	0.6007
chr19	59128983	1923618	0.0325	0.4903
chr20	63025520	1800549	0.0286	0.3698
chr21	48129895	1211007	0.0252	0.3488
chr22	51304566	929549	0.0181	0.2794
chrMT	16571	80376	4.8504	4.8148
chrX	155270560	6293563	0.0405	0.4637
chrY	59373566	305709	0.0051	0.1574

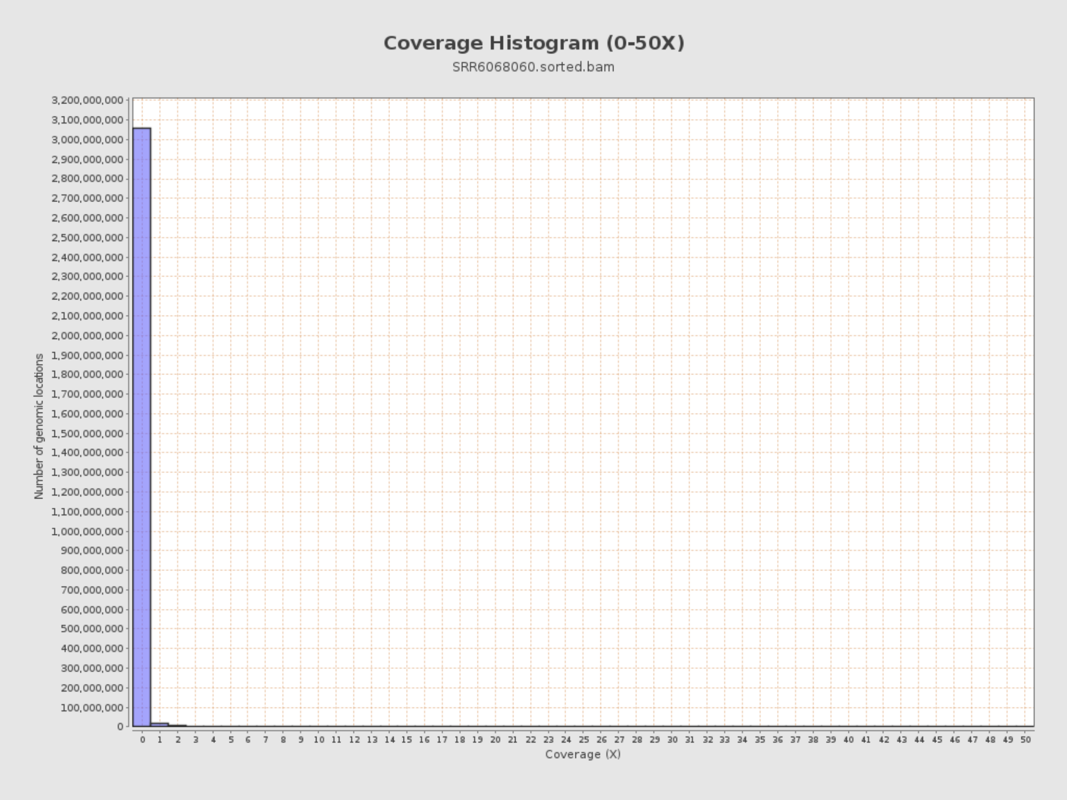
