

SnEff: Variant analysis

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Summary

Genome	aloSap
Date	2025-06-13 15:21
SnEff version	SnEff 5.2e (build 2024-10-04 18:09), by Pablo Cingolani
Command line arguments	SnEff aloSap Asap001.filtered.noMito.vcf.gz
Warnings	53,435
Errors	0
Number of lines (input file)	3,681,253
Number of variants (before filter)	3,810,930
Number of non-variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	3,810,930
Number of known variants (i.e. non-empty ID)	0 (0%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	129,677
Number of annotations	11,247,571
Genome total length	903,581,644
Genome effective length	903,538,095
Variant rate	1 variant every 237 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
NC_055957.1	56,504,578	221,283	255
NC_055958.1	44,392,265	166,064	267
NC_055959.1	41,744,500	173,625	240
NC_055960.1	40,364,483	164,111	245
NC_055961.1	40,211,269	163,261	246
NC_055962.1	39,814,911	166,396	239
NC_055963.1	39,350,476	168,091	234
NC_055964.1	38,912,301	156,852	248
NC_055965.1	38,593,806	162,092	238
NC_055966.1	38,583,819	152,654	252
NC_055967.1	38,440,066	167,136	229
NC_055968.1	38,278,902	156,598	244
NC_055969.1	37,159,020	165,564	224
NC_055970.1	36,832,652	155,469	236
NC_055971.1	35,536,770	152,056	233
NC_055972.1	35,201,806	159,125	221
NC_055973.1	34,941,941	150,200	232
NC_055974.1	32,793,614	144,636	226
NC_055975.1	32,206,363	139,492	230
NC_055976.1	32,252,668	142,850	225
NC_055977.1	32,081,259	142,943	224
NC_055978.1	31,742,902	149,466	212
NC_055979.1	31,227,213	149,228	209
NC_055980.1	30,811,943	137,516	224
NW_024582116.1	22,192	7	3,170
NW_024582117.1	295,807	268	1,103
NW_024582118.1	49,702	382	130
NW_024582119.1	32,330	268	120
NW_024582120.1	165,757	2	82,878

NW_024582121.1	165,182	3	55,060
NW_024582122.1	160,283	15	10,685
NW_024582123.1	153,101	97	1,578
NW_024582124.1	136,442	12	11,370
NW_024582125.1	101,966	16	6,372
NW_024582126.1	90,783	5	18,156
NW_024582127.1	61,195	10	6,119
NW_024582128.1	49,942	4	12,485
NW_024582129.1	48,894	409	119
NW_024582130.1	34,726	3	11,575
NW_024582131.1	32,711	199	164
NW_024582132.1	31,232	218	143
NW_024582133.1	30,872	181	170
NW_024582134.1	28,555	2	14,277
NW_024582135.1	26,883	179	150
NW_024582136.1	26,475	128	206
NW_024582137.1	25,366	99	256
NW_024582138.1	23,797	144	165
NW_024582139.1	23,679	130	182
NW_024582140.1	21,437	110	194
NW_024582141.1	21,148	150	140
NW_024582142.1	403,292	30	13,443
NW_024582143.1	20,263	83	244
NW_024582144.1	19,870	174	114
NW_024582146.1	16,842	80	210
NW_024582147.1	16,283	85	191
NW_024582148.1	375,854	42	8,948
NW_024582149.1	14,855	132	112
NW_024582150.1	12,808	13	985
NW_024582151.1	11,095	58	191
NW_024582153.1	2,376	13	182
NW_024582154.1	375,752	49	7,668
NW_024582155.1	311,703	50	6,234
NW_024582156.1	269,695	31	8,699
NW_024582157.1	269,301	47	5,729
NW_024582158.1	266,092	30	8,869
NW_024582159.1	251,813	28	8,993
NW_024582160.1	233,926	116	2,016
NW_024582161.1	225,682	20	11,284
NW_024582162.1	218,598	3	72,866
NW_024582163.1	197,639	59	3,349
NW_024582164.1	184,372	38	4,851
Total	903,538,095	3,810,930	237

Number variants by type

Type	Total
SNP	2,459,115
MNP	0
INS	631,239
DEL	720,576
MIXED	0
INV	0
DUP	0
CNV	0
BND	0
INTERVAL	0
Total	3,810,930

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	9,611	0.085%
LOW	203,004	1.805%
MODERATE	92,666	0.824%
MODIFIER	10,942,290	97.286%

Number of effects by functional class

Type (alphabetical order)	Count	Percent
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MISSENSE	82,458	35.229%
NONSENSE	479	0.205%
SILENT	151,127	64.567%

Missense / Silent ratio: 0.5456

Number of annotaitons and region counts

Annotation			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent
3_prime_UTR_truncation	4	0%	DOWNSTREAM	1,308,231	11.631%
3_prime_UTR_variant	198,486	1.756%	EXON	279,012	2.481%
5_prime_UTR_premature_start_codon_gain_variant	5,374	0.048%	GENE	183	0.002%
5_prime_UTR_truncation	2	0%	INTERGENIC	1,333,729	11.858%
5_prime_UTR_variant	48,467	0.429%	INTRON	6,735,815	59.887%
bidirectional_gene_fusion	114	0.001%	SPLICE_SITE_ACCEPTOR	2,411	0.021%
conservative_inframe_deletion	3,133	0.028%	SPLICE_SITE_DONOR	2,067	0.018%
conservative_inframe_insertion	3,633	0.032%	SPLICE_SITE_REGION	49,769	0.442%
disruptive_inframe_deletion	2,025	0.018%	TRANSCRIPT	17,788	0.158%
disruptive_inframe_insertion	1,777	0.016%	UPSTREAM	1,266,334	11.259%
downstream_gene_variant	1,308,237	11.571%	UTR_3_PRIME	198,432	1.764%
exon_loss_variant	6	0%	UTR_5_PRIME	53,800	0.478%
frameshift_variant	4,161	0.037%			
gene_fusion	69	0.001%			
initiator_codon_variant	12	0%			
intergenic_region	1,333,729	11.797%			
intragenic_variant	17,312	0.153%			
intron_variant	6,784,697	60.009%			
missense_variant	82,217	0.727%			
non_coding_transcript_exon_variant	34,310	0.303%			
non_coding_transcript_variant	476	0.004%			
splice_acceptor_variant	2,492	0.022%			
splice_donor_variant	2,320	0.021%			
splice_region_variant	54,412	0.481%			
start_lost	132	0.001%			
start_retained_variant	13	0%			
stop_gained	638	0.006%			
stop_lost	248	0.002%			
stop_retained_variant	151	0.001%			
synonymous_variant	151,071	1.336%			
upstream_gene_variant	1,266,334	11.2%			



Quality:

Min	30
Max	228
Mean	197.831
Median	222
Standard deviation	50.335
Values	30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79
Count	5076,5226,5707,4762,4943,4968,5230,7939,4750,4677,4619,4675,4728,4712,5671,4687,4747,4719,4684,4545,4623,4736,4761,4653,4968,4621,4590,461



Insertions and deletions length:

Min	0
Max	46
Mean	2.816
Median	1
Standard deviation	4.511
Values	0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Count	111981,866314,33756,73304,27245,51873,11970,38385,10052,26251,6633,20830,4383,13307,3946,10792,2406,7929,1971,6359,1808,4299,1230,3576,10



Base changes (SNPs)

	A	C	G	T

A	0	142,615	341,781	127,599
C	150,655	0	83,995	384,016
G	382,597	83,366	0	150,341
T	127,537	341,369	143,244	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	1,943,011
Transversions	1,348,358
Ts/Tv ratio	1.441

All variants:

Sample ,Asap-001,Total
Transitions ,1943011,1943011
Transversions ,1348358,1348358
Ts/Tv ,1.441,1.441

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

No results available (empty input?)

