

SnpEff: Variant analysis

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Summary

Genome	ncbi_drosophila
Date	2025-12-29 00:14
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/output2/results/variants/
Warnings	62,658
Errors	0
Number of lines (input file)	80,261
Number of variants (before filter)	80,261
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	80,261
Number of known variants (i.e. non-empty ID)	80,261 (100%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	0
Number of annotations	421,829
Genome total length	143,726,002
Genome effective length	139,397,114
Variant rate	1 variant every 1,736 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
AE013599.5	25,286,936	14,225	1,777
AE014134.6	23,513,712	16,295	1,443
AE014135.4	1,348,131	147	9,170
AE014296.5	28,110,227	17,105	1,643
AE014297.3	32,079,331	16,788	1,910
AE014298.5	23,542,271	14,207	1,657
CP007074.1	76,224	3	25,408
CP007075.1	11,983	20	599
CP007077.1	36,913	60	615
CP007078.1	22,604	3	7,534
CP007079.1	23,238	16	1,452
CP007080.1	86,267	2	43,133
CP007081.1	88,768	5	17,753
CP007084.1	62,570	1	62,570
CP007085.1	45,120	8	5,640
CP007086.1	22,882	2	11,441
CP007087.1	46,986	5	9,397
CP007089.1	16,157	1	16,157
CP007091.1	20,763	10	2,076
CP007101.1	24,503	2	12,251
CP007103.1	33,320	37	900
CP007104.1	27,447	7	3,921
CP007106.1	3,667,352	39	94,034
CP007108.1	66,731	4	16,682
CP007111.1	34,521	1	34,521
CP007115.1	21,921	1	21,921
CP007120.1	76,973	13	5,921
DS483562.1	50,625	16	3,164

DS483629.1	15,417	40	385
DS483641.1	14,503	32	453
DS483646.1	14,098	1	14,098
DS483648.1	13,940	2	6,970
DS483655.1	13,549	3	4,516
DS483659.1	13,416	42	319
DS483660.1	13,394	24	558
DS483670.1	12,827	4	3,206
DS483675.1	12,536	2	6,268
DS483677.1	12,513	2	6,256
DS483681.1	12,368	1	12,368
DS483698.1	11,522	2	5,761
DS483711.1	14,687	1	14,687
DS483724.1	13,501	24	562
DS483746.1	9,341	31	301
DS483749.1	8,007	21	381
DS483751.1	7,314	26	281
DS483753.1	7,123	4	1,780
DS483758.1	6,860	1	6,860
DS483770.1	6,193	8	774
DS483773.1	6,062	5	1,212
DS483776.1	6,000	1	6,000
DS483781.1	5,952	11	541
DS483783.1	5,891	3	1,963
DS483784.1	5,832	1	5,832
DS483789.1	5,555	4	1,388
DS483803.1	5,232	4	1,308
DS483805.1	5,182	1	5,182
DS483808.1	5,060	6	843
DS483809.1	5,057	3	1,685
DS483817.1	4,933	19	259
DS483818.1	4,917	6	819
DS483819.1	4,903	1	4,903
DS483824.1	4,820	1	4,820
DS483843.1	4,515	6	752
DS483845.1	4,465	2	2,232
DS483851.1	4,395	3	1,465
DS483853.1	4,381	17	257
DS483854.1	4,378	2	2,189
DS483866.1	4,273	7	610
DS483870.1	4,231	1	4,231
DS483880.1	4,150	7	592
DS483885.1	4,085	3	1,361
DS483888.1	4,072	10	407
DS483892.1	4,013	5	802
DS483893.1	4,012	1	4,012
DS483897.1	3,984	6	664
DS483903.1	3,941	2	1,970
DS483904.1	3,932	1	3,932
DS483905.1	3,926	5	785
DS483906.1	3,924	5	784
DS483907.1	3,921	1	3,921
DS483908.1	3,913	2	1,956
DS483909.1	3,913	1	3,913
DS483918.1	3,818	1	3,818
DS483920.1	3,806	14	271
DS483927.1	3,737	2	1,868
DS483928.1	3,730	2	1,865
DS483940.1	3,648	7	521
DS483944.1	3,622	9	402
DS483946.1	3,603	1	3,603
DS483951.1	3,574	9	397
DS483954.1	3,554	4	888
DS483955.1	3,553	2	1,776
DS483956.1	3,553	6	592
DS483961.1	3,527	5	705
DS483963.1	3,523	2	1,761
DS483970.1	3,490	2	1,745
DS483971.1	3,478	3	1,159
DS483974.1	3,473	2	1,736

DS483975.1	3,466	1	3,466
DS483982.1	3,402	1	3,402
DS483992.1	3,365	1	3,365
DS484000.1	3,302	15	220
DS484002.1	3,290	3	1,096
DS484004.1	3,277	17	192
DS484012.1	3,254	2	1,627
DS484013.1	3,252	1	3,252
DS484022.1	3,209	5	641
DS484039.1	3,162	1	3,162
DS484041.1	3,157	12	263
DS484042.1	3,156	12	263
DS484045.1	3,129	1	3,129
DS484046.1	3,123	1	3,123
DS484050.1	3,100	1	3,100
DS484051.1	3,100	2	1,550
DS484057.1	3,076	3	1,025
DS484058.1	3,073	24	128
DS484060.1	3,065	3	1,021
DS484061.1	3,059	2	1,529
DS484064.1	3,044	12	253
DS484068.1	3,013	2	1,506
DS484069.1	3,010	5	602
DS484070.1	3,009	6	501
DS484084.1	2,956	1	2,956
DS484085.1	2,945	1	2,945
DS484089.1	2,928	11	266
DS484099.1	2,910	5	582
DS484102.1	2,903	3	967
DS484116.1	2,860	16	178
DS484124.1	2,846	6	474
DS484125.1	2,844	2	1,422
DS484126.1	2,841	1	2,841
DS484130.1	2,834	3	944
DS484131.1	2,833	2	1,416
DS484138.1	2,822	2	1,411
DS484140.1	2,819	5	563
DS484143.1	2,814	1	2,814
DS484148.1	2,795	16	174
DS484153.1	2,793	1	2,793
DS484159.1	2,784	1	2,784
DS484165.1	2,751	2	1,375
DS484178.1	2,698	3	899
DS484180.1	2,697	4	674
DS484185.1	2,686	2	1,343
DS484187.1	2,671	3	890
DS484188.1	2,670	5	534
DS484197.1	2,642	1	2,642
DS484198.1	2,641	4	660
DS484202.1	2,636	1	2,636
DS484203.1	2,635	2	1,317
DS484216.1	2,603	3	867
DS484219.1	2,591	4	647
DS484225.1	2,577	4	644
DS484235.1	2,557	1	2,557
DS484244.1	2,536	15	169
DS484246.1	2,529	2	1,264
DS484253.1	2,520	1	2,520
DS484255.1	2,516	2	1,258
DS484258.1	2,510	7	358
DS484260.1	2,505	1	2,505
DS484263.1	2,487	1	2,487
DS484268.1	2,475	4	618
DS484271.1	2,470	1	2,470
DS484272.1	2,464	1	2,464
DS484276.1	2,447	4	611
DS484277.1	2,442	12	203
DS484278.1	2,439	1	2,439
DS484279.1	2,438	12	203
DS484280.1	2,438	3	812

DS484281.1	2,438	1	2,438
DS484282.1	2,435	9	270
DS484285.1	2,431	4	607
DS484289.1	2,425	9	269
DS484296.1	2,417	1	2,417
DS484297.1	2,413	2	1,206
DS484300.1	2,400	2	1,200
DS484316.1	2,379	1	2,379
DS484319.1	2,372	4	593
DS484320.1	2,369	1	2,369
DS484322.1	2,366	2	1,183
DS484330.1	2,353	1	2,353
DS484343.1	2,325	7	332
DS484345.1	2,318	1	2,318
DS484346.1	2,317	3	772
DS484348.1	2,308	1	2,308
DS484354.1	2,293	1	2,293
DS484358.1	2,286	1	2,286
DS484362.1	2,273	1	2,273
DS484367.1	2,259	1	2,259
DS484369.1	2,253	10	225
DS484371.1	2,247	1	2,247
DS484377.1	2,232	2	1,116
DS484382.1	2,223	4	555
DS484383.1	2,221	4	555
DS484387.1	2,210	2	1,105
DS484388.1	2,209	1	2,209
DS484393.1	2,201	2	1,100
DS484394.1	2,200	3	733
DS484395.1	2,198	1	2,198
DS484396.1	2,198	5	439
DS484406.1	2,177	1	2,177
DS484417.1	2,139	1	2,139
DS484419.1	2,132	1	2,132
DS484431.1	2,113	1	2,113
DS484434.1	2,108	1	2,108
DS484447.1	2,089	1	2,089
DS484450.1	2,087	1	2,087
DS484454.1	2,084	5	416
DS484458.1	2,079	1	2,079
DS484462.1	2,068	1	2,068
DS484472.1	2,046	1	2,046
DS484486.1	2,014	1	2,014
DS484497.1	1,998	1	1,998
DS484507.1	1,978	2	989
DS484526.1	1,956	1	1,956
DS484528.1	1,947	1	1,947
DS484533.1	1,944	1	1,944
DS484541.1	1,933	1	1,933
DS484552.1	1,920	1	1,920
DS484556.1	1,916	2	958
DS484563.1	1,903	3	634
DS484566.1	1,900	10	190
DS484568.1	1,899	1	1,899
DS484578.1	1,872	1	1,872
DS484588.1	1,863	8	232
DS484593.1	1,849	5	369
DS484594.1	1,843	1	1,843
DS484600.1	1,841	1	1,841
DS484601.1	1,832	4	458
DS484608.1	1,818	1	1,818
DS484609.1	1,818	1	1,818
DS484610.1	1,813	2	906
DS484611.1	1,813	1	1,813
DS484614.1	1,806	3	602
DS484625.1	1,787	1	1,787
DS484632.1	1,775	4	443
DS484644.1	1,747	1	1,747
DS484646.1	1,747	8	218
DS484673.1	1,696	8	212

DS484682.1	1,680	1	1,680
DS484697.1	1,636	2	818
DS484702.1	1,623	1	1,623
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
DS484732.1	1,556	1	1,556
DS484737.1	1,550	3	516
DS484739.1	1,549	4	387
DS484765.1	1,516	1	1,516
DS484768.1	1,509	2	754
DS484777.1	1,489	1	1,489
DS484787.1	1,475	1	1,475
DS484789.1	1,473	1	1,473
DS484803.1	1,461	1	1,461
DS484809.1	1,453	1	1,453
DS484817.1	1,445	4	361
DS484842.1	1,416	1	1,416
DS484857.1	1,402	2	701
DS484869.1	1,391	4	347
DS484880.1	1,380	1	1,380
DS484894.1	1,375	1	1,375
DS484904.1	1,366	2	683
DS484907.1	1,361	2	680
DS484913.1	1,355	1	1,355
DS484948.1	1,328	1	1,328
DS484963.1	1,315	5	263
DS484970.1	1,310	1	1,310
DS484978.1	1,306	1	1,306
DS484979.1	1,304	2	652
DS484982.1	1,304	4	326
DS484990.1	1,301	1	1,301
DS485010.1	1,286	8	160
DS485015.1	1,283	1	1,283
DS485017.1	1,281	3	427
DS485025.1	1,278	3	426
DS485031.1	1,275	2	637
DS485036.1	1,274	1	1,274
DS485044.1	1,271	1	1,271
DS485050.1	1,268	4	317
DS485053.1	1,266	1	1,266
DS485054.1	1,265	1	1,265
DS485056.1	1,263	1	1,263
DS485064.1	1,262	7	180
DS485077.1	1,258	2	629
DS485104.1	1,240	1	1,240
DS485119.1	1,235	2	617
DS485126.1	1,233	1	1,233
DS485141.1	1,228	1	1,228
DS485148.1	1,227	3	409
DS485172.1	1,220	1	1,220
DS485176.1	1,219	9	135
DS485201.1	1,208	4	302
DS485260.1	1,189	4	297
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	1	1,161
DS485360.1	1,159	2	579
DS485371.1	1,156	6	192
DS485384.1	1,153	2	576

DS485411.1	1,146	1	1,146
DS485415.1	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
DS485467.1	1,132	1	1,132
DS485476.1	1,130	1	1,130
DS485504.1	1,123	2	561
DS485509.1	1,123	1	1,123
DS485528.1	1,117	4	279
DS485535.1	1,116	2	558
DS485543.1	1,114	1	1,114
DS485549.1	1,112	2	556
DS485592.1	1,102	1	1,102
DS485597.1	1,100	5	220
DS485606.1	1,097	1	1,097
DS485647.1	1,086	3	362
DS485651.1	1,084	1	1,084
DS485656.1	1,083	1	1,083
DS485664.1	1,081	6	180
DS485703.1	1,071	2	535
DS485707.1	1,071	2	535
DS485723.1	1,067	1	1,067
DS485753.1	1,059	1	1,059
DS485757.1	1,058	1	1,058
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	1	1,048
DS485876.1	1,032	1	1,032
DS485879.1	1,031	9	114
DS485887.1	1,029	5	205
DS485933.1	1,019	2	509
DS485940.1	1,018	1	1,018
DS485941.1	1,018	2	509
DS485962.1	1,012	1	1,012
DS485968.1	1,011	1	1,011
DS485981.1	1,007	1	1,007
DS485996.1	1,004	1	1,004
DS486004.1	1,001	1	1,001
KJ947872.2	19,524	13	1,501
Total	139,397,114	80,261	1,736

Number variants by type

Type	Total
SNP	0
MNP	318
INS	21,896
DEL	30,145
MIXED	27,902
INV	0
DUP	0
CNV	0
BND	0
INTERVAL	0
Total	80,261

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	490	0.116%
LOW	1,076	0.255%
MODERATE	3,751	0.889%
MODIFIER	416,512	98.74%

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			
3_prime_UTR_truncation	1	0%			
3_prime_UTR_variant	7,055	1.665%			
5_prime_UTR_variant	3,179	0.75%			
bidirectional_gene_fusion	81	0.019%			
conservative_inframe_deletion	783	0.185%			
conservative_inframe_insertion	591	0.139%			
disruptive_inframe_deletion	1,432	0.338%			
disruptive_inframe_insertion	976	0.23%			
downstream_gene_variant	90,687	21.401%			
exon_loss_variant	1	0%			
frameshift_variant	205	0.048%			
gene_fusion	30	0.007%			
intergenic_region	29,627	6.992%			
intragenic_variant	151	0.036%			
intron_variant	186,974	44.124%			
missense_variant	378	0.089%			
non_coding_transcript_exon_variant	2,053	0.484%			
non_coding_transcript_variant	337	0.08%			
splice_acceptor_variant	101	0.024%			
splice_donor_variant	77	0.018%			
splice_region_variant	1,247	0.294%			
start_lost	18	0.004%			
start_retained_variant	6	0.001%			
stop_gained	27	0.006%			
stop_lost	38	0.009%			
stop_retained_variant	5	0.001%			
synonymous_variant	228	0.054%			
upstream_gene_variant	97,457	22.999%			

Type (alphabetical order)	Count	Percent
DOWNSTREAM	90,678	21.496%
EXON	5,948	1.41%
GENE	111	0.026%
INTERGENIC	29,627	7.023%
INTRON	186,128	44.124%
SPLICE_SITE_ACCEPTOR	90	0.021%
SPLICE_SITE_DONOR	65	0.015%
SPLICE_SITE_REGION	1,076	0.255%
TRANSCRIPT	488	0.116%
UPSTREAM	97,457	23.103%
UTR_3_PRIME	7,046	1.67%
UTR_5_PRIME	3,115	0.738%



Quality:



Insertions and deletions length:

Min	1
Max	48
Mean	6.438
Median	1
Standard deviation	8.195
Values	1,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48
Count	30145,3368,2412,2175,1634,2225,1087,1165,930,865,513,757,414,432,399,312,284,314,264,187,178,215,159,160,151,144,141,115,138,109,76,91,8



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	80261

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).

	-	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT	CAA	CAC	CAG	CAT	CCA	CCC
-		82	271	144	113	164	126	72	118	41	160	32	87	35	41	106	29	605	98	1,692	127	163	101
AAA	122		2	5	3					1	1		9			2							2
AAC	278		1	2	29	1	13				10	9			8				2			1	
AAG	166	21	2	3	2						2	4		2		6							
AAT	173	3	20	2	9	4	1		1		1			1									
ACA	229					13	20	3	19		15			9	4	1			1			4	
ACC	270		12		1	11		9	5		9		20		1	4							1
ACG	68					5	6		8					1				8		14			
ACT	157	1	1		2	14	14	6	5		6										1		
AGA	43		1									4	2	1									
AGC	298	5	40	3	2	2	14		12	1	5		12		8	2							
AGG	47	4								5	3												
AGT	111	2	5	3	3		9	12			17			3			4	2			4		
ATA	50		2				2								5		1						
ATC	104		1	2		2	1			2	1					1							
ATG	102		7	1				3		4	3	2	1	5	4				2				
ATT	58		1		1	1	2		6		1			1	2		8						
CAA	869																		53	293	13	2	
CAC	155																	10		38	16		
CAG	2,563																	309	29	50	52	10	8
CAT	220										1							20	3	31			
CCA	273								1									3		30	3	11	7
CCC	154													2				4		6		7	4
CCG	201							2										10	2	10		5	9
CCT	145					2			1											2		9	7
CGA	47									4									1	2			
CGC	61																		1				
CGG	93			1																			
CGT	50	2																	5	2	2		
CTA	31																	1		1			
CTC	70																	2	4		1	3	2
CTG	176								26										1	14	2		
CTT	42														3					3	5	1	

	-	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT	CAA	CAC	CAG	CAT	CCA	CCC
GAA	204																	1					
GAC	146	1																	2				
GAG	289			1				1				1											
GAT	162								1											5			
GCA	434					2																2	
GCC	218																			4			
GCG	169			4	2																		
GCT	243					1			2												4		
GGA	327																						
GGC	370				2																		
GGG	69																						
GGT	232												2										
GTA	51													1				1					
GTC	94						2																
GTG	149	1			2						1												
GTT	135	1	1																				
TAA	15	1																					
TAC	64		3																	1	3		
TAG	8																						
TAT	67																				2		
TCA	137						2			2								4				1	
TCC	252		6		2													2					
TCG	136																3				4		4
TCT	124	2					1					1											
TGA	11							1															
TGC	33														1					1	1		
TGG	32		2		1																		
TGT	38																	1					
TTA	35					2																	
TTC	61												1		3	2							2
TTG	125															2			3	4			
TTT	39							8															

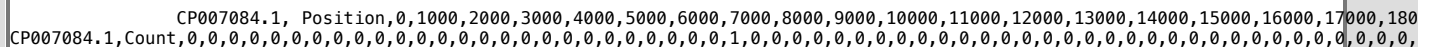
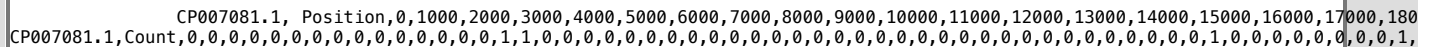
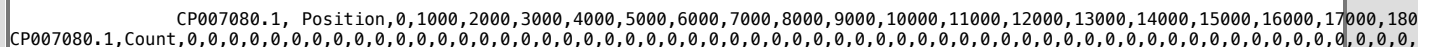
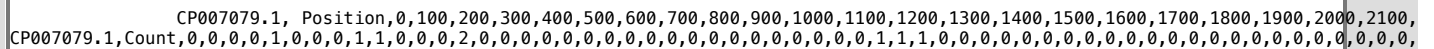
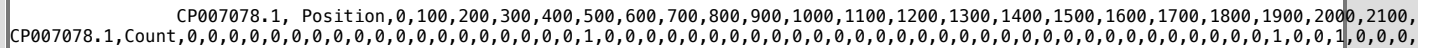
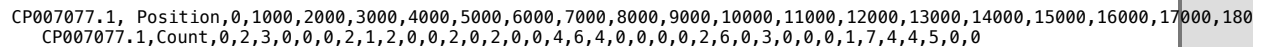
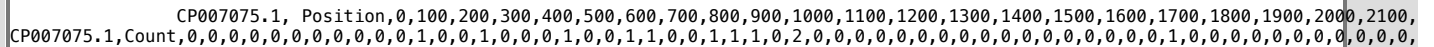
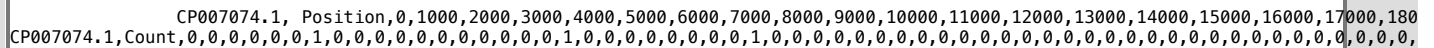
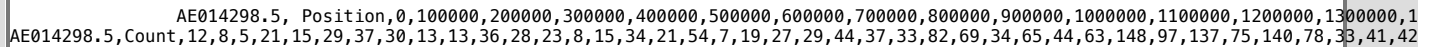
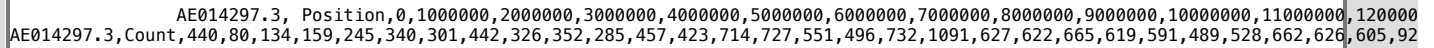
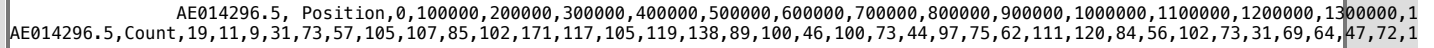
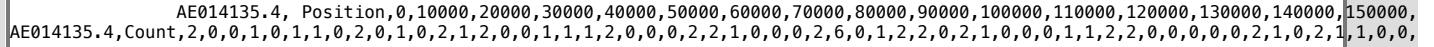
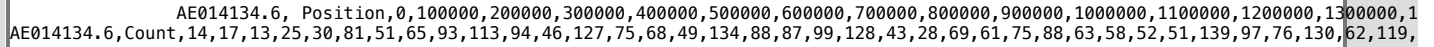
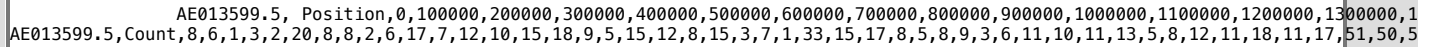
Amino acid changes

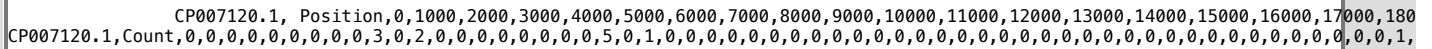
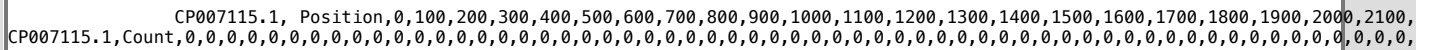
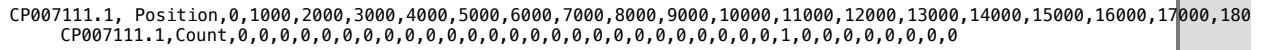
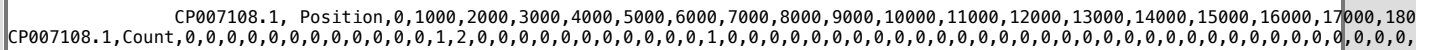
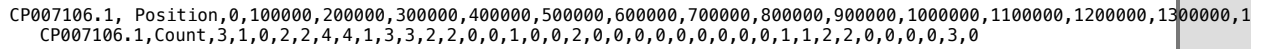
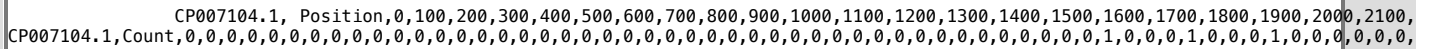
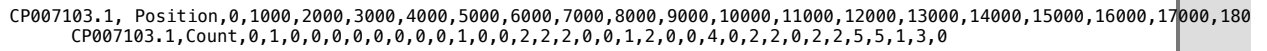
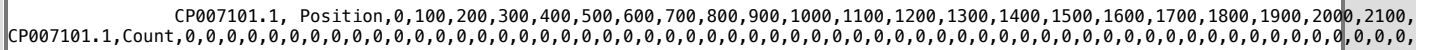
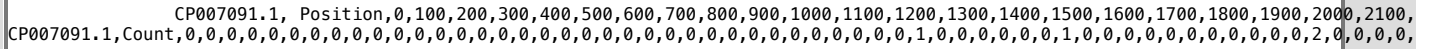
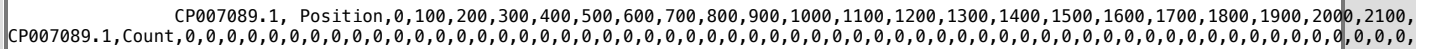
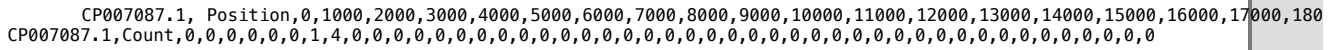
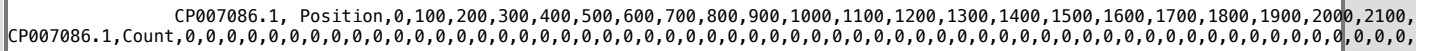
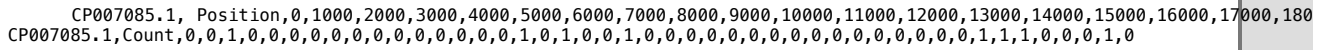
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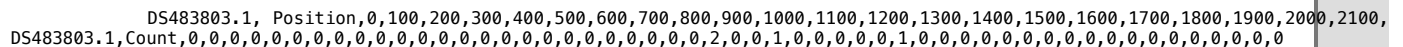
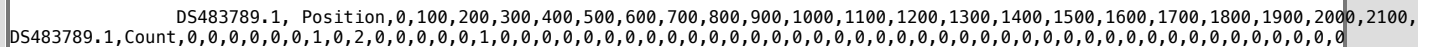
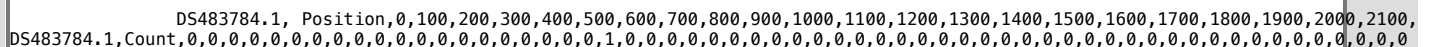
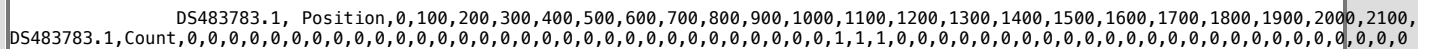
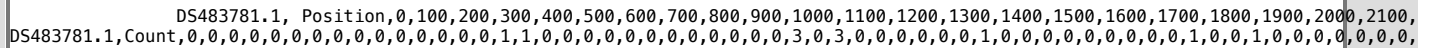
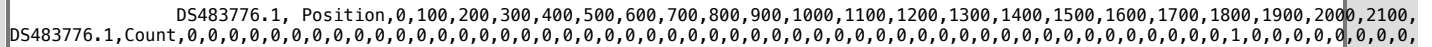
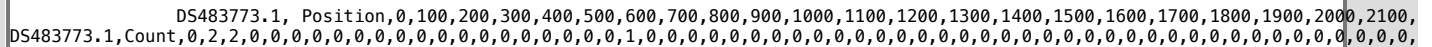
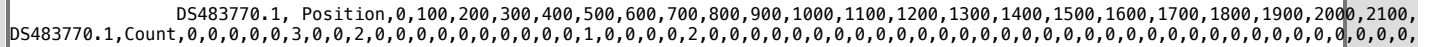
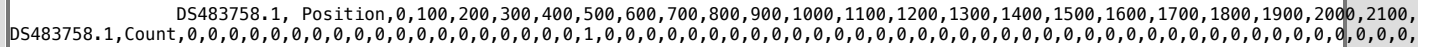
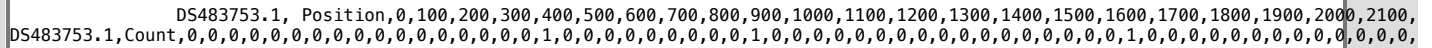
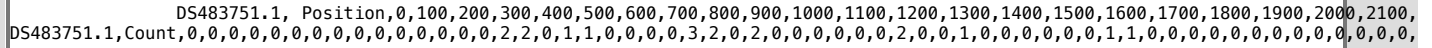
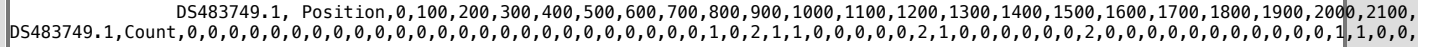
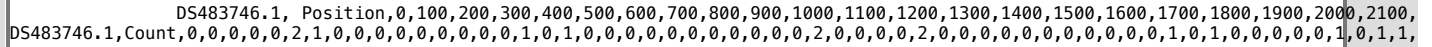
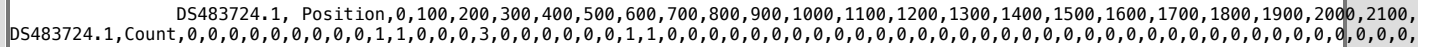
- Rows are reference amino acids and columns are changed amino acids. E.g. Row 'A' column 'E' indicates how many 'A' amino acids have been replaced by 'E' amino acids.
- Red background colors indicate that more changes happened (heat-map).
- Diagonals are indicated using grey background color
- WARNING: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

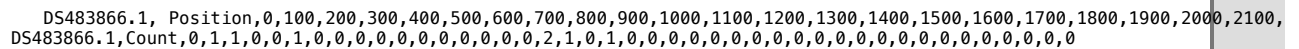
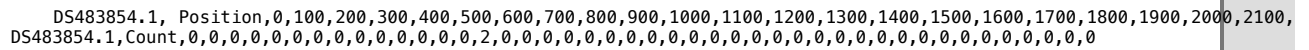
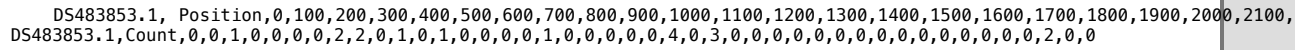
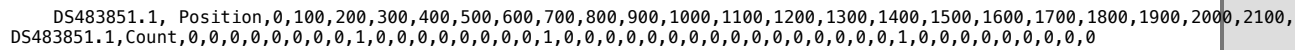
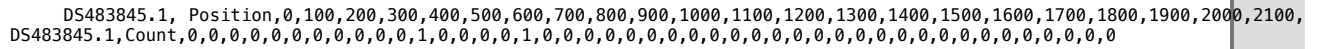
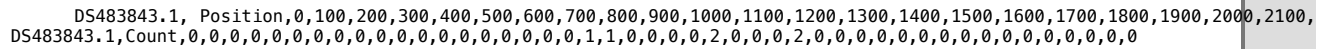
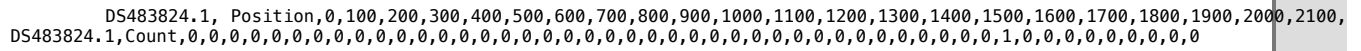
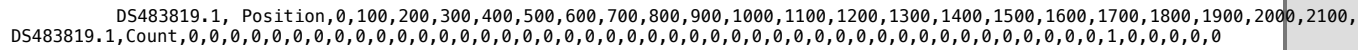
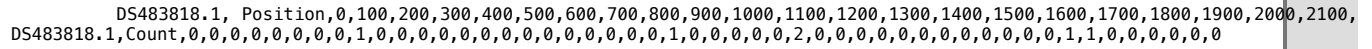
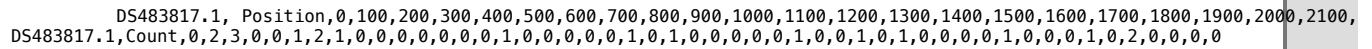
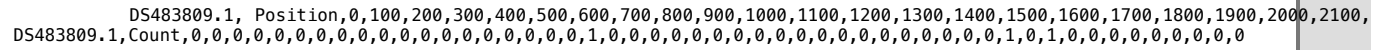
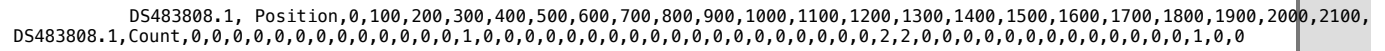
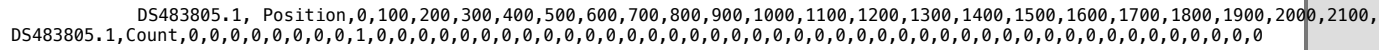
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*		30	4									1						1	1	1			1
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?																							
A		1,059	5	159		5	7		9	4		4	6		2	2	4		3	5	32		
C	1	71			7					1	1		1				2	2	2				
D		306	2	1		24	36		12	2		1	3				5			1	10		
E		493		10		50	66		9			1	5				1	1		1	15		2
F		98	2		3			6	1		3		21	2		2			10	8			
G		992	6	39	2	17	5		224				3		2	9			3		19		
H		375								19			5			6	99	6	1		1		
I		210	2								17	2	3	1	5			4	8	14	1		
K		288		8	2		2		1		2	29	1	8	9	2		5	12				
L		479		2	2	4		1	1	16	3		31	2		8	25	5	12	28	9		1
M		102								2	9	1				7		6	4	3			
N		449	2	2					2	2	9	7			59	1		9	11	20	1		8
P		773		13		4	10		6	5	2		35			135	65	4	5	6	9		
Q		3,428	4				6			147			72			32	652	10	10				
R	1	339	2	2					1	9	1	7	2		1		4	42	5		3		
S		1,056	2	19	1		1	12	5	8	18	15	7	2	58	6	8	4	109	52	8		1
T		718	6	26			3		4	2	15	1	11	5	16	7	22		50	138	2	4	1
V		426	3	35		15	6		10		1	2					1		1	2	34		
W		32														3						2	
Y	4	130	1		1		3	2	1	5			3		3		1		5		2		20

Variants by chromosome











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DS483918.1.Count,0



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DS483920.1, Count, 0, 0, 2, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 0, 0, 3, 0, 1, 0, 1, 0, 0, 0, 1, 2, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0



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DS483944.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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DS483946.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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DS483951.1	Position	0	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	2100	
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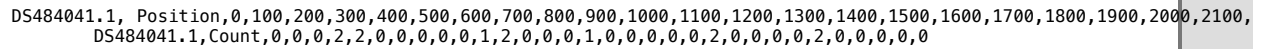
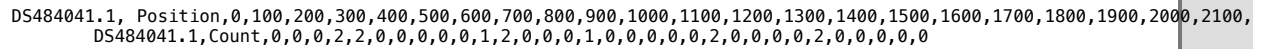
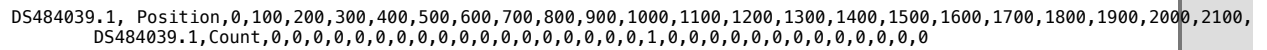
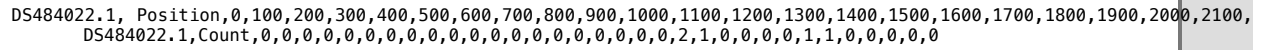
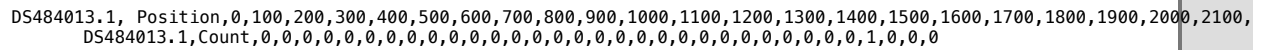
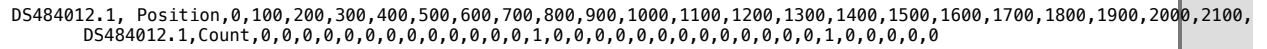
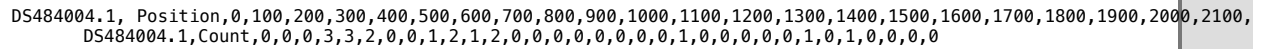
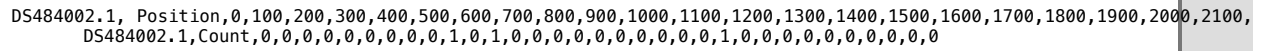
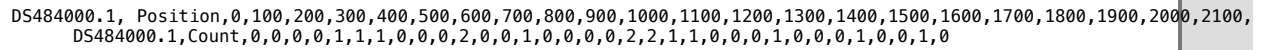
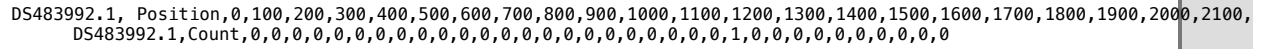
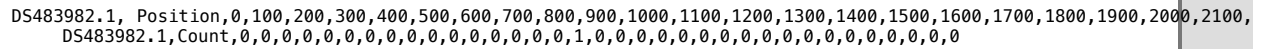
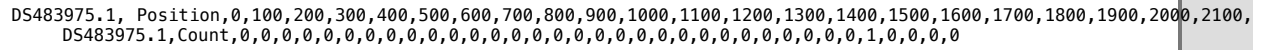
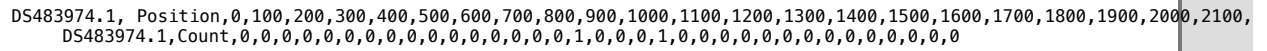
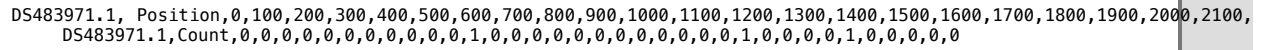
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DS483963.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,  
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DS483970.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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DS484045.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
DS484045.1,Count,0,1,0,0,0,0,0,0,0,0,0,0

DS48046.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
DS48046.1,Count,0

DS484050.1, Position,0,100,200,300,400,500,600,700,800,900,1000,1100,1200,1300,1400,1500,1600,1700,1800,1900,2000,2100,
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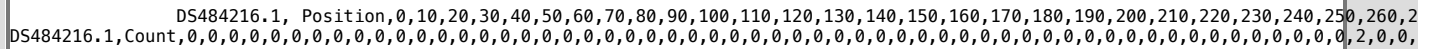
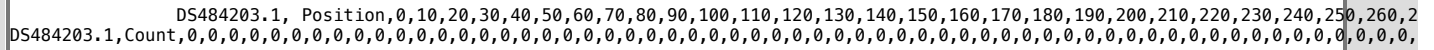
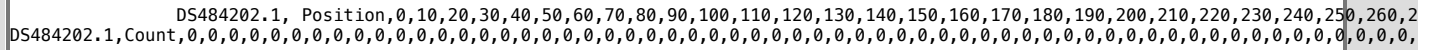
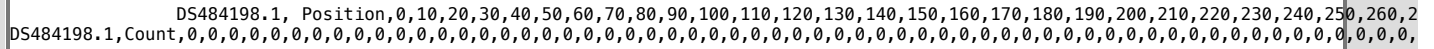
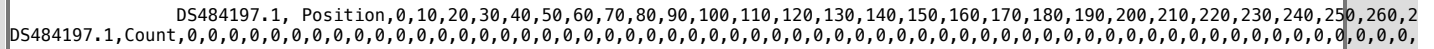
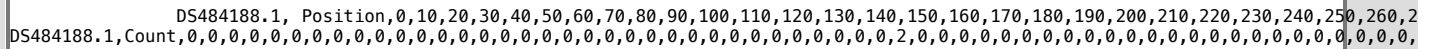
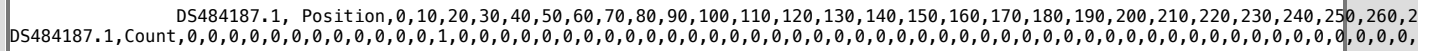
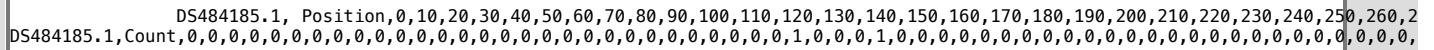
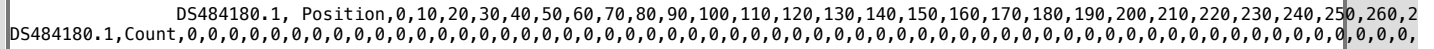
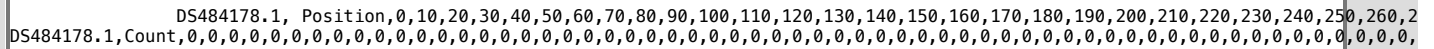
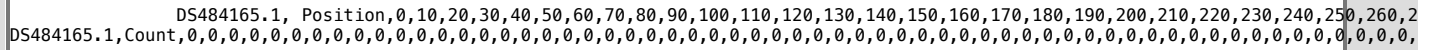
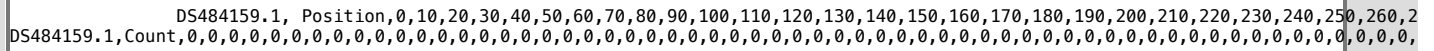
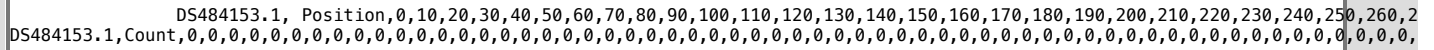
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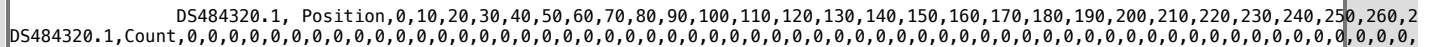
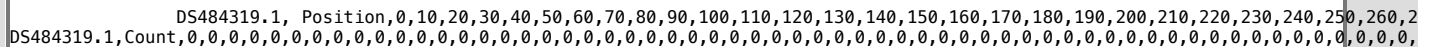
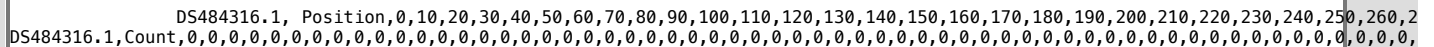
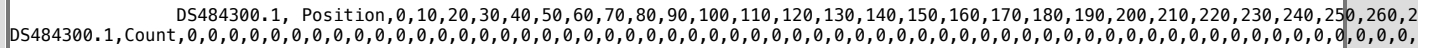
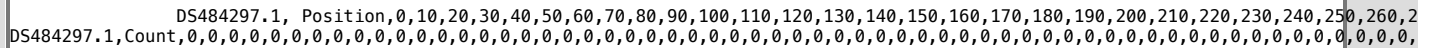
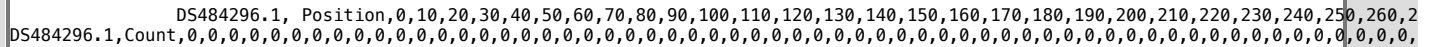
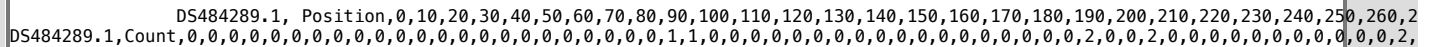
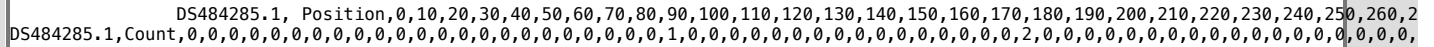
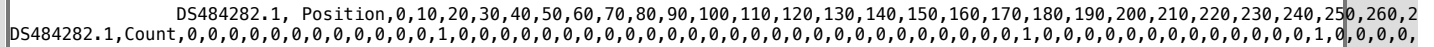
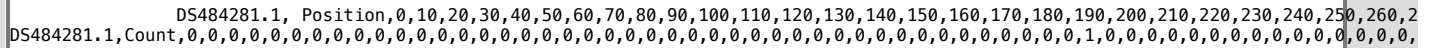
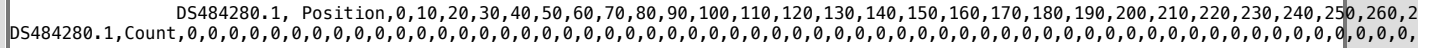
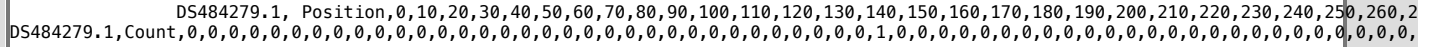
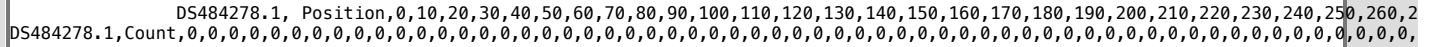
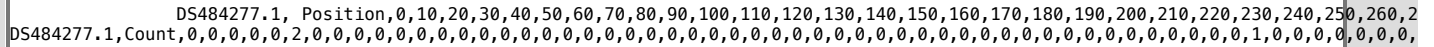
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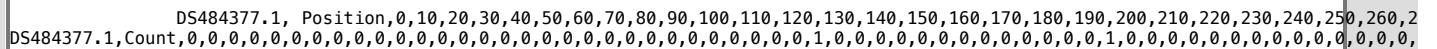
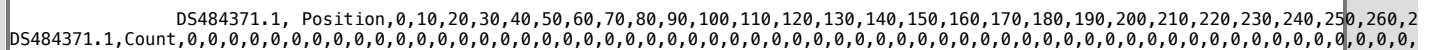
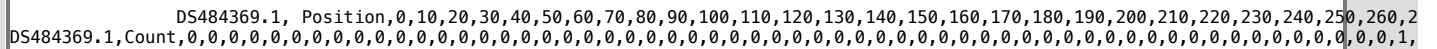
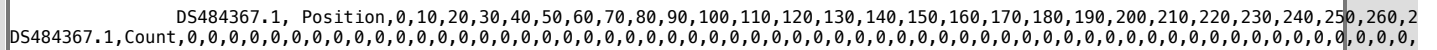
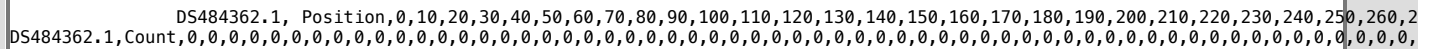
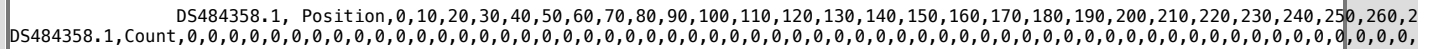
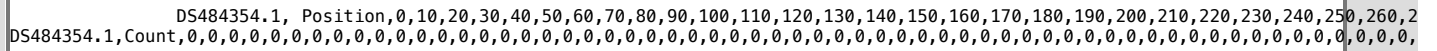
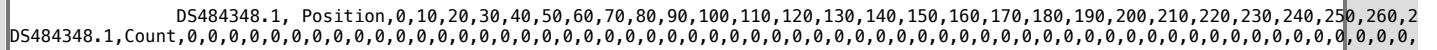
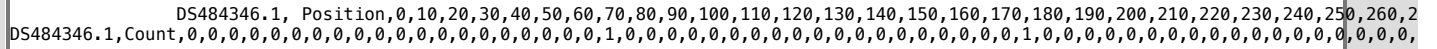
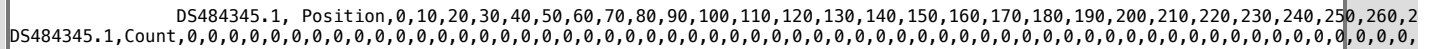
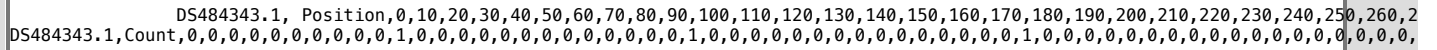
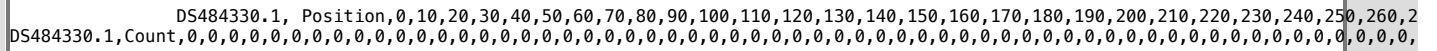
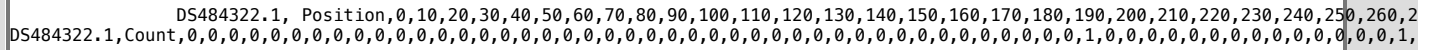
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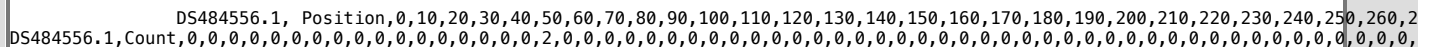
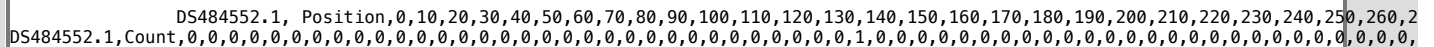
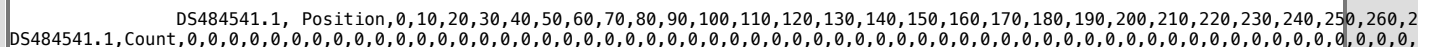
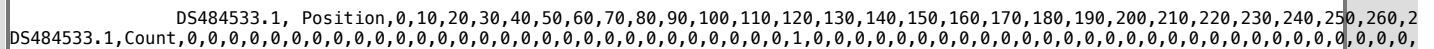
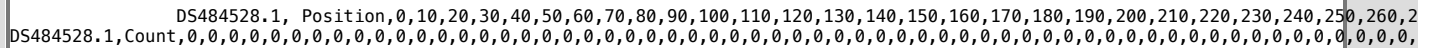
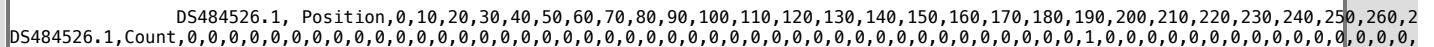
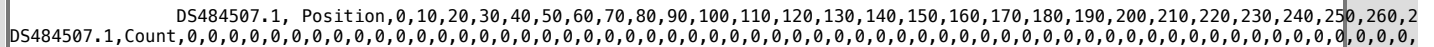
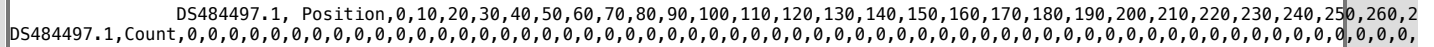
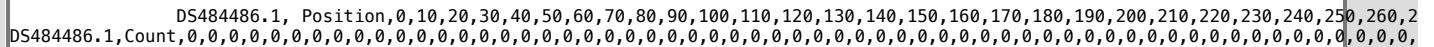
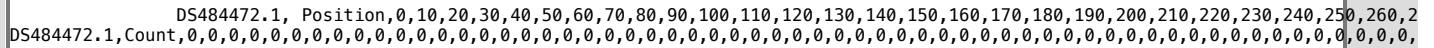
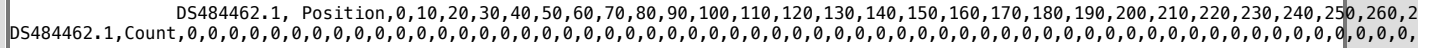
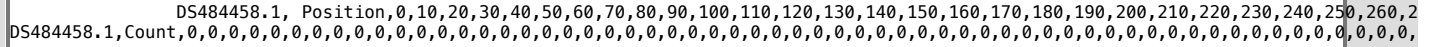
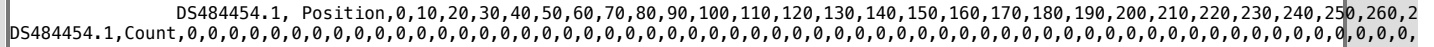
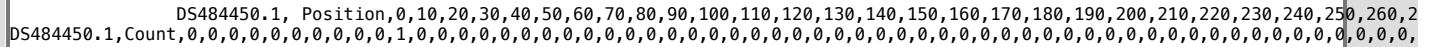
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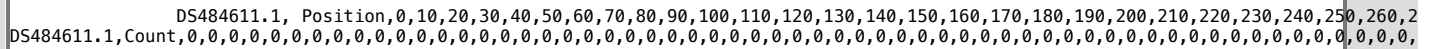
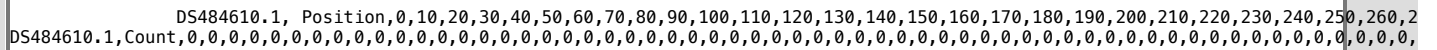
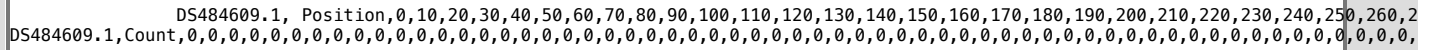
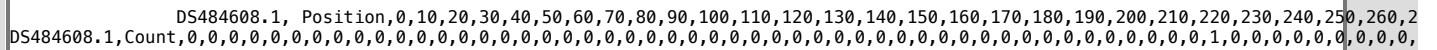
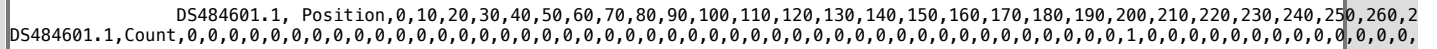
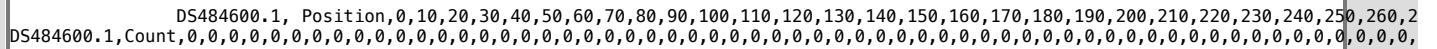
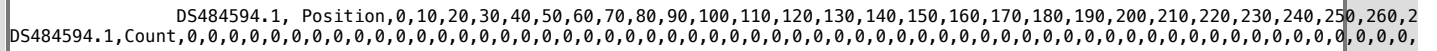
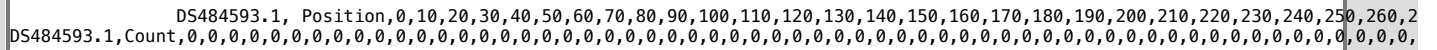
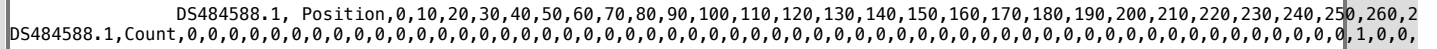
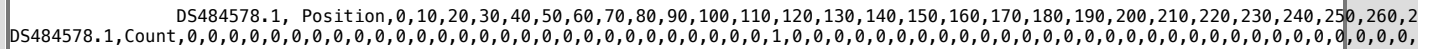
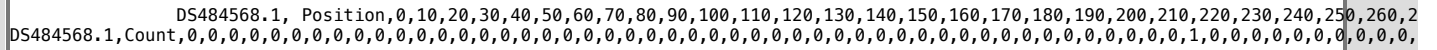
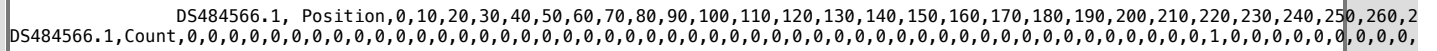
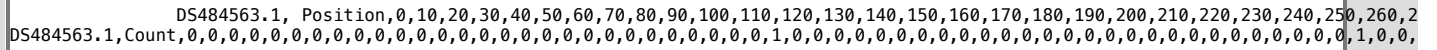
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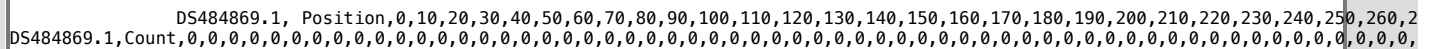
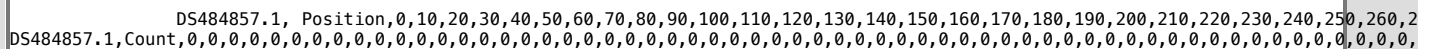
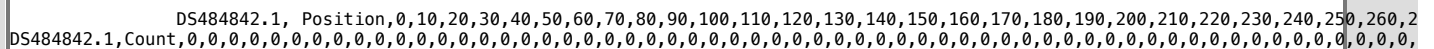
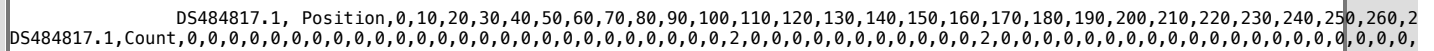
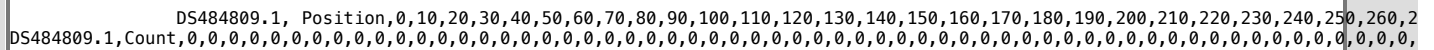
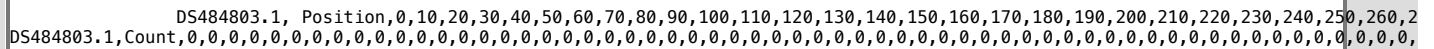
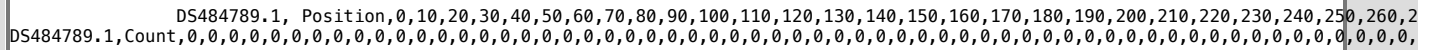
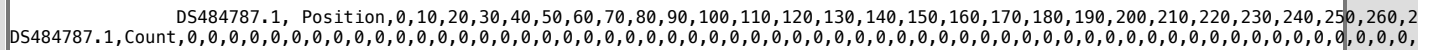
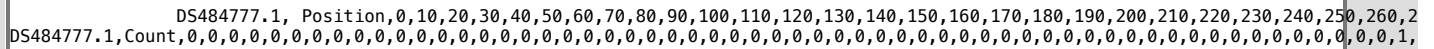
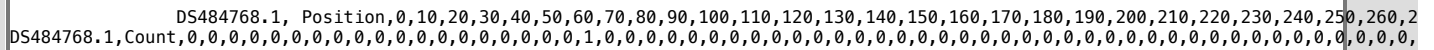
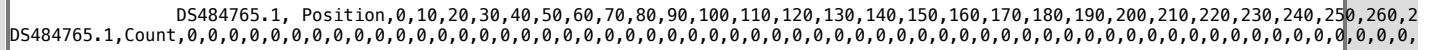
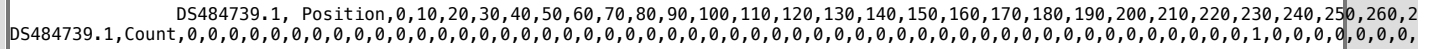
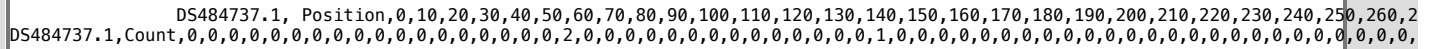
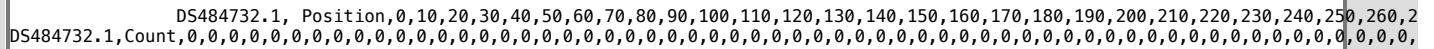


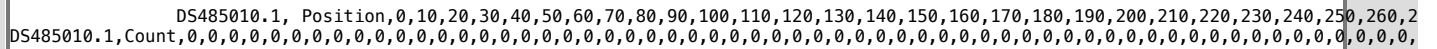
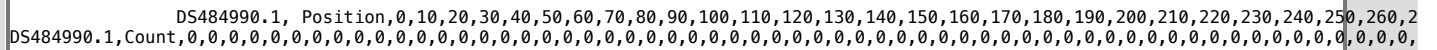
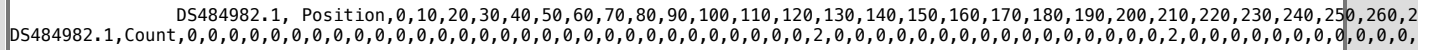
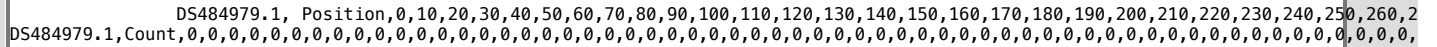
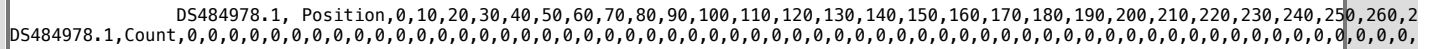
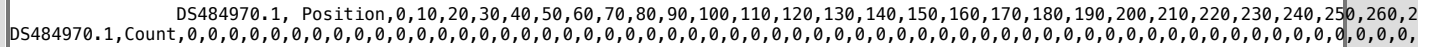
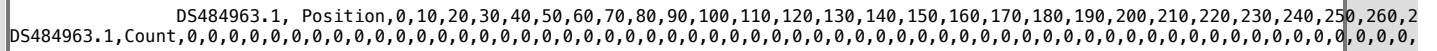
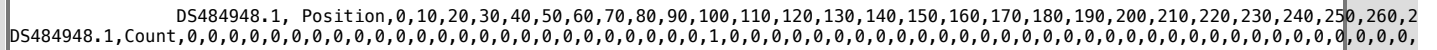
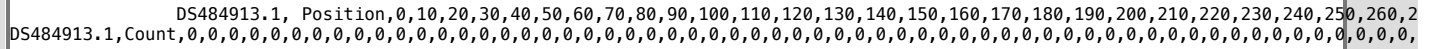
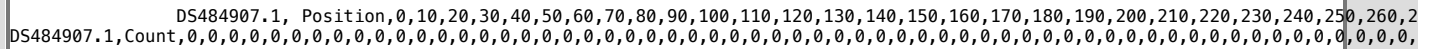
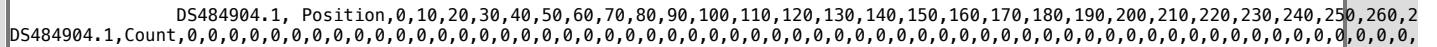
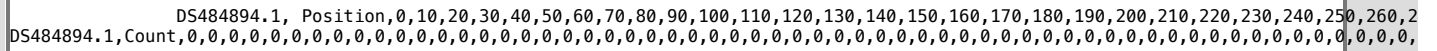
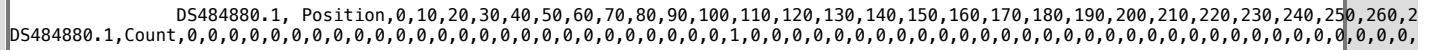


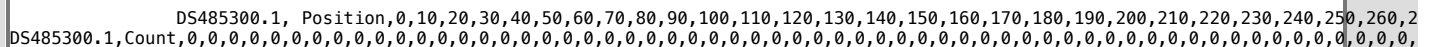
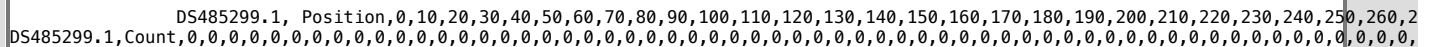
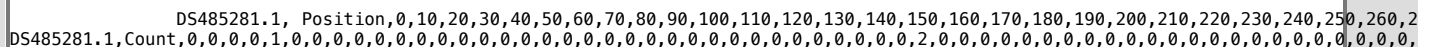
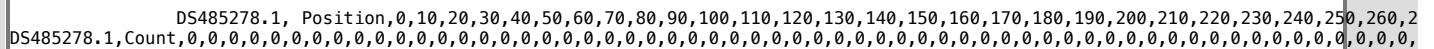
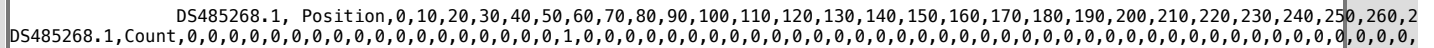
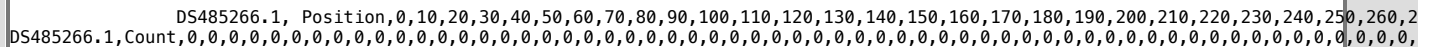
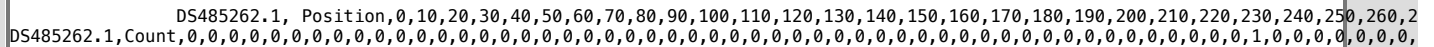
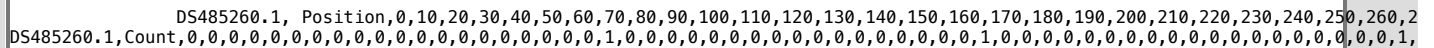
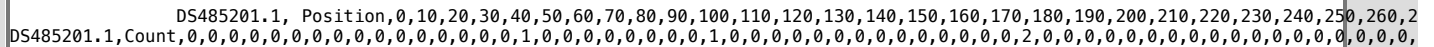
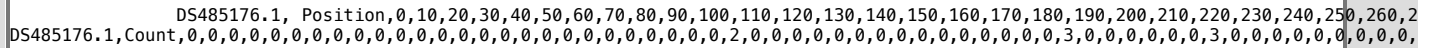
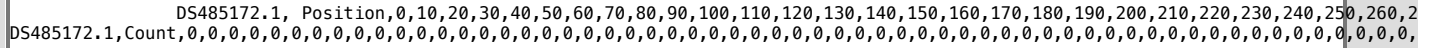
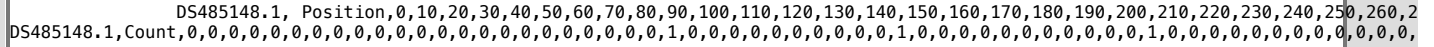
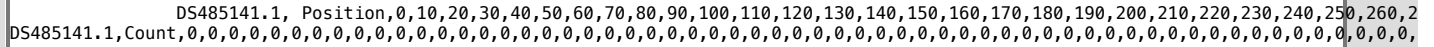
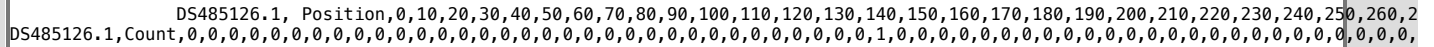


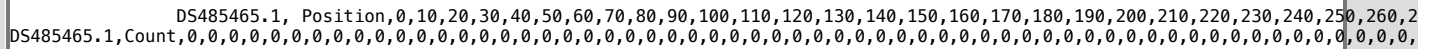
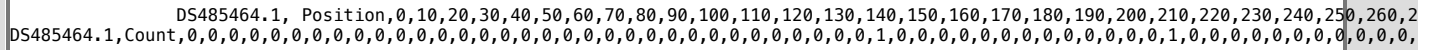
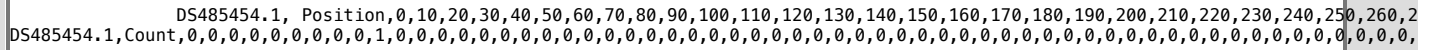
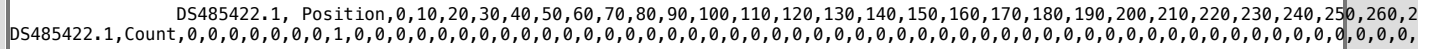
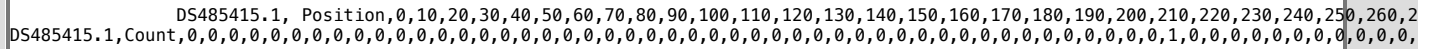
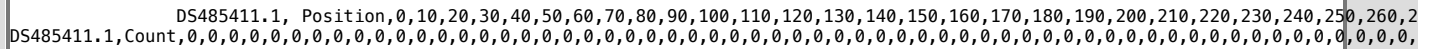
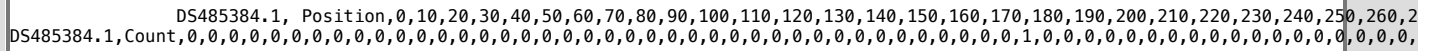
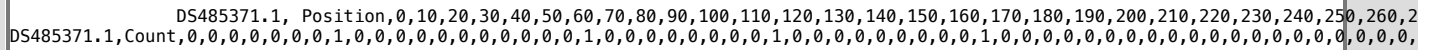
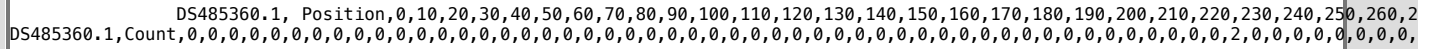
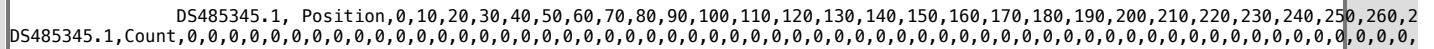
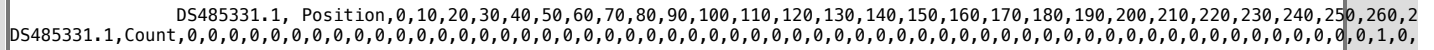
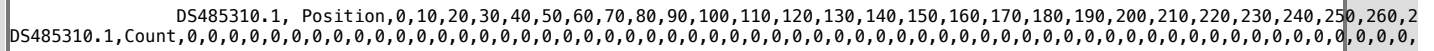
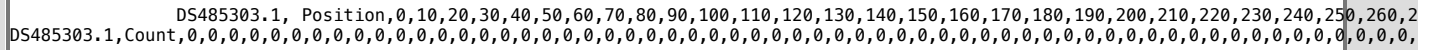


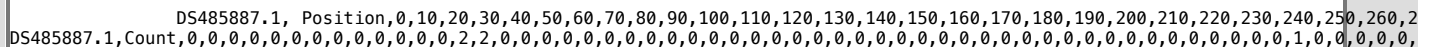
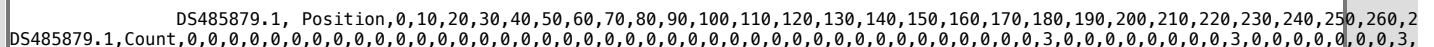
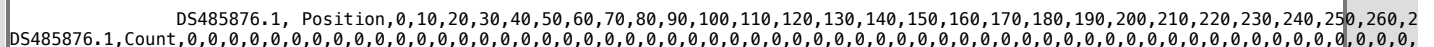
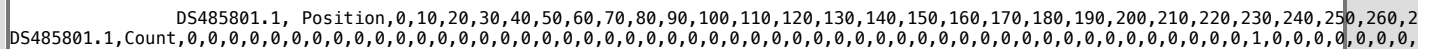
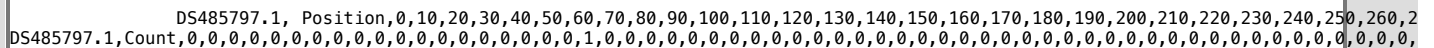
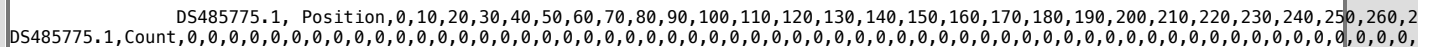
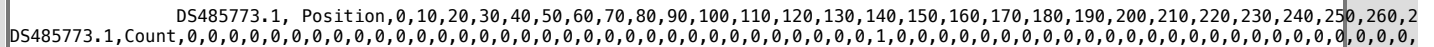
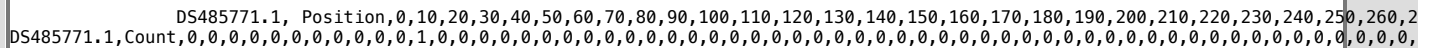
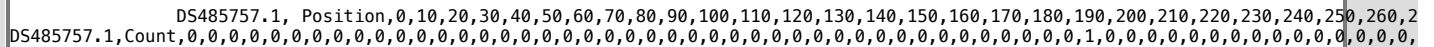
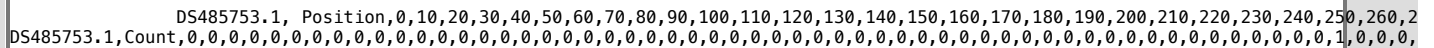
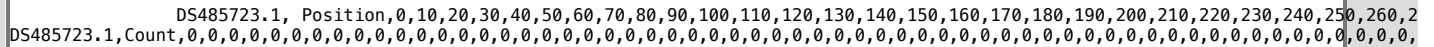
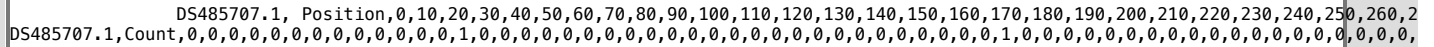
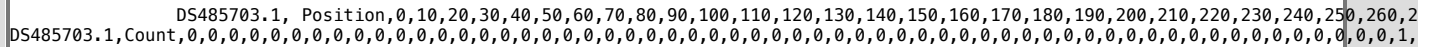
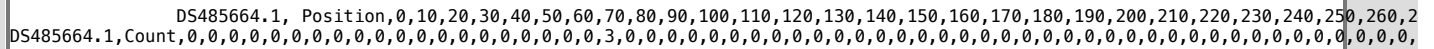


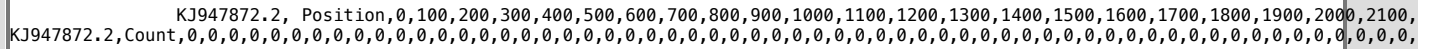
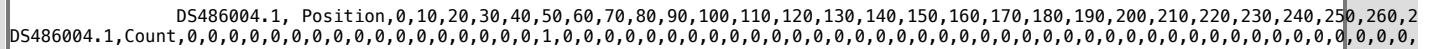
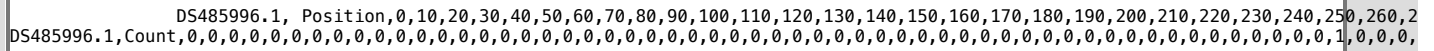
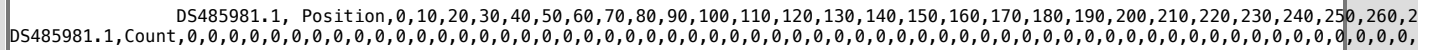
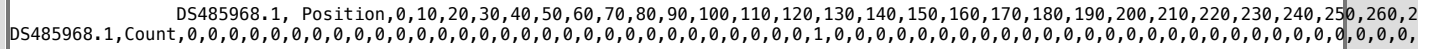
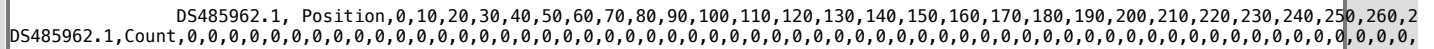
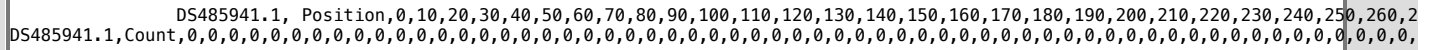
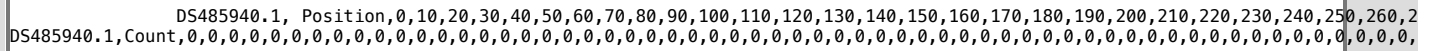
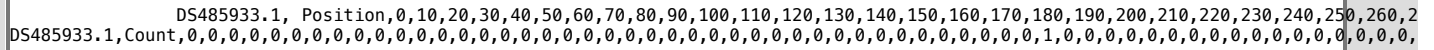












Details by gene
[Here](#) you can find a tab-separated table.