3. Results : Coverage across reference



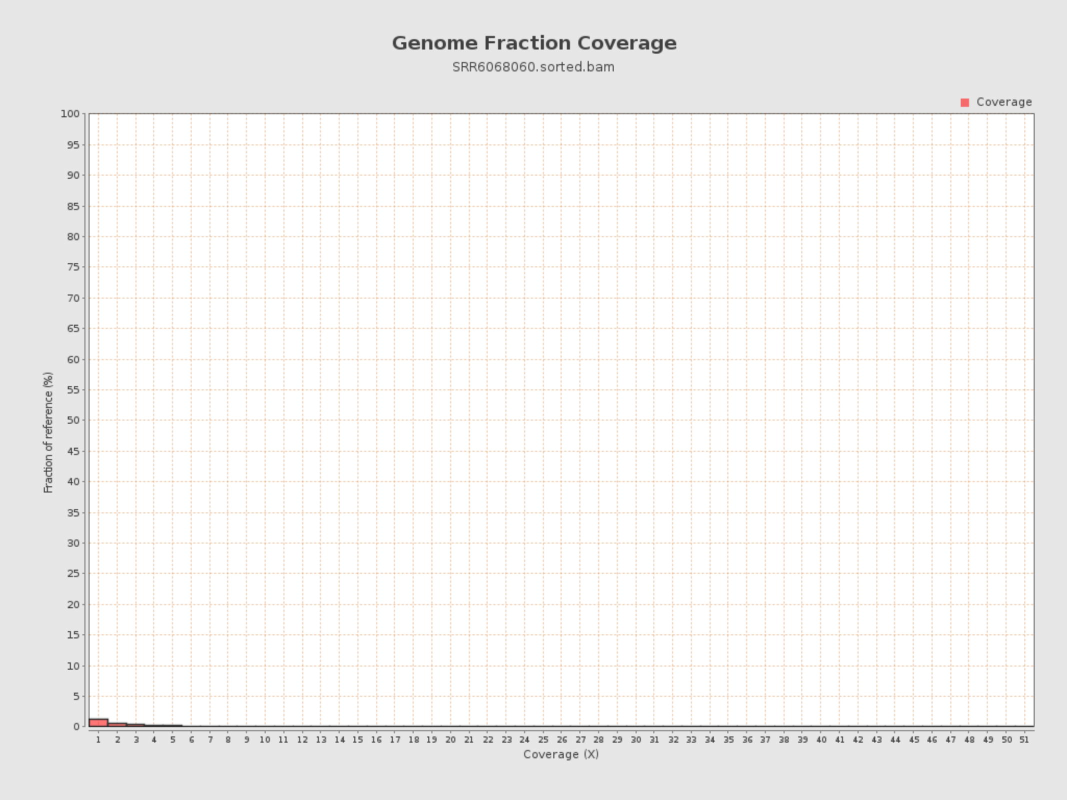
4. Results : Coverage Histogram



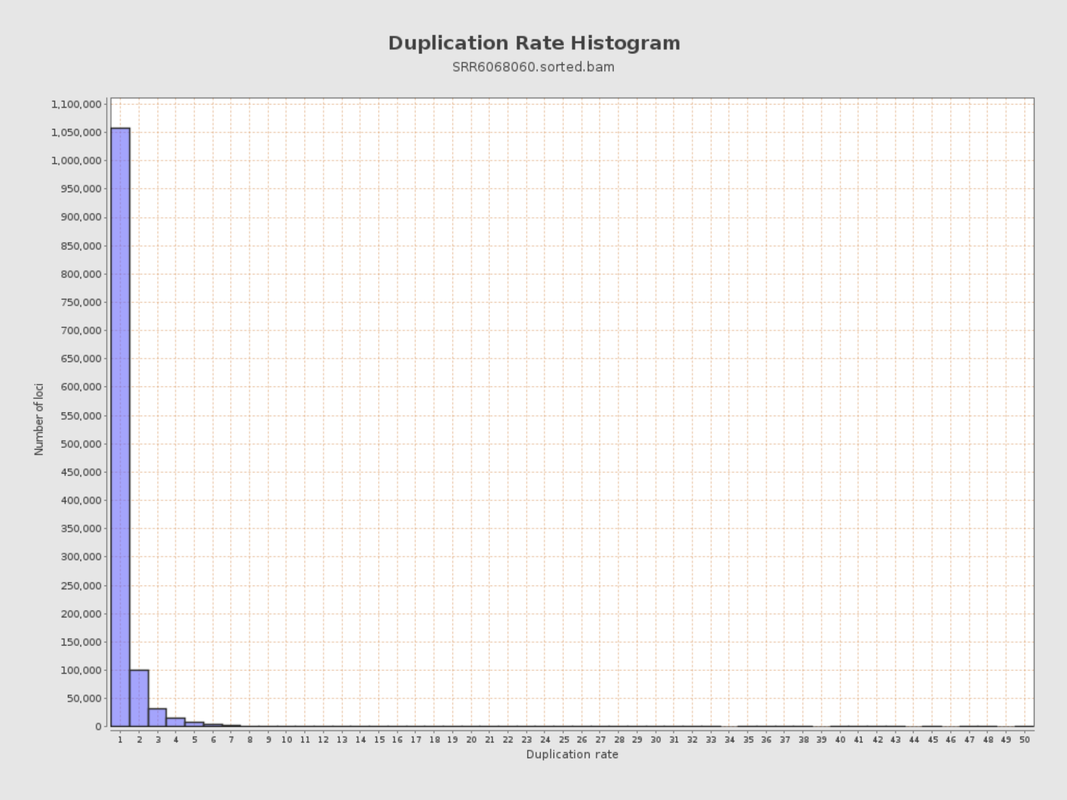
