

SnpEff: Variant analysis

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Summary

Genome	TA4
Date	2018-01-01 19:47
SnpEff version	SnpEff 4.3p (build 2017-06-06 09:55), by Pablo Cingolani
Command line arguments	SnpEff TA4 kp_all.vcf
Warnings	201,439
Errors	0
Number of lines (input file)	7,791,116
Number of variants (before filter)	9,030,162
Number of not variants (i.e. reference equals alternative)	0
Number of variants processed (i.e. after filter and non-variants)	9,030,142
Number of known variants (i.e. non-empty ID)	0 (0%)
Number of multi-allelic VCF entries (i.e. more than two alleles)	450,364
Number of effects	17,539,335
Genome total length	377,290,333
Genome effective length	377,290,333
Variant rate	1 variant every 41 bases

Variants rate details

Chromosome	Length	Variants	Variants rate
1	17,320,008	466,510	37
2	17,063,873	428,844	39
3	21,566,805	530,741	40
4	22,357,487	484,241	46
5	14,540,018	324,800	44
6	10,680,009	206,656	51
7	13,133,232	361,416	36
8	14,750,018	356,138	41
9	21,055,410	481,402	43
10	11,063,414	222,749	49
11	17,675,019	690,820	25
12	14,336,529	310,197	46
13	15,099,493	357,215	42
14	13,335,999	328,449	40
15	16,178,320	329,319	49
16	21,434,198	430,451	49
17	11,746,059	324,153	36
18	16,863,820	401,989	41
19	22,398,858	800,148	27
20	16,105,987	621,593	25
10000001	48,585,777	572,311	84
Total	377,290,333	9,030,142	41

Number variants by type

Type	Total
SNP	6,291,666
MNP	1,568,959
Total	9,030,142

Type	Total
INS	223,249
DEL	245,632
MIXED	700,636
INV	0
DUP	0
BND	0
INTERVAL	0
Total	9,030,142

Number of effects by impact

Type (alphabetical order)	Count	Percent
HIGH	13,392	0.076%
LOW	203,108	1.158%
MODERATE	235,851	1.345%
MODIFIER	17,086,984	97.421%

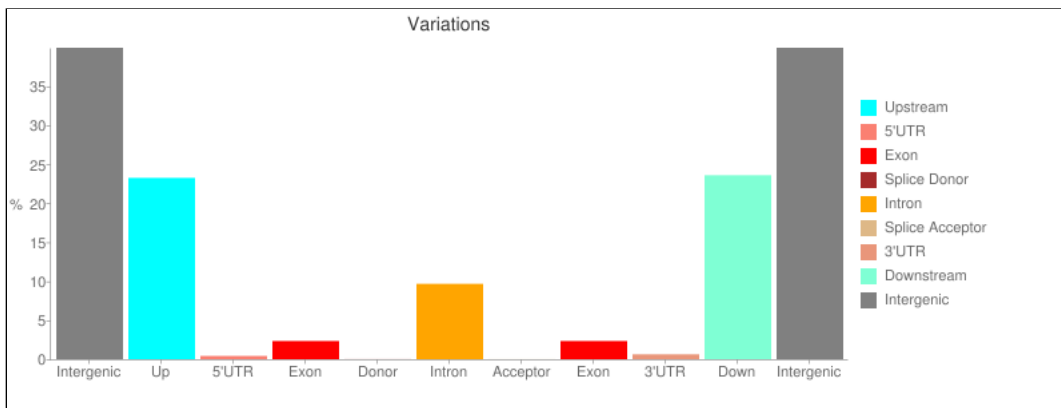
Number of effects by functional class

Type (alphabetical order)	Count	Percent
MISSENSE	201,746	55.063%
NONSENSE	2,688	0.734%
SILENT	161,956	44.203%

Missense / Silent ratio: 1.2457

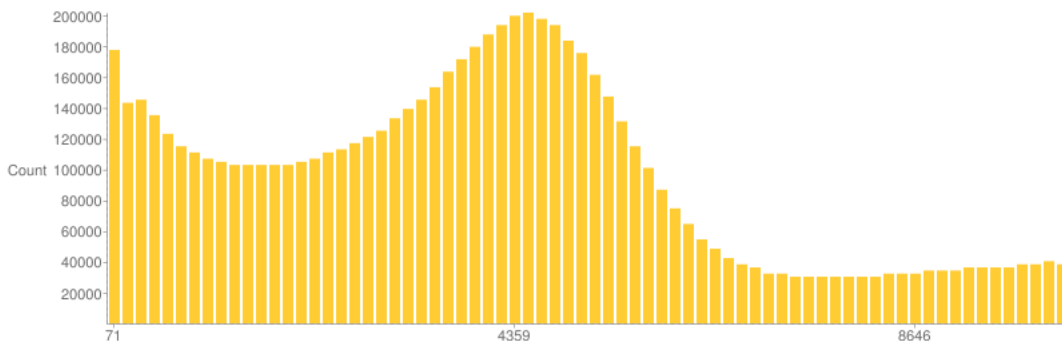
Number of effects by type and region

Type			Region		
Type (alphabetical order)	Count	Percent	Type (alphabetical order)	Count	Percent
3_prime_UTR_variant	110,313	0.627%	DOWNSTREAM	4,136,532	23.584%
5_prime_UTR_premature_start_codon_gain_variant	7,617	0.043%	EXON	408,289	2.328%
5_prime_UTR_truncation	1	0%	GENE	2	0%
5_prime_UTR_variant	65,666	0.373%	INTERGENIC	7,001,925	39.921%
bidirectional_gene_fusion	2	0%	INTRON	1,694,663	9.662%
conservative_inframe_deletion	1,268	0.007%	SPLICE_SITE_ACCEPTOR	1,965	0.011%
conservative_inframe_insertion	1,127	0.006%	SPLICE_SITE_DONOR	1,920	0.011%
disruptive_inframe_deletion	878	0.005%	SPLICE_SITE_REGION	32,557	0.186%
disruptive_inframe_insertion	560	0.003%	TRANSCRIPT	1,059	0.006%
downstream_gene_variant	4,136,549	23.526%	UPSTREAM	4,076,994	23.245%
exon_loss_variant	3	0%	UTR_3_PRIME	110,222	0.628%
frameshift_variant	5,015	0.029%	UTR_5_PRIME	73,207	0.417%
initiator_codon_variant	73	0%			
intergenic_region	7,001,925	39.822%			
intragenic_variant	284	0.002%			
intron_variant	1,725,408	9.813%			
missense_variant	233,638	1.329%			
non_coding_transcript_variant	775	0.004%			
splice_acceptor_variant	2,024	0.012%			
splice_donor_variant	2,005	0.011%			
splice_region_variant	39,208	0.223%			
start_lost	572	0.003%			
stop_gained	3,519	0.02%			
stop_lost	758	0.004%			
stop_retained_variant	317	0.002%			
synonymous_variant	166,397	0.946%			
upstream_gene_variant	4,076,994	23.187%			



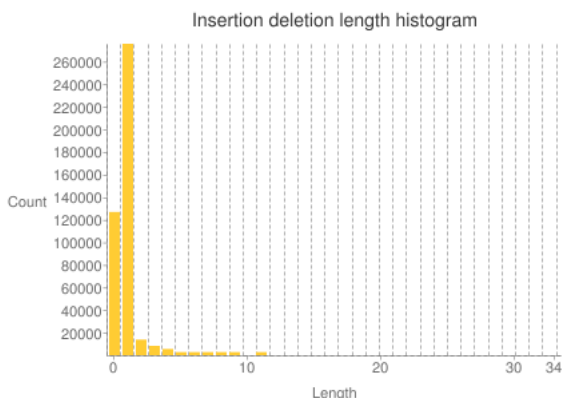
Quality:

Min	0
Max	6,264,490
Mean	5,818,445
Median	4,225
Standard deviation	49,780.119
Values	0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52
Count	25489,3136,2077,1860,1498,1297,1280,1274,1204,1139,1063,1191,1076,1151,1025,1046,1109,1053,1093,1065,1127,1096,1091,1073,1092,1182,1071



Insertions and deletions length:

Min	0
Max	34
Mean	1.467
Median	1
Standard deviation	2.71
Values	0,1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,34
Count	129104,275837,14654,10044,5974,5428,3173,3676,3183,3229,2504,2784,1787,1435,1207,993,710,698,508,457,387,267,218,166,132,102,76,57,30,33



Base changes (SNPs)

	A	C	G	T
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A	0	222,604	1,077,667	312,402
C	227,322	0	152,618	1,151,534
G	1,151,752	152,831	0	227,746
T	311,943	1,080,437	222,810	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	5,388,710
Transversions	2,200,036
Ts/Tv ratio	2.4494

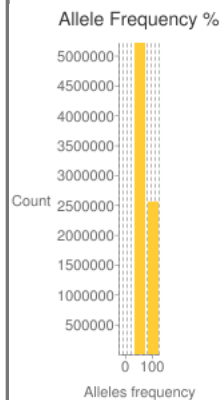
All variants:

Sample , unknown, Total
 Transitions ,5388710,5388710
 Transversions ,2200036,2200036
 Ts/Tv ,2.449,2.449

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

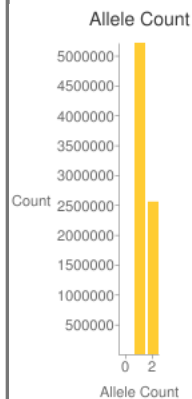
No results available (empty input?)

Allele frequency



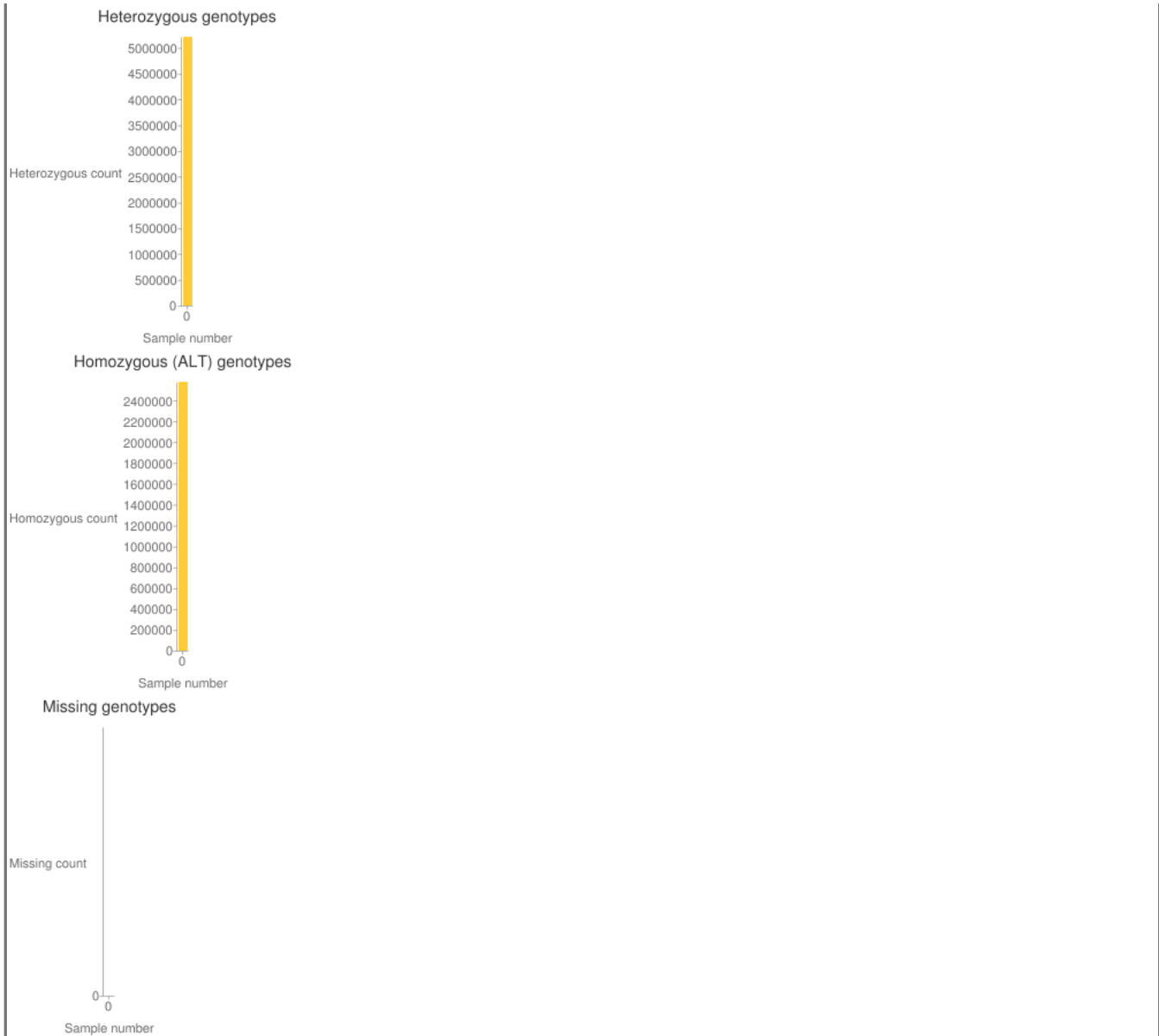
Min	0
Max	100
Mean	66.544
Median	50
Standard deviation	23.527
Values	0,50,100
Count	17,5213172,2577927

Allele Count



Min	0
Max	2
Mean	1.331
Median	1
Standard deviation	0.471
Values	0,1,2
Count	17,5213172,2577927

Hom/Het per sample



Sample_names , unknown
 Reference , 17
 Het , 5213172
 Hom , 2577927
 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
-		119	73	121	129	75	55	24	92	69	52	62	83	41	37	67	71	118	66	111	113
AAA	357	184	575	3,011	796	559	6	11	6	1,580	11	29	17	355	5	18	13	797	5	15	6
AAC	193	655	96	618	3,037	7	312	3	17	9	1,241	7	30	4	184	3	3	15	212	7	7
AAG	311	3,088	660	140	787	23	6	382	11	29	17	1,577	4	8	7	545	8	18	6	548	4
AAT	271	820	3,046	640	155	10	9	6	579	12	39	16	1,764	6	16	8	488	14	7	4	527
ACA	151	562	12	14	11	88	593	2,351	915	472	7	7	9	1,102	12	115	10	10			1
ACC	106	2	391	6	4	530	41	440	2,363	1	411	3	12	11	529	10	24		2		
ACG	45	11	5	368	7	2,329	422	17	579	7	2	201	4	32	6	1,298	14			3	2
ACT	155	14	19	5	601	987	2,610	642	87	6	10	4	777	11	19	23	1,307		3	3	6
AGA	170	1,540	4	44	18	432		10	5	100	265	1,506	262	317	3	5	5	20	1	2	
AGC	86	21	1,168	16	27	8	380	4	16	254	84	218	1,882	4	180	1	12		6	1	1
AGG	111	25	2	1,493	18	7	3	255	4	1,570	274	57	328	4	1	265	3			22	1

	-	AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT	ATA	ATC	ATG	ATT	CAA	CAC	CAG	CAT
AGT	167	12	30	22	1,764	8	13	3	743	301	1,843	282	95	4	7	7	446	2			25
ATA	112	337	2	14	15	969	7	20	11	285	4	4	9	68	663	1,385	926	9	2		1
ATC	89	4	158	3	7	7	514	2	16	1	145	2	10	716	57	403	2,538		1	1	
ATG	252	8	13	480	41	78	10	1,362	18	12	6	305	4	1,580	416	105	632			9	5
ATT	182	12	14	3	488	11	20	10	1,214	5	9	4	388	882	2,605	604	133				10
CAA	210	747	7	13	10	12		1		18	7			5		1	1	111	339	2,348	425
CAC	79	3	218	2	8	1	3		2	2	3	1			1	1		317	44	378	1,590
CAG	180	12	4	522	4	2			1			8	1	1	1	4		2,296	368	73	434
CAT	174	6	8	2	569	7			4				19			1	6	470	1,749	377	75
CCA	258	4	3	1		292	1	5	4	9				7		1		390	6	20	5
CCC	111		2			2	145		8		2					3		3	127	4	4
CCG	84			4		4		78	2			1	1			2		6	2	246	3
CCT	218				14	3	4	2	383	1			5			1	2	5	10	9	292
CGA	45	19	2		1	1	1			524	3	11		2		1	1	1,679	6	29	12
CGC	28	2	5				1	1		3	159	2				3		8	771	8	20
CGG	40			6	1	1		4		12	2	404	2			4		25	6	1,429	19
CGT	47			2	12				9	11	2	5	227				3	14	17	16	1,631
CTA	88	3		1	1	5				4		1		304	2	9	9	284		4	2
CTC	117		1				4	1			3		2	3	275	5	9	6	142	3	3
CTG	85	1	1	3	1	2		2				2		13	2	453	6	7		342	2
CTT	192	1	1	3	1		1		17				4	10	6	3	656	11	4	8	335
GAA	393	2,391	17	46	26	14	1	5	1	42		2	1	10	2		1	830	2	10	5
GAC	146	17	1,050	12	30		5	1	3	1	28	1		1	3	1	2	2	217	2	9
GAG	291	45	19	2,019	26	1		11		8	3	41	1	2		14		22	3	860	3
GAT	346	18	34	12	2,287		1	1	13	4	1	2	50	1	1	2	30	2	7	9	555
GCA	211	29				1,830	7	29	10	10	3		1	57		6		16		1	
GCC	121		9	1	1	4	1,040	3	34	1	10		1		11	1	1		3	1	
GCG	53			16	2	27		346	7	3		5				31				4	
GCT	223	1	3		21	12	41	8	1,886	1	5	2	14	1			43	4		1	5
GGA	267	46		3	3	12		2	1	1,202	4	14	14	6	1			23	1	2	1
GGC	132	6	39	1	5		4			6	895	8	29		1		1		12		
GGG	161	1	1	33	7	1	2	4	1	10	6	730	11			8		1	2	20	
GGT	291	2	2	6	41				12	9	17	9	1,616		1	2	16				25
GTA	83	8		1	1	30				3	2		1	1,368	3	24	15	4			
GTC	59		1	1			16				1		1	7	1,154	8	32	3	1	1	1
GTG	134	3		14		5	1	29				5	3	38	7	1,392	13		1	6	1
GTT	201	3			11	4	4		31	1	1		22	27	27	9	2,615	1			2
TAA	26	34												1				68	2		
TAC	90	9	243	8	4		1				4	1			5			13	561	4	25
TAG	20			19														2		59	
TAT	143	3	9		453			5	3		1		8	4		1	10	8	20		1,155
TCA	208	12	1		2	444	7	9	4	4		2		12	3	1		7			1
TCC	110		9		1	2	219		11		8				3			2	3	1	
TCG	63			3	1	4	3	91	1	2		3				8	1		1	4	
TCT	346		1		20	2	15	1	493		2		14	3			6				25
TGA	34									16			1			1		10			
TGC	80		8			1	3			1	154	1	6		2	1			34	1	
TGG	94	1		7				1		2	3	201				9		4	1	57	
TGT	117		1		5	1	1		2	2	3	1	300				8	4	3	2	55
TTA	118	6	1		2	10	1	1	1	2				369	10	8	10	3			1
TTC	165	1	2		2		5			1			1	3	252	6	13	3	14		2
TTG	187			8	2	3		11	4			3		10		615	6	2		11	
TTT	292			2	6		1		16				4	5	8	5	548	2	1	1	11

Amino acid changes

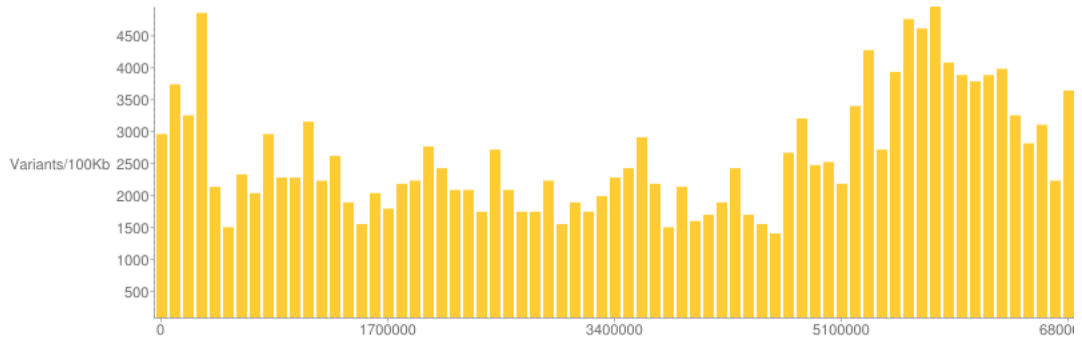
How to read this table:

- 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).

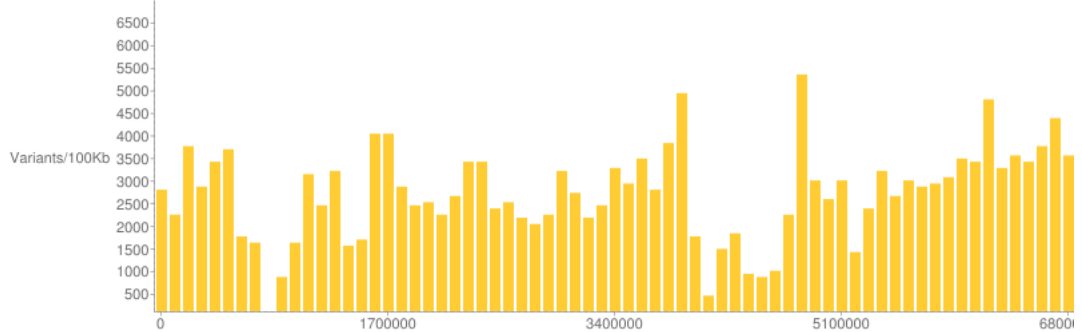
	*	-	?	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T
*	341	65	15		14	1	55	4	23	2	1	53	69	1	4	139	91	62		
-	62		2,128	236	66	211	316	172	295	179	149	240	301	67	202	321	229	200	525	246
?																				
A	8	577	31	18,121	26	612	878	27	1,744	11	113	47	69	38	36	1,276	27	32	2,059	5,284
C	99	184	13	9	3,129	13	3	536	380	93	10		42	1	14	20	7	1,332	1,205	8

	*	-	?	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T
D	15	470	22	560	25	7,370	3,344	13	1,977	788	38	59	15	3	3,401	10	15	28	101	24
E	312	649	35	879	1	3,400	6,156	10	2,308	16	15	4,501	42	14	88	14	1,722	122	12	33
F	12	423	34	24	546	20	2	5,893	12	28	829	3	3,809	11	10	33	6	8	1,519	22
G	122	805	46	1,732	542	2,127	2,164	19	13,757	45	26	98	24	10	98	10	46	2,864	2,624	39
H	10	236	17	25	129	666	26	28	36	3,458	7	13	512	2	803	382	1,542	2,140	47	17
I	5	351	32	75	6	21	11	882	31	14	8,588	373	1,565	2,392	684	22	10	312	592	2,801
K	227	625	43	42	2	60	4,026	3	75	21	396	6,423	23	563	2,818	3	1,378	3,245	66	1,004
L	228	723	64	51	42	8	25	4,172	23	489	1,700	26	27,536	1,093	11	2,641	681	760	2,495	63
M	5	238	14	27	4	7	24	18	10	5	2,628	488	1,177	105	54	8	9	319	21	1,468
N	8	440	24	24	19	3,181	71	14	80	753	701	2,733	11	11	6,334	7	40	61	3,095	943
P	16	644	27	1,254	13	8	12	27	15	452	12	9	3,013	4	19	15,176	683	784	3,218	933
Q	746	367	23	19	3	27	1,598	4	39	1,566	8	1,294	765	5	25	646	4,828	2,960	32	16
R	517	403	38	33	1,778	36	82	25	2,609	2,484	342	3,131	792	275	63	758	3,252	9,727	1,562	734
S	258	938	42	2,000	1,577	71	31	1,880	2,623	66	681	86	2,800	17	3,024	2,904	17	1,505	20,905	2,481
T	3	431	26	4,992	5	28	37	26	46	14	3,077	982	50	1,446	1,050	870	16	716	2,564	14,994
V	1	444	33	4,700	16	442	581	1,050	1,033	6	5,306	30	3,056	1,433	13	30	15	27	66	120
W	488	87	7	4	293	1	8	14	166	1		8	303	9		6	61	851	173	1
Y	363	209	24	7	1,443	664	25	1,095	24	1,761	19	20	60	1	709	6	25	36	666	9

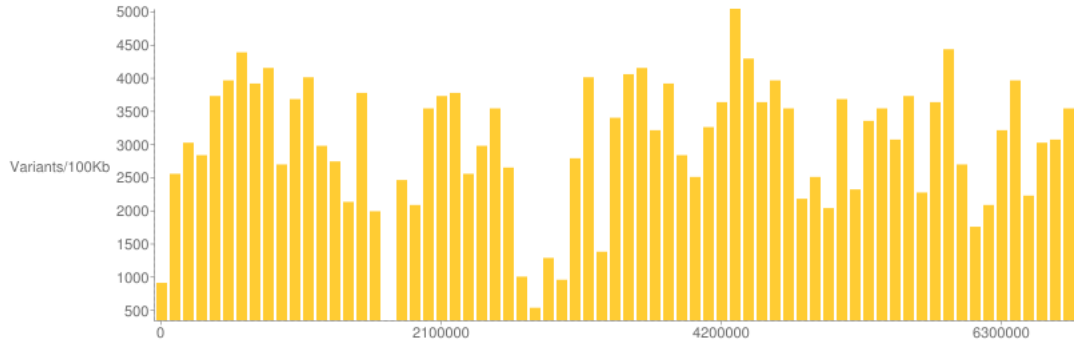
Variants by chromosome



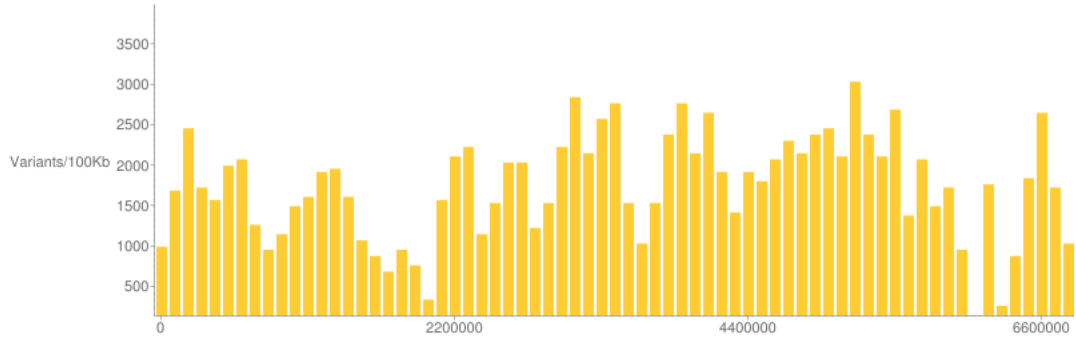
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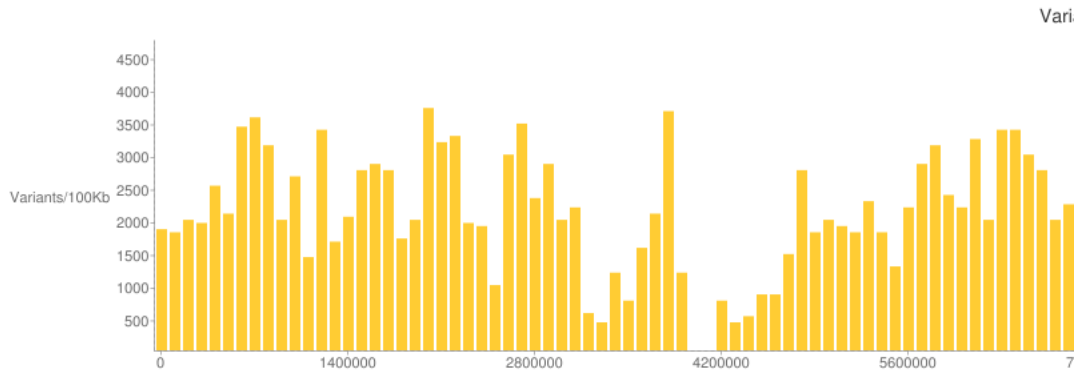
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3, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 3,Count,920,2584,3054,2855,3757,3974,4386,3914,4193,2722,3713,4044,2999,2781,2157,3791,2015,344,2489,2080,3553,3735,3780,2559,3017,3540,2661,1016,52

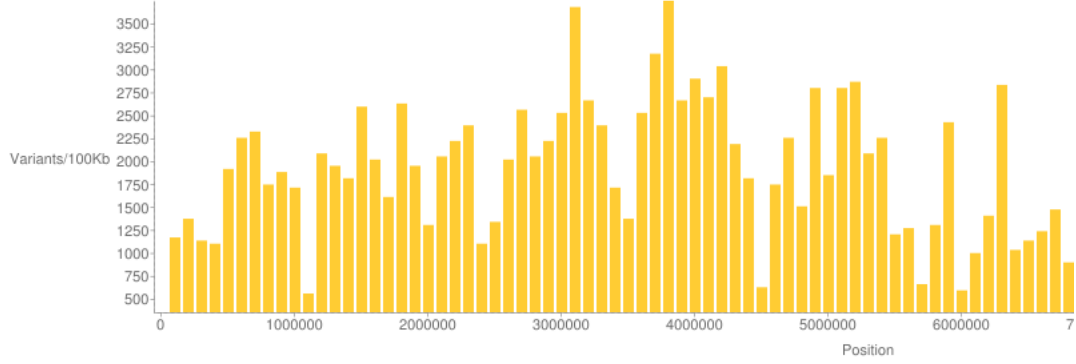


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 4,Count,1004,1677,2464,1728,1563,2017,2066,1272,970,1150,1486,1614,1939,1964,1608,1064,870,689,977,769,365,1569,2133,2233,1152,1522,2056,2043,1237,1



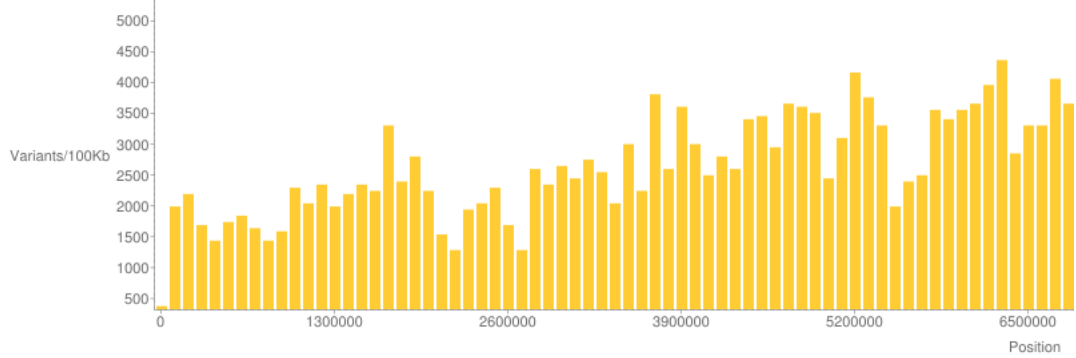
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 5,Count,1920,1869,2062,2002,2568,2135,3481,3644,3224,2064,2732,1475,3417,1745,2110,2834,2919,2830,1773,2038,3796,3260,3325,2005,1943,1062,3068,3528,1

Variants histogram: 6



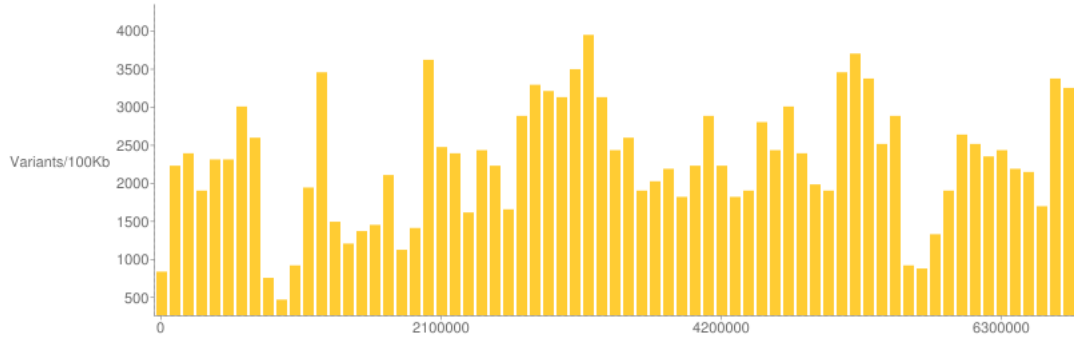
6, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000, Count,370,1178,1380,1159,1130,1917,2266,2350,1750,1906,1716,563,2091,1961,1816,2612,2020,1613,2635,1968,1315,2083,2228,2400,1115,1370,2040,2582,20

Variants histogr



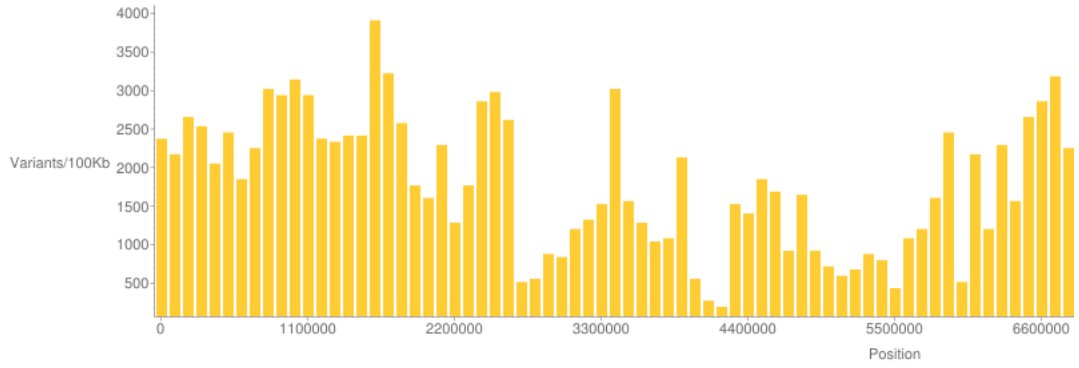
7, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000, Count,397,1991,2205,1695,1427,1756,1872,1653,1448,1583,2296,2051,2347,2014,2218,2381,2279,3338,2421,2791,2278,1575,1284,1976,2059,2289,1712,1280,2

8, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000, Count,2682,1642,2886,2396,1649,2230,2391,1835,2043,1594,2688,2463,1610,1663,2039,1310,1162,1238,1400,2105,3511,4924,4353,4943,3199,4473,4283,4478,2

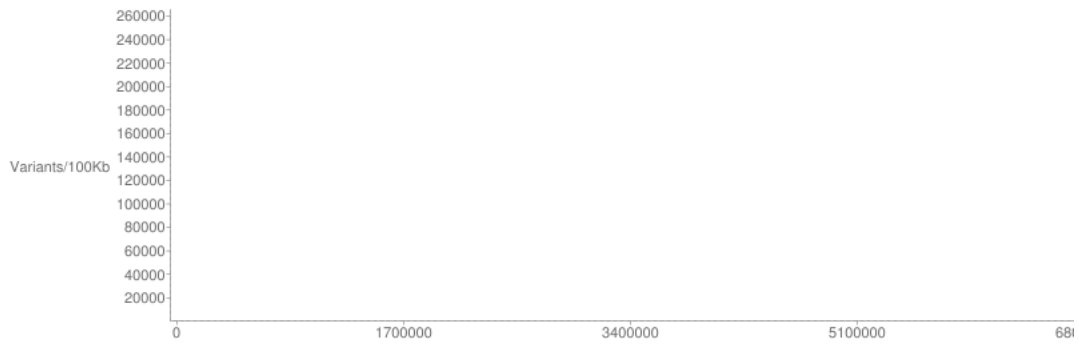


9, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000, Count,838,2233,2405,1919,2307,2311,3021,2614,759,472,914,1950,3481,1487,1218,1388,1486,2141,1143,1410,3639,2476,2401,1613,2435,2248,1651,2879,3288

Variants histogram: 10

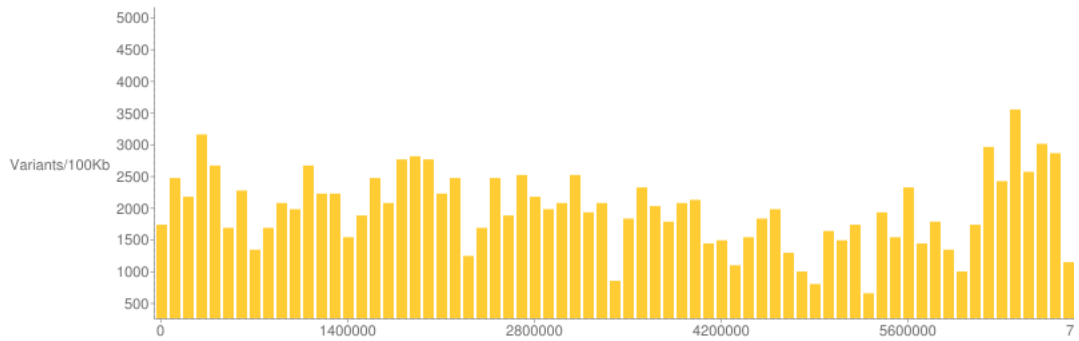


10, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 10, Count,2372,2202,2651,2558,2079,2485,1881,2272,3016,2944,3156,2969,2369,2350,2418,2431,3921,3244,2589,1797,1620,2305,1278,1779,2884,2992,2630,510,

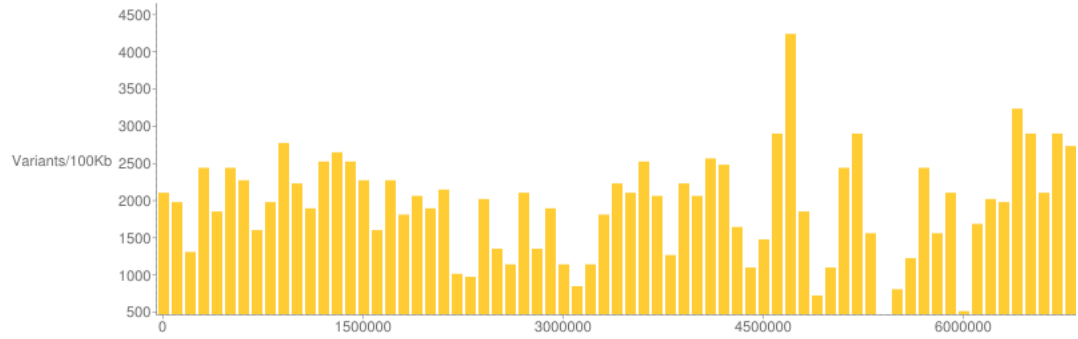


11, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 11, Count,2313,1910,1794,2412,2066,2072,1895,2009,1960,1611,1380,1884,1704,1165,1764,2015,2367,2238,2045,1606,2685,2146,2170,2173,2465,2467,1793,2440,

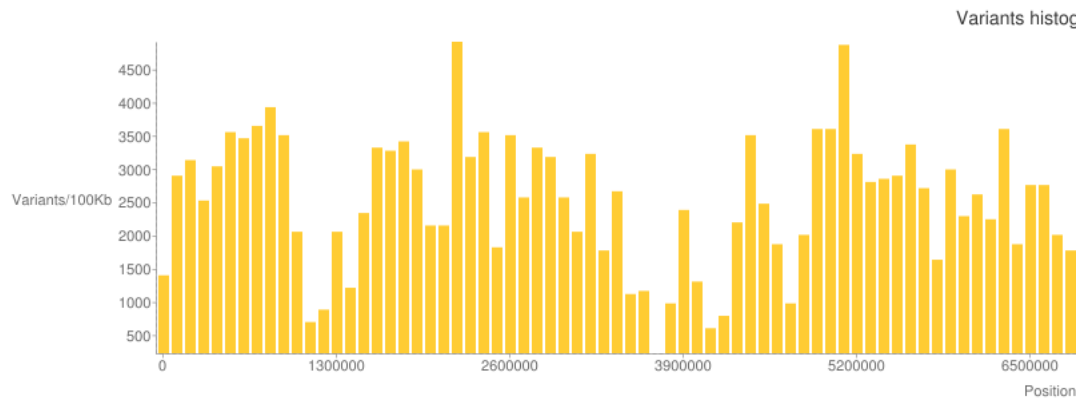
Varian



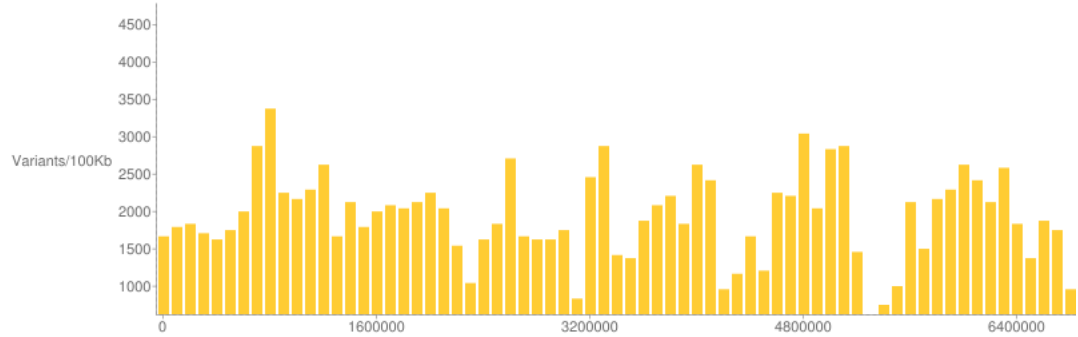
12, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 12, Count,1770,2503,2206,3202,2701,1688,2299,1379,1712,2119,2021,2664,2227,2224,1569,1916,2515,2102,2785,2836,2798,2244,2486,1284,1707,2490,1922,2555,



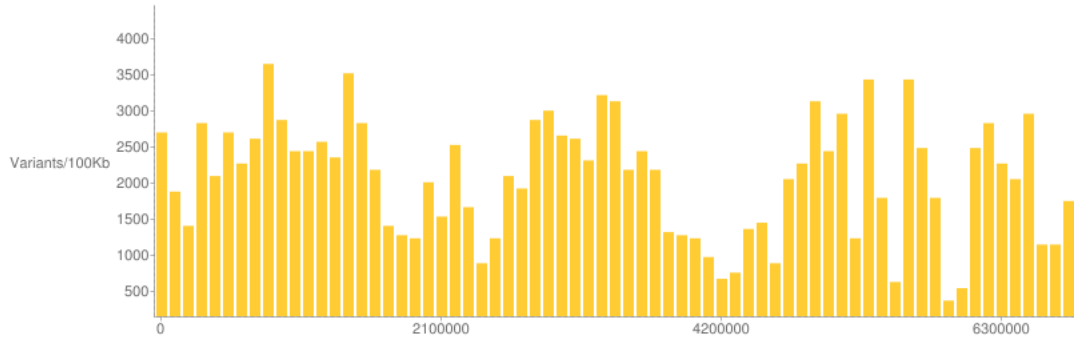
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14, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
14, Count,1417,2906,3153,2532,3046,3590,3489,3682,3935,3543,2068,722,887,2075,1249,2345,3323,3303,3429,3003,2171,2159,4915,3185,3581,1843,3548,2615,3



15, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
15, Count,1689,1809,1831,1716,1640,1760,1998,2892,3381,2249,2194,2319,2640,1669,2137,1811,2020,2096,2046,2127,2256,2049,1565,1068,1644,1863,2727,1672



16, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 16, Count,2700,1892,1435,2859,2092,2696,2289,2610,3658,2867,2447,2449,2582,2357,3520,2859,2215,1434,1301,1250,2016,1552,2548,1661,889,1249,2094,1934,

17, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 17, Count,2148,1285,2317,2320,1542,1713,2329,2272,2284,1588,2333,3296,2700,3151,3303,2914,2837,1287,1495,3364,2650,2669,2756,2712,2531,4535,3230,3253

18, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 18, Count,1099,1107,1631,187,626,1766,1266,559,2519,2365,3083,3136,3698,2255,2254,1613,2339,2442,2145,2622,2737,2774,2907,2762,2080,2333,3232,2033,23

19, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
 19, Count,2023,1647,1979,2202,2177,1629,2163,2302,1891,2360,2617,2591,2153,2464,2191,1884,2780,2744,2204,2035,1657,2280,263972,2539,2403,2213,2153,22

20, Position,0,100000,200000,300000,400000,500000,600000,700000,800000,900000,1000000,1100000,1200000,1300000,1400000,1500000,1600000
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Details by gene

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