

## SnpEff: Variant analysis

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### Summary

<b>Genome</b>	TA4
<b>Date</b>	2018-01-01 17:21
<b>SnpEff version</b>	SnpEff 4.3p (build 2017-06-06 09:55), by Pablo Cingolani
<b>Command line arguments</b>	SnpEff TA4 TA4_selfvariant.vcf
<b>Warnings</b>	128,022
<b>Errors</b>	0
<b>Number of lines (input file)</b>	5,120,815
<b>Number of variants (before filter)</b>	5,394,970
<b>Number of not variants (i.e. reference equals alternative)</b>	0
<b>Number of variants processed (i.e. after filter and non-variants)</b>	5,394,956
<b>Number of known variants (i.e. non-empty ID)</b>	0 ( 0% )
<b>Number of multi-allelic VCF entries (i.e. more than two alleles)</b>	4,368
<b>Number of effects</b>	10,095,863
<b>Genome total length</b>	377,290,333
<b>Genome effective length</b>	377,290,333
<b>Variant rate</b>	1 variant every 69 bases

### Variants rate details

Chromosome	Length	Variants	Variants rate
1	17,320,008	247,141	70
2	17,063,873	260,967	65
3	21,566,805	288,912	74
4	22,357,487	255,999	87
5	14,540,018	227,490	63
6	10,680,009	134,363	79
7	13,133,232	218,581	60
8	14,750,018	223,076	66
9	21,055,410	317,903	66
10	11,063,414	146,226	75
11	17,675,019	197,115	89
12	14,336,529	227,439	63
13	15,099,493	205,623	73
14	13,335,999	208,487	63
15	16,178,320	219,588	73
16	21,434,198	329,642	65
17	11,746,059	157,361	74
18	16,863,820	231,421	72
19	22,398,858	349,731	64
20	16,105,987	443,146	36
10000001	48,585,777	504,745	96
<b>Total</b>	<b>377,290,333</b>	<b>5,394,956</b>	<b>69</b>

### Number variants by type

Type	Total
<b>SNP</b>	3,946,854
<b>MNP</b>	1,051,633
<b>Total</b>	<b>5,394,956</b>

Type	Total
INS	138,977
DEL	146,654
MIXED	110,838
INV	0
DUP	0
BND	0
INTERVAL	0
<b>Total</b>	<b>5,394,956</b>

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	8,352	0.083%
LOW	136,667	1.354%
MODERATE	149,461	1.48%
MODIFIER	9,801,383	97.083%

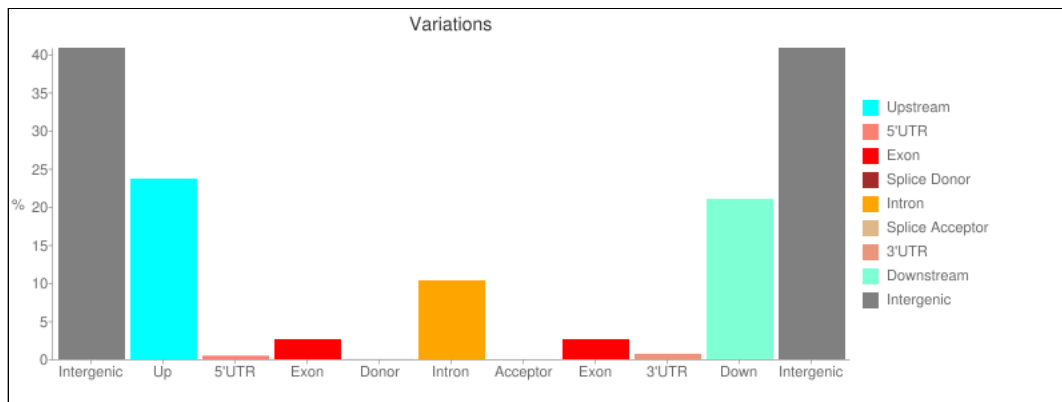
Number of effects by functional class

Type (alphabetical order)	Count	Percent
MISSENSE	129,328	53.791%
NONSENSE	1,484	0.617%
SILENT	109,615	45.592%

Missense / Silent ratio: 1.1798

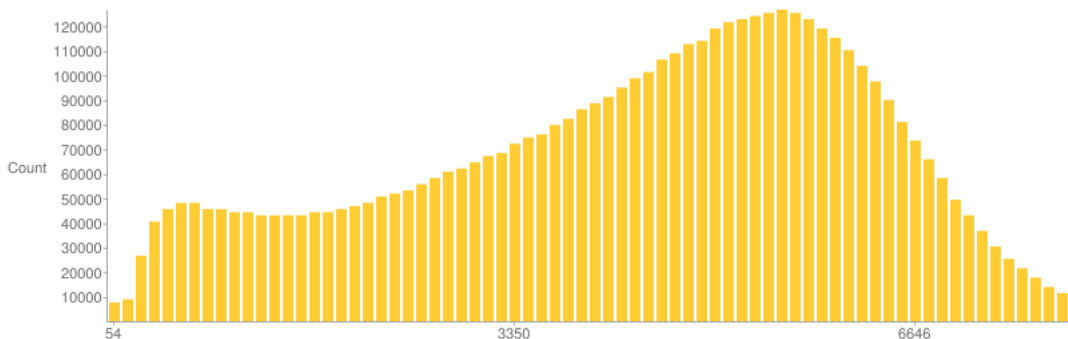
Number of effects by type and region

Type			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent
3_prime_UTR_variant	72,021	0.711%	DOWNSTREAM	2,123,353	21.032%
5_prime_UTR_premature_start_codon_gain_variant	5,080	0.05%	EXON	265,703	2.632%
5_prime_UTR_variant	42,434	0.419%	INTERGENIC	4,125,552	40.864%
conservative_inframe_deletion	815	0.008%	INTRON	1,045,061	10.351%
conservative_inframe_insertion	750	0.007%	SPLICE_SITE_ACCEPTOR	1,271	0.013%
disruptive_inframe_deletion	514	0.005%	SPLICE_SITE_DONOR	1,251	0.012%
disruptive_inframe_insertion	374	0.004%	SPLICE_SITE_REGION	21,175	0.21%
downstream_gene_variant	2,123,362	20.973%	TRANSCRIPT	608	0.006%
frameshift_variant	3,189	0.031%	UPSTREAM	2,392,499	23.698%
initiator_codon_variant	30	0%	UTR_3_PRIME	71,932	0.712%
intergenic_region	4,125,552	40.749%	UTR_5_PRIME	47,458	0.47%
intragenic_variant	156	0.002%			
intron_variant	1,065,055	10.52%			
missense_variant	148,074	1.463%			
non_coding_transcript_variant	452	0.004%			
splice_acceptor_variant	1,304	0.013%			
splice_donor_variant	1,307	0.013%			
splice_region_variant	25,421	0.251%			
start_lost	336	0.003%			
stop_gained	2,021	0.02%			
stop_lost	496	0.005%			
stop_retained_variant	195	0.002%			
synonymous_variant	112,764	1.114%			
upstream_gene_variant	2,392,499	23.631%			