5. Results : Coverage Histogram (0-50X)



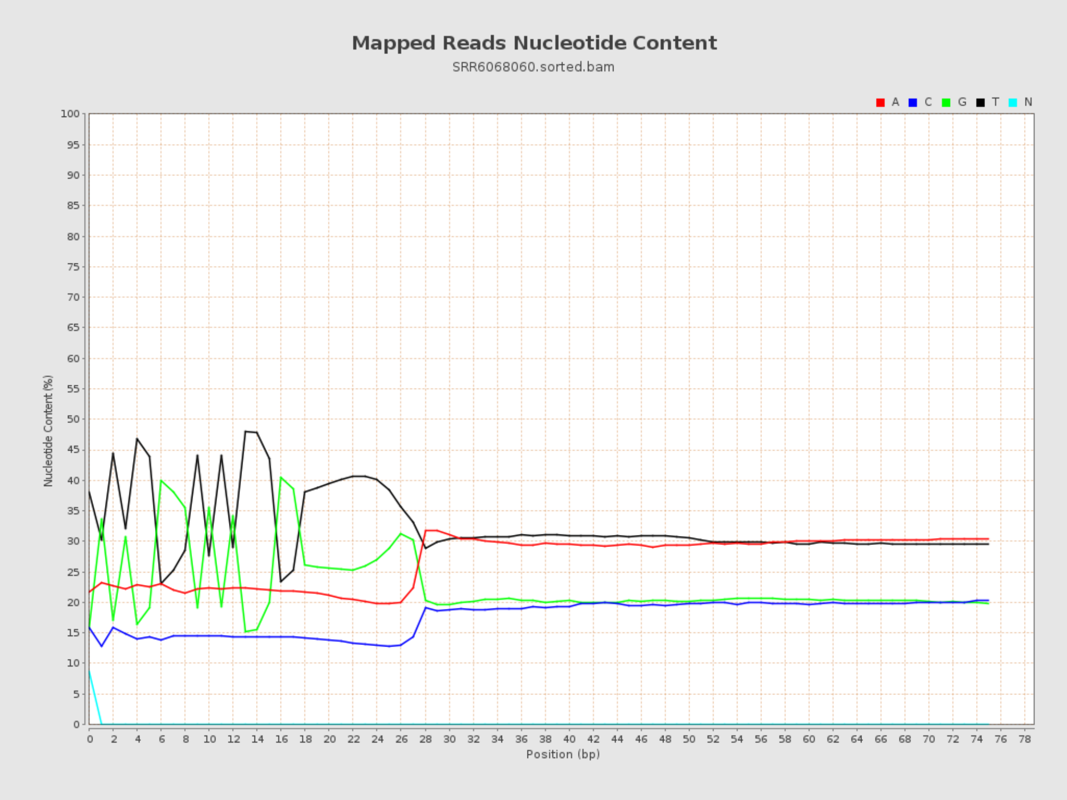
6. Results : Genome Fraction Coverage



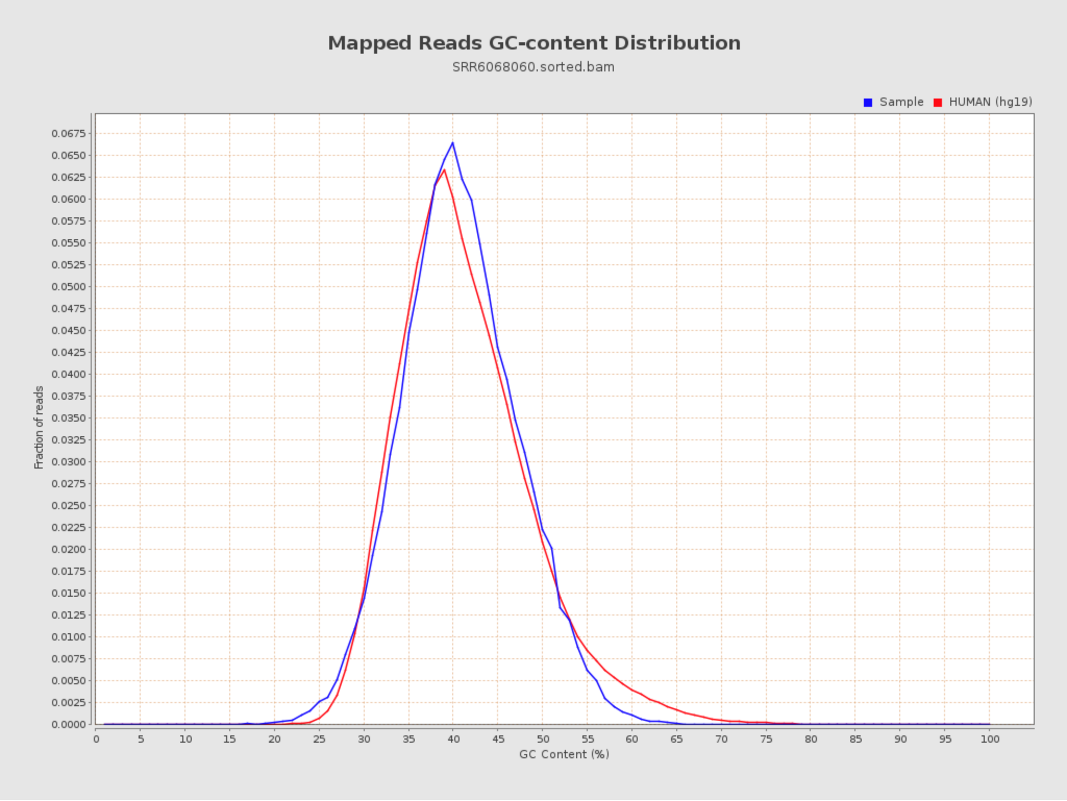