Allele frequency



Min	50
Max	100
Mean	67.454
Median	50
Standard deviation	23.834
Values	50,100
Count	2396190,1285063

Allele Count



Min	1
Max	2
Mean	1.349
Median	1
Standard deviation	0.477
Values	1,2
Count	2396190,1285063

Hom/Het per sample



Sample_names , Asap-001
Reference , 0
Het , 2396190
Hom , 1285063
Missing , 0

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	CC
-		228	171	293	106	374	315	88	105	128	267	177	104	35	70	125	50	413	411	1,331	170	2
AAA	321	76	181	1,625	126	220	10		1	267	2	3		88	5	1		193		4		
AAC	293	254	74	148	2,423	6	172			1	605	1	1	4	69		6	2	139	12		
AAG	441	1,996	105	209	196			136		1		406	1	1		139		3		190		
AAT	81	136	1,875	135	49	2		1	120		3		451				40				179	
ACA	473	271	12	13	1	75	960	2,976	314	99		12		337	1	9		1	1			1
ACC	371		154		3	867	93	282	2,069		243				338		2		1			
ACG	208		1	138		3,284	287	71	658		6	40				809			1			
ACT	147				128	470	1,656	576	48				110		1	2	280			1		

AGA	206	331		12	2	119	6	1		47	98	778	83	60	4		1			2	
AGC	396		651	2	2	5	231	1	1	127	99	83	2,680	7	126				4	9	1
AGG	239			468	2	1		40		947	83	154	144			86					
AGT	155	4			428	1	5		148	98	2,314	112	95		1		79		1	11	
ATA	77	64		2	1	290		9		77				16	413	379	199				
ATC	171	1	61				261				120	3	3	607	23	66	2,067				
ATG	186	2		162	4	1	2	852		10	1	174	1	443	118	42	219	1		9	5
ATT	99		1	1	35			3	279	3	4		58	187	1,830	266	29				
CAA	530	168	1			1					1						80	138	1,711	70	1
CAC	476	1	171			1					2						222	86	233	2,096	
CAG	1,428		1	259	2	1					2		3		1		2,062	230	460	236	
CAT	190				157												100	1,736	266	35	
CCA	466				158	1	1		2			1					143	11	20		63
CCC	575					152			2	8	2							131	31		6
CCG	221					1	57			3			1		4		19	4	229	1	3,3
CCT	536		1			1	8		89						1			3	8	106	3
CGA	97								347				1				362		1		
CGC	164									131			6					852	1	1	
CGG	119					1					423							1	679	2	
CGT	77											109								402	
CTA	71													63	1		95		8	2	2
CTC	256						1								222		2	85	12	3	
CTG	315															424		12	245		
CTT	100																88	6	1	35	
GAA	668	542				1			2								95		5		
GAC	443	1	597		4		4		1	2								101	1		
GAG	1,548			715					4		1								245		
GAT	317			1	461	8					1				1				3	78	
GCA	444			7		697															1
GCC	568					3	1,199	1			7										
GCG	322			3				604									1		2		
GCT	555					1	3		826	1	1										
GGA	559				1	2				330				1					12		
GGC	531					3		4		1	829							5	8		
GGG	359					1			1			218							2		
GGT	367										1		385		5					1	
GTA	104					1								380							
GTC	156										3				804				2		
GTG	452															877			1		
GTT	199				2			1								1	441				
NAA	2																				
NNN	8																				
TAA	32	3															3	9			
TAC	116		20					1				1		3				196			
TAG	37			4										1				4	16		
TAT	75				86												2			156	
TCA	230					145		2											1		3
TCC	420		1				189	1		1									8		
TCG	104							58													
TCT	321					1			171			1							2		
TGA	36									1											
TGC	80										77	1				2					
TGG	55							1				53							1		
TGT	183		3										79								
TTA	69													35						4	
TTC	146												1		102						
TTG	105								3							142					
TTT	93							1					1				33				

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
*	156	98	7		1		24		14	4	4	7	3				25	12	15		

-	119		1,853	1,342	766	727	1,460	100	1,533	581	155	521	527	125	277	1,335	1,744	588	1,228	882	1,439
?		10	3																		
A		1,889		16,472	2	259	332	7	713			10	5			597	3	6	848	3,334	2,772
C	61	262	1		2,625		5	118	133				2	2	3	2		492	306		2
D	5	760		293		7,712	1,538		680	179	1	2	4		1,062		4	5	2	12	135
E	125	2,216		357		1,814	6,381		733			1,257	1			3	345	8	7	1	333
F	1	239		1	127		1	3,542	1		135		758			6			317	1	144
G	12	1,816		656	126	654	816		12,364	6	5		6		1	13	22	711	1,218	11	489
H		666		2		374		2		3,953		1	160		328	312	821	915	3	1	2
I		347		1	1	2	3	107	2		5,371	68	538	711	98	3		83	187	842	1,547
K	26	762		4		5	1,171				94	3,906	1	140	608	4	390	678	7	367	8
L	21	915	1	8	3	1	2	684		141	409		16,309	566		1,143	369	238	462	1	764
M		186		4		1	3	1	5	5	780	164	358	42	4	2	10	185	4	855	702
N	11	374		7	7	975	4		8	318	119	673			4,421	2	14	4	1,065	301	
P	1	1,798		578			1	1	1	256			1,354	5	1	15,870	450	161	1,294	468	1
Q	70	1,958		4		1	450	1	11	674		427	397	1	4	440	4,313	803	15	2	1
R	40	902			714		18	2	659	1,258	65	811	233	86	4	139	1,045	10,461	656	168	2
S	52	1,626		799	336	1	9	415	1,199	8	213	6	537		1,082	1,173	29	682	18,060	959	4
T		1,199		2,785		2	11		2	3	959	422	4	820	299	471	2	153	932	14,686	4
V	1	911		2,490	1	159	374	157	385		1,625		793	878		1	3	2	6	4	8,070
W	64	55			92				155	1			46					309	30	1	
Y	59	191			288	170	1	166	1	352	3		3		106		2	2	124	1	2

Variants by chromosome



NC_055957.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055957.1,Count,4089,2949,4157,4655,5025,3598,2176,4633,4887,4075,4024,4201,4016,4322,3637,4371,3759,5366,5571,4808,4262,3923,3782,4666,



NC_055958.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055958.1,Count,2491,2699,3484,4065,3120,3441,3538,1358,557,1279,2698,3611,4823,4418,3785,5547,5212,4292,3771,3927,4440,4505,3913,4315,3



NC_055959.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055959.1,Count,1379,2035,2890,3520,3248,4058,4464,4315,4241,4251,3955,4310,4671,3033,4473,3953,4304,3381,4535,4386,3725,3636,3834,4067,



NC_055960.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055960.1,Count,703,1017,2172,3825,2499,3838,4045,2713,2111,5184,3872,4391,3328,3832,4370,4985,5640,3871,3764,4089,4193,4791,4363,4545,4



NC_055961.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055961.1,Count,1663,4122,4684,4973,4834,5230,4707,3940,4210,4082,5644,4198,4823,4896,4122,5365,4870,3573,5785,5035,4424,4257,3737,4949,



NC_055962.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055962.1,Count,394,2438,3338,3478,3988,4577,4405,1630,4294,3521,4048,5151,4820,5211,2490,3800,5502,3874,3781,4246,4483,5260,4973,4601,3



NC_055963.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055963.1,Count,2959,4053,4179,5516,3917,4869,4062,4402,5640,5242,4255,5602,4284,4772,5582,5556,3491,4726,5393,4808,4051,3238,4126,4212,



NC_055964.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055964.1,Count,1211,582,2779,3580,3619,2925,4019,3756,4507,4662,3799,4142,4608,4204,4664,3694,4543,4183,4012,3896,5166,4230,4714,4483,4



NC_055965.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000

NC_055965.1,Count,1895,2640,3216,4323,3875,4267,5470,4740,4329,5198,3583,5245,5568,5958,4338,5659,4538,4857,3429,5338,4746,4407,4809,4954,



NC_055966.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055966.1,Count,882,1343,2620,3797,3830,3120,3913,4587,3213,4134,3195,4675,3496,3442,5905,5270,2484,4759,4519,4212,3919,4133,4049,4918,4



NC_055967.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
NC_055967.1,Count,507,2854,3015,3352,3593,3965,3823,4585,4373,3318,4669,4532,4380,3466,5106,4208,4849,4375,3939,4986,5666,4587,4764,5352,5



NC_055968.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
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NC_055972.1, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000
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NC_055973.1,Count,991,1000,3153,3865,3430,4386,4510,4802,4205,5387,4937,3437,4058,4744,3928,3906,4131,3818,4660,5020,5506,5219,5008,5036,5



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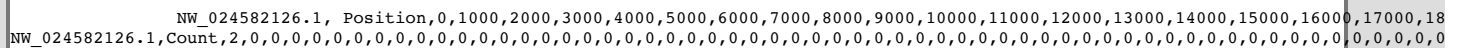
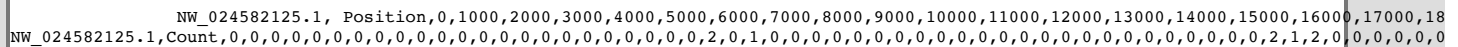
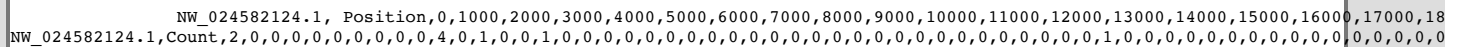
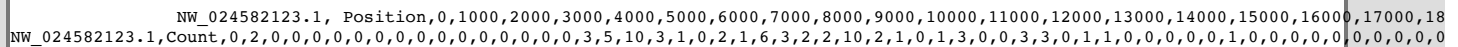
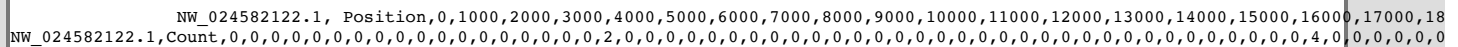
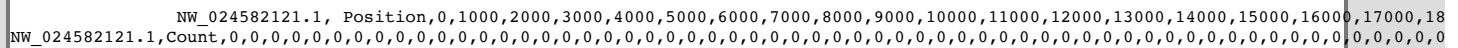
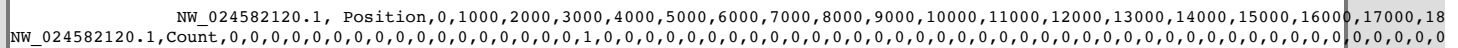
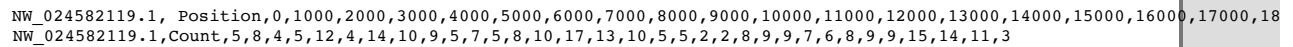
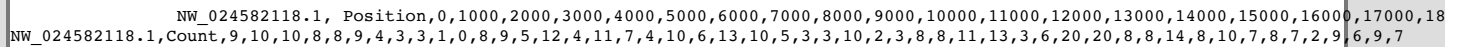
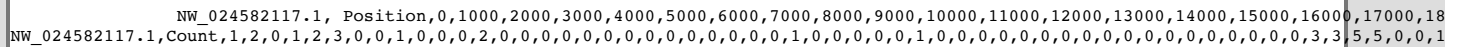
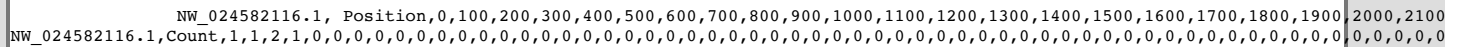
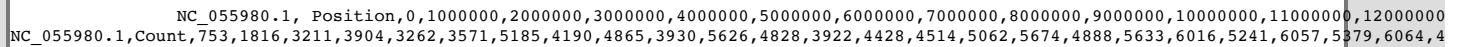
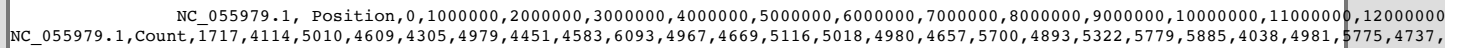
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NW_024582131.1,Count,11,7,4,2,11,7,1,1,4,3,6,5,8,2,12,1,4,13,6,5,4,5,5,15,10,2,7,7,6,4,7,8,6

NW_024582132.1, Position,0,1000,2000,3000,4000,5000,6000,7000,8000,9000,10000,11000,12000,13000,14000,15000,16000,17000,18
NW_024582132.1,Count,10,7,11,12,12,5,10,7,6,10,10,8,10,8,8,5,9,8,9,5,5,8,3,0,0,0,0,0,3,19,7,3

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NW_024582133.1, Position,0,1000,2000,3000,4000,5000,6000,7000,8000,9000,10000,11000,12000,13000,14000,15000,16000,17000,18
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NW_024582135.1	Position	0	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	2100																												
NW_024582135.1	Count	1	0	0	1	3	1	0	0	1	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	1	0	1	1	0	1	0	1	0	1	1	1	3	0	0	0	0	1

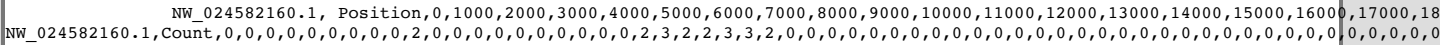
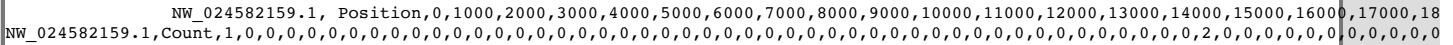
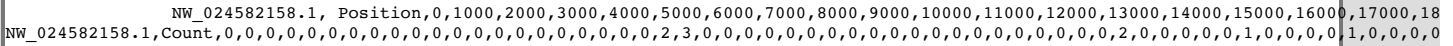
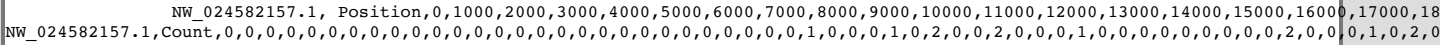
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NW_024582137.1	Count	0	0	2	0	0	0	1	0	1	0	0	2	1	1	0	1	0	0	1	0	1	0	1

	NW_024582138.1	Position,	0	,100	,	200	,	300	,	400	,	500	,	600	,	700	,	800	,	900	,	1000	,	1100	,	1200	,	1300	,	1400	,	1500	,	1600	,	1700	,	1800	,	1900		2000	,	2100									
NW_024582138.1	Count,	0	,1	,1	,2	,0	,2	,0	,0	,0	,1	,0	,0	,0	,1	,0	,0	,2	,1	,0	,0	,1	,0	,1	,0	,2	,0	,0	,2	,0	,1	,0	,0	,0	,0	,0	,1	,1	,0	,0	,0	,2	,1	,0	,0	,0	,0	,1	,1	,0	,0	,1	,1

NW_024582139.1	Position	0	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	2100																																				
NW_024582139.1	Count	2	0	1	1	0	0	3	0	0	0	3	0	1	2	1	0	0	0	1	0	0	1	2	1	1	3	0	0	4	2	1	0	0	0	3	1	2	0	2	1	1	2	0	2	0	2	0	2	0	2	1	1	2	0	2	1	0	2



[illegible]

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