

Geuvadis

24 Test samples

Marc Sultan

>80% of the Unique reads mapped in exons

Bam	Sample	All reads, M	Mapped, M	Mapped, %	Unique, M	On exons, M	On exons, %
HG00096.1.M_111124_6_sorted.bam	HG00096	62.2	53.0	85.2	46.0	40.0	87.1
HG00101.1.M_111124_4_sorted.bam	HG00101	64.6	52.7	81.7	46.6	39.1	83.9
HG00117.1.M_111124_2_sorted.bam	HG00117	136.2	108.6	79.7	92.6	81.3	87.8
HG00127.1.M_111124_2_sorted.bam	HG00127	89.9	74.0	82.3	65.0	56.4	86.7
HG00149.1.M_111124_6_sorted.bam	HG00149	74.4	61.5	82.6	52.9	44.9	84.9
HG00158.1.M_111124_8_sorted.bam	HG00158	71.3	57.2	80.2	49.9	44.6	89.4
HG00278.1.M_111124_5_sorted.bam	HG00278	54.6	46.0	84.3	39.3	36.4	92.5
HG00343.1.M_111124_5_sorted.bam	HG00343	85.9	72.0	83.8	63.0	54.9	87.2
HG00355.1.M_111124_8_sorted.bam	HG00355	72.0	60.5	84.1	52.6	45.8	87.1
HG00359.1.M_111124_6_sorted.bam	HG00359	75.1	61.3	81.7	54.2	48.2	88.8
HG00371.1.M_111124_3_sorted.bam	HG00371	60.8	50.6	83.1	43.8	39.6	90.3
HG00383.1.M_111124_1_sorted.bam	HG00383	76.8	64.4	83.9	56.2	49.9	88.9
NA06986.1.M_111124_7_sorted.bam	NA06986	61.0	52.6	86.3	44.5	39.5	88.8
NA11881.1.M_111124_5_sorted.bam	NA11881	79.8	66.4	83.3	56.4	51.7	91.6
NA11892.1.M_111124_2_sorted.bam	NA11892	59.6	49.7	83.4	42.0	37.5	89.4
NA18519.1.M_111124_3_sorted.bam	NA18519	59.3	48.3	81.5	41.2	37.2	90.4
NA19095.1.M_111124_8_sorted.bam	NA19095	75.0	62.4	83.2	54.2	48.9	90.3
NA19235.1.M_111124_6_sorted.bam	NA19235	84.4	69.8	82.7	60.7	55.1	90.8
NA20519.1.M_111124_5_sorted.bam	NA20519	87.1	72.7	83.4	62.7	54.8	87.5
NA20525.1.M_111124_1_sorted.bam	NA20525	66.3	55.5	83.8	47.7	42.9	90.0
NA20527.1.M_111124_6_sorted.bam	NA20527	83.3	70.3	84.4	61.2	53.2	86.9
NA20540.1.M_111124_2_sorted.bam	NA20540	52.9	43.3	81.9	37.1	33.2	89.5
NA20811.1.M_111124_5_sorted.bam	NA20811	55.9	47.1	84.2	41.3	35.8	86.6
NA20826.1.M_111124_1_sorted.bam	NA20826	67.6	55.9	82.8	48.3	44.2	91.7

Sample	GC, %	Dup, %	Unique Positions	Insert size	CDS Exons, reads/Kb	5'UTR Exons, reads/Kb	3'UTR Exons, reads/Kb	Intronic region, reads/Kb	TSS up 1kb, reads/Kb	TSS up 5kb, reads/Kb	TSS up 10kb, reads/Kb	TES down 1kb, reads/Kb	TES down 5kb, reads/Kb	TES down 10kb, reads/Kb
HG00096	49	60.6	45969513	167	537.8	256.7	366.5	3.2	5.7	3.0	2.6	13.9	7.0	4.6
HG00101	49	47.8	46591201	169	556.1	231.3	347.5	4.2	5.7	3.2	2.8	15.3	7.6	5.1
HG00117	50	61.1	92591114	156	1139.5	497.0	731.6	5.8	10.9	5.6	4.8	31.2	14.3	9.4
HG00127	49	66.3	64971963	148	837.6	323.2	464.3	4.6	7.9	4.2	3.6	20.5	10.0	6.6
HG00149	50	54.4	52884399	157	659.1	260.3	377.6	4.4	7.0	3.7	3.1	18.2	8.5	5.7
HG00158	48	69.2	49854043	156	637.7	266.2	381.3	2.7	5.3	2.8	2.4	14.0	6.9	4.6
HG00278	50	69.2	39317737	156	499.9	234.0	311.0	1.4	5.0	2.1	1.8	10.6	4.8	3.2
HG00343	49	68.0	62985306	156	835.3	309.1	424.1	4.4	7.6	3.8	3.2	17.6	8.5	5.7
HG00355	49	67.0	52615664	156	677.7	263.7	372.4	3.7	6.1	3.2	2.7	15.6	7.5	5.0
HG00359	49	56.5	54234998	167	726.8	266.4	401.0	3.2	6.2	3.1	2.7	15.7	7.7	5.1
HG00371	49	65.4	43808755	167	583.4	227.4	332.9	2.1	4.5	2.3	1.9	12.1	5.7	3.7
HG00383	49	68.2	56151443	167	753.9	284.0	389.0	3.3	6.5	3.2	2.7	16.2	7.6	5.0
NA06986	50	71.0	44486047	156	553.0	247.7	331.8	2.5	5.6	2.7	2.2	14.4	6.6	4.4
NA11881	50	69.0	56441403	158	764.9	300.8	417.4	2.2	7.0	3.2	2.5	17.1	7.6	5.0
NA11892	49	63.9	41992004	167	499.9	250.2	326.0	2.2	6.0	2.7	2.3	14.5	6.5	4.3
NA18519	50	59.2	41172095	146	533.2	227.8	304.8	2.0	4.6	2.2	1.8	12.2	5.4	3.5
NA19095	50	65.8	54180620	158	717.0	286.5	411.7	2.6	6.5	3.1	2.5	15.7	7.4	4.8
NA19235	49	58.6	60709143	169	823.9	320.1	435.0	2.8	6.4	3.2	2.6	16.0	7.6	5.0
NA20519	50	63.9	62669213	165	800.7	321.4	460.4	4.2	7.6	3.9	3.3	18.9	9.1	6.1
NA20525	49	63.4	47724675	146	590.6	270.6	385.4	2.4	5.8	2.8	2.4	14.7	6.9	4.5
NA20527	50	64.8	61186620	169	783.8	308.5	433.0	4.4	7.6	3.8	3.3	18.6	8.9	6.0
NA20540	50	56.7	37074656	147	455.7	210.6	295.1	2.0	4.5	2.2	1.9	11.2	5.3	3.5
NA20811	49	66.1	41317494	167	520.6	210.5	302.0	3.1	4.9	2.6	2.2	11.3	5.8	3.9
NA20826	49	57.9	48257835	158	628.1	269.6	382.7	1.9	5.4	2.6	2.2	13.9	6.4	4.2

EVER-seq 1.0.5:

Ceu vadis QC

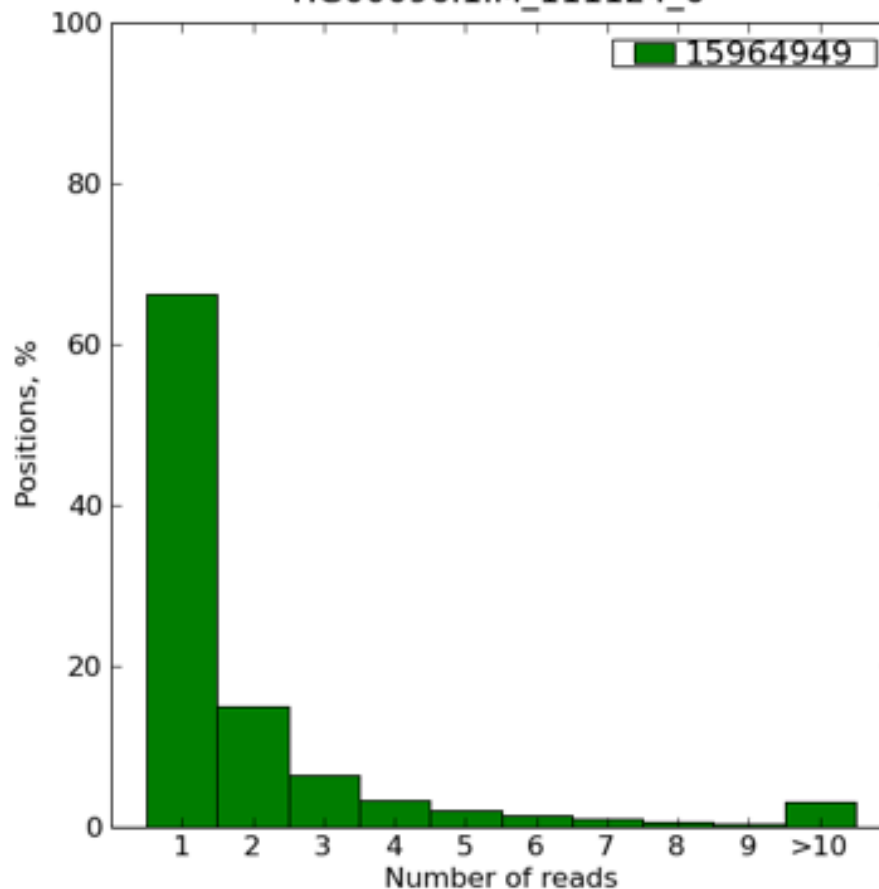
Sample	Complexity	Genes/Saturation	Genes cov	Fastqc																											
HG00096 All: Map: Ex:	<p>Mapping complexity: HG00096.1.M_111124_6</p>	<p>Genes coverage (100% of reads)</p>	<p>Genes with >5 hits and >50% coverage</p>	<table border="1"> <tr><td>Total genes</td><td>51,041</td></tr> <tr><td>Average genes coverage</td><td>45.7 %</td></tr> <tr><td>Genes not covered</td><td>24,299</td></tr> <tr><td>Genes covered</td><td>26,742</td></tr> <tr><td>Genes >50% covered</td><td>17,790</td></tr> <tr><td>Genes >70% covered</td><td>14,836</td></tr> <tr><td>Genes 100% covered</td><td>2,429</td></tr> <tr><td>Genes with only 1 read</td><td>1,495</td></tr> <tr><td>Genes with >5 reads</td><td>21,409</td></tr> <tr><td>Genes with >50 reads</td><td>15,565</td></tr> <tr><td>Genes with >100 reads</td><td>14,070</td></tr> <tr><td>Genes reads</td><td>42,168,456</td></tr> <tr><td>Mapped reads</td><td>0</td></tr> </table>	Total genes	51,041	Average genes coverage	45.7 %	Genes not covered	24,299	Genes covered	26,742	Genes >50% covered	17,790	Genes >70% covered	14,836	Genes 100% covered	2,429	Genes with only 1 read	1,495	Genes with >5 reads	21,409	Genes with >50 reads	15,565	Genes with >100 reads	14,070	Genes reads	42,168,456	Mapped reads	0	
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HG00101 All: Map: Ex:	<p>Mapping complexity: HG00101.1.M_111124_4</p>	<p>Genes coverage (100% of reads)</p>	<p>Genes with >5 hits and >50% coverage</p>	<table border="1"> <tr><td>Total genes</td><td>51,041</td></tr> <tr><td>Average genes coverage</td><td>46.9 %</td></tr> <tr><td>Genes not covered</td><td>23,696</td></tr> <tr><td>Genes covered</td><td>27,345</td></tr> <tr><td>Genes >50% covered</td><td>18,387</td></tr> <tr><td>Genes >70% covered</td><td>15,448</td></tr> <tr><td>Genes 100% covered</td><td>2,711</td></tr> <tr><td>Genes with only 1 read</td><td>1,666</td></tr> <tr><td>Genes with >5 reads</td><td>21,799</td></tr> <tr><td>Genes with >50 reads</td><td>15,565</td></tr> <tr><td>Genes with >100 reads</td><td>14,034</td></tr> <tr><td>Genes reads</td><td>41,137,818</td></tr> <tr><td>Mapped reads</td><td>0</td></tr> </table>	Total genes	51,041	Average genes coverage	46.9 %	Genes not covered	23,696	Genes covered	27,345	Genes >50% covered	18,387	Genes >70% covered	15,448	Genes 100% covered	2,711	Genes with only 1 read	1,666	Genes with >5 reads	21,799	Genes with >50 reads	15,565	Genes with >100 reads	14,034	Genes reads	41,137,818	Mapped reads	0	
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HG00117 All: Map: Ex:	<p>Mapping complexity: HG00117.1.M_111124_2</p>	<p>Genes coverage (100% of reads)</p>	<p>Genes with >5 hits and >50% coverage</p>	<table border="1"> <tr><td>Total genes</td><td>51,041</td></tr> <tr><td>Average genes coverage</td><td>50.6 %</td></tr> <tr><td>Genes not covered</td><td>22,053</td></tr> <tr><td>Genes covered</td><td>28,988</td></tr> <tr><td>Genes >50% covered</td><td>19,922</td></tr> <tr><td>Genes >70% covered</td><td>17,068</td></tr> <tr><td>Genes 100% covered</td><td>3,793</td></tr> <tr><td>Genes with only 1 read</td><td>1,574</td></tr> <tr><td>Genes with >5 reads</td><td>23,466</td></tr> <tr><td>Genes with >50 reads</td><td>17,244</td></tr> <tr><td>Genes with >100 reads</td><td>15,625</td></tr> <tr><td>Genes reads</td><td>85,622,570</td></tr> </table>	Total genes	51,041	Average genes coverage	50.6 %	Genes not covered	22,053	Genes covered	28,988	Genes >50% covered	19,922	Genes >70% covered	17,068	Genes 100% covered	3,793	Genes with only 1 read	1,574	Genes with >5 reads	23,466	Genes with >50 reads	17,244	Genes with >100 reads	15,625	Genes reads	85,622,570			
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HG00096: HG00096.1.M_111124_6

All unique starting positions	15,964,949
Mapped reads	0
Lab complexity	

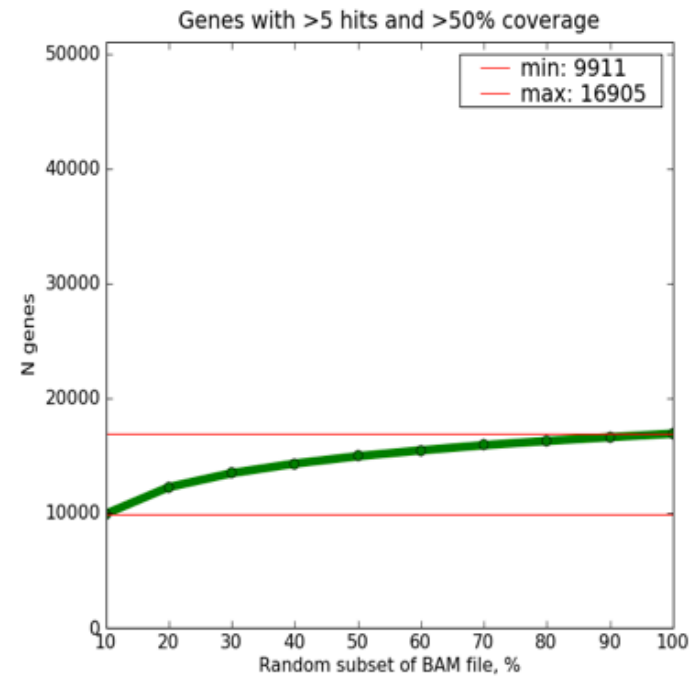
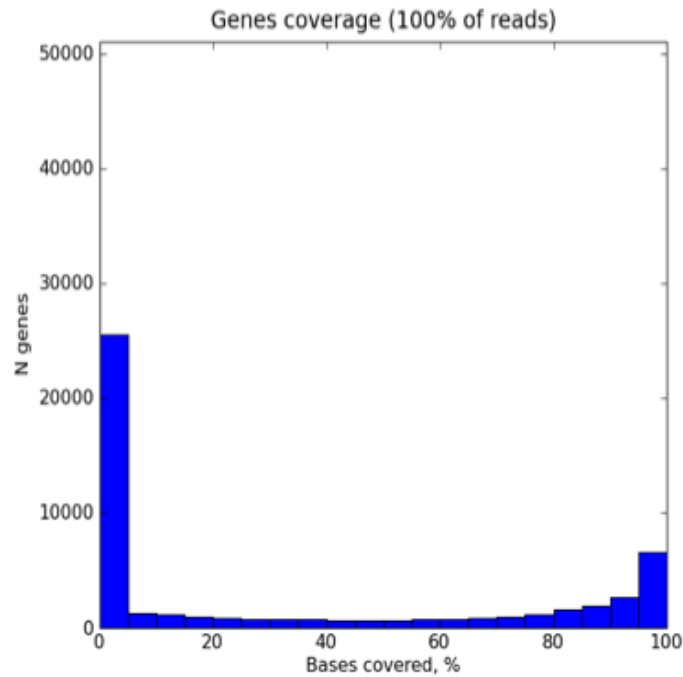
1	10,589,982
2	2,394,771
3	1,022,596
4	548,401
5	332,496
6	218,678
7	151,947
8	110,617
9	82,769
>10	512,692

Mapping complexity:
HG00096.1.M_111124_6



HG00096: HG00096.1.M_111124_6

Total genes	51,041
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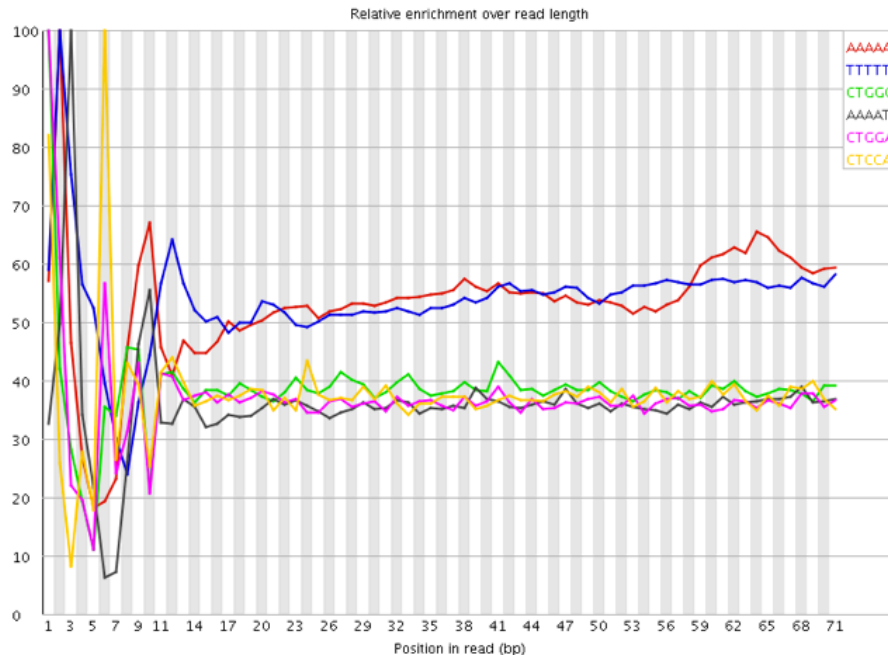
Summary

- ✔ [Basic Statistics](#)
- ✔ [Per base sequence quality](#)
- ✔ [Per sequence quality scores](#)
- ✘ [Per base sequence content](#)
- ✘ [Per base GC content](#)
- ✔ [Per sequence GC content](#)
- ! [Per base N content](#)
- ✔ [Sequence Length Distribution](#)
- ✘ [Sequence Duplication Levels](#)
- ✔ [Overrepresented sequences](#)
- ! [Kmer Content](#)

✔ Overrepresented sequences

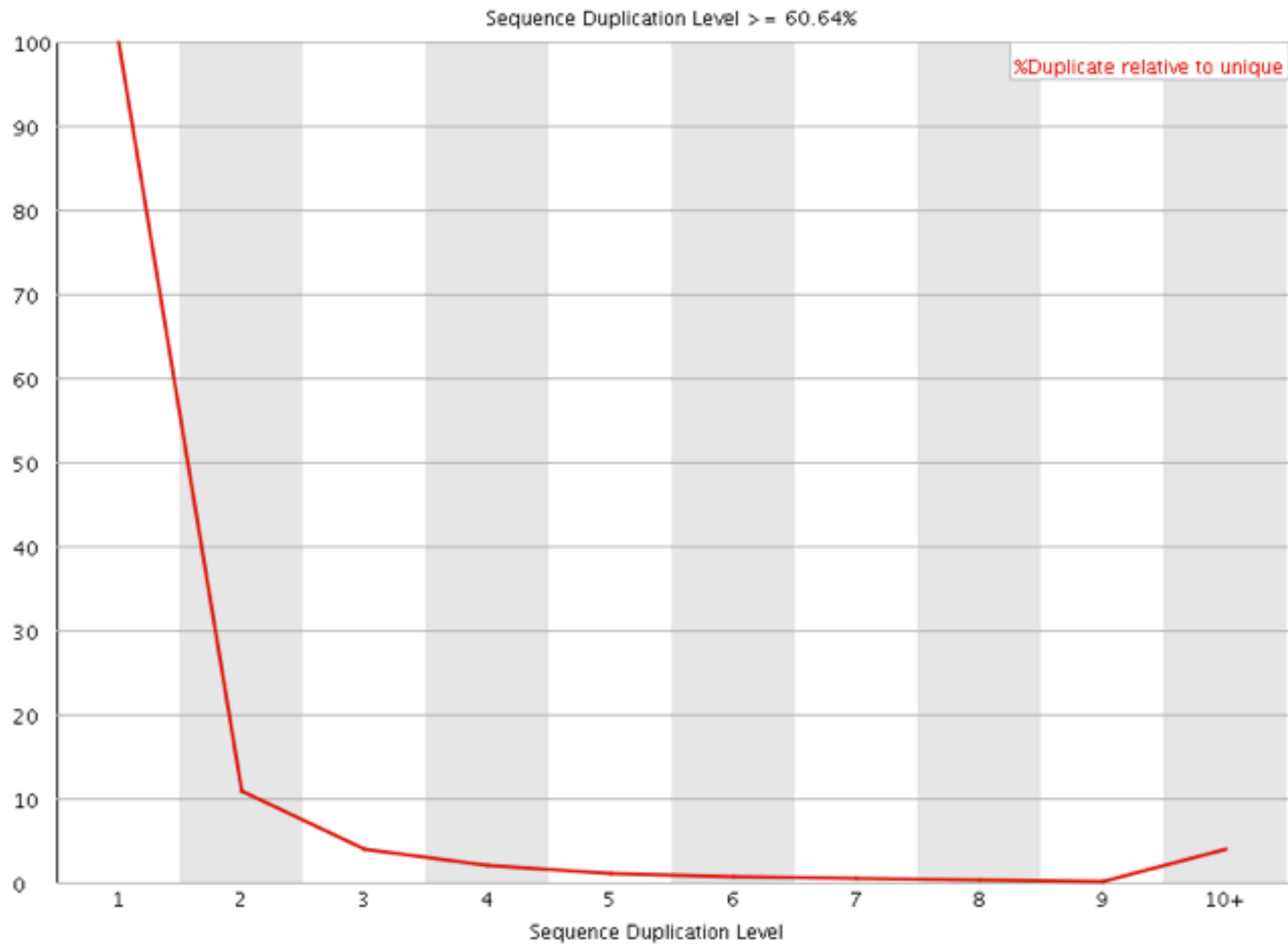
No overrepresented sequences

! Kmer Content



Sequence	Count	Obs/Exp Overall	Obs/Exp Max	Max Obs/Exp Position
AAAAA	17847095	4.0126166	7.5318594	2
TTTTT	16374005	3.618177	6.689071	2
CTGGG	9307985	2.2384932	5.784172	1
AAAAT	9032445	2.0237665	5.600858	3
CTGGA	8484580	2.0018342	5.4133735	1
CTCCA	8546220	1.9936206	5.262313	6
TCCAG	8464590	1.9858159	5.7931776	7
GAAAA	8607110	1.9725134	5.32202	1
ATCCA	5266410	1.2121191	5.285317	6

✖ Sequence Duplication Levels





Per sequence quality scores