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



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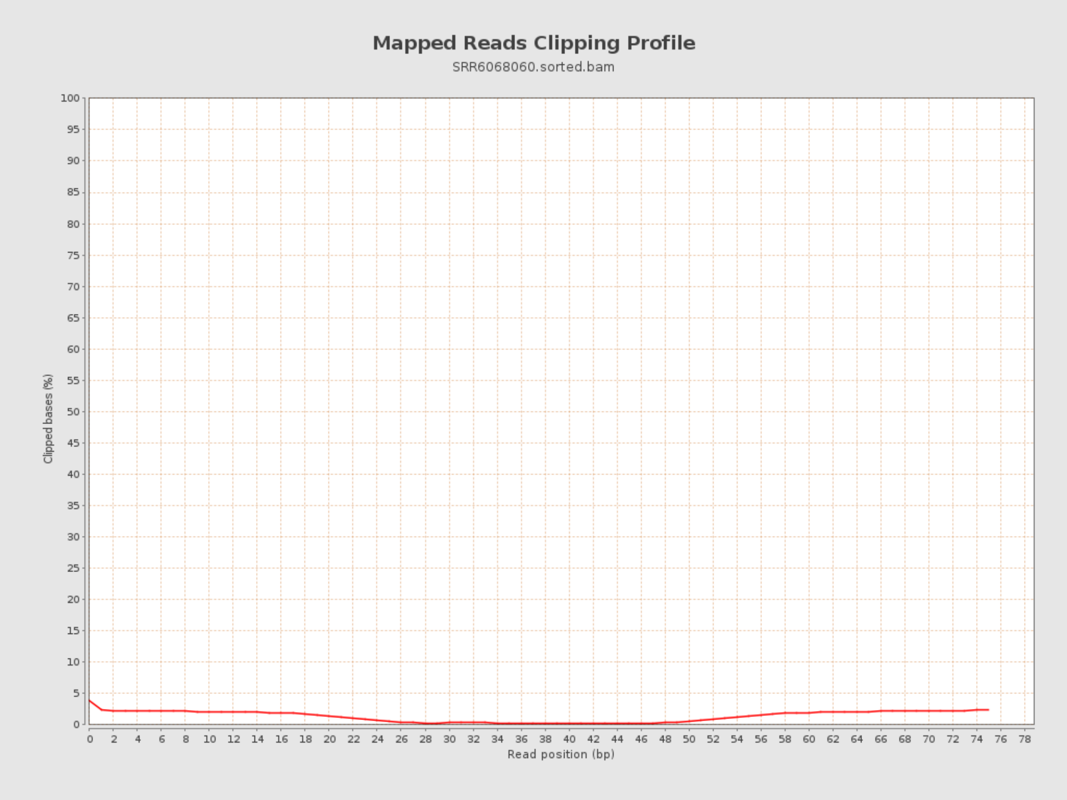