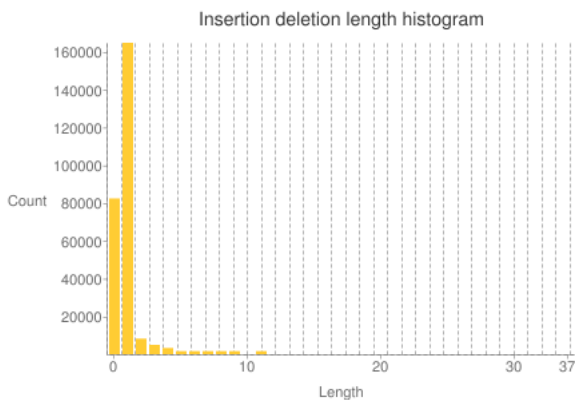
**Quality:**

<b>Min</b>	0
<b>Max</b>	2,556,390
<b>Mean</b>	5,139,301
<b>Median</b>	4,691
<b>Standard deviation</b>	25,296.375
<b>Values</b>	0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100
<b>Count</b>	1583,142,98,85,74,50,54,42,61,58,48,63,60,51,42,50,54,55,55,53,61,75,40,58,57,40,55,55,47,46,58,61,60,51,70,57,50,69,55,45,46,46,58,58,44,57,56,5



**Insertions and deletions length:**

<b>Min</b>	0
<b>Max</b>	37
<b>Mean</b>	1.435
<b>Median</b>	1
<b>Standard deviation</b>	2.626
<b>Values</b>	0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,32,33,35,37
<b>Count</b>	82444,164847,8613,5907,3582,3271,1972,2294,2011,1960,1575,1756,1079,911,744,622,463,422,299,236,190,130,100,67,44,41,23,14,3,1,3,1,1,3,2



**Base changes (SNPs)**

	A	C	G	T
A	0	142,355	691,920	196,913
C	142,764	0	99,547	697,961
G	699,883	99,884	0	143,020
T	197,267	693,330	142,010	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).

<b>Transitions</b>	2,768,385
<b>Transversions</b>	1,157,453
<b>Ts/Tv ratio</b>	2.3918

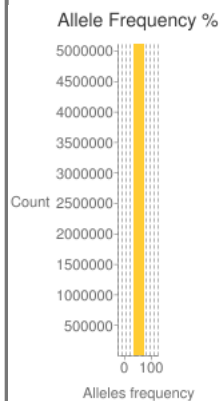
**All variants:**

Sample ,unknown>Total  
 Transitions ,2768385,2768385  
 Transversions ,1157453,1157453  
 Ts/Tv ,2.392,2.392

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

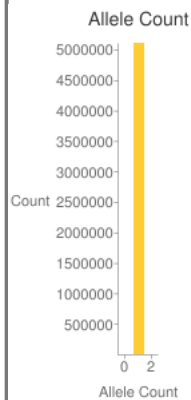
No results available (empty input?)

**Allele frequency**



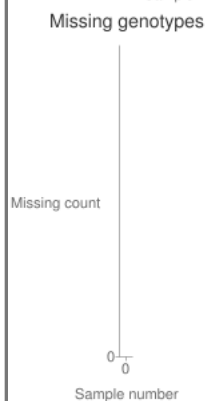
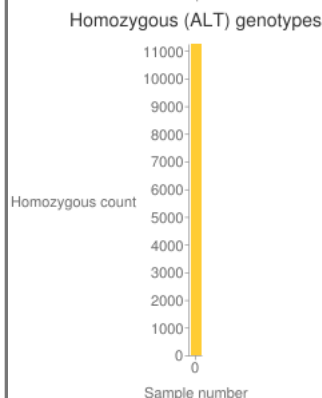
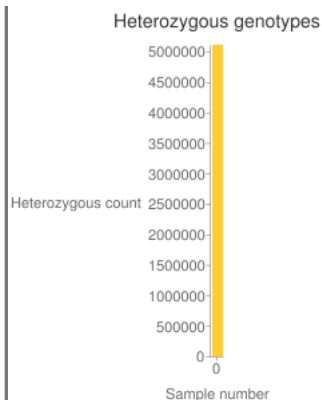
<b>Min</b>	0
<b>Max</b>	100
<b>Mean</b>	50.11
<b>Median</b>	50
<b>Standard deviation</b>	2.342
<b>Values</b>	0,50,100
<b>Count</b>	10,5109556,11249

**Allele Count**



<b>Min</b>	0
<b>Max</b>	2
<b>Mean</b>	1.002
<b>Median</b>	1
<b>Standard deviation</b>	0.047
<b>Values</b>	0,1,2
<b>Count</b>	10,5109556,11249

**Hom/Het per sample**



Sample\_names , unknown  
 Reference , 10  
 Het , 5109556  
 Hom , 11249  
 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
-		81	54	89	90	49	31	15	56	45	33	31	64	36	23	55	48	75	45	59	80
AAA	233	<b>117</b>	373	2,017	518	373	3	4	3	992	4	17	6	213	5	7	11	471	1	8	6
AAC	111	403	<b>60</b>	399	2,037	6	196	3	4	7	809	6	11	2	120	2	5	13	145	3	6
AAG	202	1,985	408	<b>95</b>	452	20	2	224	1	21	5	1,014	10	5	3	318	8	6	4	356	2
AAT	151	499	2,068	414	<b>83</b>	7	7	4	369	9	23	13	1,096	7	7	4	278	5	3	1	354
ACA	104	349	8	8	5	<b>59</b>	415	1,573	574	293	5	5	4	661	9	62	5	5			1
ACC	79	2	224	3	7	396	<b>35</b>	271	1,630		265	2	5	4	327	8	15		1		
ACG	27	4	6	231	6	1,547	295	<b>10</b>	422	1	3	141	2	24	9	825	7			3	
ACT	99	7	18	5	386	594	1,723	429	<b>47</b>	1	5	1	493	5	12	12	783		2		3
AGA	92	1,002	2	25	9	264		3	5	<b>46</b>	170	1,032	194	189	4	4	2	13		2	
AGC	62	17	760	9	15	6	241	3	11	168	<b>52</b>	148	1,236	1	122	2	9		5		
AGG	68	22	1	962	5	7		133	2	1,049	164	<b>30</b>	184	2	3	149	5			5	1

	-	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT	CAA	CAC	CAG	CAT
AGT	98	6	15	12	1,124	4	5	5	495	177	1,217	202	51	1		4	288	1			11
ATA	58	195	1	10	8	616	5	16	4	173	2	3	4	32	445	879	617	10	1		
ATC	58	6	94	1	9	7	336	5	13		93	1	2	487	29	269	1,750				1
ATG	124	8	1	341	24	58	6	848	15	3	3	201	7	1,004	288	65	421			3	1
ATT	122	5	7	2	297	4	8	14	772	4	7	3	271	568	1,762	378	90				6
CAA	119	482	3	12	1	5	1		1	8	2			5			60	231	1,586	279	
CAC	56	2	146		9	1					2					1		184	22	249	1,072
CAG	92	7	1	340	3	1	2			3	1	10	1	1	2	2		1,528	256	42	274
CAT	103	8	6	3	340	1			4				10			1	4	316	1,118	263	49
CCA	135	5	1			157	2		6	2				7				250	3	13	2
CCC	77		1			2	90	1	4		1				3			3	56	1	2
CCG	61			4		4		53	2			1				1		7	2	142	
CCT	142				3	2	4		253	1			4			1	3		4	3	200
CGA	35	10				2				356	3	4		1	1	1		1,027	5	14	14
CGC	22	1	6							1	101	1	1		4			5	465	5	14
CGG	19			5	1			3		12	1	270	1	1	1			15	3	908	9
CGT	34	1			11	2			1	7	5	2	138				4	11	13	5	974
CTA	47	1				6				1					187		3	6	193		3
CTC	70		1				2				1		2	3	166	2	7	3	83	2	3
CTG	61	1	1	4	1	1		2				3		2		282	7	3		222	1
CTT	112		2	1					13				3	6	4	2	391	5		5	226
GAA	253	1,470	5	31	13	12		1		29		1	1	7	1	2	1	517	1	3	3
GAC	104	8	621	11	23		8	1	2	1	15	3			3	2		127			4
GAG	178	18	13	1,166	14			4	1	9		21	2			8		7	1	529	3
GAT	257	7	23	13	1,370		1	1	3	4	3		13			1	12	1	5	5	365
GCA	118	13				1,160	10	15	8	10	3		1	22				11	1		
GCC	96		14	2		4	643	2	18	1	8				11		2		1	1	
GCG	32			5		15	2	225	5	2		3		1		18				3	
GCT	108		1		8	4	29	3	1,242	1	2	1	5	2	1		29	1		1	5
GGA	164	28		1	1	1			1	726	3	14	8	5		3	1	9			
GGC	88		19	1	2		3			3	580	5	15		3				5		
GGG	94	1	3	14			1	3		5	2	444	7			1		1		15	
GGT	160	2	3	1	25				8	2	11	3	996		1	2	5		1		13
GTA	54	3		1		18	3		1	8	1		1	847	6	12	10	2			1
GTC	35		2				8				2		1	5	753	5	14			1	1
GTG	75	2		7		4		17				1	2	20	7	882	3		1	2	
GTT	129	2			6	3			18	1			13	8	18	5	1,644		1		1
TAA	19	24																38		1	
TAC	53	5	129	3	6		2	1			3				2			2	334	2	9
TAG	13			13																	42
TAT	96	2	6		290	2					1		7	3			2	5	7	1	727
TCA	131	6			2	270	4	7	4	1				6	1	1	1	6			1
TCC	62				1	151		8		5	1				2		1		1		2
TCG	35				1	2	1	50	1	1						9	1				
TCT	193	2			15	3	6		325		1		9		4		11	1			13
TGA	18									14								5			
TGC	42		3		1	1	1			2	107	2	7			1			25		
TGG	50			1						2	3	135	2			6				39	1
TGT	44				2		1		1		3		234					4	4	3	36
TTA	80	6	1		2	1			2	4				226	4	6	2	3			1
TTC	88		3				1			2				2	162	3	12	1	3	1	
TTG	120			5	1	3		4	2		1			5		417	4			7	1
TTT	171				1	7		1		9	1		3	7	5	5	369		1	1	12

**Amino acid changes**

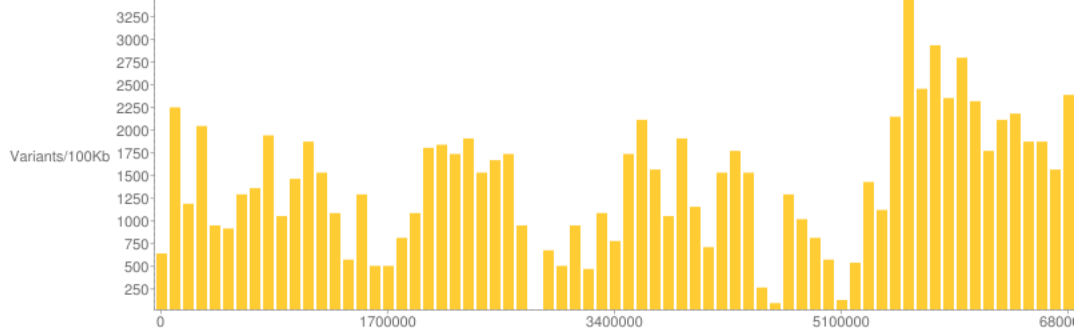
How to read this table:

- 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. mammalian DNA and mitochondrial DNA).

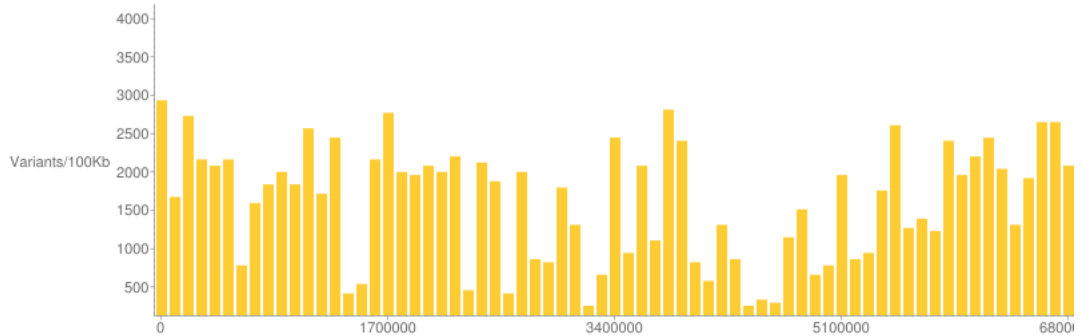
	*	-	?	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V
*	209	42	8		9	2	39	1	8			37	47				86	71	41		
-	40		1,381	154	49	148	214	126	168	125	107	170	225	55	144	210	134	122	353	151	1:
?																					
A	4	339	15	12,203	14	424	594	16	1,075	7	68	20	49	18	23	826	17	24	1,330	3,385	3,2:
C	55	76	10	5	2,001	7	1	313	252	64	4		31	1	6	8	7	917	830		4

	*	-	?	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V
D	6	343	18	355	17	<b>5,148</b>	2,174	6	1,291	501	15	39	6	3	2,037	4	6	20	48	16	21
E	185	412	19	547		2,131	<b>4,238</b>	4	1,402	8	9	2,685	17	10	45	6	1,056	72	12	18	31
F	3	243	16	19	330	15	2	<b>3,982</b>	4	16	557	1	2,420	8	10	24	3	11	1,019	11	51
G	67	486	20	1,130	306	1,320	1,398	12	<b>9,215</b>	19	15	48	21	6	53	11	25	1,736	1,635	17	71
H	6	149	10	7	93	439	11	16	24	<b>2,261</b>	4	13	326	2	501	239	1,012	1,355	25	6	
I	2	219	19	48	1	12	8	514	11	8	<b>5,780</b>	219	1,018	1,526	416	11	10	194	391	1,800	3,31
K	127	407	28	28	1	28	2,429	1	43	13	245	<b>4,214</b>	12	325	1,751	2	841	2,061	36	630	
L	147	445	45	40	22	5	22	2,446	18	318	1,020	18	<b>18,108</b>	712	9	1,814	446	471	1,669	36	1,91
M	2	115	9	12	1	5	10	12	6	1	1,713	349	712	<b>65</b>	25	1	3	206	16	927	91
N	5	244	18	16	14	2,061	47	14	42	508	419	1,715	6	6	<b>4,248</b>	5	22	48	1,955	596	
P	9	390	25	822	6	3	7	17	6	269	13	9	1,857	2	5	<b>10,285</b>	419	528	1,939	580	
Q	405	195	16	13	2	13	1,007		27	1,040	8	841	420	2	8	427	<b>3,216</b>	1,931	21	10	
R	297	246	24	23	1,036	24	40	10	1,689	1,498	217	2,028	512	154	35	495	2,010	<b>6,533</b>	979	422	
S	181	547	34	1,347	935	46	12	1,089	1,699	33	448	52	1,770	16	1,932	1,932	8	1,007	<b>13,924</b>	1,603	
T	2	293	16	3,134	5	16	26	14	32	7	1,861	609	35	907	660	623	8	449	1,606	<b>10,020</b>	
V	3	269	24	3,102	9	279	366	662	707	5	3,335	15	1,971	904	8	19	5	19	42	72	<b>8,8</b>
W	269	48	2		207	1	3	8	98	1		1	198	6		2	39	505	110		
Y	192	130	19	1	859	411	11	653	7	1,077	7	10	38		431	11	10	24	412	5	

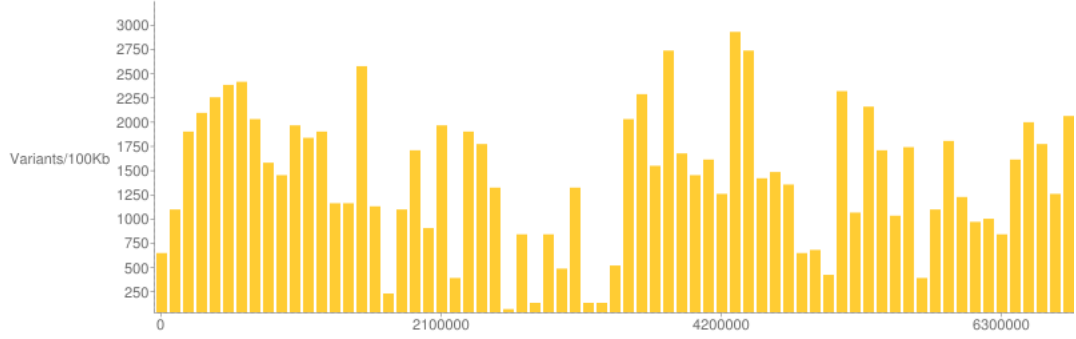
Variants by chromosome



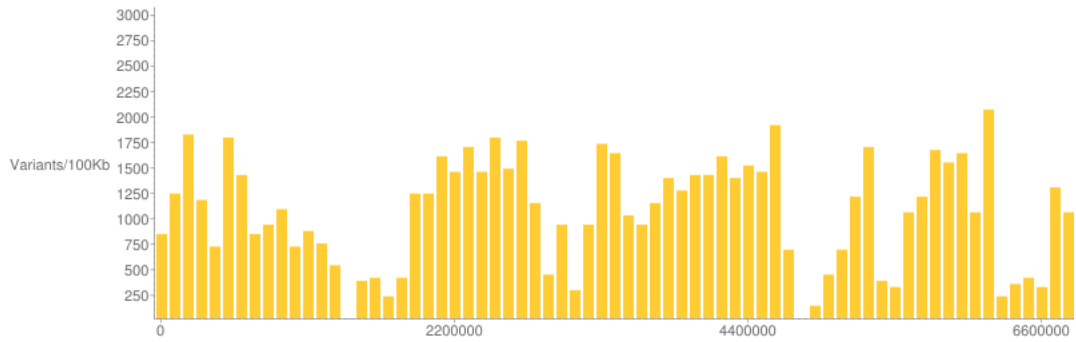
1, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 1, Count,667,2268,1211,2046,951,920,1290,1374,1943,1054,1474,1898,1538,1110,576,1288,524,506,823,1102,1825,1860,1759,1914,1542,1676,1737,973,20,700,5



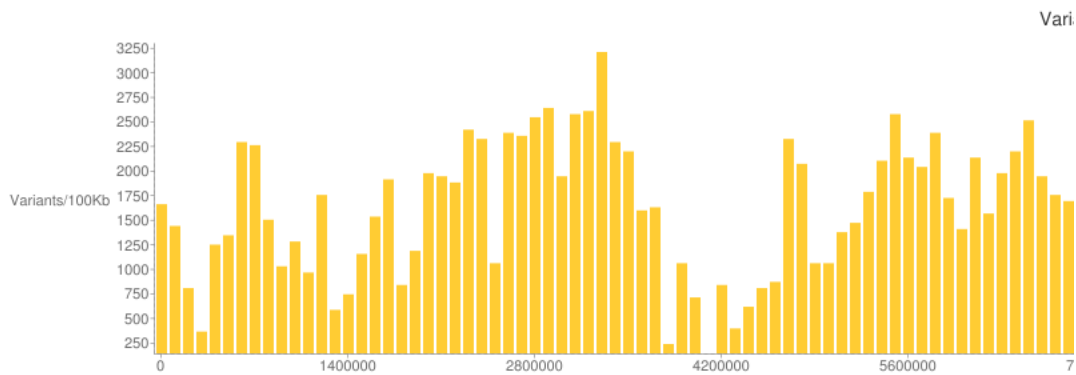
2, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 2, Count,2958,1695,2761,2161,2099,2194,775,1612,1831,2003,1870,2581,1747,2462,436,567,2168,2770,2024,1978,2083,2002,2198,487,2117,1871,415,1996,868,8



3, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 3,Count,652,1121,1919,2096,2273,2396,2425,2053,1578,1469,1963,1861,1906,1165,1189,2585,1148,240,1125,1704,925,1986,396,1926,1791,1326,72,866,141,867



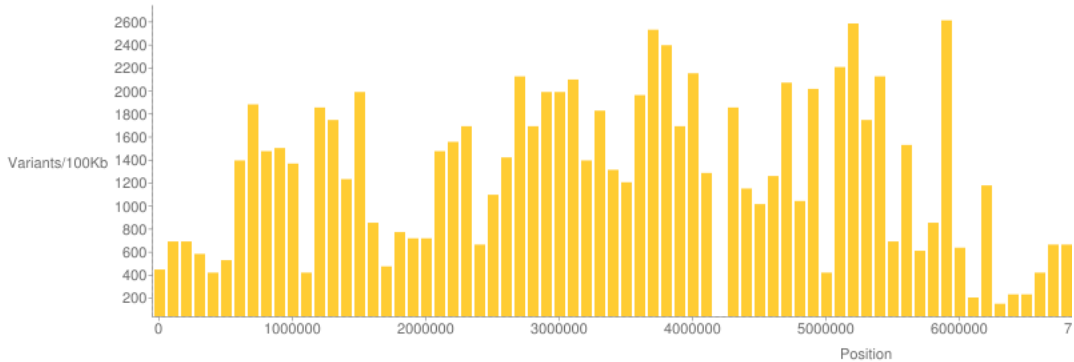
4, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 4,Count,858,1270,1834,1202,745,1794,1438,874,961,1115,747,896,781,560,45,406,434,236,437,1243,1247,1630,1481,1704,1487,1799,1498,1778,1175,476,950,3



5, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 5,Count,1663,1464,832,377,1255,1350,2294,2267,1520,1041,1300,972,1782,599,767,1171,1536,1938,861,1210,1989,1949,1890,2431,2348,1068,2407,2375,2569,2

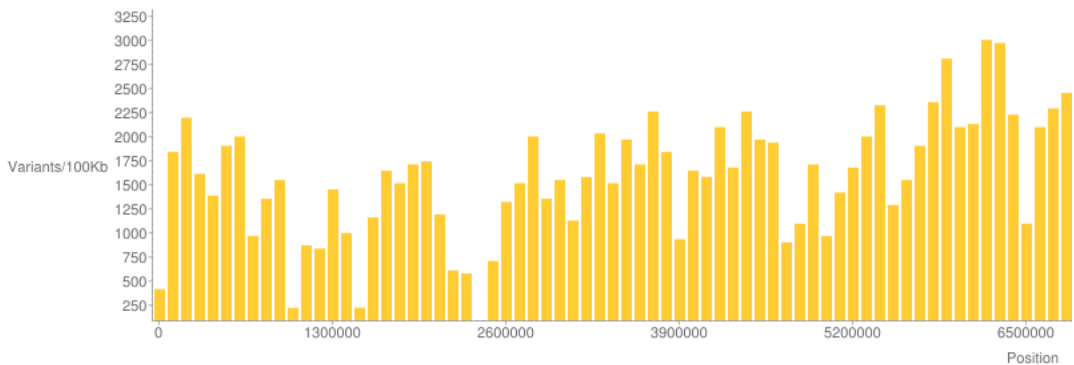


Variants histogram: 6



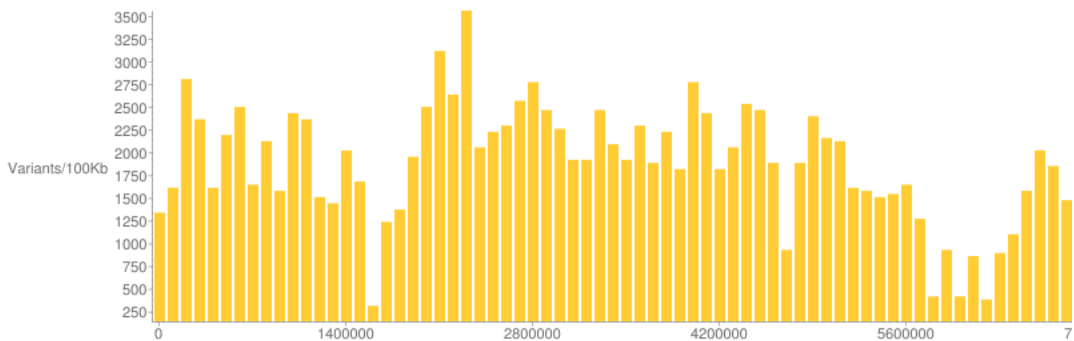
6, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 6,Count,445,714,709,583,439,537,1397,1899,1492,1511,1379,428,1869,1766,1246,2005,850,485,771,735,732,1489,1577,1705,676,1106,1442,2139,1715,2008,198

Variants histogr

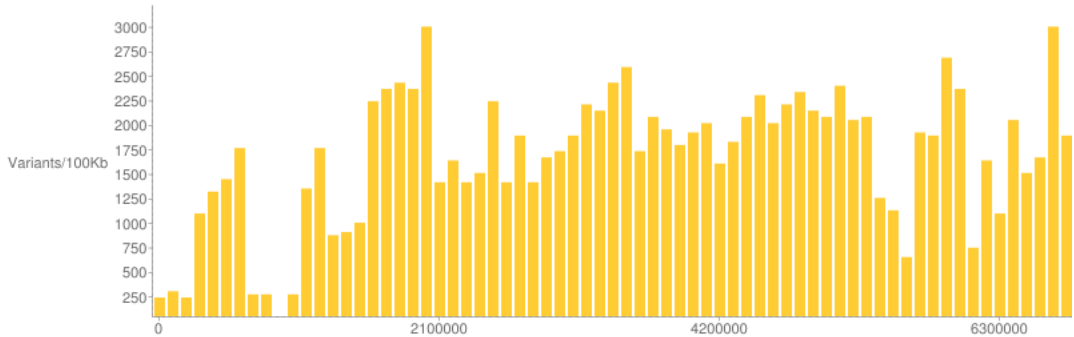


7, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 7,Count,424,1865,2210,1630,1408,1912,2002,975,1380,1574,221,883,857,1451,1005,247,1183,1647,1532,1726,1748,1196,627,592,90,709,1336,1541,2020,1356,1

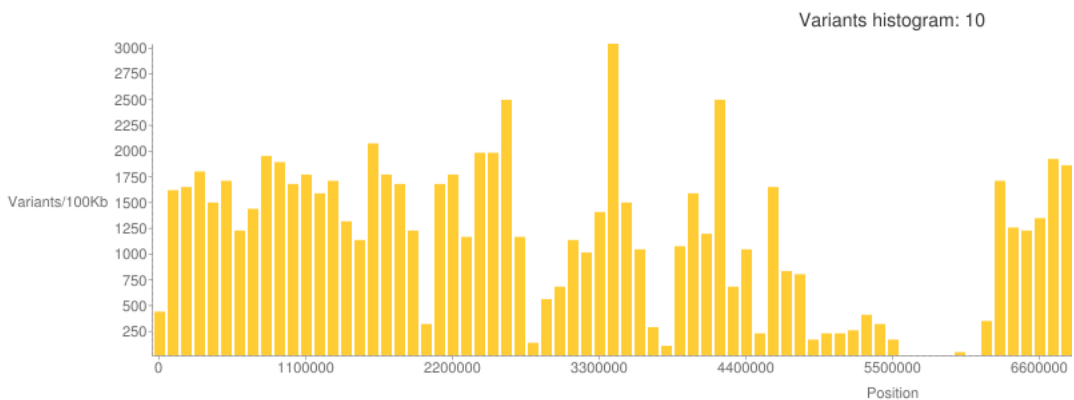
Va



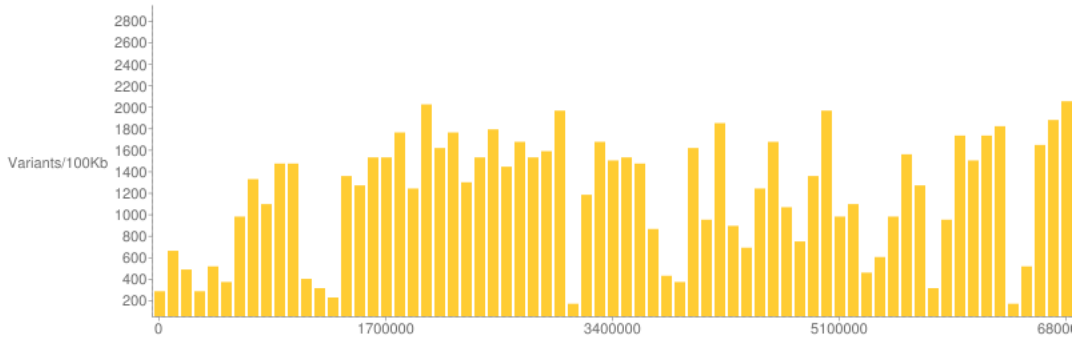
8, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 8,Count,1367,1619,2841,2381,1625,2195,2533,1678,2133,1600,2459,2367,1514,1447,2024,1706,314,1265,1405,1961,2515,3145,2647,3561,2074,2245,2320,2588,2



9, 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, Count,244,317,256,1111,1322,1476,1788,302,295,77,283,1378,1775,899,934,1030,2243,2371,2435,2385,3022,1436,1663,1438,1533,2267,1420,1914,1424,1686,

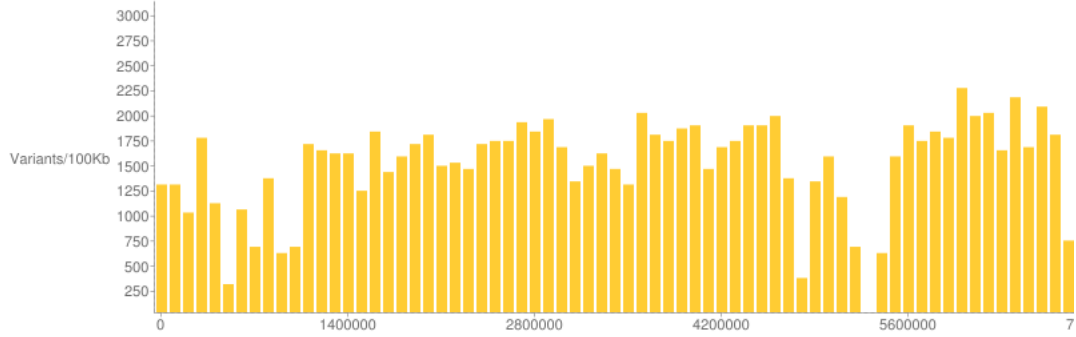


10, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000,1700000,1800000,1900000,2000000,2100000,2200000,2300000,2400000,2500000,2600000,2700000,2800000,2900000,3000000,3100000,3200000,3300000,3400000,3500000,3600000,3700000,3800000,3900000,4000000,4100000,4200000,4300000,4400000,4500000,4600000,4700000,4800000,4900000,5000000,5100000,5200000,5300000,5400000,5500000,5600000,5700000,5800000,5900000,6000000,6100000,6200000,6300000,6400000,6500000,6600000, Count,440,1630,1673,1805,1499,1718,1237,1447,1962,1916,1691,1768,1586,1707,1329,1155,2089,1790,1698,1224,324,1682,1793,1175,1980,1989,2521,1180,1



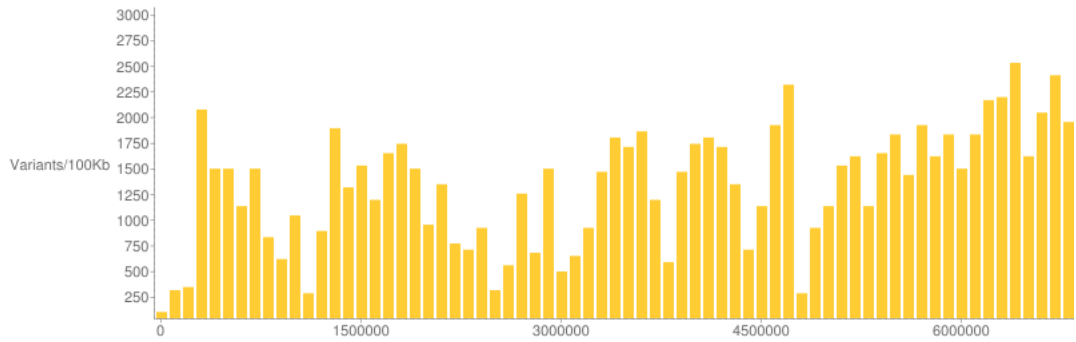
11, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000,1700000,1800000,1900000,2000000,2100000,2200000,2300000,2400000,2500000,2600000,2700000,2800000,2900000,3000000,3100000,3200000,3300000,3400000,3500000,3600000,3700000,3800000,3900000,4000000,4100000,4200000,4300000,4400000,4500000,4600000,4700000,4800000,4900000,5000000,5100000,5200000,5300000,5400000,5500000,5600000,5700000,5800000,5900000,6000000,6100000,6200000,6300000,6400000,6500000,6600000,6700000,6800000, Count,302,672,496,307,514,383,989,1337,1093,1475,1486,422,320,238,1370,1294,1551,1548,1766,1243,2044,1621,1778,1296,1546,1814,1463,1689,1546,1586,

Varian



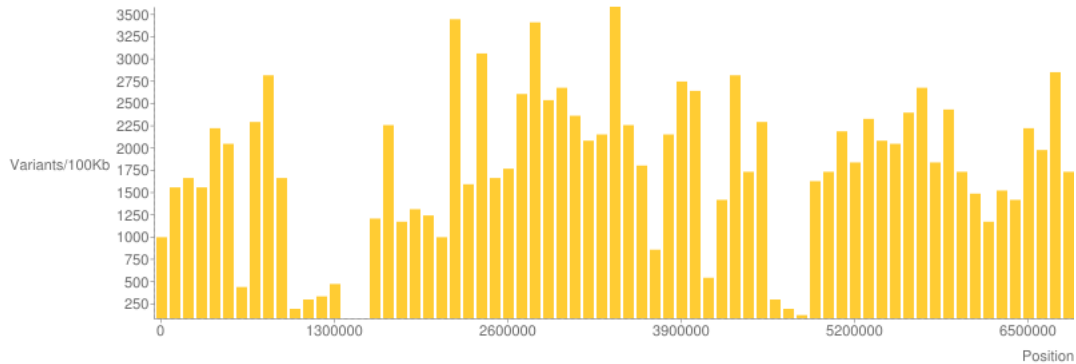
12, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 12, Count,1330,1309,1034,1780,1124,334,1091,689,1388,641,707,1738,1653,1646,1626,1272,1855,1461,1616,1726,1810,1499,1532,1467,1740,1761,1764,1936,185

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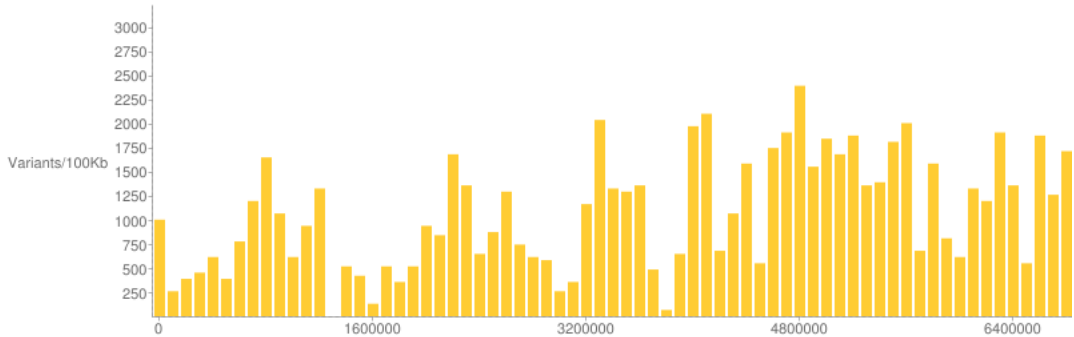


13, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 13, Count,122,324,361,2103,1499,1520,1138,1507,853,622,1060,296,907,1917,1333,1550,1196,1660,1765,1514,952,1373,787,734,938,319,571,1281,678,1506,524

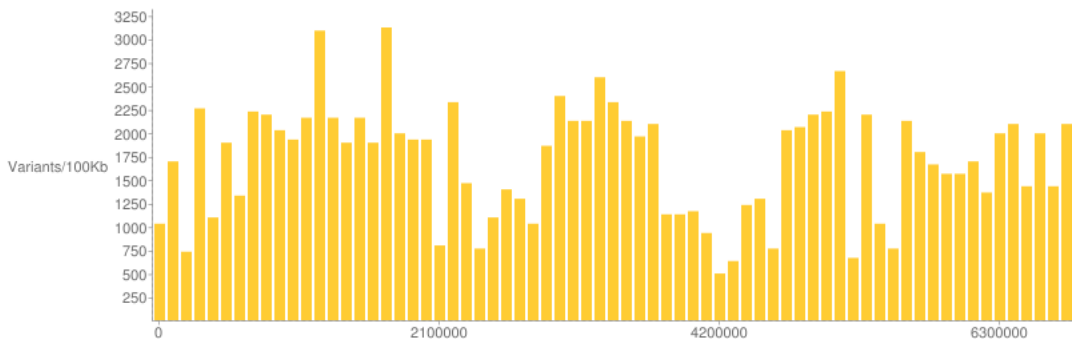
Variants histoc



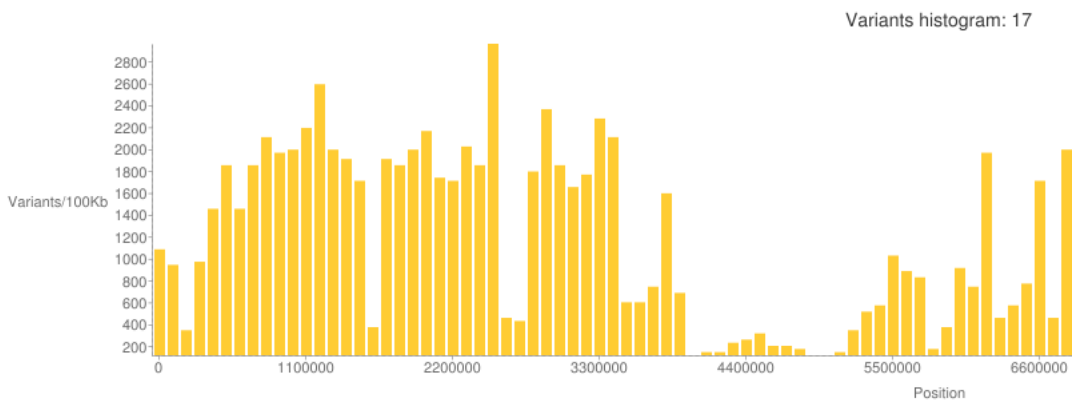
14, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 14, Count,1015,1580,1667,1551,2217,2051,459,2308,2837,1658,193,295,326,472,106,115,1210,2258,1176,1322,1258,1016,3459,1603,3090,1686,1789,2634,3435,2



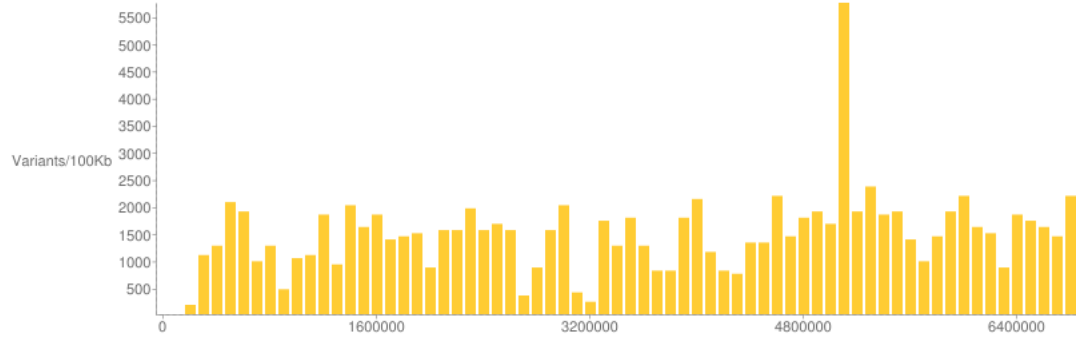
15, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
15, Count,1027,293,392,471,644,419,783,1201,1657,1093,643,942,1345,3,544,428,138,543,387,551,960,868,1686,1381,650,900,1304,774,627,614,281,374,1192,



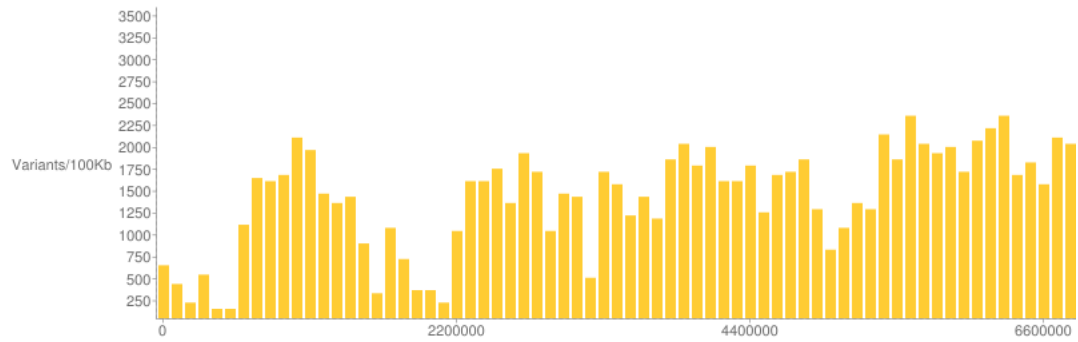
16, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
16, Count,1056,1702,769,2274,1117,1904,1357,2242,2204,2035,1964,2175,3114,2194,1901,2195,1918,3156,2018,1959,1937,837,2353,1498,783,1116,1434,1306,10



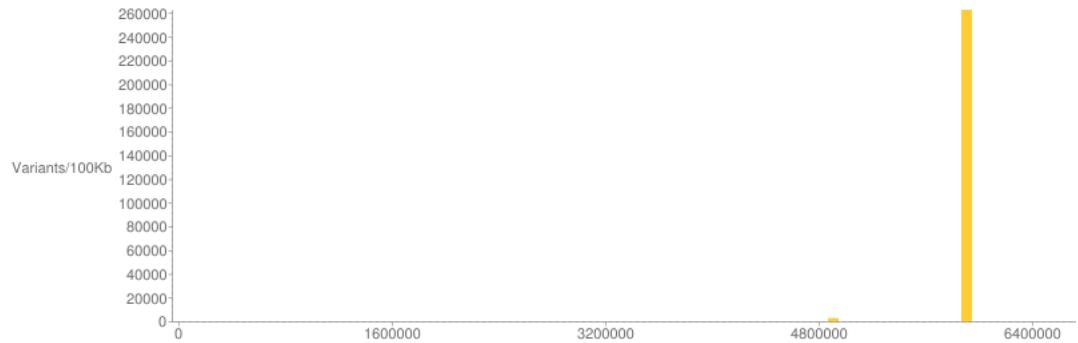
17, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
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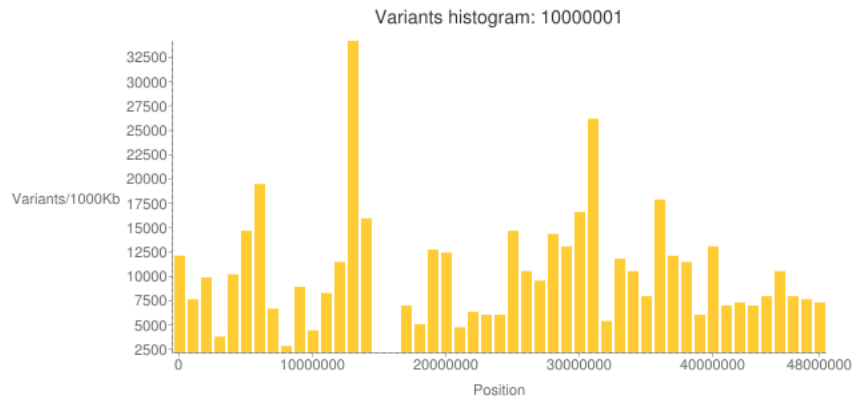
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 18, Count,26,32,210,1157,1310,2096,1971,1058,1329,525,1082,1118,1896,1000,2038,1666,1885,1405,1495,1522,906,1631,1616,1994,1587,1724,1605,409,938,161



19, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 19, Count,659,453,227,575,184,181,1145,1656,1635,1684,2119,1964,1500,1361,1463,921,341,1085,736,383,390,255,1063,1620,1628,1783,1390,1949,1722,1069,1



20, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000  
 20, Count,13,1420,108,666,1301,357,888,1702,397,1978,1629,869,626,2212,1802,970,223,391,1942,1594,1521,1699,1481,1781,1354,860,6,57,145,711,2332,2332



10000001, Position,0,1000000,2000000,3000000,4000000,5000000,6000000,7000000,8000000,9000000,10000000,11000000,12000000,13000000,14000000,15000000,16000000,17000000,18000000,19000000,20000000,21000000,22000000,23000000,24000000,25000000,26000000,27000000,28000000,29000000,30000000,31000000,32000000,33000000,34000000,35000000,36000000,37000000,38000000,39000000,40000000,41000000,42000000,43000000,44000000,45000000,46000000,47000000,48000000,Count,12374,7753,9922,4001,10389,14734,19488,6680,2819,9073,4547,8303,11689,34154,16178,2131,2350,6973,5200,12938,12571,4773,6473,6113,6212

**Details by gene**

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