

Supplemental Table 2: Details of all alterations in parathyroid tumors

SNV NO.	Gene	Predicted Protein Variants	First Priority
SNV00048	CDKN2A	L,CDKN2A:NM_001195132:exon2:c.G343T:p.V115L,C	Second
SNV00053	EZH2	9Q,EZH2:NM_001203248:exon12:c.C1409A:p.P470Q,EZ	First1
SNV00054	EZH2	6Q,EZH2:NM_001203248:exon7:c.G620A:p.R207Q,EZ	First1
SNV00003	CDC73	CDC73:NM_024529:exon1:c.3delG:p.M1fs	First1
SNV00004	CDC73	CDC73:NM_024529:exon1:c.9_18del:p.D3fs	First1
SNV00005	CDC73	CDC73:NM_024529:exon1:c.10delG:p.V4fs	First1
SNV00006	CDC73	CDC73:NM_024529:exon1:c.18delC:p.S6fs	First1
SNV00007	CDC73	CDC73:NM_024529:exon1:c.C25T:p.R9X	First1
SNV00008	CDC73	CDC73:NM_024529:exon1:c.45delG:p.K15fs	First1
SNV00009	CDC73	CDC73:NM_024529:exon1:c.G64T:p.G22X	First1
SNV00010	CDC73	CDC73:NM_024529:exon1:c.G70T:p.E24X	First1
SNV00011	CDC73	CDC73:NM_024529:exon1:c.82delG:p.G28fs	First1
SNV00012	CDC73	CDC73:NM_024529:exon1:c.84_90del:p.G28fs	First1
SNV00013	CDC73	CDC73:NM_024529:exon1:c.G85T:p.E29X	First1
SNV00014	CDC73	CDC73:NM_024529:exon1:c.104_118del:p.35_40del	Second
SNV00015	CDC73	CDC73:NM_024529:exon1:c.G128A:p.W43X	First1
SNV00016	CDC73	NM_024529:exon1:c.131+1G>C	First1
SNV00017	CDC73	CDC73:NM_024529:exon2:c.G157T:p.E53X	First1
SNV00018	CDC73	CDC73:NM_024529:exon2:c.C162G:p.Y54X	First1
SNV00019	CDC73	CDC73:NM_024529:exon2:c.T163A:p.Y55N	First1
SNV00020	CDC73	CDC73:NM_024529:exon2:c.174dupT:p.D58fs	First1
SNV00021	CDC73	CDC73:NM_024529:exon2:c.T191C:p.L64P	First1
SNV00022	CDC73	CDC73:NM_024529:exon2:c.194_202del:p.65_68del	First1
SNV00023	CDC73	CDC73:NM_024529:exon2:c.C226T:p.R76X	First1
SNV00024	CDC73	CDC73:NM_024529:exon2:c.G232C:p.A78P	First1
SNV00025	CDC73	CDC73:NM_024529:exon3:c.259_260del:p.R87fs	First1
SNV00026	CDC73	CDC73:NM_024529:exon3:c.T293C:p.L98P	First1
SNV00027	CDC73	CDC73:NM_024529:exon4:c.C362T:p.S121F	First1
SNV00028	CDC73	CDC73:NM_024529:exon7:c.549delT:p.A183fs	First1
SNV00029	CDC73	CDC73:NM_024529:exon7:c.570delG:p.M190fs	First1
SNV00030	CDC73	CDC73:NM_024529:exon7:c.C664T:p.R222X	First1
SNV00031	CDC73	CDC73:NM_024529:exon8:c.753delA:p.A251fs	First1
SNV00032	CDC73	CDC73:NM_024529:exon8:c.G817A:p.A273T	First1
SNV00033	CDC73	CDC73:NM_024529:exon14:c.G1305A:p.M435I	First1
SNV00034	CDC73	CDC73:NM_024529:exon15:c.C1394A:p.S465X	First1
SNV00035	MEN1	98L,MEN1:NM_130801:exon10:c.C1493T:p.P498L,ME	First1
SNV00036	MEN1	65+6G>A;NM_130803:exon9:c.1365+6G>A;NM_13080	First2
SNV00037	MEN1	54X,MEN1:NM_130801:exon9:c.G1360T:p.G454X,MEN	First1
SNV00038	MEN1	54X,MEN1:NM_130801:exon7:c.C1060T:p.Q354X,MEN	First1
SNV00039	MEN1	8fs,MEN1:NM_130801:exon3:c.503_510del:p.G168fs,M	First1
SNV00040	MEN1	45X,MEN1:NM_130804:exon3:c.133G>T:p.E45X,MEN	First1
SNV00042	CDKN1B	CDKN1B:NM_004064:exon1:c.280delC:p.P94fs	First1
SNV00043	HIC1	3202:exon2:c.G818A:p.S273N,HIC1:NM_006497:exon2:	First1

SNV00044	HIC1	kon2:c.1217C>T;p.A406V,HIC1:NM_001098202:exon2:	Third
SNV00045	HIC1	02:exon2:c.A1628G;p.K543R,HIC1:NM_006497:exon2:	First1
SNV00046	HIC1	kon2:c.2002G>A;p.A668T,HIC1:NM_001098202:exon2:	First1
SNV00052	EZH2	N,EZH2:NM_001203247:exon16:c.T1921A;p.Y641N,E2	First1

Calling Q	otyping Q	VCF Filter	Case_het	Case_hom	Chrs	Position	Ref Allele
M	1		1037569,1173723,		9	2.2E+07	C
H	1		1095855,		7	1.5E+08	G
H	0.9516		1037008,		7	1.5E+08	C
M	1		1131735_18B0723A,		1	1333-1930	G
H	1		877208_A2,		1	1339-1930	TGCTTA
M	1		1028591_A3,		1	1340-1930	G
M	1		1046897_A1,		1	1348-1930	C
M	1		1143390_A2,		1	1.9E+08	C
H	1		876396_A2,876415_A2,		1	1375-1930	G
H	0.9846		860550_A1,		1	1.9E+08	G
M	0.9923		1177965_A6,		1	1.9E+08	G
M	1		972291_A2,		1	1412-1930	G
H	0.9923		1028838_A,		1	1414-1930	GGAGTTG
M	1		7_A2,1155717_A3,12862,		1	1.9E+08	G
H	0.9923		1110788_A6,		1	1434-1930	GAAGACG
H	0.9923		935992_2,1172857_A2,		1	1.9E+08	G
H	0.9923		1016492_A4,		1	1.9E+08	G
H	1		1179941_A3,		1	1.9E+08	G
H	1		89_A3,1077285_F2,11404		1	1.9E+08	C
M	1		1069417_A4,		1	1.9E+08	T
H	1		972291_A2,		1	14283-1930	-
H	1		1095855_18B0723A,		1	1.9E+08	T
H	1		1209230_A3,		1	14304-1930	TAAACGTG
H	1		1012776_A3,		1	1.9E+08	C
M	0.9545		1009154_A3,		1	1.9E+08	G
H	1		876396_A2,876415_A2,		1	19325-1930	AG
H	1		867432_A,		1	1.9E+08	T
M	0.9922		935992_2,		1	1.9E+08	C
H	1		1143390_A2,		1	1016-1931	T
M	1		877208_A2,		1	1037-1931	G
H	1		1028591_A3,687917_B1,		1	1.9E+08	C
H	1		868167_A2,		1	17020-1931	A
M	1		1140404_A1,		1	1.9E+08	G
H	0.9923		700011_A4,		1	1.9E+08	G
H	1		1249519_A2,		1	1.9E+08	C
H	1		1171276,		11	6.5E+07	G
H	1		922715,		11	6.5E+07	C
M	0.9924			938331,	11	6.5E+07	C
H	0.9924		1037569,		11	6.5E+07	G
H	1		1090119,		11	5522-6457	CAGGCC
H	0		1171276,		11	6.5E+07	C
H	0.9769		974439,		12	1053-1287	C
H	1		826080,		17	1960745	G

M	0		922715,		17	1961201	C
M	0.8397		847204,1083561,876396,		17	1961555	A
M	1		876415,		17	1961986	G
H	0.9924		3365,1083561,1037503,69		7	1.5E+08	A

Alt Allele	Gene Region	Function	Strand Orientation	Protein Variation	SNP ID	q_Alts (1000G)	hg19 chr
A	exonic	nonsynonymous SNV	-		rs779913365		
T	exonic	nonsynonymous SNV	-				
T	exonic	nonsynonymous SNV	-		rs747028969		
-	exonic	frameshift deletion	+		rs1060500020		
-	exonic	frameshift deletion	+				
-	exonic	frameshift deletion	+				
-	exonic	frameshift deletion	+				
T	exonic	stopgain	+		rs4262(STR_around)		
-	exonic	frameshift deletion	+				
T	exonic	stopgain	+				
T	exonic	stopgain	+				
-	exonic	frameshift deletion	+		rs587776560		
-	exonic	frameshift deletion	+				
T	exonic	stopgain	+		DEL_around)		
-	exonic	nonframeshift deletion	+				
A	exonic	stopgain	+		rs121434263		
C	splicing		+				
T	exonic	stopgain	+				
G	exonic	stopgain	+		rs121434265		
A	exonic	nonsynonymous SNV	+				
T	exonic	frameshift insertion	+				
C	exonic	nonsynonymous SNV	+		rs121434264		
-	exonic	nonframeshift deletion	+				
T	exonic	stopgain	+		rs886041158		
C	exonic	nonsynonymous SNV	+				
-	exonic	frameshift deletion	+				
C	exonic	nonsynonymous SNV	+				
T	exonic	nonsynonymous SNV	+				
-	exonic	frameshift deletion	+				
-	exonic	frameshift deletion	+				
T	exonic	stopgain	+				
-	exonic	frameshift deletion	+				
A	exonic	nonsynonymous SNV	+				
A	exonic	nonsynonymous SNV	+				
A	exonic	stopgain	+				
A	exonic	nonsynonymous SNV	-		rs766604600		
T	splicing		-		rs746077651		
A	exonic	stopgain	-				
A	exonic	stopgain	-				
-	exonic	frameshift deletion	-				
A	exonic	stopgain	-				
-	exonic	frameshift deletion	+				
A	exonic	nonsynonymous SNV	+				

T	exonic	nonsynonymous SNV	+				
G	exonic	nonsynonymous SNV	+				
A	exonic	nonsynonymous SNV	+		99114111		
T	exonic	nonsynonymous SNV	-		267601395		

[illegible]

			2.9E-05					



ConsSites	SIFT Score	FT Score P	PolyPhen V2	POLYPHEN V2 Score Pred	MutationTas
9;Name=V	0.15	T	0.826	P	0.575
	0.366	T	0.035	B	1
	0.035	D	0.943	P	0.998
					1
;Name=V					1
;Name=V					1
5;Name=V					
5;Name=V					
5;Name=V					1
5;Name=V					
					1
					1
					1
					1
	0	D	1	D	1
	0.001	D	0.999	D	1
Name=V\$					1
9;Name=V	0.005	D	1	D	1
	0	D	1	D	1
	0.044	D	0.351	B	1
4;Name=V					
1;Name=V					1
;Name=V\$					
;Name=V\$	0.582	T	0	B	0.97
	0.336	T	0.001	B	0.992
					1
	0.305	T	0.745	P	0.998
					1
					1
Name=V\$					
Name=V\$					1
;Name=V\$					
	0.542	T	0	B	1

8;Name=V	0.457	T	0.827	P	0.959
;Name=V	0.312	T	0.989	D	1
0;Name=V	0.003	D	0.197	B	1
Name=V\$	0	D	0.998	D	1

tionTaster	Cadd_Raw	Cadd_Phre	Dann	Eigen	V_ADA_N	V_RF_S	OMIM
D	3.34673	22.9	0.982	-0.4083			er, multiple, (3); Pancreat
D	2.0944	16.82	0.952	0.0481			1573 Weaver syndrome, 2
D	4.58931	24.4	0.999	0.159			1573 Weaver syndrome, 2
							tumor syndrome, 145001
							tumor syndrome, 145001
							tumor syndrome, 145001
							tumor syndrome, 145001
A	11.0718	37	0.997	0.72			tumor syndrome, 145001
							tumor syndrome, 145001
A	12.0687	38	0.995	1.1824			tumor syndrome, 145001
A	11.3774	37	0.996	0.8455			tumor syndrome, 145001
							tumor syndrome, 145001
							tumor syndrome, 145001
A	12.3716	39	0.996	1.1731			tumor syndrome, 145001
							tumor syndrome, 145001
A	10.4893	36	0.993	0.943			tumor syndrome, 145001
D	5.10071	25.3	0.995	1.0962	1	0.94	tumor syndrome, 145001
A	12.9906	40	0.998	1.2839			tumor syndrome, 145001
A	10.4471	36	0.997	0.7081			tumor syndrome, 145001
D	6.55299	31	0.992	0.9074			tumor syndrome, 145001
							tumor syndrome, 145001
A	6.09412	28.2	0.999	0.8127			tumor syndrome, 145001
							tumor syndrome, 145001
A	12.7298	40	0.998	0.7997			tumor syndrome, 145001
D	6.61626	32	0.998	1.0038			tumor syndrome, 145001
							tumor syndrome, 145001
D	6.20825	28.7	0.999	0.8781			tumor syndrome, 145001
D	3.83905	23.4	0.993	0.2209			tumor syndrome, 145001
							tumor syndrome, 145001
							tumor syndrome, 145001
A	12.2567	39	0.998	0.7367			tumor syndrome, 145001
							tumor syndrome, 145001
D	2.76974	21.2	0.967	-0.1764			tumor syndrome, 145001
D	2.65394	20.5	0.956	-0.2838			tumor syndrome, 145001
A	13.2175	41	0.994	1.0127			tumor syndrome, 145001
D	4.26484	23.9	0.995	-0.2837			nor of lung (3); Lipoma, s
	1.72815	14.57	0.865	1.4956	0.0009	0.012	nor of lung (3); Lipoma, s
D	12.0968	38	0.991	0.8357			nor of lung (3); Lipoma, s
A	11.32	37	0.998	1.027			nor of lung (3); Lipoma, s
							nor of lung (3); Lipoma, s
A	10.5589	36	0.997	0.9838			Parathyroid adenoma, sor
							multiple endocrine neoplasia,
N	1.18692	11.68	0.979	-0.5027			17p13.3 603825

N	2.01984	16.34	0.997	-0.1876			17p13.3 603825
D	3.64685	23.2	0.988	0.0058			17p13.3 603825
D	4.39505	24.1	0.998	-0.0435			17p13.3 603825
D	6.76401	32	0.985	1.07			1573 Weaver syndrome, 2

[illegible]

equinovarus;Short ribs;Promi			ver syndrome;Weaver syndrome

[illegible]

Uncertain significance	, 0, 0, 0, 0, 0] PP=[0, 0, 0, 0, 0, 0] BA1=0 BS=[0,	
Likely pathogenic	, 0, 0, 0, 0, 0] PP=[0, 1, 1, 0, 1, 0] BA1=0 BS=[0,	



[illegible]

ing/vestibular/ear phenotype;MP:0005371 limb		ome 17p 1			lar organis
ing/vestibular/ear phenotype;MP:0005371 limb		ome 17p 1			lar organis
ing/vestibular/ear phenotype;MP:0005371 limb		ome 17p 1			lar organis
7/hematopoietic system phenotype;MP:000538		eaver synd	skin),2(pam	MELA-AU	71,histone

GO_MF	GO_CC	GG_Pathway	KING_SEQ	KING_SEQ	GOLOGY	Case(0 1 2)	t Allele Fr	3086_gen
or activity	C9,cytosol	(human)	CGATGC	CGCACC	2	129 2 0	0.00763	C/C
1490,chromasm	GO:0005575	(human)	GGAGTA	GACTCTA	1	130 1 0	0.00382	G/G
1490,chromasm	GO:0005575	(human)	TTCAA	AAACAC	1	123 1 0	0.00403	C/C
or activity	GO:0005575		ggcgagg	GACAGT	1	129 1 0	0.00385	
or activity	GO:0005575		GGCGAG	AGAAGA	1	129 1 0	0.00385	
or activity	GO:0005575		GCGAGG	CAACAT	1	129 1 0	0.00385	
or activity	GO:0005575		GGGGGG	AGAAGA	1	129 1 0	0.00385	
or activity	GO:0005575		AAGATG	GGAGAT	1	129 1 0	0.00385	
or activity	GO:0005575		GCGTCG	GACGAA	1	128 2 0	0.00769	
or activity	GO:0005575		CATCCA	GTTCTC	1	129 1 0	0.00385	
or activity	GO:0005575		GAAGAA	CTGGCC	1	129 1 0	0.00385	
or activity	GO:0005575		TGTGGT	TGTGAA	1	129 1 0	0.00385	
or activity	GO:0005575		TGGTGA	CCAAC	1	129 1 0	0.00385	
or activity	GO:0005575		GGTGA	GAAGAC	1	127 3 0	0.01154	
or activity	GO:0005575		ATCTTC	GCATGG	0	129 1 0	0.00385	
or activity	GO:0005575		AAGAAT	GGCCCA	1	128 2 0	0.00769	
or activity	GO:0005575		ATGTGA	CAGGGG	1	129 1 0	0.00385	
or activity	GO:0005575		CAGGACT	TTTATT	1	130 1 0	0.00382	
or activity	GO:0005575		TGGAA	TTCTAC	1	124 7 0	0.02672	
or activity	GO:0005575		TGGAAC	TCTACT	1	130 1 0	0.00382	
or activity	GO:0005575		GCCAAC	AACGTG	1	131 1 0	0.00379	
or activity	GO:0005575		CTACAC	CCTGTT	1	131 1 0	0.00379	
or activity	GO:0005575		CACATT	CCGACG	1	131 1 0	0.00379	
or activity	GO:0005575		CGTGCA	TTCAATT	1	131 1 0	0.00379	
or activity	GO:0005575		CCTTTC	TTTACT	1	131 1 0	0.00379	
or activity	GO:0005575		GTTTTA	CTTGGA	1	129 2 0	0.00763	
or activity	GO:0005575		CCTGAT	CTTTT	1	130 1 0	0.00382	
or activity	GO:0005575		TGCTCC	CATATT	1	128 1 0	0.00388	
or activity	GO:0005575		CTGAAG	CTAAGA	1	131 1 0	0.00379	
or activity	GO:0005575		AAATTG	GAGACTG	1	131 1 0	0.00379	
or activity	GO:0005575		TTTTGT	AGTATG	1	130 2 0	0.00758	
or activity	GO:0005575		TTTAGA	GAGAAG	1	131 1 0	0.00379	
or activity	GO:0005575		TGCAC	TTACTG	1	131 1 0	0.00379	
or activity	GO:0005575		GAGTAG	CTCTATA	1	129 1 0	0.00385	
or activity	GO:0005575		GTTTGA	AGTAA	1	131 1 0	0.00379	
histone-lys	reticulum	regulation in	CTTGTC	CCGCCG	1	130 1 0	0.00382	G/G
histone-lys	reticulum	regulation in	GTAGTG	CTAGGG	1	130 1 0	0.00382	C/C
histone-lys	reticulum	regulation in	ACCTCT	ACAAGA	1	130 0 1	0.00763	C/C
histone-lys	reticulum	regulation in	CAGGCC	CAGGCC	1	130 1 0	0.00382	G/G
histone-lys	reticulum	regulation in	GGTGA	GGAGCT	1	130 1 0	0.00382	CCC/GCA
histone-lys	reticulum	regulation in	ATGACC	AGGAGC	1	123 1 0	0.00403	C/C
ming grow	31464,Cule	asles - Ho	GCCCGA	GCCGGC	1	129 1 0	0.00385	C/C
:0003700,	oplasm GO		CTGCCG	GAGCCC	1	130 1 0	0.00382	G/G

0003700,	plasm GC		CTCGAG	GGTGAC	1	130 1 0	0.00382	C/C
0003700,	plasm GC		CCCTAC	ACGCGC	1	128 3 0	0.01145	A/A
0003700,	plasm GC		CACGCA	GGCCAA	1	124 1 0	0.004	G/G
1490,chr	asm GO:0	an) hsa05	GGTTAT	TGCACA	1	127 4 0	0.01527	A/A

[illegible]

798:0	C/C	441:0	C/C	457:0	C/C	613:0	C/C	531:0
793:0	A/A	433:0	A/A	185:0	A/A	196:0	A/A	527:0
121:0	G/G	1611:0	G/G	1573:0	G/G	836:0	G/G	825:0
55:0	A/A	143:0	A/A	154:0	A/A	280:0	A/A	191:0

[illegible]

C/C	170:0	C/C	321:0	C/C	568:0	C/C	504:0	C/C
A/A	87:0	A/A	155:0	A/A	314:0	A/A	159:0	A/A
G/G	712:0	G/G	431:0	G/G	1374:0	G/G	1124:0	G/G
A/A	159:0	A/A	266:0	A/A	280:0	A/A	98:0	A/A



[illegible]

509:0	C/C	292:0	C/C	527:0	C/C	463:0	C/C	635:0
184:0	A/A	283:0	A/A	417:0	A/A	316:0	A/A	417:0
860:0	G/G	989:0	G/G	798:0	G/G	682:0	G/G	1679:0
59:0	A/A	34:0	A/A	190:0	A/A	167:0	A/A	195:0

[illegible]

C/C	365:0	C/C	416:0	C/C	309:0	C/C	511:0	C/C
A/A	357:0	A/A	410:0	A/A	302:0	A/A	4495:0	A/A
G/G	799:0	G/G	731:0	G/G	902:0	G/G	866:0	G/G
A/A	221:0	A/A	356:0	A/A	114:0	A/A	125:0	A/A

[illegible]

493:0	C/C	332:0	C/C	345:0	C/C	253:0	C/C	253:0
237:0	A/A	328:0	A/A	2106:0	A/A	111:0	A/A	73:0
1150:0	G/G	1412:0	G/G	512:0	G/G	785:0	G/G	541:0
177:0	A/A	51:0	A/A	43:0	A/A	78:0	A/A	20:0

[illegible]

C/C	480:0	C/C	354:0	C/C	432:0	C/C	576:0	C/C
A/A	293:0	A/A	205:0	A/A	320:0	A/A	7931:0	A/A
G/G	1199:0	G/G	305:0	G/G	326:0	G/G	76:0	G/G
A/A	181:0	A/A	293:0	A/A	281:0	A/A	329:0	A/A



[illegible]

316:0	C/C	655:0	C/C	530:0	C/C	283:0	C/C	227:0
151:0	A/A	246:0	A/A	302:0	A/A	280:0	A/G	464:78
544:0	G/G	733:0	G/G	668:0	G/G	462:0	G/G	141:0
73:0	A/A	294:0	A/A	165:0	A/A	92:0	A/A	70:0

[illegible]

C/C	267:0	C/C	616:0	C/C	330:0	C/C	760:0	C/C
A/A	267:0	A/A	3752:0	A/A	65:0	A/A	4186:0	A/A
G/G	744:0	G/G	737:0	G/G	450:0	G/G	884:0	G/G
A/A	120:0	A/A	33:0	A/A	34:0	A/A	46:0	A/A

[illegible]

622:0	C/C	341:0	C/C	209:0	C/C	350:0	C/C	423:0
481:0	A/A	134:0	A/A	94:0	A/A	135:0	A/A	116:0
1252:0	G/G	1564:0	G/G	843:0	G/G	1412:0	G/G	1594:0
123:0	A/A	49:0	A/A	60:0	A/A	67:0	A/A	63:0

[illegible]

C/C	361:0	C/C	442:0	C/C	507:0	C/C	454:0	C/C
A/A	358:0	A/A	441:0	A/A	300:0	A/A	251:0	A/A
G/G	2136:0	G/G	1773:0	G/G	887:0	G/G	1019:0	G/G
A/A	77:0	A/A	129:0	A/A	181:0	A/A	200:0	A/A



[illegible]

644:0	C/C	479:0	C/C	568:0	C/C	311:0	C/C	422:0
624:0	A/A	159:0	A/A	564:0	A/A	171:0	A/A	417:0
2481:0	G/G	1571:0	G/G	3090:0	G/G	2592:0	G/G	1054:0
172:0	A/A	112:0	A/A	58:0	A/A	104:0	A/A	143:0

[illegible]


[illegible]


[illegible]




[illegible]


[illegible]


[illegible]


[illegible]




[illegible]


[illegible]


[illegible]


[illegible]




[illegible]


[illegible]


[illegible]


[illegible]




[illegible]


[illegible]


[illegible]


[illegible]




[illegible]


[illegible]






[illegible]

C/C	506:0	C/C	360:0	C/C	427:0	C/C	224:0	C/C
A/A	266:0	A/A	349:0	A/A	5908:0	A/A	2017:0	A/A
G/G	1340:0	G/G	708:0	G/G	566:0	G/G	146:0	G/G
A/A	46:0	A/A	220:0	A/A	297:0	A/A	36:0	A/A



[illegible]

386:0	C/C	360:0	C/C	541:0	C/C	286:0	C/C	481:0
303:0	A/A	236:0	A/A	4434:0	A/A	73:0	A/A	137:0
590:0	G/G	1109:0	G/G	1666:0	G/G	968:0	G/G	566:0
417:0	A/A	227:0	A/T	193:65	A/A	54:0	A/A	75:0

[illegible]

C/C	551:0	C/C	272:0	C/C	500:0	C/C	473:0	C/C
A/A	184:0	A/G	1494:163	A/A	268:0	A/A	471:0	A/A
G/G	851:0	G/G	344:0	G/G	359:0	G/G	787:0	G/G
A/A	180:0	A/T	20:16	A/A	233:0	A/A	173:0	A/A

[illegible]

448:0	C/C	340:0	C/C	585:0	C/C	462:0	C/C	325:0
5277:0	A/A	335:0	A/A	244:0	A/A	457:0	A/A	316:0
518:0	G/G	1627:0	G/G	817:0	G/G	520:0	G/G	856:0
139:0	A/A	45:0	A/A	257:0	A/A	220:0	A/A	150:0

[illegible]

C/C	524:0	C/C	627:0	C/C	600:0	C/C	633:0	C/C
A/A	292:0	A/A	251:0	A/A	596:0	A/A	265:0	A/A
G/G	179:0	G/G	753:0	G/G	764:0	G/G	3342:0	G/G
A/A	329:0	A/A	195:0	A/A	217:0	A/A	39:0	A/A



[illegible]

525:0	C/C	614:0	C/C	545:0	C/C	517:0	C/C	398:0
4804:0	A/A	249:0	A/A	337:0	A/A	319:0	A/A	4877:0
487:0	G/G	330:0	G/G	386:0	G/G	200:0	G/G	426:0
180:0	A/A	342:0	A/A	248:0	A/A	181:0	A/A	210:0

[illegible]

C/C	527:0	C/C	666:0	C/C	389:0	C/C	461:0	C/C
A/A	167:0	A/A	657:0	A/A	182:0	A/A	6693:0	A/A
G/G	745:0	G/G	939:0	G/G	264:0	G/G	102:0	G/G
A/A	164:0	A/A	57:0	A/A	289:0	A/A	332:0	A/A

[illegible]

369:0	C/C	333:0	C/C	255:0	C/C	312:0	C/C	464:0
6028:0	A/A	5197:0	A/A	251:0	A/A	311:0	A/A	449:0
204:0	G/G	89:0	G/G	390:0	G/G	139:0	G/G	1044:0
169:0	A/A	485:0	A/A	97:0	A/A	159:0	A/A	93:0

[illegible]

C/C	303:0	C/C	408:0	C/C	376:0	C/C	169:0	C/T
A/A	152:0	A/A	404:0	A/A	152:0	A/A	166:0	A/A
G/G	498:0	G/G	1389:0	G/G	1123:0	G/G	893:0	G/G
A/A	115:0	A/A	134:0	A/A	41:0	A/A	30:0	A/A



[illegible]

130:16	C/C	230:0	C/C	679:0	C/C	184:0	C/C	83:0
998:0	A/A	1587:0	A/A	196:0	A/A	1291:0	A/A	441:0
230:0	G/G	865:0			G/G	453:0	G/G	175:0
26:0	A/A	24:0	A/A	183:0	A/A	32:0	A/A	24:0

69110_gen	69110_rea	72291_gen	72291_rea	80268_gen	80268_rea	90451_gen	90451_rea	808_A2_g
C/C	2059:0	C/C	1905:0	C/C	1643:0	C/C	1727:0	
G/G	887:0	G/G	1337:0	G/G	1710:0	G/G	1601:0	
C/C	42:0	C/C	66:0	C/C	29:0	C/C	46:0	
								G/G
								AGC/CGT
								G/G
								C/C
								C/C
								G/G
								G/G
								G/G
								TTC/GGA
								G/G
								ACT/ATC
								G/G
								G/G
								G/G
								C/G
								T/T
								-/-
								T/T
								TGC/ATA
								C/C
								G/G
								AG/AG
								T/T
								C/C
								T/T
								G/G
								C/C
								A/A
								G/G
								G/G
								C/C
G/G	284:0	G/G	228:0	G/G	89:0	G/G	77:0	
C/C	1124:0	C/C	1258:0	C/C	787:0	C/C	1008:0	
C/C	1124:0	C/C	1258:0	C/C	787:0	C/C	1008:0	
G/G	503:0	G/G	927:0	G/G	645:0	G/G	946:0	
CCC/GCA	42:0	CCC/GCA	76:0	CCC/GCA	112:0	CCC/GCA	212:0	
C/C	45:0	C/C	267:0	C/C	94:0	C/C	155:0	
C/C	252:0	C/C	403:0	C/C	250:0	C/C	387:0	
G/G	467:0	G/G	167:0	G/G	177:0	G/G	220:0	

C/C	622:0	C/C	517:0	C/C	412:0	C/C	363:0	
A/A	613:0	A/A	167:0	A/A	178:0	A/A	218:0	
		G/G	1262:0	G/G	2467:0	G/G	1621:0	
A/A	128:0	A/A	251:0	A/A	93:0	A/A	214:0	

[illegible]


[illegible]




[illegible]


[illegible]


[illegible]


[illegible]




[illegible]


912_B2_g	912_B2_r	517_C2_g	517_C2_r	05746_ge	05746_rea	08008_ge	08008_rea	08625_ge
				C/C	2883:0	C/C	2082:0	C/C
				G/G	1622:0	G/G	1001:0	G/G
				C/C	45:0	C/C	23:0	C/C
G/G	6354:0	G/G	2066:0					
AGC/CGT	6354:0	AGC/CGT	2066:0					
G/G	6354:0	G/G	2066:0					
C/C	6354:0	C/C	2066:0					
C/C	6354:0	C/C	2066:0					
G/G	6354:0	G/G	2066:0					
G/G	6354:0	G/G	2066:0					
G/G	6354:0	G/G	2066:0					
G/G	6354:0	G/G	2066:0					
TTC/GGA	6354:0	TTC/GGA	2066:0					
G/G	6354:0	G/G	2066:0					
ACT/ATC	6354:0	ACT/ATC	2066:0					
G/G	6354:0	G/G	2066:0					
G/G	6354:0	G/G	2066:0					
G/G	3491:0	G/G	3154:0					
C/C	3491:0	C/G	3547:749					
T/T	3491:0	T/T	3156:0					
-/-	3491:0	-/-	3156:0					
T/T	3491:0	T/T	3156:0					
TGC/ATA	3491:0	TGC/ATA	3156:0					
C/C	3491:0	C/C	3156:0					
G/G	3491:0	G/G	3156:0					
AG/AG	817:0	AG/AG	281:0					
T/T	817:0	T/T	281:0					
C/C	684:0	C/C	921:0					
T/T	2554:0	T/T	2794:0					
G/G	2554:0	G/G	2794:0					
C/C	2554:0	C/C	2794:0					
A/A	595:0	A/A	293:0					
G/G	595:0	G/G	293:0					
G/G	865:0	G/G	1571:0					
C/C	4321:0	C/C	4507:0					
				G/G	118:0	G/G	89:0	G/G
				C/C	813:0	C/C	465:0	C/C
				C/C	813:0	C/C	465:0	C/C
				G/G	818:0	G/G	582:0	G/G
				CCC/GCA	204:0	CCC/GCA	92:0	CCC/GCA
				C/C	28:0	C/C	26:0	C/C
				C/C	319:0	C/C	152:0	C/C
				G/G	287:0	G/G	182:0	G/G

				C/C	924:0	C/C	667:0	C/C
				A/A	240:0	A/A	182:0	A/A
				G/G	805:0	G/G	154:0	G/G
				A/A	72:0	A/A	42:0	A/A

[illegible]

894:0	C/C	931:0	C/C	800:0	C/C	782:0	C/C	993:0
265:0	A/A	927:0	A/A	7655:0	A/A	6968:0	A/A	169:0
100:0	G/G	210:0	G/G	48:0	G/G	31:0	G/G	1374:0
118:0	A/T	128:19	A/A	81:0	A/A	39:0	A/A	98:0

[illegible]

C/C	668:0	C/C	1093:0	C/C	849:0	C/C	806:0	C/C
A/A	8087:0	A/A	1086:0	A/A	845:0	A/A	249:0	A/A
G/G	29:0	G/G	252:0			G/G	13:0	G/G
A/A	103:0	A/A	37:0	A/A	114:0	A/A	170:0	A/A



[illegible]

1058:0	C/C	588:0	C/C	879:0	C/C	1109:0	C/C	1046:0
77:0	A/A	5098:0	A/A	6831:0	A/A	1103:0	A/A	292:0
59:0			G/G	10:0	G/G	26:0	G/G	203:0
53:0	A/A	30:0	A/A	112:0	A/A	43:0	A/A	64:0

[illegible]

C/C	914:0	C/C	1176:0	C/C	952:0	C/C	785:0	C/C
A/A	68:0	A/A	132:0	A/A	437:0	A/A	8173:0	A/A
G/G	55:0	G/G	90:0	G/G	486:0	G/G	156:0	G/G
A/A	28:0	A/A	93:0	A/A	95:0	A/A	44:0	A/A

[illegible]

835:0	C/C	535:0	C/C	559:0	C/C	397:0	C/C	262:0
244:0	A/A	6299:0	A/A	7517:0	A/A	71:0	A/A	3948:0
1057:0			G/G	10:0	G/G	94:0		
84:0	A/A	120:0	A/A	134:0	A/T	6:18	A/A	38:0

[illegible]

C/C	976:0	C/C	183:0	C/C	838:0	C/C	717:0	C/C
A/A	173:0	A/A	795:0	A/G	4067:547	A/A	3263:0	A/A
G/G	484:0	G/G	11:0	G/G	15:0	G/A	9:5	G/G
A/A	37:0	A/A	46:0	A/A	34:0	A/A	41:0	A/A



[illegible]

702:0	C/C	1012:0	
126:0	A/A	220:0	
403:0	G/G	445:0	
34:0	A/A	54:0	