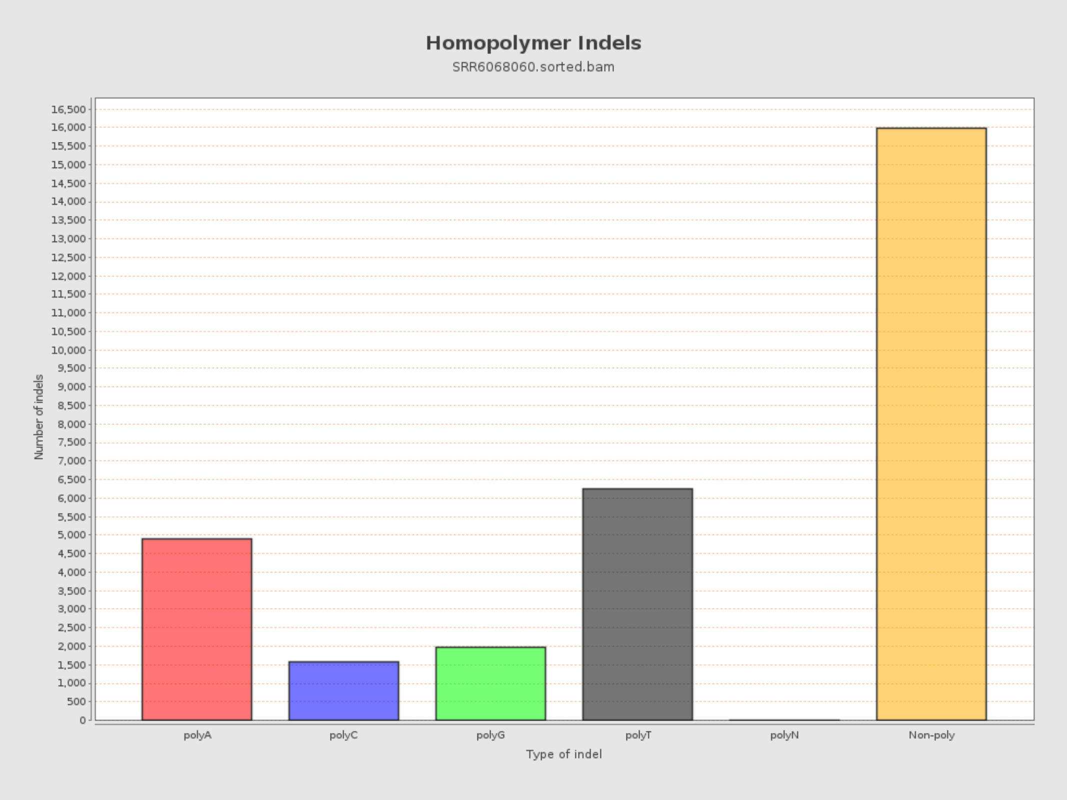
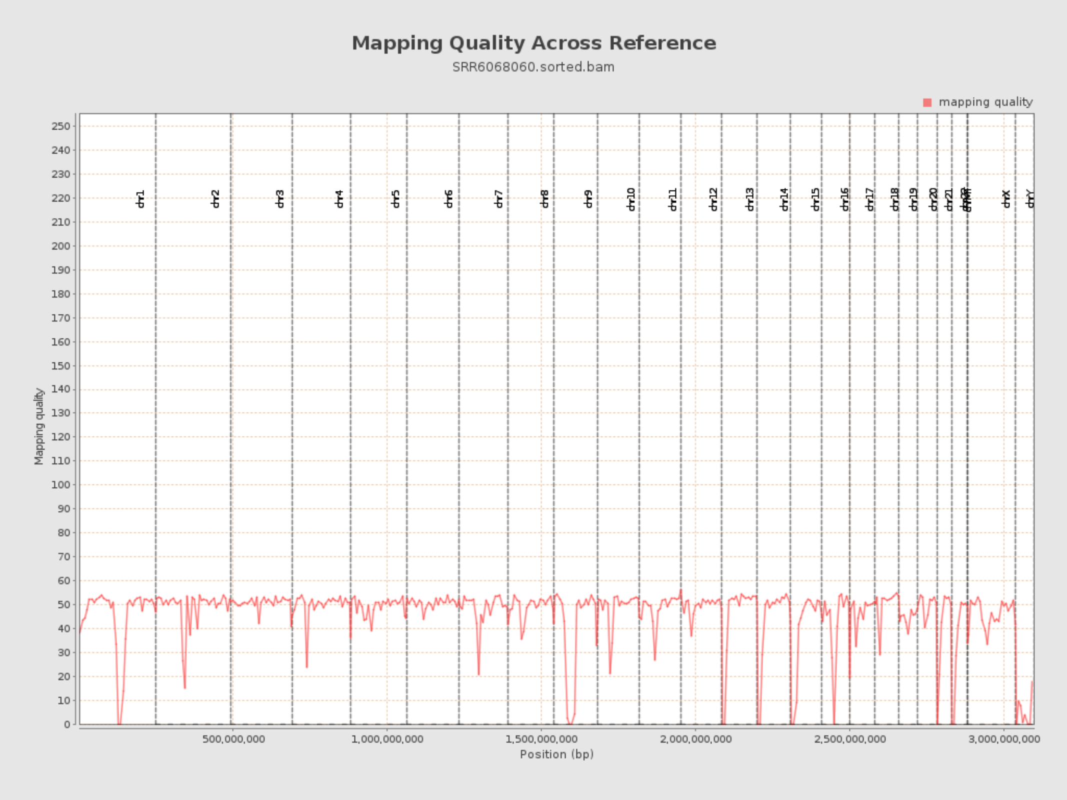
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram