

SnpEff: Variant analysis

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Summary

Genome	ncbi_drosophila
Date	2025-12-29 00:16
SnpEff version	SnpEff 5.3a (build 2025-09-02 10:24), by Pablo Cingolani
Command line arguments	SnpEff -stats smallIndels_annotation_summary.html ncbi_drosophila /Volumes/Crucial X9/Manta-Output-Processing/MantaTestOutput/output/results/variants/c
Warnings	57,182
Errors	37
Number of lines (input file)	75,296
Number of variants (before filter)	75,296
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	75,296
Number of known variants (i.e. non-empty ID)	74,510 (98.956%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	0
Number of annotations	531,234
Genome total length	143,726,002
Genome effective length	139,541,032
Variant rate	1 variant every 1,853 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
AE013599.5	25,286,936	13,489	1,874
AE014134.6	23,513,712	15,123	1,554
AE014135.4	1,348,131	134	10,060
AE014296.5	28,110,227	15,483	1,815
AE014297.3	32,079,331	15,740	2,038
AE014298.5	23,542,271	13,428	1,753
CP007074.1	76,224	2	38,112
CP007075.1	11,983	23	521
CP007076.1	87,365	1	87,365
CP007077.1	36,913	83	444
CP007078.1	22,604	5	4,520
CP007079.1	23,238	13	1,787
CP007081.1	88,768	6	14,794
CP007084.1	62,570	2	31,285
CP007085.1	45,120	10	4,512
CP007086.1	22,882	1	22,882
CP007087.1	46,986	5	9,397
CP007089.1	16,157	1	16,157
CP007091.1	20,763	8	2,595
CP007095.1	25,560	2	12,780
CP007100.1	10,091	2	5,045
CP007101.1	24,503	1	24,503
CP007103.1	33,320	41	812
CP007104.1	27,447	8	3,430
CP007106.1	3,667,352	30	122,245
CP007108.1	66,731	3	22,243
CP007111.1	34,521	4	8,630
CP007120.1	76,973	32	2,405

DS483562.1	50,625	23	2,201
DS483629.1	15,417	42	367
DS483641.1	14,503	38	381
DS483646.1	14,098	1	14,098
DS483648.1	13,940	4	3,485
DS483650.1	13,906	1	13,906
DS483655.1	13,549	7	1,935
DS483659.1	13,416	49	273
DS483660.1	13,394	23	582
DS483670.1	12,827	4	3,206
DS483675.1	12,536	1	12,536
DS483677.1	12,513	2	6,256
DS483680.1	12,399	1	12,399
DS483681.1	12,368	1	12,368
DS483698.1	11,522	1	11,522
DS483707.1	25,840	1	25,840
DS483711.1	14,687	1	14,687
DS483724.1	13,501	30	450
DS483736.1	14,006	1	14,006
DS483746.1	9,341	52	179
DS483749.1	8,007	18	444
DS483751.1	7,314	33	221
DS483753.1	7,123	9	791
DS483758.1	6,860	2	3,430
DS483770.1	6,193	7	884
DS483773.1	6,062	6	1,010
DS483776.1	6,000	1	6,000
DS483781.1	5,952	15	396
DS483783.1	5,891	4	1,472
DS483784.1	5,832	5	1,166
DS483789.1	5,555	8	694
DS483792.1	5,465	1	5,465
DS483793.1	5,463	1	5,463
DS483803.1	5,232	4	1,308
DS483808.1	5,060	4	1,265
DS483809.1	5,057	3	1,685
DS483817.1	4,933	32	154
DS483818.1	4,917	7	702
DS483819.1	4,903	1	4,903
DS483821.1	4,879	3	1,626
DS483828.1	4,785	1	4,785
DS483833.1	4,701	2	2,350
DS483843.1	4,515	9	501
DS483845.1	4,465	3	1,488
DS483851.1	4,395	7	627
DS483853.1	4,381	17	257
DS483854.1	4,378	1	4,378
DS483865.1	4,289	1	4,289
DS483866.1	4,273	6	712
DS483870.1	4,231	1	4,231
DS483872.1	4,222	1	4,222
DS483880.1	4,150	12	345
DS483885.1	4,085	12	340
DS483886.1	4,081	1	4,081
DS483892.1	4,013	7	573
DS483893.1	4,012	1	4,012
DS483897.1	3,984	6	664
DS483903.1	3,941	2	1,970
DS483905.1	3,926	10	392
DS483906.1	3,924	5	784
DS483907.1	3,921	1	3,921
DS483908.1	3,913	2	1,956
DS483913.1	3,871	1	3,871
DS483918.1	3,818	2	1,909
DS483920.1	3,806	15	253
DS483923.1	3,775	3	1,258
DS483927.1	3,737	2	1,868
DS483928.1	3,730	3	1,243
DS483940.1	3,648	13	280
DS483944.1	3,622	8	452

DS483946.1	3,603	1	3,603
DS483951.1	3,574	8	446
DS483954.1	3,554	4	888
DS483955.1	3,553	1	3,553
DS483956.1	3,553	9	394
DS483961.1	3,527	7	503
DS483963.1	3,523	3	1,174
DS483970.1	3,490	2	1,745
DS483971.1	3,478	4	869
DS483974.1	3,473	3	1,157
DS483982.1	3,402	2	1,701
DS483992.1	3,365	1	3,365
DS484000.1	3,302	13	254
DS484002.1	3,290	2	1,645
DS484004.1	3,277	8	409
DS484005.1	3,275	1	3,275
DS484022.1	3,209	6	534
DS484023.1	3,206	1	3,206
DS484039.1	3,162	1	3,162
DS484041.1	3,157	8	394
DS484042.1	3,156	17	185
DS484046.1	3,123	1	3,123
DS484051.1	3,100	2	1,550
DS484054.1	3,080	1	3,080
DS484057.1	3,076	3	1,025
DS484058.1	3,073	27	113
DS484060.1	3,065	6	510
DS484061.1	3,059	2	1,529
DS484064.1	3,044	16	190
DS484068.1	3,013	1	3,013
DS484069.1	3,010	6	501
DS484070.1	3,009	8	376
DS484074.1	2,999	1	2,999
DS484077.1	2,984	1	2,984
DS484084.1	2,956	1	2,956
DS484089.1	2,928	7	418
DS484099.1	2,910	5	582
DS484102.1	2,903	3	967
DS484116.1	2,860	19	150
DS484124.1	2,846	7	406
DS484125.1	2,844	2	1,422
DS484130.1	2,834	3	944
DS484131.1	2,833	2	1,416
DS484138.1	2,822	2	1,411
DS484140.1	2,819	6	469
DS484143.1	2,814	1	2,814
DS484148.1	2,795	26	107
DS484153.1	2,793	6	465
DS484159.1	2,784	1	2,784
DS484165.1	2,751	1	2,751
DS484169.1	2,736	1	2,736
DS484178.1	2,698	4	674
DS484180.1	2,697	4	674
DS484185.1	2,686	5	537
DS484187.1	2,671	7	381
DS484188.1	2,670	2	1,335
DS484197.1	2,642	2	1,321
DS484198.1	2,641	4	660
DS484200.1	2,639	1	2,639
DS484202.1	2,636	2	1,318
DS484203.1	2,635	2	1,317
DS484205.1	2,629	1	2,629
DS484212.1	2,612	1	2,612
DS484216.1	2,603	5	520
DS484219.1	2,591	1	2,591
DS484225.1	2,577	5	515
DS484226.1	2,576	1	2,576
DS484235.1	2,557	1	2,557
DS484244.1	2,536	24	105
DS484246.1	2,529	7	361

DS484258.1	2,510	2	1,255
DS484260.1	2,505	1	2,505
DS484263.1	2,487	1	2,487
DS484267.1	2,476	1	2,476
DS484268.1	2,475	8	309
DS484271.1	2,470	2	1,235
DS484272.1	2,464	1	2,464
DS484276.1	2,447	3	815
DS484277.1	2,442	15	162
DS484278.1	2,439	1	2,439
DS484279.1	2,438	22	110
DS484280.1	2,438	2	1,219
DS484281.1	2,438	1	2,438
DS484282.1	2,435	14	173
DS484285.1	2,431	3	810
DS484289.1	2,425	4	606
DS484296.1	2,417	1	2,417
DS484297.1	2,413	3	804
DS484300.1	2,400	2	1,200
DS484303.1	2,390	1	2,390
DS484309.1	2,384	1	2,384
DS484314.1	2,381	1	2,381
DS484316.1	2,379	1	2,379
DS484319.1	2,372	5	474
DS484322.1	2,366	3	788
DS484330.1	2,353	1	2,353
DS484343.1	2,325	9	258
DS484345.1	2,318	3	772
DS484346.1	2,317	5	463
DS484348.1	2,308	2	1,154
DS484354.1	2,293	1	2,293
DS484358.1	2,286	1	2,286
DS484361.1	2,282	3	760
DS484362.1	2,273	1	2,273
DS484367.1	2,259	1	2,259
DS484369.1	2,253	16	140
DS484371.1	2,247	1	2,247
DS484377.1	2,232	2	1,116
DS484382.1	2,223	6	370
DS484383.1	2,221	4	555
DS484387.1	2,210	1	2,210
DS484388.1	2,209	1	2,209
DS484393.1	2,201	3	733
DS484394.1	2,200	9	244
DS484396.1	2,198	8	274
DS484397.1	2,196	1	2,196
DS484406.1	2,177	1	2,177
DS484414.1	2,157	1	2,157
DS484417.1	2,139	2	1,069
DS484419.1	2,132	1	2,132
DS484429.1	2,113	2	1,056
DS484430.1	2,113	1	2,113
DS484431.1	2,113	1	2,113
DS484447.1	2,089	1	2,089
DS484450.1	2,087	2	1,043
DS484454.1	2,084	12	173
DS484458.1	2,079	1	2,079
DS484462.1	2,068	3	689
DS484469.1	2,060	2	1,030
DS484472.1	2,046	5	409
DS484486.1	2,014	1	2,014
DS484487.1	2,010	1	2,010
DS484496.1	1,998	1	1,998
DS484507.1	1,978	1	1,978
DS484526.1	1,956	1	1,956
DS484528.1	1,947	1	1,947
DS484533.1	1,944	1	1,944
DS484552.1	1,920	1	1,920
DS484556.1	1,916	5	383
DS484563.1	1,903	3	634

DS484566.1	1,900	13	146
DS484568.1	1,899	1	1,899
DS484578.1	1,872	1	1,872
DS484588.1	1,863	5	372
DS484593.1	1,849	3	616
DS484594.1	1,843	1	1,843
DS484600.1	1,841	1	1,841
DS484601.1	1,832	8	229
DS484608.1	1,818	1	1,818
DS484609.1	1,818	1	1,818
DS484610.1	1,813	3	604
DS484611.1	1,813	1	1,813
DS484614.1	1,806	3	602
DS484618.1	1,800	2	900
DS484623.1	1,792	1	1,792
DS484628.1	1,785	1	1,785
DS484632.1	1,775	7	253
DS484644.1	1,747	2	873
DS484646.1	1,747	5	349
DS484672.1	1,703	2	851
DS484673.1	1,696	2	848
DS484697.1	1,636	1	1,636
DS484702.1	1,623	2	811
DS484718.1	1,586	4	396
DS484719.1	1,586	1	1,586
DS484722.1	1,577	4	394
DS484724.1	1,575	1	1,575
DS484725.1	1,573	1	1,573
DS484737.1	1,550	3	516
DS484739.1	1,549	10	154
DS484748.1	1,538	1	1,538
DS484751.1	1,533	1	1,533
DS484765.1	1,516	1	1,516
DS484768.1	1,509	1	1,509
DS484777.1	1,489	1	1,489
DS484779.1	1,487	1	1,487
DS484782.1	1,484	1	1,484
DS484787.1	1,475	1	1,475
DS484789.1	1,473	1	1,473
DS484803.1	1,461	2	730
DS484817.1	1,445	4	361
DS484837.1	1,423	1	1,423
DS484857.1	1,402	3	467
DS484869.1	1,391	5	278
DS484880.1	1,380	1	1,380
DS484894.1	1,375	4	343
DS484904.1	1,366	2	683
DS484907.1	1,361	2	680
DS484913.1	1,355	1	1,355
DS484948.1	1,328	3	442
DS484963.1	1,315	7	187
DS484970.1	1,310	3	436
DS484978.1	1,306	2	653
DS484979.1	1,304	2	652
DS484982.1	1,304	4	326
DS484990.1	1,301	1	1,301
DS485010.1	1,286	5	257
DS485015.1	1,283	1	1,283
DS485017.1	1,281	9	142
DS485025.1	1,278	5	255
DS485031.1	1,275	5	255
DS485044.1	1,271	1	1,271
DS485050.1	1,268	4	317
DS485054.1	1,265	1	1,265
DS485056.1	1,263	1	1,263
DS485064.1	1,262	5	252
DS485071.1	1,260	2	630
DS485077.1	1,258	5	251
DS485102.1	1,240	2	620
DS485119.1	1,235	3	411

DS485126.1	1,233	2	616
DS485141.1	1,228	2	614
DS485148.1	1,227	9	136
DS485172.1	1,220	1	1,220
DS485176.1	1,219	8	152
DS485190.1	1,211	1	1,211
DS485249.1	1,192	1	1,192
DS485255.1	1,190	1	1,190
DS485260.1	1,189	7	169
DS485262.1	1,189	1	1,189
DS485266.1	1,186	1	1,186
DS485268.1	1,186	1	1,186
DS485278.1	1,184	1	1,184
DS485281.1	1,184	3	394
DS485299.1	1,178	3	392
DS485300.1	1,178	2	589
DS485303.1	1,175	3	391
DS485310.1	1,173	2	586
DS485331.1	1,165	7	166
DS485345.1	1,161	3	387
DS485360.1	1,159	4	289
DS485362.1	1,158	3	386
DS485371.1	1,156	3	385
DS485384.1	1,153	3	384
DS485411.1	1,146	1	1,146
DS485422.1	1,144	1	1,144
DS485454.1	1,135	1	1,135
DS485464.1	1,133	2	566
DS485465.1	1,133	1	1,133
DS485476.1	1,130	1	1,130
DS485478.1	1,129	2	564
DS485504.1	1,123	1	1,123
DS485509.1	1,123	1	1,123
DS485514.1	1,121	1	1,121
DS485528.1	1,117	4	279
DS485535.1	1,116	1	1,116
DS485537.1	1,115	1	1,115
DS485543.1	1,114	2	557
DS485547.1	1,112	1	1,112
DS485549.1	1,112	2	556
DS485562.1	1,109	3	369
DS485572.1	1,107	1	1,107
DS485592.1	1,102	1	1,102
DS485597.1	1,100	7	157
DS485599.1	1,100	2	550
DS485606.1	1,097	1	1,097
DS485647.1	1,086	1	1,086
DS485651.1	1,084	1	1,084
DS485656.1	1,083	2	541
DS485664.1	1,081	10	108
DS485678.1	1,077	2	538
DS485703.1	1,071	3	357
DS485707.1	1,071	2	535
DS485753.1	1,059	1	1,059
DS485757.1	1,058	1	1,058
DS485769.1	1,055	1	1,055
DS485771.1	1,055	1	1,055
DS485773.1	1,054	1	1,054
DS485775.1	1,053	1	1,053
DS485797.1	1,049	1	1,049
DS485801.1	1,048	5	209
DS485802.1	1,048	1	1,048
DS485808.1	1,047	1	1,047
DS485848.1	1,040	3	346
DS485876.1	1,032	1	1,032
DS485879.1	1,031	9	114
DS485887.1	1,029	9	114
DS485933.1	1,019	2	509
DS485940.1	1,018	1	1,018
DS485941.1	1,018	1	1,018

DS485952.1	1,014	3	338
DS485954.1	1,014	1	1,014
DS485962.1	1,012	1	1,012
DS485968.1	1,011	3	337
DS485981.1	1,007	1	1,007
DS485997.1	1,004	3	334
DS486004.1	1,001	1	1,001
DS486008.1	1,001	1	1,001
KJ947872.2	19,524	55	354
Total	139,541,032	75,296	1,853

Number variants by type

Type	Total
SNP	0
MNP	259
INS	19,961
DEL	28,248
MIXED	25,807
INV	0
DUP	235
CNV	0
BND	786
INTERVAL	0
Total	75,296

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	52,024	9.793%
LOW	8,660	1.63%
MODERATE	86,561	16.294%
MODIFIER	383,989	72.282%

Number of effects by functional class

Type (alphabetical order)	Count	Percent
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Missense / Silent ratio: 0

Number of annotaitons and region counts

Annotation			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent
3_prime_UTR_truncation	17	0.003%	CHROMOSOME	37	0.007%
3_prime_UTR_variant	6,352	1.187%	DOWNSTREAM	84,264	15.862%
5_prime_UTR_truncation	59	0.011%	EXON	8,049	1.515%
5_prime_UTR_variant	2,842	0.531%	GENE	25,922	4.88%
bidirectional_gene_fusion	3,149	0.589%	INTERGENIC	35,640	6.709%
chromosome_number_variation	21	0.004%	INTRON	168,731	31.762%
conservative_inframe_deletion	682	0.127%	SPLICE_SITE_ACCEPTOR	189	0.036%
conservative_inframe_insertion	567	0.106%	SPLICE_SITE_DONOR	189	0.036%
disruptive_inframe_deletion	1,383	0.258%	SPLICE_SITE_REGION	1,192	0.224%
disruptive_inframe_insertion	879	0.164%	TRANSCRIPT	107,059	20.153%
downstream_gene_variant	84,273	15.751%	UPSTREAM	90,914	17.114%
duplication	83,581	15.621%	UTR_3_PRIME	6,309	1.188%
exon_loss_variant	2,022	0.378%	UTR_5_PRIME	2,739	0.516%
feature_ablation	5,513	1.03%			
feature_fusion	7,306	1.365%			
frameshift_variant	1,337	0.25%			
gene_fusion	1,853	0.346%			
intergenic_region	28,334	5.296%			
intragenic_variant	374	0.07%			
intron_variant	169,728	31.722%			
missense_variant	326	0.061%			
non_coding_transcript_exon_variant	1,878	0.351%			
non_coding_transcript_variant	574	0.107%			
splice_acceptor_variant	219	0.041%			
splice_donor_variant	267	0.05%			
splice_region_variant	1,715	0.321%			
start_lost	63	0.012%			
start_retained_variant	6	0.001%			
stop_gained	113	0.021%			

Type (alphabetical order)	Count	Percent
stop_lost	61	0.011%
stop_retained_variant	6	0.001%
synonymous_variant	200	0.037%
transcript_ablation	38,429	7.182%
upstream_gene_variant	90,914	16.992%



Quality:



Insertions and deletions length:

Min	1
Max	509
Mean	7.741
Median	1
Standard deviation	17.943
Values	1,4,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54
Count	28248,211,2866,2140,1877,1407,1979,939,998,811,759,434,656,354,368,346,282,245,283,239,160,171,196,140,136,129,128,117,108,118,97,66,75,7



Base changes (SNPs)

	A	C	G	T
A	0	0	0	0
C	0	0	0	0
G	0	0	0	0
T	0	0	0	0

Ts/Tv (transitions / transversions)

Note: Only SNPs are used for this statistic.

Note: This Ts/Tv ratio is a 'raw' ratio (ratio of observed events).

Transitions	0
Transversions	0
Ts/Tv ratio	0

All variants:

No results available (empty input?)

Only known variants (i.e. the ones having a non-empty ID field):

No results available (empty input?)

Allele frequency



Allele Count



Min	1
Max	1
Mean	1
Median	1
Standard deviation	0
Values	1
Count	75296

Hom/Het per sample



Sample_names
Reference
Het
Hom
Missing

Codon changes

How to read this table:

- Rows are reference codons and columns are changed codons. E.g. Row 'AAA' column 'TAA' indicates how many 'AAA' codons have been replaced by 'TAA' codons.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

-	-	AA<	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACN	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATN	ATT	CAA	
-	-		2,458	1,872	1,588	1,562	2,014	1,475	1,395		1,704	2,054	2,337	2,429	1,484	973	1,631	1,604	2	1,386	3,328	
AA<																						
AAA	427		98	25	52	52	22	28	12		13	39	83	32	49	44	24	17		36	60	
AAC	554	3	30	82	65	53	64	57	35		66	65	54	68	15	23	65	31		31	38	
AAG	712		98	82	209	95	61	36	64		97	64	58	162	102	42	33	99		76	146	
AAT	576		74	38	23	45	34	27	87		15	27	107	71	52	18	14	79		13	28	
ACA	850		65	2	30	22	66	38	46		41	61	83	40	7	19	24	11		32	38	
ACC	783		51	60	42	37	77	82	51		49	65	70	24	91	11	28	50		29	116	
ACG	419		19	25	20	15	52	29	13		57	23	66	28	32	15	28	23		12	29	
ACN																						
ACT	908		31	11	26	8	37	64	50		115	18	20	37	19	3	29	6		5	40	
AGA	316		20	8	51	4	8	3	14		16	48	10	80	21	3		7		17	17	
AGC	557		74	55	107	57	46	77	31		42	43	89	20	104	13	95	20		46	43	
AGG	195		28	1	79	53	40	25	38		23	63	47	76		8	12	12		13	19	
AGT	420		50	24	31	22	18	18	50		55	30	61	21	53	10	21	7		36	50	
ATA	255		48	24	34	1	26	11			8	16	12	7	7	5	19	19		13	4	
ATC	388		20	32	30	44	86	19	92		62	36	46	25	45	24	35	44		47	64	
ATG	426		42	62	68	52	67	16	64		59	66	73	47	12	33	34	38		25	73	
ATN																						
ATT	391		28	12	38	17	49	25	14		45	42	45	41	14	19	28	37		51	34	
CAA	1,183		27	69	59	20	23	38	43		25	84	49	31	10	21	17	23		41	28	
CAC	368		37	45	20	15	35	44	19		37	21	79	39	44	15	33	19		8	51	
CAG	2,793		38	70	57	47	139	112	79		77	146	79	101	113	8	71	118		62	326	
CAT	373		25	22	7	20	26	10	14		29	37	26	10	12	10	43	47		35	40	
CCA	762		45	22	36	10	39	46	28		52	20	42	25	27	7	31	16		28	52	
CCC	522		17	25	56	60	50	35	24	4	66	6	59	35	26	10	23	13		74	46	
CCG	366		34	16	42	32	34	45	33		34	27	55	14	35	10	26	43		26	63	
CCT	469		21	31	61	11	4	18	2		60	26	22	12	23	29	30	5		20	2	
CGA	164		18	2	26	10	20	17	2		10	6	15	55	4	18	26	13		8	35	
CGC	203		6	23	3	15	24	32	36		27	73	40	72	33	6	49	86		24	31	
CGG	198		7	4	31	14	12	18	17		15	8	14	10	4	6	19			22	32	
CGT	139		2	16	36	31	22	21			8	67	27	34	12	4	28	2			39	
CTA	201		16	8	9	2	31	1	8		15	13	42	16	12	1	20	23		16	35	
CTC	246		10	18	49	9	17	10	23		29	8	16	33	21	3	35	26		17	56	
CTG	570		50	100	31	53	118	60	75		99	141	109	66	64	60	117	64		43	114	
CTN																						
CTT	228		71	12	18	11	2	3	5		18	11	6	45	25	5	18	16		14	44	
G>S																						
GAA	833		88	17	117	57	52	46	17		105	46	34	62	21	27	30	22		68	58	
GAC	479		91	56	39	56	99	75	27		54	51	57	82	42	15	46	29		46	62	
GAG	817		183	132	200	52	77	94	91		110	66	107	146	69	70	72	92		98	101	
GAT	591		87	64	50	56	79	15	62		68	63	92	102	31	21	65	88		60	111	
GCA	669		30	53	25	13	14	26	12		29	24	10	8	33	4	34	27		26	33	
GCC	579		81	64	18	79	81	58	74		127	95	126	135	38	27	79	40		40	85	
GCG	280		30	27	40	41	14	34	50		25	23	28	6	20	36	74	9		26	46	
GCN																						
GCT	523		20	48	69	8	37	22	44		38	11	33	15	23	8	26	34		24	29	
GGA	835		68	41	25	39	32	32	35		20	23	61	81	27	8	7	91		43	53	
GGC	616		65	36	66	59	57	43	60		50	52	110	75	39	61	98	75		50	47	
GGG	165			12	11	8	6		4		12	49	4	7	4		16	6			12	
GGT	538		18	23	23	22	32	6	30		18	19	37	47	21	3	29	29		15	63	
GT>																						
GTA	222		12	4	26	10	26	18	5		20	15	5	10	2	10	2	9		3	15	
GTC	301		27	14	46	34	26	29	27		24	34	47	48	21	11	40	26		20	49	
GTG	487		73	48	38	27	55	67	105		83	47	78	79	64	25	35	55		33	99	
GTT	494		24	26	20	28	50	34	14		42	6	53	16	20	15	57	27		51	20	
INS																						
NGC																						
NI<																						
NNC																						
NNN																						

	-	AA<	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACN	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATN	ATT	CAA
NNT																					
NTT																					
SNI																					
TAA	60		10			14	1				1					1					6
TAC	330		59	39	40	80	28	34	25		15	45	70	39	22	43	40	33		19	59
TAG	28		4		1				1				2							3	
TAT	283		7	16	17	18	26	13	12		20	34	26	31	12	2	35	6		17	25
TCA	538		47	13	6	15	40	66	15		42	32	41	8	7	2	25	38		7	50
TCC	528		22	49	64	48	74	36	36		62	42	106	55	82	21	19	26		63	72
TCG	329		45	26	18	8	49	24	28		30	51	108	28	54	14	6	31		39	49
TCN																					
TCT	374		37	29	22	4	35	17			24	5	31	4	23	2	9	12		24	12
TG>																					
TGA	42			3	1		3		1			1				4					1
TGC	224		24	29	14	20	11	16	14		8	76	26	41	17	23	41	63		43	15
TGG	186		26	16	17	42	10	21	2		14	8	28	8	22	24	14	22		13	11
TGN																					
TGT	160		12	6		2	2	9	8		13	4	62	10	4	16	3			11	8
TTA	209		36	7	4	15	31	14	28		2	12	16	4	3	12	14	2		8	4
TTC	396		23	18	22	27	45	20	82		68	47	32	28	21	18	41	42		41	65
TTG	380		16	43	19	20	47	18	35		21	37	44	113	22	6	45	22		22	50
TTT	313		34	26	19	16	26	20	13		27	23	49	23	41	16	18	14		17	7

Amino acid changes

How to read this table:

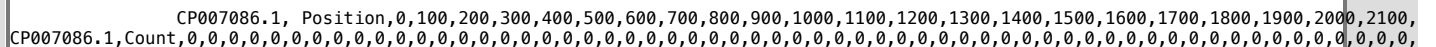
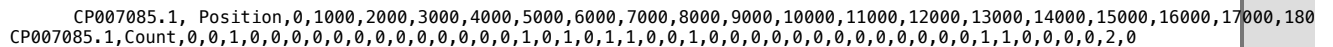
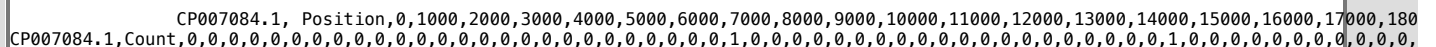
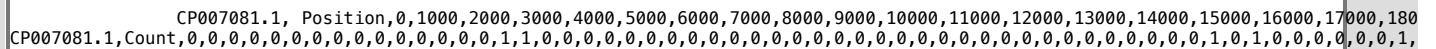
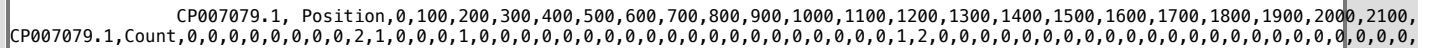
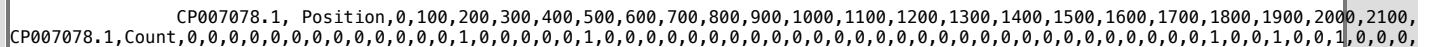
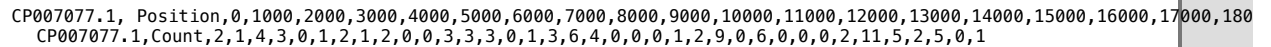
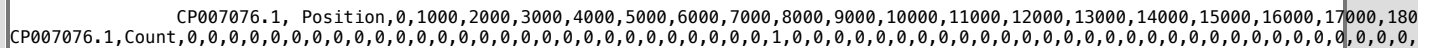
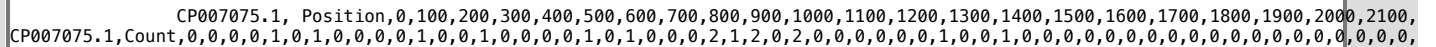
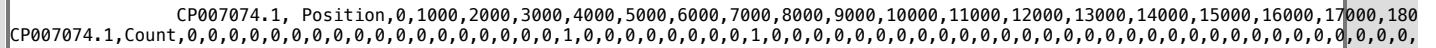
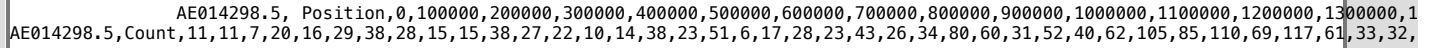
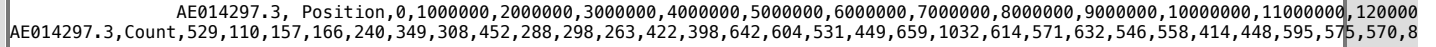
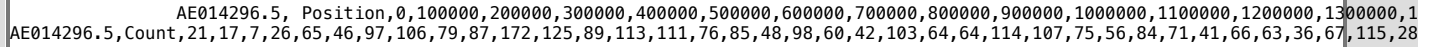
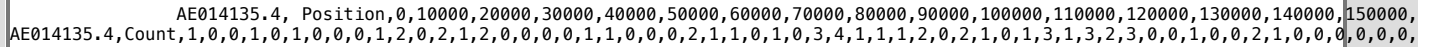
- Rows are reference amino acids and columns are changed amino acids. E.g. Row 'A' column 'E' indicates how many 'A' amino acids have been replaced by 'E' amino acids.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: This table may include different translation codon tables (e.g. mamalian DNA and mitochondrial DNA).

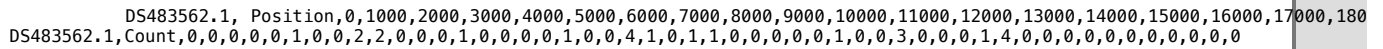
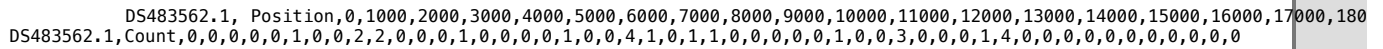
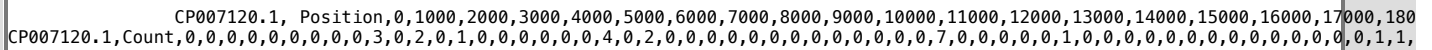
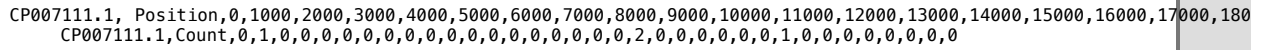
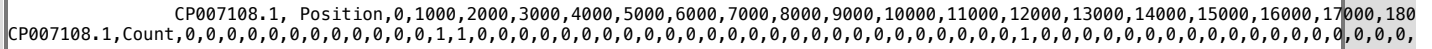
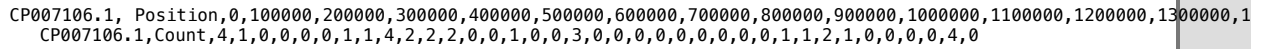
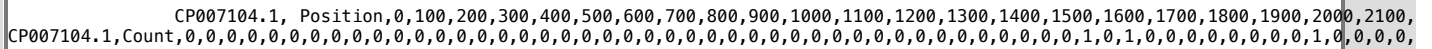
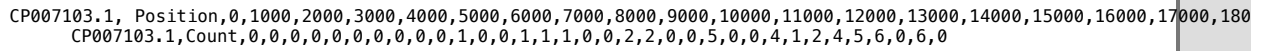
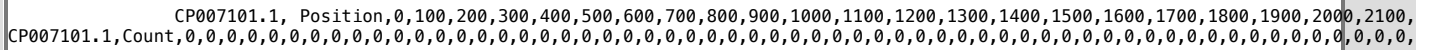
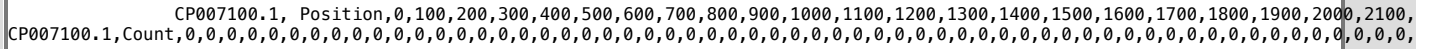
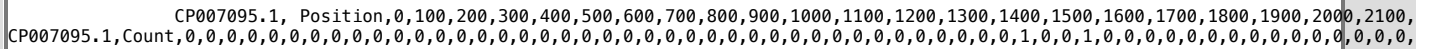
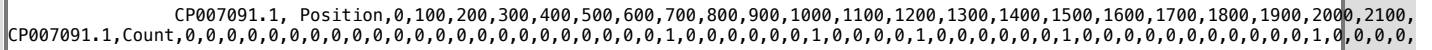
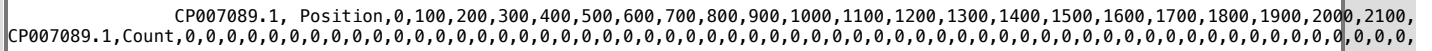
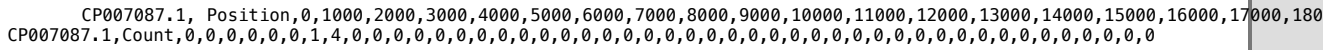
	*	-	?	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V
*	35	129	5	28	3	4	3	9	5	18	8	16	16		17	6	24	2	6	7	25
-	4,077		3,102	9,803	3,739	3,312	3,934	3,011	8,735	4,287	3,990	4,046	8,218	1,604	3,434	9,273	6,998	11,222	9,875	6,588	5,126
?	2	8																			
A	262	2,047	52	943	358	347	476	184	681	281	404	313	732	110	333	668	418	915	933	685	484
C	55	384	1	181	93	62	52	75	127	35	137	50	100	63	57	177	51	243	229	81	58
D	193	1,063	28	528	180	254	425	138	382	162	253	267	325	117	232	575	276	686	553	479	331
E	299	1,650	16	818	266	427	734	184	509	186	365	588	678	114	258	825	329	917	764	592	515
F	89	706	3	394	129	116	83	117	285	118	151	98	199	56	87	248	124	352	382	301	214
G	270	2,149	28	849	331	299	334	191	838	238	330	276	346	201	240	618	316	791	698	437	397
H	100	741	12	347	56	108	101	88	206	134	144	89	293	66	102	226	179	330	409	214	95
I	158	1,032	22	405	211	214	211	114	275	208	241	198	272	100	130	509	189	423	448	437	295
K	176	1,137	26	545	129	182	344	122	440	159	255	457	438	116	254	544	315	723	710	333	292
L	387	1,834	1	958	409	266	326	320	642	286	456	329	720	153	298	747	574	1,239	1,005	710	502
M	60	423	11	160	81	46	88	95	140	106	92	110	124	38	114	178	88	245	227	206	167
N	106	1,127	14	545	193	144	153	99	218	144	164	192	360	110	218	358	141	506	472	385	119
P	238	2,115	8	629	250	273	395	100	380	292	314	312	400	77	207	770	361	567	954	570	289
Q	180	3,972	12	608	217	199	344	150	571	400	220	181	517	141	206	566	923	779	599	536	254
R	297	1,204	31	885	271	380	334	143	446	206	263	307	412	120	181	769	339	1,261	692	448	303
S	500	2,742	62	1,604	352	389	580	376	829	331	452	523	552	134	350	1,011	475	1,187	1,958	915	616
T	301	2,952	38	585	202	312	448	156	439	139	235	284	442	90	180	666	375	666	1,014	867	486
V	174	1,500	61	673	229	262	301	194	420	142	302	266	428	117	191	535	302	701	701	625	400
W	46	186		144	46	23	39	32	49	16	51	43	78	22	58	75	25	87	101	47	83
Y	73	611	10	305	123	70	130	47	170	96	156	123	184	39	153	238	140	344	315	173	115

Variants by chromosome



AE013599.5, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000,1700000,1800000,1900000,2000000,2100000,2200000,2300000,2400000,2500000,2600000,2700000,2800000,2900000,3000000,3100000,3200000,3300000,3400000,3500000,3600000,3700000,3800000,3900000,4000000,4100000,4200000,4300000,4400000,4500000,4600000,4700000,4800000,4900000,5000000,5100000,5200000,5300000,5400000,5500000,5600000,5700000,5800000,5900000,6000000,6100000,6200000,6300000,6400000,6500000,6600000,6700000,6800000,6900000,7000000,7100000,7200000,7300000,7400000,7500000,7600000,7700000,7800000,7900000,8000000,8100000,8200000,8300000,8400000,8500000,8600000,8700000,8800000,8900000,9000000,9100000,9200000,9300000,9400000,9500000,9600000,9700000,9800000,9900000,10000000,10100000,10200000,10300000,10400000,10500000,10600000,10700000,10800000,10900000,11000000,11100000,11200000,11300000,11400000,11500000,11600000,11700000,11800000,11900000,12000000,12100000,12200000,12300000,12400000,12500000,12600000,12700000,12800000,12900000,13000000,13100000,13200000,13300000,13400000,13500000,13600000,13700000,13800000,13900000,14000000,14100000,14200000,14300000,14400000,14500000,14600000,14700000,14800000,14900000,15000000,15100000,15200000,15300000,15400000,15500000,15600000,15700000,15800000,15900000,16000000,16100000,16200000,16300000,16400000,16500000,16600000,16700000,16800000,16900000,17000000,17100000,17200000,17300000,17400000,17500000,17600000,17700000,17800000,17900000,18000000,18100000,18200000,18300000,18400000,18500000,18600000,18700000,18800000,18900000,19000000,19100000,19200000,19300000,19400000,19500000,19600000,19700000,19800000,19900000,20000000,20100000,20200000,20300000,20400000,20500000,20600000,20700000,20800000,20900000,21000000,21100000,21200000,21300000,21400000,21500000,21600000,21700000,21800000,21900000,22000000,22100000,22200000,22300000,22400000,22500000,22600000,22700000,22800000,22900000,23000000,23100000,23200000,23300000,23400000,23500000,23600000,23700000,23800000,23900000,24000000,24100000,24200000,24300000,24400000,24500000,24600000,24700000,24800000,24900000,25000000,25100000,25200000,25300000,25400000,25500000,25600000,25700000,25800000,25900000,26000000,26100000,26200000,26300000,26400000,26500000,26600000,26700000,26800000,26900000,27000000,27100000,27200000,27300000,27400000,27500000,27600000,27700000,27800000,27900000,28000000,28100000,28200000,28300000,28400000,28500000,28600000,28700000,28800000,28900000,29000000,29100000,29200000,29300000,29400000,29500000,29600000,29700000,29800000,29900000,30000000,30100000,30200000,30300000,30400000,30500000,30600000,30700000,30800000,30900000,31000000,31100000,31200000,31300000,31400000,31500000,31600000,31700000,31800000,31900000,32000000,32100000,32200000,32300000,32400000,32500000,32600000,32700000,32800000,32900000,33000000,33100000,33200000,33300000,33400000,33500000,33600000,33700000,33800000,33900000,34000000,34100000,34200000,34300000,34400000,34500000,34600000,34700000,34800000,34900000,35000000,35100000,35200000,35300000,35400000,35500000,35600000,35700000,35800000,35900000,36000000,36100000,36200000,36300000,36400000,36500000,36600000,36700000,36800000,36900000,37000000,37100000,37200000,37300000,37400000,37500000,37600000,37700000,37800000,37900000,38000000,38100000,38200000,38300000,38400000,38500000,38600000,38700000,38800000,38900000,39000000,39100000,39200000,39300000,39400000,39500000,39600000,39700000,39800000,39900000,40000000,40100000,40200000,40300000,40400000,40500000,40600000,40700000,40800000,40900000,41000000,41100000,41200000,41300000,41400000,41500000,41600000,41700000,41800000,41900000,42000000,42100000,42200000,42300000,42400000,42500000,42600000,42700000,42800000,42900000,43000000,43100000,43200000,43300000,43400000,43500000,43600000,43700000,43800000,43900000,44000000,44100000,44200000,44300000,44400000,44500000,44600000,44700000,44800000,44900000,45000000,45100000,45200000,45300000,45400000,45500000,45600000,45700000,45800000,45900000,46000000,46100000,46200000,46300000,46400000,46500000,46600000,46700000,46800000,46900000,47000000,47100000,47200000,47300000,47400000,47500000,47600000,47700000,47800000,47900000,48000000,48100000,48200000,48300000,48400000,48500000,48600000,48700000,48800000,48900000,49000000,49100000,49200000,49300000,49400000,49500000,49600000,49700000,49800000,49900000,50000000,50100000,50200000,50300000,50400000,50500000,50600000,50700000,50800000,50900000,51000000,51100000,51200000,51300000,51400000,51500000,51600000,51700000,51800000,51900000,52000000,52100000,52200000,52300000,52400000,52500000,52600000,52700000,52800000,52900000,53000000,53100000,53200000,53300000,53400000,53500000,53600000,53700000,53800000,53900000,54000000,54100000,54200000,54300000,54400000,54500000,54600000,54700000,54800000,54900000,55000000,55100000,55200000,55300000,554





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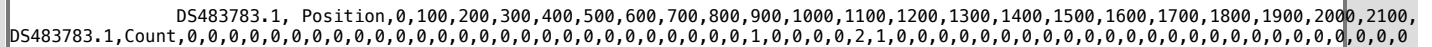
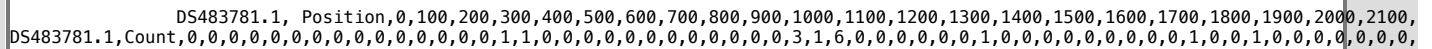
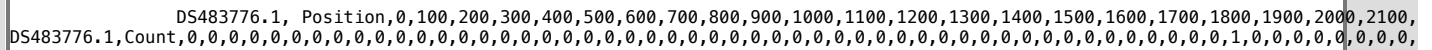
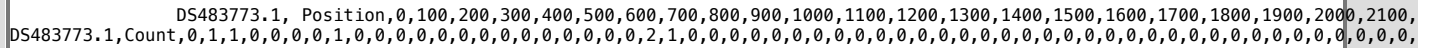
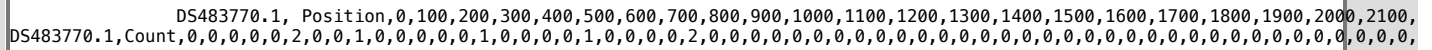
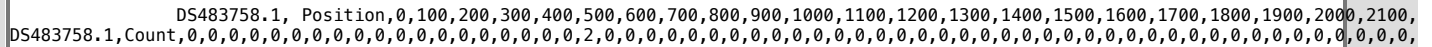
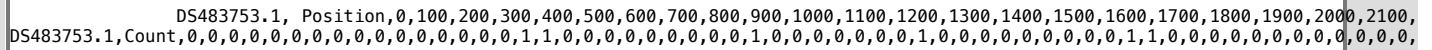
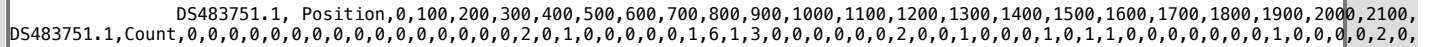
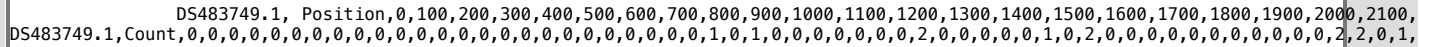
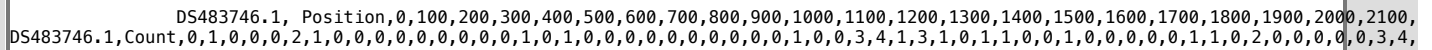
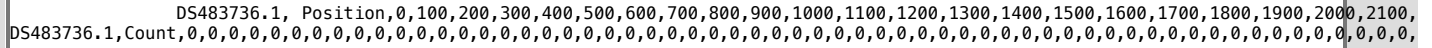
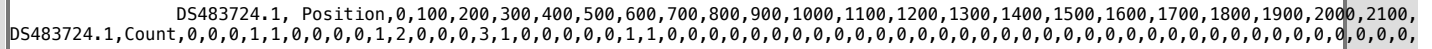
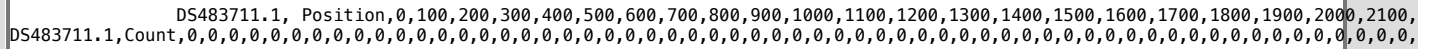
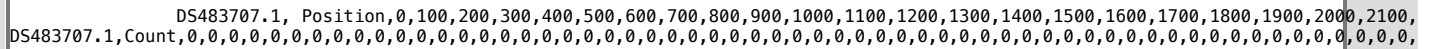
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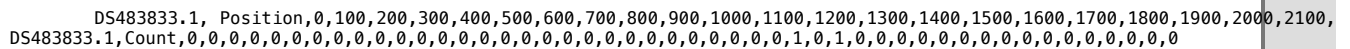
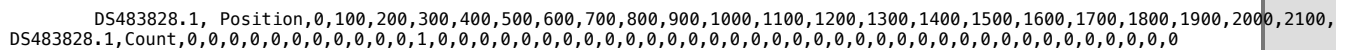
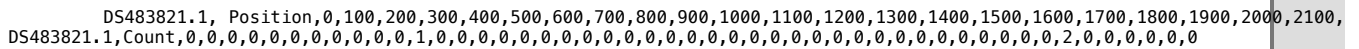
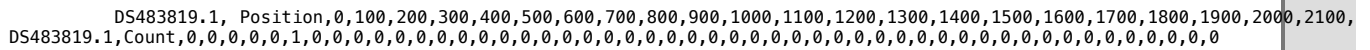
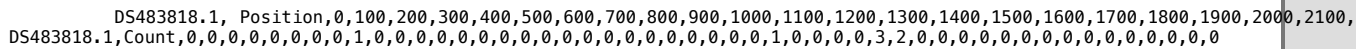
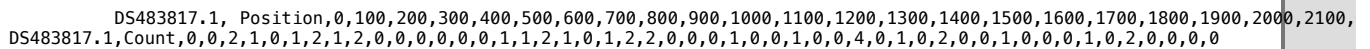
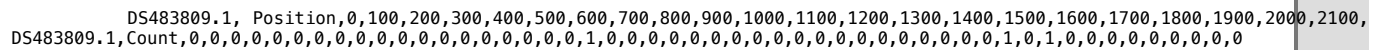
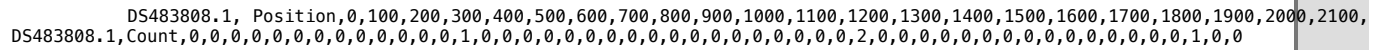
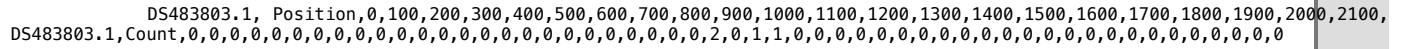
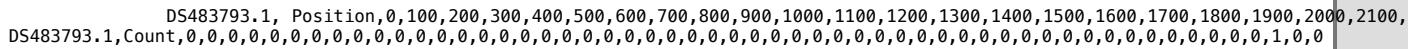
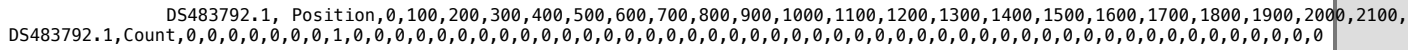
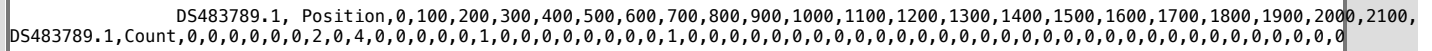
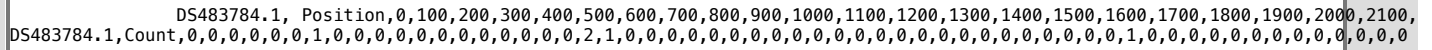
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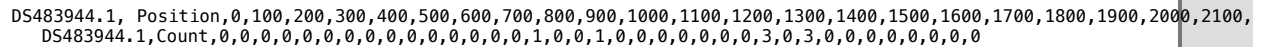
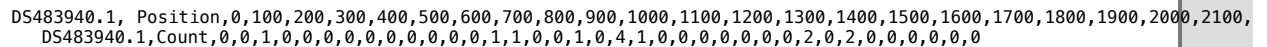
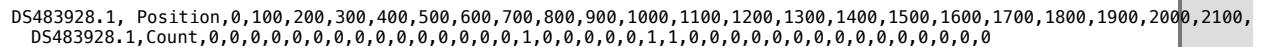
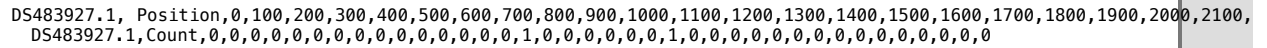
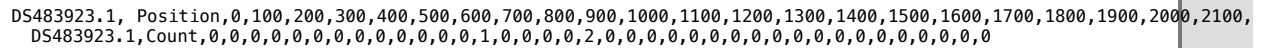
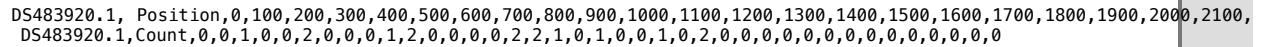
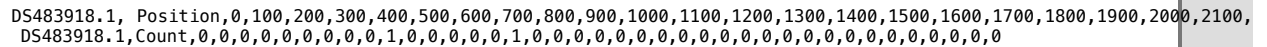
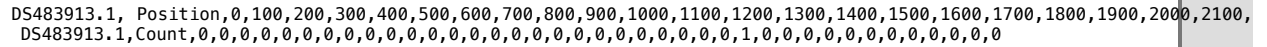
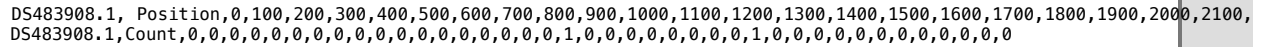
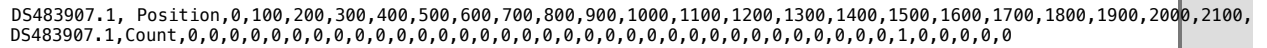
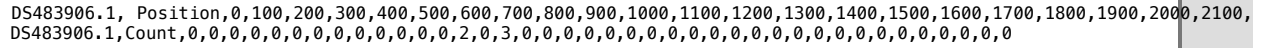
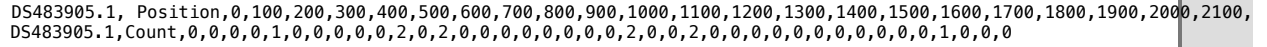
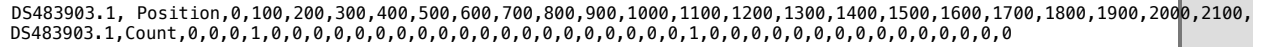
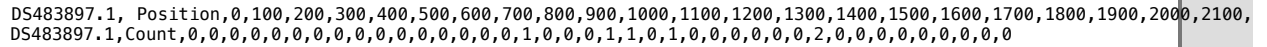


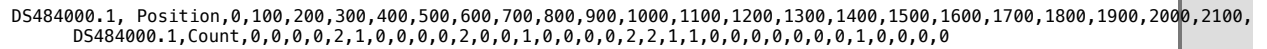
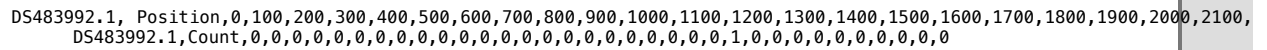
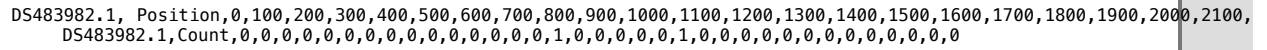
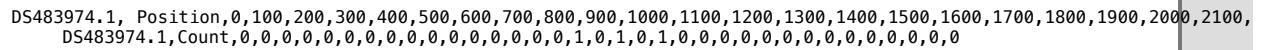
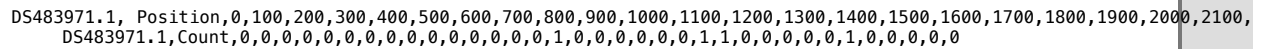
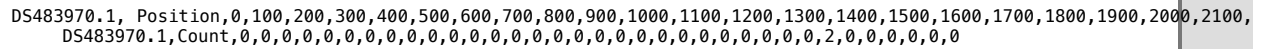
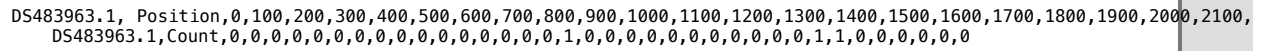
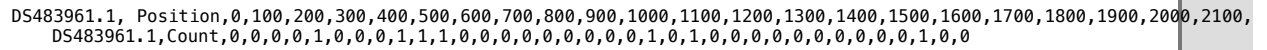
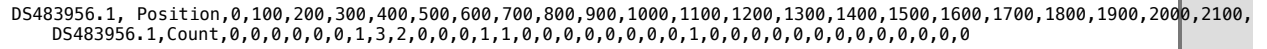
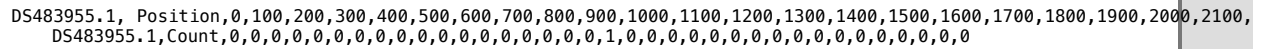
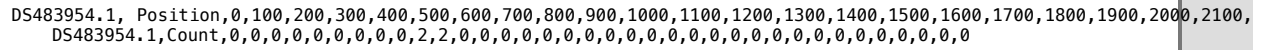
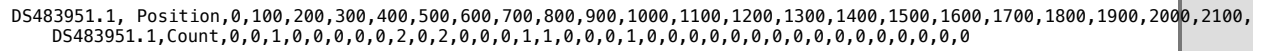
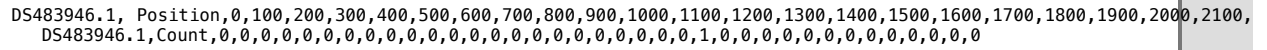
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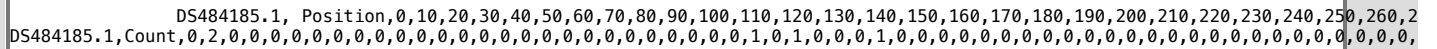
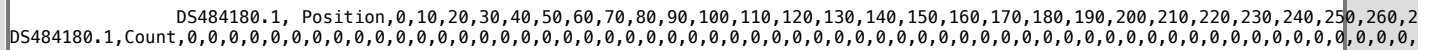
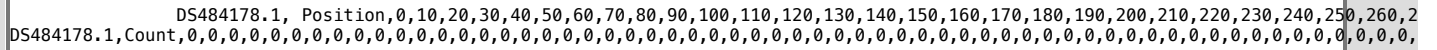
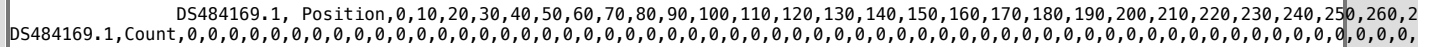
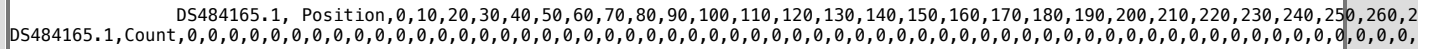
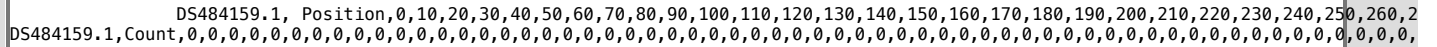
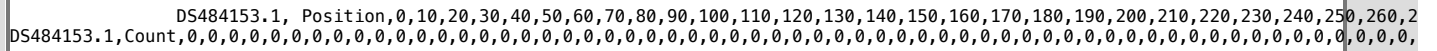
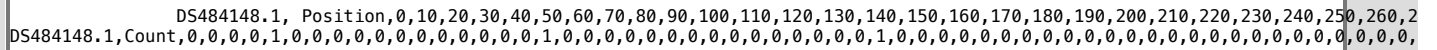
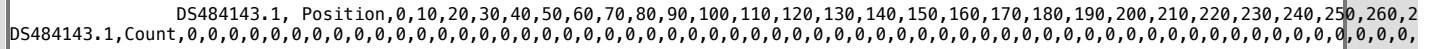
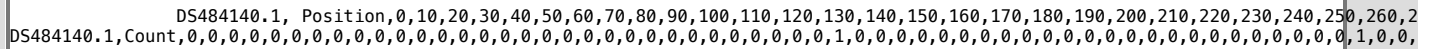
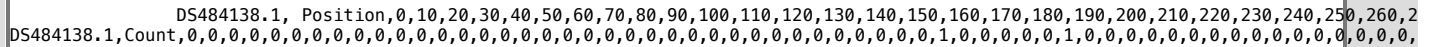
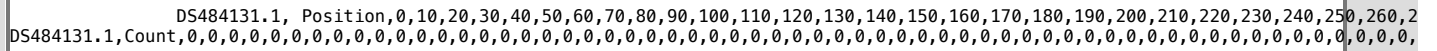
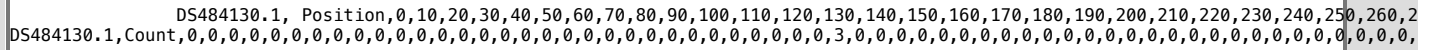


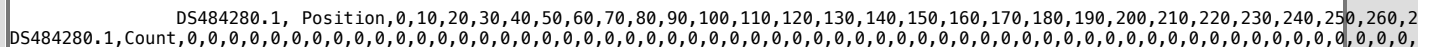
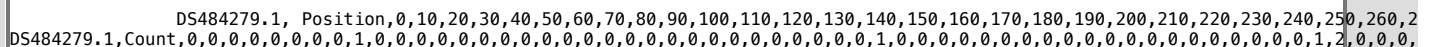
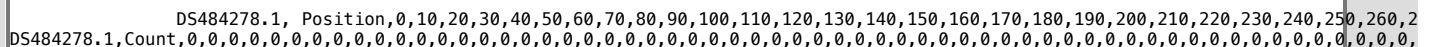
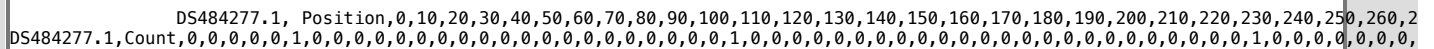
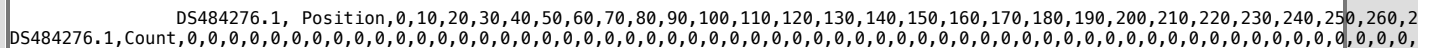
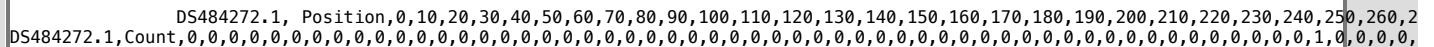
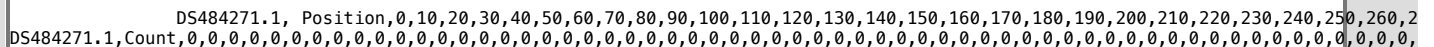
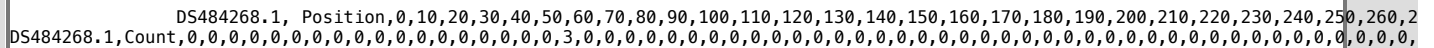
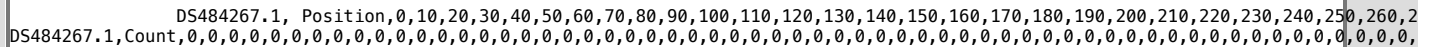
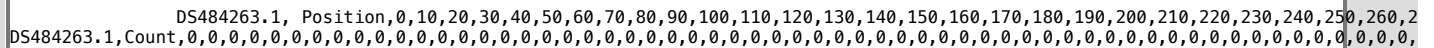
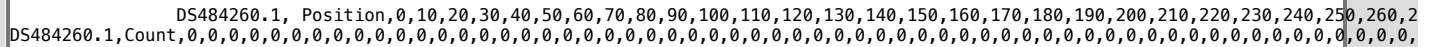
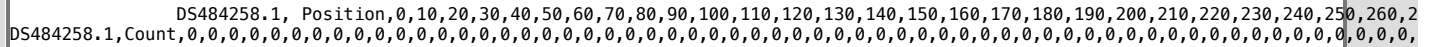
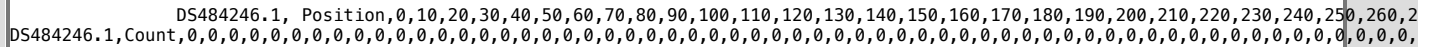
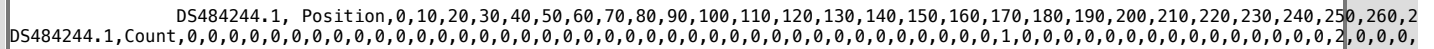


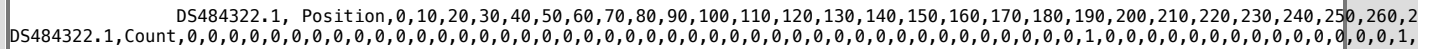
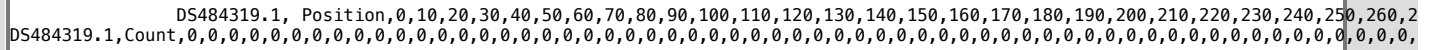
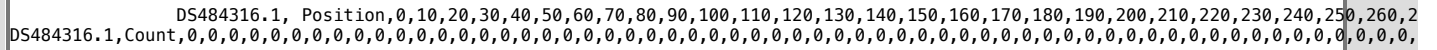
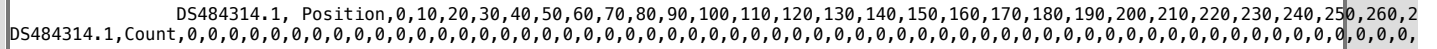
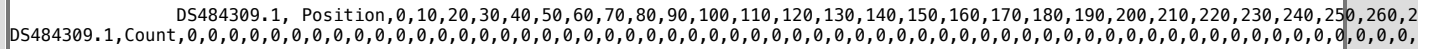
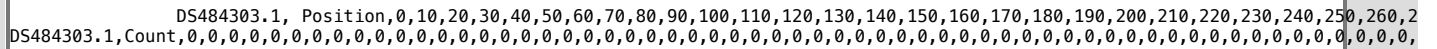
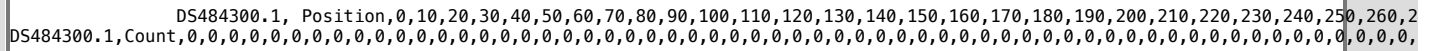
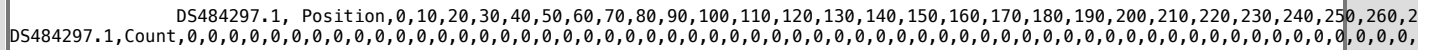
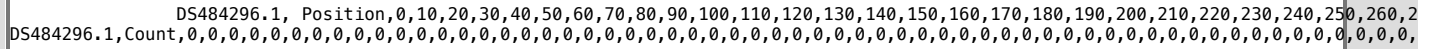
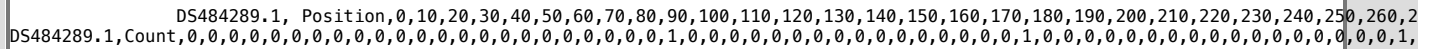
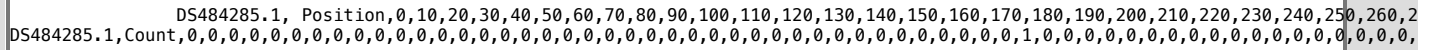
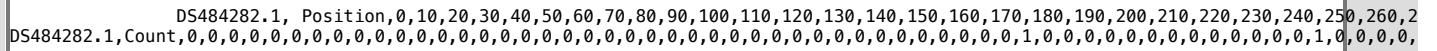
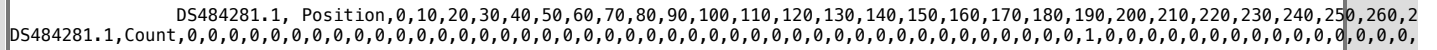


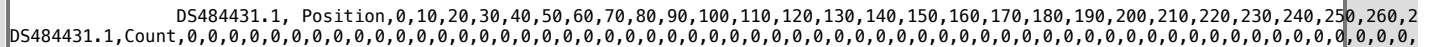
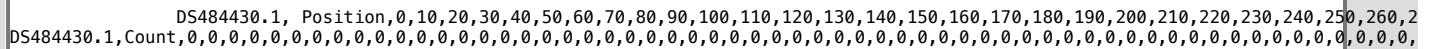
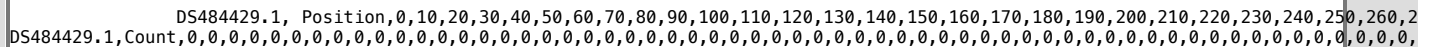
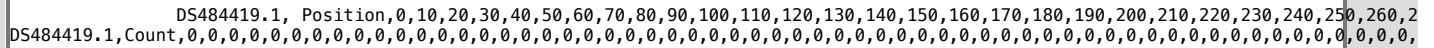
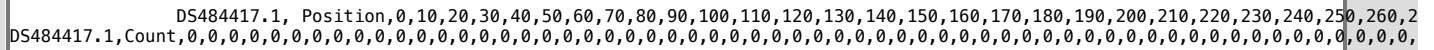
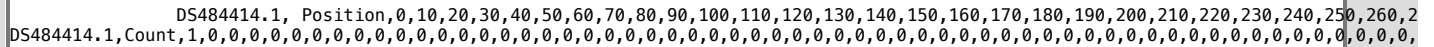
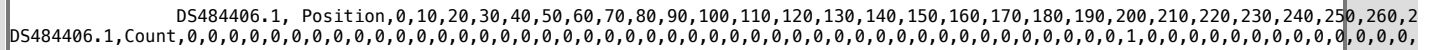
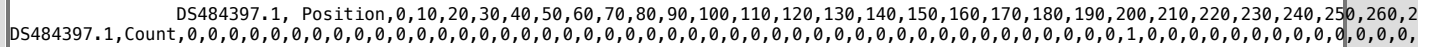
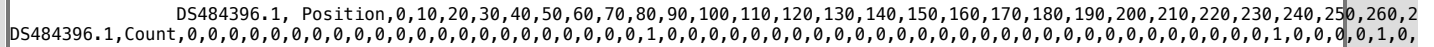
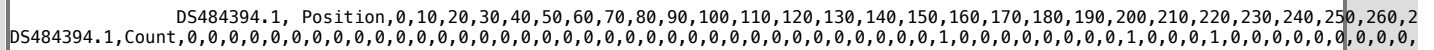
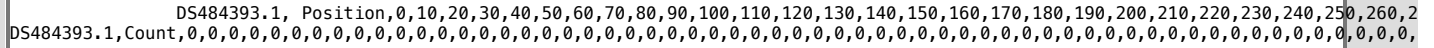
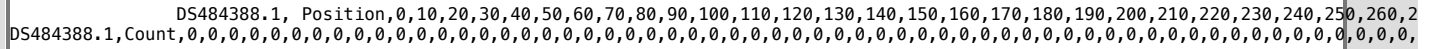
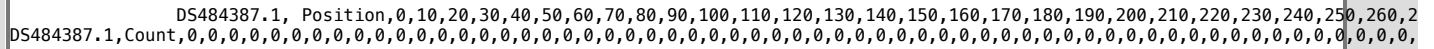
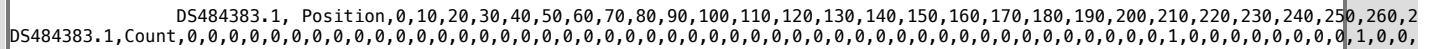


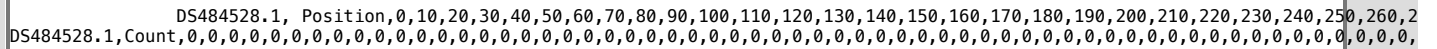
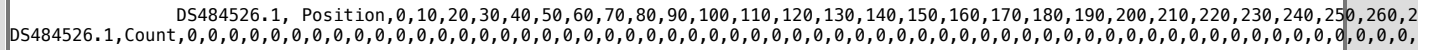
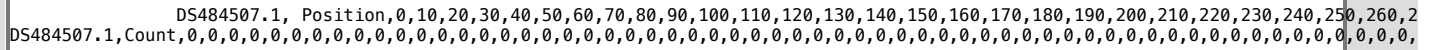
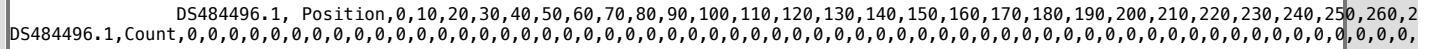
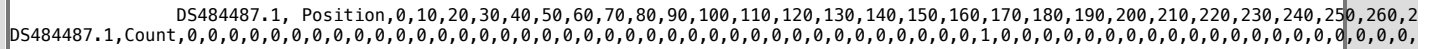
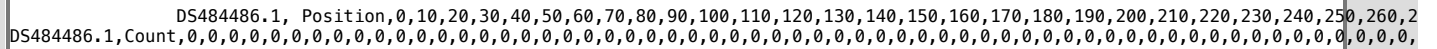
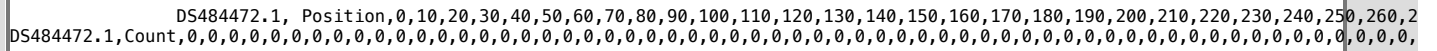
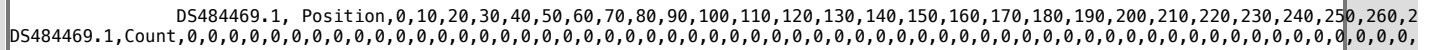
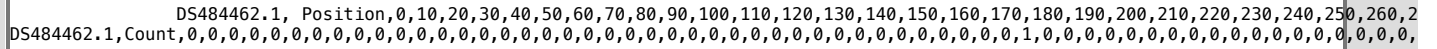
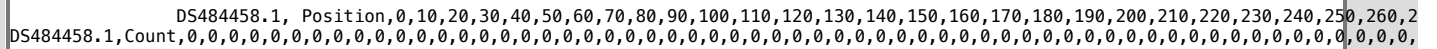
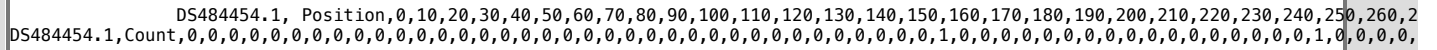
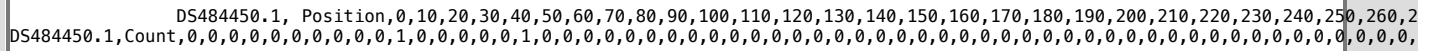
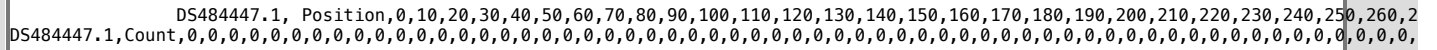
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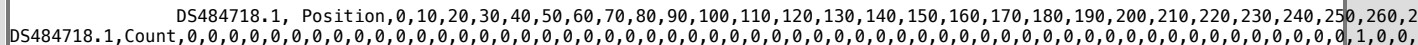
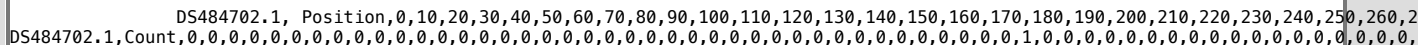
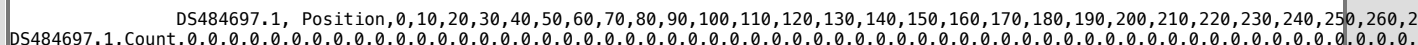
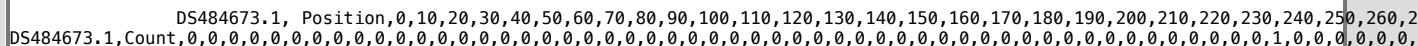
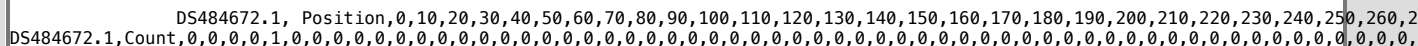
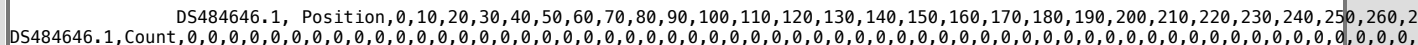
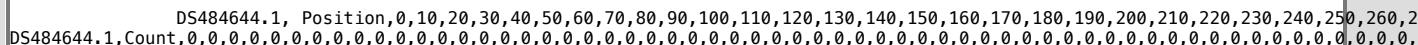
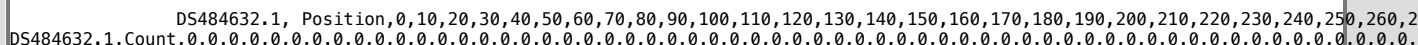
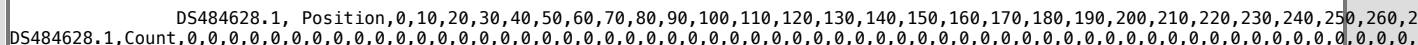
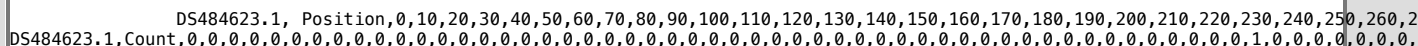
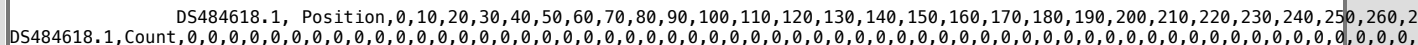
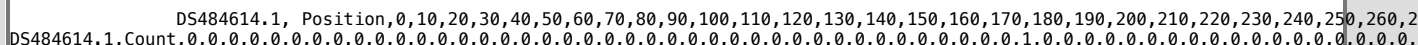
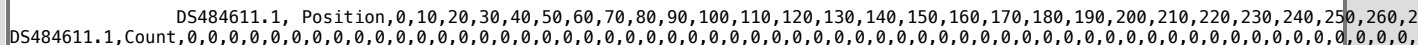
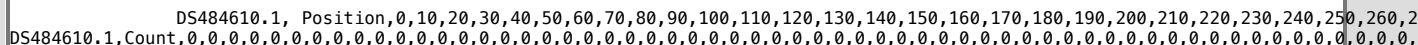


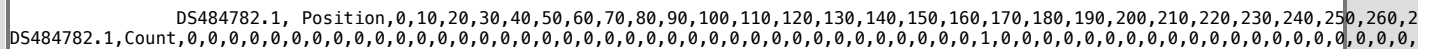
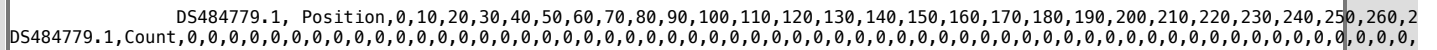
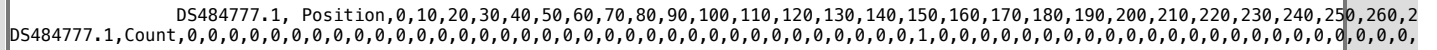
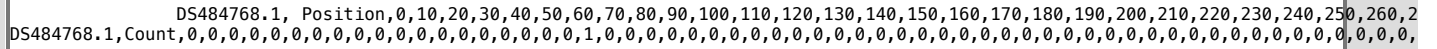
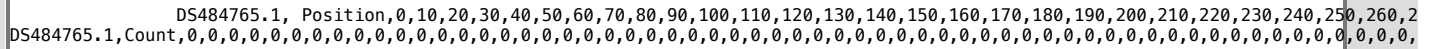
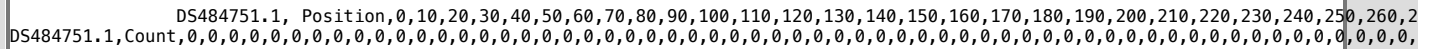
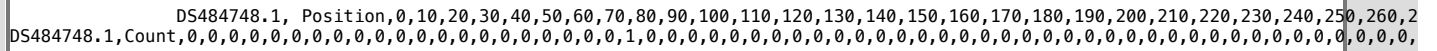
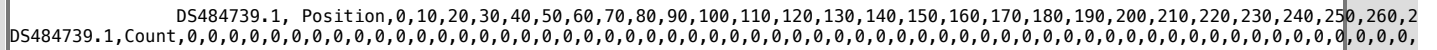
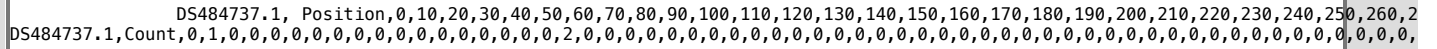
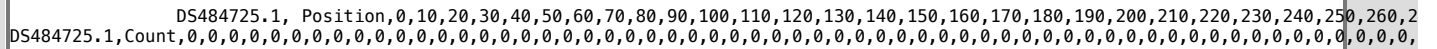
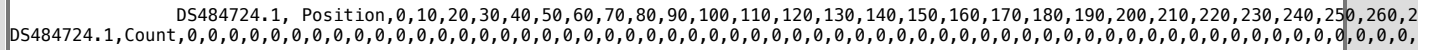
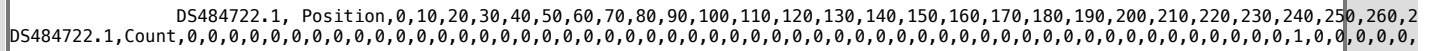
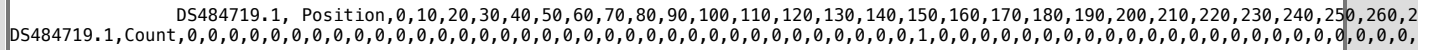


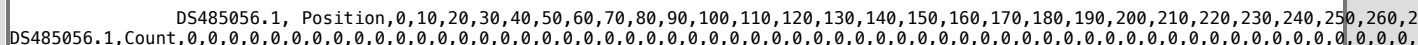
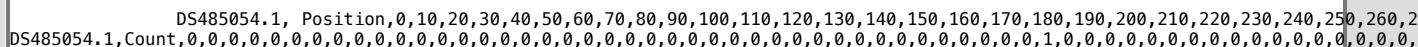
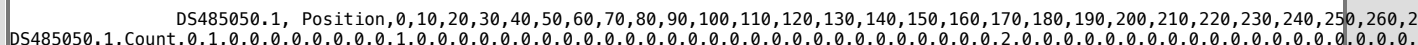
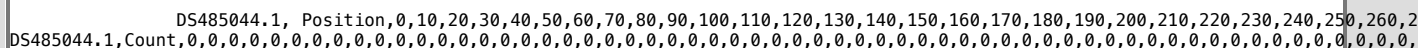
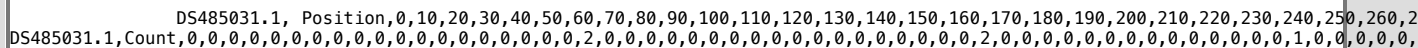
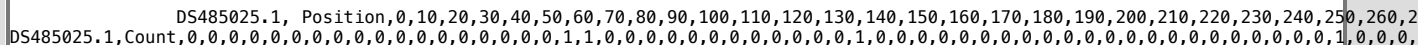
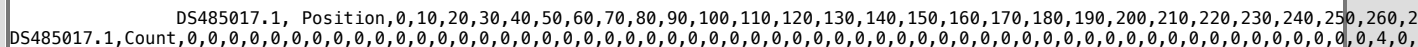
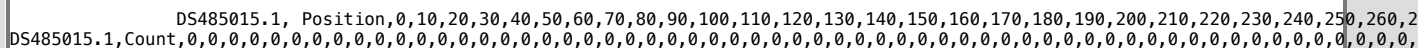
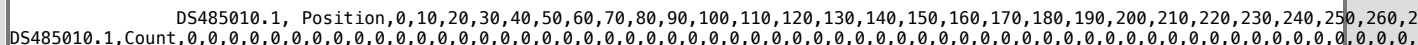
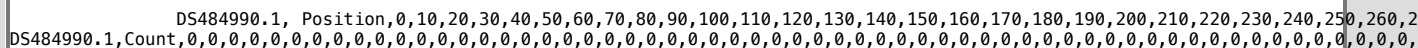
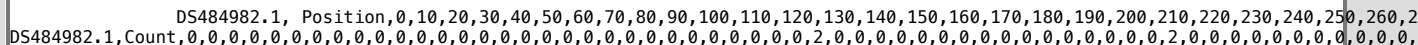
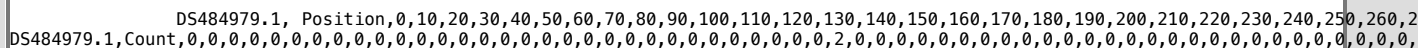
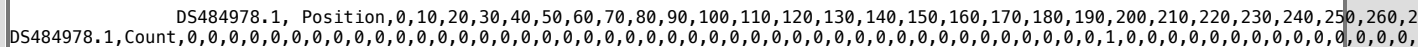
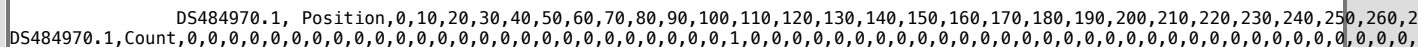


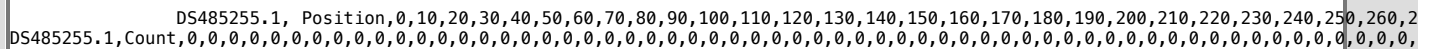
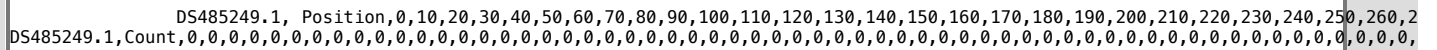
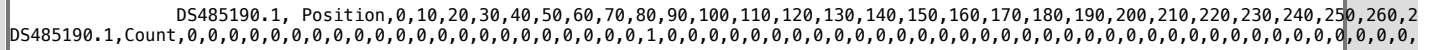
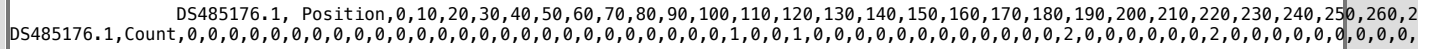
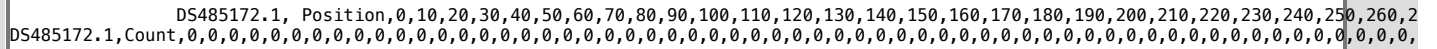
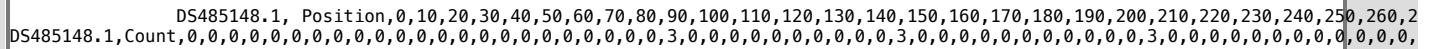
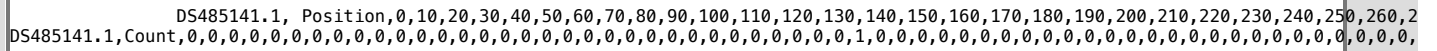
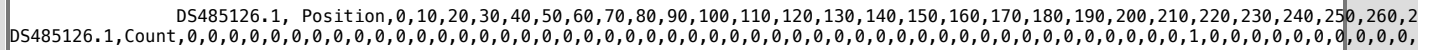
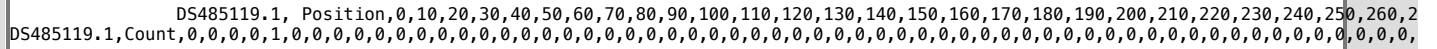
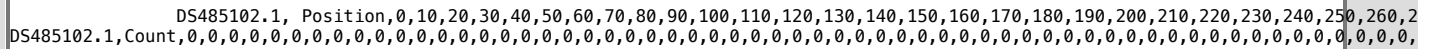
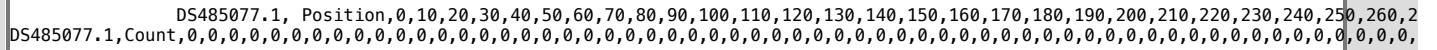
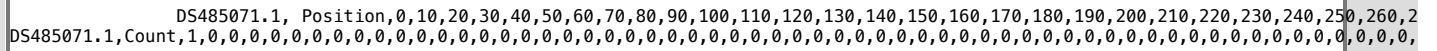
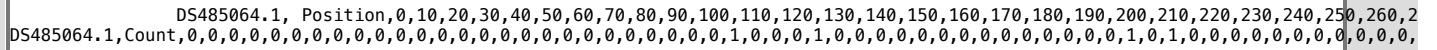


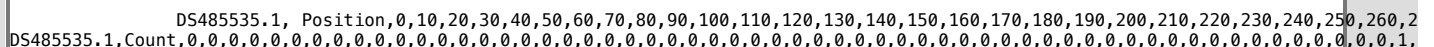
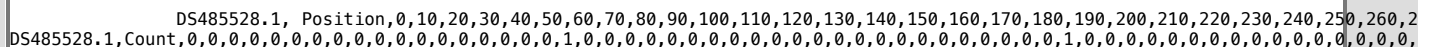
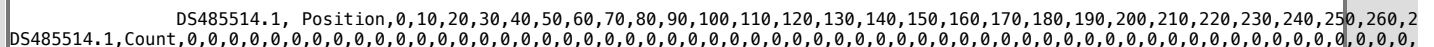
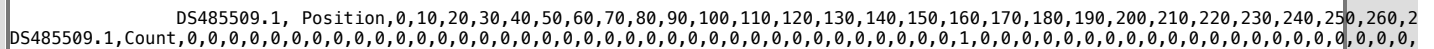
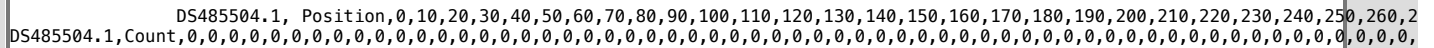
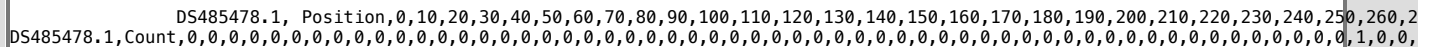
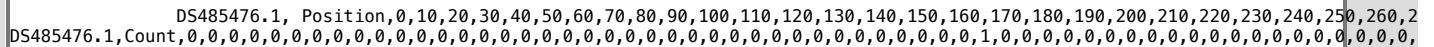
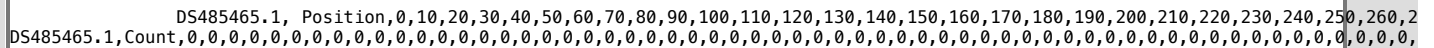
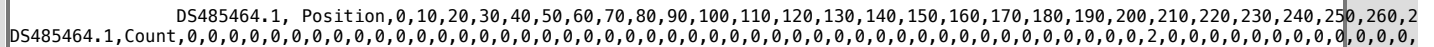
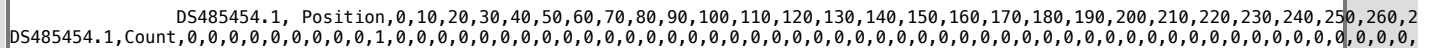
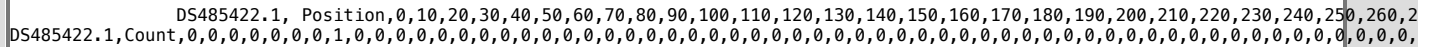
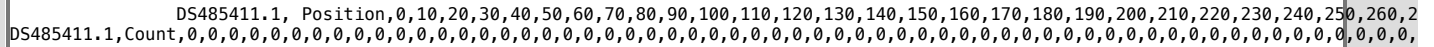
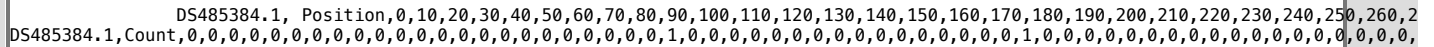
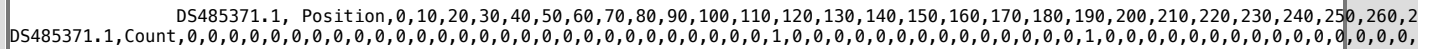


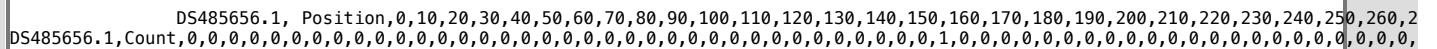
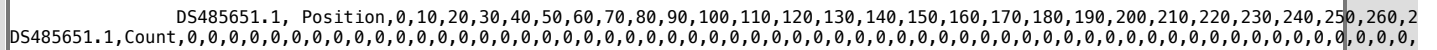
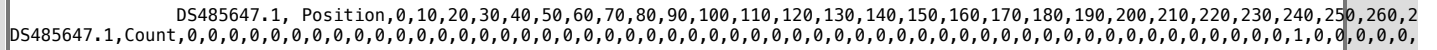
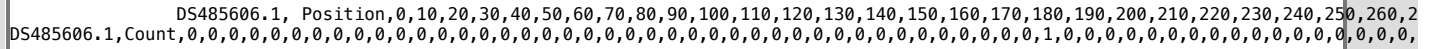
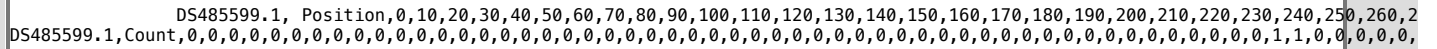
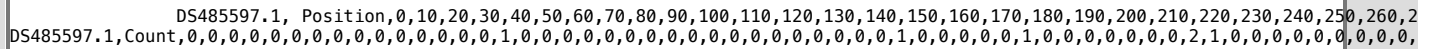
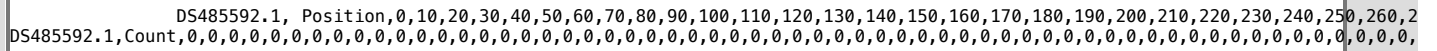
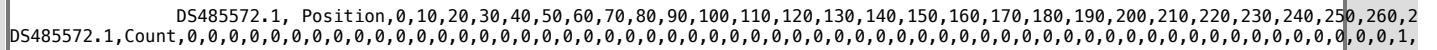
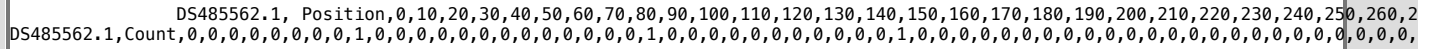
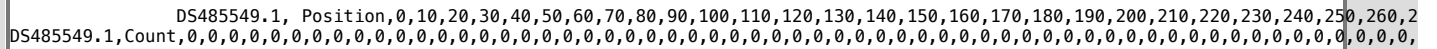
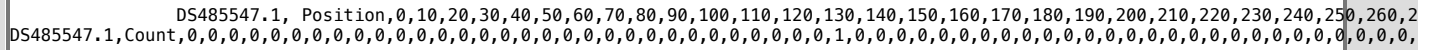
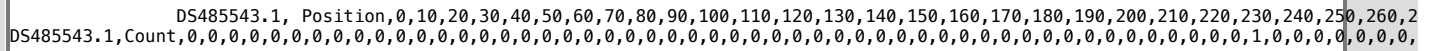
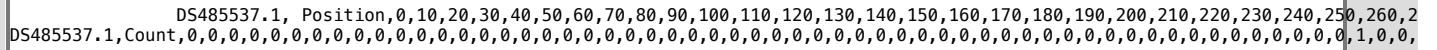


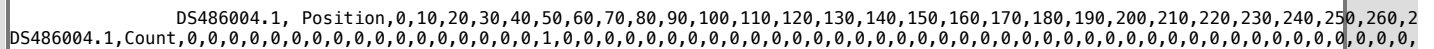
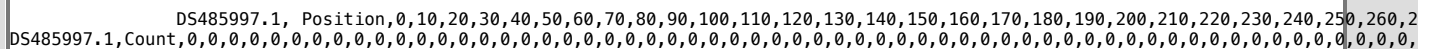
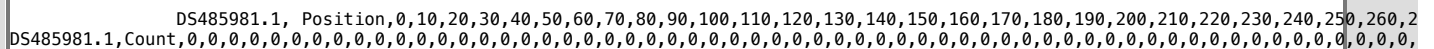
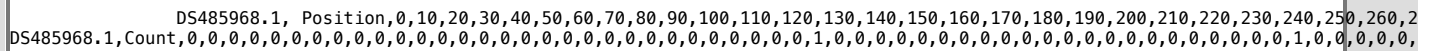
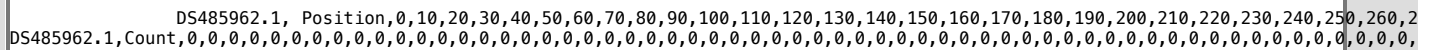
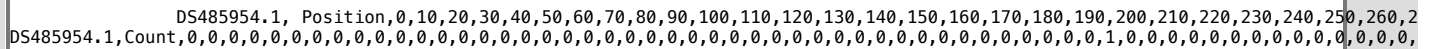
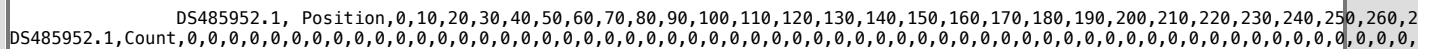
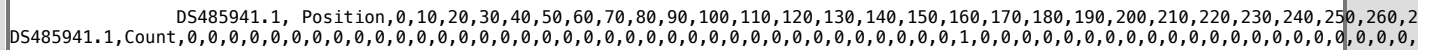
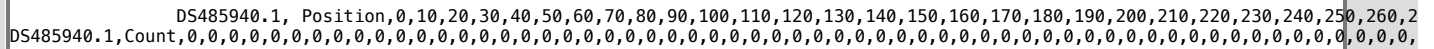
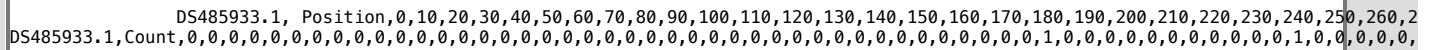
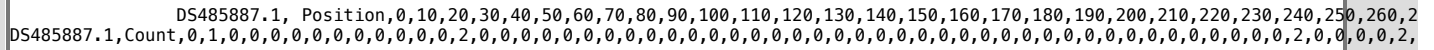
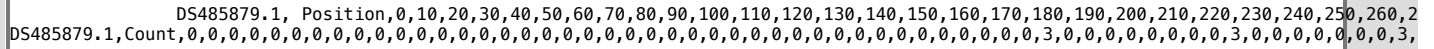
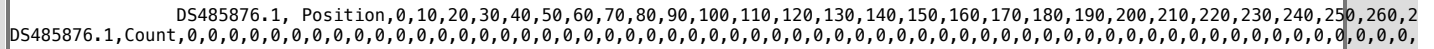
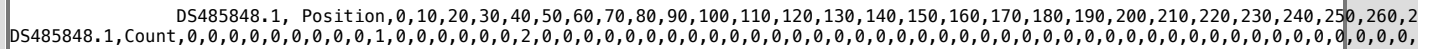


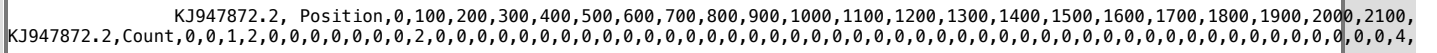
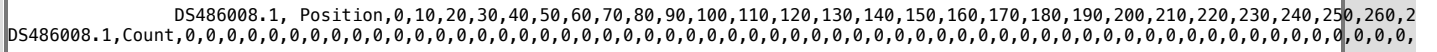












Details by gene
[Here](#) you can find a tab-separated table.

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